

## Epitope prediction

Highlights in yellow depict epitope regions predicted by the Bepipred 2.0 tool. Highlights in red fonts show epitope regions predicted by the ABCpred tool (shown only score  $\geq 0.8$ ). Epitope regions predicted by the SVMTriP tool are shown in bold and underline (shown only recommended sequences).

### **Bepipred 2.0**

**<http://tools.iedb.org/bcell/>**

### **ABCpred (score $\geq 0.8$ )**

**[https://webs.iiitd.edu.in/raghava/abcpred/ABC\\_submission.html](https://webs.iiitd.edu.in/raghava/abcpred/ABC_submission.html)**

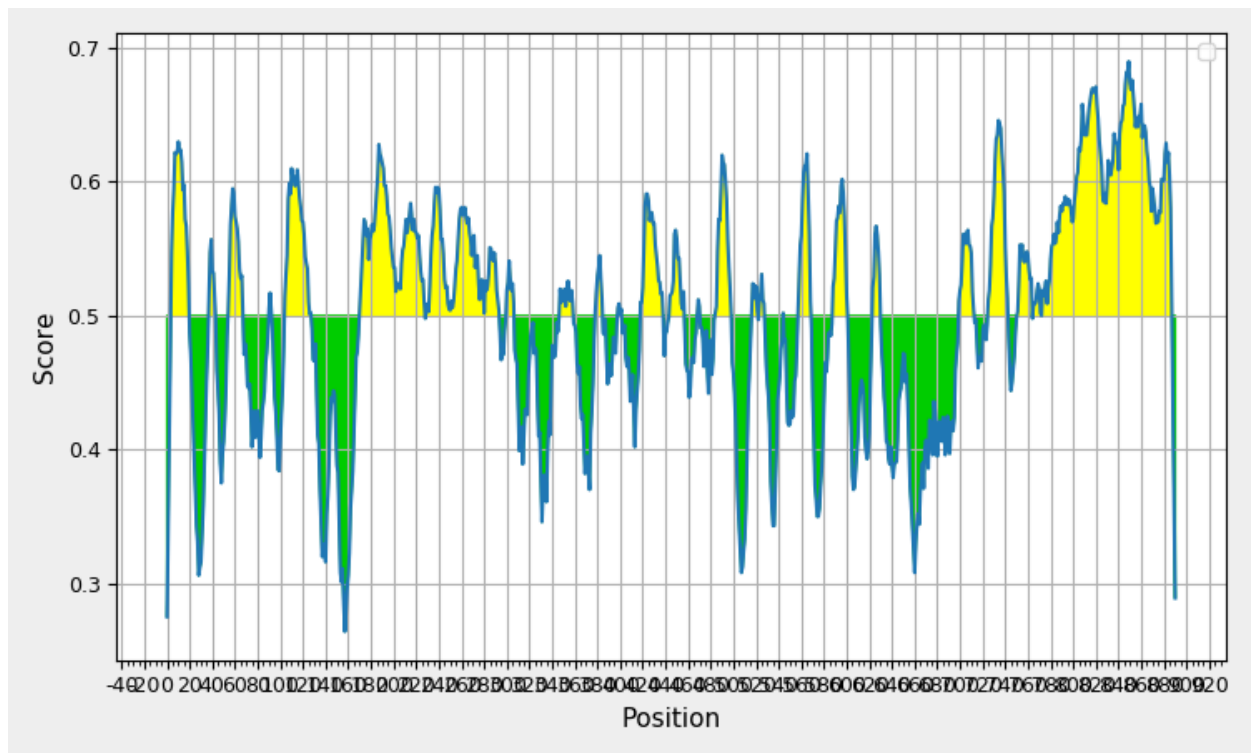
### **SVMTriP (Only flag = highest score and recommended)**

**<http://sysbio.unl.edu/SVMTriP/prediction.php>**

### P3 TmHam13

>XP\_002149306.1 conserved hypothetical protein [Talaromyces marneffei ATCC 18224]

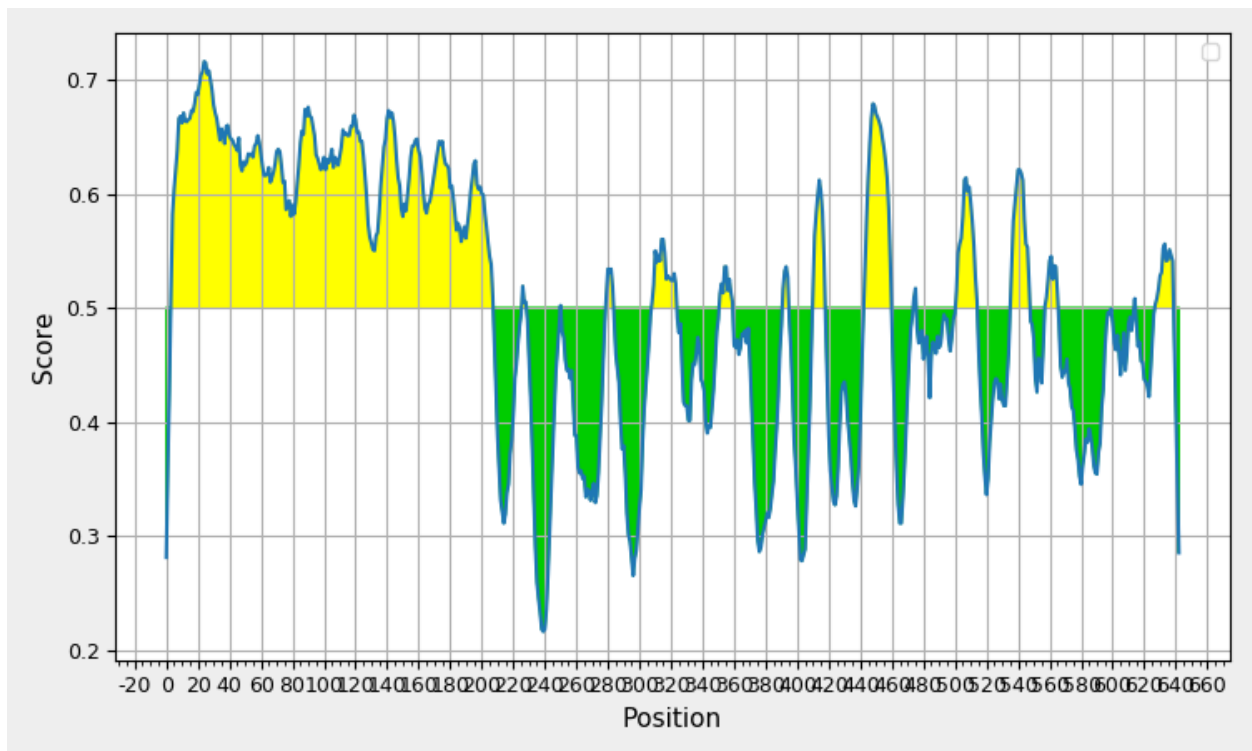
MGAKKSAVNRPMNAQQRDADISTKLQIYGIYSAFANGKLPNSKQCDVALNSAIKSKWLSSPPKELSEDGR  
TLVKDLRDVIDKTKLLFLTKNELIQEFIWDAQQITGEEFQRITGVPVSKESARGDADQAAEGFKTLGLTL  
LITNGEFRKLLSDAVTLLRDIAGDTASKAASKLRPDEDALAQIDQPAEENVVHDKPDLNKESLKAQFKEQ  
TDRFKPASKQDVQEAANAATTAATGGQQDASVSQIDARAGVNAAKETLQQRAEQNVAPEDRDQVRQVTEQ  
AQAVSSEYNRRIKDFLASKMPKERREQIVWRLKMMIVEIQGHSQYQAIETLLSLAESYAGHGRDISSQG  
TTATKGARETTIIHKAETNLRILIERFANSTSTDDFFDSLNTIYRDADQDPRLKKEWFRGVDTYIRKCLRE  
QGFIMQDEANDQWNKLYDEGRFLLRDRYRSHTDRIADEAKFLATQFDEDPQNRFRQSLERLKFKDLGQDQ  
YGKPTFKPHLIKDITNVIVPEIFENASYIPIPRIEVS~~DP~~AVDMVIENLIIESDNLMPNVLEFGTDNYWRW  
GRKKISSFDHKVMISASGIQADLRDVSYYFKKKQGFPSLTDIGVMDILLGGSGFGFKIAASKAQKNDHN  
AVFKLDSVKVNVKNLTIKLLKSKHKMLFSIFRPMLLNVRPVLEKVLEAQIREAFQKADAFAYQVQTEAQ  
RAQETMREDPENAKNIFARYADATRHVITEKKKQAEAIAERGTKVHMAMTHQDAMFKDIKLPGGVTNKAT  
EFKELSAKGDRWQSPVFNWGGASPTSNFPKASAVSRKPHTAAESHLEKSTDGVNGV GASAVNGLHGVST  
TGATARGSSGKAMPLPTNGVTNGQSATNGTFQKEVERAFDANGTTLPTLGGV



## P6 TmMon1

>XP\_002144612.1 conserved hypothetical protein [Talaromyces marneffei ATCC 18224]

METANDAPSTTLEGQHEADAQNSRTQQPQQSPDSQEDDAEEVRRPPLPPRPETIDLLNEGIAFRTSTARPN  
LQSHATTALSLTDITGQTNADGRDGFVAGFGRTLLGRGLRAKASLSQLNSARGSEAGDTASVLSFAPNSE  
EGQDESLFGEFANETNAQDISGNI EVLGYDEYPQDGNEYEFVVEEFEPIGELDEDGQNEESLLQKWKEKRK  
HYLILSAAGKPIYTRHGDSGLVSGYIGIIQTIISFYQDADDTLRSFSAGDTKIVILSKTPLYLVVAISRLL  
EESHRLRLQDALYMQILSTLTLPALNHLFSIRPSTD LKRPLQG TETLLSSLADSFTKGSPTLLSALEC  
LKLKRAHRQVINNILLRNRAEKLLYGLVAAGGRLVSVVRPKKHS LHPGDLQLLFNMI FEADGVKAGGGES  
WIPVCLPGFNSSGYLYMYVSFIDLNDESGGVIMNDDTPKDESVAIVLISADKESFFQLQEMRNKLVGQMR  
KSGSLNIMKESIKKGRPSPTDIVPD TVLRHF LYSKAHVQFVMSAYAPDFTSLTRHRLISTYNSLHESV  
HARNTHVKIHYGTSKSASVFAWVTPIFELYCVAGPDATRTPISQ GANKIRQWVQKEERLFIIGGAVSSI  
FHDLKDKRCSNML



## P7 TmFus1

>XP\_002146157.1 SH3 domain protein [Talaromyces marneffeii ATCC 18224]  
MSHAHFHRHERRNFISDVEDFFGVNYAKGPQSTVTETASIVYVTASPTFTGPIGGYITGTDTASPADPTT  
TAGKGAPVAQSSTKTTAASSKSDTSTTTKAPATHTTTSTLSTTSTLSDLLTTLSDPPATTFLTSSSTQ  
SASSTSTDTALDQLSSPTASPTTSAASTSNGLTGAKAGIAIGVLFVGLIAGLILFWLHKQKKNREE  
AAAAAAAAAENEKFTPSQPPPMQSAQSPQSMAYSSAPSTPATAPQVSLRPITQFNPLLSQPGGANPYAAG  
AVGAAVGGAAAAAGGLQVNRSAERPYSAGSAHVPPQSPRQDPFTDPVNPFDNGAQTASPPMPPAKDASSPV  
RDLTPSPTGSAHNLASPIAEEPSAGSVEAAAAAGAVAGAAVAAAAAASDDKPAESRTPSPEYVENA  
GSRPQSPVVGAGAPVSNVHRVQMDFTPSLADEMELRAGQLVRLKSYDDGWTQCSMDGQSVQGIAPRTC  
LSARPLQPRRSPGPNGPGGPRGPPIMAPNGRPMSAGGRMGPPPQMKGAPPRFYNDGRPMTPTGSGMPQF  
PPPPGTPRAMSPGPGRGVDVPRPLTPGGRSPASAGGRSRNSASVAQMGRPAMHRGSQSPLAPPTGPL  
PGPPMQPVQSPATAAPAAPAPQVQNDARPEPAIERKPVPGQQ

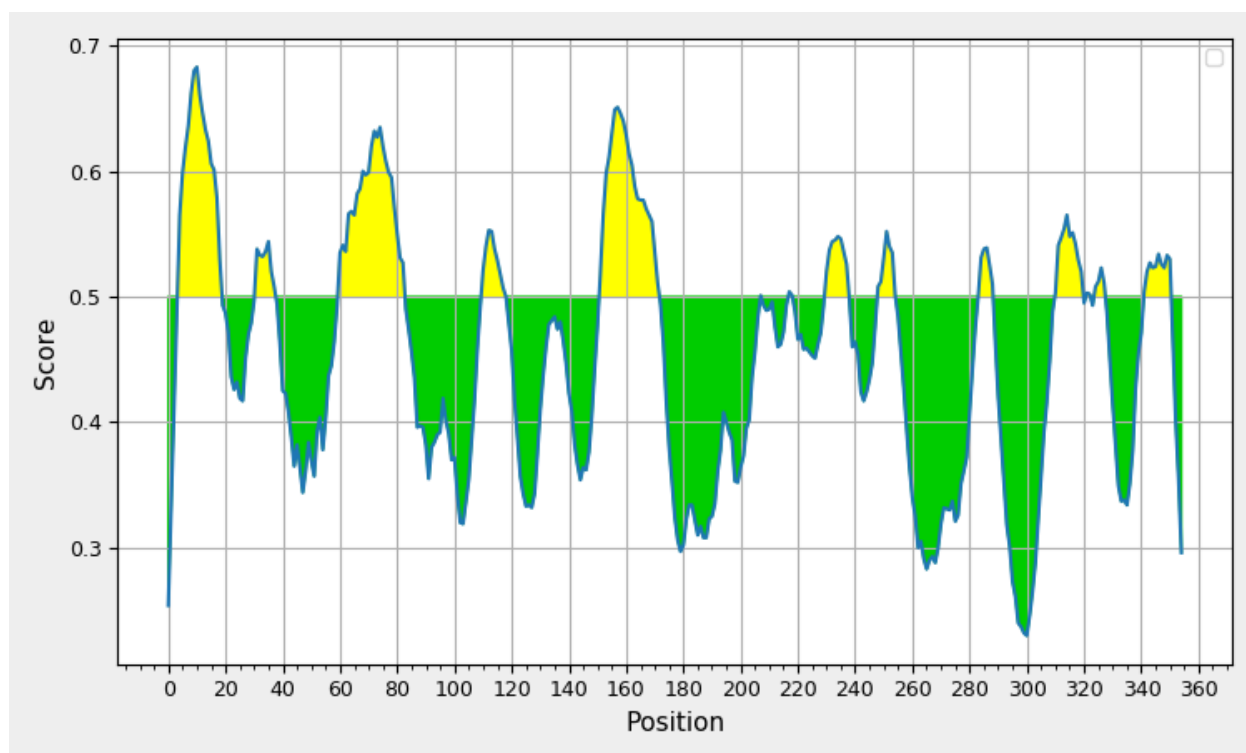
>> Cannot be identified by Bepipred 2.0

>> Below threshold by Bepipred 3.0

## P9 Fbp

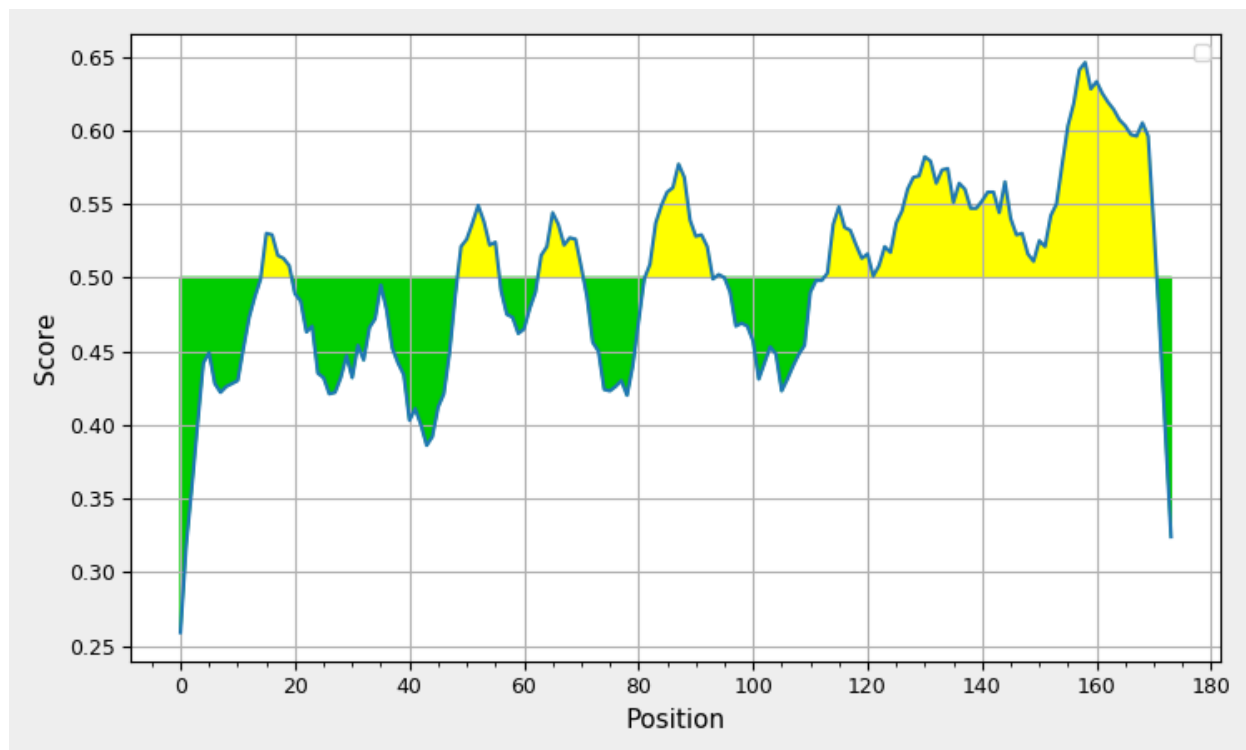
>XP\_002151273.1 fructose-1,6-bisphosphatase Fbp1, putative [Talaromyces marneffeii ATCC 18224]

MAANGNGGSGVGVQENINTDIITLTRFLTEEQLRVPEATGDFTELLCHALQFAFKSIAYYIRRASLINLTGL  
AGSSNITGDDQKKLDVIGNDVFIAMRGSGKVRLVSEEEEAEIFDEHPNARYAVVCDPIDGSSNLDAG  
VSVGTFIFGIFRLPDEILGPNKTVSAKDILRDGTELVASGFTMYGASAQLVITMRGGSVNGFTMENSLGEF  
ILTHPKMQLPTKRAIYSVNEGNSMYWDDWVKDYFHSLKYP AEGDKPYSARYIGSMVADAYRTLLYGGIFA  
YPADKKS PKGLRILYECAPMAMVFENAGGLAINSHGERLLTVLPEHIHDRSGVFLGSKDEVQKAIDVYN  
KHHKK



## P10 RPL20A

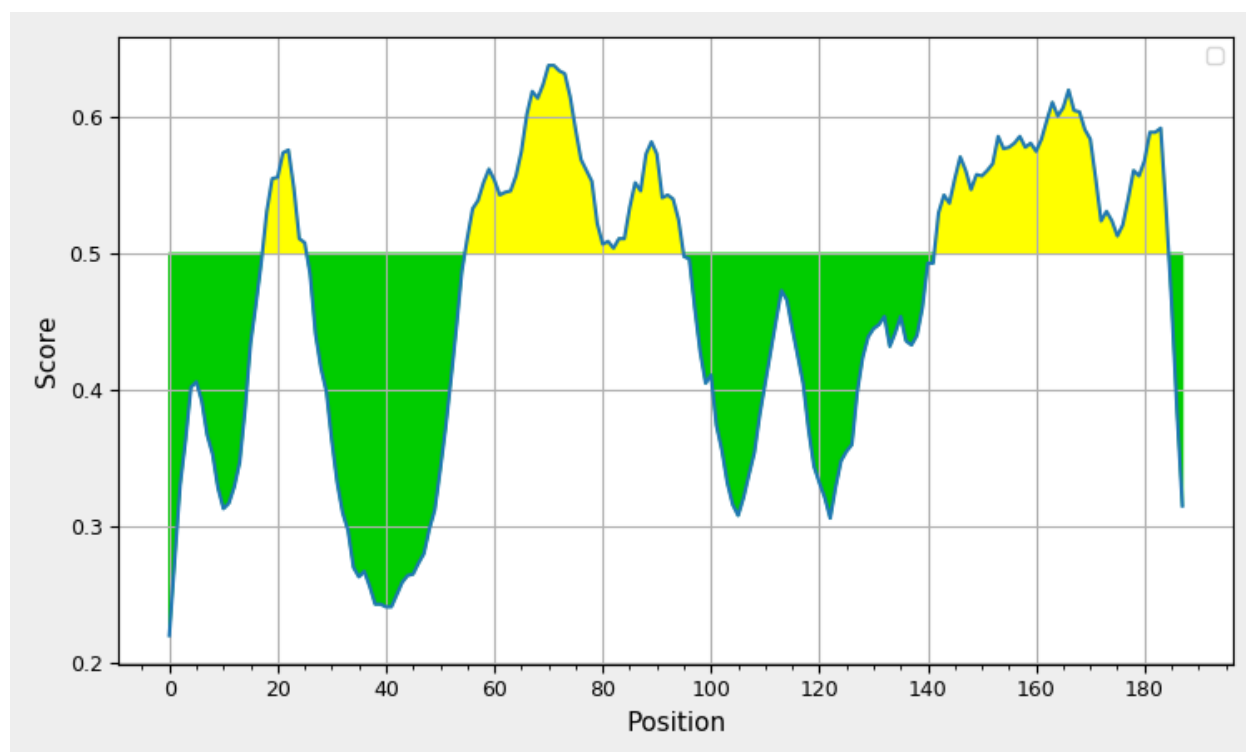
>XP\_002150233.1 60S ribosomal protein L20 [Talaromyces marneffeii ATCC 18224]  
MGRLLNEYQVIGRHLPT**TEAN**PTPKLYRMRI**FAPNTVVAKSRFWYFLTKLKKVKKANGEIVSLN**VISE**EKRPT**  
**KVKNFGIWLRYSRS**GTHNMYKE**FRELSRTDAVDSLYQDMAARHRARFGS**IHILRVIEIEDNESIRRPYI  
KQLLTKGLKFPLPHRVPA**QSSKKVFAYKRPS**TFA



## P11 Pho88

>XP\_002151103.1 phosphate transporter (Pho88), putative [Talaromyces marneffei ATCC 18224]

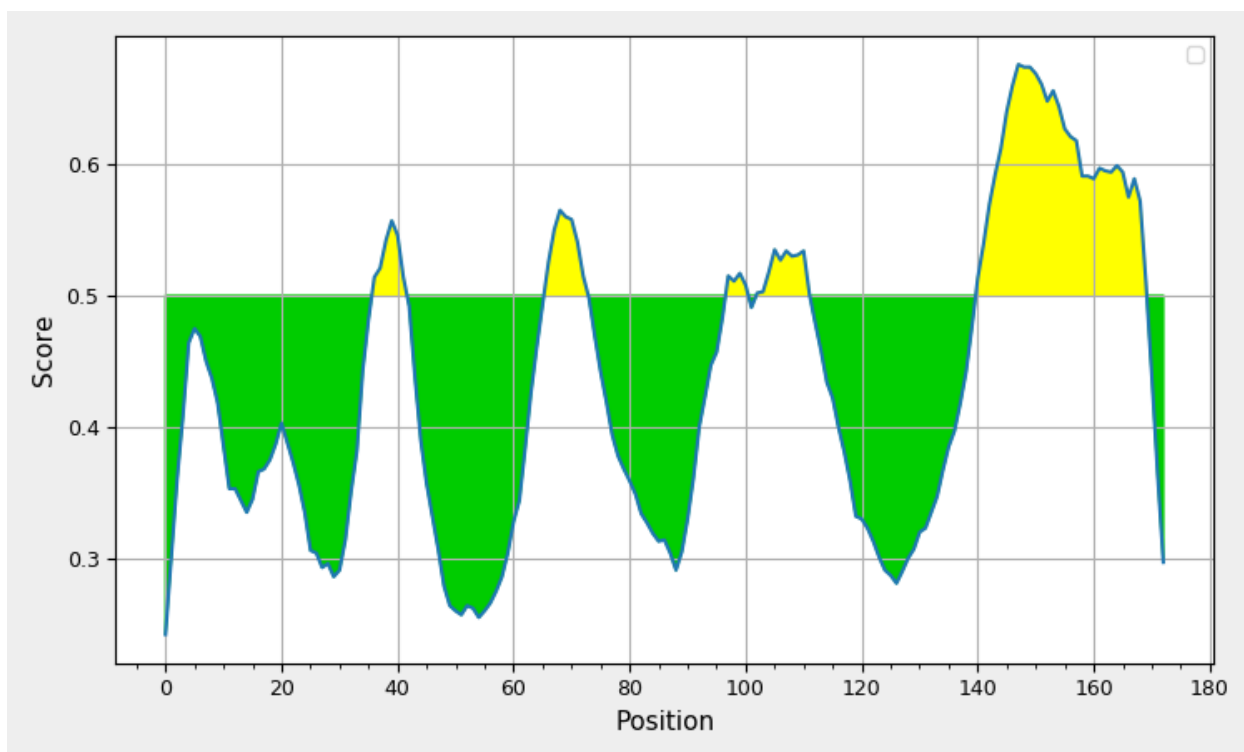
MAAQVTNLVILGMMQVSKRIPFENPDVLLGVRALYIVSNVLILGIYLYVQSKISKKKDLTTLKYVEPAP  
MGSGEPRPVTTTVM EYDKQQLRQLMRSQLMGVGMMAVMHLYFKYTNPLLIQSILPVKSALESNLVKIHV  
LGKPATGDLQRPFKAAAGFMGMGQGEIKSDKAS IENAEKNWRGGVKEE



## P12 Marvel

>XP\_002152818.1 conserved hypothetical protein [Talaromyces marneffeii ATCC 18224]

MAMLSSSLSRPILLGIRTMQWASSVIALGIYAYFVHHQ<sup>1</sup>RS<sup>2</sup>GNPIFNLVISVLSVVF<sup>3</sup>FIPAFVSPF<sup>4</sup>MTVL<sup>5</sup>  
SKWVALIDMVFSYLWLTAFVLAQAQSYNYGDVYLKAPSGVRVSIKHAAESFTFLAFIFT<sup>6</sup>FFGLL<sup>7</sup>TEV<sup>8</sup>ATRW<sup>9</sup>  
TDADDT<sup>10</sup>PVTREKHNGDTRAPLDAPANPTGPAAV

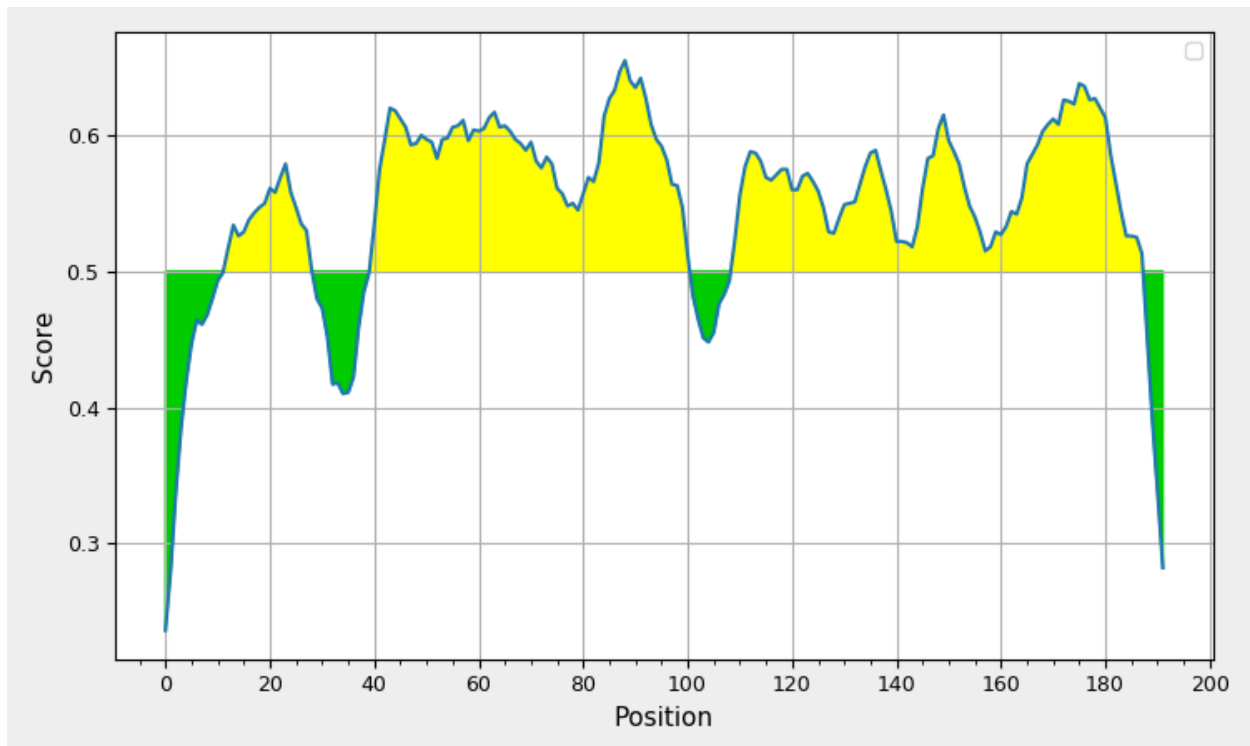




## P13 Nuo21.3

>XP\_002144515.1 NADH-ubiquinone oxidoreductase 21 kDa subunit, putative  
[Talaromyces marneffeii ATCC 18224]

MSREVAKAAKSASNAIAVSKKYTVQSTGIWEVIRRTLAVDPTRSTGVPLNSQFRNPAPGALPPQSYDEPV  
TLPAADLADNPNYWKRDVRRNYPQLSVFSQGDVAGLLTFGNKQAPKEDALQLGEAGEKQLIAAKQEGDEKG  
LAAQFEKDKNSVKSVLGPDGLPPLPVRLNNLAKYELGSGQGYPEKYPCRTFV



## P14 C2H2 zinc finger protein

>XP\_002150081.1 C2H2 finger domain protein, putative [Talaromyces marneffeii ATCC 18224]

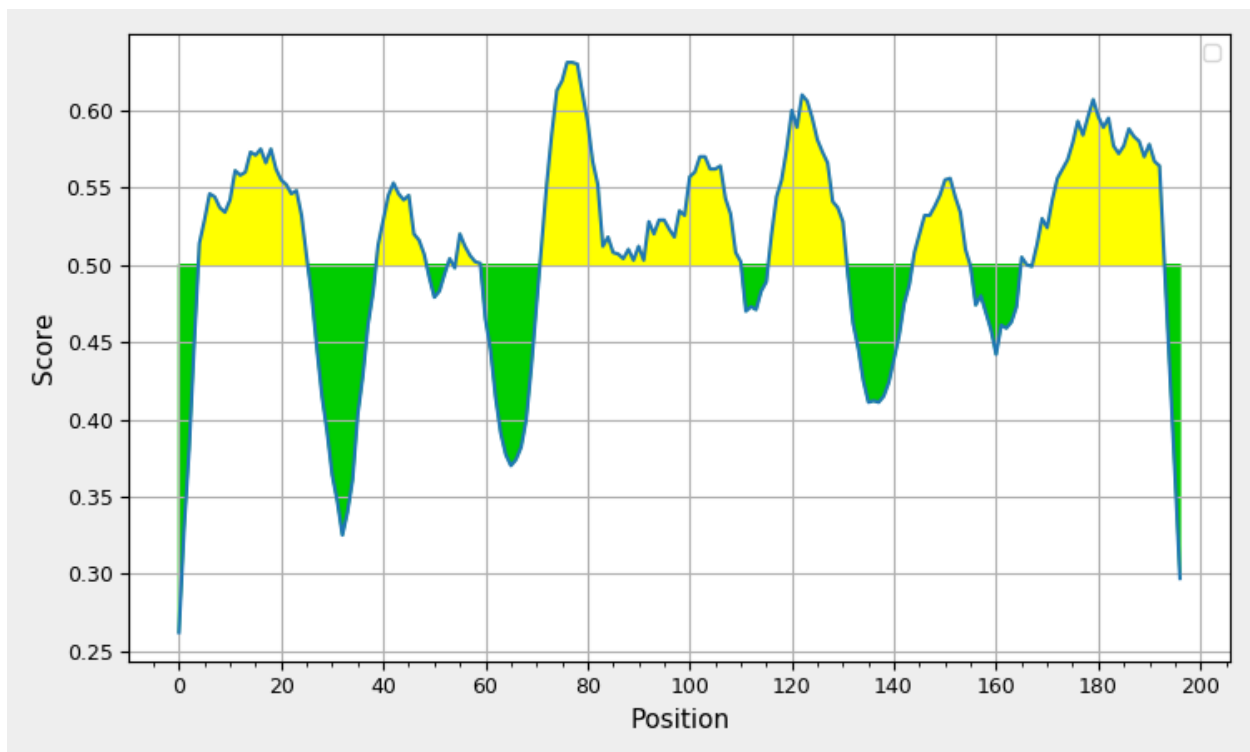
MS SYPKYNSYRFPNSQNEENSRRNHHPAQQQQQQPVPQPPRGYMEANYSWNNENTNRSYLNTNNAYSRAQ  
DSLSSFPHPVELSRYSQHGTRTDENTQRSAGLYRYPSQSNSAVNAQATTTYNQPPQHVSNAVSLTSLAS  
YTYRNTSVNNAQPKWRPSPKANQRGQRNTENDKSPLVTQPSTNTSLNARSYSQMSHGYSLYTTNTSSVA  
NPSHTVISIETLPTVTQDYPQVSETRTTDQISSNVQYINPTDLYIQQYFLAQERARATEPEQMAGEEAR  
KKEVEAQTQVQAEAVARAAEEASSTNAQATPTSTAKGTVKPKPAKNTSKKRSSAKKDAAPADPLDPEGDH  
DMALEMRRMMEKLSMRSKDPSLFAKLWDDFKNPAASTQTATSEQAAAGPSQSTTNPPPSTRTLTKTPK  
GQAQAQDGF PDLGKFFPAQRKREKQSDVAEVAANSQLDASAPVSVQVNVNSMRNQQHQSAPVPASVAK  
KTAAKSLQKASTAASSASKPKATPAQEATWPVATQKLAQAVSGYLSKGAANNNGKECSPELMLLLRNNP  
TYPDLCAQLESRGFVLDLQAMARFLLVAVPALLSGKNGQEKKAIAIKNTPSAQASRSLPPTMTQPPHPP  
SLPPQPVQPTQASQLVPPAQSTIPRPPALPQGVPTSDLDVVYYQPGAPAHKPHAPKNVDPTI STARPQSN  
QKGT SWQRPRRSDGAWISNHPVGPKAAMARKRFFSEIVDMSQASDEEGI PSDDDDDEDFSGRPNAS  
MNMSISQPPNFPDSDGPDMDIDTDSYPPIEQDLSDSHAAIPEPDIEFNPDES VLCEIKRLPNITKPLNP  
SDALKRVYYNPKSIARDIMLATGRHPSERPLNFHLMHFTQTFSGVTVRS DLETFKWNLVDPGGPSMPVVE  
LEDILVEPPEFTRKKRRRRDVGSRDDADVKGPTSESQPQPSGTVATPGQPLSTSVSTPHGVRDSMVGTP  
TGQRTGRRGRPPGAKNKNPTKATLKALVKTTAGSSTRDAQPAVPAPAPATSVPELSYPMFTCEWASCPAQ  
HDVHTLERHVKNHISGQTTCLWQNCPLATEYSGEGLKEHLAQAHIQPLAWKYGDGASVNGNVQLDLDR  
YLNANGLIVTPDAITAGENDALIFVPEPIPIRAF NKLYGDQKATDRARQVLRVQKRRRRVIGIGLEQEGC  
EFSTPVRNKL FVNDEEFYEVVT DGEQGTDDWFSQGETY

>> cannot be identified by Bepipred 2.0

## P17 Gpx1

>XP\_002152894.1 glutathione peroxidase Hyr1, putative [Talaromyces marneffeii ATCC 18224]

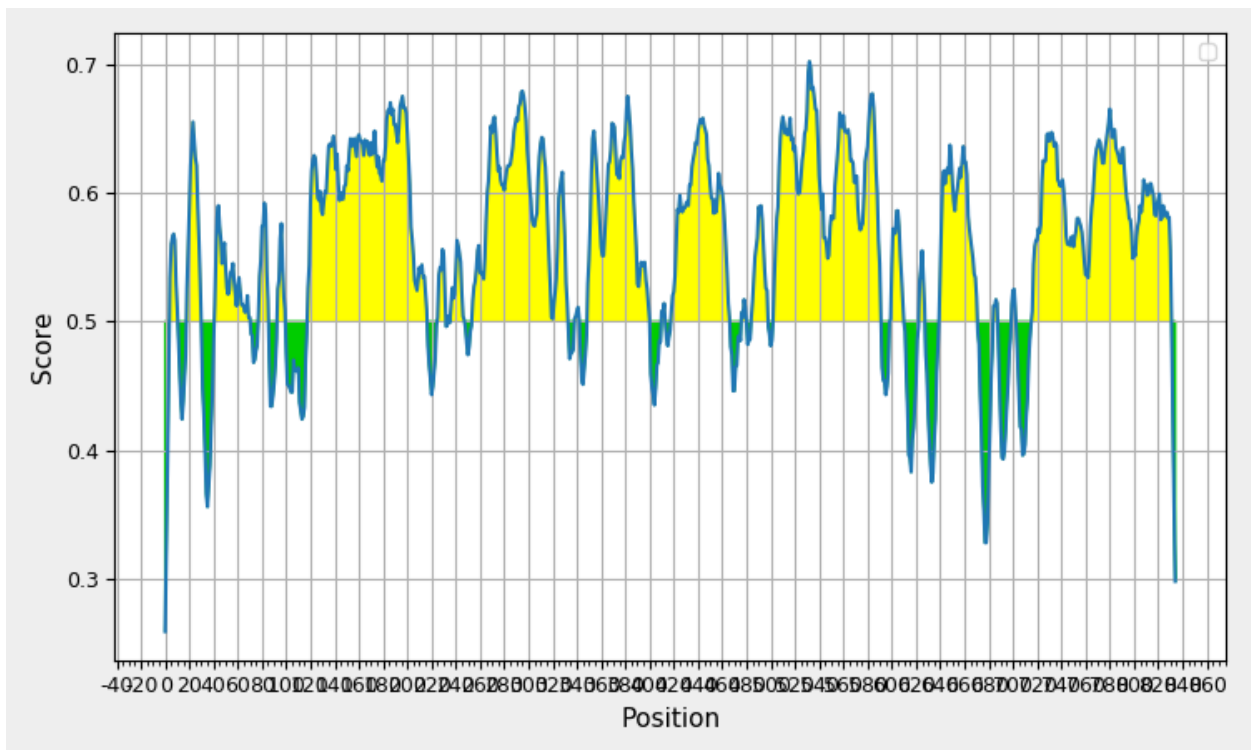
MASATTFYDFSPDCKGNPYPLTDYKGVVLLVNTASKCGFTPQFAGLEKLYKSI**EA**KHPGAFTILGFPC  
NQFGNQDPGSNDEIQSFCQVNYGVTFPVLGKIDVNGSKAEP**LFEWIKSEK**PGLLGVKRVLWNFEKALING  
KGEVVGRWRSITKPE**SLEATILKEIDIASKDVKGE**VVPTATETAASAAPAEEAKEA



## P21 TmNbr1

>XP\_002152652.1 ZZ type zinc finger domain protein [Talaromyces marneffeii ATCC 18224]

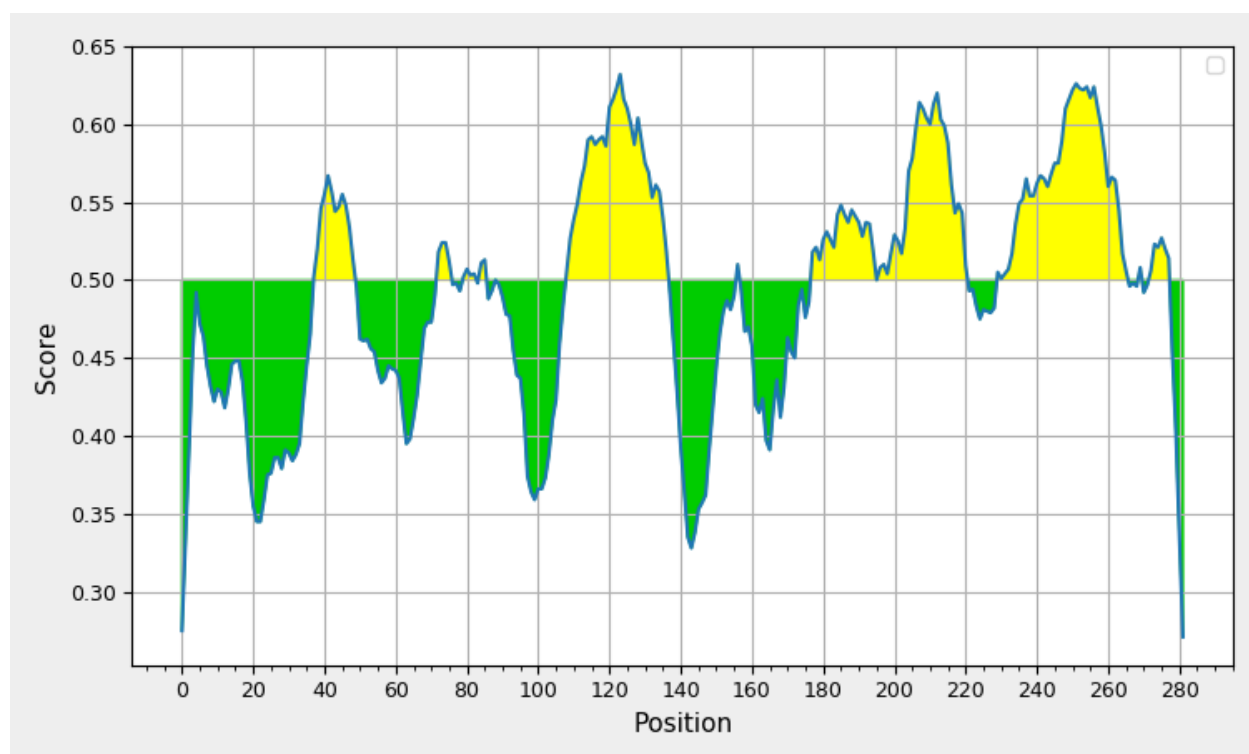
MSDLVPLSKSSAILSTSMATPSPSAPAVGPDTLITIKILHNSVNRRFKIPLRDLGARVFPQKVRYLLAV  
APTDSLVLERYSDSLANYIVLDSENPAVYKQLYRAAKAKLKLRIKATTKPQESTDSPVVTAPIEEPRIQE  
QSHQRFRYLETVLSPTTASAQTKNMTSPLTSRARAFSPVSSVHEKQQAFLRFSDNNYLGNAFCIDCNN  
CGGSIPSEHYHCGICDDGDYDLCCLNCVDAGVSCPGDDHLLKRVVQNGVIINSVTEIAPKRLGSLEPVAT  
EKPAPVKEPEEEPKVEEKEAIVPEPEVKKEPKVADERTCNACFRFSESSMVHCDNCEDYDLCIGCLL  
KNSHGHNPAHAFSIIQENQLGLKLNVLSSRCRPGRRHYHAAICDGCEKRIVGVRHKCLSCPWDYCWSCAK  
TADQSHPQHRFVPIYGPISSEYSFSQDVHYGIYCDGPLCRGKPKSTSYITGVRYKCAVCHDTDFCAACEALP  
TNTHNQTHPMIKFRTAVRNVTVNTLGDDGFGGQTMVMGDRTPPAVRSSANVTPTSPVEAPSVVEKVEPEA  
VKEETAEEEEPAPETPETPATPRRSSVDFTDDYSAYFMKDTVSDGTAMAPSQVFQQTWTLYNPGPTTWVPG  
TSRYVGGDAMFNINTEHPSSVVALAVAMSSNELVHPVAPSESADFSVTCLKTPQRIGSSISYWRMKLPNG  
TPFGHKLWCDVKVVEQPIAATEPVVPVVEEAEESVSEYSEATVVDAATETESAEMAGSNMVFPKLEKE  
SPVSSHTLAQNPAPSYTAPSVDDQALPDDMESLTLSDSDDDGFFTDEEYDILDASDQESINGKH



## P24 Nmt1

>XP\_002145167.1 thiamine biosynthesis protein (Nmt1), putative [Talaromyces marneffeii ATCC 18224]

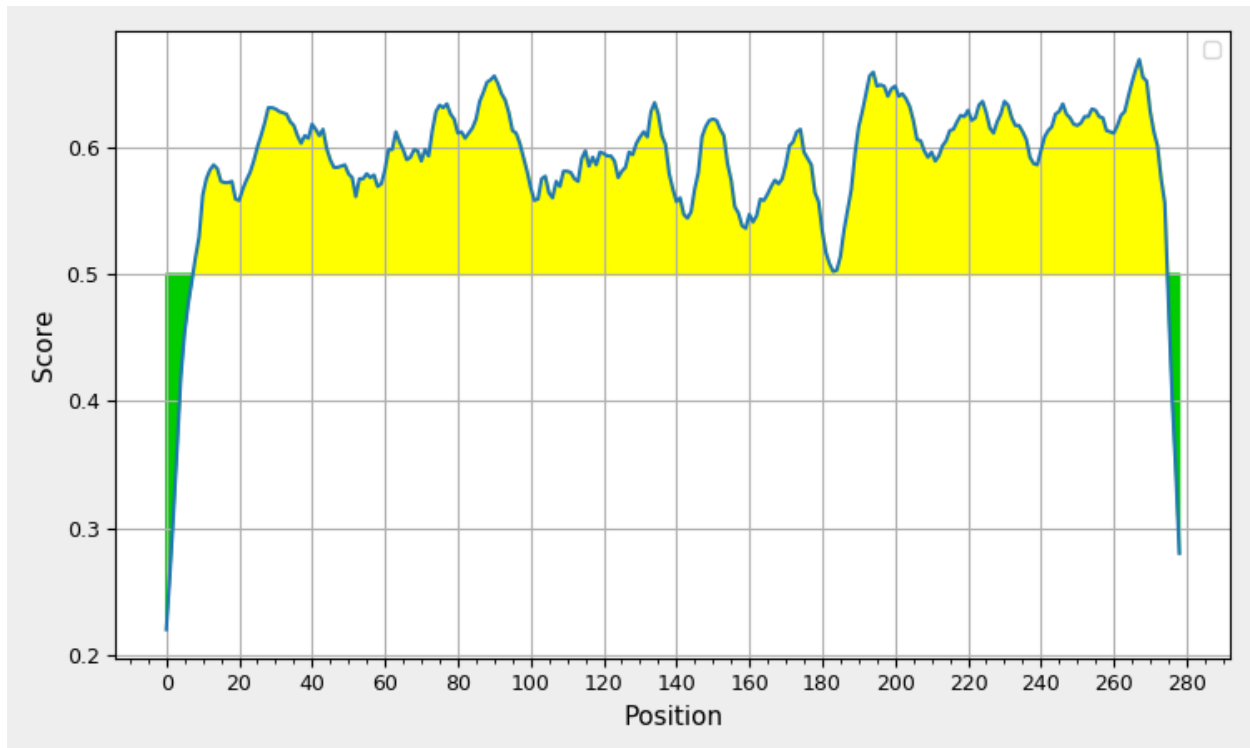
MGFKAMIHTLAAKARNFPVTSFGSLLDEPFTGVVYLKDSGITTDFKTLK**GKRIGYVGEFGKIQIDELTKY**  
YGMTPDDY**TAVRCGMNVT**KAIIEGNIDAGIGLENVQMVELEEWLAAQGRPRDDVQMLRIDQLAELGCCF  
CSILYIAN**DSFLAANGDKVMKFLRAIKRAT**DFVIAEP**KKAYEEYVDFKPI**MGTEVNRK**IFERSYAYFSRD**  
LKNVPRDWQKV**TNYGKRLG**ILDASFQPNYTNELLTWDLADSTDPIGDQQRMAELQ**KKVA**TEGGFQRLEI  
AA



## P26

>XP\_002153087.1 conserved hypothetical protein [Talaromyces marneffeii ATCC 18224]

MRSILISAALIGSALAYPGGYWAERRHYGTGIGTGTQPHPPPQTSTLTTTSMPPASTTTTTTSVSEWSTV  
TETETNTKTVFVPCSTSVGTRGSSTVYSTWLTTTTSVWTTTHTTTTPVYGTTPVGGVGPVGSETGLAC  
PLPVTTTHTETKTTTATVTVTVAVTAPGAPETTTTKPAVAIPPPPPPPVESTSTSTLHTSTSTATATA  
TTTATGTETSVEPTSTHTTTTTTKPASTTTTITTHLGTGTITGPVGTGTGSPSWVHKRNEMKKPIIHRVL



## P28 SdeA

>XP\_002152122.1 stearic acid desaturase (SdeA), putative [Talaromyces marneffeii ATCC 18224]

MSATADARPRPAADTKKVHIADTKMTLKNWYKHVDWLN~~VYFIIGIPLYGCIQSLWVPLQLKTA~~VWAVLY  
YFYTGLGITAGYHRLWAHCSYSATLPLQIFLAAAGGGAVEGSIRWWARGHRAHHR~~YTDTKDP~~YSVRKGL  
LYSHLGWMMVKQNPKRIGRTDITDLNEDPIVKFQHRHYIKIVAFMGLVFPMMVAGLGWGDWGGFVYAGI  
LRIFFVQQATFCVNSLAHWLGDQPFDDRNSPRDHVITALITLGEGYHNFHHEFPSDYRNAIEWHQYDPTK  
WFIWTKQLGLAYDLKQFRANEIEKGRLLQQLQKKLDRRTQLDWGIPLDQLPVMWDDYVEQAKNGRGLI  
AIAGVIHDVTD~~FIKDH~~PGGRAMINSGIGKDATAMFNGGVYFHSNAAHNLLSTMRVGVIRGGCEVEIWKRA  
QKENTNV~~DYVR~~DTNGQRVVRAGEQVTKIPQPVATADAA

