Supplementary Table S1. Top BLAST hits for *P. brevicompactum* MPA gene cluster in *Phaeosphaeria nodorum* and *Talaromyces stipitatus*.

	P. nodorum SN15 (taxid:321614)				T. stipitatus ATCC 10500 (taxid:441959)				
Query (P. brevicompactum)	Protein ID (top BLAST hit)	BLASTP E- value	BLASTP Identity	Identity (ClustalW)	Protein ID (top BLAST hit)	BLASTP E- value	BLASTP Identity	Identity (ClustalW)	
MpaA	SNOG_05304	7.00E-17	30%	17.38%	gi 242821326	1.00E-16	20%	17.12%	
MpaB	SNOG_14971	2.00E-89	39%	33.72%	gi 242779340	2.00E-120	50%	42.06%	
MpaC (PKS)	SNOG_06682	0	39%	36.90%	gi 242760313	0.00E+00	49%	42.50%	
MpaD	SNOG_06679	2.00E-109	47%	31.22%	gi 242760308	1.00E-113	55%	53.13%	
MpaE	SNOG_06681	1.00E-81	50%	45.90%	gi 242760293	3.00E-87	50%	47.89%	
MpaF (IMPDH-B)	SNOG_00421	0.00E+00	73%	70.45%	gi 242786825	0.00E+00	79%	76.64%	
MpaG	SNOG_08626	2.00E-60	31%	30.35%	gi 242781136	0.00E+00	63%	61.85%	
МраН	SNOG_15010	5.00E-50	37%	26.05%	gi 242768952	2.00E-84	39%	36.59%	

1. MpaD and MpaE (shown in green) were together identified as a single fusion protein in the current study. BLAST search for the fusion protein MpaDE did not find any good hits. 2. BLASTP search was performed on the NCBI BLAST server (<u>http://blast.ncbi.nlm.nih.gov/Blast.cgi</u>, 16th March 2012) against the two genomes of interest and with the default settings. 4. For MpaC/D/E, amino acid sequence based on the coding region was used for the search. For the rest, protein sequences available in the NCBI gene bank were used.

Supplementary Table S2: ¹H and ¹³C NMR data (extracted from HMBC experiment) for 5methylorsellinic acid and 5,7-dihydroxy-4-methylphtalide^a

OH

4

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	5-methylo	rsellinic acid	5 7-dihydroxy-4-methylphtalide			
	3-meanyion		3, <i>i</i> -diriyuroxy-4-metriyipntallue			
Position	$\delta_{ m C}$ (ppm)	δ_{H} mult	$\delta_{ m C}$ (ppm)	δ_{H} mult		
2	18.6	2.28 (3H, s)	67.5	5.11 (3H, s)		
3	138.9		149.0			
4	115.1		108.5			
5	159.2		162.1			
6	100.2	6.23 (1H, s)	102.0	6.41 (1H, s)		
7	nd		155.6			
8	108.9		nd			
9	172.0		168.6			
10	12.1	1.93 (3H, s)	10.1	1.91 (3H, s)		
5-OH		9.81 (1H, s)		10.32 (1H, s)		
7-OH		10.92 (1H, bs)		10.18 (1H, s)		

^a recorded in DMSO- d_6 at 25 °C, referenced to 2.50 ppm

 δ_{C} : carbon chemical shift values

 δ_{H} : proton chemical shift values

Mult: multiplicity of proton NMR peaks (s: singlet, bs: broad singlet)

HMBC: Heteronuclear Multiple Bond Correlation (nd: not detected via HMBC experiment)



Supplementary Figure S1.

Integration of expression cassette into integration site II on *A. nidulans* chromosome I by homologous recombination using bipartite transformation. A) Schematic drawing of BGHA P127, BGHA P146 and BGHA P123. TSI and TSII are the sequences for homologous integration in IS2. The selection marker is *pyrG* from *A. fumigatus* shown in bipartite gene targeting configuration. PgpdA and TrpC define promoter and terminator of native *gpdA* and *trpC*, respectively, controlling and enabling constitutive *mpaDE* expression. Transformation substrates are generated by SwaI digest of the constructs. B) Integration of the *mpaDE* expression cassette into *A. nidulans* by homologous recombination. Control strain is generated by bipartite transformation with SwaI digested BGHA P146 and BGHA P123. Drawing is not to scale.

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Supplementary Figure S2.

¹H NMR spectrum of 5-methylorsellinic acid (5-MOA) measured in DMSO- d_6 (¹H at 500 MHz, ¹³C at 125 MHz) and referenced to solvent residual signals and solvent signals at 2.50 ppm (¹H NMR).



Supplementary Figure S3.

¹H NMR spectrum of 5,7-dihydroxy-4-methylphatalide (DHMP) measured in DMSO- d_6 (¹H at 500 MHz, ¹³C at 125 MHz) and referenced to solvent residual signals and solvent signals at 2.50 ppm (¹H NMR).

		20		40		60		80		100	
MpaD_MpaE		MKSLSLTWIT	AVAVVLYLVQ	RYVRSYWRLK	DIPGPV-LAK	LTDLQRVWWV	-KTGRAHEFH	RDMHAMYGP I	VRFGPNM	VSVSDPRVIP	85
2ij2 3k9v		MTIK	APKEVPLCPL	MTDGETRNVT	EMPQPKTFGE DLPGPTNWPL	LKNLPLL LGSLLEIFWK	- NTDKPVQAL GGLKKQHDTL	AEYHKKYGQI	FREAPGRVT	RYLSSQRLIK VHLGSPSLLE	50 84
2f9q		MAKK	TSSKGKL		- PPGPLPLPG	LGNLLHV	- DFQNTPYCF	DQLRRRFGDV	FSLQLAWTPV	VVLNGLAAVR 6	66
TSTA_060710 SNOG 06679	MDSMNIFPGY	RQADSIVFIA GMAGGVAVVA	VGSILGLSLL	HLLRTYWRLR	YIPGPF-LAR HIPGPF-LAS	FTNLQRVYWV ITDLYRMNWV	-KTTRAHEIH	QQMHEKYGNV	VRFGPNM VRIGPNT	VSLGDPALIP S	95 95
3dha											-
2r2d 1sml											-
TST_060680											-
SNOG_06681		120		140		160		180		200	-
MaaD MaaE	TIVESPECE	KODEVRTOKR	VTRNKGAMRA	VENT ODEDI			RIERIVOETI		EVGTNDKRED		100
2jj2	EACDESRFDK	NLSQALKEVR	DFAGDG	LFTSWTHEKN	WKKAHNILLP	SFSQQ AMK	GYHAMMVDIA	VQLVQKWERL	NADEH I E	VPEDMTRLTL	151
3k9v	ALYRTESAHP	QRLEIKPWKA	YRDHRNEAYG	LMIL-E-GQE	WQRVRSAFQK	KLMKP-VEIM	KLDKKINEVL	ADFLERMDEL	CDERGRI-PD	LYSELNKWSF	180
TSTA 060710	SLYPIRPGFP	KSDFYRSLMP	YTRKGGSLPA	VFNT-RDENL	HKVIKTPIAP	LFSLSNIL	PLEVFVNRVL	EVLFQQLDTR	FVSSGDT-FD	LADWLQYFAF	191
SNOG_06679	EVYPMRAGMP	KSDFYVTLRP	YT-SGQALHA	VFNT-TEESI	LKQIKPPIAP	LFNISSAA	TLEPLVDEVL	ECIRGRFDER	FVGTGQI-FD	MGQWLQFFAF	190
2r2d											-
1smi 1smi											-
SNOG_06681											-
		220		240 I		260		280 I		300 I	
MpaD_MpaE	DSMGTLTFSR	RYG-FLEQGR	DMHGILQ	EIWNFMTRVA	VMGQIPWFDE	IWNKNSFITL	FKRPTGFGVL	KVVDNF	ISQR	VSSRENDEKA	268
21j2 3k9v	ESICLVLYEK	RFG LLQKE	TEEEALTFIT	AIKTMMSTFG	KMMVTPVELH	KRLNTKVWQA	HTLAWD	-TIFKS-VKP	CIDNRLQRY -		261
2f9q	NVIASLTCGR	RFE YDDPR	-FLRLLDLAQ	EGLKEESGFL	REVLNAVPVD	RHIPALAGKV	LRFQ	-KAFLTQLDE	LLTEHRMTWD	PAQ	244
SNOG 06679	DVMGTMTFSK	RYG-FLDKGR	DVGGMLG	AIVDEMRTAA	PMTQSPLLDK		LRQYIRPTAS	LTILSF-VGQ	AIKEKKEKME	SKTSKSE	282
- 3dha											-
2r2d 1sml											-
TST_060680											-
SNUG_06681		320		340		360		380		400	•
MpaD MpaE	DEKDMLSQFL	I DIQASNPH	SIMPWAPR	AWTFSNVMAG	SDSTANVMRT	MMYNLLVDRD	TLRSLRAELL	EAENSNGL	SRSLPSWDGV	RSLPYLDACV	362
2ij2	QSDDLLTHML	NGKDPETG	-EPLDDENIR	YQIITFLIAG	HETTSGLLSF	ALYFLVKNPH	VLQKAAEEA-	ARVLV	D-PVPSYKQV	KQLKYVGMVL 3	319
3k9v 2f9a	PPRDLTEAFL	AEMEKAKGNP	ESSFNDENLR	IVVADLFSAG	WETTANSLMW MVTTSTTLAW	GLLLMILHPD	VQRRVQQEI-	QSVLP	QVRRPEMGDQ	AHMPYTTAVI	338 338
TSTA_060710	SDRDMLSRFF	ELQEKDSK	IPRWAVT	AWAFSNVIAG	SDSTAVTMRT	TWFGLLSHPE	TLKTLRKELL	DQDSKLEGGI	TRPFPAWKDI	CNLAYLDACV	377
SNOG_06679 3dha	GQIDFLTRYI	ELQKHNPS	IPPWAPT	AWTFSNVIAG	SDSVGTCMRT	MLYHLLAYPN	TFDRLYKEL-	LAAKT	SRPFPSYSEV	RELPYLEACV	371 -
2r2d											-
1smi TST_060680											-
SNOG_06681											-
		420 I		440 		460 		480 		500 I	
MpaD_MpaE 2ii2	LEALRLHPPF NEALRLWPTA	CLPFERVVPE P-AFSLYAKE	-DTVLGGEYP	LPAGTVVGIS	PYLANRDKQT I POLHRDKT I	FGDDADKWRP	SRWLDLSRED ERFENPSA	RVKLENSILT	FGAGRRTCLG	KNIAILEIKK 4 QOFALHEATL 4	461 413
3k9v	KESMRLTPSV	P-FTTRTLDK	- PTVLGE - YA	LPKGTVLTLN	TQVLGSSEDN	F-EDSHKFRP	ERWLQKEK	K-INPFAHLP	FGIGKRMCIG	RRLAELQLHL 4	442
2f9q TSTA 060710	HEVQRFGDIV NEAVRLHPPF	PLGMTHMTSR	-DIEVQG-FR GGLTIGG-TY	IPKGTTLITN FPAGTVVGMS	LSSVLKDEAV PWVINRHRPT	W-EKPFRFHP FGHDAESWRP	EHFLDAQG ERWMVPEE-H	HFVKPEAFLP RRKLEQSVLT	FSAGRRACLG	EPLARMELFL 4	433 475
SNOG_06679	QEAIRVHPPF	ALPLERVVPD	GGMTVLG-YF	LPGGTVIGGS	PYVVNRDTSM	FGEDAEFWRP	ERWLGGDAAH	KRSLEASMLT	FGAGRRICLG	RHVGILEIKK 4	470
3dha 2r2d											-
1sml											-
TST_060680 SNOG 06681											2
-		520		540 I		560		580		600	
MpaD_MpaE	LFPMLLLNYE	IEIVNPENYQ	TTNAWFFRQW	GLQAVIRKLP	APERDDTIEQ	KASIPPALNI	PPSSSTVEVR	IIDSGTLLDL	RPDLFWTPDL	PGLLK	556
2ij2 3k9v		FEDHTNYELD	MUNICITY	GFVVKAKSKK	IPLGGIPSPS	TEQSAKKV					471 482
2f9q	FFTSLLQHFS	FSVPTGQPRP	SHHGVFAFLV	SPSPYELCAV	PR						475
TSTA_060710 SNOG_06679	LIAFLVLTYE	FDLLDPKRFK	VENGWFFRQY	GMDVKARKAT	VWEEDKKQ						523 512
3dha					MTV	KKLYFIPAGR	CMLDHSSV		NSALTPGK		29
2r2d 1sml					MG-	TLLAFALAVA	LPAAHTSAAE	VPLPQLRAYT	VDASWLQPMA	PLQIADHTWQ	37 53
TST_060680					MNSSHL - A	SPIAPPQLNI	PHSTYTVDIR	VIDTETLIYL	DPKLFWQPEL	DGFDG	52
SNUG_00081		620		640	MSQPPFSA	QSTAAPALGG 660	THPMITVDVR	VIDIQUERE 680	DPKLFWQPSL	700	53
MpaD MpaF	-VTAPTYCEL	ISNGTRHVLF			SOTVIGEPRN	1 SDV	LDSDESS-LG	VRSKDIEAII	WSHAHFDHIG	DPSTEPPSTE (648
2ij2										4	471
3k9v 2f9q											482 475
TSTA_060710									•••••		523
3dha	LLNLPVWCYL	LETEEGPILV	DTGMPESAVN	NEGLF	-NGTFVEGQI	LPKMTEEDRI	VNILKR VG				J12
2r2d	LIDIPVSAYL	IQCTDATVLY	DTGCHPECMG	TNGRWPAQSQ	INAPYIGAS.			YEPDDLLYII	SSHLHFDHAG	GNGAFTNTPI	121
TST_060680	-VHAPIYCEL	VUIPDGAVLL			ENAL LIGHT	ECNL	PERLRQLG	YEPDDLLYII LSPDDISTVV	SSHLHFDHAG LSHLHNDHAG	GNGAFTNTPI CVEYFGKSRL	121 128 122
SNOG_06681		ISHGQQHVVF	DLGVRRDWEN	YAPRIVSLIK	ATTEVIVGKD	·····ECNL ·····SHL V····AEV	PERLRQ LG LDNMKA RG LDGDQSGEVN	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI	SSHLHFDHAG LSHLHNDHAG LSHAHADHAG WSHNHFDHIG	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE	121 128 122 145
MpaD Mar -	-LDAPVYCFL	I SHGQQHVVF I THKDTHMVF	DLGVRRDWEN DLGVRTDWEN	YAPRIVSLIK YPPNIVSLIK	ATTEVIVGKD ATTRITPGKA	·····ECNL ·····SHL V·····AEV V·····AHI	PERLRQLG LDNMKARG LDGDQSGEVN LDESSV	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV	SSHLHFDHAG LSHLHNDHAG LSHAHADHAG WSHNHFDHIG WSHNHFDHIG	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE DIATLP-QAE	121 128 122 145 141
wipau MpaE	-LDAPVYCFL	I SHGQQHVVF I THKDTHMVF 720		YAPRIVSLIK YPPNIVSLIK 740	ATTEVIVGKD	ECNL SHL VAEV VAHI 760	PERLRQLG LDNMKARG LDGDQSGEVN LDESSV	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV 780 I HSVGHIC A	SSHLHFDHAG LSHLHNDHAG LSHAHADHAG WSHNHFDHIG WSHNHFDHIG	GNGAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE DIATLP-QAE 800 1	121 128 122 145 141
2ij2	- LDAPVYCFL LVVGPGIRDT	ISHGQQHVVF ITHKDTHMVF 720 I HWPGFPTNPD	DLGVRRDWEN DLGVRTDWEN	YAPRIVSLIK YPPNIVSLIK 740 I RNVREISFEK	ATTEVIVGKD ATTRITPGKA TQKGATKIGS	ECNL SHL VAEV VAHI 	PERLRQ - LG LDNMKA - RG LDGDQSGEVN LDESSV	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV 780 I HSVGHIG-AL	SSHLHFDHAG LSHLHNDHAG LSHAHADHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE DIATLP-QAE 800 1 SPVSFVFM	121 128 122 145 141 739 471
2ij2 3k9v	- LDAPVYCFL LVVGPGIRDT	ISHGQQHVVF ITHKDTHMVF 720 HWPGFPTNPD		YAPRIVSLIK YPPNIVSLIK 740 I RNVREISFEK	ATTEVIVGKD ATTRITPGKA TQKGATKIGS	ECNL 	PERLRQ LG LDNMKA RG LDGDQSGEVN LDESSV	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV 780 I HSVGHIG-AL	SSHLHFDHAG LSHLHNDHAG LSHAHADHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE DIATLP-QAE I SPVSFVFM Z	121 128 122 145 141 739 471 482
2ij2 3k9v 2f9q TSTA_060710	- LDAPVYCFL	ISHGQQHVVF ITHKDTHMVF ITHKDTHMVF I HWPGFPTNPD		YAPRIVSLIK YPPNIVSLIK 740 I RNVREISFEK	ATTEVIVGKD ATTRITPGKA TQKGATKIGS	ECNL SHL VAEV VAHI 760 FDAVDYFGDG	PERLRQLG LDNMKARG LDGDQSGEVN LDESSV SFYL-LDAAG	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV 1 HSVGHIG-AL	SSHLHFDHAG LSHLHNDHAG USHAHADHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE DIATLP-QAE 800 SPVSFVFM7	121 128 122 145 141 739 471 482 475 523
2ij2 3k9v 2f9q TSTA_060710 SNOG_06679 2dba	- LDAPVYCFL	ISHGQQHVVF ITHKDTHMVF 720 HWPGFPTNPD	AINLNTDIQG	YAPRIVSLIK YPPNIVSLIK 70 RNVREISFEK	ATTEVIVGKD ATTRITPGKA TQKGATKIGS		PERLRQLG LDNMKARG LDGDQSGEVN LDESSV SFYL-LDAAG	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV 1 HSVGHIG-AL	SSHLHFDHAG LSHLHNDHAG USHAHADHAG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE DIATLP-QAE 800 - SPVSFVFM 	121 128 122 145 141 739 471 482 475 523 512
2ij2 3k9v 2f9q TSTA_060710 SNOG_06679 3dha 2r2d	- LDAPVYCFL LVVGPGIRDT 	I SHGQQHVVF I THKDTHMVF 720 HWPGFPTNPD LHR VRYFATGDHS	AINLNTDIQG EEYMKECILP SPYIVKDIEA	YAPRIVSLIK YPPNIVSLIK RNVREISFEK HLNYK- WLATPRNWD-	ATTEVIVGKD ATTRITPGKA TQKGATKIGS		PERLRQ - LG LDMMKA - RG LDGDQSGEVN LDESSV	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI WSVGHIG-AL	SSHLHFDHAG LSHLHNDHAG USHAHADHAG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE IATLP-QAE 800 SPVSFVFM 	121 128 122 145 141 739 471 482 475 523 512 197 219
2ij2 3k9v 2f9q TSTA_060710 SNOG_06679 3dha 2r2d 1sml	- LDAPVYCFL LVVGPGIRDT 	I SHGQQHVVF I THKDTHMVF 720 HWPGFPTNPD LHR VRYFATGDHS V-LLARGGSD	AINLNTDIQG AINLNTDIQG EEYMKECILP SPYIVKDIEA DLHFGDGIT	YAPRIVSLIK YPPNIVSLIK 700 I RNVREISFEK HLNYK- WLATPRNWD YPPANAD- PUVPEISEE	ATTRITPGKA TQKGATKIGS		PERLRQLG LDNMKARG LDGDQSGEVN LDESSV SFYL-LDAAG 	YEPDDLLYII LSPDDISTVV VTPRDLRLIL VHSRDISSVI VRSDNIDTVV 7800 HSVGHIG-AL HSPGHQS-LF HASGMLG-LA HTPGSTAWTW	SSHLHFDHAG LSHLHNDHAG LSHAHADHAG USHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE IATLP-GAE 00 	121 128 122 145 141 739 471 482 475 523 512 197 219 210 220
2ij2 3k9v 2f9q TSTA_060710 SNOG_06679 3dha 2r2d 1sml TST_060680 SNOG_06681	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDT	I SHGQQHVVF I THKDTHMVF 720 PHVPGFPTNPD LHR VRYFATGDHS V-LLARGGSD SWPGYPSRAD LFPGWPNNPD	AINLNTDIQG AINLNTDIQG EEYMKECILP SPYIVKDIEA DLHFGDGIT- AGLDSDADG SPVKNSDMQG	YAPRIVSLIK YPPNIVSLIK RNVREISFEK HLNYK WLATPRNWD- -YPPANAD RVVREISFE RSIREIVFD	ATTRITPGKA ATTRITPGKA TQKGATKIGS 		PERLRQ - LG LDMMKA - RG LDGDQSGEVN LDESSV SFYL - LDAAG 	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV RSDNIDTVV HSVGHIG-AL SPGHQS-LF HASGMLG-LA HTPGSTAWTW HAIGHIC-GL	SSHLHFDHAG LSHLHDDHAG LSHAHADHAG WSHNHFDHIG ARVTT	GNGAFTHTPI CVEYFGKSRL DPSTFPVSTE DIATLP-QAE 0 SPVSFVM 7 SPVSFVM 7 SPVSFVM 7 	121 128 122 145 141 739 471 482 475 523 512 197 219 210 239 226
2ij2 3k9v 2f9q TSTA_060710 SNOG_06679 3dha 2r2d 1sml TST_060680 SNOG_06681	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDT	ISHGQQHVVF ITHKDTHMVF 720 HWPGFPTNPD LL-HR VRYFATGDHS V-LLARGSD SWPGYPSRAD LFPGWPNNPD 820	A I NLNTDI QG LGVRROWEN A I NLNTDI QG EEYMKECI LP SPYI VKDI EA DLHFGDGI T- AGLLDSDADG SPVKNSDMQG	YAPRIVSLIK YPPNIVSLIK 740 RNVREISFEK HLNYK- HLNYK- WLATPRNWD- YPPANAD- RVVREISFE- RSIREISFE- 810	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLRGLG LDNMKARG LDDDQSGEVN LDESSV SFYL-LDAAG VQLLYTPG VNLL-NFGTG SFYL-LDSPG SLFL-LDAPG	YEPDDLLY11 LSPDD1STVV VTFRDLRLIL VHSRD1SSV1 VRSDN1DTVV 780 780 780 780 14SVGH1G-AL HSVGHQS-LF HASGMLG-LA HAIGHIC-GL HALGHMC-AL HALGHMC-AL	SSHLUFDHAG LSHLHDHAG LSHLHDHAG LSHAADHAG WSHNHFDHIG ARVTT	GNGAFINTPI PVAELKRATG DPSTFPVSTE DIATLP-QAE 600 SPVSFVFN SPVSFVFN SPVSFVFN 	121 128 122 145 141 739 471 482 475 523 512 219 210 239 226
2ij2 3k9v 2f9q TSTA_660710 SNOG_06679 3dha 2r2d 1sml TST_060680 SNOG_06681 MpaD_MpaE	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDT GGDSCHH	ISHGQQHYUF ITHKDTHMUF 720 HWPGFPTNPD 	DGUMPQMA- DLGVRROWEN AINLNTDIQG 	YAPRIVSLIK YPPNIVSLIK 740 741 RNVREISFEK 	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLRGLG LDMNKARG LDGDQSGEVN LDESSV	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV 1700 HSVGHIG-AL HSVGHIG-AL HASPGHQS-LF HASGMLG-LA HTPGSTAWTW HAIGHIG-GL HALGHMC-AL 800 -TLSP-ALPT	SSHLHFDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE DIATLP-QAE 500 	121 128 122 145 141 739 471 482 475 523 512 197 219 210 239 226 803 471
2ij2 3k9v 219q TSTA_060710 SNOG_06679 3dha 2r2d 1smi TST_060880 SNOG_06681 MpaD_MpaE 2ij2 3k9v	LUAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LVVGPGVRDT GGDSCHH	ISHGQQHVVF ITHKDTHMVF 720 HWPGFPTNPD LHR V.YFATGHT VYFATGHT SWPGYPSRAD LFPGWPNNPD LFPGWPNNPD LFPGWPNNP AGVLRPTKYL	DGUMPGMA- DLGVRROWEN DLGVRTOWEN AINLNTDIQG EEYMKECILP EEYMKECILP EEYKKEDIEA DLHFODGIT- AGLLDSDADG SPVKNSDMQG P	YAPRIVSLIK YPPNIVSLIK YPNIVSLIK 740 747 RNVREISFEK HLNYK- WLATPRNWD YPPANAD YPANAD RVVREISFE- RSIREIVFD 640	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 	CONTRACTOR	PERLRQ - LG LDNNKA - LG LDNNKA - LG DSSV	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV 700 HSVGHIG-AL HSVGHIG-AL HASGMLG-LA HASGMLG-LA HAIGHIC-GL HALGHMC-AL S00 -TLSP-ALPT	SSHLHFDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFVSTE DIATLP-QAE 600 	121 128 122 145 141 739 471 482 475 523 512 219 210 239 226 803 471 482
2ij2 3k9v 2f9q TSTA_060710 SNOG_06679 3dha 2r2d 1sml TST_06080 SNOG_06681 MpaD_MpaE 2ij2 3k9v 2f9q 2f9T	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDT GGD - SCHH	ISHGQQHVVF ITHKDTHMVF 720 HWPGFPTNPD LHR V.LLARGGSD SWPQYPSRAD LFPGWPNNPD 820 AGVLRPTKYL	DGUMPGMA- DLGVRROWEN DLGVRTOWEN A INLNTDIQG 	YAPRIVSLIK YPPNIVSLIK RNVREISFEK HLNYK WLATPRNWD -YPPANAD RVVREISFE SIREIVFD 840	ATTEVIVGKD ATTRITFGKA TQKGATKIGS 	ECNL SHL V AEV V AHI FDAVDYGDG 	PERLROLG LDNNKARG LDGDQSGEVN LDESSV SFYL-LDAAG VQLLYTPG VQLLYTPG VILL-NFGTG IVFTAHFMAG SFYL-LDSPG SFYL-LDAPG SDSVF	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV I HSVGHIG-AL HSVGHIG-AL HSVGHQS-LF HASGMKG-LA HTPGSTAWTW HAIGHIC-GL ALGHMC-AL 800 -TLSP-ALPT	SSHLUFDHAG LSHLHDHAG LSHLHDHAG LSHANADHAG WSHNHFDHIG ARVTT	GNGAFINTPI CVEYFGKSRL DPAELKRRTG DPAELKRRTG DIATLP-QAE 000 SPVSFVFM 	121 128 122 145 141 739 471 482 475 523 512 219 210 239 226 803 471 482 475 529 210 239 226 803
2ij2 3k9v 219q TSTA_060710 SNG_06679 3dha 2r2d 1sml TST_060680 SNOG_06681 MpaD_MpaE 2ij2 3k9v 219q TSTA_060710 SNOG_06679	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEYEAA AKVAANAESA LVVGPGVRDA LIVGPGVRDT GGD - SCHH	ISHGQQHVVF ITHKDTHMVF 720 HWPGFPTNPD L L VRYFATCDHS VRYFATCDHS VRYFATCDHS SWPGYPSRAD LFPCWPNNPD B20 AGVLRPTKYL	DGUMPGMA DLGVRRØWEN A INLNTDIQG EEYMKECILP SPYIVKDIEA DLHFGDGIT- AGLLDSDADG P	YAPRIVSLIK YPPNIVSLIK 740 RNVREISFEK HLNYK- WLATPRIND YPPANAD RVVREISFE RSIREIVFD- 640	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLRQLG LDNMKARG LDDNKARG LDDDQSGEVN LDESSV	YEPDDLLY11 LSPDD1STVV VTFRDLRL1L VHSRD1SSV1 VRSDN1DTVV 780 780 780 780 780 780 780 780 780 780	SSHLHFDHAG LSHLHDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFINTPI PVAELKRRTG DPSTFPVSTE DIATLP-GAE 500 SPVSFVFN -	121 128 122 145 141 739 471 4475 523 512 210 239 226 803 471 482 475 523 512 803 471
2ij2 3k9v 219q TSTA_060710 SNG_06679 3dha 2r2d 1sml TST_060680 SNOG_06681 MpaD_MpaE 2ij2 3k9v 2f9q TSTA_060710 SNGG_06679 3dha 2r2d	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDA LIVGPGVRDT GGD SCHH	ISHGQCHVUF ITHKDTHMVF 720 HWPGFPTNPD LHR VRYFATCDHS WPGYPSRAD LFPGWPNPD LFPGWPNPD AGVLRPTKYL 	DGUMPGMA- DLGVRROWEN DLGVRTOWEN AINLNTDIQG 	YAPRIVSLIK YPPNIVSLIK 740 741 742 743 744 744 744 744 744 744 744 744 744	ATTEVIVEKD ATTEVIVEKD ATTEVIVEKD ATTRITPGKA TQKGATKIGS 		PERLRGLG LDNMKARG LDDNGSGEVN LDDDSSGEVN LDESSV	YEPDDLLY11 LSPDD15TVV VTFRDLRL1L VHSRD15SV1 VRSDN1DTVV 700 	SSHLHFDHAG LSHLHDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNAAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE DIATLP-QAE 60 SPVSFVFM SPVSFVFM CVENCONTRACTOR LTIDASYTKE LVSDACYAT IAVADSLSAP SSESSFVFM SPVFM 500 NIKELDACED	121 128 122 145 141 739 482 475 523 512 210 220 803 471 482 220 803 471 482 220 803 471 482 220 803 471 482 250 220 803 220 803 220 803 803 803 803 803 803 803 803 803 80
2ji2 3k9v 2f9q TSTA_060710 3dha 2r2d 1sm1 TST_060880 SNOG_06681 MpaD_MpaE 2jj2 3k9v 2f9q TSTA_060710 SNOG_06679 SNOG_06679 3dha 2r2d 1sm1	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDA LIVGPGVRDA NFE - DEVPF NYG - PPARR	ISH00QHVVF ITHKDTHMVF 70 70 70 70 70 70 70 70 70 70 70 70 70	DGUMPGMA- DLGVRROWEN DLGVRTOWEN AINLNTDIQG EEYMKECILP SPYIVKDIEA DLHFGDGIT- AGLLDSDADG SPVKNSDMQG P LSSIKRL DRTVSHI FATVRALPCD	YAPRIVSLIK YPPNIVSLIK 740 741 740 740 740 740 740 740 740 740 740 740	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLRQ - LG LDNNKA - LG LDNNKA - LG LDNSKA - LG STSL - LDAAG STL - LDAAG VQLL - YTPG VQLL - YTPG VQLL - YTPG VQLL - YTPG SLFL - LDAPG SLFL - LDAPG SLFL - LDAPG GLFL - E GHD LEQ - E GHD LEQ - E GHD LEQ - E	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV 1700 HSVGHIG-AL HSVGHIG-AL HASPGHQS-LF HASGMLG-LA HTPGSTAWTW HAIGHIG-GL HALGHMC-AL TLSP-ALPT 	SSHLHFDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE DIATLP-QAE 600 SPVSFVFM SPVSFVFM 	121 128 122 145 141 739 471 482 475 523 512 210 239 226 803 482 475 523 512 239 226 803 482 475 523 512 226 250 2276 290
2812 3892 2194 5TA_060710 SNOG_06679 3dha 272d 1smi TST_060680 SNOG_06681 MpaD_MpaE 2812 3892 2194 TSTA_060710 SNOG_06679 2194 1smi TST_060880 SNOG_06679 SNOG_06679	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVQPGVRDA GGD - SCHH NFE - DEVPF NYG - PPARR GYQLOGNRRY GAD - ACH	ISH00QHVVF ITHKDTHMVF 720 721 722 723 724 725 725 725 725 725 725 725 725 725 725	DGUMPGMA- DLGVRROWEN DLGVRROWEN AINLNTDIQG 	YAPRIVSLIK YPPNIVSLIK 740 RNVREISFEK HLNYK- 	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLEGLG LDBNBKAKG LDGDQSGEVN LDESSV SFYL-LDAAG VQLLYTPG VQLLYTPG VYLL-NFGTG IVFTAHFMAG SFYL-LDAPG SDSVF SDSVF GHDIEQE- GHDIEQ-E- GHDIEQ-ESSEPVF	YEPDDLLY11 LSPDD1STVV VTFRDLRLIL VHSRD1SSV1 VRSDN1DTVV 1 BVGH1G-AL STORMAR STORMAR STORMAR STORMAR STUDE STORMAR STUDE STORMAR STUDE STORMAR STUDE STORMAR STO	SSHLHFDHAG LSHLHDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRRTG DPSTFPVSTE DIATLP-QAE 600 	121 128 122 145 141 739 471 482 552 512 210 239 226 803 471 239 226 803 471 482 552 226 803 471 229 220 803 226 220 226 220 226 220 226
212 3160% 2196 2196 2196 2196 2197 2197 2197 2197 2197 2197 2197 2197	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDA LIVGPGVRDA NFEDEVPF NFEDEVPF NFEDEVPF QAD - ACHH GAD - ACHH	ISHGQCHVUF ITHKDTHMVF 70 70 70 70 70 70 70 70 70 70 70 70 70	DGUMPGMAL DLGVRROWEN DLGVRROWEN AINLNTDIQG EEYMKECILP SPYINSONGGIT AGLLDSDADG P	YAPRIVSLIK YPPNIVSLIK 740 RNVREISFEK HLNYK- WLATPRNWD- -YPPANAD RVVREISFE RSIREIVFD- 810 VLITPHPGAS FFFELEANYA SLQGN-340	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLROLG LDNMKARG LDGDQSGEVN LDESSV	YEPDDLY11 LSPDD1STVV VTFRDLRLIL VHSRD1SSV1 VRSDN1DTVV 780 780 780 780 780 780 780 780 780 780	SSHLHFDHAG LSHLHDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG HSH	GNAAFINTPI PVAELKRRTG DPSTFPVSTE DIATLP-QAE 900 SPVSFVFN SPVSFVFN SPVSFVFN SPVSFVFN SPVSFVFN SPVSFVFN SSVSSFVFN SSSSFVFN DSFVFN SSSSFVFN DSFVFN SSSSFVFN	121 128 122 145 141 739 471 482 475 523 512 210 226 803 471 229 226 803 471 482 2250 226 803 471 229 226 803 471 220 226 803 471 220 226 803 471 220 226 803 471 220 226 803 471 220 226 803 803 803 803 803 803 803 803 803 803
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212 3.66% 2.16% 2.	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDA LIVGPGVRDA MFG DEVPF NYG PPARR GQL_GQNPRY GAD ACHH VFVVLAHDAT	ISHGQQHVUF ITHKDTHMVF 70 70 70 70 70 70 70 70 70 70 70 70 70	A INLNTDIQG DLGVRROWEN A INLNTDIQG EEYMKECILP SPYIVKDIEA DLHFGDGIT- AGLLDSDADG SPVKNSDMQG P LSSIKRL LSSIKRL FATVRALPCD PLPQSIRPPL KINDWKAKEY	YAPRIVSLIK YPPNIVSLIK 740 741 742 743 744 744 744 744 744 744 744 744 744	ATTEVIVEKD ATTRITPEKA TQKGATKIGS 		PERLRQ - LG LDNNKA - LG LDNNKA - LOAG STYL - LDAAG VQLL - YTPG VQLL - YTPG VQLL - YTPG VVLL - NTFGTG IVFTAHFMAG SLFL - LDAPG - SDSVF	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV 700 	SSHLHFDHAG LSHLHDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG IETEQSGSVL VRLEKQPGFL TDTRNGKPVR TDTRNGKPVR TDTRNGKPVR DYTAALRTVE EYI EYI EE	GNAAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE JOTATLP-QAE 500 	121 128 122 145 141 739 471 445 523 512 226 803 471 229 803 471 2226 803 471 482 226 803 471 2250 226 803 471 2290 306
212 3.6% 216q 216q 216q 216d 216d 212d 212d 212d 212d 212d 212d	- LDAPVYGFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA GGD - SCHH NFE - DEVPF NYG - PPARR GQD - SCHH GAD - ACHH GAD - ACHH YFVVLAHDAT	ISHGQQHVUF ITHKDTHMVF 720 721 721 722 722 723 723 724 724 724 724 725 725 725 725 725 725 725 725 725 725	DGUMPGMA- DLGVRROWEN DLGVRROWEN AINLNTDIQG 	YAPRIVSLIK YPPNIVSLIK RNVREISFEK HLNYK- WLAPPRNWD RVVREISFE SIREIVFD SIREIVFD SIREIVFD VLLTPHPGAS FRFELEANVA SLQGN- GKKTKWLFYK	ATTEVIVGKD ATTRITPGKA TQKGATKIGS 		PERLRQLG LDNBKARG LDDDSGEVN LDESSV SFYL-LDAAG VQLL-YTPG VQLL-YTPG VVLL-NFGTG IVFTAHFMAG SLFL-LDAPG SLFL-LDAPG SLFL-LDAPG GSLFL-LDAPG GSLFL-LDAPG GSLFL-LDAPG CSSSVF SSSSPVF	YEPDDLLY11 LSPDD1STVV VTFRDLR11L VHSRD1SSV1 VRSDN1DTVV 700 HSVGH1G-1L HSVGH1G-4L HASGMLG-LA HTF0STAWTW HA1GH1G-GL HALGHMC-AL TLSP-ALPT 	SSHLHFDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG ARVTT	GNGAFTNTPI CVEYFGKSRL PVAELKRTG DPSTFPVSTE DPSTFPVSTE DIATLP-QAE 600 	121 128 122 145 141 739 471 482 475 521 210 229 803 471 220 803 471 220 803 471 220 803 471 220 226 803 471 220 226 803 471 220 220 200 200 200 200 200 200 200 20
212 346% 2154, 066710 340a 222d 1517_060680 340a 212 2154 346% 212 2154 2154 2154 2154 2154 2154 2154	- LDAPVYGFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVQPGVRDA LIVQPGVRDA LIVQFQVRDA NFE - DEVPF NFE - DEVPF NFE - DEVPF NFE - ACHH GAD - ACHH GAD - ACHH	ISHGQQHVUF ITHKDTHMVF 720 721 722 722 723 724 724 724 725 725 725 725 725 725 725 725 725 725	DGUMPGMA- DLGVRROWEN DLGVRROWEN A INLNTDIQG SPYTVKDIEA DLHFGDGIT- AGLLDSDADG SPVKNSDMQG P- SVKNSDMQG P- SVKNSDMQG P- SVKNSDMQG P- SVKNSDMQG P- SVKNSDMQG P- SVKNSDMQG RUSSI SVKNSDMQG SVKN	YAPRIVSLIK YPPNIVSLIK RNVREISFEK HLNYK WLATPRNWD -/YPPANAD RVVREISFE RSIREIVFD BANKIKISFE VLLTPHPGAS FRFELEANVA 	ATTEVIVOKD ATTRITPGKA TQKGATKIGS II. LVGR LVGR CPLDS KEV KEV RQY NWDYAAGRAR CPEDI DIENSIEGQK		PERLROLG LDNBKARG LDGDQSGEVN LDESSV SFYL-LDAAG VQLLYTPG VILL-NFGTG VFTAHFMAG SFYL-LDSPG SFYL-LDSPG SDSVF SDSVF SSSVF SSSPVF	YEPDDLLYII LSPDDISTVV VTFRDLRLIL VHSRDISSVI VRSDNIDTVV 1 HSVGHIG-LS HASGMLG-LA HASGMLG-LA HASGMLG-LA HASGMLG-LA TISP-ALPT 	SSHLHFDHAG LSHLHNDHAG LSHLHNDHAG LSHAHADHAG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG HITL HITL WSHNHFDHIG HITL HITL HITL HITL HITL HITL HITL HITL	GNAAFINTPI PVAELKRTG DPSTFPVSTE DIATLP-QAE 00 SPVSFVFM SPVSFVFM SPVSFVFM SPVSFVFM SPVSFVFM SSVSFVFM SSVSFVFM SSSSFVFM S	121 128 122 145 141 739 471 239 475 552 210 239 226 803 471 252 250 2512 250 2512 250 2512 250 306
212 316/w 216q 216q 216q 216q 216q 217d	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVGPGVRDA LIVGPGVRDA LIVGPGVRDA LIVGPGVRDA NFE - DEVPF NFE - DEVPF NFE - DEVPF QAD - ACHH GAD - ACHH VFVVLAHDAT	ISHGQCHVUP ITHKDTHMVF 720 721 722 722 722 723 723 724 724 724 725 725 725 725 725 725 725 725 725 725	DGUMPGMA DLGVRROWEN DLGVRROWEN AINLNTDIQG EEYMKECILP SPYINKDIEA DLHFGDGIT AGLLDSDADG P LHSIKRL DSNKRD P LSSIKRL LSSIKRL DETVSHI- FATVRALPCD NLPESVLA- KINDWKAKEY	YAPRIVSLIK YPPNIVSLIK RNVREISFEK HLNYK- WLATPRNWD- -YPPANAD RVVREISFE SIREIVFD- 800 VLLTPHPGAS FFFELEANVA -SLQGN- GKKTKWLFYK	ATTEVIVOKD ATTRITPGKA TQKGATKIGS II. LYGR CLUS GKLKIGG CPLDS KEV RQY NWDYAAGRAR CPGEF CPGDI DIENSIEGQK		PERLROLG LDNNKARG LDGDQSGEVN LDESSV SFYL-LDAAG VQLL-YFPG VNLL-NFGTG VNLL-NFGTG SFYL-LDSPG SFYL-LDSPG SFYL-LDSPG GHDREQ-FA ADAAEQKFDG DPADPFF	YEPDDLLY11 LSPDD1STVV VTFRDLR1L VHSRD1SSV1 VRSDN1DTVV 700 	SSHLHFDHAG LSHLHNDHAG LSHLHNDHAG LSHLANDHAG WSHNHFDHIG WSHNHFDHIG WSHNHFDHIG USHNHFDHIG USHNHFDHIG USHNHFDHIG LETEQSGSVL VRLEKQPGFL VRLEKQPGFL VRLEKQPGFL DTRNGKPVR ARTTAAGDGL ARTTP	GNAAFINTPI PVAELKRATG DPSTFPVSTE DIATLP-QAE 900 SPVSFVFN -	121 128 128 122 145 141 739 471 4482 5523 5512 210 226 803 471 4482 5523 512 226 803 471 4482 5523 5523 2266 2306
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212 3.66% 2.86% 2.86% 2.86% 3.66%3.66% 3.66% 3.66%3.66% 3.66% 3.66%3.66% 3.66%3.66% 3.66%3.66% 3.66%3.66% 3.	- LDAPVYCFL LVVGPGIRDT IVQRTEYEAA IAHEDEFATA AKVAANAESA LVVOPGVRDA LIVGPGVRDA LIVGPGVRDA GGD - SCHH 	ISHGQQHVUF ITHKDTHMVF 70 70 70 70 70 70 70 70 70 70 70 70 70	DIGVIRROWEN DIGVIRROWEN AINLNTDIQG EEYMKECILP EEYMKECILP EEYKKECILP EEYKKECILP EEYKKECILP EEYKKECILP EEYKKECILP EEYKA SPYIVKDIEA DLHFODGIT- SPYKNSDMQG P	YAPRIVSLIK YPPNIVSLIK 740 741 740 741 741 742 742 742 742 742 742 742 742 742 742	ATTEVIVEKD ATTRITPGKA TQKGATKIGS I. 		PERLRQLG LDNNKALG LDNNKALG LDNSKALG STSULDAAG 	YEPDDLLY11 LSPDD1STVV VTFRDLR11L VHSRD1SSV1 VRSDN1DTVV 700 	SSHLHFDHAG LSHLHDDHAG LSHLHDHAG LSHLHDHAG WSHNHFDHIG WSHNHFDHIG ARVTT	GNGAFTNTPI PVAELKRTG DPSTFPVSTE DDTTLP-QAE 60 0 0 0 0 0 0 0 0 0 0 0 0 0	121 1228 1222 145 147 147 523 512 210 2226 803 471 219 2226 803 471 219 2226 803 471 2226 803 471 2226 803 471 226 803 471 227 208 226 803 803 803 803 803 803 803 803 803 803

Supplementary Figure S4. Alignment of MpaDE with the CYPs; *Bacillus megaterium* P450 BM3 (2ij2), *Rattus norvegicus* CYP24A1 (PDB 3k9v), *Homo sapiens* CYP2D6 (PDB 2f9q), *Talaromyces stipitatus* TSTA_060710 and *Phaeosphaeria nodorum* SNOG_06679, *Bacillus thuringiensis serovarkurstaki* lactone hydrolase (PDB 3dha), *Agrobacterium tumefaciens* lactone hydrolase (PDB 2r2d), *Stenotrophomonas maltophilia* lactone hydrolase (PDB 1sml), *Talaromyces stipitatus* TSTA_060680, *Phaeosphaeria nodorum* SNOG_06681. The last three amino acids in the MpaD expressed in this study are marked in green.





Supplementary Figure S5.

MpaD catalyses the conversion of 5MOA to 4,6-dihydroxy-2-(hydroxymethyl)-3methylbenzoic acid. UHPLC-UV/VIS-HRMS analyses NID210, NID211, NID410, NID416 and NID944. For each strain, two extracts were analysed, resulting in two chromatograms for each strain for each compound. Left column: extracted ion chromatogram, m/z 197.0455 ± 0.005 corresponding to the $[M+H]^+$ ion of 4,6-dihydroxy-2-(hydroxymethyl)-3methylbenzoic acid. To the right: extracted ion chromatogram, m/z 181.0495 ± 0.002 corresponding to the [M+H]⁺ ion of 5,7-dihydroxy-methyl-phthalide (DHMP).