

File S3: Sequences and alignment of arabinoxylan alpha arabinofurano hydrolases (GH43 AXH-like)

>Apiotrichum.siamense_AXH arabinoxylan alpha arabinofuranohydrolase
MPSPLVSHIYTADPSAHVFDGRIYVYPSHRETDIGFNDNGDQYDMVDYHVLSDMTIGGPVTDHGVALAAKDVPWVDKQLWAP
DAAKGADGRYYLYFPARAHDGIFRIGVAVSDKPEGPFPTQPEAIKSSFSIDPASFVDEDGTPYLYFGGLWGGQLQKYNADGTV
FTADAPEEPSGPGVRALGPRVARLRGDMLEFDETVKEILIVDDAGEPIPADDHERRFFEAAMHKRNGVYYFSYSTGDTHLLA
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>Apiotrichum.porosum_XP_028476455.1
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DAAKGADGRYYLYFPARAHDGVFRIGVAVSDKPEGPFAPQPEAIKGSFSIDPASFVDEDGTAYLYFGGLWGGQLQRYNADGTV
SDPKAPEEPTGAGVRALGPRVARLRGDMLEFDETVREILIVDDEGNPILADDHERRFFEAAMHKRNGKYYSYSTGDTHLLA
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>Cutaneotrichosporon.oleaginosum_XP_018280189.1_xylosidase/arabinosidase
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DCARGKDGRHYLYFPARGHDGIFRIGVAVGDRPEGPFKAQPEPIKGSFSIDPATFVDDDGAAICYFGGLWGGQLQCYNSDGT
YTPDVADEPSGAGVRAYGPRVARLRDDMLEFAEGVRELIVITVGGQVPADDHERRFFEAAMVHKHNGRYYSYSTGDTHLLAY
AIGDSPYGPFEYAGTILEPVVGWTTTHHSIVENFKGKTYLFYHDCELSKGVDHLRSVKMREITYDKDGKIIKQKP

>Trichosporon.asahii var. asahii CBS2479_XP_014181348.1
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DCAEKNGKYYFYFPAKADGKFKMGVAVSDKPEGPFPTQPEAMKGSFSIDPAAFVDDDGAYLYFGGLWGGQLQCYNSDGT
DGSKQGPQEPTEGDALGPRVARLTDMLFAEPVREISITYQGKVPASDHEKRFFEAAMHKRNGKYYSYSTGDTHLIAYA
TGDSPPYGPFEYQGTVLTPPIGWTHHSMVHFKGKDYLFYHDCSLSKGVDHLRSVKAKEMKFDGDKIVTMDP

>Humicola.insolens_AHC72382.1 Xyl43A
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FDAEWSGPKPSGSAKALGPRVAKLTDDMRQFAEEVREIVILAPETGEPLAADDHRRFFEAAMHKNYNGKYYFSYSTGD
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>Aspergillus.clavatus_NRR1_1_XP_001276579.1
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>Penicillium.rokeforti_XP_038925552.1
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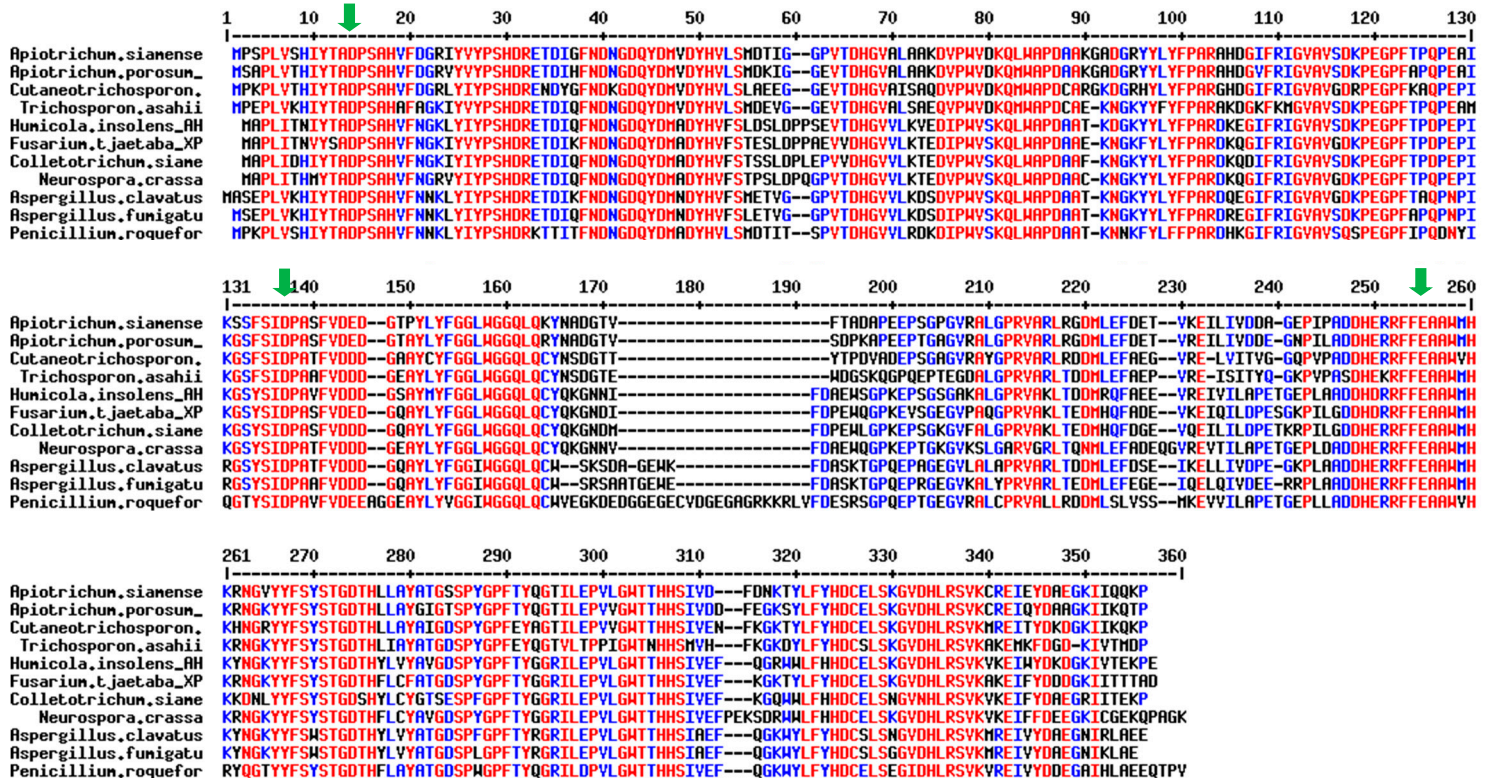
>Aspergillus.fumigatus_Af293_XP_747277.1
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EWEFDASKTGPEPRGEGVKALYPRVARLTEDMLEFEGEIQELQIVDEERRPLAADDHERRFFEAAMHKNYNGKYYFSWSTGD
THYLVIYATGDSPLGPFTYRGRILEPVLGWTTHHSIAEFQGWLYFYHDCSLSGVDHLRSVKMREIVYDAEGNIKLA

>Fusarium.tjaetaba_XP_037205011.1
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FDPEWQGPKEVSGEGVPAQGPRAVLKTEDMHQFADEVKEIQILDPESGKPI LGDDHRRFFEAAMHKRNGKYYFSYSTGDTH
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>Neurospora.crassa_OR74A_EAA36295.3
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FDAEWQGPKEPTGKGVKSLGARVGRILTQNMLEFADEQGVREVTILAPETGEPLDADDHERRFFEAAMHKRNGKYYFSYSTGD
THFLCYAVGDSPPGPFPTYGGRILEPVLGWTTHHSIVEFPEKSDRWLFHHDCELSKGVDHLRSVKKEIFFDEEGKICGEKQ
AGK

>Colletotrichum.siamense_XP_036490221.1

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FDPEWLGPEPSGKGVFALGPRVAKLTEDMHQFDGEVQEILILDPETKRPILGDDHERRFFEAAMHKKDNLYYFSYSTGDSH
YLCYGTSESFPFGPTYGGRILEPVLGWTTHHSIVEFKGQWWLFHHDCELSNGVNLHRSVKVKEIFYDAEGRIITEKP



Alignments were performed with the Multalin server (<http://multalin.toulouse.inra.fr/multalin/>). The *Apiotrichum siamense* Axh1 predicted protein was aligned with Axh1 proteins from Basidiomycetes: *Apiotrichum porosum* XP_028476455.1, *Cutaneotrichosporon oleaginosum* XP_018280189.1 and *Trichosporon asahii* var. *asahii* CBS2479 XP_014181348.1 and Axh1 proteins from Ascomycetes: *Humicola insolens* AHC72382.1 Xyl43A, *Aspergillus clavatus* NRRL 1 XP_001276579.1, *Penicillium roqueforti* XP_038925552.1, *Aspergillus fumigatus* Af293 XP_747277.1, *Fusarium tjaetaba* XP_037205011.1, *Neurospora crassa* OR74A EAA36295.3 and *Colletotrichum siamense* XP_036490221.1.

↓ Acidic amino acids that form the active sites as defined for the conserved domain cd08990 (Pons et al., 2004): D in position 13, D in position 134 and E in position 225 for the *A. siamense* Axh1 protein.