>**gb|ACS84568.1| glycoside hydrolase family 1 [Dickeya dadantii Ech703]**MSKVSIALPEGFILGAAASAWQTEGWSGKKTGQDSYLDLWYQRDRQVWHDGYGPAVATDFYNRYREDVALMKQVGLTHYRTSINWSRFMLDYENGVVDEEYAGYIDNLIDEMLRQGIEPMLCLEHYELPAVLFEKYQGWSSKQVVEWFVQYAAAVFARYAGRVKRWFTFNEPIVVQTRVYLDAVRYPYEQNTHTWMQWNHHKNLATAKVVQLFRAQGYHRQGGSIGVILNPEVTYPRSSAPHDVDAARIYDLFYNRVFLDPAIKGEYPPELVALLEKHQVRWDYTDEELTIIRNNTVDEVGINLYYPHRVKAPSRAWNSATPFHPAYYYEHFELPGRRMNKSRGWEINPRIIYDMAQRLRLEYGNIPWFVAENGMGIENESQFKDADGVVQDDYRIAFIVEHLYWTLRARQEGANCQGYMLWAFTDNVSPMNAFKNRYGLIEIDLEHDRQRRPKKSADWFRRVRDAGVLEFERDDENK  
  
>**gb|ACS84575.1| glycoside hydrolase family 1 [Dickeya dadantii Ech703]**MSVSNAFPPDFLWGGATAANQLEGAWNVGGKGLSVSDVYTFDSQTPKERWLDQWLFMTHQQVAEAQDPHSKKYYPKRKGNGFYYHYKEDIALFAEMGFTCFRMSIAWTRIFPRGDETEPNEAGLAFYDRVLDTLLAHHIQPIVSLSHYEMPLCLVTEYGGWPNRKLVDFYVRFATTVFERYKHKVKYWMTFNEINCVKHHPYVSVGVIEEDHPNLEQDKYQGAHHQFVASALATKACHQIIPGSQVGCMISYQILYPNTCHPDDLQACEEAQRVSLFFSDVQARGYYPAYTDRMLAEKGVVLQKQQGDDDILRQYPVDYVSFSYYMSSTVSAHPERLEGVTGNLITGGIRNPYLPTSEWGWQIDPQGLRLALNQLYDRYQKPLFIAENGLGAVDTVNPDGTIDDEYRIDYLRQHVAQMKEALADGVKLFGYTWWGPIDVVSAGTAQISKRYGFIYVDQDDEGHGTQQRSRKKSFYWYRKLIATNGDDLS  
  
>**gb|ACS84576.1| 6-phospho-beta-glucosidase [Dickeya dadantii Ech703]**MTRFPQGFLWGGAIAANQAEGAWNEDGKGPSIADVVRGGIVAGAPDEAVDPARYYPSHEAIDFYHRYPEDIALFAEMGFKCFRTSIAWSRIFPQGDETEPNEAGLRFYDRLFDELLKYGIEPVITLSHYETPLALYQRYGGWQDRRLVDFFIRYCETVFHRYRDKVKYWMTFNELNNMHRIPFATGAIRPAPEARLQAIYQASHHMFVANALANQLCHRIIPQAKIGCMLSLSTLYPHSCHPDDVFATLQIRRRSLFYADVMMRGHYPAYSQRLWRENGIEPVMDAGDLALLAAHPSDYLGFSYYRSATYQADMPVLADTGGVVGLDNPYLKSSAWGWTIDPKGLRQVCNELADRYEKPLFIVENGFGAVDTPDANGAIDDDDRISYGRQHLQEVAEAIADGCEIMGYTWWGPIDIVSAGTGEMKKRYGFIYVDKDNDGQGTLARRKKKSFDWYRQVIATNGEQL  
  
>**gb|ACS85209.1| glycoside hydrolase family 1 [Dickeya dadantii Ech703]**MQKTFPDGFLWGGSMAANQVEGAWDDAGKGVSTSDLQPQGVHGHAVERANRPANIKDVAIDFYHRYPEDIQLFAEMGFKVLRTSIAWTRIYPNGDETEPNEAGLGFYDRLFDEMIRHGIQPLITLSHYEMPYGLVEKYDGWGGRETIACFERYARTVFSRYRDKVKYWLTFNEINMALHAPFTGVGLRGERTKQAIYQAIHHQLVASARAVKACHEIIPDAKIGNMLLGGVRYPITCKPADVLKAQSVNREWLFFGDVQARGAYPNWIQRYFRENDIHVQMTEQDSADLRETVDFISFSYYMSGCAAAEPEQYPTSRGNIMKMIPNPHLASSEWGWQIDPEGLRYLLNELHDRYQKPLFIVENGLGAKDVPQADGTIHDDYRIQYLKEHLIQVREAIADGVDLLGYTSWGPIDLVSAGTAQMSKRYGFIYVDRDDDGQGTLERRRKQSFFWYQQVIKSNGGSLA  
  
>**gb|ACS85465.1| glycoside hydrolase family 1 [Dickeya dadantii Ech703]**MSSIFPEHFLWGGAIAANQVEGAYLDDGKGLSTSDLQPQGIFGDIKARHSGDFSLKDVAIDFYHRYPQDIALFAEMGFSCLRVSIAWTRIFPQGDETQPNEAGLAFYDRLFDELARYGIQPLVTLSHYEMPYGLVQNHGGWGNRQTIDCFERYARTVFQRYQHKVKLWLTFNEINMSLHEPFTGVGLARGSELPAIYQAIHHQLVASARAVKACHDIIPDARIGNMMLGALLYPLTCKPQDVMESLHQNREWLFFGDVQVRGAYPAYMRRFFKEKNITLDITEQDRLDLQSTVDFISFSYYMTGCVSADEAEVEKARANILNMVPNPYLESSEWGWQIDPEGLRYLLNFLYDRYQKPLFIVENGLGARDNIEADGSINDDYRIKYLNDHLVQVGEAIEDGVDVLGYTCWGPIDLVSASKAEISKRYGFIYVDRDDQGNGSLERKRKKSFFWYQSVISSKGDMLKK  
  
>**gb|ACS85617.1| glycoside hydrolase family 1 [Dickeya dadantii Ech703]**MSASTFPDGFLWGGALAANQSEGAYLEGGKGLTTVDMIPHGPNRLPVKLGLEKRVALRNDEFYPSHQAIDFYHRYKEDIALMAEMGFTVFRTSIAWSRLYPNGDDAAPNPAGIAFYRDVFNECRKYGIEPLVTLCHFDVPMHLVTEYGSWRNRKMVDFFTRYARTCFEAFDGLVKYWLTFNEINILLHSPFSGAGLVFEAGENQDQVKYQAAHHELIASALATRIAHEVNPVNQVGCMLAGGNFYPWSCKPEDVWAALEKDRENLFFIDVQARGAYPSYSARVFREKGVHIDMLDGDAEILKNTVDFVSFSYYASRCASADMNEHNSSAANIVKSLTNPHIQRSEWGWGIDPLGLRITMNMMYDRYQKPLFLVENGLGARDDINVDGKIEDDYRISYLREHIRAMADAIADGVPVMGYTTWGCIDLVAASTGEMSKRYGFVYVDRDDHGNGTLARRKKKSFGWYRKVIASNGRDLD  
  
>**gb|ACS87325.1| glycoside hydrolase family 1 [Dickeya dadantii Ech703]**MSKLPDGFLWGGAVAAHQLEGGWQEGGKGVSVVDVLTAGAHGTLRRITEGVLPGESYPNHEAIDFYHRYKDDIALFAEMGFTCFRTSIAWTRIFPRGDELEPCEAGLRYYDDLIDELLKHGIEPVMTLSHFEMPLHLVQQYDGWMSRKTLECFVHFATTVIERYKHKVKYWMTFNEINNQKNVAAEIFGWMCSGVRFPQKEKPEEAMYQAVHHQFVASARVVKRAHDINPAIKVGCMCSFVPFYPYSCHPEDVMLAARSMHDRFYFSDVHVRGRYPGYARREWALKGYNIRMEPEDEQILREGKADYIGFSYYMSSVVKHDVQNAIAASMDGSSEHSIPNPHLTASDWGWQIDPVGLRYALVTLYERYDVPLFIVENGLGALDKPDETGVCQDDYRIDYLRSHIEAMKAAVWEDGVELMGYTPWGCIDLVSFTTGEMAKRYGFIHVDKHDDGTGTLKRTPKKSFYWYQKAIASNGEML  
  
>**gb|ACT05617.1| glycoside hydrolase family 1 [Dickeya zeae Ech1591]**MSKVSMTLPEGFILGAASSAWQTEGWSGKKSGQDSYLDLWYKRDRQVWHNGYGPAVATDFYNRYREDVALMKQTGLTHFRTSINWSRFMLDYENGVVDEEYAAYIDNLIDELHRQGIEPMLCLEHYELPAVLFEKYQGWSSKQVVEWFVQYADAVFARYAGKVKRWFTFNEPIVVQTRVYLDAVRYPYQQDSGVWMQWNHHKNLATAKVVQLFRDKGYHRDGGSIGVILNPEVTYPRSSAAHDVEAARLYDLFYNRVFLDPALKGEYPAELLALLEKHQVHWDYTEEELAIIRANTVDEVGINLYYPHRVKAPSRAWNSNTPFHPAYYYEHFELPGRRMNKSRGWEINPRIIYDMAMRLKDEYGNVPWFVSENGMGIENEGQFKDSRGVIQDDYRIAFIAEHLYWTLKAREDGANCLGYMLWAFTDNVSPMNAFKNRYGLIEIDLEHDRQRRAKKSAGWFSQVRDGGVLSFELDDEDK  
  
>**gb|ACT05628.1| glycoside hydrolase family 1 [Dickeya zeae Ech1591]**MSVSKTCPPDVNAFPPDFLWGGATAANQLEGAWNVGGKGLSVSDVYTFDSRTPKERWLDQWLFMTHQQVAEAQDPHSQKYYPKRKGNGFYYHYKEDIALFAEMGFKCFRMSIAWTRIFPRGDETEPNEAGLAFYDRVLDALLAHHIQPIVSLSHYEMPLCLVTEYGGWPNRKLVDFYVRFATTVFERYRHKVKYWMTFNEINCVKHHPYVSVGVIEEGNPHLEQDKYQGVHHQFIASALATKACHRIIPGSQVGCMISYQMLYPHTCHPDDLQACEEAQRVSLFFSDVQARGYYPAYTDRMLAEKGVVLQKEQGDDEILRQYPVDYVSFSYYMSSTVSAHPEQLEGATGNLITGGIRNPYLPTSEWGWQIDPKGLRLALNQLYDRYQKPLFIAENGLGAVDSVNPDGSVDDDYRIDYLRQHVQQMKEALADGVKLFGYTWWGPIDVVSAGTSQISKRYGFIYVDQDDDGHGTQQRSRKKSFYWYRKLIASNGADLD  
  
>**gb|ACT05629.1| glycoside hydrolase family 1 [Dickeya zeae Ech1591]**MARFPQGFLWGGAIAANQAEGAWNEGGKGPSIADVVRGGIVAGKPDAAVDPTQYYPSHEAIDFYHRYQEDIALFAEMGFKCFRTSIAWSRIFPQGDEAQPNEAGLRFYEQLFDELLKYGIQPVVTLSHYETPLALYQRYGGWQDRRLVDFFIRYCDTVFHRYRHKVKYWMTFNELNNMNRIPFATGAIQPAAEDRLQAIYQASHHMFVANARANRLCHQIIPEARIGCMLSLSTVYPHSCRPEDVFETMQMRRRSLFYADVMMRGHYPAYSQRMWREHGIQLTMEADDLTLLAAHPSDYLGFSYYRSATYQAGMPVLADTGGVIGKENPYLQSTDWGWPIDAKGLRLVCNELADRYEKPLFIVENGFGGVDTPDADGAINDDDRIRYGQQHLHEVAEALADGCDIMGYTWWGPIDIVSAGTGEMKKRYGFIYVDKDNDGHGTLARRRKKSFDWYRQVIAGNGEQL  
  
>**gb|ACT06558.1| glycoside hydrolase family 1 [Dickeya zeae Ech1591]**MSNPFPAHFLWGGAIAANQVEGAYLTDGKGLSTSDLQPQGIFGRIVERTPGDSGIKDVAIDFYHRYPQDIALFAEMGFTCLRVSIAWTRIFPQGDEAEPNEAGLAFYDRLFDELAKYGIQPLVTLSHYEMPYGLVKKHGGWGNRLTIDCFERYARSVFTRYRHKVKRWLTFNEINMSLHAPFTGVGLPPDSDKAAVYQAIHHQLVASARAVKACHEIIPDAQIGNMLLGAMLYPLTSKPEDVMESLHQNREWLFFGDVQVRGAYPGYMHRYFREQGITLNITEQDKQDLTATVDFISFSYYMTGCVSTDEAQHEKTRGNILNMVPNPYLASSEWGWQIDPLGLRYLLNFLYDRYQKPLFIVENGLGAKDKIEANGEIHDDYRIRYLNDHLVQVSEAIADGVDVLGYTCWGPIDLVSASKAEMSKRYGFIYVDRDDAGQGTLERRRKKSFYWYQSVIASRGKTLTR  
  
>**gb|ACT08535.1| glycoside hydrolase family 1 [Dickeya zeae Ech1591]**MSQLPAGFLWGGAVAAHQLEGGWNEGGKGISVVDVLTAGAHGKLRRITDGVIPGESYPNHEAIDFYHRYKDDIALFAEMGFKCFRTSIAWTRIFPNGDDAEPCEAGLKFYDDLIDELLKHGIEPVLTLSHFEMPLHLVQQYDGWMSRKTLDCFVHFADTVIARYQHKVKYWMTFNEINNQKNVSAEIFGWMCSGVKFPQKAQPEEAMYQAVHHQFVASALIVKKAHDINPDIKVGCMCAFLPYYPYSCHPEDVMLAAQAMHDRFYFTDVQVRGHYPAYARREWALKGYQIHMEPEDERILREGKADYIGFSYYMSNVVKHDVQNRIDASMDGSSEHSIPNPHLKASDWGWQIDPTGLRYALTTLYERYEVPLFIVENGLGAVDKPDANGMCQDDYRIDYLRSHIDAMKAAVWEDGVDLMGYTPWGCIDLVSFTTGEMAKRYGFIHVDKHDDGTGTLARTPKKSFYWYQRVIASNGEEL  
  
>**gb|ACZ75273.1| glycoside hydrolase family 1 [Dickeya dadantii Ech586]**MSQLPAGFLWGGAVAAHQLEGGWNEGGKGPSVVDVLTAGAHGTLRRITDGVIPGESYPNHEAIDFYHRYKDDIALFADMGFKCFRTSIAWTRIFPHGDEAEPCEAGLQFYDDLIDELLKHGIEPVLTLSHFEMPLHLVQQYDGWMSRKTLDCFVHFAETVITRYQHKVKYWMTFNEINNQKNVSAEIFGWMCSGVKFPQKAKPEEAMYQAVHHQFVASALIVKKAHDINPDIKVGCMCAFVPYYPYSCHPQDVMLATRAMHDRFYFTDVQVRGHYPAYARREWALKGYHIHMEPEDEQILREGKSDYIGFSYYMSNVVKHDVHNHIAASMDGSSEHSVVNPHLKASDWGWQIDPTGLRHALVTLYERYEVPLFIVENGLGAIDKPDANGVCQDDYRIDYLRSHIEAMKAAVWEDGVDLMGYTPWGCIDLVSFTTGEMAKRYGFIYVDKHDDGTGTLARTPKKSFYWYQRVIASNGEEL  
  
>**gb|ACZ76526.1| glycoside hydrolase family 1 [Dickeya dadantii Ech586]**MSNPFPEHFLWGGAIAANQVEGAYLTDGKGLSTSDLQPQGIFGSIVERQPGDSGIKDVAIDFYHRYPQDIALFAEMGFTCLRVSIAWTRIFPEGDELEPNEAGLAFYDRLFDELAKHGIQPLVTLSHYEMPYGLVKKHGGWGNRLTIDCFERYARTVFTRYQHKVKRWLTFNEINMSLHAPFTGVGLPSDSSKAAIYQAIHHQLVASARAVQACHDIIPDAKIGNMLLGAMLYPLTSKPEDVMESLHQNREWLFFGDVQVRGAYPGYMQRYFREQGITLVITEQDKQDLAATVDFISFSYYMTGCVSTDEAQREKTRGNILNMVPNPYLESSEWGWQIDPLGLRYLLNFLYDRYQKPLFIVENGLGAKDKIEDNGEIQDDYRIRYLNDHLVQVSEAIADGVEVVGYTCWGPIDLVSASKAEMSKRYGFIYVDRDDTGKGTLERRRKNSFYWYQSVIASHGKTLTR  
  
>**gb|ACZ78240.1| glycoside hydrolase family 1 [Dickeya dadantii Ech586]**MSKVSMTLPEGFILGAAASAWQTEGWSGKKNGQDSYLDLWYKRDRQVWHNGYGPAIATDFYNRYREDVALMKQTGLTHFRTSINWSRFMLDYENGVVDEEYAAYIDNLIDEMQREGIEPMLCLEHYELPAVLFEKYQGWSSKQVVEWFVQYADAVFARYAGKVKRWFTFNEPIVVQTRVYLDAVRYPYQQDTGTWMQWNHHKNLATAKVVQRFRDKGYHLQGGSIGVILNPEVTYPRSSEAHDVEAARLYDLFYNRVFLDPALKGEYPAELLALLEKHQVKWDYDAQELAIIRANTVDEVGINLYYPHRVKAPSRAWNSNTPFHPAYYYEHFELPGRRMNKSRGWEINPRIIYDMAMRLKDEYGNVPWFVSENGMGIENEGQFKDSHGVIQDDYRIAFIAEHLYWTLKAREDGANCQGYMLWAFTDNVSPMNAFKNRYGLIEIDLEHDRQRRAKKSAGWFRQVRDSGVLAFELDDEEK  
  
GH1

>**gb|ACZ79036.1| glycoside hydrolase family 1 [Dickeya dadantii Ech586]**MIYQQRTRFPDGFLWGASTSAYQVEGAWNEDGKGPSVVDMLDHPPGTADFRIASDHYHHVEEDVALMAEMGLKAYRFSVSWSRVIPDGDGVVNPAGLAFYHRLIDALTRHRITPIVTLYHFDLPWALELKGGWLNRNTGAAFVRYARLLFSEFADKVPLWLTINEQNTMILHPGAIGVPTDRTLPDKKALYQQNHHMMLAQAQIFALCRREFPGLRIGPAINTTSMYAQSCKPEDAIAAHNWETLRCWSFLDVAVHGRYNALAWAYLQDRGLAPDMQVDDLSILQQGRPDFIAINYYSTATIAASRGDGADVAPRAGDQQIMLGEEGVYRPAENPWVGKTPYGWVVDPVGLRLTLRKVCERYGLPILISENGMGAPDKLEHDGTVNDDYRIAFLDAHIEQMRLAIADGVELMGYCPWAALDVVSTHQGYAKRYGFIYIDRGEDDLKSLQRIRKRSFWWYKDVIAQNGSYGESQR  
  
>**gb|ADM96608.1| 6-phospho-beta-glucosidase [Dickeya dadantii 3937]**MRGKNMSQLPAGFLWGGAVAAHQLEGGWNEGGKGISVVDVLTAGAHGKLRRITDGVIPGESYPNHEAIDFYHRYKDDIALFAEMGFKCFRTSIAWTRIFPNGDEAEPCEAGLKFYDDLIDELLKHGIEPVLTLSHFEMPLHLVQQYDGWMSRKTLDCFVHFAATVIARYQHKVKYWMTFNEINNQKNVSAEIFGWMCSGVKFPQKAKPEEAMYQAVHHQFVASALIVKKAHDINPDIKVGCMCAFLPYYPYSCHPEDVMLAAQAMHDRFYFTDVQVRGHYPAYARREWALKGYQIHMEPEDERILREGKADYIGFSYYMSNVVKHDVQNRIDASMDGSSEHSIPNPHLKASDWGWQIDPTGLRYALTTLYERYEVPLFIVENGLGAVDKPDANGMCQDDYRIDYLRSHIDAMKAAVWEDGVDLMGYTPWGCIDLVSFTTGEMAKRYGFIHVDKHDDGTGTLARTPKKSFHWYQRVIASNGEEL  
  
>**gb|ADM98908.1| phospho-beta-glucosidase [Dickeya dadantii 3937]**MMSNPFPAHFLWGGAIAANQVEGAYLTDGKGLSTSDLQPQGIFGEIVTRQPGDSGIKDVAIDFYHRYPQDIALFAEMGFTCLRISIAWTRIFPQGDEAEPNEAGLAFYDRLFDELAKYGIQPLVTLSHYEMPYGLVEKHGGWGNRLTIDCFERYARTVFTRYRHKVKRWLTFNEINMSLHAPFTGVGLPPDSDKAAVYQAIHHQLVASARAVKACHDIIPDAQIGNMLLGAMLYPLTSKPEDVMESLHQNREWLFFGDVQVRGAYPGYMHRYFREQGITLNITAQDTQDLKATVDFISFSYYMTGCVSTDEAQLEKTRGNILNMVPNPYLESSEWGWQIDPLGLRYLLNFLYDRYQKPLFIVENGLGAKDKIEENGDIHDDYRIRYLNDHLVQVGEAIDDGVEVLGYTCWGPIDLVSASKAEMSKRYGFIYVDRDDAGQGSLERRRKKSFYWYQSVIASHGKTLTR  
  
>**gb|ADM99899.1| Beta-glucosidase; 6-phospho-beta-glucosidase [Dickeya dadantii 3937]**MIMARFPQGFLWGGAIAANQAEGAWNEDGKGPSIADVVRGGIVAGKPDAAIDPASYYPSHEAIDFYHRYRDDIALFAEMGFKCFRTSIAWSRIFPQGDEAQPNEAGLRFYDNLFDELLKYGIQPVITLSHYETPLALYQRYGGWHNRKLVEYFVRYCDTVFRRYRHKVKYWMTFNELNNMNRIPFATGAIQPEPEARLQAIYQAGHHMFVANALANQLCHQIIPDARIGCMLSLSTVYPHSCHPDDVFETMQMRRRSLFYADVMMRGHYPAYSQRMWRDHGIELAMEEGDLALLAAHPSDYLSFSYYRSATYQAGMPVLADTGGVIGKENPYLQSTDWGWPIDAKGLRLVCNELADRYEKPLFIVENGFGGVDVPDADGLINDDDRIRYGQQHLREVAEALADGCDIMGYTWWGPIDIVSAGTGEMKKRYGFIYVDKDNDGHGTLARRRKKSFDWYRQVIASNGEQL  
  
>**gb|ADM99900.1| Beta-glucosidase; 6-phospho-beta-glucosidase [Dickeya dadantii 3937]**MSVSKTCPPDVNAFPPDFLWGGATAANQLEGAWNVGGKGLSVSDVYTFDSRTPKERWLDQWLFMTHQQVADAQDPQSKKYYPKRKGNGFYYHYKEDIALFAEMGFTCFRMSIAWTRIFPRGDETEPNEDGLAFYDRVLDTLLAHHIQPIVSLSHYEMPLCLVTEYGGWPNRKLVDFYVRFATTVFERYRHKVKYWMTFNEINCVKHHPYVSVGVIEEDNPHLEQDKYQGVHHQFIASALATKACHQIIPGSQVGCMISYQILYPHTCHPDDLQACEEAQRVSLFFSDVQARGYYPAYTDRMLAEKGVVLEKQQGDDEILRQYPVDYVSFSYYMSSTISAHPEQLEGATGNLITGGIRNPYLLTSEWGWQIDPKGLRLALNQLYDRYQKPLFIAENGLGAVDSVNPDGSVDDDYRIDYLRQHVEQMKEALADGVKLFGYTWWGPIDVVSAGTSQISKRYGFIYVDQDDDGHGTQQRSRKKSFYWYRKLIASNGADLD  
  
>**gb|ADM99910.1| Beta-glucosidase [Dickeya dadantii 3937]**MSKVSMTLPEGFILGAASSAWQTEGWSGKKSGQDSYLDLWYKRDRQVWHNGYGPAVATDFYNRYREDVALMKQTGLTHFRTSINWSRFMLDYENGVVDEEYAAYIDNLIDELHRQGIEPMLCLEHYELPAVLFEKYQGWSSKQVVEWFVQYADAVFARYAGKVKRWFTFNEPIVVQTRVYLDAARYPYQQDTGVWMQWNHHKNLATAKVVQLFRDKGYHRHGGSIGVILNPEVTYPRSSAAHDVEAARLYDLFYNRVFLDPALKGEYPAELLALLETHQVHWDYTEEELAIIRANTVDEVGINLYYPHRVKAPSRAWNSNTPFHPAYYYEHFELPGRRMNKSRGWEINPRIIYDMAMRLKDEYGNLPWFVSENGMGIENEGQFKDGRGVVQDDYRIAFIAEHLYWTLKAREDGANCLGYMLWAFTDNVSPMNAFKNRYGLIEIDLEHDRQRRPKKSASWFRQVRDSGVLAFELDDEDK

GH2

>**gb|ACS85063.1| glycoside hydrolase family 2 TIM barrel [Dickeya dadantii Ech703]**MSITATPPTLAQILARRDWENPACSQVNRLDAHPPFSSWRNLQHARDDEPSRRRQPLNGEWVFSYFPRPEAVPESWLTQDLPQADRTIVPSNWQLSGYDAPIYTNVKYPIPVNPPLVPAENPTGCYSLTFKVDDSWRQHGQTRIIFDGVNSAFHLWCNGCWIGYSQDSRLPAEFDLSNALQEGDNRLAVMVLRWSDGTYLEDQDMWRMSGIFRDVWLLHKPTTQLRDIQLTTPLSRDYTHGTLCVQASASLLPETAANWRLHVQLWRHGQLEAEAIAPFGSAPIDERGNYHDRVDIQLDIDNPALWSAETPHLYRVVAALEYADGMLVEAEAYDVGFREVSISNGRLKLNGKPLLIRGVNRHEHHPEHGQVMDEATMLQDILLMKQHNFNAVRCSHYPNHPLWYRLCDRYGLYVVDEANIETHGMQPMNRLSDDPRWLPAMAERVTRMVQRDRNHPCIIIWSLGNESGYGRAHSALYQWVKQQDPTRPVQYEGGGADTPATDILCPMYARVDQDQPFPAVPKWAIKKWIGLPDESRPLILCEYAHAMGNSFGGFARYWQAFRQYPRLQGGFVWDWVDQALTRYDRHPPHWAYGGDFGDTPNDRQFCLNGLVFPDRTPHPALYEAQRAQQFFQFESLSAEPLTIAVTSEYLFRASDNEILQWRIMQDNLTLAEGRVELSLPPEGRQIITLLDTLPTVRHPAAMWLNLDVIQPTATAWSPAGHCCAWDQWALPAPMPTPALMPSTGAAPRLSSTEEAVEITHGDQSWTFHRHSGLLTHWQQDHRQRLLSPLRDNLTRAPLDNDIGISEVDRIDPHAWVERWKLAGLYQYETDCLEIRADALGDGVVVNTTHAGRYQQQTLFVSRKQWRIDNQGRLSVSVDVEVSPHLPPLARVGLSCQLAEVFPQVSWRGLGPHENYPDRRLSARHGRWQLPLEAMHTPYIFPSENGLRCDTEELNYGDWTIDGDFHFGIGRYSQQQLMNCSHHHLLQPETGVWLNLDGFHMGVGGDDSWSPSVAPDFLLTRPRYHYQLRITLG  
  
>**gb|ACT07558.1| glycoside hydrolase family 2 TIM barrel [Dickeya zeae Ech1591]**MSTASAYAPLSGLSLADILARRDWENPACPHIRRLDAHPPFSSWRNLNAARDDQPSDRRQMLNGEWTFSYFSRPEAVPEQWLTQDLTDANPLAVPSNWQLAGYDAPIYTNIKYPIPVNPPFVPQDNPTGCYSLTFSVNGDWLTQGQTRIVFDGVNSAFHLWCNGQWVGYSQDSRLPAEFDLTSCLQPGENRLAVMVLRWSDGTYLEDQDMWRMSGIYRDVYLLHKPAVHLRDVQLTTPLRHSYTQGTLCVTALANLPEDQAQAWQLAVQLWRGGQLVGEQRAPFGTPAIDERGAYHDRVSLQLEVAQPALWSAEEPNLYRAVVALEYDGTLVEAEAYDVGFREVAIRNGLLLLNGQPLLIRGTNRHEHHPQYGQAIDEATMRQDILLMKQHNFNAVRCSHYPNHPLWYRLCDRYGLYVVDEANIETHGMQPMSRLSDDPRWLPAYAERVTRMVQRDRNHPCIIIWSLGNESGYGPTHSALYQWVKQQDPTRPVQYEGGGADTPATDILCPMYARVDQDQPFPAVPKWSIKKWIGLPGEHRPLILCEYAHAMGNSFGGFDRYWQAFRQYPRLQGGFVWDWVDQALTREQDGKTHWAYGGDFGDKPNDRQFCLNGLVFPDRTPHPALYEAQRAQQFFQFNHHENAPLTLTITSEYLFRRSDNEELHWRIMQDDVQLASGRVPLDITPQGCQTLTLLEQLPAPQHHADMWLTVEVIQPNATDWSPAGHRCAWDQWQLPMPLARPTPRRDGSERPTLTQNDDQFEVIHGQQRWAFNRHNGLLTQWWRDGQAQLLSPLQDNLARAPLDNDIGISEVDRIDPNAWVERWKLAGLYRYDTDCRHIHADTLSDGVLITTEHIGHYQQQVLFISRKQWRIDAQGVLTVSVEVDVARHLPSLARVGLSMQLAAVTPQVSWLGLGPHENYPDRRLAALHGRWQQPLEAMHTPYIFPSENGLRCHTRELRYGDWLIEGDFHFGIGRYSRQQLMDCTHHHLLQPEPGTWLNLDGFHMGIGGDDSWSPSVAPDFLLTAPRYRYQLQLQLR  
  
>**gb|ACZ77478.1| glycoside hydrolase family 2 TIM barrel [Dickeya dadantii Ech586]**MSTVSAYVPLSDISLADILARRDWENPACPHIRRLDAHPPFSSWRDLNAARDDKPSDRRQLLNGEWTFSYFDRPQAVPEQWLTQDLNDAERITVPSNWQLAGYDAPIYTNVKYPIPVNPPFVPEDNPTGCYSLTFSVTPDWLAQGQTRIVFDGVNSAFHLWCNGQWVGYSQDSRLPAEFDLTPCLHVGENRLAVMVLHWSDGTYLEDQDMWRMSGIYRDVYLLHKPVVHLRDVQLTTPLRHSYTQGTLCVTALANLPEDQAEHWQLAVQLWRGEHLVGEQRKPLGTPAIDERGAYHDRLSLQLEVAQPALWSAEEPNLYRAVVALECNGSLVEAEAYDVGFREVTIRNGLLLLNGQPLLIRGANRHEHHPQHGQAIDEATMRQDILLMKQHNFNAVRCSHYPNHPLWYRLCDRYGLYVVDEANIETHGMQPMSRLSDDPRWLPAYAERVTRMVQRDRNHPCIIIWSLGNESGYGHTHSALYQWVKQHDPTRPVQYEGGGANTPATDILCPMYARVDQDQPFPAVPKWSIKKWIGLPGEHRPLILCEYAHAMGNSFGGFDRYWQAFRQYPRLQGGFVWDWVDQALVREQDGKTHWAYGGDFGDKPNDRQFCLNGLVFPDRTPHPALYEAQRAQQFFQFSHHDDAPLTLNVTSEYLFRHSDNEELHWRIMQDDVQLASGRVPLDIAPQGSQTLTLLEQVPAPQHHADMWLTVEVIQPKATDWSPAGHRCAWNQWQLPMPLARSLPPVHDGKSPSLSQTDEQFEVTQGQQRWVFNRHSGLLTQWWRDGQPQLLSPLQDNVTRAALDNDIGISEVDRIDPNAWVERWKLAGLYQYDTDCQHIHADTLSDSVLITTEHISHYQQQVLFISRKQWQIDACGVLRVNVEVEMARHLPSPARIGLSVQLAAVNPQVSWLGLGPHENYPDRRLAALHGRWQQPLESMHTPYIFPSENGLRCHTQELRYGNWLIEGDFHFGIGCYSQQQLMSCTHHHLLQPEAGTWLNLDGFHMGVGGDDSWSPSVAPDFLLTAPRYRYQLQLRLR  
  
>**gb|ADM97757.1| Beta-galactosidase [Dickeya dadantii 3937]**MSTASAYAPLSDISLADILARRDWENPACPHVRRLDAHPPFSSWRGLDAARDDQPSERRQQLNGAWTFSYFPRPEAVPEQWLTQDLTDADAITVPSNWQLAGYDAPIYTNIKYPIPVNPPFVPQDNPTGCYSLTFSVNADWLTQGQTRIVFDGVNSAFHLWCNGKWVGYSQDSRLPAEFDLTPCLQPGENRLAVMVLRWSDGTYLEDQDMWRMSGIYRDVYLLHKPAVHLRDVQLTTPLRHSYTQGTLCVTAQANLPEDQAQAWRLNVQLWRDGQLVGERRAPFGTPAIDERGAYHDRVNLQIEVERPALWSAEEPNLYRAVVALEYADGTLAEAEAYDVGFREVAIRNGLLLLNGQPLLIRGVNRHEHHPQRGQAIDEATMRQDILLMKQHNFNAVRCSHYPNHPLWYRLCDYYGLYVVDEANIETHGMQPMSRLSDDPRWLPAYAERVTRMVQRDRNHPCIIIWSLGNESGYGPTHSALYQWVKQQDPSRPVQYEGGGANTPATDILCPMYARVDQDQPFPAVPKWSIKKWIGLPGENRPLILCEYAHAMGNSFGGFDRYWQAFRQYPRLQGGFVWDWVDQALLREQDGKTHWAYGGDFGDKPNDRQFCLNGLVFPDRTPHPALYEAQRAQQFFQFTRHESAPLTLTVTSEYLFRHSDNEELRWRIMQDDVPLASGTVPLDIAPQGCQTLTLLDQLPAPQHHADMWLTVEVVQPHATDWSPAEHRCAWDQWPLPMPLAHSAPHRNDGACPTLTRDDDHFDIIHDQQRWSFDRRSGLLTQWWRDGQPQLLSPLQDNLTRAPLDNDIGISEVDRIDPNAWVERWKLAGLYQYQTDCRQIRADTLSDSVLITTEHVGHYQQQTLFISRKQWRIDAQGVLTVSVEVDVARHLPPLARIGLYGQLAAVNPQVSWLGLGPHENYPDRRLAALHGRWQQPLEAMHTPYIFPSENGLRCHTRELRYGDWLIEGDFHFGISRYSLQQLMDCTHQHLLQPEPGTWLNLDGFHMGIGGDDSWSPSVAPNFLLTAPRYRYQLQLRLQ

GH3

>**gb|ACS85403.1| glycoside hydrolase family 3 domain protein [Dickeya dadantii Ech703]**MKNQEVFVGPLMLDVAGYALDAEDRDVLEHPLVGGVILFSRNFHDADQLAELVRQIREASRERLVVAVDQEGGRVQRFRQGFTALPAAQSFAALNDLPQAQQLAEEAGWVMAAEMISMDIDISFAPVLDVGHQSAAIGDRAFHDEPDTLLAVAGGFIQGMRQAGMKATGKHFPGHGAVSADSHQETPRDDRPLALIQKRDMHIFRALNDANLLDAVMPAHVIYSDADPRPASGSPYWLKQVLRQSLGFDGIIFSDDLSMEGAAVMGNYVDRAQASLDAGCDMILVCNQRQGAISVLDNLPLINVDRLARLYHQGRFTRRELLDSSRWKQSSQALTTLSERWLAYKATR  
  
>**gb|ACS86184.1| glycoside hydrolase family 3 domain protein [Dickeya dadantii Ech703]**MKWLTSLTLAVGLACSPVWANHVDSTPPAATLTSQQQRDAFVNDLLNKMTLEEKIGQLRLISVGPDNPKHAIREMIRNGQVGGIFNTVTRPDIRVMQDQVMQLSRLKIPLFFAYDVVHGQRTVFPIGLGLASSWDMDTVETSARIAAYEATEDGLNMTWAPMVDITRDPRWGRVSEGFGEDTYLTSEIARVMVKGFQGDDLTGRHSLMTSVKHFALYGAAEGGRDYNTVDMSPQRMFQDYMPPYKAAIDAGSYGVMASLNSINGVPATANRWLLKDVLRDQWHFKGITISDHGAIKELIKHGVAADPSDAARIAVHAGIGMSMSDEYFERYLPDLVKRGVVNIKDIEDACRQVLNMKYDMGLFQDPYRHLGPVGSDPLDTNAESRLHRAEARDVARRSLVLLKNRLNILPLAKSGTIAVVGPLADSKRDIIGSWSAAGRPAQAVTVYEGIRKAVGYNARVYYAKGSNVTNHPGLIKFLNEYDESVVVDPRSPQAMIDEAVDAAKKSDVVIAVVGESQGMAHEASSRAKITIPPEQKALIAALKATGKPLVLVLMNGRPLDLSREDQQANAILETWFSGTEGGNAIADVLFGDYNPSGKLPMTFPRSVGQIPMYYNQLPTGRPYSAEAPNKYTSHYFDEANGPLYPFGYGLSYTTFAVSDVALSSPTMKRNGSVNASVTVTNTGKRAGETVVQLYLHDVVASVSRPVKELRGFRKVMLQPGESQQVNFTITPQALMFYNQQMQQVVEPGQFDVMIGLDSQRVKHGSFTLQ  
  
>**gb|ACS86228.1| glycoside hydrolase family 3 domain protein [Dickeya dadantii Ech703]**MTRLPTICRTPTVLALSAALPLLFSPLASAVQQAVLETRDIRLISVDGLQFRDLNRDGKLNPYEDWRLPAAVRTADLVSRMTLAEKAGVMMHGSAPTAGSVIGAGAHYDRQSARALIADLHINSFITRLSGDNPAQMADENNALQQLAEATRLGIPITISSDPRNAFQSLAGASSAAGKFSKWPETLGLAAIGDETLVRRFADIVRQEYRAVGITEALSPQADLATEPRWPRIDGTFGEDPALTKKMVHGYVAGMQNGTGGLNDGSVIAVVKHWVGYGAAQDGWDSHNAYGKYARYGKDGLQSHIEPFTGAFAAHAAGIMPTYSILRGATWRGVPIEPVGAGFNKFLLTDLLRDQYGFDGVILSDWLITNDCKGDCVTGVGPGEKPVPRGMPWGVEHLTSYERFIKAVNAGIDQFGGVTDSAMLVKAVREGRLRESRLDASVTRILQQKFQTGLFERPFVKAEQAGNVVGNPQSQQLANNAQAQALVLLQNKQLLPLRPGSRLWVYGIDPAAVKNAGFIPATRLEEADIALIRTRTPYEQPHKNYFFGSRHHEGSLAFSADNPDYQAIVRASARVPTVVTLYLERPAVLANVVNKTQALVANFGVSDAVLLQRLSSSADYTARLPFELPSSMQAVLKQRSDLPHDSAAPLFPFGFGLPR  
  
>**gb|ACT06490.1| glycoside hydrolase family 3 domain protein [Dickeya zeae Ech1591]**MVPPGRPCKRFDNQSDVQLTKEVFVGPLMLDVAGYELDAEDREVLAHPLVGGVILFSRNFHDADQLAELVRQLRRASRERLVVAVDQEGGRVQRFRNGFTALPAAQSFAALNPLALAQQLAEEAGWVMAAEMTALDIDISFAPVLDVGHQSAAIGDRAFHDDPDTLLAVAERFITGMRTAGMKATGKHFPGHGAVTADSHKETPRDERSLAQIRERDMWVFRELIARQRLDAVMPAHVIYSDADPRPASGSPYWLRQVLRQELGFGGIIFSDDLSMEGAAVMGGYAERAQAALDAGCDMILVCNQRQGAISVLDNLSPVKVPGLETLYHRGVITRRELLNSPRWKQATSQLTALSERWQAHKAAG  
  
>**gb|ACT07337.1| glycoside hydrolase family 3 domain protein [Dickeya zeae Ech1591]**MKWFTPLALAVGLACSPLWAQTSLQQTAPQAAPAQQQRDAFVSDLMKKMTLDEKIGQLRLISVGPDNPKHAIREMIHNGQVGGIFNTVTRQDIRVMQDQVMQLSRLKIPLFFAYDVVHGQRTVFPIGLGLASSWDMSAVELSAKIAAYEATEDGLNMTWAPMVDITRDPRWGRVSEGFGEDTYLTSEIARVMVKGFQGDDLTGRHSLMTSVKHYALYGAAEGGRDYNTVDMSPQRMFQDYMPPYKAAIDAGSYGVMASLNSINGVPATANRWLLKDVLRDQWHFKGITISDHGAIKEMIKHGVAADPSDASRIALQSGIGMSMSDEYFVRYLPDLVKRGLVSMKDIDDACRQVLNMKYDMGLFEDPYRHLGPAGSDPVDTNAESRLHREEARDVARRSLVLLKNRLDILPLKKSGTIAVVGPLADSQRDIIGSWSAAGRKAQAVTVYEGIRKAVGYNARVYYAKGSNVTNHPGLLKFLNEYDESVVVDPRSPQAMIDEAVDVAKKSDVVVAVVGESQGMAHEASSRAKITIPPEQKALISALKATGKPLVLVMMNGRPLDLSREDQQANAILETWFSGTEGGNAIADVLFGDYNPSGKLPMTFPRSVGQIPMYYNHLPTGRPYSAEAPNKYTSHYFDEANGPLYPFGYGLSYTTFDVSEVKLSSPTMKRNGSIKASVTITNTGKRAGETVAQLYLHDVVASISRPVKELRGFQKVMLQPGESRTLTFTLSPQDLMFYNAQMQQVAEPGKFDVMIGLDSQRVKTSSFTLL  
  
>**gb|ACT07381.1| glycoside hydrolase family 3 domain protein [Dickeya zeae Ech1591]**MKSRFSPHVAAALPWVATLPLLFSPLAEAVQQATLDTRGAPLITVNGLTFKDLNRDGKLNPYEDWRLPAAQRAADLVSRMTLAEKAGVMMHGSAPTAGSVTGAGTQYDLNAAKTMIAERYVNSFITRLSGDNPAQMAEENNKLQQLAEATRLGIPATISTDPRSSFQSLVGVSVSVGKFSKWPETLGLAAIGDEERVRRFADIVRQEYRAVGITEALSPQADLSTEPRWPRIDGTFGEDPDLTKKMVRGYVTGMQNGSNGLNAQSVISIVKHWVGYGAAQEGWDSHNVYGKYAQFRQNNLQWHIDPFTGAFEAHAAGIMPTYSILRNARWHGKPIEQVAAGFNRFLLTDLLRGQYGFDGVILSDWLITNDCKGDCITGVKPGEKPIPRGMPWGVENLTPAERFIKAVDAGVDQFGGVTDSALLVQAVQDGRLSEARLDASVNRILKQKFQIGLFERPYVNAAQASDIVGKADWQQLADDTQARSLVLLQNNNLLPLRKGSRVWLHGIAATAAQAAGFVVVDTPEQADVALIRTQTPYEQPHKNFFFGSRHHEGSLAFRADNPDYQAIVRASARVPTLVSLYMERPAILTNVVDKTRALVANFGVSDSVLLDRLTSGAAYTAKLPFELPSSMQAVRKQQPDLPYDSAKPLFPFGYGLPH  
  
>**gb|ACZ76466.1| glycoside hydrolase family 3 domain protein [Dickeya dadantii Ech586]**MGPLMLDVAGYELDAEDREVLAHPLVGGVILFSRNFHDADQLTELVRQMRRASRERLVVAVDQEGGRVQRFRHGFTPLPAAQSFAALNSLEQAQQLAQEAGWVMAAEMITLDIDISFAPVLDVGHQSAAIGDRAFHDDPDTLLAVAEHFIAGMRAAGMKATGKHFPGHGAVTADSHKETPQDNRPMAQIRERDMRVFRELIARQQLDAIMPAHVIYRDADPRPASGSPYWLKQVLRQELGFGGIIFSDDLSMEGAAVMGGYAERAQAALDAGCDMILVCNQRQGAISVLDNLSAVKVPGLETLYHRGMITRRELLNSSRWKQATSQLTALSERWQAHKAAG  
  
>**gb|ACZ77292.1| glycoside hydrolase family 3 domain protein [Dickeya dadantii Ech586]**MKWFTPLALAVGLACSPLWAQTPLQQTAAPQATPAHQQQRDAFVNDLMKKMTLDEKIGQLRLISVGPDNPKQAIREMIHNGQVGGIFNTVTRQDIRVMQDQVMQLSRLKIPLFFAYDVVHGQRTVFPIGLGLASSWDMNAVELSAKIAAYEATEDGLNMTWAPMVDITRDPRWGRVSEGFGEDTYLTSEIARMMVKGFQGDDLTGRHSLMTSVKHYALYGAAEGGRDYNTVDMSPQRMFQEYMPPYKAAIDAGSYGVMASLNSINGVPATANRWLLKDVLRDQWHFKGITISDHGAIKELIKHGVAADPSDASRIAVQSGIGMSMSDEYFARYLPDLVKRGVVSMKDIDDACRQVLNMKYDMGLFEDPYRHLGPAGSDPVDTNAESRLHREEARDVARRSLVLLKNRLDILPLKKSGTIAVVGPLADSQRDIIGSWSAAGRKAQAVTVYEGIRKAVGYNARVYYAKGSNITNHPGLIKFLNEYDESVVVDPRSPQAMIDEAVDVAKKSDVVIAVVGESQGMAHEASSRAKITIPPEQKALIAALKATGKPLVLVLMNGRPLDLSREDQQANAILETWFSGTEGGNAIADVLFGDYNPSGKLPMTFPRSVGQIPMYYSHLPTGRPYSADAPNKYTSHYFDEANGPLYAFGYGLSYTTFAVSDVKLSSPTMKRNGSITASVTITNTGKRAGETVAQLYLHDVVASVSRPVKELRGFQKVMLMPGESRTVTFTLSPKDLMFYNAQMQQVVEPGKFDVMIGLDSQRVKTSSFTLL  
  
>**gb|ACZ77342.1| glycoside hydrolase family 3 domain protein [Dickeya dadantii Ech586]**MEKSATRQKALLIALPLLFSPLASAVQQAVLDTRGAPLITVNGLTFKDLNRDGKLNPYEDWRLPAAERAADLVSRMTLAEKAGVMMHGSAPTAGSVTGAGTQYDLNAAKTMIADRYVNSFITRLSGDNPAQMAEENNKLQQLAEATRLGIPLTISTDPRSSFQSLVGVSVSVGKFSKWPETLGLAAIGDEELVRRFADIVRQEYRAVGITEALSPQADLATEPRWPRIDGTFGEDPDLTKKMVRGYVTGMQNGKNGLNAQSVISIVKHWVGYGAAKDGWDSHNVYGKYAQFRQNNLQWHIDPFTGAFEAHAAGIMPTYSILRNASWHGKPIEQVGAGFNRFLLTDLLRGQYGFDGVILSDWLITNDCKGDCLTGVKPGEKPVPRGMPWGVEKLTPAERFVKAVNAGVDQFGGVTDSALLVQAVQDGKLSEARLDTSVNRILKQKFQTGLFERPYVNATQANDIVGRADWQQLADDTQARSLVLLQNNNLLPLRKGSRVWLHGIAANAAQEVGFIVVNTPEQADVALIRTHTPYEQPHKNFFFGSRHHEGSLAFRNDNPDYQAIVRASAKVPTLVTVYMERPAILTNVVDKTRAVVANFGVSDSVLLNRLMSGAAYTAKLPFELPSSMSAVRNQQPDLPYDSAKPLFPFGYGLPH  
  
>**gb|ADM98002.1| Beta-glucosidase (Gentiobiase) (Cellobiase) / Beta- xylosidase [Dickeya dadantii 3937]**MKYDGYIHNEKNHMTSRFSPHTAVVLPWVATLPLLFSPLAEAVQQATLDTREAPLINVDGLTFKDLNRDGKLNPYEDWRLPPAQRAADLVSRMTLDEKAGVMMHGSAPTAGSVTGAGNQYDLNAAKTMIAERHVNSFITRLSGDNPAQMAEENNKLQQLAEATRLGIPATISTDPRNSFQSLVGVSVSVGKFSKWPETLGLAAIGDEERVRIFADIVRQEYRAVGITEALSPQADLSTEPRWPRIDGTFGEDPDLTKKMVRGYVTGMQNGKNGLNSQSVISVVKHWVGYGAAQDGWDSHNAYGKYALFRQNNLQWHIDPFTGAFEAHAAGIMPTYSILRNARWHGKPIEQVGAGFNRFLLTDLLRDQYGFDGVILSDWLITNDCKGDCLTGVKPGEKPVPRGMPWGVENLTPAERFIKAVNAGVDQFGGVTDSAVLVKAVQDGLLSEARLDTSVNRILKQKFQTGLFERPYVNAGQADDIVGRTDWQQLADDTQARALVLLQNNNLLPLRKGSRVWLHGIDAKAAQEAGFVVVNVPEQADVALIRTHTPYEQPHKNFFFGSRHHEGSLAFRADNPDYQAIVRASARVPTLVTVYMERPAVLTNVVDKTRTLIANFGVSDSVLLNRLISGAAYTAKLPFELPSSMQAVLKQQPDLPYDSDKPLFPFGYGLPH  
  
>**gb|ADM98059.1| Periplasmic beta-glucosidase [Dickeya dadantii 3937]**MKWFTSLALAVGLACSPLWAQTPLQQTAPQAASAQQRDAFVNDLMKKMTLDEKIGQLRLISVGPDNPKQAIRDMIRNGQVGGIFNTVTRQDIRVMQDQVMQLSRLKIPLFFAYDVVHGQRTVFPIGLGLASSWDMSAVELSAKIAAYEATEDGLNMTWAPMVDITRDPRWGRVSEGFGEDTYLTSEIARVMVKGFQGDDLTGRHSLMTSVKHYALYGAAEGGRDYNTVDMSPQRMFQDYMPPYKAAIDAGSYGVMASLNSINGVPATANRWLLKDVLRDQWHFKGITISDHGAIKELIKHGVAADPSDASRIAVQSGIGMSMSDEYFVRYLPDLVKRGLVSMKDIDDACRQVLNMKYDMGLFQDPYNHLGPVGSDPVDTNAESRLHREEARDVARRSLVLLKNRLDVLPLKKSGTIAVVGPLADSKRDIIGSWSAAGRQAQAVTVYEGIRKAVGYNARVYYAKGSNVTNHQGLVQFLNQYDQSVEIDPRTPQAMIDEAVDAAKKSDVVIAVVGESQGMAHEASSRAKITIPPEQKALISALKATGKPLVLVLMNGRPLDLSREDQQANALLETWFSGTEGGNAIADVLFGDYNPSGKLPMTFPRSVGQIPMYYNQLPTGRPYSAQAPNKYTSHYFDEANGPLYPFGYGLSYTTFEVSDVKLSSPTMKRNGSVKASVTVTNTGKRAGETVAQLYLHDVVASISRPVKELRGFQKVMLQPGESRTLTFTLSPQDLKFYNAQMQQVAEPGKFEVMIGLDSQRVKTGSFTLL  
  
>**gb|ADM98979.1| beta-N-acetylglucosaminidase [Dickeya dadantii 3937]**MGPLMLDVAGYELDAEDREVLAHPLVGGVILFSRNFHDADQLAELVRQMRRASRERLVVSVDQEGGRVQRFRDGFTALPAAQSFAALNPLPQAQVLAEEAGWVMAAEMIALDIDISFAPVLDVGHQSTAIGDRSFHDDPDTLLAVAERFIAGMRAAGMKATGKHFPGHGAVTADSHKETPRDERPLAHIQQRDMRVFRELIARQQLDAVMPAHVIYTDADPRPASGSPYWLKQVLRQELGFGGIIFSDDLSMEGAAVMGGYAERGQAALDAGCDMILVCNQRQGAISVLDNLSPVKVPGLETLYHRGLITRRELLNSSRWKQATSQLTALSERWQAHKAAG

GH5

>**gb|ACS85678.1| Cellulase [Dickeya dadantii Ech703]**MSLLDLNKTTFLSREKIISHRHFSLATVCFGLVMTCFSGTVMASVEPLSVNGNKIYAGEQVKSFAGNSLFWSNNGWGGEKFYTAETVARLKSEWGASIVRAAMGVQESGGYLQDPSGNKAKVEKVVDAAIANDMYVIIDWHSHHAEDNQNEAISFFQEMAKKYGDKPNIIYEIYNEPLQVSWGNTIKPYAEAVISAIRAIDSDNLIIVGTPTWSQDVDEASLNPISGTNIAYTLHFYAGTHGESLRNKALKALNNGIALFVTEWGAVNADGNGGVNASSVDTWVTFMRDNNISNANWALNDKDEGASTYYPDSLTLTESGKKVKEIIQNWPYNTGTSTSSTATGSSSSGDAETSSSSCSSASASTSSSDTGTSASTTTTTADSTATTATTVSCSNVNVYPNWVSKDWSGGEYTHNNAGEQMVYQGTLYSANWYTASVPGSDGSWTLVGTCG  
  
>**gb|ACT06384.1| Cellulase [Dickeya zeae Ech1591]**MPIFDLDKKNTSNKKHYSSRKSLYFSGIFLGLSITCLSGSAWASVEPLSVSGNKIYAGEKAQSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWGSSIVRAAMGVQDAGGYLQDPAGNKAKVEKVVDAAIANDMYVIIDWHSHSAENNRNEAISFFQEMARKYGKNPNVIYEIYNEPLQVSWSNTIKPYAEAVISAIRAIDPDNLIIVGTPSWSQNVDEASRDPINANNIAYTLHFYAGTHGESLRNKARQALNNGIALFVTEWGAVNADGNGGVNQTETDAWVTFMKDNNISNANWALNDKNEGASTYYPDSKNLTESGKKVKSIIQNWPYKINGTSSTTTEPSTEPTPTPTTDEPVTTDEPATTNCSNTNVYPNWVSKDWAGGQPNHNEAGQSIVYKGNLYTANWYTTSTPGSDSSWTLVGSCN  
  
>**gb|ACZ76357.1| Cellulase [Dickeya dadantii Ech586]**MPLFDSKNDATVNRKKHTFRQKLFFSCSCVGLSLICLSSNTWASVEPLSVSGSNIYAGGKVRSFSGNSLFWSNTGWNAEKFYTAETVASLKKDWKSSIVRAAMGVQEYGGYLQDPTNNKARIEKVVNAAIANDMYVIIDWHSHSAENNRSEAISFFQEMARKYGDKPNVIYEIYNEPLQVSWSYTIKPYAEAVISAIRAIDPDNLIVVGTPSWSQNVDEASRDPINARNIAYTLHFYAGTHGESLRNKARQAINNGIALFVTEWGSVNADGNGGVNYSETDAWVTFMRDNNISNANWALNDKNEGASTYYPDSKNLTESGKKVKSIIQSWPYKTSNTASAMSESSSDVSTDMTSDNANAPDSSATTSCANVNIYPNWVSKDWAGGQPDHNEAGQSIVYQGNLYTANWYTTSVPGSDSSWTLVGSCN  
  
>**gb|ADM99099.1| endo-1,4-beta-glucanase precursor [Dickeya dadantii 3937]**MPLSYLDKNPVIDSKKHALRKKLFLSCAYFGLSLACLSSNAWASVEPLSVNGNKIYAGEKAKSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWKSSIVRAAMGVQESGGYLQDPAGNKAKVERVVDAAIANDMYAIIGWHSHSAENNRSEAIRFFQEMARKYGNKPNVIYEIYNEPLQVSWSNTIKPYAEAVISAIRAIDPDNLIIVGTPSWSQNVDEASRDPINAKNIAYTLHFYAGTHGESLRNKARQALNNGIALFVTEWGTVNADGNGGVNQTETDAWVTFMRDNNISNANWALNDKNEGASTYYPDSKNLTESGKKVKSIIQSWPYKAGSAASATTDPSTDTTTDTTVDEPTTTDTPATADCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN

GH8

>**gb|ACS87644.1| Cellulase [Dickeya dadantii Ech703]**MIKPVWRVGMVLLMMWFSMAASAASGWDSYKSRFMTQDGRILDTGNKNISHTEGQGFAMLMAVYFNDRSAFDGLWTWTQTHLQDNKSGLFYWRYNPMDSNPVVDRNNAADGDVLIAWALLKAGEKWQENRYLLASDVIQKAILARNVVQFAGRTVMLPGANGFNKNSYVILNPSYFLFPAWQDFARHSHLQAWRQLIDDGLALLGEMRFGKVELPVDWVALNADGTMAPATNWPPRFSYDAIRIPLYLYWYDAKTLALVPFQLYWRNYSRLNTPAWIDVLNNNTAPYSMRDGLLAIRDLTMGSPGDIPASLNASEDYYSSSLHLLAYIASGR  
  
>**gb|ACT08877.1| Cellulase [Dickeya zeae Ech1591]**MLKLMWRGWILMLMVWFSVSATAATGWETYKSRFMTADGRIQDTGNKNVSHTEGQGFAMLMAVHYDDRAAFDNLWNWTQSHLKNTVNGLFYWRYDPAASNPVADRNNASDGDVLIAWALLKAGNKWQDNRYLQASDGIQKAIISNEIIQFAGRTVMLPGAYGFNKNSYVVLNPSYFLFPAWRDFANRSHLQVWRQLIDDSLSLVGEMRFGQTGLPTDWVALNADGSMAPATAWPSRFSYDAIRIPLYLYWYDAKTMALVPFQLYWRNYPRLATPAWVDVLSNNTAPYSMQGGLLAVRDLTMGSFGALSDQPGAAEDYYSSSLRLLVALARGQ  
  
>**gb|ACZ78883.1| Cellulase [Dickeya dadantii Ech586]**MIKPMWRGWVLIAMMWFSVSATAATGWETYKSHFMTPDGRIQDTGNKNVSHTEGQGFAMLMAVHYGDRAAFDSLWNWTQSHLRDTSSGLFYWRYDPSAANPVVDKNNASDGDVLIAWALLKAGNKWQDNSYLQASDTIQKAVISHEIIQFAGRTVMLPGAYGFNKNSYVVLNPSYFLFPAWQDFARRSHLQVWRQLIDDGLSLIGEMRFGQVGLPTDWVALNADGTMAPATAWPSRFSYDAIRVPLYLYWYDAKTTALVPFQLYWRNYSRLSTPAWIDVLSNNTAPYTMQGGLLAVRDLTMGNLDALSDQPGAAEDYYSSSLRLLAMMAARHQ  
  
>**gb|ADM96331.1| endoglucanase Y [Dickeya dadantii 3937]**MGKPMWRCWALMLMVWFSASATAANGWEIYKSRFMTTDGRIQDTGNKNVSHTEGQGFAMLMAVHYDDRIAFDNLWNWTQSHLRNTTSGLFYWRYDPSAANPVVDKNNASDGDVLIAWALLKAGNKWQDNRYLQASDSIQKAIIASNIIQFAGRTVMLPGAYGFNKNSYVILNPSYFLFPAWRDFANRSHLQVWRQLIDDSLSLVGEMRFGQVGLPTDWAALNADGSMAPATAWPSRFSYDAIRIPLYLYWYDAKTTALVPFQLYWRNYPRLTTPAWVDVLSSNTATYNMQGGLLAVRDLTMGNLDGLSDLPGASEDYYSSSLRLLVMLARGK

GH 13

>**gb|ACS84094.1| 1,4-alpha-glucan branching enzyme [Dickeya dadantii Ech703]**MSGFSDQRVINLLFSGHYADPFAVLGMHDTPAGLEVRALLPGALEAHVVDAHNGRKVGKLERQDERGFFASVIPRRKHHFSYRLAVTWPRDTCIIDDPYRFGTLLQELDVWLLAEGRHLRPFEQMGAHLRTLDGVDGACFSVWAPNAQRVSVVGDFNFWDGRRHPMRLRRESGIWELFVPGVGVGDLYKFELIDCYGNLLLKSDPYAFESQMRPDNASLVTRLPAPLPASPERQQANDLQSPISIYEVHLGSWRRHTDDNFWLSYRELAEQLVPYVKSMGFTHVELMPVHEHPFDGSWGYQPLGLYAPTRRFGSPEEFRQLVDAFHEAGINVLLDWVPGHFPADSYGLARFDGTALYEYADPKEGFHQDWNTLIYNFDRHEVRNYLTGNAVYWAERFGADGLRVDAVASMIYRDYSRRDGEWVPNHYGGKENLEAISFLRYTNQTVGQHCPGLITIAEESTDYAGVTLPPEHNGLGFHYKWNMGWMHDTLAYMQLDPVHRKFHHDLLTFGMLYAYSENFVLPLSHDEVVHGKRSLLDRMPGDPWQKFANLRAYYGFMWAYPGKKLLFMGGEFAQGKEWNHDISLDWHLLDEPEGWHAGVQNLVRDLNHCYCQHPPLYQCDYLHQGFEWVVVDDRENSVFAFIRRDNDGNEMLVVSNFTPVPREGYRIGINQPGRWREVLNTDSLHYHGGNLGNAGAVNSEPVGSHSRPQSLVLTLPPLATLYLVREA  
  
>**gb|ACS84095.1| glycogen debranching enzyme GlgX [Dickeya dadantii Ech703]**MTVLQAGHPYPLGAHFDGRGVNFALSSADAVGVELCLFDGAYEQRVPMTARTDAIWHGYLPGARPGLQYGFRVDGPFDPARGLRFNRNKLLLDPCARMMMGTVRDNERLHGGYHRPDPRDDADVMPRCVVVDERYDWRDDSFPMTPWPRTVLYEAHVRGLTKRHPDIPQAIRGTYAALAHPVMLAYFARLGVTALELMPVHQHADEPRLQAMGLRNYWGYNTLLPFAADNLLSASEHPLNEFRDMVRVLHKAGIEVILDVVFNHSAELDLDGPTLTLRGMDNASYWLTDDGDYHNWTGCGNVLRLDYPATLDWVVSCMVFWRDVCHVDGFRLDLATVLGRSPDFSSRAPFFAVLRNHPSLRDIKLIAEPWDVGPGGYQLGRFPAPFAEWNDRFRDDMRRFWLHRDVPVGVFARRFAASSDVFDHDGRHPWASVNLLTSHDGFTLRDLVCFNHKHNEANGEQNRDGTNSNFSNNHGVEGEQADQETQARRHVSQRALLTTLLLSQGTPMLLAGDEFGNSQQGNNNAYCQDNALAWLHWDQADDTLIAFTSGLIRLRRSIPVLQGGGWWRDGESDVRWLNEQGTPMTPQDWEQGERRLQIPLSECWLLLINATEQACDFLLPAGAWRVSPPFDAVANPVEGRVWRGEANAVCVLVKQ  
  
>**gb|ACT05116.1| 1,4-alpha-glucan branching enzyme [Dickeya zeae Ech1591]**MSGFSDRNIINLLFSGHYADPFAVLGMHVTSSGLEVRALLPDASDVHVVDAHSGRKVAHLQRLDPRGFFVAVIPRRKKPFSYRLAVTWQQDTHVIDDPYRFGPLLQELDIWLLAEGRHLRPFETLGAHPSTLDGVGGTCFAVWAPNAQRVSVVGDFNFWDGRRHPMRLRCENGVWELFVPGVGVGQLYKFEIIDCYGNVLVKSDPYAFASQMRPDTASVVSALPPALPVDEARQSANDLQSPISIYEVHLGSWRRHDDNNFWLSYRELADQLVPYVKDMGFTHVELMPVHEHPFDASWGYQPLGLYAPTRRFGSPEDFRYLVSAFHEAGINVLLDWVSGHFPTDSYGLARFDGTALYEYADPKEGYHQDWNTLIYNFDRHEVRNYLAGNALYWTERFGVDGLRVDAVASMIYRDYSRRDGEWVPNHYGGKENLEAIGFLRYTNQMLGQNRAGAVTIAEESTDYAGVTLPPEHSGLGFHYKWNMGWMHDSLAYMQQDPVHRKYHHDLLTFGMLYAYSENFVLPLSHDEVVHGKRSLLDRMPGDAWQKFANLRAYYGFMWAYPGKKLLFMGGEFAQGREWNHDTSLDWHLLDEPEGWHVGVQQLVRDLNHCYRQHPPLYQCDYLHQGFEWVVVDDRENSVFAFIRRDAEGNEILIISNFTPVPREGYRVGINQPGHWREVLNTDSMHYHGSNLGNQGLVRSEAVGSHSRPQSLVLTLPPLSTLYLVKEA  
  
>**gb|ACT05117.1| glycogen debranching enzyme GlgX [Dickeya zeae Ech1591]**MVELLAGRPRPLGSHFDGEGVNFALFSSRASRVELCIFDGLRELRLPLTARTGDIWHGYLPDAQPGLCYGYRVDGAFDPQRGLRFNANKLLLDPCARQMDGWVVDDERLHGGYDYPDAVDSAEVMPRSVVVDERYDWQGDAFPRTPWSQTVLYEAHVRGLTRRHPRIPAAIRGTYAALAHPVMLDYLTKLGVTALELMPVQQHADEPRLQAMGLRNYWGYNTLLPFAVDSSLAAGDEPLNEFRDMVRALHNAGIEVILDVVFNHSAELDADGPTLTLRGIDNASYYWLTQDGAYHNWAGCGNVLRLEHPAVLQWVIECLTFWHETCRVDGFRFDLATILGRMPDFSSSAPFFTALRNHRSLRNCKLIAEPWDIGPGGYQLGKFPSPFVEWNDRFRDDIRRFWLHGDLPVGVFARRFAASSEVFERNGRLPWASVNMLTSHDGFTLRDLVSFNYKHNQANGEQNRDGTNSNFSFNHGTEGLEADEATQARRRASQQALLTTLLLSQGTPMLLAGDEFGSSQQGNNNAYCQDNALAWLHWETADTELIAFTAGLLRLRRAIPALQKAGWWRDDEDDVRWLNAQGEPLTPYEWEQGEHRLQIQLSKHWLLLINATSQTSDFSLPKGEWRVAPPFDAADHPLNERVWRGQANAVCVLVKK  
  
>**gb|ACZ78670.1| glycogen debranching enzyme GlgX [Dickeya dadantii Ech586]**MVELLAGRPRPLGSYFDGEGVNFALFSSGASKVELCIFDGLREQRLPLTARTGDIWHGYLPDAQPGLCYGYRVDGVFDPKRGLRFNARKLLLDPCARQMDGWVVDDERLHGGYDYPDAADSAEVMPRSVVVDERYDWQGDAFPRTPWHHTVLYEAHVRGLTRRHPRIPASIRGTYAALAHPVMLEYLTQLGVTALELMPVQQHADEPRLQSMGLRNYWGYNTLLPFAVDSSLAAGDDPLNEFRDAVRALHKAGIEVILDVVFNHSAELDVDGPTLSLRGIDNTSYYWLTGEGDYYNWAGCGNVLRLDSPAVLQWVIECLKFWHETCHVDGFRFDLATILGRSPDFSSSAPFFTALRNHRSLRECKLIAEPWDIGPGGYQLGQFPALFAEWNDRFRDDMRRFWLLGDMPVGVFARRFAASSEVFERNGRLPWASVNMLTSHDGFTLRDLVCFNHKHNEANGEQNRDGSNSNFSFNHGTEGLEADDATQARRRASQQALLTTLLLSQGTPMLLAGDEFGNSQQGNNNAYCQDNALAWLHWDQADTDLLAFTAGLIRLRRAIPALRKAAWWRDGGNDVQWLNAQGEPLTPYEWEQGAHQLQIQLSERWLLLLNATTQTSEFSLPAGEWRVSPPFSAADHPLKGRVWHGQANAVCVLVKQ  
  
>**gb|ACZ78671.1| 1,4-alpha-glucan branching enzyme [Dickeya dadantii Ech586]**MSGFSDRNIINLLFSGHYADPFAVLGMHVTSSGLEVRALLPDASEVHVVDVHSGRKVAHLQCRDPRGFFASVIPRRKKPFSYRLAVTWQQETYVIDDPYRFGPLLQELDIWLLAEGRHLRPFETLGAHPSTLDGVEGTCFAVWAPNAQRVSVVGDFNFWDGRRHPMRLRRENGVWELFVPGVGIGQLYKFEIIDCYGNVLVKSDPYAFASQMRPDTASVVSGLPTALPVDEARQSANDLQSPISIYEVHLGSWRRHTDNNFWLSYRELADQLVPYVKEMGFTHVELMPVHEHPFDGSWGYQPLGLYAPTRRFGSPEDFRYLVNAFHEAGINVLLDWVSGHFPTDSYGLARFDGTALYEYADPKEGYHQDWNTLIYNFDRHEVRNYLAGNALYWTERFGVDGLRVDAVASMIYRDYSRRDGEWVPNHYGGKENLEAIGFLRYTNQMLGQHHAGAVTIAEESTDYAGVTLPPEHGGLGFHYKWNMGWMHDSLAYMQQDPVHRKYHHDLLTFGMLYAYSENFVLPLSHDEVVHGKRSLLDRMPGDAWQKFANLRAYYGFMWAYPGKKLLFMGCEFAQGREWNHDTSLDWHLLDEPEGWHAGVQQLVRDLNHCYRQHPPLYQCDYLHQGFEWVVVDDRENSVFAFIRRDADGNEMLIISNFTPVPRDGYRVGINQPGQWREVLNTDSMHYHGSNIGNQGLVRSEAVGSHSRPQSLVLTLPPLSTLYLVREA  
  
>**gb|ADN00396.1| Glycogen debranching enzyme [Dickeya dadantii 3937]**MGELLAGRPRPLGSHFDGEGVNFALFSSGASRVELCIFDGLREQRLPLTARTGDIWHGYLPDAQPGLCYGYRVDGVFDPSRGQRFNANKLLLDPCARQMDGWVVDDERLHGGYHQPDPSDSAEVMPRSVVVDEHYDWQDDRLPRTPWSQTVLYEAHVRGLTRRHPGIPAAIRGTYAALAHPVMLDYLTQLGVTALELMPVQQHADEPRLQSMGLRNYWGYNTLLPFAVDSSLAASDDPLNEFRDTVRALHQAGIEVILDVVFNHSAELDVDGPTLTLRGIDNASYYWLTESGDYHNWAGCGNVLRLEHPAVLHWVIECLTFWHEVCHVDGFRFDLATILGRLPDFSSSAPFFTALRNHRSLRDCKLIAEPWDIGPGGYQLGQFPAPFAEWNDRFRDDMRRFWLHGDLPVGVLARRFAASSEVFERGSRQPWASVNMLTSHDGFTLRDLVCFNHKHNDANGEQNRDGTNSNFSFNHGTEGLEADEATQARRRVSQQALLTTLLLSQGTPMLLAGDEFGNSQQGNNNAYCQDNALAWLHWEQADDALLAFTSGLIRLRRSIPALQRGRWWRDDEDDVRWLNAQGEALTPYEWEQGAHQLQIQLSERWLLLVNATPQVSDFSLPEGEWRVAPPFSAADHLLDGQTWRGQANAVCVLVKQ  
  
>**gb|ADN00397.1| 1,4-alpha-glucan branching enzyme [Dickeya dadantii 3937]**MSGFSDQNIINLLFSGHYADPFAVLGMHDTASGLEVRALLPDASDVWVVDAHSGRKVANLQCRDPRGFFASAIPRRKKPFSYRLAVTWPQDTQVIDDPYRFGTLLQELDIWLLAEGRHLRPFETLGAHPSTLDGVVGTCFAVWAPNAQRVSVVGDFNFWDGRRHPMRRRRENGVWELFVPGVGPGQLYKFEIIDCYGNVLVKSDPYAFESQMRPDTASVVSRLPPALPVDEARQHANDLQSPISIYEVHLGSWRRHTDNNFWLSYRELADQLVPYVKEMGFTHVELMPVHEHPFDGSWGYQPLGLYAPTRRFGSPDDFRYLVSAFHEAGINVLLDWVSGHFPADSYGLARFDGTALYEYADPKEGYHQDWNTLIYNFDRHEVRNYLAGNALYWTERFGVDGLRVDAVASMIYRDYSRRDGEWVPNYFGGKENLEAIGFLRYTNQMLGQHHAGAVTIAEESTDYAGVTLPPEHGGLGFHYKWNMGWMHDSLAYMQLDPVHRKYHHDLLTFGMLYAYSENFVLPLSHDEVVHGKRSLLDRMPGDVWQKFANLRAYYGFMWAYPGKKLLFMGGEFAQGREWNHDTSLDWHLLDEPEGWHAGVQQLVRDLNHCYRQHPPLYQCDYLHQGFEWVVVDDRENSVFAFIRRDADGNEMLIISNFTPVPRDSYRVGINQPGAWREVLNTDSWHYHGGNLGNKGLVYSETVGSHSRPQSLVLTLPPLATLYLVKEA

GH19

>**gb|ACS84172.1| glycoside hydrolase family 19 [Dickeya dadantii Ech703]**MALDITQEKLQQLMPNASAEDIALFQPALQQECLEAGINTSLRFAHFIAQIAHESAELRARSENLNYSAKGLRAVFGRYFTTDQMAEQYARKPEAIANVVYANRLGNGATESGDGWAFRGRGLIQLTGRDNYRTCGEAIGHKLTDDPDVIGQKPEISVAVAIWFWNRNQLNVLADQDDLNAITRRINGGLNGLEDRKAYLEKAKRLF  
  
>**gb|ACT05168.1| glycoside hydrolase family 19 [Dickeya zeae Ech1591]**MTLEISQEKLKKVMTAASADDLALFQPALQQECNTAGINTPLRFAHFIAQVAHESNELRARVENLNYSAKGLRSVFGRYFTTDEMAAQCERKPESIANIVYANRLGNGATETGDGWKYRGRGLIQLTGRDNYRTCGSAIGQDLVTNPDLISQNPEVSVAAAIWFWKKNGLSEFADQDDINTITRRINGGLNGLADRKNYLAKAKRAFG  
  
>**gb|ACZ78613.1| glycoside hydrolase family 19 [Dickeya dadantii Ech586]**MTLEISQEKLKKVMTAASADDLTQFQPALQQECNAAQIDTPLRFAHFIAQIAHESNELRARVENLNYSAKGLRSVFGRYFTTDEMAAQCERNPEAIANIVYANRLGNGATQTGDGWKYRGRGLIQLTGRDNYRACGSAIGQDLVTNPDLISQNPDVSVAAAIWFWKKNGLNELADQDDINGITRRINGGLNGLADRKNYLAKAKRAFN  
  
>**gb|ADM98823.1| EF hand domain protein [Dickeya dadantii 3937]**MKKNNTTRKQLVVVIKKTRSFAKKTEITTQSRQNTTAANSTAANYPNAPSSTGLDNIRLSAPEPGQSGAPATAAGQPTPPAAPPVTTVPPLPKFNPPRAETTTPPSAPPAQPSTPSAPQPSLPSPAPAPVAAAPAAEPPTAQEPATPPFAPDYAAVGNQLSKLMSGMAAPLSRLAGSFQSFAHATNQALLNPAQSVAPKTEPKPVTPATEPKPVAPAPASAKPISLPVALIKKIRTQVPADKVEEVLRALVTGAAYKQGDIAGLDDAHTRALVASTAATESAGGKLDIRNSAGYLGRYQAGASWLADAGLIAGGANAVIAAMKADGFTNEYKWGKSGGMTRFLKNKNNWKNGLDYDKYLSSAEVQDTAFKTNSDKAYKQLLKEGTIKPNMSQGEIAGILKARHIGGIGGARKAAKGIAGPTDANGTSALKYKNDLAAGNVFIESYQSGTQTTSNIDANTSKTPPVETVEKPVAKTDRDVPQRAQSGRRIIDKTQQEKKEGVDDVPKNEEHPNNKRVTISMLRKIWKNRKNVSDEKLRKIADELNANLEKSHLNTEERLSHFIAQMYQETGGSLSFSENMNYKPEVLISNFGYYKKNSAEAFSDGRTSSHIANQDAIANKVYGHRLGNSLPDDGSRYRGRGMVHLTGRNNYKDFTSYHKENWGENQDFEKNPELISSDVKYAVRAALYFWEKNGLYKIADKGFNDQATNSITKVINEKTGSYSERRKNLEKIAKERIFKEAF  
  
>**gb|ADN00340.1| Lytic enzyme [Dickeya dadantii 3937]**MTLEISQEKLKKIMTAASADDLALFLPALQQECNAAEINTPLRFAHFVAQIAHESNELRARVENLNYSAKGLRSVFGRYFTTDEMAAQCERKPESIANIVYANRLGNGATETGDGWKYRGRGLIQLTGRDNYRACGSAIGQDLVTNPDLISQNPAVSVAAAIWFWKKNGLSALADQDDINGITRRINGGLNGLADRKDYLAKAKRAFG  
  
>**gb|ADN00571.1| EF hand domain protein [Dickeya dadantii 3937]**MRHEPDGWWLASSNRQWHGGIHISRHSAPESVLTSINADKAVPLQCIASGNVVAWRINKNYCTAPYDKYQLRYSSTFLLVRSEHKPNPDDQSTWLTFYTLYMHLAPVSAYPALMNCYRVKPNVNSLPTNEYNGREISGQKLPKAGNITLKENDLLVVSKQETFKVERETSNDVFGLAQRLKDGKVSEEKFWVSLQDKFVEQTAPRYHRMPEWMTKAVEQGKYDTVVIPEETFAINAGDAIGFLAEDNAPDKSDSNRVEVDFYSHIEVISVDTNMPGFLSNPKGIKTGRAFVKIKEGKPLYQRSGEGAETTFTPTNDMTKGMNAGRILPRDKTNQIEAQGTTWFQITADSWIKCEDVDELSQHDLSKLGFTALEEASTDDFGSLLKENFLKGIFDWVSQSIRGDTEFECQQGSETYKKLVKVIDQNNDGNLSQYELAAFERRIFEGLHSGENNAPELVRRLIVKHDSEWFGDSKHKHWQSFLNNDSYPKMMPYLKKWRDDMAWMSEVPEFKSGKPVWHFHPMEFLDAISSTNGPITINMILAANLGMNKNQCDIVLPYMNKYAIKYKINDDIEIAHLLSQIGHESQFKPSEEGLSYSAKRMREFFGCKEGKYDDTRDECVIGRLREKLWTHETYYARNPVNLGNYVYAKRLGNDNEDSGDGYKYRGRGMIQLTGKDNYHKFTTQHNANNPDDIRDFVKNPDLLTEIEYAVESAFFFWCNKKDKNGKSLRDIAKTGSVLDVTLVVNGGKNGYNDRDERYSRVSKIIKEGK

GH 23

>**gb|ACS84375.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech703]**MFKVGYWRYIVAGVCLVGASCQVFADSLDEQRQRYQQIKLAWDSNQLDVVSQLMPTLRDYPLYPYLEYRALTQDVSLLSTVQVKQFIATHPTLPAVRTLNNNFINELARRQDWSGLLSFSPEQPKPVAARCNYLYARLMVNQPQGIWDQTRDIWLTGRSLPPSCDKLFTAWQQSGGMTSMMVLERMRLAMGEGNSGLVSHLARQLPPDYKTITDALLRLQNTSTKTVERFARSVGPTDFTRKALLAAFSRIARQDPDSARSLLPQLVRLQRFGSQDRQTMDEDVAWRFMGTDVSDEQARWRDVVIAKSKSAPLIERRVRLALGQDDHQGLSQWLTRLPAEVLQKDEWRYWRAVLLIEQGQREDGENQLRDLMKQRGFYPMAAAQRLNLNYPLTTVISARPDRSIGQLPEIARIRELMYWRLESLARSEWAGLVASRDRPQQEALARFAFEQRWYDLSVQATIVAKLWDNLEERFPLAWNDEFRQATQGKGISQSYAMAIARQESAWNPQARSSVGAAGLMQLMPATAQHTAQMFNVTSYSDSSQLLDPQMNIQLGSSYLEYVYQSFGQNRILASAAYNAGPSRVSTWLKNSEGRIDAVAFVESIPFSETRGYVKNVLAYDVFYRNLLSRPTQLMTDSEWRRRY  
  
>**gb|ACS86549.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech703]**MKRLTINYFFIGVIALLLTLALWPNIPWRSNQEFQLRQILSRGELRISTIASPLTYTPNNGSPTGLDYELAKRFADYLGVKLVVSVRQNVDELFNDLDNGDADLLCAGLIYNHERLNRFRTGPAYYSVSQQLVYRLGNPRPATLDKLQGRLTLLSGSAHIATLRALKSARYPQLSWEAAADISEQDLLKQVADGKLDYTIADSVTIGLMQRIHPQLAVAFDLSDEEPVTWYLRRTHDDSLSAALLDFFSQAMEDGTLARLEEKYLGHVGNFDYVDTTTFLNAIDSTLPGLRPLFEKYAREIDWKLLAAISYQESHWNPLATSPTGVRGLMMLTRNTADSLDVADRLNPEESIRGGAQYLSRMMQLIPASIPADERIWFALAAYNMGYAHMMDARKLTETQKANPDSWAEVKTRLPLLSQKRYYAQTANGYARGQEAYNYVENIRRYMVSLVGYLSEKESKEQQQQLLARAYPVVPPEQIPPTKPAP  
  
>**gb|ACS86619.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech703]**MKTKATLIASVLLTGCQVSPYDTSQPRQHAQSLSSAGQSEARMYTNGRETDARWLDDNSLAQRDLWNFIGDELKMEVPDNARIREQKARYLKNKSYLHDVTLRAEPYMYWIVEQIKQRKMPMELVLLPIVESAFDPNARSSANAVGLWQIVPHTGRNYGLKQNQWYDGRRDVVASTTVALDMMQRLNRMFDGDWLLTVAAYNAGEGRIMQAVKASKAKGRPVNYWALALPYETSTYVPKMLALSEILKHSKKYGVELPKPNENRALARVELGQQMELTQAAELAGLSVSKLKSYNTGYKRDMTAPNGPHYIMVPKSHVAQLKDSLADGDIAVAVQPVKMAQASLSTTYKVRSGDTLSSIAKRMKVSTQDLQKWNRLKGNSLKIGQNLQIAQVSASSATVKLSSSKQSSIVYRVQKGDSLASIAKRHGVNTTDVMRWNSVINKNANIQPGDRLTLFVTDKQSPES  
  
>**gb|ACS86802.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech703]**MKKLFVLLLVAPLLISCSGKKGNEYNEEFVKDTNAFDILMGQFANNIENIWGLNEVLIAGPKDYVKYSDQYLTRSHVNFDAGTITVETISATNYQASLRQAIITTLLMGDDASNTDLYSDANDIQISREPLLYGQVLDNTGQPIRWEGRAGSYADYLLQTRLQQRTSGMKVIWSVTIQLVPNHLDKRAHKFLPIVRKASERYGIDIPLILAIMQTESSFNPYAVSRSDALGLMQVVQHSAGRDVFKMKGKWGQPSRNYLFDPENNIDTGTAYLAMLKNVYLAGIQNPTSQRYAMITAYNGGAGSVLRVFSSDKENAVSIINRMSPGDVYQTLTTRHPSSESRNYLYKVNNAQKNYRVYNR  
  
>**gb|ACT05337.1| putative signal peptide [Dickeya zeae Ech1591]**MAASALTSMRRRWILLVNILLSSLAQGQEIPPPAYQLAAQRAGIPSVVLYVVALQESGVRRAERIVPWPWSLNVDGQSCRYASQVQACAGIHQALRDVPPTRIDVGLGQINLGWQKHRYRQPCDLLNPYNNLAIAAQILKEQYIPGEDWLLAIGRYHRPSGGTPAARYRHGVSQHLQRVLGPQQAFTNTNSKETSP  
  
>**gb|ACT05407.1| Lytic transglycosylase catalytic [Dickeya zeae Ech1591]**MFKIGYWRYVAAVLCLVGASCQVLADSLDEQRQRYQQIKSAWDNNQMDVVSQLMPTLRDYPLYPYLEYRALTQDLSTLSAAQVRQFIAAHPTLPAVRTLNNSFINELARRQDWNGLLAFSPNQPKPVASLCNYLYAKVMVGQSQGVWEQTRDIWLTGRSLPPTCDKLFSNWQQQGGQTSIMVLERMRLAMDAGSAGLVNHLARQLPAEYRTITDALLKLQSNPKTIERFARSVGPTDFTRRAVLSAFGRIARQDPDEARALLPQLVRLQKMRPQERQSMEEDVVWRMMGSDVTDEQARWRDAVILRSTSAPLLERRVRMALGQGDKAGLAQWIARLPADVQQKDEWRYWRASLLLDQGQQQEGENQLRELMKIRGFYPMAAAQKLNVNYPLTVVIAAKPERTIGQLPEVARVRELMFWGLESLARSEWSGLVASRERPQQEALARFAFEQRWYDLSVQATIVAKLWDNLEERFPLAWNDDFRQATQGKGISQSYAMAIARQESAWNPQARSTVGASGLMQLMPATAQHTAEMFNIASYTNSNQLLDPQMNIQIGTSYLDYVYNAFGQNRILASAAYNAGPSRVSSWLKDSNGQIDAIAFVESIPFSETRGYVKNVLAYDVFYRSLMQQRQTALLMDNEWRRRY  
  
>**gb|ACT05879.1| Lytic transglycosylase catalytic [Dickeya zeae Ech1591]**MKTKAIFIASVVLTGCQVPPNDTSQPRQHGQSLSSAGQSEAGKYTDGRETGARWLDDDSLAQQDLWNFIGDELKMEVPENSRIREQKQRYLKNKSYLHDVTLRAEPYMYWIVGQIKERKMPMELVLLPIVESAFDPNARSSSNAVGLWQIVPGTGRNYGLKHTQWYDGRRDVVASTTAALDMMQRLNRMFDGDWLLTVAAYNAGEGRIMQAVKANKAKGRPTNYWALALPYETSTYVPKMLALSDILKHSRKYGVELPKPNENRALARVDLGQQMELTQAAELAGLSVTKLKSYNSGYTRDVTAPNGPHYIMVPKSHVGQLKDSLADGDITAVQPAKATQPMAITRTVGYKVRTGDTLSSIAKRMNIRTQDLQNWNHLKGSALKVGQTLQVAKVTAPVTAGTIASNKSNSITYQVRKGDSLASIAKRHGVNIADVMRWNTVIKDANLQPGDRLTLYVTKKQSPDS  
  
>**gb|ACT05953.1| Lytic transglycosylase catalytic [Dickeya zeae Ech1591]**MKRLTINYVFIGVIALLLTLALWPNIPWRSHQDVQLRQILSRGELRISTVTSPLTYTLSNGSPSGLDYELAKRFADYLGVRLVVSVRQNVDDLFSDLDNDNADLLAAGLIYNQERLNRFQAGPSYYSVSQQLVYRMGSARPASLDKLQGKLTVLSGSAHAATLRDLKTEKYPQLSWEVATDVSELDLLKQVADGKLDYTIADSINIGLMQRIHPQLAVSFDLSDEEPVTWYMRQNRDDSLSAALLDFFSQVMEDGTLARLEEKYLGHVGEFDYVDTTTFLSAIDNTLPGLRPLFEKHAKEIDWKLLAAISYQESHWNPLATSPTGVRGLMMLTRNTAESLDVVNRLNPEESIRGGARYLSQMMQQVPATIPADERIWFALAAYNMGYAHMMDARKLTEKQQGNPDSWADVKIRLPMLSQKRYYSQTANGYARGQEAYNYVENIRRYMVSLVGYLSEKESRALQQQLAASAYPAVPPEQLTATQPH  
  
>**gb|ACT06347.1| Lytic transglycosylase catalytic [Dickeya zeae Ech1591]**MLSPTAFLAAAMQCAASIHPSTAFDVAKVESGFNPYAIAEIVPKQERMPGSAGVISHQPTRDETAVSIINRIEAKGRRYSVGLMQITSTHFQHYGVTARALLDPCTNLSVFERILTDCYQRGGTLQRALSCYYAGNFTAGQQPESTFNQTSYLQRIGYAVPSTQEDRTRRTNSQATSAMHYPATVLRGELAAPSTPVSTTLRYPNAVLRGDVSPL  
  
>**gb|ACT08030.1| Lytic transglycosylase catalytic [Dickeya zeae Ech1591]**MKKLFVLLLVAPLLISCSSKKGGENNEAFIKDTNAFDILMGQFANNIENIWGLNEVLIAGPKDYVKYSDQYMTRSHVNFDAGTITIETISSTNYQASLRQAIITTLLMGDNASNTDLYSDANDIQISREPLLYGQVLDNAGQPIRWEGRAGNFADYLLQNKLQRRTSGMRVIWSVTIQLVPNHLDKRAHKYLPMVRQASERYGIDASLILAIMQTESSFNPYAVSRSDALGLMQVVQHSAGRDVFKMKGKWGQPSRSYLFDPENNIDTGTAYLSMLKNVYLSGIQDPTSQRYAVITAYNGGAGSVLRVFSSDKDTAFSLINNMSPGEVYQTLTTRHPSAESRHYLYKVNTAQKNYRGYSR  
  
>**gb|ACZ75771.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech586]**MKKLLALLLVAPLLISCSSKKGGENNEAFIKDTNAFDILMGQFANNIENIWGLNEVLIAGPKDYVKYSDQYMTRSHVNFDAGTITIETISSTNYLASLRQAIITTLLMGDNASNTDLYSDANDIQISREPLLYGQVLDNTGQPIRWEGRAGNFADYLLQNKLQRRTSGMKVIWSVTIQLVPNHLDKRAHKYLPMVRQASERYGIDASLILAIMQTESSFNPYAVSRSDALGLMQVVQHSAGRDVFKMRGKWGQPSRSYLFDPENNIDTGTAYLAMLKNVYLSGIQDPTSQRYAMITAYNGGAGSVLRVFSSDKDTAFGIINTMSPSQVYQTLTTRHPSAESRHYLYKVNTAQKNYRGYSR  
  
>**gb|ACZ76329.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech586]**MLSPTAFLAAAMQCAASIHPSTALDVAKVESGFNPYAIAEIVPKKERTPGSAGVISHQPTRDEMAVNIINRIEARGRRYSVGLMQITSTHFRHYGVTARALLDPCTNLSVFERILTDCYQRGGTLQRALSCYYAGNFTAGQQPESAFSQTSYLQRIGYAVPSTQEDRTRSRASQATSAMHYPATVLRGELADTTTPVSTTLRYPNAVLRGDVSPL  
  
>**gb|ACZ77506.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech586]**MLSTTAFLAAAMQCAASIHPSTALDVARVESGFNPYAIAEIIPKATRSLGDNNVISHQPASREKAEHIIRRLMAQGRRYSVGLMQITSTNFHHYGVTASDLLDPCTNLSVFERILSDCYQRGGSLKRALSCYYSGNFRTGQQPEAAFSGTSYVQRIGYVSASPRYAVPGTRADKSTTPTPLEAIPVDKPSPPRLIWPGTVVRGVPAKLRQGKTAIAQTSAPSVRRSLSQSPREEE  
  
>**gb|ACZ77928.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech586]**MKRLTINYVFIGVIALLLTLALWPNIPWRSHQDVQLRQILSRGELRISTVTSPLTYTLSNGSPTGLDYELAKRFADYLGVRLVVSVRQNVDDLFSDLDNDNADLLAAGLIYNQERLNRFQAGPSYYSVSQQLVYRMGSARPTSLDKMQGKLTVLSGSAHAATLRDLKAEKYPQLSWEVATDVSELDLLKQVADGKLDYTIADSINIGLMQRIHPQLAVSFDLSDEEPVTWYMRQNRDDSLSAALLDFFSQVMEDGTLARLEEKYLGHVGEFDYVDTTTFLSAIDNTLPGLRPLFEKYAREIDWKLLAAISYQESHWNPLATSPTGVRGLMMLTRNTAESLDVVNRLNPEESIRGGARYLSQMMQQVPATIPVDERIWFALAAYNMGYAHMMDARKLTEKQQGNPDSWADVKIRLPMLSQKRYYSQTANGYARGQEAYDYVENIRRYMVSLVGYLSEKESRALQQQLAGSAYPAVPPEQLTATRSR  
  
>**gb|ACZ77995.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech586]**MKTKAIFIASVVLTGCQVPPNDTSQPRQHAQSLSSAGQGEAGKYTDGRETGTRWLDDESIAQQDLWNFIGDELKMEVPENTRIREQKQRYLKNKSYLHDVTLRAEPYMYWIVGQIKERKMPMELVLLPIVESAFDPNARSSSNAVGLWQIVPGTGRNYGLKHTQWYAGRRDVVASTTAALDMMQRLNRMFDGDWLLTVAAYNAGEGRIMQAVKANKAKGRPTNYWALALPYETSTYVPKMLALSDILKHSRKYGVELPKPNENRALARVDLGQQMELTQAAELAGLSVTKLKSYNTGYTRDVTAPNGPHYIMVPKSHVGQLKGSLADGDIAAIQPTKTAQPTVATRSAGYKVRSGDTLSSIAKRMNVRTQDLQNWNHLKGSALKVGQTLQVAKATIPVTAGVVASNKSNSIIYQVRKGDSLASIAKRHGVNIADVMRWNTVIKDANLQPGDRLTLYVTRRQSPDS  
  
>**gb|ACZ78441.1| Lytic transglycosylase catalytic [Dickeya dadantii Ech586]**MFKIGYWRSVAAVLCLVGVSYQVLADSLDEQRQRYQQVKSAWDNNQMDIVSQLMPTLRDYPLYPYLEYRSLTQDLSTVSTVQVRQFMTSHPTLPAVRTLNNSFINELARRQDWSGLLAFSPQQPKPVASLCNYLYAKVMTGQPQGVWEQTQEIWLTGRSLPPTCDKLFSAWQQQGGLTSLMVLERMRLAMDAGSAGLVNHLARQLPADYKTITDALLKLQSNTKSIERFARSVGPTDFTRRVVVSAFSRIARQDPNEALALLPQLVRLQKMRPQDRQSMEDDIAWRLMSSDATDEQARWRDAVILRSASAPLLERRVRMALGQGDRVGLAQWMARLPADVQQKDEWRYWRAVLLLEQGQKQEGENQLRELMKIRGFYPMAAAQKLNVNYPLTIIIAAKPERSIGQSPEVARVRELMFWGLESLARSEWAGLVASRERPQQEALARFALEQHWYDLSVQATIVAKLWDNLEERFPLAWSDDFRQAIQGKGISQSYAMAIARQESAWNPQARSAVGAAGLMQLMPATAQHTAEMFNIASYSNSSQLLDPQMNIQLGTSYLDYVYQSFGQNRILASAAYNAGPSRVNNWLKDTNGRIDAIAFVESIPFSETRGYVKNVLAYDVFYRSLMQQRQTALLMDNEWQRRY  
  
>**gb|ADM97232.1| membrane-bound lytic murein transglycosylase C [Dickeya dadantii 3937]**MKKLFALLLVAPLLISCSSKKGGENNEAFIKDTNAFDILMGQFANNIENIWGLNEVLIAGPKDYVKYSDQYMTRSHVNFDAGTITIETISSTNYEASLRQAIITTLLMGDNASNTDLYSDANDIQISREPLLYGQVLDNTGQPIRWEGRAGNFADYLIQNKLQRRTAGMRVIWSVTIQLVPNHLDQRAHKYLPMVRQASERYGIDASLILAIMQTESSFNPYAVSRSDALGLMQVVQHSAGRDVFKMKGKWGQPSRSYLFDPENNIDTGTAYLSMLKNVYLSGIQDPTSQRYAVITAYNGGAGSVLRVFSSDKDTAFGRINNMSPGEVYQTLTTRHPSAESRHYLYKVNTAQKNYRGYSR  
  
>**gb|ADM99153.1| VirB1 [Dickeya dadantii 3937]**MAICNPNDVTEAIMLSPTALLVAAMQCAASIHPSTAFDVAKVESGFNPYAIAEIVPKQERTPGSAGVISHQPTRHETAVNIINRIEAKGRRYSVGLMQITSTHFRHYGVTALALLDPCTNLSVFERILTDCYQRGGTLQRALSCYYAGNFTAGQQPESAFNQTSYLQRIGYAVPSTREDRARSSTSQATSTIHYPSTVLRGELAAPSTPVSTTLHYPNAVLRGDVSPQ  
  
>**gb|ADM99560.1| lytic transglycosylase [Dickeya dadantii 3937]**MKRLTINYVFIGVIALLLTLALWPNIPWRSHQDVQLRQILSRGELRISTVTSPLTYTLSNGSPTGLDYELAKRFADYLGVRLVVSVRQNVDDLFGDLDNDNADLLAAGLIYNRERLSRFRAGPSYYSVSQQLVYRMGTARPSALDKLQGKLAVLSGSAHAATLRDFKAGKYPQLSWEVATDLSELDLLKQVAEGKLDYTIADSINIGLMQRIHPQLAVSFDLSDEEPVTWYMRQNHDDSLSAALLDFFSQMMEDGTLARLEEKYLGHVGEFDYVDTTTFLSAIDNTLPGLRSLFEKYAREIDWKLLAAISYQESHWNPLATSPTGVRGLMMLTRNTADSLDVADRLNPEESIRGGARYLNQMMQQVPATIPTDERIWFALAAYNMGYAHMMDARKLTEKQKGNPDSWADVKVRLPMLSQKRYYAQTANGYARGQEAYNYVENIRRYMVSLVGYLSEKESRALQQQLAASAYPAVPPEQLTANPSR  
  
>**gb|ADM99642.1| membrane-bound lytic murein transglycosylase D [Dickeya dadantii 3937]**MKTKAIFIASVVLTGCQVPPNDTSQPRQHAQSLSSAGQSEAGKYTDSRETGTRWLDDESIAQRDLWNFIGDELKMEVPENIRIREQKQRYLKNKSYLHDVTLRAEPYMYWIVGQIKERKMPMELVLLPIVESAFDPNARSSSNAVGLWQIVPGTGRNYGLKHTQWYDGRRDVVASTTAALDMMQRLNRMFDGDWLLTVAAYNAGEGRIMQAVKANKAKGRPTNYWALALPYETSTYVPKMLALSDILKHSKKYGVELPKPNENRALARVDLGQQMELTQAAELAGLSVTKLKSYNTGYTRDVTAPNGPHYIMVPKSHVGQLKDSLADGDIAAIQPAKAVQPVVSTRSVGYKVRSGDTLSSIAKRMNVRTQDLQSWNRLKGSALKVGQTLQVAKATVPVTAGIAANSNKSNSIVYQVRKGDSLASIAKRHGVNIADVMRWNTVIKDANLQPGDRLTLYVTNRQSPDS  
  
>**gb|ADN00131.1| lytic murein transglycosylase, soluble [Dickeya dadantii 3937]**MYGAMVVSVDGGVRRVMAETITSEVRAVMFKLGYWRYVAAALCLIGVSCQALADSLDEQRQRYQQIKSAWDNNQMDVVSQLMPTLRDYPLYPYLEYRALTQDLSTVSEAQVKQFMASHPTLPAVHTLNNSFINELARRQDWNGLLVFSPEQPKPVASLCNYLYAKVMVGQQQGVWEQTRDIWLTGRSLPPTCDKLFSAWQQQGGLTSLMVLERMRLAIDAGSAGLVNHLSRQLPADYKTITDALLRLQSNPKTIERFARSVGPTDFTRRAVLSAFSRIARQEPDEARALLPQLIRLQKIRPQERQSMEDDIAWRLMGSDTTDEQARWRDAVILRSASAPLLERRVRMALGQGDRPGLKQWIARLPADVQQKDEWRYWRAILLIEQGQKQEGETQLRELMSIRGFYPMAAAQKLNVNYPLTIMIAAKPERSIGQLPEVARVRELMFWGLESLARSEWAGLVASRDRPQQEALARFAFEQHWYDLSVQATIVAKLWDNLEERFPLAWNDDFRRATQGKGISQSYAMAIARQESAWNPQARSAVGAAGLMQLMPATAQHTAEMFNIASYSNSSQLLDPQMNIQLGTSYLDYVYQSFGQNRILASAAYNAGPSRVTNWLKDSDGRIDAIAFVESIPFSETRGYVKNVLAYDVFYRSLMQQRPTTLLMDNEWQRRY

GH24

>**gb|ACS87579.1| glycoside hydrolase family 24 [Dickeya dadantii Ech703]**MKTAIKRCSIALIVALGVTLSPGALRTSQEAQQKTASWEDCRASPYYCPAGVLTVGIGSTGSVQNRPYGNDEIARRWVNDMQRAENCVNGNFNGAAMPQSAFEAMTDTAFNLGCSGLMWFTNRQGSKQRTTIWKHAQAQEWPAMCERLTDFVNSGGQRSAGLVNRRSDFKAWCLRDLAGVP  
  
>**gb|ACT08849.1| Peptidoglycan-binding domain 1 protein [Dickeya zeae Ech1591]**MNTIESSVGLRGSNRRNDVTLVQEILKKNGFPHLRVDGICGRNTKRAIIEYQKKFHLLPDGMINPGGKTIESLTSTSNTESLPTPHGSTATNPNGERKRASLMSPSFQCINLMKQYEVLKTKPYDDQTGRDTEYWKVGATIGYGHLIRESEFEKYKQGIDFSDADVLFNQDIRRFIAAVRDFVKVDVTQNEFDALVMFSFNIGTKDSQHQRGLYYSSVLKIINGESSENIDNAWMRYTISQGHQMRGLINRRRSELNVYHKGIYIKL  
  
>**gb|ADN00213.1| Phage lysozyme, putative [Dickeya dadantii 3937]**MNAIESSVGLGGINRKNDVTIVQQLLKNSGFPYLRVDGICGRNTKRAIIAYQKYFHFSPYGIIEPGGKTIENLTSTSHTDSLPNPHGATGINPRGERKRASLMSPSSQCIYLMKQYEKLKTKPYDDQTGRETTFWKVGATIGYGHLISENEFERYKQGIALSEADTLFSQDISRFILAVRNFVKVDITQNEFDALVMLSFNIGIKDRQRHRGLYYSTVLKIINGESSENIDNAWMRYTISQGHQMQGLVNRRRSELNVYHKGIYIKL

GH26

>**gb|ADN00246.1| Mannan endo-1,4-beta-mannosidase precursor [Dickeya dadantii 3937]**MRPRHFPFTNRIYCMRRTYQLFRRISLAACLMTATISQVGAHTVSPVTANAMATTRAIYNWMAHLPNRSDSRLLSGAFGGYANIGGDDAFSLTEAENIAARTGQYPAIYACDYARGWDRTSAGNEADLVDYSCNSTLIDYWKKGGLVQISHHLPNPVFAGNDPGTGEGGLKKAVSNEQLAAVLQSGTPERTRWLAILDKVAAGLAQLQQQGVVVLYRPLHEMNGEWFWWGATGYNTHDTTRMNLYIRLYRDIYTYFTQTKGLNNLLWVYAPDANRQDKTGFYPGDAYVDIAGLDMYLDNPANLSGYDEMLRLNKPFALTEVGPSTTNQQFDYARLVSIIKSNFPKTVYFLPWNNVWGPVKNLNASAAYNDSSVVNRGGIWNGSQLTPIVEAN

GH28

>**gb|ACS84017.1| glycoside hydrolase family 28 [Dickeya dadantii Ech703]**MSTPSLPRNTFCLATLIPLLLLAPPTLAASRQAPQKLQVPTLAYDDHSVVLVWDAPEDTAAITDYQVYQNGRLVGLASQIADKYSPAQPYITAFYRADTRSFHHKIVLQNARIEGLKADTEYRFTVRTVYADGTVSADSNAVVAKTAAPPQIINITHYGAKGDGTTLNTTAIQNAINACNTGCRIDIPAGVFKTGALWLKSDMTLNLMEGATLLGSENAADYPAAYQIYSYSSQMRPASLLNAIDKHHSTVGTFQNIRIIGKGVIDGNGWKRDTATEAKDETGAVIPHYVKSNNSKVGKDGILASSQVAAAIADGLDAKTAYGQARSSLITLRGVKNVYLADITIRNPAFHGMMFLENQHVVVNGVTHHTYDANNGDGIEFGNSQDTMVFNSVFDTGDDCINFAAGMGKSAEHQEATQTSWLFNNAFIHGHGAVVLGSHTGAGIADVLAENNVMNQTDIGLRAKSATSIGGGAHNITFRNNAMKNLAKQAVIVTLSYSDANSTTDYTPAATSARFYNFMVKNVTVQNSTGKSPSIDITGDSKNGIWHSQLNFSNMKLDNVMPVAISDLADSQFTHLTFTHLQSGNTPWNFGAVKNVSVDGKTVTP  
  
>**gb|ACS84778.1| glycoside hydrolase family 28 [Dickeya dadantii Ech703]**MRISLDEVTINRDGSVLVTALLQRMIDKIHDAGGGTLIVTPGIYRTGTLVLPSDFCLQLDAGATLLASADYGDYAAAQTLTTAELSNSALLYARGQQNITLCGAGKIDGNADAFFSSQADEQGYRLPHSHRPRMVVFEDCQAIRLQDITLTQSPMWTVHLVSCAQVFIARICVDNDLTMANTDALDIDSCQQVHISDCHFSAADDGICLKTTRKTPQIQRPLRNVTVTNCTLRSKSCAIKIGTETFADIENVTISNCSIYESNRGIGIISRDGGRFSRLIFSNITYSCAYAHACHWGKSDPIFISVRFRDPEIRPGNISDVAFNNIVGVTEGAINLHSEIQGAIENIAFNAVSIRQLPSDNHAQGEYDIRPPCNPERPTGMGLDNAYRVNPQTGRAFGVEKYPGGLPAIFAKGVASLHLNDIQIIRPDHLPPGWNPQAIVMEDAITAP  
  
>**gb|ACT05045.1| glycoside hydrolase family 28 [Dickeya zeae Ech1591]**MTTISRRHALASLVSVCLFGTPALAATSTTQAPQKLQIPTLSYDDHSVMLVWDTPEDTSNITDYQIYQNGQLIGLASQNNDKNSPAKPYISAFYKSDAANFHHRIILQNAKVDGLKAGTDYQFTVRTVYADGTTSADSNTVTATTTAVPKVINITQYGAKGDGTTLNTSAIQKAIDACPTGCRIDVPAGVFKTGALWLKSDMTLNLLQGATLLGSDNAADYPDAYKIYSYVSQVRPASLLNAIDKNSSAVGTFKNIRIVGKGIIDGNGWKRSADVKDELGNTLPQYVKSDNSKVSKDGILAKNQVAAAVATGMDTKTAYSQRRSSLVTLRGVQNAYIADVTIRNPANHGIMFLESENVVENGVIHQTFNANNGDGVEFGNSQNIMVFNSVFDTGDDSINFAAGMGQDAQKQEPSQNAWLFNNFFRHGHGAVVLGSHTGAGIVDVLAENNVITQNDVGLRAKSAPAIGGGAHGIVFRNSAMKNLAKQAVIVTLSYADNNGTIDYTPAKVPARFYNFTVKNVTVQDSTGSNPAIEITGDSSKDIWHSQFIFSNMKLSGVSPTSISDLSDSQFNNLTFSNLRSGSSPWKFGTVKNVTVDGKTVTP  
  
>**gb|ACT05046.1| glycoside hydrolase family 28 [Dickeya zeae Ech1591]**MEIIILPRRFVLASMAALCLIGTPMLAAAFPVPQKLQIPTLSYDDHSVVLVWDAPENTEVIADYQIYQNDQLIGLASKNNDINSPAKPYINAFYKNDTGNFHHRVIMQNAKVSGLKASTEYAFTVRAVYADGSISANSNTVTVTTTAAPPVINITQYGAKGDGTTLNTAAIQKAIDACQIGCRVDIPPGVFKIGALWLKSDMTLNLLQGATLLGSDKPSDYPDTYSNNAYSSLSRPASLINAIDKNHASGGKLKNIRITGKGIIDGNGWKRSANVNDELGNGLPQYVKSDSDRVSLDGILAKNQVEAAVASGVNIKTAYNQRRSSLISLSNVQNVYIADVTIRNPANHGVMILENSNVVENGVTHQTFNTNNGDGVEFGSSQNIMVFNSVFDTGDDCINFASGMGQQAQSQAPVKNVWLFNNYFRHGHGAVVLGSHTGAGIIGIQAENSVMSQTDIGLRAKSAPDIGGGAHDIIFRNNAMKNLARQAVMVTLNYVDNTGTINYTPARIPARFYNFTVKNVTVQDSTGKNPSIEIVGDSSKNIWHSQLNFSDMKLSGVMPTSISDLSDSQFNNLVFSNLRSGTSPWNFGTVRNVTVNGQTVPAAF  
  
>**gb|ACT05703.1| glycoside hydrolase family 28 [Dickeya zeae Ech1591]**MRLFIRAYHPAADGITPDTALFQQAIDELAAQGGGTLVVEPGRYLLGGLHLPSNFCLQLDAGAELIASADYDDFAQNTTVSVAELSDRAFLYARQQRNITLSGQGKIIGNADAYFSAQPDEQGYRLPARHRPRILVLEDCEQVKIQGVTIENAPMWTVHLVSCRQVNVERLTVDNDMTMANTDALNLDSCQDVTVRDCHLSAADDALCIKTTAKPPAMQYKAQRMTVSHCRLRSRSCALKIGTETFADIEDLTVSHCAIYDSNRGIGLISRDGGAFRRICFSDITFECVAAPPCHWGKADPIFISVRYRDPAIEPGVVEDVRFVRLSGVSEGAINLHSTPAGYIRHIHFDDITLEQRPSHSPEQGLYDVRPPCNPARPTGMGLDNAYLVNPDTGRAYGVETYPTGLPALFARGVNDLTWHKMTLQRPSPLPVGWSPDAIVELAE  
  
>**gb|ACT07852.1| glycoside hydrolase family 28 [Dickeya zeae Ech1591]**MKHCFTYGVIMHKGIAFSLLASCALAGMSAQSAEKVAFPDRVCDVTRYGAEGHRLQIALNTSSFQKAIDECAAAGGGTVLVPAGNYLVEPLFLKSNVRLHLEKHATLVASTGESAYRATDSTRYAQAENGWLPFISIADAQNVAITGEGTIDGQGAVWWERWREAIRATGKKGGTDRPRLIYITRSSQVLVDGVTLTNSPSFHVVMRYARDVTVNGTSIIAPWHAPNTDAIDPIDSQNIRITNNVIDCNDDHIAIKAEKPDSRFPDGVVDNVYIANNVLKQGRGISIGSETSGGVNNVLVENNRFEGSMYGIRIKSLRGKGGEVKNVTYRHTRMVNVEVPLVFSGYYQAAPIVQAEVDKLLQAGGFTLGEQIYPPDTEPAQPFDKVKTPHFSNITIVDLESTGRSKAAGYIIGVPEAPLSGFHFEQVRIEAEKGLRVRNAELVTQGLTLNAKQGEALLLDKGANVTR  
  
>**gb|ACZ78152.1| glycoside hydrolase family 28 [Dickeya dadantii Ech586]**MTLSFRTYQPAADGITPDTARFQQALNDLDIQGGGTLVVESGRYLLGGLRIPSNCCLQLDEGAELIASACYDDFAHTTTLSVAELSDRAFLYARQQRNITLCGKGKITGSADAYFSAQPDEQGYRLPAQHRPRIVVLEDCEQITIQDITIEHAPMWTIHLVSCRQVNVERLTVDNDMTMANTDALNLDSCQDVIVHDCHLSAADDALCIKTTAKPPAMQYKAQRMSVSHCRLRSRSCALKIGTETFADIEDLNVSHCTLYDSNRGIGLISRDGGAFRRICFSDITLECVTAPPCHWGKADPIFISVRYRDPTIEPGVIEQIRFVRITGVSEGAINLHSTPAGYVRDIHFEDITLTQQSVDSTEQGLYDVRPPCNPARPTGMGLDNAYLVNPDTGRAYGVEAYPGGMPALFARGINGLTLHNMTLQRPSPLPVGWNHNAIIELAE  
  
>**gb|ACZ78734.1| glycoside hydrolase family 28 [Dickeya dadantii Ech586]**MKTFTFSRRHTLASMVSACLLSLPVLAIASPTQAPQKLQVPTLSNDDHSVVLVWDAPEDTSNITDYQIYQNGQLIGLASQNNDKNSPAKPYISTFYKNDTASFHHRIVVQNAKIDGLKANTDYQFTVRAVYADGTTSTDSNAVTATTSATPTVINITQYGAKGDGTTLNTSAIQKAIDACPTGCRIDVPAGIFKTGALWLKSNMTLNLLQGATLLGSDNAADYPDAYKIYSYSSQMRPASLINAIDKTSSAVGTFTNIRIVGKGVIDGNGWKRSADAKDELGNSLPQYVKSDNSKVSKDGILAKNQVAAATATGMDTKTAYSQRRSSLITLRGVQNAYVADVTIRNPANHGVMFLESQNVVENGVTHQTFNANNGDGVEFGNSQNIMVFNSVFDTGDDSINFAAGMGQAAQKQEPSQNAWLFNNYFRHGHGAVVLGSHTGAGIVDVLAENNVISQSDIGLRAKSAPDIGGGAHGIIFRNSALKNLAKQAVIVTLSYADNNGTTDYTPATVPARFYDFTVKNITVQDSTGSSPSIEISGDSSKDIWHSQFTFSNMKLSGVSPTSISDLSDSQFNNLTFSNLRSGSSPWKFGTVKNVTVDGKTVTP  
  
>**gb|ADM97429.1| Exo-poly-alpha-D-galacturonosidase [Dickeya dadantii 3937]**MKRCFTYGVIMHKGVAFSLLASCALASVAAQAAEKVAFPDRVCNVTRYGAEGHRLQIALNTESFQKAIDECAAAGGGTVLVPAGNYLVEPLFLKSNVRLHLEKNATLVASTGENAYRATDSTRYAEAENGWLPFISIADAQNVAITGEGTIDGQGAVWWERWRAAIRATGKKGGTDRPRLIYVTRSNRVLIDGVTLTNSPSFHVVMRYAHDVTVNGTHIIAPWHAPNTDAIDPIDSQNIRITNNVIDCNDDHIAIKAEKPDSRFPNGVVDNIYIANNVLKQGRGISIGSETSGGVNNVLVENNRFEGSMYGIRIKSLRGKGGEVKNVTYRHTRMLDVEVPLVFSGYYQAAPIVQAEVDKLLQAGGFTLGEQIYPPDTEPAQPFDKVKTPHFSQVTIVDLESTGRSKAAGYIIGVPEAPLSGFHFEQVRIDAEKGLRVRNAELAAKGLTLNVKQGDALLLDKGANVTR  
  
>**gb|ADM99816.1| Polygalacturonase [Dickeya dadantii 3937]**MLEWLSFPYRNRIKTMRLSIRSYTPAADGVTPDTELFQRAIDDLTAQGGGTLVVEPGRYLLGGLRLPSNFCLQLDAGAELIASACYDDFAQTTTVSVAELSDRAFLYARRQRNITLCGKGKITGNADAYFSAEPDEQGYRLPAQHRPRILVLEDCEQVNLQDLTIEQAPMWTVHLVSCRQVNVERLTVDNDMTMANTDALNLDSCQDVTVHHCHLSAADDALCIKTTAKPPAMQYKAQRMTVSHCRLRSRSCALKIGTETFADIEDLTVSRCAIYDSNRGIGLMSRDGGAFRRICFSDITFECVAAPPCHWGKADPVFVSVRYRDPTIEPGVIEDVRFVRLSGVSEGAINLHSTPAGYIRDIHFDGITLEQRPSHSPEQGLYDVRPPCNPKRPTGMGLDNAYLVNPDTGRAYGVETYPTGLPALFARGVSGLTLHHMTLRRPSPLPAGWSHDAVIELTE  
  
>**gb|ADN00465.1| Exo-poly-alpha-D-galacturonosidase precursor [Dickeya dadantii 3937]**MKAIRLSQCHALALTATVCLFTSQALAMPTNEQTPPALEALTPSLDNHSVVLVWKAPEDTSDIIDYQIYQDNQFVGLASQNSNQHSPAQPYINMFYKNDTGNFQHRIVIQSAKIDGLQPSTDYHFTVRAVYTDSSVTADSNTVDITTTAVPQIIDITRYGAKGNGTTLNTSAIQKAIDACPSGCQVNVPAGVFKTGALWLKSNMTLNLSPGATLLGSENAADYPGGYTIGKSSTDMRPASLLNVTDKTSSKGGVFQNIRITGKGAIDGSGWKRSADGQDELGNKLPQYVKSDNANVNNDGILAKNQVAAARAKGIDLKTAYRQYRSSLITLRGANNVYIADITIRNPADHGIVFMKSQNVIENGVIHQTFDANNGDGVEFSNSQDITVLNSVFDTGDDCINFAAGLGQEGQKQSPTQNARLFNNYFRHGHGAIVMGSHTAATIANILAENNVMNKTDIGLRAKSSPDIGGGAHHVVFRNNAMANLAMQAVFVTLNYVDVNGSGVYTPADVPAHFYDFTVKNITVLNSADISPSIQIEGNSNKQVWNSNFNFCDMKLSGIMPASVSDLEDSEFNNIAFSDLRGGTSPWKFGAVKNVTLDGKIVSPNP  
  
>**gb|ADN00467.1| Exo-poly-alpha-D-galacturonosidase precursor [Dickeya dadantii 3937]**METITFSRRPALASIVAACLISTPALAATAQAPQKLQIPTLSYDDHSVALVWDAPEDTSNITDYQIYQNGQLIGLASQNNDKNSPAKPYISAFYKNDTGNFHRRVVIQNAKIDGLKANTDYQFTVRTVYADGSTSADSNAVTATTAATPQVINITQYGAKGDGTTLNTTAIQKAIDACQTGCRVDIPAGVFKTGALWLKSDMTLNLLQGATLLGSDNAADYPDAYKIYSYSSQVRPASLINAIDKTSSAVGTFKNIRIIGKGVIDGNGWKRSADAKDELGNSLPQYVKSDSSKVSKDGILAKNQVAAAVAKGMDTKTAYSQRRSSLVTLRGVKNVYIADVTIRNPANHGVMFLESQNVVENGVIHQTFDANNGDGVEFGNSQNIMVFNSVFDTGDDSINFAAGMGQDAQSQEPSQNAWLFNNYFRRGHGAVVMGSHTGAGIIDVLAENNVISQNDVGLRAKSAPAIGGGAHGIVFRNSAMKNLAKQAVIVTLSYSDSNGTIDYTPAKVPARFYDFTVKNVTVQDSTGSSPVIEITGDSGKGIWHSQFTFSNMKLSGVTPASISDLSDSQFNNLTFSKLRSGSSPWKFGTVKNVSVDGKIVTP

GH30

>**gb|ACS85921.1| Glucuronoarabinoxylan endo-1,4-beta-xylanase [Dickeya dadantii Ech703]**MNGKVNDWVRHCLRATVLVSATTIALSVHAATVSIDADVNYQTIQGFGGMNGVGWINDLTTDQINTAFGNDTGQIGLSIMRIRIDPDSNKWNKQVSSARQVSTLGAKIMATPWTPPAYMKSNNSLINGGRLLTEHYSGYTSHLLDFSNYMQNQGAPIYAISIQNEPDWKPDYESCEWSGDDFKNYLKSQGAKFGSLKVIVGESLNFNHNLTDPTLNDSDASQYVAIVGGHLYGTTPKSYPLAQNAGKQLWMTEHYVDSKQSANNWSSALDVATELNASMVANYNAYVWWYIRRSYGLLTEDGNVSKRGYVMAQYAKFVRPGFQRIQATENPQTNVHLTAYKNAEGKMVIVAVNTNDSDQLLTLNISHADVGKFAKYSTSETLNVGYGGSYQVDNSGKTNVWLNPLSVTTFVSQ  
  
>**gb|ACZ76867.1| Glucuronoarabinoxylan endo-1,4-beta-xylanase [Dickeya dadantii Ech586]**MNGNVSLWVRHCLHAALFVSATAGSFSVYADTVKIDANVNYQIIQGFGGMSGVGWINDLTTEQINTAYGSGVGQIGLSIMRVRIDPDSSKWNIQLPSARQAVSLGAKIMATPWSPPAYMKSNNSLINGGRLLPANYSAYTSHLLDFSKYMQTNGAPLYAISIQNEPDWKPDYESCEWSGDEFKSYLKSQGSKFGSLKVIVAESLGFNPALTDPVLKDSDASKYVSIIGGHLYGTTPKPYPLAQNAGKQLWMTEHYVDSKQSANNWTSAIEVGTELNASMVSNYSAYVWWYIRRSYGLLTEDGKVSKRGYVMSQYARFVRPGALRIQATENPQSNVHLTAYKNTDGKMVIVAVNTNDSDQMLSLNISNANVTKFEKYSTSASLNVEYGGSSQVDSSGKATVWLNPLSVTTFVSK  
  
>**gb|ADM98550.1| xylanase [Dickeya dadantii 3937]**MNGNVTCWVRHCLSAAIVVSVTAGAFSAYADTVKIDAKVNYQTIQGFGGMNGAGWINDLTTEQINTAFGNDAGQIGLSIMRIRIDPDSNKWNIQVPSARKAVSLGAKLMATPWTPPAYMKSNNSLINGGRLLPAHYSAYTSHLLDFSKYMQTNSAPIYAISIQNEPDWKPDYESCEWSGDEFKNYLKSQGSKFGSLKVIVAESLGFNPALTDPVLKDSDASKYVSIIGGHLYGTTPKPYPLAQNAGKQLWMTEHYVDSKQSANNWTSALDVGTELNASMVSNYSAYVWWYIRRSYGLLTEDGKVSKRGYVMSQYARFVRPGALRIQATENPQSNVHLTAYKNSDGKMVIVAVNTNDSDQMLSLNISNANVGKFEKYSTSEVLNVEYGGSYQVDDSGKATVWLNPLSVTTFVGK

GH31

>**gb|ACS85409.1| Glucan 1,3-alpha-glucosidase [Dickeya dadantii Ech703]**MKTLKNWEFHQQTADRIELCVEGKHIFQLYVLAPGLMRVLIKQHGMLRLNRTWSIAPEADVPWEGRRRDSAEGFPLPGYELDWQEETLWVTADRLRVAIHQPLWLEWQYQAEDGTWKTLAADRPTSAYQLNAHGDGVAHYQRRFAEERCYGLGEKAGDLNRSGRRFEFRNLDAMGYNAATTDPLYKHLPFTIVNHDGVSYGLFYDNLSSTWMDLGNEIDNYHQPYRRYQAEAGDLDYYFLFGPKIADVTKAFVRLTGKTCFGPKWSLGYSGSTMHYTDAPDAQQQLQQFIALCRQHEIPCDSFQLSSGYTSIGNKRYVFNWNYDKVPQPERMSQSFHDAGMKLAANIKPCLLQDHPRYAEVAERGMFVQDSESGQPERSSFWDDEGSHLDFTNPETVAWWQENVTRQLLEKGIDSTWNDNNEFEIWDGEARCHGFGEPITIKHIRPLMPLLMMRASMEAQQRFAPEQRPYLISRSGSAGMQRYVQTWSGDNRTSWQTLRYNTRMGVGMSLSGLYNVGHDVGGFAGNKPDAELFVRWVQNGVMHPRFTIHSWHDDGSVNEPWMYPEVTPMIRDAIRLRYRLLPYLYTLLWQASADDEPMLRPMFLDHEQDARTFDESDDFMLGQDLLVASVMEPGQRRRQVYLPDNHTGWYDFYCGDWYPGGQMVELDAPLDRLPLLARAGAMIPVSAREAFVDQAADDQRAFLVFPSQEGCHQGMLFEDDGETHGWREGQALWLRWEMRCDAQRIEVTFTPQGRFRPAWQSVDLRLPQGETRALYINGKPACRYELSL  
  
>**gb|ACT06496.1| Glucan 1,3-alpha-glucosidase [Dickeya zeae Ech1591]**MKTLKHWVLHHQAEDRVELLVDGAHRFMLYVLAPGLMRVLIKQDDALRLNRTWSIAPQQDVPWQGRVRESSDGFALPGYTLSWQGDALQISTAQLRVTVHQPLWLSWEYRDAHGQWQPLASDRSTGAYLLNRHGDGVAHYQRRAAQERCYGLGEKAGDLNRAGRRFEFRNLDAMGYNAYSTDPLYKHLPFTIVNQPGASYGVFYDNLSSTWLDLGNEIDNYHQAYRRYQAEAGDLDYYFLFGPAILDVTKAFVRLTGKTCFGPKWSLGYSGSTMHYTDAPDAQRQLLSFIALCRQHTIPCDSFQLSSGYTSIGNKRYVFNWNYDKVPQPEQMSQAFHDAGLHLAANIKPCLLQDHPRYQEVAAKGLFVRDSESDSPERSSFWDDEGSHLDFTNPDTVNWWQENVTRQLLEKGIDSTWNDNNEFEVWDGEARCHGFGQPIAIKHIRPLMPLLMMRASMEAQQRFAPALRPYLISRSGSAGMQRYVQTWSGDNRTSWQTLRYNTRMGVGMSLSGLYNVGHDVGGFAGNKPDAELFVRWVQNGVMHPRFTIHSWNDDATVNEPWMYPAVTPIIRDAIQLRYRLLPYLYTLLWQAHADDEPMLRPTFLDHEHDPQTFEETDDFLLGRDLLVASVVEPGQRQRQVYLPDNDDGWYDFYHGDWFSGGQTVTLDAPLERLPLLVRAGAMIPLSARTDFVCPASDDQRTMLLFPQTGNGIRQGVLFEDDGETHRWRDGQALWLRWEVCCSAQRIDVTFRAEGAFIPAWQQLTVQLPPDERRALYINGERTTQYQLPSRR  
  
>**gb|ACZ76472.1| Glucan 1,3-alpha-glucosidase [Dickeya dadantii Ech586]**MKTLKHWVLHHQAEDRVELLVDGAHRFMLYVLAPGLMRVLIKQDDELRLNRTWSIAPEQDVPWQGRVRESSDGFALPGYSLSWQDDALQVSTAQLRVTVHQPLWLSWEYCDAQGQWQPLASDRPTGAYLLNRHGDGVAHYQRRTAQERCYGLGEKAGDLNRAGRRFEFRNLDAMGYNAQSTDPLYKHLPFTIVNQPGASYGVFYDNLSSTWLDLGNELDNYHLAYRRYQAEAGDLDYYFLLGPAILDVTKAFVRLTGKTYFGPKWSLGYSGSTMHYTDAPDAQQQLLSFIELCRQHAIPCDSFQLSSGYTSIGNKRYVFNWNYDKVPQPEQMSQAFHDAGLHLAANIKPCLLQDHPRYQEVAAKGLFVRDSESDNPERSSFWDDEGSHLDFTNPDTVAWWQENVTRQLLEKGIDSTWNDNNEFEVWDGEARCHGFGQPIAIKHIRPLMPLLMMRASMEAQQRFAPELRPYLISRSGSAGMQRYVQTWSGDNRTNWQTLRYNTRMGVGMSLSGLYNVGHDVGGFAGNKPDAELFVRWVQNGVMHPRFTIHSWNDDATVNEPWMYPAVTPIIRDAIQLRYRLLPYLYTLFWQAHTDDEPMLRPTFLDHEHDPRTFEESDDFMLGKDLLVASVVEPGQRQRQVYLPDNGDGWYDFYRGDWFSAGQTVTLDAPLERLPLLVRAGAMIPMSARTDFVSPQSDDQRTMLLFPLMGNGTRQGLLFEDDGETHRWRDGQALWLRWELCCSAGRIDVTFQSEGAFVPAWRQLTVQLPPDEQRVLYINGERATQYTLPSRN  
  
>**gb|ADM98973.1| Alpha-glucosidase [Dickeya dadantii 3937]**MKTLKHWVLHHQAEDRVELLVDGAHRFLLYVLAPGLMRVLIKQRGELRLNRTWSIAPQHDVPWQGRERESSEGFALPGYTLCWQGDALQISTGQLRVTVHQPLWLSWEYLDVHGQWQPLASDRPTGAYLLNMHGDGVAHYQRRTPQERCYGLGEKAGDLNRAGRRFEFRNLDAMGYNAQNTDPLYKHLPFTIVNQPGANYGVFYDNLSSTWLDLGNEIDNYHPAYRRYQAEAGDLDYYFLLGPAILDVTKAFVRLTGKTCFGPRWSLGYSGSTMHYTDAPDAQQQLLSFIELCRQHAIPCDSFQLSSGYTSIGNKRYVFNWNYDKVPQPEQMSQAFHNAGMHLAANIKPCLLQDHPRYQEVAAKGLFVRDSESDNPERSSFWDDEGSHLDFTNPDTVAWWQENVTRQLLEKGIDSTWNDNNEFEIWDGEARCHGFGQPVAIKHIRPLMPLLMMRASMEAQQRFAPALRPYLISRSGSAGMQRYVQTWSGDNRTSWQTLRYNTRMGVGMSLSGLYNVGHDVGGFAGNKPDAELFARWVQNGVMHPRFTIHSWNDDATVNEPWMYPTVTPIIRDAIQLRYRLLPYLYTLLWQAHADDEPMLRPTFLDHEHDPRTFEETDDFMLGKDLLVASVVEPGQRQREVYLPDNGDGWYDFYRGDWFSGGQTVTLDAPLERLPLLVRAGAMLPLSARTDFTCPEADDQRTLLLFPLTGNGVRQGVLFEDDGETHRWRDGQALWLRWEVRCSAQRIDITFRPEGAFVPAWRTLAVQLPPDERRALYINGECGTEYQLPADR

GH32

>**gb|ACS87353.1| sucrose-6-phosphate hydrolase [Dickeya dadantii Ech703]**MKEIHLLKRMAQTLMSGQSRQTYDPWRPQWHLSPLVGLMNDPNGFIQHNGRYHLFYQWNPLACAHGAKCWGHWSSADLVHWRHEPVALLPVERYESHGCYSGSAVADNGVLTLIYTGNVKYDDGSRTAYQCLATENADGEFDKLGPVLTLPEGYTGHVRDPKVWRYQDCWYMVLGAQDATLQGKILLYRSDNLRQWQLLGEIAGSRLNGLGDFGYMWECPDLFPLDGWDVLICCPQGLAAEDERYLNTYQSGYFVGHLEGEQGRFTHQAFNELDHGFEFYAPQTTLSDDGRRLLFGWMGVPDQNEFQQPTIAHGWIHTMTCPRELTLRDGRLYQLPARELQRLRLREYQWQGTASYAPALPAGSAELSLDIQGEFQAHFADQMTLNWDGERLSLSRRHRLTGEPEHRYWRGTTLYHLQILCDRSSVEIFINHGQAVMSSRYFPDGDATIRFQGSGSILLRHWLLSPCVIE  
  
>**gb|ACT08558.1| sucrose-6-phosphate hydrolase [Dickeya zeae Ech1591]**MKEIHLIKRMACALMSASSKQAFDPHRPLWHLSPQVGLLNDPNGFIQHKGRYHLFYQWNPLACAHGAKFWGHWSSTDLVHWRHEPVALVPAESYESHGCYSGSAVVDNDTLMLVYTGNVKYDNGSRTAYQCLAQANEHGEFDKLGPVLSLPEGYTGHVRDPKVWRHQDNWYMVLGAQDLDLQGKVLLYRSADLRQWYLLGEIAGSRLNGLGDFGYMWECPDLFTLENREVLICCPQGLSAEEERYLNTYQSGYFIGSLDYENGRFTHHAFHELDLGFEFYAPQTTQSEDGRRLLFGWMGVPDQNEFFQPTLTHGWIHTMTCPRELTLRDDRIYQQPARELQSLRHLEHLWQGVADYAPALPASNAELMMDTQGEFQINFAGVMVLCWDGERLTLSRRNRRTNEPEHRYWHDGPLYHLQILCDRSSVEIFINHGQAVMSSRYFPTCDAMISFSGSGRITLQHWLLAPCVVE  
  
>**gb|ACZ75240.1| sucrose-6-phosphate hydrolase [Dickeya dadantii Ech586]**MKEIHLVKRMACALMSASAKQTYDPHRPQWHLSPSVGLLNDPNGFIQHKGRYHLFYQWNPLACAHGAKFWGHWSSADLVHWRHEPVALVPAESYESHGCYSGSAVADNDTLTLIYTGNVKYDNGTRTAYQCLARANENGEFDKLGPVLSLPDGYTGHVRDPKVWRYQDSWYMVLGAQDLDLQGKVLLYRSPDLLQWQALGEIAGSRLNGLGDFGYMWECPDLFTLGNREVLICCPQGLPAEEERYLNTYQSGYFVGSLDYDNACFPHQAFHELDLGFEFYAPQTTQSEDGRRLLFGWMGVPDQNEFFQPTLTHGWIHTMTCPRELTLCDDRVYQQPARELQSLRHLEHLWQGVADYAPALPASSAELMLDTQGEFQINFADILVLCWDGERLTLSRRNRRTNEPEHRYWHEGALHHLQILCDRSSVEIFINHGQAVMSSRYFPTSDAMVRFSGSGRITLRHWLLATCVIE  
  
>**gb|ADM96585.1| Sucrose-6-phosphate hydrolase [Dickeya dadantii 3937]**MKEIHLLKRMAYALMSGPSRQTYDPHRPQWHLSPLVGLLNDPNGFVQHKGRYHLFYQWNPQACAHGAKFWGHWSSADLVHWRHEPVALVPAESYESHGCYSGSAVVDNDALALIYTGNVKYDDGSRTAYQCLARANGDGEFDKTGPVLSLPEGYTGHVRDPKVWRHQDNWYMVLGAQDMDLQGKVLLYRSSDLLQWHALGEIAGSRLNGLGDFGYMWECPDLFALENHDVLICCPQGLPAEEERYLNTHQSGYFIGSLDYDSGRFTHQAFHELDLGFEFYAPQTTQSEDGRRLLFGWMGVPDQNEFFQPTIVHGWIHTMTCPRELTLRDDRIYQQPVRELQSLRHLEHLWQGVADYAPALPASSAELVLDTQGEFQLNFAGVMVLCWDGERLTLSRRNRRTNESEHRYWHDGPLHHLQILCDRSSVEIFINHGQAVMSSRYFPTSDAMVSFSGSGRITLQHWLLAPCVIE

GH33

>**gb|ACS84498.1| conserved hypothetical protein [Dickeya dadantii Ech703]**MTTETVTVERSGIVHQAEGDNQRIEAYIPSECPQNHAANLLHLPNGDLLCVWFGGTQEGVADISIYMSRLPQGSQQWTPAEKLSEDPTRSEQNPVLFLAPDGVLWLLYTAQKSGNQDTAIVRYRQSTDLGHTWGDIGVLLEQPGTFIRQPITVLPNGNWLLPVFYCRTRPGEKWVGNDDISAVKISSDQGKTWRESVVPNSTGCVHMNITLLQDGTLLALYRSRWADAIYLSRSTDGGESWSDPVATDLPNNNSSIQVTTLRNGHLALVFNHMNADGATERRVSLYDEIEDEEDEGQNAVMPEITSERSAFWGAPRAPMTVAISEDGGRSWPWQRNVEIGDGYCMTNNSTEKLNREFSYPSIKQGPDDKLHMAFTYFRQAIKYVCVSEAWVKG  
  
>**gb|ACS87671.1| conserved hypothetical protein [Dickeya dadantii Ech703]**MMLTTVKQQFVLPTDHRYFGNCHASTIAALPDGRLRAAWFAGEKEGSGDTAIWLANYQQGQWHAPVRLAWEDGLPHWNPVLHRQDGALWLFYKVGADVHHWQTRVMVSGDDGLSWSAPRMLVPGDSAPRGPVKNKLLVMSNGEWLAPGSVEDDRDWDAFVDISGDRGEHWQATPIPLAHQAPGDGQHDALWQGLEHAALWENDLTRVFQWDGVIQPSAWESAPGQVHVLMRSTRGAIYRSDSPDYGRRWCDAYATALPNNNSGIDVVHLGAGRLVLVYNPVTGNWRSRYPLTAAYSADNGEHWENLIDLEQEPGEFSYPAIIADGDTLHVTYTWNRKNIVYCALKFGKQS  
  
>**gb|ACT05526.1| conserved hypothetical protein [Dickeya zeae Ech1591]**MTTETITIERDGLVRPADADNQRIDAYIPSECPQNHAANLLHLPNGDVLCVWFGGTQEGVSDISIYLSRLVKGSEQWTPAVKLSDDPTRSEQNPVLFLAPDGVLWLLYTAQKSGNQDTAIVRYRQSLDQGYTWGEIGVLLEQPGTFIRQPITVLPNGDWLLPVFYCRIQPGEKWVGNDDISAVKISSDQGKTWRESVVPNSTGCVHMNITLLKDGTLLALFRSRWADFIYRSHSTDGGESWSEPEATTLPNNNSSIQVTTLDNGHLALVFNAMNADGATERRLSLYDEIEDEEETDAKMPDISSGRSAFWGAPRAPMTLAISEDGGKSWPWQRNLEVGDGYCMTNNSTDKRNREFSYPSIKQGPDGKLHVAFTYFRQAIKYVCVSEEWVKG  
  
>**gb|ACZ78328.1| conserved hypothetical protein [Dickeya dadantii Ech586]**MTTETTETITIERDGLVRPADADNQRLDAYIPSECPQNHASNLLHLPNGDVLCVWFGGTQEGVSDISIYLSRLVNGSGQWTPAVKLSDDPTRSEQNPVLFLAPDGVLWLLYTAQKSGNQDTAIVRYRQSQDQGYTWGEIGVLLEQPGTFIRQPITVLPNGDWLLPVFYCRIQPGEKWVGNDDISAVKISSDRGQTWRESVVPNSTGCVHMNITLLKDGTLLALFRSRWADFIYRSHSTDGGETWSEPEATDLPNNNSSIQVTTLDNGHLALVFNAMNADGATERRLSLYDEIEDEEESDAKMPEIATGRSAFWGAPRAPMTLAISEDGGKTWPWQRNLEVGDGYCMTNNSTDKRNREFSYPSIKQGPDGKLHIAFTYFRQAIKYVCVSEEWVKG  
  
>**gb|ACZ78906.1| conserved hypothetical protein [Dickeya dadantii Ech586]**MRLTTTTRQYVLPEGHDYFGNCHASTVVALPGGRLRVAWFAGEKEGSGDTAIWLASHEQGRWSPPVRVAWEDGLAHWNPVLHWQAGTLWLFYKVGADVHHWQTRVQLSTDEGASWSAPRPLVPGDSAPRGPVKNKLLVMSNGEWLAPASVEDDRHWDAFVDLSADQGQRWQTAPIPLAHRLPGEHGREALWSGLEQAALWENDLTRVFQWDGVIQPSAWESSPGRVHVLMRSTRGALYRSDSDDYGRHWCEAYAVDLPNNNSGVDLVHLGAGRLVLVYNPVTGNWHRRYPLAVACSTDNGEHWQDALCLEQEPGEFSYPAIIADGDTLHVTYTWNRKNIVYCALIFSG  
  
>**gb|ADM96302.1| Putative cytoplasmic protein [Dickeya dadantii 3937]**MRACSGWARRWRRSSRHRSGNLKDTLMKLTMTTQQFVLPEGHDYFGNCHASTVAVLPEGRLRVAWFAGEKEGSGDTAIWLACAEQGRWLQPVRVAWEDGVAHWNPVLHWQAGTLWLFYKVGADVHHWQTRVAVSTDDGASWSAPRLLVPGDSAPRGPVKNKLLVMSNGEWLAPASVEDDRHWDAFVDLSGDRGRSWQTAPIPLTHRTPGERDGEALWQGLEQAALWENDLTRVFQWDGVIQPSAWESSPGQVHVLMRSTRGALYRSDSDDYGRRWREAYAIDLPNNNSGVDLAHLGAGRLVLVYNPVTGNWRHRYPLTVACSTDNGEHWENSIDLEQEPGEFSYPAIIADGDTLHVTYTWNRKNIVYCALIFSG  
  
>**gb|ADN00006.1| expressed protein [Dickeya dadantii 3937]**MTTETITIERSGLVHPADNDSQRIDAYIPSERPQNHAANLLHLPNGDVLCVWFGGTQEGVSDISIYLSRLVKGSGQWTPAVKLSDDPTRSEQNPVLFLAPDGVLWLLYTAQKSGNQDTAIVRYRQSLDQGYTWGDIGTLLEQPGTFIRQPITVLPNGDWLLPVFYCRTQPGEKWVGNDDISAVKISSDQGKTWRESVVPNSTGCVHMNITPLKDGSLLALFRSRWADFIYRSHSTDSGATWSEPVPTVLPNNNSSIQVTTLDNGHLALVFNAMSAEGATERRLSLYDEIEDEEETDAKMPEVSSGRSAFWGAPRAPMTLAISEDGGKTWPWQRNLEVGDGYCMTNNSTEKLNREFSYPSIKQGPDGKLHIAFTYFRQAIKYVCVSEEWVKG

GH36

>**gb|ACS85133.1| glycoside hydrolase clan GH-D [Dickeya dadantii Ech703]**METTLVRLASPVTDVIVRCRPAAEILYWGPHLAAFSPQDVDSLSRPVPNGRLDVDVPVTLAAETGRGLFGSPGIEGHRNGLDAFAVLTTVEVRQPDPQQLVVVAEDSQAGLRLTTELRLHADSGVLQLRHGLTNLHPGDWQVQRLALTLPLPESAAEVMAFHGRWVREFQPHRALLAHGSLVQENRRGRTSHEYFPAMISGEPGFAEQHGRVWGVHLGWSGNHRLRAEVKTDGRRLLQAEALYLPGEIALAQGESLTTPWLYAACSGQGLNGMSQQFHRFLRQEIIPFPRASARPVHLNTWEGIYFEHDPAYIMQMATQAAALGVERFIIDDGWFRGRDHDRAALGDWYVDPHKYPQGLMPVINHVRSLGMEFGIWVEPEMINPDSDLYRAHPDWLLALPGYLQPTGRYQYVLDLSHPEVFDYLLMRLSWLLGEHPIDYVKWDMNRELVQPTHQGRAAADRQTQAFYRLLDVLGERFPQVEFESCASGGGRIDYEVLRRCHRFWASDNNDALERQTIQRGMSYFFPPEVMGAHIGHHRCHATGRRHSIAFRGLTALFGHMGIELDPVRADAQEQDGFRHYVALHQRYRTLLHTGCLWRVDMSDATTQVQGVVSDDRAQALFLVAQLAMPEYALAGVLRFPGLDLQARYRLSVVDHPDLKPVIDGGSTMRQLPAWMASPTEFSGEWLMNAGLRLPILNPETALLLALDRL  
  
>**gb|ACT07487.1| glycoside hydrolase clan GH-D [Dickeya zeae Ech1591]**METTLIRLTSPVTDVIVRCRPAAEILYWGPHLAAFSPQDAESLSRPVANGRLDVDVPVTLAAETGRGLFGSPGIEGHRNGLDAFAVLTTVAVRQPDPQQLVIEAEDRQAGLRLTSELRLHADSGVLQLRHCLTNLHPGDWQVQRLAVTLPLPESAAEVMAFHGRWVREFQPHRTLLAHGSLVQENRRGRTSHEYFPAMVSGEPGFAEQHGQVWGAHLGWSGNHRLRTEVKTDGRRLVQAEALYLPGEITLAQGESLTTPWLYAACSEQGLNGMSQQFHRFLRQEIIRFPHAKARPVHLNTWEGIYFKHDPAYIMQMATQAAALGVERFIIDDGWFRGRDHDRAALGDWYVDSDKYPQGLMPVINHVRDLGMEFGIWVEPEMINPDSDLYRAHPDWLLALPGYDQPTGRYQYVLDLSNPEAFDYLLARLSWLLGEHPIDYVKWDMNRELVQPAHQGRAAADRQTKAFYRLLDVLGERFPQVEFESCASGGGRIDYEVLRRCHRFWASDNNDALERQTIQRGMSYFFPPEVMGAHIGHHRCHATGRQHGIAFRGLTALFGHMGIELDPVRADAQEQAGFRHYVALHRQYRTLLHTGCLWRVDMADAATQVQGVVSEDRRQALFLITQLAMPDYALAGVLRVPGLDAQARYRLTVVDHPDLKPVIEGGSTMRQLPTWMAAPAEYSGEWLMKAGLRLPILNPETALLLELERL  
  
>**gb|ACZ77401.1| glycoside hydrolase clan GH-D [Dickeya dadantii Ech586]**METTLIRLTSSVTDVIVRCRPAAEILYWGSHLATFSPQDVQSLSRPVANGRLDVDVPVTLAAETGRGLFGSPGIEGHRNGLDAFAVLTTVSVEQPSPQHLIIEAEDRQAGLRLRSEFKLHADSGVLQLRHCLTNLHPGDWQVQRLAVTLPLPESAAEVMAFHGRWVREFQPHRTLLSHGSLVQENRRGRTSHEYFPAMVSGEPGFSEQQGRVWGAHLGWSGNHRLRAEVKTDGRRLVQAEALYLPGEIALAQGESLTTPWLYAACSEQGLNGMSQQFHRFLRQEIIRFPRANARPVHLNTWEGIYFKHDPDYIMQMATQAAALGVERFIIDDGWFRGRDHDRAALGDWYVDVEKYPQGLMPVINHVRALGMEFGIWVEPEMVNPNSDLYRAHPDWLLAVPGYEQPTGRYQYALDLANPEVFDYLLARLSWLLGEHPIDYVKWDMNRELVQPAHQGQAAADRQTKAFYRLLDVLGERFPQVEFESCASGGGRIDYEVLRRSHRFWASDNNDALERQTIQRGMSYFFPPEVMGAHIGHYRCHATGRQHSIAFRGLTALFGHMGIELDPVRADAQEQAGFRHYVALHRQYRTLLHTGRLWRVDMPDATTQVQGVVSEDSRQALFLVAQLAMPDYALAGVLRFPGLDAQARYRLTVVDHPDLKPVIEGGSTMRQLPSWMATPAQYSGEWLMKAGLRLPILNPETALLLELERL  
  
>**gb|ADM97865.1| Alpha-galactosidase [Dickeya dadantii 3937]**METTLIRLASPATDVIVRCRPAAEILYWGPHLAAFSPQDADSLSRPVANGRLDVDVPVTLAAETGRGLFGSPGIEGHRNGLDAFAVLTTVAVRQPDPQQLVIEAEDRQAGLRLTTELRLHADSGVLQLRHCLTNLHPGDWQVQRLAVTLPLPESAAEVMAFHGRWVREFQPHRTLLSHGSLVQENRRGRTSHEYFPAMISGEPGFAEQHGRVWGAHLGWSGNHRLRTEVKTDGRRLLQAEALYLPGEIALAQGESLTTPWLYAACSEQGLNGMSQQFHRFLRQEIIRFPRAKARPVHLNTWEGIYFKHDPDYIMQMASQAAALGVERFIIDDGWFRGRDHDRAALGDWYVDPRKYPQGLMPVINHVRELGMEFGIWVEPEMINPDSDLYRAHPDWLLALPGYDQPTGRYQYVLDLSNPEVFDYLLARLSWLLGGHPIDYVKWDMNRELVQPAHQGRAAADRQTQAFYRLLDVLGERFPQVEFESCASGGGRIDYEVLRRCHRFWASDNNDALERQTIQRGMSYFFPPEVMGAHIGHHRCHATGRQHSIAFRGLTALFGHMGIELDPVRADAQEQAGFRHYVALHRRYRALLHTGCLWRVDMPDATTQVQGVISADRGQALFLVAQLAMPDYALAGVLRFPGLDPQARYRLTVVDHPDLKPVVDGGSTMRQLPAWMAAPAEYSSEWLMKAGLRLPILNPETALLLALERL

GH38

>**gb|ACS84508.1| glycosyl hydrolase 38 domain protein [Dickeya dadantii Ech703]**MFFTEEKLSQRLDEVAQYRWREAIEVELADICFDREGENGTPPPPDAADWQPCQRGFQWREKDIYVWLRLRIALPAHWATEIIAARFDFSLGVQRRDFEALLYLNGEPWQGLDQNHVETVIPSALAGQTIECCCRVWSGILEGKVRKHFQAFHVGNGFERVSIAVRDEAATNLFYTTEAILQSLAVLPENDPHRVLLLAAADRAYNLIDWREPGSAECYHSLAQAAASLEREYPRSGGVQPVTVHCVGHTHIDVAFLWQLKHTREKCARSFSTVLRLMERYPEYVFFQSQPQLYDYLKQDYPAIYRQIKQRIAEGRWEVDGAMWVEADCNLPSGESFVRQILLGTRFMQQEFGVTPRCLWLPDVFGYSWALPQILRKSGIRYFMTTKISWNEFNQMPHDTFTWRGIDGSEVLAHFITTPEEGHPRYTYNGMVNAMSVQGLWDNYKDKPLNQELMLAYGYGDGGGGPTEEMLELLRRFEKVPALPNIRHGRVDDYFTRLEQRLADSDAWQHVWDGELYFESHRGTYTSQAQVKKANRRGELTYRRLEWLHAQAAVSHADWPAYPQVTLNAGWQILLRNQFHDIIPGSSIAEVYRDAADEYRQAEQLADEMLAQCQPRLLSARADAVSVLNSAAWPRSDLAFIAGDGAGGWMQADGQPLASQAVAGGWLVALREIPALSGVALYRRAEQEAGDLPFSVGERQVETPFYQISWNEHGQLTRIFDRQHQRDVLADCGNVLTVYEDKPLKYDAWDIEIFYIQKQRPVTELLSATVREQGELCCSIEFVWRYHHSRIVQQMRLYRDSRRIDFHTQVDWQDYNQLLKVGFPVAVRATEATYDIQFGNVKRPTTWNTSWDYARFESVAHQWADLSEYGYGVSLLNDCKYGHAIRDNLMQLTLIKSAVSPDAHADRGQHEFTYSLLPHAGDWREAGTAQQAFFLNEPLLPLPGEWLPEAPLVAFDHPYIQLDALKKAEDGNWLVVRLHEFAGGRQNVVLRCARPVRWWAESDLLENLSAKQMDAGQTLELHFAPYEIKTLVLCLAD

GH42

>**gb|ACT06143.1| Beta-galactosidase [Dickeya zeae Ech1591]**MKRFSPLNPKVEGLLHGADYNPEQWENYPGIIDDDIAMMKQVKCNVMSVGIFSWAKLEPQEGVYRFDWLDEVIDKLYQQGISVFLATPSGARPAWMSQRYPDVLRVGRDRVAALHGGRHNHCLSSPVYRDKVQKINTLLAERYGHHPAVIGWHVSNEYSGECHCERCQQAFRTWLKARYQTLDNLNHAWWSDFWSHTYSDWSQIESPAPQGEVSIHGLNLDWRRFNTAQATDFCAQEIAPLKRVNPAIPATTNFMEYFYDYDYWQLSQVLDFISWDSYPMWHRDKDDATLACYIALFHDLMRSLKQGKPFVLMESTPSVTNWQPLSKLKKPGMHILSSLQAVAHGADAVQYFQWRKSRGSVEKFHGAVVDHVGHIDTRVGREVAQLGQILSQLSAVAGSRVEAQVAILFDWESRWAMDDAQGPRNAGLEYEKTVAEHYRPFWEQGVAVDVINADGDFSGYRLLVAPMLYMVRPGFAERVEQFVRQGGQVVVTYWSGIVNDSDLCYQGGFPGPLRPLLGIWSEEIDCLADGEYNRVLGLADNDIGLKGPYQARHLCELIHLEGATALASYCDDFYAGRPAVTVNRVGDGKAWYVTSRNDLAFQRDFFAAIISELALPRALDIPLPPAVTAHRRTNGDEEFIFIENYSAVPQPIRLPAGYSDMLTGLPLADVVLSAWDCRVIRRRLV  
  
>**gb|ACZ77765.1| Beta-galactosidase [Dickeya dadantii Ech586]**MKRFPPLNPKVEGLLHGADYNPEQWENYPGMIDDDIAMMKQVKCNVMSVGIFSWSKLEPQEGVYRFDWLDAVIDKLYQQGISVFLATPSGARPAWMSQRYPEVLRVGRDRVPALHGGRHNHCLSSPVYRDKVQKINTLLAERYGHHPAVIGWHISNEYSGECHCPRCQQAFRHWLQARYQTLENLNHAWWSDFWSHTYSDWLQIESPAPQGEVSIHGLNLDWRRFNTAQAKDFCAQEIAPLKRVNPAIPVTTNFMEYFYDYDYWQLSQVLDVISWDSYPMWHRDKDDATLACYIALFHDLMRSLKQGKPFVLMESTPSVTNWQPLSKLKKPGMHILSSLQAVAHGADAVQYFQWRKSRGSVEKFHGAVVDHVGHVDTRVGREVAQLGQILSQLADVAGSRVDAQVAILFDWESRWAMDDAQGPRNLGLEYEKTVAEHYRPFWEQGIAVDVINADCDFSGYRLLIAPMLYMVRSGFAERLEQFVRQGGQVVVTYWSGIVNDSDLCYLGGFPGPLRPLLGIWSEEIDCLADGEFNRILGLSDNDIGLKGPYQARHLCELIHLEGATALASYCDDFYAGRPAVTVNRVGDGKAWYVTSRNDQAFQRDFFAAIIRELNLPRALDMPFPEAVTAHRRTNGDDEFIFIENYSALPQTLPLPAGYRDMLTGAPLSDVVLSAWDCRVIRRRLV  
  
>**gb|ADM99399.1| 1,4-beta-exogalactanase [Dickeya dadantii 3937]**MKRFTPLNPKVEGLLHGADYNPEQWENYPGIIDDDIAMMKQVKCNVMSVGIFSWAKLEPQEGVYRFDWLDEVIDKLYRQGIAVFLATPSGARPAWMSQRYPEVLRVGRDRVPALHGGRHNHCLSSPVYRDKVAKINTLLAERYGHHPAVIGWHISNEYSGECHCDRCQQAFRNWLQARYQTLDNLNHAWWSDFWSHTYSDWSQIESPAPQGEVSIHGLNLDWRRFNTAQATDFCAQEIVPLKRVNPAIPVTTNFMEYFYDYDYWQLSRVLDFISWDSYPMWHRDKDDATLACYIAMFHDLMRSLKQGKPFVLMESTPSVTNWQPLSKLKKPGMHILSSLQAVAHGADAVQYFQWRKSRGSVEKFHGAVVDHVGHIDTRVGREVAQLGQILSQLDAVAGSRVEAQVAILFDWESRWAMDDAQGPRNAGLEYETTVAEHYRPFWEQGIAADIINADCDFSGYRLLIAPMLYMVRPGFAERVEQFVRQGGQVVVTYWSGIVNESDLCYQGGFPGPLRAVLGIWSEEIDCLADGEYNRVQGLADNDIGLKGPYQARHLCELIHLEGATALASYCDDFYAGRPAVTVNRVGAGKAWYVTSRNDLAFQRDFFGAIIRELALPRALDIPLPPAVTAHRRTNGDDEFIFIENYSAQPQPIQLPAGYSDMLTGLPLVDVVLSAWDCRVIRRRLI

GH43

>**gb|ACT06297.1| glycoside hydrolase family 43 [Dickeya zeae Ech1591]**MKCTAGLLAFIALAAYGEGPVAPCGDSAVVSWAQGIEHQRKADLGNGCYLNPIMSGDHPDPTILKDGHDYYMTFSSFDAIPGLVIWHSQDLINWQPVGPAVTTPVDSIWAPELVKHNDKYYLYFITNKTDPVSGAKTKKFYVITTDNIRGAWTPPREIVVKSDKGDNGATSDPGHAVGEDGKRYIFMSGGVRVQLKDDGLAVADGEAGIAKTVYAGWQYPEQWDVESFSQEGPKMLKHGDYFYMVLAEGGTAGPPTGHMVIAARSRSINGPWENSPYNPIIRTQSASEKWWSRGHATLVEGMDGQWYMVYHGYENSFMTLGRQALLEPITWTADGWFISAGYDVGKPIPRPVGGHAVPHGMAFSDSFRPEVFDSVWSFYMPGENEKARIRFDDGSLLLRAKGRSPKDTTPLFINAGDLAYQVDVEIAFEPKAQAGLLLFYSNRLYAGLAFNANGTVMHRYGLERNGAKIADITGNTVHLRLVNRRNILTLYTSPDGEKWTKYGVQMEVSGYNQNVGYDFQALRPAIYASGEGNVRFSHFRYTALP  
  
>**gb|ACT08169.1| glycoside hydrolase family 43 [Dickeya zeae Ech1591]**MNPSQITSPWNPDLGNGRYRNPVLFADYSDPDIIRVGNDIYLVSSSFNHMPALPILHSRDLVNWTLINHVFTGFDLPGYERFQPGKGVWAPSIRYHAGKFWVFFSTPDEGIFMCQTDDPRGKWSTPHCVKSAKGWIDPCPFWDDDGSAWLIHAFAFSRSGRKHLLQLCRMSGDGRQLLDDGRIIVDGTASQPTLEGPKLYKRRGWYYIFAPAGGVPTGWQTVLRASSLEGPWQSRIVLHQGGTAVNGPHQGGWVELESGESWFVHFQDRHAYGRVVHLQPMKWQDDWPLIGAQTGDDGIGEPVTEAAIPNVGRPYMPVQPATSDDFTDDRLGLQWQWQANPDAGWYELCRPGLRLFCQPMPQRNGVPSWYDVPHLLMQKFPAETFTVTTRLQPSLANVGDRCGLIVYGERFAFLGLEKTADGVALTSGYGWMTDAQELRQYAGPTLPVGEEVHALELRVTVLPNARCQFACRTPDGGFTPVGEPFAAGPGKWVGAKIGLYALSLPEQRGPGRVDVDFFHVTP  
  
>**gb|ADM96955.1| Xylosidase/arabinosidase [Dickeya dadantii 3937]**MVRPDSEGEKINVEPSLTTSPWNPDRGDGRYRNPILFADYSDPDIVRVGEDIYLVSSSFNHMPALPILHSRDLVNWTLINHVFTRFDLPGYERFQPGKGVWAPSIRYHAGKFWVFFSTPDEGIFMCQADDPRGDWSAPHCVQPAKGWIDPCPFWDDDGSAWLVHAFAFSRSGRKHQLQLCRMSSDGRQLLDEGRIIVDGTAAQPTLEGPKLYKRNGWYYIFAPAGGVPTGWQTVLRAASLQGPWQARVALHQGRSAVNGPHQGGWVELENGESWFVHFQDRHAYGRVVHLQPMRWQDDWPLIGAQSGDGGPGEPVENAAMPAVRADNIRAQPATSDDFTADRLGLQWQWQANPDAGWYEMCRPGLRLFCQPMPQRHGAPSWYDVPNLLMQKFPAETFTVTTRLQAALENVGDRCGLMVYGERFAFLGLEKTADGVALTSGYGWMTDAQELRQYAGPALPVGEEAHTLELRVTVLPNARCQFAWRTPDGGFTPVGEPFAAGPGKWVGAKIGLYALSLPEQRGPGRVDVDFFHVTP

GH53

>**gb|ACT06142.1| Arabinogalactan endo-1,4-beta-galactosidase [Dickeya zeae Ech1591]**MKKMIPTLLAVSLSLGAMPLMAAESVVIKPLRNAPADFIKGADISTLLEVERQGGVFYDENHVRVDPVALLKKNGVNYIRLRLWVDPHDAAGRPYGGGDNDLATTLALAKRVKAAGMKLLLDFHYSDFWTDPGKQFKPKAWANLSYEQLKTAVHDYTRDTIARFKREGVLPDMVQIGNEANGGILWPEGKSWGQGGGEFDRLAGLLNAAIAGLRENLSSPGQVKIMLHLAEGTKNDTFRWWFDEITQRGVPFDVIGLSMYTYWDGPISSLKANMDDISQRYNKDVIVVEAAYGYTLANCDNAENSFGEKEAAAGGYPATVQGQADFIRDLMQSVIDVPKKHGKGVFYWELAWITPAGNTWATEAGMNYINDHWKLGNARENQALFNCQGEVLPSIKAFK  
  
>**gb|ACZ77766.1| Arabinogalactan endo-1,4-beta-galactosidase [Dickeya dadantii Ech586]**MKKMIPALLAVSLSLGAMPLMAAESVVIKPLRNAPADFIKGADISTLLEVERQGAVFYDENHTRVDPVALLKKNGVNYIRLRLWVDPKDSAGHPYGGGDNDLATTLALAKRAKAAGMKLLLDFHYSDFWTDPGKQFKPKAWANLSYDQLKTVIHDYTRDTIARFKREGVLPDMVQIGNEANGGILWPEGKSWGQGGGEFDRLAGLLNAAIAGLRENLSSPGQVKIMLHLAEGTKNDTFRWWFDEITKRGVPFDVIGLSMYTYWNGPISALKANMDDISQRYNKDVIVVEAAYGYTLANCDNAENSFGEKEAAAGGYPATVQGQADFVRDLMQSVIDVPKKRGKGVFYWEPAWITPPGNTWATEAGMTYINDHWKLGNARENQALFNCQGEVLPSIKVFK  
  
>**gb|ADM99400.1| periplasmic 1,4-beta-endogalactanase [Dickeya dadantii 3937]**MKKMIPALLAVSLALGAAPLMAAESVVIKPLRNAPADFIKGADISTLLEVERQGGVFYDENRARVDPIALLKKNGVNYIRLRLWVDPRDAAGHPYGGGDNDLATTLTLAKRAKAQGLKLLLDLQFSDFWTDPGKQFKPKAWAHLSYDQLKVVIHDYTRDTIARFKREGVLPDMVQIGNEANGGILWPEGKSWGQGGGEFDRLAGLLNASIAGLRENLSSPGQVKIMLHLAEGTKNDTFRWWFDEITKRGVPFDVIGLSMYTYWNGPISALKANMDDISQRYNKDVIVVEAAYGYTLANCDNAPNSFGAKEAAAGRYPATVQGQADFIRDLMQSVIDVPNRRGKGVFYWEPTWIIAAGNTWATEAGMDYINDHGFIGNARENQALFNCQGEALPSIKVFN

GH73

>**gb|ACS85333.1| flagellar rod assembly protein/muramidase FlgJ [Dickeya dadantii Ech703]**MIPLDKSVDQQASAAYDVKSLNKLRNDAGKSDPAALKKVAQQVEGLFVNMMLKSMRSALPQDGIMDSQQTRMFTSMYDQQISQDLSAKGLGLADMMVKQLGKNFKGEVGDDVGKTAMPLTSDDFSPTALTPALAGELMRRSGQSSDREGDGREYSELPPVSANFTDRLSIPSMIASLKTGIPHYLIMAQAALESGWGKKEIMTSEGKTSHNLFGVKAGNSWDGKVTEIWTTEFENGRSYRVKEKFRVYDSYLESINDYISLLTNNSRYKDVVNAGNAEEAAYALQRAGYATDPRYGDKLVQIIGQIKNVSQKAVKAYTHDISGLF  
  
>**gb|ACT06415.1| flagellar rod assembly protein/muramidase FlgJ [Dickeya zeae Ech1591]**MSEMKAFNNPAYETQSLNSLKRDVSNHPQGREGIRAVAKQLEGVFVQMMMKSMRDTLPKDGIFSSDQTRMLTSMYDQQLAQQMSSGKGVGLASLIEKQMMGQGIAGTEQAASPTPFKPDSQLAREMPSLVMEQMVRKAMPKLPEKSSPLPMSSSDFISRLSTPAMLVSQQSGIPHHLIMAQAALESGWGQHEIPTSDGRRSHNIFGIKAGSSWDGPVTEITTTEYEQGVAKKVTAAFRVYGSYLEALNDYAKLLTQNPRYAAVSSAATAEQAAVALQQAGYATDPAYAKKLVSMIQQMKNSGEKAVQAYTHDLSGIF  
  
>**gb|ACZ76391.1| flagellar rod assembly protein/muramidase FlgJ [Dickeya dadantii Ech586]**MSDMKTFNNPAYETQSLNALKRDVSSHPQSREGIRAVAKQLEGVFVQMMMKSMRDTLPKDGMFSSDQTRMITSMYDQQLAQQMSSGKGVGLAALIEKQMMGQGIVGIEQPAPSTPFKPDGQLARNMPSFVMEQMVRKAMPKLPEKSSPLPMNSADFISRLSTPAMLVSQQSGIPHHLIMAQAALESGWGQHEIPTTDGRRSHNIFGIKAGSNWDGPVTEITTTEYEQGVAKKVTAAFRVYGSYLEALNDYAKLLTQNPRYVGVSAAATAEQAAVALQQAGYATDPAYAKKLVSMIQQMKNSGEKAVQAYTHDLSGIF  
  
>**gb|ACZ76599.1| Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase [Dickeya dadantii Ech586]**MKKNNTTRKQLFVVIKKTRSFTKKTEINSQSRQNNSEANNTATGYSVSPATGLDNIRSSAPESARPSSAPAAASQPTPPTTPPVTTVPPLPKFSPPQTPTPPVETPTQPAATNTAPPSQPTPAPTAAAPTTEPAAPQEPATEPFAPDYAAAGSQLSKLMSGMAAPLSRLTSSLQGFTSQSLLKSATSKPADNTGAPPSRIDSISLPTAPAQKINTPIPAGRSGTIQRALATGAAYKQGNIEGLDDAHTRALVASTAATESAGGKLDIRNSAGYLGRYQAGAGWLAEAGLIAGGANAVTAAMKADGFTNEYKWGKSGGMTRFLKNKNNWKNGLDYDKYLSSAEIQDNAFKTNSDKAYAYLVKKGIIKPGMTQNEIAGILKARHIGGIGGAIKAAKNIEGPKDANGTSALKYKNDLADGNVFIESYQSGNTVLSEPIHADLDLAPQVSNAKKPETKKTEAKNTSSKGQKPKKLNLSKENNDFVEKIYKEALALETETGVPAAITAAQAILESGYGKRVPVDINTKEVSNNLFGIKANDKYIKNGGKYVNILTTEYVPVTGEKENKKIKIVGKFRSYQSSEDSLRDHASFLRGNKRYKNLFTSKNPMKWAEGLQASGYATDPEYAKKLQNVILKFGWDKKDNNN  
  
>**gb|ADM99063.1| flagellum-specific muramidase [Dickeya dadantii 3937]**MSDMKTSNNAAYETQSLNALKRDVSSHPQSREGIRAVAKQLEGVFVQMMMKSMRDALPKDGIFSSDQTRMLTSMYDQQLAQQMSSGKGLGLASVIEKQMMGQGIAGNEPASAAPFKPDGQLARAMPSFVLEQMVRKAVPKLPEKSSALPMSSTDFISRLSTPAMLVSQQSGIPHHLIMAQAALESGWGQREISIADGRRSHNIFGIKAGSSWDGPVTEVTTTEYEQGVAKKVKAAFRVYGSYLEALNDYAKLLTQNPRYAGVSAASTAEQAAVALQQAGYATDPAYAKKLVSMIQQMKNSGEKAVQAYTHDLSGIF

GH77

>**gb|ACS84131.1| 4-alpha-glucanotransferase [Dickeya dadantii Ech703]**MVLKAKKSVRYPVGLVDTYKDAYGNEQVIAEETREKLMQLLAPQDIAGARLPPVCVFRQGKAMTLKPGGEGDYGWIITYEKGGGTEGKVSAGQVLSLPDTLPIGYHQLVLEQGEKQWSCRIIVAPSGCYEPEPLTNGRRWWGITVQLYTLRSQHNWGIGDFGDLKSLVENVARRGGAFVGFNPLHSLYPAEPEAASPYSPSSRHWLNIIYIDVNQVEDFHHSEAAQAWWRRDDIQRQVLVARTNRWVDYTSVTTLKLAALRLAFQHFCRRSPLDHRKTALQQFIRNGGESLQQQATYDALLVYLKAQGDIPADWRRWPEEYREAGGDAVMRFRQENAEEIQFYCWLQWVAHEQLAACFERSRQLGMPIGLYRDLAVGGAQGGVDTWGDRQLYCLDVTLGAPPDPLGPQGQNWNLTPMHPYALQQRGYQPFIDMLRRNMASSGALRIDHVMGLLRLWWIPGGDTAAGGAYVRYPVDDLLAIVALESQRYRCLVIGEDLGTVPEEVVQRLEENGIYSYKVLFFEKDRKNRYRAPCEYPRRSMATITTHDLPTLRGFWQGMDLTLGKDLGLYPSDEILQLQLEERELAKQGMLDALHEQGLLPQRVGRNAALTSMSSHLNRGVQRYLADSASALLGLQLEDWLDMATPVNVPGTDREYPNWRRKLSRTLDSIFTDRNLERLIRDIDLRRGGPVPVRGRKKKTDATPSADA  
  
>**gb|ACT05126.1| 4-alpha-glucanotransferase [Dickeya zeae Ech1591]**MALKAKKSVPHQMGIADTYKDAYGNERAIDNETRQALLQLLEVTEPSTAPLPSVCVLRQEQQNRLPLRHAGDYVWTLTYEKGGIIEGRITGQAVLALPDNLPLGYHQLMLMQGEQQWPCRVIVAPTRCYEPEPLTQGKRWWGVMVQLYTLRSSDNWGIGDFGDLKTLVEQVARRGGAFVGLNPLHALYPAQPEAASPYSPSSRNWLNIVYIDVNQVDDFHQSDAARAWWKQDDIQQQLTAARANRWVDYTAVTRLKLAALRLAFSHFTNRNALDPRKTAFQQFLKTHDESLLQQATYDALQAWMHQQGKPTADWRQWPQEYHAARSDATLAFRQEHADDVQFYCWLQWLAHEQLAACFSHSKQLGMPIGLYRDLAVGVAQGGVDTWGDQQLYCMSVTIGAPPDPLGPGGQNWNLTPVHPTLLRQRGYQPFIDLLRSNMAHSGALRIDHVMGLLRLWWILNGNDATHGAYVFYPVDDLLGILALESHRHRCLVIGEDLGTVPEEIVNKLPDNSVYSYKVLFFEKDQQDRFRAPDEYPPRSMATITTHDLATLRGYWQGVDLTLGKDLGLYPDAAALQRQHEARECAKQGLLDALHEQALLPQRVGRNASLTTMSAQLNRGVQRYLADSASALLGLQLEDWLDMSTPVNVPGTDQEYPNWRRKLSRPLDSIFTDRYLERLIRDIDLRRGGPVPSRSKKTVKPAETPVDNGKQKETKKPE  
  
>**gb|ACZ78657.1| 4-alpha-glucanotransferase [Dickeya dadantii Ech586]**MALKAKKSVPHYQGIADTYKDAYGNEQAIDSDTRKALLHLLDVAEPTASPLPSVCVFRQGQQHRLPLRGEGDYIWTLIFEKGGIIEGRSGGQATLVLPDTLPLGYHQLMLTQGEQQWSCRVIVAPTRCYEPDPLIQGKRWWGVMVQLYTLRSSDNWGVGDFGDLKTLVEQVARRGGAFVGLNPLHALYPAEPEAASPYSPSSRNWLNIIYIDVNQVDDFHQSQAAQAWWMQDDIQRQLTAVRASRWVDYTAVTHLKLTALRLAFGHFTGRSALDPRKTAFLQFLKTHDESLLQQATYDALQDWMKLQGKPAADWLQWPQEYHDARSDATLRFRQEHADDVQFYCWLQWLAHEQLATCFSHSKQLGMPIGLYRDVAVGVAQGGVDTWSDQQLHCLSVTIGAPPDPLGPGGQNWNLTPMHPTRLRQRGYQPFIDLLRSNMAHSGALRIDHVMGLLRLWWILNGGTANRGAYVLYPVDDLLGILALESHRHRCLVIGEDLGTVPEEIVNKLRDNSIYSYKVLFFEKDQHDRFRTPDEYPARSMATITTHDLATLRGYWQGVDLTLGKDLGLYPSEALLKQQHDARERAKQGLLDALHEQGLLPQRVGRNASLTTMSAQLNRGVQRYLADSASALLGLQLEDWLDMATPVNVPGTNQEYPNWRRKLSRPLDSIFTDRYLERLIRDIDLRRGGPVPSRTKKTVKPADTPEDNGKQEQTKKPE  
  
>**gb|ADN00380.1| 4-alpha-glucanotransferase (amylomaltase) [Dickeya dadantii 3937]**MALKAKKSVPQHPGIADTYKDAYGNEQAIDQETREKLLQLLDVAEPTVAPLPSVCVFRQGQQNRLPLRDEGEYGWTLTYEKGGIIEGRSTGQAELALPDNLPLGYHQLILTQGEQQWSCRVIVAPARCYEPDPLTQGKRWWGVMVQLYTLRSSDNWGIGDFGDLKTLVEQVARRGGAFVGLNPLHALYPAEPEAASPYSPSSRNWLNIIYIDVNQVDDFHQSDAAGEWWKQDDVQRRLTAARASRWVDYTAVTSLKLTALRLAFNHFNRRNALDPRKTAFQQFLKTHDESLLQQATYDALQAWLKQQGEPAADWLQWPREYHDARSDASLRFRQEHADDVQFYCWLQWLAHEQLAACFSHSKQLGMPIGLYRDLAVGVAQGGVDTWGDQQLHCMSVTLGAPPDPLGPGGQNWNLTPMHPMLLRQRGYQPFIDLLRSNMAHSGALRIDHVMGLLRLWWILSGNTATRGAYVLYPVDDLLGILALESHRHRCLVIGEDLGTVPEEIVNKLRDNSVYSYKVLFFEKDQHDRFRAPDAYPTRSMATITTHDLATLRGYWQGVDLTLGKDLGLYPTDALLQQQHDARESAKQGLLDALHEQGLLPQRVGRNASLTTMSAQLNRGVQRYLADSASALLGLQLEDWLDMATPVNVPGTHQEYPNWRRKLSRSLDSIFTDRYLERLIRDIDLRRGGPVPSRNRKTAKPAGDETPEETKKEVQKETNKEAKKDTKKA

GH78

>**gb|ACT05921.1| alpha-L-rhamnosidase [Dickeya zeae Ech1591]**MVSITKPMLRINCKSNSIVVDKLPLHLSWSVDFKQKAYEVSVIKNDKVIYFAEQISNNTVLMIDSFELDKNSEYVVEVCAYNQDEQYDILRNTFKTGNFGHFIGQWISGGKTLATESDYYLENRNSILRKVFVVDQDIVDSNINIVGLGYYKLYINGEEVGDSELNTDWTNYNETVYYDTYDVNRYLKKGDNEILIELGNGWFNPAPLTLFGKYNLRNVLSIGEPQTIADLVIKYAKETVTVSSDESWEVCDGPYLFNNIYLGEVLDFRLIKGQNTFLVTKPVWRPVVINHGPRGRLIPSFIPKIKKSAQLTPHHIHVVDENEIIVDFGEVLTGFIDITLAAYDAQEIELIYSEEINNDYILQTASTLAGFIGEEVDNGVVIPGGPGAPHRAEQKDKIICKNGFNRFLNKFTYHSFRYMQIKGLTLDQIHDVRAVYVHTDLAENGTFNCSDVYLNKLLKTGNITKLNNIHSVFSDCARERFAYGGDIVALANSQVYQFDTASLYEKTIYDFVDDIRLNGGFPETAPFVGIKTNGTGEEAGPLGWQLAFSYLLNIHYRHYGNLQLIKDMFPYFEKQVIYLNGFNLDELSLCCLGDWGSRDKNSEDYKSSSPAIRFTTACFYYFHILLMAKFSTYLSFDEKSEFYLSQASALKNKIINQYRNTDGSFSDKSQTSYIFAVYFNLVDDISDAVNQLVALIRNNNYVMRCGIFGQSFSYEILRQHGHNDVVYHWLNSEDGFKSMLGSEYRTLKEYFGDNKHGSCNHAMFSSYISWLYQGLGGISIQEHAIASDQVVISPFIIDSLDYVECEYQSVRGLISCKWHRVEAHVELVIKVPFNLKGCMLSLDKRYNIHVNNVIEIYSDESKRYFDITDMGEVEIILTPALH

GH94

>**gb|ACZ77398.1| glycosyltransferase 36 [Dickeya dadantii Ech586]**MKTNIKQWLTAHKPEKAQPEKPVWKDNASAYDLAIKAELFSRAQMERYGQKLAHSHKLSPTRQPYYLLQRLKDNEAMITRNCYVLNAAAQSSITPEGEWLLDNYYLIEEQIRMVRHHLPKNFGKGLPVLAPPHDCPRIYDIASEAIAHGDGRWDTTSLTGYIAAYQQVTPLSLGELWALPGMLRLAIIENLRRISIEVANAQKARNLADAWVTRILECAENTPVDVIMVIADLARSRPPLSSAFVAEMVRRLQGRGAMLALPLTWVEQRLAESGITTDVLIRRFNQQLAASQLSVSNSIAGLRQLSETNWTDFAEAMSLVEQTLRQDPAGVYPDMHFDTRDNYRHSIETLARHSRHSELDIARHILTQAQAANTATPGYHVGYYLIGAGRPELERQLAVNTSWITRLRQGFNQVSLLSWLGSLSLLTLTLTADMVLKTHEQGMHWPLWLMALPLAVVISQLASHLLSEAVTRWRTPLPLPRMDFSTGIPPQFSAMVVIPCLLTHRESTDRLINSLEVCYLGNNSANLYFALLTDFTDSPTENTPENRVLLSWVGSQIQNLNHRYAKGSRPLFYLLHRSPQWNPQQGVWMGYERKRGKLSMLNSWLRQPGAQFSTVVGDEQGLPERVKYVITLDSDTVLPRDTAHKLVATLAHPLNHPVYDPTKRRVVTGYGILQPGLAEEIPRNGQGRYAAICSSVAGNNPYSMMSSDVYQDLFGEGSFVGKGIYDVDTFVEATHNTCPENLVLSHDLLEGCYARSGLLSEVLLYEHYPNNYLTDVARHSRWIRGDWQLLNWLTPRVKTADGSWVKNPLSALSYWKLLDNLRRSLVAPSLWGLLFCALLLVPNPFYWLGILAMTLLLPTLLAVTLDLVNKPMRRPFWPHLILVSSGVVKRLIRIGLDFATLPHKAGYSLYAILTTLWRLGISHRNLHQWASIDQCADGEEASPWRFYQTMWLNVVSGLALIALTAQFAPMWLLFALPIGTLWCLAPLLLSWLSRPPRRRPPTISIGQTRFLRQTSREIWAFFDTFATAKDNWLPPDNYQEIPRAMLAHRTSPTNIGLALMANLTAWDFGYIPLSDVLRRVTHTLDTLDKMAHYRGHLYNWYDTRTLAPLNPRYISSVDSGNMASHLLTLSAGLTLSRHQPILNSSQMLAGLEDTLCLLETAWGRNAPTSLRQLHKHCTRAATLPPALLFAELNNMRAQCRRLHALCNREDSRIRRWVDHLRHQLARFCREWSSLLGWITPDWRAATLPSLTWLAQATPDAEGAPSPAAIGRARRRLNIITELELRLNAHARMDFTFLYNPVTSLLSIGYHSDHQKLDTSYYDLLPSEIRLTSFLAITTNQLPLKSWFALGRLFTTINNETALMSWSGSMFEYLMPSLVMPTYPGSLLEAMNHSAVNRQIDWGKARGVPWGISESGYYAFDAQQNYQYHAFGVPGLGLRRGLADDMVIAPYATLMALMVVPQKAYENLVNLEKIGARGEYGFYEALDYTPSRLANGQQYAVVRSWMAHHQGMAFQALSHLLLNAPMVDRFMSCPAFQSARLLLQERTPDAIELYSPRRHFESHEGALPSARYEAREFTGVGNLPPEVQLLSNTRYHLMVTQSGGGYSHWNDLALTRWRSDTTCDDQGTFCYISDPKTGDVWSNAWQPLGGPVSQYHVIFTDASAEFRRTEGTLSIKTEIVVSPEDDIELRRVTLLHRGRQPRTLELTTYAEVVLAYAASDLAHPAFSKLFVQTELIPEQDTILCHRRPRSPDDPCVWLFHMMVVRGQTPEQKTSFETDRARFLGRGRTTANALALRQNGPLSNTAGPVLDPIFAIRQSVVLQPGKPVIVDMVYGVADNRQRSQALLEKYRDHPIAERVFELAWSHSQVMLRQINANEDDATLFNRLASALLFPGPELRADASIISRNRRGQPGLWGWAISGDLPIVILNVTRNDSLAEIATLIQAHHYWRQKGLSVDLVILNDSQGGYQQELYHQIMDLIGTVSATSQMDKPGGIFVRNGELLSADDRLLLLSVAHILLDDRAGGLKEQLNQRVQATVAMQPTLIPHTGLPVNQHEPWQPDTRDLLFFNGYGGFSANGREYQITLADNAPTPAPWSNVLANAQFGTVISEAGQAYTWYENAHEYRLTPWENDPVSDNAGEAFYLRDEESGAVWSPTPLPVRGSGHYLTRHGFGYSVFTHRETGIDSELTVLVAEHAPVKFAILTLSNNSGRTRRISATGYVEWTLGESRTHSAMHVVTSPAAVTNGCGVLAHNFYRSNGSERTAFFAVTGVHCSVTGDRREFLGRNGSRREPAAMTQRTLSDNTGAGLDPCAAVQSTTKLIDGDQRTFVFVLGVGQRHQHAELMIAQYLSEDAARVELACVHRYWRNLLDNIVVDTPDPAVNLLANGWLLYQTLASRIMARSGYYQSGGAFGFRDQLQDALALSHAAPERLREQILLCASRQFIEGDVQHWWHPPLGNGVRTHCSDDYLWLPFALCHYVETTGDAAILEQRQPYLEGRQLQPGEESLYEQPTVSTLEETLWQHGVKAIRYGLRFGRHGLPLMGSGDWNDGMNRVGLAGLGESVWLGFFLYDVLQRFARLAEQKQEHDIVALCRTQAARLQTSLETAGWDGNWYRRGYFDRGEPLGSKTSPECQIDAIAQSWAVLSGAGSPEHCAQAMQALDQQLVDDDAGLIKLLTPPFDGRGPSPGYIQGYPPGVRENGGQYTHGALWAVMAFAHRGDTARAWQLWSLINPINHALNADAVERYKVEPYVMAADVYSVEPHTGRGGWSWYTGSAGWAYRLIVEALLGVKRHGTTIAVHPLLPQNWPSVSLRYQHGNSHYQITVTRGDDDYCVTLDGNVLPGDRIPLVDDGQSHKVDIVQR

GH102

>**gb|ACS86778.1| MltA domain protein [Dickeya dadantii Ech703]**MLTGVVIAVLAGCQSRPTDRGQQYKDGHLNQPLALVNEPNANGKPVNAGDFTHQISQIQSASPSLYYRNSDTFQAIRNWVQAGGDTRELSRFGLNAWQMEGVDNFGNVQFTGYYTPVVQARHYRQGEFRYPLYAMPRAARNHRLPDRAAIYSGALSDNLAIAWTNSLMDNFMMEVQGSGYVDFGDGSPLTFFGYAGKNGHAYRSIGKVLIDRGEVPKEEMSMQAIRQWAERHSEAEVRGLLEQNPSFVFFKPMASMPVKGASAVPLVAKASVASDRSLIPAGTTLLAEVPLLDNQGKFTGQYEMRLMVALDVGGAIKGQHFDIYQGIGPEAGHAAGYYNHYGRVWVLRNAQAQSGMLFSANAGEALSPQSN  
  
>**gb|ACT08009.1| MltA domain protein [Dickeya zeae Ech1591]**MKGWWGKYVLTGVVIAILAGCQTRPSDRGQQYKDGRLDQPLEWVNAPNANGKPVNAVDFSQQVSQIQSSSPGLYSRNSDIFQAVQNWIQAGGDTRHLAQFGLNAWQMEGVDSFGNVQFTGYYTPVVQARRYRQGEFRFPLYAMPRVRKNGRLPDRTAIYSGALSNELAIAWTNSLMDNFMMEVQGSGYVDFGDGSPLTFFGYAGKNGHAYRSIGKVLIDRGEVPREEMSMQAIRQWADRHSEAEVRDLLVQNPSFVFFKSMASMPVKGASAVPLVARASVASDRSLIPAGTTLLAEVPLLDNQGKFTGQYEMRLMVALDVGGAIKGQHFDIYQGIGTDAGHAAGFYNHYGRVWVLKNAQSSSAMPLLSAGNNNTAGNTGGLVSNPNE  
  
>**gb|ACZ75794.1| MltA domain protein [Dickeya dadantii Ech586]**MKGWWGKYVLTGVVIAILAGCQTRPSDRGQQYKDGRLDQPLEWVNTPNANGKPVNAGDFSQQISQIQASSPGLYSRNSDIFQAVQNWLQSGGDTRQLTQFGLNAWQMEGVDSFGNVQFTGYYTPVVQARRYRQGEFRFPLYAMPRVRKNGRLPDRAAIYSGALSNELAIAWTNSLMDNFMMEVQGSGYVDFGDGGPLTFFGYAGKNGHAYRSIGKILIDRGEVPREEMSMQAIRQWADRHSEAEVRDLLVQNPSFVFFKSMASMPVKGASAVPLVARASVASDRSLIPAGTTLLAEVPLLDAQGKFTGKYEMRLMVALDVGGAIKGQHFDIYQGIGPEAGHAAGFYNHYGRVWVLKNAQSSSAMPLLSASNGAATSTGGLMGSNPH  
  
>**gb|ADM97258.1| membrane-bound lytic murein transglycosylase A [Dickeya dadantii 3937]**MKGWWGKYVLTGVVIAILAGCQTRPSDRGQQYKDGRLDQPLEWVNAPNANGKPVNTVDFSQQISQIQASSPGLYSRNSDVFQAIHNWIQAGGDTRQLTQFGLSAWQMEGVDSFGNVQFTGYYTPVVQARRYRQGEFRFPLYAMPRVRKNGRLPDRAAIYSGALSNELAIAWTNSLMDNFMMEVQGSGYVDFGDGSPLTFFGYAGKNGHAYRSIGKVLIDRGEVPKEEMSMQAIRQWADRHSEAEVRELLVQNPSFVFFKSMASMPVKGASAVPLVAKASVASDRSLIPAGTTLLAEVPLLDNQGKFTGQYEMRLMVALDVGGAIKGQHFDIYQGIGSEAGHAAGFYNHYGRVWVLKNAQSASAMPLLSAGNGSGTGGGLVGNPN

GH103

>**gb|ACS87000.1| lytic murein transglycosylase B [Dickeya dadantii Ech703]**MAATLFLAELYGYLMRRLIAVVPLLVMLSACSNTPSESQPDAMITGTPSSTSPTPTGGFFNPGAQSGMLANGDFANSPDVDRFIGKMAQQYGFDRQQLHTILGQAQRLDWVIRLMDKQAPAPSTAVPSNIPNGAWLRYRKQFITPDNLQNGVAFWNQYADALERARQIYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLAFAYPRRAEYFQSELEYFLLMAREDGFDPLSLRGSFAGAMGYGQFMPSAFKKYAVDFNGDGIPNLWDPVDAIGSVANYFKSNGWQPNEQIAVPASGQTFSLDTGFKTRYSLSTLAAAGLRPTASLGGYQEASLLRLDMGSYYQFWYGLPNFYAITRYNHSVHYAMAVWQLGEEVRKARQGY  
  
>**gb|ACT06752.1| lytic murein transglycosylase [Dickeya zeae Ech1591]**MVNNRTRCSSMMAKVTVLLLVTGVLSSCAHKHAPPGECRDIDGLLKSHGVTDTPTGLPTPDESFEQWKAKVRQEALSKGITADTFDKAFADLTPDNDVVAATQKQPEVITPVWTYIEQRVTPDNIAQGKTLLKQYAKVAARIEQRYQVEPSLLFAFLAIESHYGANTGDKAVVRSLATLDYYNYRRAFNRQNLIAALRMIQNGDARPEQIKGSWAGAMGMPQFIPTSYLQYAVDFDGDRRPDIWTSFPDTLASVANYMQQAKWKAGVPWGFEVTLPAGFDYAASGLDSQKTVADWQALGVKAAKPRDLSSLSVENASILLPTGKNGPAFLVTGNYRAILRYNNYMSYALTVGLLSDNYQRDTPVLKPWPRQETPLTRKEREALQILLQEKQLYQGAIDGNMGRGTIQAIRAYQQQQGLPADGYPDHALLDRLRCD  
  
>**gb|ACT08148.1| lytic murein transglycosylase B [Dickeya zeae Ech1591]**MAATLFLTELYGYLMRRLVAVFPLLLALSACSNKSTEPAGAEIIGTPAANAPSGGFLLSPAHAGAMLTNGDFANSPEVNRFVDKMVQQHGFERQQLHDVLAQAQRLDWVIRLMDKQAPAPSTATPSNIPNGAWLRYRKQFITPDNLQNGVAFWNQYQDALARAQQVYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLAFAYPRRAAYFQSELEYFLLMAREDGFDPLSLRGSFAGAMGYGQFMPSAFKKYAVDFNGDGIANLWDPVDAIGSVANYFKSNGWQPDGQVAVTASGQTFALETGFKTRYSVSTLAAAGLRPTASLGGAQEASLLRLDMGSYYQFWYGLPNFYAITRYNNSVHYAMAVWQLGDEVRKARQGY  
  
>**gb|ACZ75609.1| lytic murein transglycosylase B [Dickeya dadantii Ech586]**MRRLVAVLPLLLALSACSNKSAEPAGAEIIGTPPSSAPSGGFLLSPGHSGGLLTNGDFANSPDVDRFVDKMVRQYGFERQQLHDVLAQAQRLDWVIRLMDKQAPAPSTATPSNIPNGSWLRYRKQFITPDNVQNGVAFWNQYQDALARAQQVYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLSFAYPRRAEYFQSELEYFLLMAREDGFDPLSLRGSFAGAMGYGQFMPSAFKKYAVDFNGDGIANLWDPVDAIGSVANYFKSNGWQPNQQVAITASGQTFSLETGFKTRYSLSTLAAAGLRPTASLGGYQEASLLRLDMGSYYQFWYGLPNFYAITRYNHSVHYAMAVWQLGEEVRKARQGY  
  
>**gb|ACZ76758.1| lytic murein transglycosylase [Dickeya dadantii Ech586]**MVNSGTQTSSMMSMAKVMKVVVVLLGTGVLSSCAHQHKPPGECRDINSLLTAHGITDTPTGLPTPDESFEQWKAEVRQDALAQGITADTFDSAFAGLTPDNDVVAATQKQPEVIVPVWTYIAQRVTPDNLAQGKALLKQYQKVTARIEQRYQVDPPLLFAFLSIESNYGANTGNKAVVRSLATLDYYNYRRAFNRQNLIAALRMIQNGDARPEQIKGSWAGAMGMPQFIPTSYLQYAVDFDGDHHPDIWTSFPDTLASVANYMQQAKWKAGVPWGMEVNLPARFDYAVSGLDNQKTVADWQALGVKTAVPRDLTSLSAEKASILLPVGKNGPAFLVTGNFRAILRYNNYVSYALTVGLLSDNYQHDTPVLKPWPQRETPLTRKEREALQILLQEKQLYQGAIDGNIGSGTMQAIRTYQQQQGLAADGYPDHALLDRLRCG  
  
>**gb|ADM96987.1| membrane-bound lytic murein transglycosylase B [Dickeya dadantii 3937]**MRRLVAVFPLLLALSACSNKSAEPAGAEIIGTPAANAPSGGFLLSPAHAGGLLTSGDFANSPDVDRFVDKMARQYGFERQQLHDVLAQAQRLDWVIRLMDKQAPSPSTATPSNIPNGAWLRYRKQFITPDNVQNGVAFWNQYQDALDRAQQVYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLAFAYPRRAAYFQSELEYFLLMAREDGFDPLSLRGSFAGAMGYGQFMPSAFKKYAVDFNGDGIPNLWDPVDAIGSVANYFKSNGWQPGGQVAVTASGQTFALETGFKTRYSLSTLAAAGLRPTASLGGVQEASLLRLDMGSYYQFWYGLPNFYAITRYNNSVHYAMAVWQLGEEVRKARMGY  
  
>**gb|ADM98672.1| Membrane-bound lytic murein transglycosylase B [Dickeya dadantii 3937]**MVNNRMQTSPMMSMARVLVVVLGAGLLSSCAHRPTPPGECRNIDSLLKSHGITDTPAGLPTPDESVEQWEAALRQQALSQGITADTFDKAFAGFTPDSDVVAATQKQPELVTPVWTYIEQRVTPENIAQGKTLLKQYAKVTNRIEQRYQVEPPLLFAFLSIESGYGANTGDKAVIRSLATLDYYNYRRAFNRQNLIAALRMIQNGDARPEQIKGSWAGAMGMPQFIPTSYLQYAVDFDGDRHPDIWTSFPDTLASVANYMQQAKWKAGVPWGFEVNLPAGFDYSLSGLDNQKTVADWQARGVRASVPRDLTALSSENASILLPVGKNGPAFLVTANYRAILRYNNYLSYALTVGLLSDNYQRDTPVLKPWPRQETPLTRKEREALQILLQEKQLYQGAIDGNIGRGTTQAIRTYQQQQGLPADGYPDHALLDRLRCG

GH104

>**gb|ACS85898.1| Lysozyme [Dickeya dadantii Ech703]**MSNNSPNITAFLDMLAFSEGTATHPLTQNRGYDVIVTGIDGKPEIFTDYHDHPFADGRPAKVFNRQGQRSTAAGRYQQLYRYWPAYKNRLRLPDFSPASQDTLAIQLIREQKALDAVIAGRIACAIGLCNNIWASLPGAGYGQREHNLDRLLTCYQQSGGRLA  
  
>**gb|ACT06381.1| Lysozyme [Dickeya zeae Ech1591]**MLNNSPNLIAFLDMLAFSEGTATHPLTRNRGYDVIVTGIDGKPEIFTDYHDHPFANGRPGKIFNKQGQRSTAAGRYQQLYRYWPAYKTQLKLQDFGPDSQDTLAIQLIRERNALEDIRQGRIASAINRCNNIWASLPGAGYGQREHNTARLLDIYQQAGGELA  
  
>**gb|ACZ76354.1| Lysozyme [Dickeya dadantii Ech586]**MPTNAPNLTAFLDMLAFSEGTATHPLTRNRGYDVIVTGIDGKPEIFTDYHDHPFANGRPGKIFNKQGQRSTAAGRYQQLYRYWPTYKALLKLPDFGPDSQDTLAIQLIREQQALEDIAQGQIANAITRCSNIWASLPGAGYGQREHSIDRLLTAYQQAGGGLA  
  
>**gb|ACZ77250.1| glycoside hydrolase family 24 [Dickeya dadantii Ech586]**MSQTIDELLISLGLKMDAKSFQAANDAIKGVSDKVLQLAAVAGTGMGLRALTSGVAQTALEMKRVADNTGFTIRQIQGLEMAMNRLKINPEAAQDIAKMIPALQLKARFGQLGDKAYWGAAFNPTEFASMGAMNGLKYFINAYSKMNYDQRTFLRQGAETGQDSPLIRLSEKGSGFLDESMKMAGNMPFPIDNELLKNAQVFNDEMAQFKNNLDALAISLGKGIIPVVNDLLKAANKFIQENPGAAAGVLATAGVGSVVAGSGILKRLLRPTPPKGLAPTASRGLLSRLLFNPLTLEAAAAFTPGNIFTSTDEARAMSNPLLNRGGSGGGVSPREAYQRQTSGEIGKLVDNPNARAYLDAISKAEGTAGYMNNGYNTLFGGEQFANMSDHPRIMKPFTQTDGVQNKTSAAGRYQFTQKSWDEAASALGLTDFSPRSQDMAALWLIQRAGQLDNVVNGDFMSATNGLGGVWASLPSSPYAQPKRSQEDMANYLGDYGYRAGSVPTPAALPVIGQGGSAGGGMVVNQQNEFNISGAGLNEQQMKDAAAAAIGETAKRWQQSYALGR  
  
>**gb|ADM98125.1| Lysozyme [Dickeya dadantii 3937]**MAQTIDELLISLGLKMDAKSFQKANDAIKGVSDKILQLAAVAGTGMGLRALTSGVAQTALEMKRVADNTGFTIRQIQGLEMAMNRLKINPEAAQDIAKMIPALQLKARFGQLGDKAYWGAAFNPTEFASMDAMNGLKYFINAYSKMNYDQRTFLRQGAETGQDSPLIRLSEKGSGFLDESMKMAGNMPFPIDNELLKNAQVFNDEMAQFKNNLDALAISLGKGIIPVVNDLLKVTNRFIQENPGAAKGMLTVAGVGSVVAGSGMLKWLLRPTPPKGPVPTASRGLLSRLLFNPLTLEAAAAFTPGNIFTSTDEARAMSNPLLNRGGSGGGVSPREAYQRQTSGEIGKLVDNPNARAYLDAIAKAEGTAGHMNSGYNTLFGGEQFANMSDHPRILKPFTQTDGVQNKTSAAGRYQFTQKSWDEAASALGLTDFSPRSQDMAALWLIQRAGQLDNVVNGDFMSATNGLGGVWASLPSSPYAQPKRSQEDMANYLGDYGYRAGAVPTPAALPVIGQGGSAGGGMVVNQQNEFHISGAGLNEQQMKDAAAAAIGETAKRWQQSYALGR  
  
>**gb|ADM99103.1| Lysozyme [Dickeya dadantii 3937]**MLNNPNLIAFLDMLAFSEGTSTHPLTGNRGYDVIVTGIDGKPEIFTDYRDHPFANGRPGKIFNKQGQRSTAAGRYQQLYRYWPAYKTQLALPDFGPDSQDTLAIQLIREQRALDDIMQGRLTSAITRCNNIWASLPGAGYGQREHNAERLIAVYRQAGGKLA

GH 105

>**gb|ACS84524.1| glycosyl hydrolase family 88 [Dickeya dadantii Ech703]**MTVQLSRQQTDALLDKVALAFCRLKAIDSVTTDASQSDGLTIQFEEWDWEVGVGLYGFWKLARLRQDDAMLAALEQWYEQKLQAGLPPRQINSTAPMLVLALLCRDNPRPHWLAAVTEWADWLLTSLPKTEDGGFQHTVKERPNTGQLWDDTLFMAGLFLVVAAGVLKRRDLQDEAEYQVLTHARYLADAATGLWYHGWTFIGRHHYAGAFWGRGNAWITLVLPEMCGLADMLLSTPVRRTLEAILEQQTRTLARCQHASGLWHTLLNDPDSPLETSASAGFVAGILTARQMGMLNDFPQDVLEKGLAAVVAQIDEQGVVQGVSDGTAMGHDLQFYHDIPNVAVPYGQALAMLMLLAQRHSV  
  
>**gb|ACS84664.1| glycosyl hydrolase family 88 [Dickeya dadantii Ech703]**MTIFPVKQSALLCQPEYFISREELKALICRITDNLINIEDKTGEFLLRLDDGRVIDTKGWAGWEWTHGIGLYGMYQYYRQTGDDSMRAIIDDWFSARLAEGTPTKNVNTVCPFLTLAYRYEETGNSHWQPYLERWAEWVMYDMPRTRKNGLQHIVYNSENTDQLWDDTLMMSVLPLAKIGKLFNRPEFVEEATYQFLLHVQYLMDRQSGLWFHGWTFDGNHNFAQARWARGNSWLTMVIPEFIELLDLPEHNATRRFLVQVLESQIEALATYQDDSGLWHTLLDDPNSYLESSATAGFAYGILKAVRKRYIDRRYAEMAEKAVRGVVGNINAEGELLQVSFGTAMGKDLDYYRQIPLTSMPYGQAMAILCLSEYLRVYL  
  
>**gb|ACT05542.1| glycosyl hydrolase family 88 [Dickeya zeae Ech1591]**MTTQAMSAAAGSRQIDALLDKVALAFCRLKAIDSVSVTDSAQTRDALTIQFEEWDWEVGVGLYGFWKLAQQRQDHAMLAALEQWYEQKLQAGLPPRQINSTAPMLVLALLCRDNPRPHWLAAVEEWADWLLHSLPKTEDGGFQHTVKERPNTGQLWDDTLFMAGLFLVVSAGVLKRRELLEEAEYQLLTHARYLADATTGLWYHGWTFLGRHHYAGAFWGRGNAWVTLVLPEICSLADSPLSVPVRRTLEAILTQQTRALAVCQHPSGLWHTLLNDPDSPLETSASAGFIAGILTARRLGMLADFPQEVLDKGLAAVVAQIDEQGVVQGVSDGTAMGHDLQFYHDIPNVAVPYGQALVMLMLLAQRHSV  
  
>**gb|ACT05699.1| glycosyl hydrolase family 88 [Dickeya zeae Ech1591]**MTIFPVKHSALLRQPEYFISRDELKALICRVTDNLVNIEDKTGEFLLRLDDGRVIDTKGWAGWEWTHGIGLYGIYQYYRQTGDDKMRAIIDDWFTARLEEGTPTKNVNTVCPFLTLAYRYEETGDSRWVPYLERWAEWVMYDMPRTHKNGLQHIVYNSENTDQLWDDTLMMSVLPLAKIGKLLNRPEFVEEATYQFLLHVQYLMDRQSGLWFHGWTFDGNHSFAQARWARGNSWLTIVIPEFIELLDLPEHNATRRFLIQVLESQVEALAKYQDDSGLWHTLLDDPNSYLESSATAGFAYGILKAVRKRYIDRRYAEVAEKAMRGVVANISEHGELLNVSFGTAMGKDLDYYRQIPLTSMPYGQAMAILCLSEYLRVYL  
  
>**gb|ACZ76699.1| glycosyl hydrolase family 88 [Dickeya dadantii Ech586]**MEKRTLNKNIDLLLSGFTELKDNGRFNEPNLDGSIGDYISFASWEWPQGVGLFGLVRLWENNKSNDLYQIIDNWFQKNIEKGLPGLNVNTTAPMLPLSLFWSHHRQPHYQQVLDNWATRVMTELPRTPEQGFQHVVSDGINEMELWDDTLFMVVLFLAHYGTVSGRKELVDEAVRQFLLHARYLNDPQTGLWYHGWSFVENSNFANARWARGNAWITVGILELLDLADVDTGVREYLIECLKKQVNTLIDLQADNGAWHTLLDHPDSYTEISATAGFGYGLLKGTRMGIGDERWQQAGMKALAIVQDNIDAKGTVHNVSYGTRMGRTLQFYKDIPLQPTGYGQALAILCLSEGLHFVN  
  
>**gb|ACZ78156.1| glycosyl hydrolase family 88 [Dickeya dadantii Ech586]**MTIFPVKHSALLRQPEYVISRDELKALICRVTDNLVNIEDKTGEFLLRLDDGRVIDTKGWAGWEWTHGIGLYGIYQYYRQTGDEQMRAIIDDWFTARLEEGTPTKNVNTVCPFLTLAYRYEETGDSRWVPYLERWAEWVMYDMPRTHKDGLQHIVYNSENTDQLWDDTLMMSVLPLAKIGKLLNRPEFVEEATYQFLLHVQYLMDRQSGLWFHGWTFDGNHSFAQARWARGNSWLTIVIPEFIELLDLPEGNATRRFLIQVLESQVDALAKYQDDSGLWHTLLDDPNSYLESSATAGFAYGILKAVRKRYIDRRYAEVAEKAMRGVLANISESGELLNVSFGTAMGKDLDYYRQIPLTSMPYGQAMAILCLSEYLRVYL  
  
>**gb|ACZ78308.1| glycosyl hydrolase family 88 [Dickeya dadantii Ech586]**MTIQSINRSAGSQPIDALLDKVALAFCRLKAINSVTDGAPTGDTLTIQFEEWDWEVGVGLYGFWKLARQRQDTAMLAALEQWYEQKLQAGLPPRQINSTAPMLVLALLCRDNPKPHWLAAVEEWADWLLHSLPKTEDGGFQHTVKERPNTGQLWDDTLFMAGLFLVVSAGVLKRRELLEEAEYQLLTHARYLADATTGLWYHGWTFLGRHHYAGAFWGRGNAWVTLVLPEMCWLTDSPLSAPVRRTLEAILTQQTRALALCQHQSGLWHTLLNDPDSPLETSASAGFIAGILTARQLGMLTDFPQEVLDNGLAAVMAQIDEQGVVQGVSDGTAMGHDLQFYRDIPNVAVPYGQALAMLMLLAQRHSV  
  
>**gb|ADM99820.1| Rhamnogalacturonides degradation protein RhiN [Dickeya dadantii 3937]**MTIFPVKHSALLRQPEYFISRDDLKALICRVTDNLINIEDKTGEFLLRLDDGRVIDTKGWAGWEWTHGIGLYGIYQYYRQTGDERMRDIIDDWFTARLAEGTPTKNVNTVCPFLTLAYRYEETGDSRWLPYLERWAEWVMYDMPRTHKDGLQHIVYNSENTDQLWDDTLMMSVLPLAKIGKLLNRPEFVEEATYQFLLHVQYLMDRQSGLWFHGWTFDGNHSFAQARWARGNSWLTIVIPEFIELLDLPEHNATRRFLIQVLESQVEALAKYQDDSGLWHTLLDDPTSYLESSATAGFAYGILKAVRKRYIDRRYAEVAEKAMRGVVANISENGELLNVSFGTAMGKELDYYRQIPLTSMPYGQAMAILCLSEYLRVYL  
  
>**gb|ADM99981.1| predicted glycosyl hydrolase [Dickeya dadantii 3937]**MTIQSMNGLSEQSMNGLSDSRQIDALLDKVALAFCRLKAINSVTDLNDGAPAGEALTIQFEEWDWEVGVGLYGFWKLARQRRDHAMLAALEQWYEQKLQAGLPPRQINSTAPMLVLALLCRDNPRAHWLAAVEEWADWLLHSLPKTEDGGFQHTVKERPNTGQLWDDTLFMAGLFLVVSAGVLKRRELLEEAEYQLLTHARYLADATTGLWYHGWTFLGRHHYAGAFWGRGNAWVTLVLPEICCLADSPLSASVRRTLEAILTQQTRALAACQHDSGLWHTLLNDPDSPLETSASAGFIAGILTARQLGMLADFPQAVLDKGLAAVMAQIDEQGVVQGVSDGTAMGHDLQFYHDIPNVAVPYGQALVMLMLLAQRHSV