

A0A9P5L1K9 <i>P. crustosum</i>	maprftwtalwaltlghavmaap--qilaprATGSLDTWLASESAVARQGILDNIGS	54
G3Y7U0 <i>A. niger</i>	-----msfrsllalsglvctg--lanviskrATLDSWLSNEATVARTAILNNIGA	48
XP_006960925.1 <i>H. jecorina</i>	mhvltstavllgsvavqkvlgprpgssglSDVTKRSVDDFISTETPIALNNLLCNVGP	56
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A0A9P5L1K9 <i>P. crustosum</i>	AGAYAANAKPGVVVASPSTSDPDYYYTWTRDSALVFKTLVDMFKN-GDSALLDVIE	109
G3Y7U0 <i>A. niger</i>	DGAWVSGADSGIVVASPSTDNPDYFYTWTTRDSGLVLKTLVDLFRN-GDTSLLSTIE	103
XP_006960925.1 <i>H. jecorina</i>	DGCRAFGTSAGAVIASPSTIDPDYYMWTRDSALVFKNLIDRFTETDYDAGLQRRIE	112
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	■N95	
A0A9P5L1K9 <i>P. crustosum</i>	EYISAQAYIQTVS■PSGALSGGSGLGEPKFNADETAFTGSWGRPQRDGPALRATAL	165
G3Y7U0 <i>A. niger</i>	NYISAQAIQGIS■PSGDLSSGAGLGEPKFNVDETAFTGSWGRPQRDGPALRATAM	159
XP_006960925.1 <i>H. jecorina</i>	QYITAQVTLQGLS■PSGSLADGSGLGEPKFELTLKPFTGNWGRPQRDGPALRAIAL	168
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	173N■ ◆E181	
A0A9P5L1K9 <i>P. crustosum</i>	ISFGQWLIDNEYTTYATDIVWPVVRNDLSYVAQYWNQ■TGYDLW■EVS■GSSFFTVAA	221
G3Y7U0 <i>A. niger</i>	IGFGQWLIDNGYTSTATDIVWPLVRNDLSYVAQYWNQ■TGYDLW■EVS■GSSFFTIIV	215
XP_006960925.1 <i>H. jecorina</i>	IGYSKWLINNNYQSTVSNVIWPIVRNDLNYVAQYWNQ■TGF■DLW■EVS■GSSFFTVAN	224
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	212C C215 C224	
A0A9P5L1K9 <i>P. crustosum</i>	QHRALVEGSTFASQVGSS■PY■CDSQAPQVL■CFLQSFWTGSYILAN----FGGGRSG	273
G3Y7U0 <i>A. niger</i>	QHRALVEGSAFATAVGSSCSWCDSQAPEILCYLQSFWTGSFILAN----FDSSRSG	267
XP_006960925.1 <i>H. jecorina</i>	QHRALVEGATLAATLGQSGSAYSSVAPQVLCFLQRFWVSSGGYVDSNINTNEGRTG	280
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	C264 C272	
A0A9P5L1K9 <i>P. crustosum</i>	KDANTLLGSIETFDPEAG■CDDTT■FQPC■SARALANHKVVTDSEFRSIYSVNSGIAAGK	329
G3Y7U0 <i>A. niger</i>	KDANTLLGSIHTFDPEAACDDSTFQPCSPRALANHKVVDSFRSIYTLNDGLSDSE	323
XP_006960925.1 <i>H. jecorina</i>	KDVNSVLTSIHTFDPNLGCDA■GTFQPCSDKALS■NLKVVVDSFRSIYGVNKGIPAGA	336
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A0A9P5L1K9 <i>P. crustosum</i>	AVSVGRYPEDSYNGNPWYLCTLA■AEQLYDAIYTWNRIGSLTITSVLSFFQDLY	385
G3Y7U0 <i>A. niger</i>	AVAVGRYPEDTYNGNPWFLCTLA■AEQLYDALYQWDKQGSLEVTDVSLDFFKALY	379
XP_006960925.1 <i>H. jecorina</i>	AVAIGRYAEDVYNGNPWYLATFA■AEQLYDAIYVWKKTGSI■TVTATSLAFFQELV	336
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	◆E402	
A0A9P5L1K9 <i>P. crustosum</i>	SSAATGTYS■SSSDTYSSIVA■AVKEYADGYVSIVEQYAPSTGSLSE■QFSKSDGSQLS	441
G3Y7U0 <i>A. niger</i>	SDAATGTYS■SSSSTYSSIVDAVKT■FADGFVSIVETHAAS■NGSMS■EQYDKSDGEQLS	435
XP_006960925.1 <i>H. jecorina</i>	PGVTAGTYS■SSSSTFTNI■NAVSTYADGFLSEAAKYVPADGSLA■EQFDRNSGTPLS	392
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	C451	
A0A9P5L1K9 <i>P. crustosum</i>	ASDLTWSYAALLTANERRNAIVPAPWGETSASSVPGQ■QY■TSAIGTFSSATNTAWP	497
G3Y7U0 <i>A. niger</i>	ARDLTWSYAALLTANNRRNSVVPASWGETSASSVPGTCAATS■AIGTYSSVTVTSWP	491
XP_006960925.1 <i>H. jecorina</i>	ALHLTWSYASFLTATARRAGIVPPSWANSSASTIPSTCSGASVVGSYSRPTATSFP	448
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	507C	
A0A9P5L1K9 <i>P. crustosum</i>	ATLTSG----SGSGTTGSSGVT■TTKTAT■TTT■TKATST■TTS■TPTAVAVTFNVIA	549
G3Y7U0 <i>A. niger</i>	SIVATGGTTTTATPTGSGSVTSTSKTTATASKTSTST■SST■SCTPTAVAVTFDLTA	547
XP_006960925.1 <i>H. jecorina</i>	-----PSQTPKPGVPSGTPY■TPLPCATPT■SAVTFHEL■V	482
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	Y525 W541 Y554	
A0A9P5L1K9 <i>P. crustosum</i>	TTT■Y■GQNIKLAGSISQ■LG■S■WSTSSAIALSASS■Y■TSSNNLWFVTVTL■PVGTS■SFTYKY	605
G3Y7U0 <i>A. niger</i>	TTT■Y■GENIYLVGSISQ■LG■D■WETSDGIALSADK■Y■TSSDPLWYVTVTL■PAGES■SFEYKF	603
XP_006960925.1 <i>H. jecorina</i>	STQFGQTVK■VAGNAA■AL■GN■WSTSA■AVALDAVN■Y■ADNHPLWIGTVNLEAGDVVEYKY	538
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	W588 ■N593 C602	
A0A9P5L1K9 <i>P. crustosum</i>	IRVASDGTVT■WESDP■NLSYTVPTT■GTTAVAI■SDTWR-	642
G3Y7U0 <i>A. niger</i>	IRIESDDSV■WESDPNREYTV■PQACGTSTATVTD■TWR-	640
XP_006960925.1 <i>H. jecorina</i>	INVGDG■SVT■WESDPNHTYTV■PAVACVTQVVKEDTWQS	632
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Supplementary Figure 4. Sequence analysis of *P. crustosum* G10 glucoamylase (UniProt A0A9P5L1K9). Sequence alignment of the *P. crustosum* glucoamylase amino acid sequence with homologous enzymes from *A. niger* (AlphaFold G3Y7U0) and *H. jecorina* (*T. reesei*) (PDB 2VN7). The catalytic domain is underlined in blue, the CBM20 domain in green, and the linker peptide in red. Signal peptide sequences are shown in dark brown lowercase letters. The two catalytic Glu residues in the active site are highlighted in bold red and marked with black diamonds. The Asn residues highlighted in bold magenta (Asn95, Asn173, and Asn593) and marked with black squares correspond to the predicted *N*-glycosylation sites in the *P. crustosum* enzyme. Tryptophan (Trp541 and Trp588) and tyrosine (Tyr525 and Tyr554) residues in the CBM20 domain, which are essential for raw starch binding, are shown in purple and dark brown, respectively. Cysteine residues involved in disulfide bond formation are highlighted in green (Cys212-Cys215, Cys264-Cys272, Cys224-Cys451, and Cys507-Cys602).