

## Supplementary Materials

### Identification and characterization of dextran $\alpha$ -1,2-debranching enzyme from *Microbacterium dextranolyticum*

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**Table S1. Putative GHs detected by LC-MS/MS.**

Accession	-10logP	Coverage (%)	No. of peptides	Signal peptide	Average mass	GH family	Description
MBM7461785.1	338.32	29	43	Yes	113904	GH9	endoglucanase
MBM7463898.1	206.35	13	15	Yes	131812	GH65	trehalose/maltose hydrolase-like predicted phosphorylase
MBM7461588.1	180.35	11	13	No	123490	GH97	hypothetical protein
MBM7463772.1	54.35	2	2	Yes	130172	GH92	putative alpha-1,2-mannosidase

1 MKPVSPTAGE PEMRRAPRRT RAAMGALLTA PLLVTGVLGA GAAAESGSA PTGANTSNGW EMATTDPFSA DYHPTFTGNG ■ Carbamidomethylation (+57.02)

81 NFAARVPAQG QGYSAADVAT QFQVAGLYAA HLPNEARASA PAWTGLTVSD GSGSFDQAFS APCVVGSICQ LEDAQLSGGV

161 SVASDHGGYQ GSGFTQGWGN ASAGALLYAN GAQPDAAYDL IVR**YAAGNPG DNSANVR**SLH VSVGDTSAI ALPPSPQGDW

241 DTWMQAR**LPL GALTDRALT LSCSSTPGAD CRVNVDSIAI VPRDGALPTT PPDLTMDAR**G LADYRQSLDV STGAIITSAR

321 WTSPSGNVSD VAYTVLTD RG HDDRALVRVD VTPQWSGDLE VTDVLDTRPA TFVAGTVTHR DDAAGTIGVD AAITGSGITA

401 SIASTLAGPG QR**AEARPVGL PSGSIAQ**KL T QSVESGKTY S FVKYVGLTT HDGADTAGLA **KAASTAAAQ GYDAVRASND**

481 **GAWADIWK**GD IQVTGDDALQ QQIRASRFYL LASVNADRPW SPSPAGLSSD GYGGHVFDW ETWMWPSLVA QDPEIAAAVL

561 KYRSDRIDDA RANAAAGHD GIRFPWEGAL DGTEQTATL FGETEQHITA DVALAFWQYY LSTGDRTWLQ NEGWPVISGA

641 ADFWASRVEL GDDGQYHNG VTPPDEWAGK HDSAYTNVA AAQTMRMATR **AAGVLGTSAK PAWQTIADK**M FMPHDDALGI

721 TPEYAGYNHG VIKQADVMT TYPWGYEQSD ELTAR**NLAYY ASR**VTTSGGP SMTDAIHSIV SAELGNVCDA WYYTQQSGTP

801 **FMRAPFDQFS EER**EGGAFTT TTGAGGLQE FYYGYTGLRM QEDGITLAPI LPPSLTDMTV AGLHYQGRTF DVKIGTSTD

881 VTLTSGPALT VHTADGDKTV STDAALRIPT RTANDCEATS GYGTLLGSLS APAGGDNGAG TLQYPGSSNF PTGTFDMTDF

961 DVYRDGDTLR YVTVSGEIT NPWGGNGMSV QLLHTYLRLP SNDSAPARSG AVPALPGTNA DLESPWDLVL VGNGRATGSG

1041 PGTGLYDASG ALVAVVELSV TPRRHQIVLS FPESALKGAD FVKVGYVAAM LVNAESNEGL SNIRPALDCE APGSPDWVSQ

1121 WRICGGLGTI SSASPYD TDT RDPNIIK**VFV PEGR**TQQGDV LK**TEGPSILP FVALK**AAPGP SPSPSDSGSA SPNPSDSGSA

1201 SPSPSDSGPG SPSASASASP TTSGAAAGGP SADRLGATGG ESPLPLAVIG GVLLLLGAAG VLMRRRSLRR DGA

#### Supporting Peptides:

Peptide	Uniq	-10lgP	Mass	ppm	m/z	z	RT	Scan	#Spec	Start	End	PTM
K.AASTAAAQGYDAVR.A	Y	82.23	1421.6898	31.9	711.8749	2	-	532	2	462	476	
R.AALTLSG(+57.02)SSTPGADC(+57.02)R.V	Y	71.23	1665.7450	27.9	833.9030	2	-	569	1	257	272	Carbamidomethylation
R.VNVDSIAIVPR.D	Y	63.76	1181.6768	27.5	591.8619	2	-	655	1	273	283	
R.YAAGNPGDNSANVR.S	Y	57.69	1404.6382	28.8	703.3466	2	-	466	1	204	217	
R.ASNDGAWADIWK.G	Y	55.54	1332.6099	27.6	667.3306	2	-	710	1	477	488	
R.LPLGALTDR.A	Y	55.52	954.5498	27.3	478.2952	2	-	615	1	248	256	
R.AAGVLGTSAKPAWQTIADK.M	Y	54.21	1884.0105	30.2	629.0297	3	-	657	1	691	709	
K.TEGPSILPFVALK.A	Y	49.94	1370.7809	26.7	686.4160	2	-	749	1	1163	1175	
R.APFDFSEER.E	Y	40.92	1224.5410	31.2	613.2969	2	-	598	1	804	813	
L.PSGSIAQK.L	Y	38.90	786.4235	30.4	394.2310	2	-	558	1	421	428	
R.DGALPTTTPDLTMDAR.G	Y	37.46	1669.7981	27.3	835.9291	2	-	671	1	284	299	
R.AEARPVGLPSGSIAQK.L	Y	32.12	1579.8682	34.2	527.6480	3	-	557	1	413	428	
R.NLAYYASR.V	Y	19.27	956.4716	30.6	479.2577	2	-	531	1	756	763	
K.PAWQTIADK.M	Y	19.14	1028.5291	29.9	515.2872	2	-	579	1	701	709	
K.VFVPEGR.T	Y	16.38	802.4337	32.1	402.2370	2	-	501	1	1148	1154	
<b>total 15 peptides</b>												

**Figure S1. Peptides of *M. dextranolyticum* GH65 protein (MddDE) identified by LC-MS/MS.** Coverage map (*top*) and properties (*bottom*) of MddDE-derived peptides identified by LC-MS/MS are shown.