

Cmn00144_CEL_A_GENE

NE3 MAVGATFGAFAAPASAATAAGPGSGGSESQPGPAKPGAISAKWQPGGSWA 50
HF4 MAVGATFGAFAAPASAATAAGPGSGGSESQPGPAKPGAISAKWQPGGSWA 50

NE3 SGYVANLDVTATDAVTGWTVSWASPETTGVVNSWGMRCVASNTVTCTGT 100
HF4 SGYVANLDVTATDAVTGWTVSWASPETTGVVNSWGMRCVASNTVTCTGT 100

NE3 DWASELAAGQTVSVGVQLAGGPAPSSPQISATAAGTPPSQPTPPSQTPTP 150
HF4 DWASELAAGQTVSVGVQLAGGPAPSSPQISATAAGTPPSQPTPPSQTPTP 150

NE3 SQPTPPSQ-----SATHGRATHYSLGTGNTIANGNCMPAVPADRMVA 200
HF4 SQPTPPSQPTPPSQSATHGRATHYSLGTGNTIANGNCMPAVPADRMVA 200

NE3 VSSPEYSGAAACGSYLLVTGPKGTVRVQIVDQCHECEIGHLDLSEEAFFRA 250
HF4 VSSPEYSGAAACGSYLLVTGPKGTVRVQIVDQCHECEIGHLDLSEEAFFRA 250

NE3 VGDFDAGVIPISYTTVRDPDVPDVAVRVKEGSSRWWAGLQILNAGNPIDH 300
HF4 VGDFDAGVIPISYTTVRDPDVPDVAVRVKEGSSRWWAGLQILNAGNPIDH 300

NE3 VEVQADGQWLGLSRTDYGWVTPSPIPDGPMTVRVTDQYGRSVVLPGIRM 350
HF4 VEVQADGQWLGLSRTDYGWVTPSPIPDGPMTVRVTDQYGRSVVLPGIRM 350

NE3 APGEIQSTARRFYPVHZ 367
HF4 APGEIQSTARRFYPVHZ 367

Cmn02650_Endoglucanase_gene

GIL1 MQHHRHPIRTATTLVLGLLALTAGILTAASPASAATTGPAPTVASGAPTVS 50
HF4 MQHHRHPIRTATTLVLGLLALTAGILTAASPASAATTGPAPTVASAAPTVS 50

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GIL1 DARLRFGVATPGGPTDTGELDAVAQQVGEDPSIVLAYADFTQAPPAAALD 100
HF4 DARLRFGVATPGGPTDTGELDAVAQQVGEDPSIVLAYADFTQAPPAAALD 100

GIL1 SVAARGAETLLTWEPWTAGAGVDQPTFTNASIAAGDHDAYIREWGAALAK 150
HF4 SVAARGAETLLTWEPWTAGAGVDQPTFTNASIAAGDHDAYIREWGAALAK 150

GIL1 WGGPVSLRYAHEMNGDWYPWADGVNGNAPGSYAAAFRHHVDVVVGAGATN 200
HF4 WGGPVSLRYAHEMNGDWYPWADGVNGNAPGSYAAAFRHHVDVVVGAGATN 200

GIL1 VRVWVTPNVPYTGSTALAGLYPGAGYVDVVGLDGYNWGSVAGQSWTAPSD 250
HF4 VRVWVTPNVPYTGSTALAGLYPGAGYVDVVGLDGYNWGSVAGQSWTAPSD 250

GIL1 LFGAGLEQLRAIAPGKPIVIAETASSEVGGSKAQWDGELVSFLQAQTDVV 300
HF4 LFGAGLEQLRAIAPGKPIVIAETASSEVGGSKAQWDGELVSFLQAQTDVV 300

GIL1 AFVWFDMDKEADWRIGSSASSATAIHDAALAARRLQZ 336
HF4 AFVWFDMDKEADWRIGSSASSATAIHDAALAARRLQZ 336

Cmn02651_Endoglucanase_gene

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NE3 MPTRRRLKCAVVTAVAPAVVTATVLVAPAAGARAASAQAAPTAPAATVLS 50
HF4 MPTRRRLKCAVVTAVAPAVVTATVLVAPAAGARAASAQAAPTAPAATVLS 50

NE3 VASGPVGTPTVVTGTGTFPAKKAHVAVGSTTKRITTTATGRFTTAITIPR 100
HF4 VASGPVGTPTVVTGTGTFPAKKAHVAVGSTTKRITTTATGRFTTAITIPR 100

NE3 TSLSTIRITATAGTRSAGAPFTVTTAKSNGSARLGASAPAPTTTPAPAPT 150
HF4 TSLSTIRITATAGTRSAGAPFTVTTAKSNGSARLGASAPA----- 140
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NE3 GAPSTAAPAPATSSPAPAASAAPAISSARLRLGLSTPGGPTANGELDAA 200
HF4 -----TSSPAPAASAAPAISSARLRLGLSTPGGPTANGELDAA 178
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NE3 STTLGESPSIVMSHVDFTHPAPIAGLRSVAARGADSLITWEPWQGGAGVD 250
HF4 STTLGESPSIVMSHVDFTHPAPIAGLRSVAARGADSLITWEPWQGGAGVD 228

NE3 QPAYANARIVAGDYDSYIRSWGADLAKYGQPVYLRFGHEMNGNWYPWSDG 300
HF4 QPAYANARIVAGDYDSYIRSWGADLAKYGQPVYLRFGHEMNGNWYPWSDG 278

NE3 VNGNASGSYVQAWKHVHDLVAAQGATNVKVVWSPNVPYPGSTDLASLYPG 350
HF4 VNGNASGSYVQAWKHVHDLVAAQGATNVKVVWSPNVPYPGSTDLASLYPG 328

NE3 ADQVDVVALDGYNWGAVPGQRWTAPADLFGPGMAQLRAVAPGKPLIIGEV 400
HF4 ADQVDVVALDGYNWGAVPGQRWTAPADLFGPGMAQLRAVAPGKPLIIGEV 378

NE3 ASGETGGSKADWDRDLVAYLQSQPDVLFVWFDFKKEEDWRIDSSAASAT 450
HF4 ASGETGGSKADWDRDLVAYLQSQPDVLFVWFDFKKEEDWRIDSSAASAT 428

NE3 ALRDALALRRGZ 462
HF4 ALRDALALRRGZ 440
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XylanaseB_GENE

GIL1 MSIPRTDTSALADVSPRLGRSRFAPRRRRRRGLAALTALGLIAGAGA 50
HF4 MSIPRTDTSALADVSPRLGRSRFAPRRRRRRGLAALTALGLIAGAGA 50

GIL1 LTAPAAQAADAAAPAGIGSDFESGTGAWAPRGDGVRIAPSTEARTGSGSL 100
HF4 LTAPAAQAADAAAPAGIGSDFESGTGAWAPRGDGVRIAPSTEARTGSGSL 100

GIL1 LVTDRTOEWHGAALDVTGALTVGQQVEVTVWARLAAGEEPASLKVSVQRD 150
HF4 LVTDRTOEWHGAALDVTGALTVGQQVEVTVWARLSAGEEPASLKVSVQRD 150
*

GIL1 TGGGSGYDGVAGAAARVTADAWTELTGTYTLGGPVDKAQVYVEGTVGADF 200
HF4 TGGGSGYDGVAGAAARVTADAWTELTGTYTLGGPVDKAQVYVEGTVGADF 200

GIL1 LLDDFQLGEAVSTPVQTDIPALQDVLGARGIEHVGVAIDGRETVGAGADL 250
HF4 LLYDFQLGEAVSTPVQTDIPALQDVLGARGIEHVGVAIDGRETVGAGADL 250
*

GIL1 VGRQFNAFTPENAGKPESVQPEEGRFTFAQIDQLLDYADRTGTKVYYHVL 300
HF4 VGRQFNAFTPENAGKPESVQPEEGRFTFAQIDQLLDYADRTGTKVYYHVL 300

GIL1 FWHSQTPAWFFLDGDRPLTDSPADQALLRAMEAHVKG IADHVAARYPDG 350
HF4 FWHSQTPAWFFLDGDRPLTDSPADQALLRAMEAHVKG IADHVAARYPDG 350

GIL1 GSPIWAMDVVNEVIDDGPNDNAHDMRDSRWYQVLGEGFVDEGFRLARAYF 400
HF4 GSPIWAMDVVNEVIDDGPNDNAHDMRDSRWYQVLGEGFVDEGFRLARAYF 400

GIL1 PGVKLFINDYNTELPTKRADYLELISALVARGVPIDGVGHQAHVDFARPV 450
HF4 PGVKLFINDYNTELPTKRADYLELISALVARGVPIDGVGHQAHVDFARPV 450

GIL1 SWLRDSIRAVERIDTRLLQAITELDVNASNQNEGADVSGAPQDPYTPVYA 500
HF4 SWLRDSIRAVERIDTRLLQAITELDVNASNQNEGADVSGAPQDPYTPVYA 500

GIL1 DDADAGAEVGHYYRDLFQMIROQAASIDSVTFWGVSNARSWLRTWPIARP 550
HF4 DDADAGAEVGHYYRDLFQMIROQAASIDSVTFWGVSNARSWLRTWPIARP 550

GIL1 WEQPLPFDDDLQAAPAYWGIVDAKRLPARPADLSAPRIADVDDITAVATK 600
HF4 WEQPLLFDDDLQAAPAYWGIVDAKRLPARPADLSAPRIADVDDITAVATK 600
*

GIL1 AAGVRVPYALPSAIDTRDGNLRVLCAPPRSGIFPVGTTT VTCTAKDRAGN 650
HF4 AAGVRVPYALPSAIDTRDGNVRVLCAPPRSGIFPVGTTT VTCTAKDRAGN 650
*

GIL1 VRTSEFDVIVTRAGSZ 666
HF4 VRTSEFDVIVTRAGSZ 666

Cmn02654_Pectate_lyase

GIL1 MRIRLLPAALAGALLLVALTGTGPTAPASAATASGTSATASASADSGSGS 50
HF4 MRIRLLPAALAGALLLVALTGTGPTAPASAATASGTSATASASADSGSGS 50

GIL1 AATGAGPTARVASVAALRDIAIQHVHHIVITTSLYGGTSPVYVDVLDSAS 100
HF4 AATGAGPTARVASVAALRDIAIQHVHHIVITTSLYGGTSPVYVDVLDSAS 100

GIL1 SGTVIEGATPTVELVNIQLRIFDLTYAGAIHDVTVRDLTMHGRIQDLVAL 150
HF4 SGTVIEGATPTVELVNIQLRIFDLTYAGAIHDVTVRDLTMHGRIQDLVAL 150

GIL1 TGAATKPYGVGVNYEAISVRGAAHVTIDHIVAYDTTDDLMSVTRGADDVT 200
HF4 TGAATKPYGVGVNYEAISVRGAAHVTIDHIVAYDTTDDLMSVTRGADDVT 200

GIL1 ISNSTFSYSRAYADIDPSITWDWGFGLQPLASERLGILVGANAKDSYAVT 250
HF4 ISNSTFSYSRAYADIDPSITWDWGFGLQPLASERLGILVGANAKDSYAVT 250

GIL1 GHLHVNLVDDHIGPLVRGRPLLRGDVDVKGVTFDNTQAGSEQYAAIEVGS 300
HF4 GHLHVNLVDDHIGPLVRGRPLLRGDVDVKGVTFDNTQAGSEQYAAIEVGS 300

GIL1 GGRVVVEGCEFDHSNNPIAIHLDSPSDT 328
HF4 GGRVVVEGCEFDHSNNPIAIHLDSPSDT 328