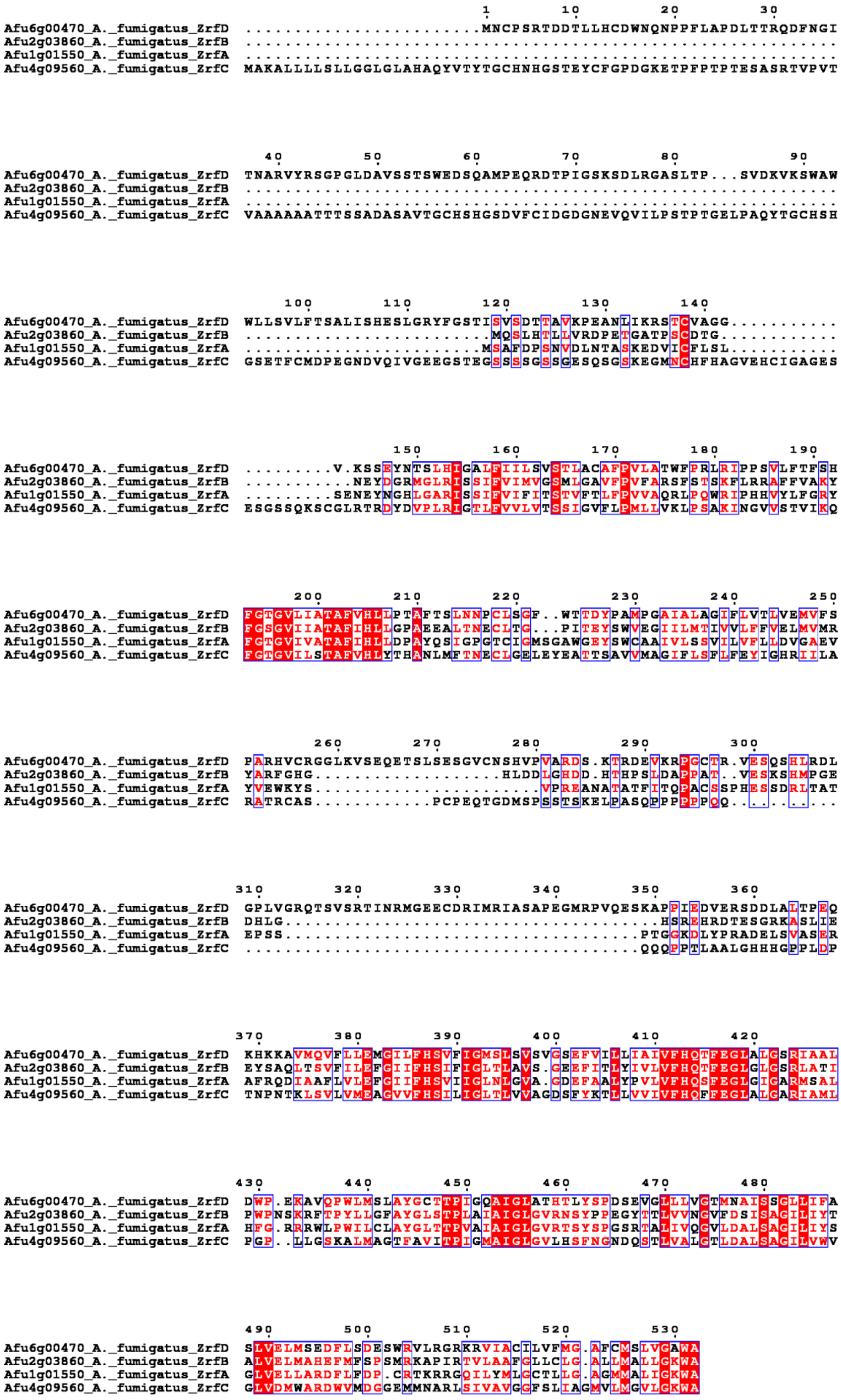
Supplementary Figure S1. Alignment of amino acid sequences of *A. fumigatus* zinc importers, ZrfA, ZrfB, ZrfC and ZrfD.



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                                                     1       10        20        30
Afu6g00470_A._fumigatus_ZrfD ........................MNCPSRTDDTLLHCDWNQNPPFLAPDLTTRQDFNGI
Afu2g03860_A._fumigatus_ZrfB ............................................................
Afu1g01550_A._fumigatus_ZrfA ............................................................
Afu4g09560_A._fumigatus_ZrfC MAKALLLLSLLGGLGLAHAQYVTYTGCHNHGSTEYCFGPDGKETPFPTPTESASRTVPVT

                               40        50        60        70        80           90
Afu6g00470_A._fumigatus_ZrfD TNARVYRSGPGLDAVSSTSWEDSQAMPEQRDTPIGSKSDLRGASLTP...SVDKVKSWAW
Afu2g03860_A._fumigatus_ZrfB ............................................................
Afu1g01550_A._fumigatus_ZrfA ............................................................
Afu4g09560_A._fumigatus_ZrfC VAAAAAATTTSSADASAVTGCHSHGSDVFCIDGDGNEVQVILPSTPTGELPAQYTGCHSH

                                  100       110       120       130       140
Afu6g00470_A._fumigatus_ZrfD WLLSVLFTSALISHESLGRYFGSTISVSDTTAVKPEANLIKRSTCVAGG...........
Afu2g03860_A._fumigatus_ZrfB .........................MQSLHTLLVRDPETGATPSCDTG............
Afu1g01550_A._fumigatus_ZrfA ........................MSAFDPSNVDLNTASKEDVICFLSL...........
Afu4g09560_A._fumigatus_ZrfC GSETFCMDPEGNDVQIVGEEGSTEGSSSSGSSGESQSGSKEGMNCHFHAGVEHCIGAGES

                                             150       160       170       180       190
Afu6g00470_A._fumigatus_ZrfD .........V.KSSEYNTSLHIGALFIILSVSTLACAFPVLATWFPRLRIPPSVLFTFSH
Afu2g03860_A._fumigatus_ZrfB ...........NEYDGRMGLRISSIFVIMVGSMLGAVFPVFARSFSTSKFLRRAFFVAKY
Afu1g01550_A._fumigatus_ZrfA .........SENEYNGHLGARISSIFVIFITSTVFTLFPVVAQRLPQWRIPHHVYLFGRY
Afu4g09560_A._fumigatus_ZrfC ESGSSQKSCGLRTRDYDVPLRIGTLFVVLVTSSIGVFLPMLLVKLPSAKINGVVSTVIKQ

                                   200       210       220         230       240       250
Afu6g00470_A._fumigatus_ZrfD FGTGVLIATAFVHLLPTAFTSLNNPCLSGF..WTTDYPAMPGAIALAGIFLVTLVEMVFS
Afu2g03860_A._fumigatus_ZrfB FGSGVIIATAFIHLLGPAEEALTNECLTG...PITEYSWVEGIILMTIVVLFFVELMVMR
Afu1g01550_A._fumigatus_ZrfA FGTGVIVATAFIHLLDPAYQSIGPGTCIGMSGAWGEYSWCAAIVLSSVILVFLLDVGAEV
Afu4g09560_A._fumigatus_ZrfC FGTGVILSTAFVHLYTHANLMFTNECLGELEYEATTSAVVMAGIFLSFLFEYIGHRIILA

                                     260       270       280        290        300
Afu6g00470_A._fumigatus_ZrfD PARHVCRGGLKVSEQETSLSESGVCNSHVPVARDS.KTRDEVKRPGCTR.VESQSHLRDL
Afu2g03860_A._fumigatus_ZrfB YARFGHG...................HLDDLGHDD.HTHPSLDAPPAT..VESKSHMPGE
Afu1g01550_A._fumigatus_ZrfA YVEWKYS.......................VPREANATATFITQPACSSPHESSDRLTAT
Afu4g09560_A._fumigatus_ZrfC RATRCAS............PCPEQTGDMSPSSTSKELPASQPPPPPPQQ...........

                             310       320       330       340       350       360
Afu6g00470_A._fumigatus_ZrfD GPLVGRQTSVSRTINRMGEECDRIMRIASAPEGMRPVQESKAPPIEDVERSDDLALTPEQ
Afu2g03860_A._fumigatus_ZrfB DHLG......................................HSREHRDTESGRKASLIE
Afu1g01550_A._fumigatus_ZrfA EPSS....................................PTGGKDLYPRADELSVASER
Afu4g09560_A._fumigatus_ZrfC ........................................QQQPPTLAALGHHHGPPLDP

                             370       380       390       400       410       420
Afu6g00470_A._fumigatus_ZrfD KHKKAVMQVFLLEMGILFHSVFIGMSLSVSVGSEFVILLIAIVFHQTFEGLALGSRIAAL
Afu2g03860_A._fumigatus_ZrfB EYSAQLTSVFILEFGIIFHSIFIGLTLAVS.GEEFITLYIVLVFHQTFEGLGLGSRLATI
Afu1g01550_A._fumigatus_ZrfA AFRQDIAAFLVLEFGIIFHSVIIGLNLGVA.GDEFAALYPVLVFHQSFEGLGIGARMSAL
Afu4g09560_A._fumigatus_ZrfC TNPNTKLSVLVMEAGVVFHSILIGLTLVVAGDSFYKTLLVVIVFHQFFEGLALGARIAML

                             430        440       450       460       470       480
Afu6g00470_A._fumigatus_ZrfD DWP.EKAVQPWLMSLAYGCTTPIGQAIGLATHTLYSPDSEVGLLLVGTMNAISSGLLIFA
Afu2g03860_A._fumigatus_ZrfB PWPNSKRFTPYLLGFAYGLSTPLAIAIGLGVRNSYPPEGYTTLVVNGVFDSISAGILIYT
Afu1g01550_A._fumigatus_ZrfA HFG.RRRWLPWILCLAYGLTTPVAIAIGLGVRTSYSPGSRTALIVQGVLDALSAGILIYS
Afu4g09560_A._fumigatus_ZrfC PGP..LLGSKALMAGTFAVITPIGMAIGLGVLHSFNGNDQSTLVALGTLDALSAGILVWV

                              490       500       510       520        530
Afu6g00470_A._fumigatus_ZrfD SLVELMSEDFLSDESWRVLRGRKRVIACILVFMG.AFCMSLVGAWA
Afu2g03860_A._fumigatus_ZrfB ALVELMAHEFMFSPSMRKAPIRTVLAAFGLLCLG.ALLMALLGKWA
Afu1g01550_A._fumigatus_ZrfA GLVELLARDFLFDP.CRTKRRGQILYMLGCTLLG.AGMMALIGKWA
Afu4g09560_A._fumigatus_ZrfC GLVDMWARDWVMDGGEMMNARLSIVAVGGFSLIAGMVLMGVLGKWA
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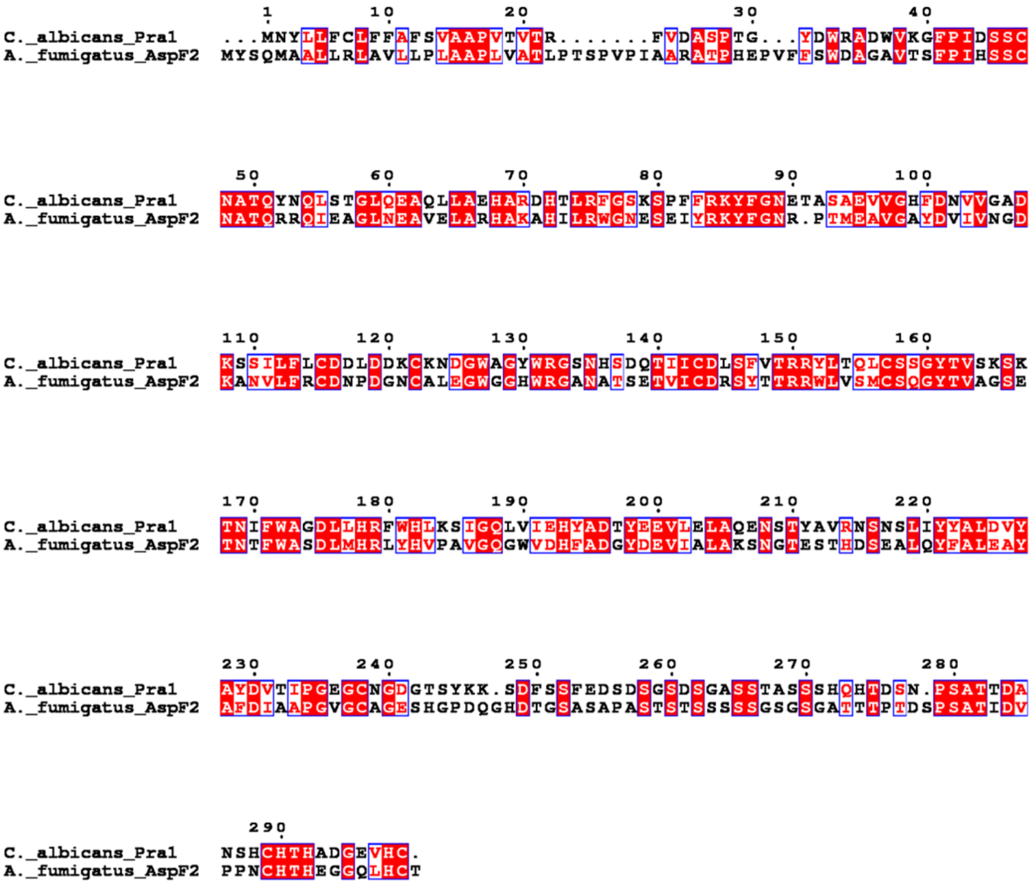
Figure S2. Alignment of *C. albicans* Pra1 and *A. fumigatus* AspF2.



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                       1       10        20               30           40
C._albicans_Pra1    ...MNYLLFCLFFAFSVAAPVTVTR.......FVDASPTG...YDWRADWVKGFPIDSSC
A._fumigatus_AspF2  MYSQMAALLRLAVLLPLAAPLVATLPTSPVPIAARATPHEPVFFSWDAGAVTSFPIHSSC

                     50        60        70        80        90       100
C._albicans_Pra1    NATQYNQLSTGLQEAQLLAEHARDHTLRFGSKSPFFRKYFGNETASAEVVGHFDNVVGAD
A._fumigatus_AspF2  NATQRRQIEAGLNEAVELARHAKAHILRWGNESEIYRKYFGNR.PTMEAVGAYDVIVNGD

                    110       120       130       140       150       160
C._albicans_Pra1    KSSILFLCDDLDDKCKNDGWAGYWRGSNHSDQTIICDLSFVTRRYLTQLCSSGYTVSKSK
A._fumigatus_AspF2  KANVLFRCDNPDGNCALEGWGGHWRGANATSETVICDRSYTTRRWLVSMCSQGYTVAGSE

                    170       180       190       200       210       220
C._albicans_Pra1    TNIFWAGDLLHRFWHLKSIGQLVIEHYADTYEEVLELAQENSTYAVRNSNSLIYYALDVY
A._fumigatus_AspF2  TNTFWASDLMHRLYHVPAVGQGWVDHFADGYDEVIALAKSNGTESTHDSEALQYFALEAY

                    230       240        250       260       270        280
C._albicans_Pra1    AYDVTIPGEGCNGDGTSYKK.SDFSSFEDSDSGSDSGASSTASSSHQHTDSN.PSATTDA
A._fumigatus_AspF2  AFDIAAPGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSGSGSGATTTPTDSPSATIDV

                      290
C._albicans_Pra1    NSHCHTHADGEVHC.
A._fumigatus_AspF2  PPNCHTHEGGQLHCT
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For both figures, sequences were aligned using ClustalW (www.ebi.ac.uk/Tools/msa/clustalw2/) and rendered using ESPript [1].

1. Robert X, Gouet P (2014) Deciphering key features in protein structures with the new ENDscript server. Nucleic Acids Res 42: W320-324.