

ScVps15 MGAQLSLVVQASP-----SIAIFSYIDVLEEVHYVSQLNSSRFLKTCALDP 47
PfVps15 MGNLTLYSNIGHSTTELDDVYCKYLNKLFIYNYLFKYEHFFFMNSYTLNFFYHVLEGINN 60

ScVps15 NGEIVIKVFIKPKDQYSLRPFQIRAQSFKLGQLPHVLNYSKLIETNRAGYMIRQHLKN 107
PfVps15 NEGHVLIKICKLKSEAPKIKRILYTLKFLFSFDLFPNVLPYNRMSVYENNIYIYRRFIFK 120

ScVps15 NLYDRLSLRPYLQDIELKFIAFQLLNTLKDINHNLNIVHGDIKTENILVTSWNWCILTDFA 167
PfVps15 NLDHYLSNKINTNFFYY-FYIFQIFLSIIQLHSLGIYHGHIKRENVLIQNNMHIFLTDIN 179

ScVps15 AFIKPVYLPEDNPGEFLFYFDTSKRRTCYLAPERFNSKLYQDGKSNNGRLTKEMDIFSLG 227
PfVps15 ILNDYLYFIFP-----KIRYEDERKGRMLKQLQEDIFNLG 212

ScVps15 CVTAEIFAEGRPIFNLSQLFKYKSNYSVDNREFLMEEMNSTDLRNLVLDMIQLDPSKRLS 287
PfVps15 ILILEILLRDK---DVSYFFLNENCAKNDNFYSGRRKQSGLT-FLKKMESIDEDDKND 268

ScVps15 CDELLNKYRGIFFPDYFYTFIYDFRNLVTMTTSTPISDNTCTNSTLEDNVKLLDETTEK 347
PfVps15 VENYHHDSDNDYHHNENYNNMNHQYDY-----HSDNYKCNRSNYKEEYTNDENKK 318

ScVps15 IYRDFSQICHCLDFPLIKDGGEIGSDPPILESYKIEIEISRFLNLTNLYFPQNYHLVLQOF 407
PfVps15 NGEYQKKYVHALSLPSIKK-----KKKQIKNEEYPYFNK----- 352

ScVps15 TKVSEKIKSVKEECALLFISYLSHSIRSIVSTATKLNLELLAVFAQFVSDENKIDRVVP 467
PfVps15 ---NQNIKMNIDKYKYNYHYIN-----NVNYINIYNDIYNNVSPFSSIDY 395

ScVps15 YFVCCFEDSDQDVQALSLLTTLIQLVTSVRKLNQLNENIFVDYLLPRLKRLNISNRQNTNY 527
PfVps15 NGENIFYENDSNFFKRQPIKYSNTHNIKEQLN---DDFQENIKYNDKNIYRQKQNEQVT 451

ScVps15 LRIVFANCLSDLAIINRFQEFQFAQHCDNSMDNNTIMESSTKYSAKLIQSVEDLTVS 587
PfVps15 QKKSQGINIYNVTDLFDNDKDDKYNTGGGDENDNHGKNKDNRGNKNDNDGEKYNNDGEKN 511

ScVps15 FLTDNDTYVKMALLQNILPLCKFFGRERTN---DILSHLITYLNDKDPALRVSLIQTI 643
PfVps15 YNDGEKNYNDGEKNYNDGEKNYNDGEKNYNDGDKNNISNNADIYNNLHNSNYNNVYTK 571

ScVps15 SGISILLGTVTLEQYILPLLIQTITDSEELVVISVLQSLKSLFKTGLIRKKYYIDI SKTT 703
PfVps15 KTPNKIKKNDHKDPHMVYKIKWVFN--QVKNPLIISLINHFFSYKNNNKNILKIFNYW 629

ScVps15 SPLLLHPNNWIRQFTLMIIEIINKLSKAEVYCI LYP IIRPF FEFDFVEFNFKSMISCKQ 763
PfVps15 S-YYIFPSTYKIFFPPLSILQLHPLFKNSDFFILLLHFNLPFILFHLDLFSN----- 680

ScVps15 PVSRSVYNLLCSWSVRASKSLFWKKIITNHVDSFGNRIEFITKNYSSKNYGFNKRDTKS 823
PfVps15 -KEQDKYILLNMLNRRNNKSGYVSTGKG-SDPAYEKSDNDDDDDDNNNYNNYNNNNNN 738

ScVps15 SSSLKGIKTSSTVYSHDNKEIPLTAEDINWIDKFHIGLTEKDIWKIVALRGYVIR TARV 883
PfVps15 NNNNYNNYHYDDYGNVVRNHHIGTYLGRNLNYFNI VRTH TTSINKHQMKAYIINTNIN 798

ScVps15 MAANPDFPYNNSNYRPLVQNSPPNLTNIMPRNIFFDVEFAEESTSEGQDSNLENQQIY 943
PfVps15 NQIKKQILKQWHSYKKEKKQEYAYVNNKN--NVHNNIYIHKKTINNNNNYNNNNYNN 856

ScVps15 KYDESEKDSNKLNINGSKQLSTVMD-INGSLIFKNSIATTTSNLKNVVFVQLEPTSYHMH 1002
PfVps15 KRSYHLSYFPPFILSYKNVHAFYKNFLNFYQFLYYSIFYEKSYMDVFKCMEYKREIY 916

ScVps15 SPNHGLKDANVVKPERKVVVSNSEYEGDVESEIEKFLSTFKILPPLRDYKEFGPIQIEIVRSP 1062
PfVps15 SPLFNDFYKQDRKKKETSMMNMPMKRDLGNEIFACANNIQSNKIHLKKGKKEETCNYYI 976

ScVps15 NMGNLRGKLIATLMENEPNSITSSAVSPGETPYLITGSDQGVIKIWNLKEIIVGEVYSSS 1122
PfVps15 NNNNKE-----RNNNEHNNNNNPRANENVVRWQFN-----EDICQLINIIICCYN--S 1022

ScVps15 LTYDCSSTVTQITMIPNFDAFVSSKDGQIIVLKVNHYYQEQESE-VKFLNCECIRKINLKN 1181
PfVps15 LTYNFVKMLTIEIYCIILHISENRLNNE LISFLLYCFNKENEKIKIMVIKCFYKIINNS 1082

ScVps15 FGKNEYAVRMRAFVNEEKSLLVALTNLSRVIIFDIRTLERLQIENS PRHGAVSSICIDE 1241
PfVps15 MNNR---PNMQLYIEKFLPKYYLLKNQD--IYEKYYYSKYLPLFSYITIQYIYNESLLK 1136

ScVps15 ECCVILIGTTRGIIDIWDIRFNVLIRSWSFGDHAPITHVEVCQFYGKNSVIVVGGSSKTF 1301
PfVps15 NNITKQKKN TLSQIPYMEILNDIKTEIQFILLNTQQNYENLFEFYN-HIFPFCKIMNKW 1195

ScVps15 LTIWNFVKGHCQYAFINSDEQPSMEHFLPIEKGLEELNFCGIRSLNALSTISVSNDKILL 1361
PfVps15 VKIY-----ILPYLLTNIYKSKNNFIKASCARKVTLKIVFYINQKKVYHIFLQYLNKLL 1248

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ScVps15      TDEATSSIVMFSLNELSSSKAVISPSRFSDVFIPTQVTANLTMLLRKMKRTSTHSVDDSL 1421
PfVps15      FSQNEQ-IIEFLLCELN----HILKKTWQKYKQEQKKSKKFWIFLKKIQLDHLY-IHPSI 1302

ScVps15      YHHDIIINSISTCEVDETPLLVACDNSGLIGIFQ 1454
PfVps15      IIQQLVDKIKN-KLKNIEYRTTNKNNKMIFM-1332

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Figure S3. Sequence alignment of Vps15 proteins. The yeast (ScVps15) and *P. falciparum* (PfVps15) Vps15 protein sequences were aligned using the Clustal W2 program. The conserved amino acid residues are shown in red, the predicted kinase domain of yeast Vps15 is shown in grey shaded bold letters, and the catalytic aspartate residues are highlighted. Notably, PfVps15 has His in place of the first catalytic aspartate residue.