File S2: ***DIM-1 orthologs are highly conserved.*** Protein alignment of DIM-1 from *Neurospora crassa* with orthologs in *Saccharomyces cerevisiae* (Yta7), *Schizosaccharomyces pombe* (Abo1), *Caenorhabditis elegans*, *Mus musculus* (ATAD2), and *Homo sapiens* (ATAD2). To determine orthologs in these species in an unbiased manner, the entire genome of that species was BLASTed for the NCU06484 protein sequence. The table below the alignment presents the E-value of the match between DIM-1 from Neurospora and the indicated ortholog, as well as the NCBI reference sequence number; the reference sequence for DIM-1 (NCU06484) from Neurospora is XP\_957124.1. The sequences used for this alignment are provided at the end of this file.

Neurospora MSKRKKDFLTDFDPNKSDPE----------------DENFDPIAEKQRTPRSARKQANTR

S\_cerevisiae ------------------------------------------------------------

S\_pombe ------------------------------------------------------------

C\_elegans -----------------------------MPR----SDGFSPRK--N-LRRSARDHSRSY

Mus MVNTRKSSLRLLGSKSPGPGPGPGAGAGAEPGATGGSSHFISSR--TRS-------SKTR

Homo\_sapiens MVVL-RSSLELHNHS-----------AASATGSLDLSSDFLSLE--HIGRRRLR--SAGA

Neurospora ---RP----------KNRGAAGGARRRNSRYKGSDIEDDEDISDSEQDISFGEEEDEEEE

S\_cerevisiae ------------------------------------------------------------

S\_pombe ------------------------------------------------------------

C\_elegans AGQCNEDFDDMYAPSSRRRSSGGVDGNGYTRSGRKI------------------------

Mus AASCPA---------AK---AGG-S-------GGAL------------------------

Homo\_sapiens AQKKPA---------ATT-AKAG-D-------GSSV------------------------

Neurospora EDSDAPVNATGRRMRQAAARHQSYRESSEDEDGIQSSDQDKDVVQEPDEEHRVPSIESPE

S\_cerevisiae ------------------------------------------------------------

S\_pombe ------------------------------------------------------------

C\_elegans --------------NHNRYYEEEYH------EAIS-SEEDERRYRTRR------------

Mus --------------DEARKAEVDGS----LSDSHV-SPPAKRTLKQPDS-------VCKD

Homo\_sapiens --------------KEVETYHRTR---------------ALRSLRKDAQ-------NSSD

Neurospora QSPSKKKSRIVVL--SVKKGAKPSSQRPRRGA----AAKEPATMVPPTRRS-----TRAR

S\_cerevisiae ---------------------MARNLRNRRGS----DVEDASN-----------------

S\_pombe ------------------------------------------------------------

C\_elegans ----------------SSNSMTYRQQVMQAI----DESKRNQKVPPAKRKRIYLSDEE-E

Mus ----KSKSR--------STGQREEWNIPSGQT---RLTSQPGATLPNGHSSLSLRSHPLR

Homo\_sapiens ----SSFEKNVEITEQLANGRHFTRQLARQQADKKKEEHREDKVIPV------TRSLRAR

Neurospora TEETDEPLLELSNSGRHTRVTRASTRSKSPEALTHAT-RATRG----------------S

S\_cerevisiae ------A-----KVGYETQ-------IKDENGIIHTTTRSLRKINYAEIEK--VFDFLED

S\_pombe ------------------------------------------------------------

C\_elegans EDFAEAAHVENTVPERATR---RSTR----------------------------------

Mus GEKKGDGDLSCINGDIEVR---KSCRS--------------RKNRFESVNQSLLFDQLVN

Homo\_sapiens NIVQSTEHLHEDNGDVEVR---RSCRI--------------R-SRYSGVNQSMLFDKLIT

Neurospora KGVKKQQPPPIPEASHE-------E--DDDEFKVETDIPNADDVDELAGQANMVDAPADH

S\_cerevisiae DQVMDKDETPVDVTSDEHHNNNQKGDDEDDDVDLVSPHENARTNEELTNERNLRKRK---

S\_pombe ---MKE-------------EASEHGGSADETQ-ELSPVSDS--SDEMPNNAKRRRRSQS-

C\_elegans -------------------------------------------------------RRSS-

Mus ----ST---------------------------------AEAVLQEMDNINIRRNRRSG-

Homo\_sapiens ----NT---------------------------------AEAVLQKMDDMKKMRRQRMR-

Neurospora PDEHQEGRAEQVAEEGAAQQVSEEQPAQTESQPAAE--DADGDDEDDRPITRRTRGARAV

S\_cerevisiae ----------AHDPEEDDESFHEEDVDDDEEEEEADEFEDEYLDEDSKDNNRRRRAADR-

S\_pombe ----------MIANKRIHQAFQEDEGDEDWEE------------EEHKPKAKRR------

C\_elegans ----------MH----------E--ELGVSE-------------QEESPVRRTRKAAKRL

Mus ----------EV----------E--RLRMWT-------------DTE-------------

Homo\_sapiens ----------EL----------E--DLGVFN-------------ETE-------------

 \* :

Neurospora TSTTAASTTTTVTAVEPEGEGLRSRLRRGSRLKKRSLAEP--SSDFEPGEESGDNECYAS

S\_cerevisiae ---------------------------------KFVVPDPDDDEEYDEDDEEGDRISHSA

S\_pombe ----------------------------------YNT---RSNESFSEGDDEPFEVSESS

C\_elegans GSEQPEENLAADDPLPMEGGGE------------IVLPIA----------E-----ID--

Mus -----FENM------DMYSRVKR---------RRKSLRRN----------------SY--

Homo\_sapiens -----ESNL------NMYTRGKQ---------KDIQRTDE----------ETTDN-QE--

Neurospora --EASVKK--SGRKGSSADESAATPVRGRSTRARAAKRPRRNQDSGDE---E----VELD

S\_cerevisiae -SSKRLKRANSRRTRS-SRHPETPPPVRRALRSR----TRHSRTSNEENDDENDN-SRNE

S\_pombe ALEDELSDSEDSFIRSVRSKPKYKPGTRRSTRLR----NRRSQD----------------

C\_elegans --------------GMAEQ----------ENEDLIEKIGREEEEEGAEED---EQSGEKD

Mus ------------------------------------GIQNHHEVSTEGEEEE--------

Homo\_sapiens --------------GSVES----------SE----EGEDQEHEDDGEDEDDEDDDDDDDD

 .. .

Neurospora REELAEELEELRESSRSRPRRAATRRRRSPSIQYEEPAGKRRRTTQRVDYTIPAIDLAAL

S\_cerevisiae ALTLADEIRELQEDSPIREKRF------------------LRERTKPVNYKLPPPLTASN

S\_pombe -----------EEESEEEHRPI------------------LRERTSRINYSVPLAFPPVD

C\_elegans PEEEEDDSSNAESSEESTAPRQYSLRRRQPVVQFNASEARENRRARLE-----HH-----

Mus -SQEEDGDIEVEEAEGEENDRPYNLRQRKTVDRYQAPPIVPAHQKKRENTLFDIH-----

Homo\_sapiens DDDDDDEDDEDEEDGEEENQKRYYLRQRKATVYYQAPLEKPRHQRKPN-IFYSGP-----

 .. .

Neurospora EAE-----EDEEPVATPARGRKRN-----GGNAGWDRPLNTTYGPFGGAGIGALLGGPWG

S\_cerevisiae AEEFIDKNNNALSFHNPSPARRGRGGWNASQNSGPTRRLFPTGGPFGGNDVTTIFGKN-T

S\_pombe EMD--GD---PSSQVNQSRSRKTHSEL----------------------AITKLLRQQVS

C\_elegans --------------RVANQN---------------------------------------R

Mus --------------RSPAR----------------------------------------R

Homo\_sapiens --------------ASPARPRYRL--S----SAGPR--------------------SPYC

Neurospora T----GATGG--VDSD----SSDDEMVQRTGPGQNPIGM-----TPTSAAPPVGLSNPAA

S\_cerevisiae NFYNQVPSAF----SD----NNNNKLILDSDSSDD-------------------------

S\_pombe SFMPYIDSSG--SESE----SDNTRI-KK--SSAK-------------------------

C\_elegans HHRNRNGSRRRRSDSDS---DSDDMVLPRPDKRQSRPHMHNRGERERGRFMPINMTEKE-

Mus SHIRRKKHAIHSSDTT----SSDEERFER--------RKSKSMARARNRCLPMNFRAED-

Homo\_sapiens KRMNRRRHAIHSSDSTSSSSSEDEQHFER--------RRKRSRNRAINRCLPLNFRKDE-

 : ..:

Neurospora QTHNVDGLGGIGGATPNVGKVKNLKAFADADPLGVDTSVDFSKVGGLQGHIDQLKEMVQL

S\_cerevisiae -EILPLGVTPKTKKENTQKKKKKKPEIADLDPLGVDMNVNFDDIGGLDNYIDQLKEMVAL

S\_pombe -TIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDSSLSFESVGGLDNYINQLKEMVML

C\_elegans -----L-QSAQHILMDRMRKTDAGQGASDIDPMSVDSSVGFDQVGGLGHHIQSLKEVVLF

Mus -----L-AS--GILRERV---KVGASLADVDPMNIDKSVRFDSIGGLSHHIHALKEMVVF

Homo\_sapiens -----L--K--GIYKDRM---KIGASLADVDPMQLDSSVRFDSVGGLSNHIAALKEMVVF

 :\* \*\*: :\* .: \*..:\*\*\* :\* \*\*\*:\* :

Neurospora PLLYPELFTRFHVTPPRGVLFHGPPGTGKTLLARALANSVGSGGRKISFYMRKGADALSK

S\_cerevisiae PLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKITFFMRKGADILSK

S\_pombe PLLYPEIFQRFNMQPPRGVLFHGPPGTGKTLMARALAAACSSENKKVSFYMRKGADCLSK

C\_elegans PMLYPEVFEKFRINPPKGVVFYGPPGTGKTLVARALANECRRGANKVAFFMRKGADCLSK

Mus PLLYPEIFEKFKIQPPRGCLFYGPPGTGKTLVARALANECSQGDKKVAFFMRKGADCLSK

Homo\_sapiens PLLYPEVFEKFKIQPPRGCLFYGPPGTGKTLVARALANECSQGDKRVAFFMRKGADCLSK

 \*:\*\*\*\*:: .\*.: \*\*:\* :\*:\*\*\*\*\*\*\*\*\*:\*\*\*\*\* .:::\*:\*\*\*\*\*\* \*\*\*

Neurospora WVGEAEKQLRLLFEEARRTQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDGMDG

S\_cerevisiae WVGEAERQLRLLFEEAKKHQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDGMDN

S\_pombe WVGEAERQLRLLFEEAKSTQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDGMES

C\_elegans WVGESERQLRLLFDQAYAMRPSIIFFDEIDGLAPVRSSKQDQIHASIVSTLLALMDGLDG

Mus WVGESERQLRLLFDQAYLMRPSIIFFDEIDGLAPVRSSRQDQIHSSIVSTLLALMDGLDN

Homo\_sapiens WVGESERQLRLLFDQAYQMRPSIIFFDEIDGLAPVRSSRQDQIHSSIVSTLLALMDGLDS

 \*\*\*\*:\*:\*\*\*\*\*\*::\* :\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*:\*\*\*:\*\*\*\*\*\*\*\*\*\*\*\*::.

Neurospora RGQVIVIGATNRPDNIDPALRRPGRFDREFYFPLPDIEGRRSILEIHTKDWG---LSNEF

S\_cerevisiae RGQVIVIGATNRPDAVDPALRRPGRFDREFYFPLPDVKARFKILQIQTRKWSS-PLSTNF

S\_pombe RGQVIIIGATNRPDAVDPALRRPGRFDREFYFPLPDRDARKKIIEIHTRNWDP-PVPEWL

C\_elegans RGEVVVIGATNRLDTLDPALRRPGRFDRELRFSLPDLNARRQILDIHTSKWEENKPIPET

Mus RGEIVVIGATNRLDSIDPALRRPGRFDREFLFNLPDQRARKHILQIHTRDWNP-KLSDAF

Homo\_sapiens RGEIVVIGATNRLDSIDPALRRPGRFDREFLFSLPDKEARKEILKIHTRDWNP-KPLDTF

 \*\*::::\*\*\*\*\*\* \* :\*\*\*\*\*\*\*\*\*\*\*\*\*: \* \*\*\* .\* \*:.\*:\* .\*

Neurospora KDQLAEFTKGYGGADLRALCTEAALNAIQRTYPQIYTSKEKLVVNPQKISIQASDFMHSI

S\_cerevisiae IDKLAFLTKGYGGADLRSLCTEAALISIQRSFPQIYRSNDKLLVDPSKIKVKVSDFMLAL

S\_pombe CSMLAEKSKGYGGADLRALCTEAALNSIKRTYPQLYRSTKRLQIDPKTIKVKVKDFVMSM

C\_elegans LDAIAERTSGYCGADLKFLCTEAVLIGLRSRYPHIYMCSERLKLDVATIKITSEHFGHAM

Mus LGELAEKCVGYCGADIKALCTEAALTALRRRYPQIYASSHKLQLDVTSIVLSAHDFYHAM

Homo\_sapiens LEELAENCVGYCGADIKSICAEAALCALRRRYPQIYTTSEKLQLDLSSINISAKDFEVAM

 :\* \*\* \*\*\*:: :\*:\*\*.\* .:: :\*::\* ..:\* :: .\* : .\* ::

Neurospora KKMVPSSERSASSSAMTIPKMVKPLLEKQFEALVAQLDKILPRSKKTTALEE--AMFEPY

S\_cerevisiae KKIVPSSARSTGSSPQPLPELIKPLLADQLNNLKNKLDYMLNIKDTTFQRNT--SLLQNF

S\_pombe KRMIPSSERSSISPSKPLSPELKPLLNEAFQDIEKTLQKLMPVASKLNPL----------

C\_elegans RRITPASRRDLTIPSRPLDERTSILLGDTVSNLISLRI---PQG-----------YRC--

Mus QNIVPASQRAVMSSGQALSPIIRPLLERSFNNILAVLQKIFPHAETSQSDKKED-VGSLI

Homo\_sapiens QKMIPASQRAVTSPGQALSTVVKPLLQNTVDKILEALQRVFPHAEFRTNKTLDSDISCPL

 :.: \*:\* \* : \*\* .. :

Neurospora KD-----------------------------LDGGFEREQMS-QDFQRSRVYRPRLLLCG

S\_cerevisiae IDYEEYSGEEEEHDKY-----------GGNEDTSSFRSYEFF-ESMAESQICKPRLLING

S\_pombe -EEVMYDDP----------------------KENDFEYQQRL-ETFETLRIYKPRFLICG

C\_elegans VENAMATASS--------------------------ELEQVVRALEPNPTVPAIRLLLCG

Mus LDDS---EEENALSIFEMSCHSGSPKKSLPAAAVTKPYLHFTMSPYHQPTSYRPRLLLSG

Homo\_sapiens LESDLAYSDDDVPSVY----ENGLSQKSSHKAKDNFNFLHLNRNACYQPMSFRPRILIVG

 : . \*:\*: \*

Neurospora GA---GMGH-GYLSKAVLHYLESVHVQDFGLPVLLNDS-RPPEQVIVSLF---TEVRRHK

S\_cerevisiae PK---GNGQ-QYVGAAILNYLEEFNVQNLDLASLVSESSRTIEAAVVQSF---MEAKKRQ

S\_pombe RK---GLGQ-TALGPAILQQYEGVHVQSFDMSTLLQDSTQSIETSIIHLF---LEVRRHT

C\_elegans SEQLADGGQTSYVLPAILAKLDHLPVFSLSVSSLLTD--GRPEEAFSNAIQSAMRASATG

Mus ER---GSGQTSHLAPALLHTLERFSVHRLDLPALYSVSAKTPEESCAQIF---REARRTV

Homo\_sapiens EP---GFGQGSHLAPAVIHALEKFTVYTLDIPVLFGVSTTSPEETCAQVI---REAKRTA

 . \*: : \*:: : . \* :.: \* \* : ..

Neurospora PSVIFIPNVDAWWTTLGYATLTTFTTMLRQISPTDPVLVFGTAESMPDLLPPEMLTELFG

S\_cerevisiae PSVVFIPNLDIWINTIPENVILVLSGLFRSLQSNEKILLLCLAENLDISEVKNGILSDFA

S\_pombe PSIIYIPDIDNWLNVLPLTAITTFSSMLERLDFSDQILFLALSS-SPLSELHPQLREWFS

C\_elegans PCIMLLPSIDEWIKVIPVSVQHMLITCLESMTGFTPILFLSTLD-TSFEDAPEYVTEIFR

Mus PSIVYMPHIGDWWDAVSDTVRATFLTLLQDIPSFSPIFLLSTSE-TMYSELPEEVKCIFR

Homo\_sapiens PSIVYVPHIHVWWEIVGPTLKATFTTLLQNIPSFAPVLLLATSD-KPHSALPEEVQELFI

 \*.:: :\* : \* : : :. : ::.: . : \*

Neurospora FSKKNRAAIWRPDREQRVAFFLPIIQNLWKAPEEFPDLSSRKKRVLEILPVAP-----PP

S\_cerevisiae FD-KNIFQLHKPSKENITRYFSNLIELLKTKPSDIPMKKRRVK-PLPELQKVTSNA--AP

S\_pombe SK-QSVYSLQYPTRDSIIAFFQPILELIKASPTELPGGIPRKRRVLPELPLA---P--DP

C\_elegans HANCITLN--PSRRTIRQKYFEHVIEKINTP-PK--VFDPT-VY---EMPLPDDDSPDSK

Mus IQYEEVLYIQRPIEEDRRKFFQELILHQASMAPP--RRKHTALRAMEVLPLAL-----PS

Homo\_sapiens RDYGEIFNVQLPDKEERTKFFEDLILKQAAKPPI--SKKKAVLQALEVLPVAP-----PP

 . :\* :: :

Neurospora PPRV----------PTKEEIKAQRQIDFHHLNLLKARLQPIMDQIQRRYRKFRQPVIPLN

S\_cerevisiae TNFDENGEPLSEKVVLRRKLKSFQHQDMRLKNVLKIKLSGLMDLFKNRYKRFRKPPIDDA

S\_pombe PPFTS----------QKITLKQTKQADMRLLNKLKIKLNALLGSLRARYRKFKKPLIDFN

C\_elegans PSRKLNDDETRE--LLKMYTALQRQMRLFFKE----RLTRL--MRDRRFVEFVEPVDPDE

Mus PPRQLSESEKNR--MEDQEENTLRELRLFLRD----VTKRL--ATDKRFNIFSKPVDIEE

Homo\_sapiens EPRSLTAEEVKR--LEEQEEDTFRELRIFLRN----VTHRL--AIDKRFRVFTKPVDPDE

 :. : : : \*: \* :\*

Neurospora TISYLFQESDPNFVRPDVGEQEQRPFVIAKDDKGVDGILETKTGKFYYNLDSTTIEERLA

S\_cerevisiae FLVHLFEPETSND--PNWQ---------PAYIKDENMILEVSTGRKFFNMDLDIVEERLW

S\_pombe DIYC-VDPETGHSYRSREE---------CHYEFVDDVVKQIGSDQKFSMMSLEEIEKRTW

C\_elegans AEDYYEII--------------------------------------ETPICMQDIMEKLN

Mus VSDYLEVI--------------------------------------KEPMDLSTVITKID

Homo\_sapiens VPDYVTVI--------------------------------------KQPMDLSSVISKID

 : : :

Neurospora NGYYARPMDFYEDIKRLFLDVKTIG------DKDYLPKASEMVTNVEIDVYDINLSFKTQ

S\_cerevisiae NGYYSEPKQFLKDIELIYRDANTIG------DRERVIKASEMFANAQMGIEEISTPDFIQ

S\_pombe DNCYCTPKQFVHDIKLILRDALQLE------DSETIKRAQEMYANVLLGVEDMEDDQFSQ

C\_elegans NCEYNHADKFVADLILIQTNALEYNPSTTKDGKLIRQMANTLRDAIDDLIECELDESFVE

Mus KHNYLTAKDFLQDIDLICSNALEYNPDKDPGDKIIRHRACTLKDTAHAIIAAELDPEFNK

Homo\_sapiens LHKYLTVKDYLRDIDLICSNALEYNPDRDPGDRLIRHRACALRDTAYAIIKEELDEDFEQ

 \* .: \*: : :. . \* : : :

Neurospora GINFEDIYQRQLERTRKAEERHRKKAAFQPM-----VDKIQSDLAETQDDSESQGPVGIG

S\_cerevisiae EC--KATRQRDLERQELFLE------------------DE-----EKRAA--------ME

S\_pombe RC--ERMALREAERRKLRHG------------------KLQKHLDETKAD--------MQ

C\_elegans RIE--TVSRMLQDA-------GVTPTSD--KLLTEIPKGFAR------------------

Mus LCE--EIKEARIKR-------GLSVTAEQIT-----PHGAGARKTETRVEEA--------

Homo\_sapiens LCE--EIQESRKKR-------GCSSSKYAPSYYHVMPKQNSTLVGDKRSDPE--------

 .

Neurospora FPMNKPAHTTAARFQVITSPKS-TGNPNSSGSHPLTNGTSHPSNQGETGQTVEEESTLLF

S\_cerevisiae LEAKEQSQE-----NILQEPDL-KDNK--ANEFGVAAGNQ---LQAQLQTTINTASIVNN

S\_pombe FTSEKPSVD-----ESITEVD---D--------AIKDGPP---VLAE---TLT-NSLME-

C\_elegans --------------------KKAWSMTNS--------L-------------AKEIE--QW

Mus FR------------HKQRNPMDAWHNSANKCAFRVRRK-------------SRRRS--QW

Homo\_sapiens QN------------EKLKTPST---PVACSTPAQLKRK-------------IRKKS--NW

 .

Neurospora SQGVEISSPLRYRQAQRQLQQNRVITETNRETIGTFSQTSALTSVPPGVSPAAI-QNDAS

S\_cerevisiae S---EVPQPIDT----------N-----------LYKK------EIPAAIPSAV-DKEKA

S\_pombe D---VGPENVDM-----DIEDNE-----------IFTN------QSTMSVPSML-VEN--

C\_elegans TSEREAE---------------------NQKMLSKLG--VAAPTLELVVVPV-EDMKSEE

Mus GKGIIKK-----RK------VNNLKKDEEDTKFTDYDHTEDRKLLENGEFEVSTDCHEEN

Homo\_sapiens YLGTIKK-----RR------KISQAKDDSQNAI---DHKIESDTEETQDTSV---DHNET

 ..

Neurospora STRTSDPSSGRG----EWNTQQTNGVQSISRG--TSQLLESQETTVNPPAAAFPVESNSQ

S\_cerevisiae V--IPEDSGANE----EYTT----------------ELIQ--------------------

S\_pombe -----EESPKPD----EYIDQKDK-VQ--------SPLLN--------------------

C\_elegans GTSTSTDGVPASAGNKKKLLKKKKG-QKKS------------------------------

Mus GEETGDLSMTND-ESSCDIMDMDQG-QRLNSGAGTKENFASTEE--ESSNESLLV-----

Homo\_sapiens G-NTGESSVEEN-EKQQN-----------------------------ASESKLEL-----

 .

Neurospora SQSQSNSSSSGPWPHSQMAGIAQGILLPAVPEEAE---------A----HDTNEVPAGGL

S\_cerevisiae -----------------------ATCTSEITTDDD---------E----RARKE-PKENE

S\_pombe -----------------------GKSPVGVPSEAA---------L----RVST-------

C\_elegans -----------------------KTGESEEHDEDS----TVEDAGEDTIVENLEIKKNQE

Mus ----HSSSSLNPEQTSKKEPFLKGTCLNGEASTDSSEGIPVLECQNGRVLEVVPLPDGGE

Homo\_sapiens ----RNN---------------SNTCNIENELEDSRK---TTACTELRD----KIACNGD

Neurospora RSSSSKDQPQQGSSNNDSQNSKPSNDDSQNS---KPSNDTPDSQRSLLEARRLRDLAIAD

S\_cerevisiae -----DSLQTQVTEENFS--KIDANTNNINHVKEIQSVNKPNSLHETV-EKRERS-----

S\_pombe ------DVSTNISSNGRA--DIPVD--TLITSPADVPNNAPTDAHNITSADGHIE-----

C\_elegans TPNSEHDIEM--------------------------------------------------

Mus KSSSEQKIALE-----------------------EQLKDKPETWNENR-GDAAEKLEVLE

Homo\_sapiens AS-SSQIIHI--------------------------------------------------

Neurospora CMERVLQ-----------GPVRPGSTGGKKTDSSPYSNNSPALGRNNVYLPFGRRDTSVS

S\_cerevisiae ---PIPK-----------EVVE------------------P--------------EQGKK

S\_pombe ---NIEQ-----------EVV---------------------------------------

C\_elegans ----------------------------KDASKDST-----------------PSVQISI

Mus CSSSEKPEPGPDAEGKETELDREGASKVKKYRKLLLEQAKP----TNLEL---VPEEPSE

Homo\_sapiens ---------SDENEGKEMCVLR-----MTRARRSQVEQQQL----ITVEK---ALAILSQ

Neurospora SQQQPILNDGKVCEFWSTLVDRTAGCNIEQMEQIHRELMDAIWQYRHEWNRMRVLSTLAD

S\_cerevisiae SDKELILTPEQIKKVSACLIEHCQNFTVSQLEDVHSSVAKIIWKSKSAWDKTGTVDEIIK

S\_pombe -FPDLVFDEDRLTPLKQLLIDSTTGFTVDQLLHLHSFLYQIIWNTKSEWNRNSVVDECER

C\_elegans AEKELIVSKPATCELIQCCVEKSEGWSVSELERLSSVLSHTIERFRDEWNRENLPAQLTQ

Mus PAPPLVVDHERLQKLLDLLVDKSNNLTVDQLERLYSLLSQSIYRHRKDYDKSQLVEEMER

Homo\_sapiens PTPSLVVDHERLKNLLKTVVKKSQNYNIFQLENLYAVISQCIYRHRKDHDKTSLIQKMEQ

 :. . :. . .: :: : : . \* . : ::

Neurospora VFDDTVTDIELVQ----GILIDAQGREQREYERKELEKREAEAAKSSSSTSAQSRAATQT

S\_cerevisiae FLSE--------------------------------------------------------

S\_pombe AVKEFMINALQ-------------------------------------------------

C\_elegans IVREWQTADDSNNTIVNGTLNKSNGNLANGH-----------------------------

Mus TVHMFETFL---------------------------------------------------

Homo\_sapiens EVENFSCSR---------------------------------------------------

 .

Neurospora QAAVAAVPVDAAASSTGVAAGSVAAPGPAAVAAARGVPTPAPTVVSASAPSAVSANVAAV

S\_cerevisiae ------------------------------------------------------------

S\_pombe ------------------------------------------------------------

C\_elegans ------------------------------------------------------------

Mus ------------------------------------------------------------

Homo\_sapiens ------------------------------------------------------------

Neurospora AGNGSESQGTSGSGTGSTNNSQKSHSSQKSKSNNSGKSSSQKTPTSNSTSQKRNKAAAEE

S\_cerevisiae ------------------------------------------------------------

S\_pombe ------------------------------------------------------------

C\_elegans ------------------------------------------------------------

Mus ------------------------------------------------------------

Homo\_sapiens ------------------------------------------------------------

Neurospora ERLPYIWLK

S\_cerevisiae ---------

S\_pombe ---------

C\_elegans ---------

Mus ---------

Homo\_sapiens ---------

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | *Saccharomyces cerevisiae* | *Schizosaccharomyces pombe* | *Caenorhabditis elegans* | *Mus musculus* | *Homo sapiens* |
| E-value | 0.0 | 0.0 | 1.0 e -122 | 1.0 e -156 | 4.0 e -159 |
| % identity | 42% | 47% | 40% | 43% | 43% |
| NCBI ref#  | NP\_011786.1 | NP\_001342853.1 | NP\_502289.2 | NP\_001349278.1 | NP\_054828.2 |

>XP\_957124.1 hypothetical protein NCU06484 [Neurospora crassa OR74A]

MSKRKKDFLTDFDPNKSDPEDENFDPIAEKQRTPRSARKQANTRRPKNRGAAGGARRRNSRYKGSDIEDD

EDISDSEQDISFGEEEDEEEEEDSDAPVNATGRRMRQAAARHQSYRESSEDEDGIQSSDQDKDVVQEPDE

EHRVPSIESPEQSPSKKKSRIVVLSVKKGAKPSSQRPRRGAAAKEPATMVPPTRRSTRARTEETDEPLLE

LSNSGRHTRVTRASTRSKSPEALTHATRATRGSKGVKKQQPPPIPEASHEEDDDEFKVETDIPNADDVDE

LAGQANMVDAPADHPDEHQEGRAEQVAEEGAAQQVSEEQPAQTESQPAAEDADGDDEDDRPITRRTRGAR

AVTSTTAASTTTTVTAVEPEGEGLRSRLRRGSRLKKRSLAEPSSDFEPGEESGDNECYASEASVKKSGRK

GSSADESAATPVRGRSTRARAAKRPRRNQDSGDEEVELDREELAEELEELRESSRSRPRRAATRRRRSPS

IQYEEPAGKRRRTTQRVDYTIPAIDLAALEAEEDEEPVATPARGRKRNGGNAGWDRPLNTTYGPFGGAGI

GALLGGPWGTGATGGVDSDSSDDEMVQRTGPGQNPIGMTPTSAAPPVGLSNPAAQTHNVDGLGGIGGATP

NVGKVKNLKAFADADPLGVDTSVDFSKVGGLQGHIDQLKEMVQLPLLYPELFTRFHVTPPRGVLFHGPPG

TGKTLLARALANSVGSGGRKISFYMRKGADALSKWVGEAEKQLRLLFEEARRTQPSIIFFDEIDGLAPVR

SSKQEQIHASIVSTLLALMDGMDGRGQVIVIGATNRPDNIDPALRRPGRFDREFYFPLPDIEGRRSILEI

HTKDWGLSNEFKDQLAEFTKGYGGADLRALCTEAALNAIQRTYPQIYTSKEKLVVNPQKISIQASDFMHS

IKKMVPSSERSASSSAMTIPKMVKPLLEKQFEALVAQLDKILPRSKKTTALEEAMFEPYKDLDGGFEREQ

MSQDFQRSRVYRPRLLLCGGAGMGHGYLSKAVLHYLESVHVQDFGLPVLLNDSRPPEQVIVSLFTEVRRH

KPSVIFIPNVDAWWTTLGYATLTTFTTMLRQISPTDPVLVFGTAESMPDLLPPEMLTELFGFSKKNRAAI

WRPDREQRVAFFLPIIQNLWKAPEEFPDLSSRKKRVLEILPVAPPPPPRVPTKEEIKAQRQIDFHHLNLL

KARLQPIMDQIQRRYRKFRQPVIPLNTISYLFQESDPNFVRPDVGEQEQRPFVIAKDDKGVDGILETKTG

KFYYNLDSTTIEERLANGYYARPMDFYEDIKRLFLDVKTIGDKDYLPKASEMVTNVEIDVYDINLSFKTQ

GINFEDIYQRQLERTRKAEERHRKKAAFQPMVDKIQSDLAETQDDSESQGPVGIGFPMNKPAHTTAARFQ

VITSPKSTGNPNSSGSHPLTNGTSHPSNQGETGQTVEEESTLLFSQGVEISSPLRYRQAQRQLQQNRVIT

ETNRETIGTFSQTSALTSVPPGVSPAAIQNDASSTRTSDPSSGRGEWNTQQTNGVQSISRGTSQLLESQE

TTVNPPAAAFPVESNSQSQSQSNSSSSGPWPHSQMAGIAQGILLPAVPEEAEAHDTNEVPAGGLRSSSSK

DQPQQGSSNNDSQNSKPSNDDSQNSKPSNDTPDSQRSLLEARRLRDLAIADCMERVLQGPVRPGSTGGKK

TDSSPYSNNSPALGRNNVYLPFGRRDTSVSSQQQPILNDGKVCEFWSTLVDRTAGCNIEQMEQIHRELMD

AIWQYRHEWNRMRVLSTLADVFDDTVTDIELVQGILIDAQGREQREYERKELEKREAEAAKSSSSTSAQS

RAATQTQAAVAAVPVDAAASSTGVAAGSVAAPGPAAVAAARGVPTPAPTVVSASAPSAVSANVAAVAGNG

SESQGTSGSGTGSTNNSQKSHSSQKSKSNNSGKSSSQKTPTSNSTSQKRNKAAAEEERLPYIWLK

>NP\_011786.1 Yta7p [Saccharomyces cerevisiae S288C]

MARNLRNRRGSDVEDASNAKVGYETQIKDENGIIHTTTRSLRKINYAEIEKVFDFLEDDQVMDKDETPVD

VTSDEHHNNNQKGDDEDDDVDLVSPHENARTNEELTNERNLRKRKAHDPEEDDESFHEEDVDDDEEEEEA

DEFEDEYLDEDSKDNNRRRRAADRKFVVPDPDDDEEYDEDDEEGDRISHSASSKRLKRANSRRTRSSRHP

ETPPPVRRALRSRTRHSRTSNEENDDENDNSRNEALTLADEIRELQEDSPIREKRFLRERTKPVNYKLPP

PLTASNAEEFIDKNNNALSFHNPSPARRGRGGWNASQNSGPTRRLFPTGGPFGGNDVTTIFGKNTNFYNQ

VPSAFSDNNNNKLILDSDSSDDEILPLGVTPKTKKENTQKKKKKKPEIADLDPLGVDMNVNFDDIGGLDN

YIDQLKEMVALPLLYPELYQNFNITPPRGVLFHGPPGTGKTLMARALAASCSSDERKITFFMRKGADILS

KWVGEAERQLRLLFEEAKKHQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDGMDNRGQVIVIGA

TNRPDAVDPALRRPGRFDREFYFPLPDVKARFKILQIQTRKWSSPLSTNFIDKLAFLTKGYGGADLRSLC

TEAALISIQRSFPQIYRSNDKLLVDPSKIKVKVSDFMLALKKIVPSSARSTGSSPQPLPELIKPLLADQL

NNLKNKLDYMLNIKDTTFQRNTSLLQNFIDYEEYSGEEEEHDKYGGNEDTSSFRSYEFFESMAESQICKP

RLLINGPKGNGQQYVGAAILNYLEEFNVQNLDLASLVSESSRTIEAAVVQSFMEAKKRQPSVVFIPNLDI

WINTIPENVILVLSGLFRSLQSNEKILLLCLAENLDISEVKNGILSDFAFDKNIFQLHKPSKENITRYFS

NLIELLKTKPSDIPMKKRRVKPLPELQKVTSNAAPTNFDENGEPLSEKVVLRRKLKSFQHQDMRLKNVLK

IKLSGLMDLFKNRYKRFRKPPIDDAFLVHLFEPETSNDPNWQPAYIKDENMILEVSTGRKFFNMDLDIVE

ERLWNGYYSEPKQFLKDIELIYRDANTIGDRERVIKASEMFANAQMGIEEISTPDFIQECKATRQRDLER

QELFLEDEEKRAAMELEAKEQSQENILQEPDLKDNKANEFGVAAGNQLQAQLQTTINTASIVNNSEVPQP

IDTNLYKKEIPAAIPSAVDKEKAVIPEDSGANEEYTTELIQATCTSEITTDDDERARKEPKENEDSLQTQ

VTEENFSKIDANTNNINHVKEIQSVNKPNSLHETVEKRERSPIPKEVVEPEQGKKSDKELILTPEQIKKV

SACLIEHCQNFTVSQLEDVHSSVAKIIWKSKSAWDKTGTVDEIIKFLSE

>NP\_001342853.1 putative bromodomain-containing ATPase [Schizosaccharomyces pombe]

MKEEASEHGGSADETQELSPVSDSSDEMPNNAKRRRRSQSMIANKRIHQAFQEDEGDEDWEEEEHKPKAK

RRYNTRSNESFSEGDDEPFEVSESSALEDELSDSEDSFIRSVRSKPKYKPGTRRSTRLRNRRSQDEEESE

EEHRPILRERTSRINYSVPLAFPPVDEMDGDPSSQVNQSRSRKTHSELAITKLLRQQVSSFMPYIDSSGS

ESESDNTRIKKSSAKTIKALTDPANSGGPPDFGRIREKSDLADSDPLGVDSSLSFESVGGLDNYINQLKE

MVMLPLLYPEIFQRFNMQPPRGVLFHGPPGTGKTLMARALAAACSSENKKVSFYMRKGADCLSKWVGEAE

RQLRLLFEEAKSTQPSIIFFDEIDGLAPVRSSKQEQIHASIVSTLLALMDGMESRGQVIIIGATNRPDAV

DPALRRPGRFDREFYFPLPDRDARKKIIEIHTRNWDPPVPEWLCSMLAEKSKGYGGADLRALCTEAALNS

IKRTYPQLYRSTKRLQIDPKTIKVKVKDFVMSMKRMIPSSERSSISPSKPLSPELKPLLNEAFQDIEKTL

QKLMPVASKLNPLEEVMYDDPKENDFEYQQRLETFETLRIYKPRFLICGRKGLGQTALGPAILQQYEGVH

VQSFDMSTLLQDSTQSIETSIIHLFLEVRRHTPSIIYIPDIDNWLNVLPLTAITTFSSMLERLDFSDQIL

FLALSSSPLSELHPQLREWFSSKQSVYSLQYPTRDSIIAFFQPILELIKASPTELPGGIPRKRRVLPELP

LAPDPPPFTSQKITLKQTKQADMRLLNKLKIKLNALLGSLRARYRKFKKPLIDFNDIYCVDPETGHSYRS

REECHYEFVDDVVKQIGSDQKFSMMSLEEIEKRTWDNCYCTPKQFVHDIKLILRDALQLEDSETIKRAQE

MYANVLLGVEDMEDDQFSQRCERMALREAERRKLRHGKLQKHLDETKADMQFTSEKPSVDESITEVDDAI

KDGPPVLAETLTNSLMEDVGPENVDMDIEDNEIFTNQSTMSVPSMLVENEESPKPDEYIDQKDKVQSPLL

NGKSPVGVPSEAALRVSTDVSTNISSNGRADIPVDTLITSPADVPNNAPTDAHNITSADGHIENIEQEVV

FPDLVFDEDRLTPLKQLLIDSTTGFTVDQLLHLHSFLYQIIWNTKSEWNRNSVVDECERAVKEFMINALQ

>NP\_502289.2 Tat-binding homolog 7 [Caenorhabditis elegans]

MPRSDGFSPRKNLRRSARDHSRSYAGQCNEDFDDMYAPSSRRRSSGGVDGNGYTRSGRKINHNRYYEEEY

HEAISSEEDERRYRTRRSSNSMTYRQQVMQAIDESKRNQKVPPAKRKRIYLSDEEEEDFAEAAHVENTVP

ERATRRSTRRRSSMHEELGVSEQEESPVRRTRKAAKRLGSEQPEENLAADDPLPMEGGGEIVLPIAEIDG

MAEQENEDLIEKIGREEEEEGAEEDEQSGEKDPEEEEDDSSNAESSEESTAPRQYSLRRRQPVVQFNASE

ARENRRARLEHHRVANQNRHHRNRNGSRRRRSDSDSDSDDMVLPRPDKRQSRPHMHNRGERERGRFMPIN

MTEKELQSAQHILMDRMRKTDAGQGASDIDPMSVDSSVGFDQVGGLGHHIQSLKEVVLFPMLYPEVFEKF

RINPPKGVVFYGPPGTGKTLVARALANECRRGANKVAFFMRKGADCLSKWVGESERQLRLLFDQAYAMRP

SIIFFDEIDGLAPVRSSKQDQIHASIVSTLLALMDGLDGRGEVVVIGATNRLDTLDPALRRPGRFDRELR

FSLPDLNARRQILDIHTSKWEENKPIPETLDAIAERTSGYCGADLKFLCTEAVLIGLRSRYPHIYMCSER

LKLDVATIKITSEHFGHAMRRITPASRRDLTIPSRPLDERTSILLGDTVSNLISLRIPQGYRCVENAMAT

ASSELEQVVRALEPNPTVPAIRLLLCGSEQLADGGQTSYVLPAILAKLDHLPVFSLSVSSLLTDGRPEEA

FSNAIQSAMRASATGPCIMLLPSIDEWIKVIPVSVQHMLITCLESMTGFTPILFLSTLDTSFEDAPEYVT

EIFRHANCITLNPSRRTIRQKYFEHVIEKINTPPKVFDPTVYEMPLPDDDSPDSKPSRKLNDDETRELLK

MYTALQRQMRLFFKERLTRLMRDRRFVEFVEPVDPDEAEDYYEIIETPICMQDIMEKLNNCEYNHADKFV

ADLILIQTNALEYNPSTTKDGKLIRQMANTLRDAIDDLIECELDESFVERIETVSRMLQDAGVTPTSDKL

LTEIPKGFARKKAWSMTNSLAKEIEQWTSEREAENQKMLSKLGVAAPTLELVVVPVEDMKSEEGTSTSTD

GVPASAGNKKKLLKKKKGQKKSKTGESEEHDEDSTVEDAGEDTIVENLEIKKNQETPNSEHDIEMKDASK

DSTPSVQISIAEKELIVSKPATCELIQCCVEKSEGWSVSELERLSSVLSHTIERFRDEWNRENLPAQLTQ

IVREWQTADDSNNTIVNGTLNKSNGNLANGH

>NP\_001349278.1 ATPase family AAA domain-containing protein 2B [Mus musculus]

MVNTRKSSLRLLGSKSPGPGPGPGAGAGAEPGATGGSSHFISSRTRSSKTRAASCPAAKAGGSGGALDEA

RKAEVDGSLSDSHVSPPAKRTLKQPDSVCKDKSKSRSTGQREEWNIPSGQTRLTSQPGATLPNGHSSLSL

RSHPLRGEKKGDGDLSCINGDIEVRKSCRSRKNRFESVNQSLLFDQLVNSTAEAVLQEMDNINIRRNRRS

GEVERLRMWTDTEFENMDMYSRVKRRRKSLRRNSYGIQNHHEVSTEGEEEESQEEDGDIEVEEAEGEEND

RPYNLRQRKTVDRYQAPPIVPAHQKKRENTLFDIHRSPARRSHIRRKKHAIHSSDTTSSDEERFERRKSK

SMARARNRCLPMNFRAEDLASGILRERVKVGASLADVDPMNIDKSVRFDSIGGLSHHIHALKEMVVFPLL

YPEIFEKFKIQPPRGCLFYGPPGTGKTLVARALANECSQGDKKVAFFMRKGADCLSKWVGESERQLRLLF

DQAYLMRPSIIFFDEIDGLAPVRSSRQDQIHSSIVSTLLALMDGLDNRGEIVVIGATNRLDSIDPALRRP

GRFDREFLFNLPDQRARKHILQIHTRDWNPKLSDAFLGELAEKCVGYCGADIKALCTEAALTALRRRYPQ

IYASSHKLQLDVTSIVLSAHDFYHAMQNIVPASQRAVMSSGQALSPIIRPLLERSFNNILAVLQKIFPHA

ETSQSDKKEDVGSLILDDSEEENALSIFEMSCHSGSPKKSLPAAAVTKPYLHFTMSPYHQPTSYRPRLLL

SGERGSGQTSHLAPALLHTLERFSVHRLDLPALYSVSAKTPEESCAQIFREARRTVPSIVYMPHIGDWWD

AVSDTVRATFLTLLQDIPSFSPIFLLSTSETMYSELPEEVKCIFRIQYEEVLYIQRPIEEDRRKFFQELI

LHQASMAPPRRKHTALRAMEVLPLALPSPPRQLSESEKNRMEDQEENTLRELRLFLRDVTKRLATDKRFN

IFSKPVDIEEVSDYLEVIKEPMDLSTVITKIDKHNYLTAKDFLQDIDLICSNALEYNPDKDPGDKIIRHR

ACTLKDTAHAIIAAELDPEFNKLCEEIKEARIKRGLSVTAEQITPHGAGARKTETRVEEAFRHKQRNPMD

AWHNSANKCAFRVRRKSRRRSQWGKGIIKKRKVNNLKKDEEDTKFTDYDHTEDRKLLENGEFEVSTDCHE

ENGEETGDLSMTNDESSCDIMDMDQGQRLNSGAGTKENFASTEEESSNESLLVHSSSSLNPEQTSKKEPF

LKGTCLNGEASTDSSEGIPVLECQNGRVLEVVPLPDGGEKSSSEQKIALEEQLKDKPETWNENRGDAAEK

LEVLECSSSEKPEPGPDAEGKETELDREGASKVKKYRKLLLEQAKPTNLELVPEEPSEPAPPLVVDHERL

QKLLDLLVDKSNNLTVDQLERLYSLLSQSIYRHRKDYDKSQLVEEMERTVHMFETFL

>NP\_054828.2 ATPase family AAA domain-containing protein 2 [Homo sapiens]

MVVLRSSLELHNHSAASATGSLDLSSDFLSLEHIGRRRLRSAGAAQKKPAATTAKAGDGSSVKEVETYHR

TRALRSLRKDAQNSSDSSFEKNVEITEQLANGRHFTRQLARQQADKKKEEHREDKVIPVTRSLRARNIVQ

STEHLHEDNGDVEVRRSCRIRSRYSGVNQSMLFDKLITNTAEAVLQKMDDMKKMRRQRMRELEDLGVFNE

TEESNLNMYTRGKQKDIQRTDEETTDNQEGSVESSEEGEDQEHEDDGEDEDDEDDDDDDDDDDDDDDEDD

EDEEDGEEENQKRYYLRQRKATVYYQAPLEKPRHQRKPNIFYSGPASPARPRYRLSSAGPRSPYCKRMNR

RRHAIHSSDSTSSSSSEDEQHFERRRKRSRNRAINRCLPLNFRKDELKGIYKDRMKIGASLADVDPMQLD

SSVRFDSVGGLSNHIAALKEMVVFPLLYPEVFEKFKIQPPRGCLFYGPPGTGKTLVARALANECSQGDKR

VAFFMRKGADCLSKWVGESERQLRLLFDQAYQMRPSIIFFDEIDGLAPVRSSRQDQIHSSIVSTLLALMD

GLDSRGEIVVIGATNRLDSIDPALRRPGRFDREFLFSLPDKEARKEILKIHTRDWNPKPLDTFLEELAEN

CVGYCGADIKSICAEAALCALRRRYPQIYTTSEKLQLDLSSINISAKDFEVAMQKMIPASQRAVTSPGQA

LSTVVKPLLQNTVDKILEALQRVFPHAEFRTNKTLDSDISCPLLESDLAYSDDDVPSVYENGLSQKSSHK

AKDNFNFLHLNRNACYQPMSFRPRILIVGEPGFGQGSHLAPAVIHALEKFTVYTLDIPVLFGVSTTSPEE

TCAQVIREAKRTAPSIVYVPHIHVWWEIVGPTLKATFTTLLQNIPSFAPVLLLATSDKPHSALPEEVQEL

FIRDYGEIFNVQLPDKEERTKFFEDLILKQAAKPPISKKKAVLQALEVLPVAPPPEPRSLTAEEVKRLEE

QEEDTFRELRIFLRNVTHRLAIDKRFRVFTKPVDPDEVPDYVTVIKQPMDLSSVISKIDLHKYLTVKDYL

RDIDLICSNALEYNPDRDPGDRLIRHRACALRDTAYAIIKEELDEDFEQLCEEIQESRKKRGCSSSKYAP

SYYHVMPKQNSTLVGDKRSDPEQNEKLKTPSTPVACSTPAQLKRKIRKKSNWYLGTIKKRRKISQAKDDS

QNAIDHKIESDTEETQDTSVDHNETGNTGESSVEENEKQQNASESKLELRNNSNTCNIENELEDSRKTTA

CTELRDKIACNGDASSSQIIHISDENEGKEMCVLRMTRARRSQVEQQQLITVEKALAILSQPTPSLVVDH

ERLKNLLKTVVKKSQNYNIFQLENLYAVISQCIYRHRKDHDKTSLIQKMEQEVENFSCSR