

<i>A. oryzae</i>	122	IKKADPSALGIDPNVKQYTYGLDDNGNDKHLFYWFFESRNDPKNDPVVWLWLNNGGPGCSSL
<i>A. nidulans</i>	132	IKKTDPSALGIDPDVKQYTYGLDDNENDKHLFYWFFESRNDPKNDPVVWLWLNNGGPGCSSL
<i>S. cerevisiae</i>	112	-KIKDPKILGIDPNVTQYTYGLDVEDEKHFHFWTFESRNDPAKDPVILWLNNGGPGCSSL
<i>S. pombe</i>	574	-KDSKPESLGIDT-VKQYTYGLDVED-DRHLFFWFFESRNDPENDPVVWLWLNNGGPGCSSL
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<i>A. oryzae</i>	182	TGLFMELGSSIDEN-IKPVYNDFSWNSNASVIFLDQPVNVGYSYSG-SAVSDTVAAGKD
<i>A. nidulans</i>	192	TGLFMELGSSIDEN-IKPVYNPYAWNSNASVIFLDQPVNVGYSYSG-STVSDTVAAGKD
<i>S. cerevisiae</i>	171	TGLFFELGSSIGPD-LKPIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVSNNTVAAGKD
<i>S. pombe</i>	631	TGLFMELGSSINIETLKPEYNPHSWNSNASVIFLDQPINTGFSNGD-DSVLDTVTAGKD
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<i>A. oryzae</i>	240	VYALLSLFFKQFPEYA--EQDFHIAGESYAGHYIPVFASEILAHKN-----
<i>A. nidulans</i>	250	VYALLTLFFKQFPEYA--EQDFHIAGESYAGHYIPVFTSEILSHQK-----
<i>S. cerevisiae</i>	230	VYNFLELFFDQFPEYVKNKGQDFHIAGESYAGHYIPVFASEILSHKD-----
<i>S. pombe</i>	690	VYAFNLNLFKQFPEYAH--LDFHIAGESYAGHYIPQFAKEIMEHNQGANFVVASGYEMEK
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<i>A. oryzae</i>	284	RNINLKSVLIGNGLTDGLTQYGYRPMGCGEGGYKAVLDEATCESMDNALPRCRSMIESC
<i>A. nidulans</i>	294	RNINLKSVLIGNGLTDGLTQYGYRPMACGEGGYPAVLDESSCRSMDNALGRCQSMIESC
<i>S. cerevisiae</i>	276	RNFNLTSVLIGNGLTDPLTQYNYEPMACGEGGEPVLPSEECSAMEDSLERCLGLIESC
<i>S. pombe</i>	748	QYINLKSVLIGNGLTDPLVQYFYGKMACESPYPG-IMSQEECDRITGAYDTCAKLTGTC
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<i>A. oryzae</i>	344	YNSESAWVCVPASIYCNNAIIGPYQRTGQNVYDVRSKCEDESNLCYKMGYVSEYLNKAE
<i>A. nidulans</i>	354	YNSESAWVCVPASIYCNNAIILAPYQRTGQNVYDVRGKCEDESNLCYKMGYVSEYLNKPE
<i>S. cerevisiae</i>	336	YDSQSVWSCVPATIYCNNAQLAPYQRTGRNVYDVRKCEG-GNLCYPTLQIDDYLNQDY
<i>S. pombe</i>	807	YQTGFTPVICI GASLYCNNAIIGPFTKTGLNIYDIREECDRQEHLCYPETGAIESYLNQEF
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<i>A. oryzae</i>	404	VREA VGAEVGGYDSCNF DINRNFLFHGDWMKP-YHRLVPGLL-EQIPVLIYAGDADYICN
<i>A. nidulans</i>	414	VRAA VGAEVDGYDSCNF DINRNFLFHGDWMKP-YHRLVPGIL-EQIPVLIYAGDADFICN
<i>S. cerevisiae</i>	395	VKEA VGAEVDHYE SCNF DINRNFLFHGDWMKP-YHTAVTDLLNQDLPILVYAGDKDFICN
<i>S. pombe</i>	867	VQEALGVEYD-YKGCNTEVNI GF LFKGDWMRKTFRDDVTAILEAGLPVLIYAGDADYICN
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<i>A. oryzae</i>	462	WLGKAWTEALEWPGQKEYASAELEDLKI EQNEHTGKKIGQVKSHGNFTFMRLYGGGHMV
<i>A. nidulans</i>	472	WLGKAWTEALEWPGHKEFAAAPMEDLKI V DNEHTGKKIGQIKTHGNFTFMRLYGGGHMV
<i>S. cerevisiae</i>	454	WLGKAWTDVLPWKYDEEFASQKVRNWTAS---ITDEVAGEVKS YKHFTYLRVFNNGGHMV
<i>S. pombe</i>	926	YMGNEAWTDALWAGQREFYEAELKPWSPN-----GKEAGRGKSFKNFGYLRLYEAGHMV
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<i>A. oryzae</i>	522	PMDQPEASLEFFNRWLGGGEWF-
<i>A. nidulans</i>	532	PMDQPEASLEFFNRWLGGGEWF-
<i>S. cerevisiae</i>	511	PFDPENALSMVNEWIHGGFSL
<i>S. pombe</i>	981	PFNQPEASLEMLNSWIDGSLFA
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Supplemental Fig. 2 Comparison of the predicted amino acid sequence of *A. oryzae* AoCpyA with CPYs from other organisms. The numbers show the position of the amino acid residues in each mature CPY while dashes indicate gaps introduced into the sequences to facilitate optimal alignments. Asterisks indicate amino acid residues which share identity. Residues with conserved and semi-conserved substitutions are indicated with colons and dots, respectively.