GT1

**gb|ACS86259.1| glycosyl transferase family 28 [Dickeya dadantii Ech703]**MKIFLATLGSAGDVYPFIAIGESLIQAGHDVYLCTNPYFEKTARDRKLHFIPVGSVDSYYQAVNSQRLWHHKSSYKEMCYFINTQQKMMYDALAPHVDNTSVILTSLWAFSAKMLGETKGCCIIPVRVTPSTFISSYDPPYHKKLAWIRHLPLGLRRFLLHMAEKHLLDRELAPFLNEFRNGLGLPHIERVITRWTHKTDAELLCLFPQWFASPLPDWPANLHQVGFPLFNLLNQQEQDETGAFIAQAKTVILMPSWALQVNTTLIVALAKKIRRLGYQCLVVGAPNPQFGDDSGIRFEKHINLAQYLHQFKAIIHHGGIGTIAQSFAAGIPQMVLPSAFDQFDNARRVTAMKCGLSLTEAEAGHMDRRLKRLLNDPDIAENCQRIRARFLAEPAVDTRIVNIIQTAHARHLSHTA  
  
>**gb|ACT06318.1| glycosyl transferase family 28 [Dickeya zeae Ech1591]**MRIFLSTLGSAGDVYPFILIGEALKKAGLEVYLCTNPYFEKTAEERGLHFIPVGSSEEYLRTVNSQQLWHQRSAFNEMVNYMNAQQKPAYDALEPWVDSSSVILTSLWSFSAKMFSETHGCCVIPVRVTPSTFISSYDPPHHRQLAWSRRLPIGLRRLFLYCVEKYLVDRALAPFINNFRSQLQLPRIERILTSWTHHSDSALLCLFPEWFASPLPDWPAHVHQVGFPLFNLLDNQQDDELARFIAHAPTVIFMPSWALSTKRELIVSLVKKTRQRGYQCLIISQLDHHLDDDDGIRVERHINLSQYLHQCAAILHHGGIGTMAQSFAAGIPQLVIPSAFDQFDNARRVTAMKCGTWLKDSDIDNLDEKLRQILDDPDIAENCRRTRQQCVPTQAVCEQIVATVHDAYTRHMARS  
  
>**gb|ACT08102.1| glycosyltransferase, MGT family [Dickeya zeae Ech1591]**MSHILMAAVATPGHVYPMLTIARHLLTKGHRVTLFSGALFREQAQAAGVGFIAFDEAIDFDYRYLERHFPKRATLPPGNAQMALALREFFSAPIPLIDRQLRQVLAHTQADVVMAENCFYGILPLLASEDRPPVIGIGVTPLSFSSRDSIFYGPRIPPALLPPDLTREQLIDQETRELIAGVKEAFDTVMVQSGKPPLTAPFADALISGCDRFLQLSTTELEYHRDDLPSCVRFVGPLPLKVTEEEADQAWWPVEDTRPLVIVSQGTLANVDLQQLIGPTLRALAGLPVRVLATTGGRPVEELAASAPENARVCRFVSLEHWLPRAALLITNGGYGSLNAALSHGVPLIVAGTGEDKLETAARVVFAGCGLNLGTSTPGEQQIADAVMRILEQPGYTQRARWVQADCARHDALEAIAEEVGAIK  
  
>**gb|ACZ76249.1| Sterol 3-beta-glucosyltransferase [Dickeya dadantii Ech586]**MKISIFTAGSMGDIRPFIVLGKALQQMGHECSIMSGERNEKIVTDEGLGYHTWSLDLPEARKIEQELMDGESSYKNAKKMSGVVDQLMSLWVEQAIKAASHSRLIIAANQAVPLAISIGEKLDIPVVTVYFAPLTPSSSIPPFFLKKIIRLPGPINLAVWKLLRIIMWRFVAKSFSACRTRLGLPTWSWFGPWSDKSNQTRKIIYAFSPHVVPRPPEWSEDIVKITGSWFGDIQSMQSVSPTLEQFIAEGAPPVYIGFGSMNSTDPEGLTNKIINVIKRLSVRAVIMSGGGAIKTDMIVAANLPGVICVEHVSHEWLFPRVRTVFHHGGSGTVAAALKAGTPQVIMPFIYDQFYWAWRLEALGSSGGSLDLKRSGEDDIEQALNRSFSSAVRERARVLGQQVRQERGVENTISELQCWGLL  
  
>**gb|ACZ77531.1| glycosyl transferase family 28 [Dickeya dadantii Ech586]**MRIFLSTLGSAGDVYPFIIIGEALKNAGLEVYLCTNPYFEKTAKERGLQFIPVGSSEEYLRAVNSQRLWNQKSAFNEMVMYMNAQQQAAYDALEPWVDSTSVILTSLWSFSAKMFSETRGCCVIPVRVTPSTFISSYDPPYHRQLAWGRRLPIRLRRLFLHLAEKYLIDRTLAPSINRFRNQLQLPHIERVLTSWAHRTDSTLLCLFPEWFASPLPDWPPHIRQVGFPLFNLLDNQQDDSLAQFIAHRPTVMFMPSWALSSKQALMVSLVKKIRRRGYQCLIVGKPNDDLANDTGIRIERHVNLNHYLHRCAAIIHHGGIGTMAQSFAAGIPQLVIPSAFDQFDNARRVTAMKCGTWLKDNEIDRFEDTLCQLLDDPEIAENCQRIRQQCLPGPVIGEQIVTTVCDAYARHTAKSHSSPG  
  
>**gb|ADM97127.1| N-glycosyltransferase [Dickeya dadantii 3937]**MMSHILMAAVATPGHVYPMLTIARHLLTKGHRVTLFSGALFREQAQAAGVGFIAFDEAIDFDYRYLERHFPRRATLPPGNAQMALALREFFSAPIPLIDRQLRAVLAQTGADVVMAENCFYGILPLLASEDRPPVIGIGVTPLSFSSRDSIFYGPRIPPALLPPDLTREQLIDDETRELIAGVKEAFDTVMVQSGQQPLTAPFADALISGCDRFLQLSTTELEYHRDDLPSCVRFVGPLPLKVTEEDAEQALWPPQDNRPLVIVSQGTLANVDLQQLIGPTLRALADLPVRVLATTGGRPVEALAASVPENARVCRFVSLEHWLPRAALLITNGGYGSLNAALSHGVPLIVAGTGEDKLETAARVVFAGCGLNLGTSTPGEQQIADAVTRILEQPGYTQRARWVQADCARHHALEAIAEEVAAIG  
  
>**gb|ADM99203.1| Rhamnosyltransferase I, subunit B [Dickeya dadantii 3937]**MRVFLSTLGSAGDVYPFIKIGEALKNAGLDVYLCTNPYFEQTAKERGLNFISVGNSEDYLRAVNSQRLWHHQSAFNEMVNFMNAQQQAAYDALAPWVDHASVILTSLWSFTAKMFSETRGCCVIPVRVTPSTFISSYDPPYHRQLLWVRRLPMYMRRLFLYLAEKYLADRQLAPFINTFRSRQGLPRIERVLTSWTHRTDAALLCLFPEWFASPLPDWPAHVRQVGFPLFNLLDKQQDDDLAQFIARERTVVFMPSWALSTKRPLAISLVKKIRQRGHQCLIVGKPYHELADDTGVRAESHINLGQYLHRCAAIIHHGGIGTMAQAFAAGIPQLVIPSAFDQFDNARRVTAMKCGEWLPESDIDQLGDKLHSLLGNADIAEHCQRIRQQFPSEQTVCQRIVDTVREAYARHMAQG

GT5

>**gb|ACS84097.1| glycogen/starch synthase, ADP-glucose type [Dickeya dadantii Ech703]**MRVLHVCSEFFPLLKTGGLADVVGALPNAQIETGLDVRVLLPAFPDVKRGIPDTQVVRELETFAGHVTIRYGHFNGVGVYLIDVPHLFERAGSPYHDTSMFAYTDNFLRFGLLGWVGAEMASGIDPFWRPDIVHAHDWHAGLACAYLAAKGRPAKSVFTVHNLAYQGLFDARHMADLRLPPEFFHMYGLEFYGQISYLKAGLYYADHVTTVSPTYAHEITQTEFGYGMEGLLKAREDEGRLSGILNGVDESIWNPAHDALLTATYSRDELAKKAENKRHLQTAMGLKVDDRVPVFAIVSRLTNQKGLDIALQAVPELLEQGGQLVVLGAGDAVLQEGFLAAAAEYHGRVGVQIGYHEAFSHRIIGGADVIMVPSRFEPCGLTQLYGLKYGTLPLVRRTGGLADTVADCSLENLADGLASGFVFSDCNVASLSRAIRRVFVLWSRPSLWRYVQRQAMAMDFSWQVAAQAYRALYQRLW  
  
>**gb|ACT05119.1| glycogen/starch synthase, ADP-glucose type [Dickeya zeae Ech1591]**MRVLHVCSELFPLLKTGGLADVVGALPSAQIAAGMDVRVLLPAFPDVKKGIPDAQVVRELDTFGGHVTLRYGHYNGVGIYLIDVPHLYDRAGSPYHDTSLFAYSDNVVRFGLLGWMGAEMASGADPFWRPDIVHAHDWHAGLACAYLAAKGRPAKSVFTVHNLAYQGLFDARHMSQLRLPPEYFSMYGLEFYGQISYLKAGLYYADHITTVSPTYAHEITQPEYGYGLEGLLKSREEAGRLSGILNGVDDDIWNPAHDSLLTATYSRDELARKAENKRHLQTAMGLKVDDRVPVFAIVSRLTSQKGLDIALQTVTSLLEQGGQLVVLGAGDATLQEGFLAAAAEYHGRVGVQIGYHEAFSHRIIGGADVIMVPSRFEPCGLTQLYGLKYGTLPLVRRTGGLADTVADCSLENLADGLASGFVFSDCNVASLSRAIRRVFVLWSRPSLWRYVQRQAMAMDFSWQVAAQAYRALYQRLW  
  
>**gb|ACZ78668.1| glycogen/starch synthase, ADP-glucose type [Dickeya dadantii Ech586]**MRVLHVCSELFPLLKTGGLADVVGALPGAQIAAGMDVRVLLPAFPDLKKGIPDAQVVRELDTFGGHVTLRYGHYNGVGIYLIDVPHLYERAGSPYHDTSLFAYTDNVLRFGLLGWMGAEMANGVDPFWRPDIVHAHDWHAGLACAYLAAKGRPAKSVFTVHNLAYQGLFDARHMSELRLPPEYFHMYGLEFYGQISYLKAGLYYADHVTTVSPTYAHEITQAEYGYGLEGLLKSREEEGRLSGILNGVDDEIWNPAHDALLTATYSRDELARKAENKRHLQTAMGLKVDDRVPVFAIVSRLTSQKGLDIALQAVPDLLEQGGQLVVLGAGDATLQEGFLAAAAEYHGRVGVQIGYHEAFSHRIIGGADVIMVPSRFEPCGLTQLYGLKYGTLPLVRRTGGLADTVADCSLENLADGLASGFVFSDCNTASLSRAIRRVFVLWSRPSLWRYVQRQAMAMDFSWQVAAQAYRALYQRLW  
  
>**gb|ADN00394.1| glycogen synthase [Dickeya dadantii 3937]**MRVLHVCSELFPLLKTGGLADVVGALPGAQIAAGMDVRVLLPAFPDLKKGIPDAQVVRELDTFGGRVTLRYGHYNGVGIYLIDVPHLYERAGSPYHDTSLFAYSDNFLRFALLGWMGAEMASGVDPFWRPDIVHAHDWHAGLACAYLAAKGRPAKSVFTVHNLAYQGLFDARHMSELRLPPEYFSMYGLEFYGQISYLKAGLYYADHITTVSPTYAHEITQPEYGYGLEGLLKSREDAGRLSGILNGVDDDIWNPAHDSLLTATYSRDELARKADNKRHLQTAMGLKVDDRVPVFAIVSRLTSQKGLDIALQAVPGLLEQGGQLVVLGAGDATLQEGFLAAAAEYHGRVGVQIGYHEAFSHRIIGGADVIMVPSRFEPCGLTQLYGLKYGTLPLVRRTGGLADTVADCSLENLADGLASGFVFSDCNTASLSRAIRRVFVLWSRPSLWRYVQRQAMAMDFSWQVAAQAYRALYQRLW

GT9

>**gb|ACS83985.1| glycosyl transferase family 9 [Dickeya dadantii Ech703]**MSKFAARLQIFPRAALRLLMKFRRRRPQRVSRILVAHNLLLGDTVMLTPLLAKLRRNYPDADIVLLCKPPFAEVYRLNPYGVSLMPYHPASAASVKAIVRSGPYDLAFVPGDNRYSWLALAAGSRWIVAHTPAKPDVKSWPVDEFVAYPQMPTAWSDAVADMTHGDTPVPLAWALPDVDLGLPDSPYVVLHVGASNSVRFWPSERWLALADWLAGEGFTPVWSGGGNERHIVDAIDPTRRYRSFAGELSLSQLLTLLAHARVLICADTGVAHLAKWVDTPTMTLYGPGNPTAFGPGQFWQANPIINVGFIPIACRDQKTLFSRQLPWLERCNRNEKSCLQFCDGHSACMKGIVLAEVQTAFIHLLRNTR  
  
>**gb|ACS83988.1| lipopolysaccharide heptosyltransferase III [Dickeya dadantii Ech703]**MTSPRNVEFRRILITKFRHHGDVLLTSPLFSILRQRYPEARIDALVFAETAEMLSLHPAIDQLYTVDKKWKKLGPFRHIAKEWELLKTLRQQRYDLIIHLTESMRGFWIARLARIPAGVTFRNAGRDKLSFWRNTFQFRVPRISRRHTVESHLDTLRVLGIQPEMDERRLRLVSGETADRSVERKLRDQHWQGQPFIVVHPTSRWLFKCWKSSAMAETINHLCRQGHTIVLSASPADSEMAMIAEIKSRLEYPVLDLAGQLSLKELAGLIGKAQLLLGVDSVPMHIASAMQTPVVALFGPSGETEWSPWMTVNRVIVSERHHCRPCGKDGCGGSKVSDCLQQISVQQVLLAIDSALLEAQA  
  
>**gb|ACS83989.1| lipopolysaccharide heptosyltransferase I [Dickeya dadantii Ech703]**MRVLIVKTSSMGDVLHTLPALTDAMNIIPGLQFDWVVEEGFAQIPGWHPAVDRVIPVAIRRWRKHWFSGPVRRERARFKTQLREKRYDAVIDAQGLLKSTLLVTRLARGPRHGLDWKSVREPLASWFYQYRHPVARQLHAVERIRELFAVSLNYRKPAEQGDYAIAARFLTTPPADAGRYLVFLHATTRDEKHWPEAHWRKLIALAAPSGLRIKLPWGAEHEHQRALRLAAGFPHVDVLPKLTLEQVATVLAGARAVVSVDTGLSHLSAALDRPNITLYGPTDPGLIGGYGKHQLVCRPANSRNLADLDAANVWQLCIPLIE  
  
>**gb|ACS83990.1| lipopolysaccharide heptosyltransferase II [Dickeya dadantii Ech703]**MKILVIGPSWVGDMMMSHSLYRTLKAEHPDAIIDVMAPAWCRPLLARMPEVNQALAMPLGHGALALRERRQLGRGLREQDYDRAIVLPNSFKSALVPFFAAIPRRTGWRGEMRYGLLNDIRPLDKTAFPLMVQRYVALAYARESIRRADDLPQPLLWPQLQVSETEIADVTSAFNLMDARPSIGFCPGAEFGPAKRWPHYHYGALAQRLIEQGYQVILFGSANDRQAGEDIRQTLDESTREYCINLSGQTSLDQAVVLLAACQAVVSNDSGLMHVAAALGRPLVALYGPSSPDFTPPLSHQARVIRLITGYHRVRKGDAEQGYHQSLIDIQPSQVLAALADYLPGQGEPA  
  
>**gb|ACT08747.1| lipopolysaccharide heptosyltransferase II [Dickeya zeae Ech1591]**MKILVIGPSWVGDMMMSHSLYRTLKAEHPDAIIDVMAPAWCRPLLARMPEVRQALPMPLGHGMLALGERRRLGVSLREQQYDRAYVLPNSFKSALVPFFANIPHRTGWRGEMRYGLLNDLRVLDKPAFPLMVQRYVALAYDRQRIRTSADLPQPLLWPQLTVQDAEIADIAAAFNLTDTRSLIGFCPGAEFGPAKRWPHYHYGALAQSLVEQGYQVVLFGSKNDHQAGEDIRQTLSDEAKEHCLNLAGQTTLDQAVVLIAACQAVVSNDSGLMHVAAALNRPLVALYGPSSPDFTPPLAQQAEVIRLITGYHRVRKGDAEQGYHQSLIDIQPQQVLDALSRYLPAKGEPA  
  
>**gb|ACT08748.1| lipopolysaccharide heptosyltransferase I [Dickeya zeae Ech1591]**MRVLIVKTSSMGDVLHTLPALTDAMQVIHGIQFDWVVEEGFAQIPSWHPAVDRVIPVAIRRWRKSWFSRETRAERAAFKKQLREKRYDAVIDAQGLLKSAVLVTRLALGNKHGLDWKSAREPLASWFYQYRHPVARQQHAVERIRELFSVSLNYRKPAEQGDYAIAARFSSAQPADSQPYLVFLHATTRDEKHWPEAHWRELIALAEPRGLRIKLPWGAEHEHQRAQRLAAGFSHVDVLPRLTLEQVAGVLAGAHAVVSVDTGLSHLAAALDRPNITLYGPTDPGLIGGYGQNQQVCRPAGSRNLADLHAADVWQHCASLLTE  
  
>**gb|ACT08749.1| lipopolysaccharide heptosyltransferase III [Dickeya zeae Ech1591]**MTSPRKVELRRILITKFRHHGDVLLTSPLFSILRQRYPDAQIDALVFADTAEMLSLHPAIDHLYTVDKKWKKLGVFGHLAKEWALLKTLRAQRYDAIIHLTESMRGLWIARLAGIPLGVTFRNSARDKLSFWKKTFQYRVPRIPRRHTVESHLDTLRALGIQPELEERRLQLVAGDDADQAVDQKLRAQQWQGQPFIVVHPTSRWLFKCWKSSAMAQAINTLSERGYTIVLSASPAESEMAMIADIKSQLTHPVLDLAGQLTLKQLSSLIGKAQLLLGVDSVPMHIASAMQTPVVALFGPSGETEWSPWMTVNRVIVSDRHPCRPCGKDGCGGSKISDCLQQISVQQVLLAVDSALLEAQG  
  
>**gb|ACT08752.1| glycosyl transferase family 9 [Dickeya zeae Ech1591]**MSKFAARLQIFPRGLLQLLKKPWRRAPAEVDRILVAHNLLLGDTVMLTPLLAKLRRNYPRAEIVLLCKPAFVEVYRLNPYGVVPMPYQPSSSASVSAIVSSGPYDLALIPGDNRYSWLALAAGSRWIIAHRPALHNAKSWPVNEYHDYPAEPMAWGDAMATLTHGELPEPLRWSVPACDFTPPASPFVVLHVGASNPVRFWPPEQWLALADWLTTQGYTPVWSGGGNERHIVDAIDPQRHYRSFAGELSLSQLLALLAGAKALICADTGVAHLAKWVNTPTMTLYGPGNPVAFGPGRFWQNNPIINIGFHPISCRDQHTLFGRELAWLERCNRTEARCLQFCDGQSACMRHITLPEIQSAFIHLLRKI  
  
>**gb|ACZ75056.1| glycosyl transferase family 9 [Dickeya dadantii Ech586]**MSKFSARLRIFPRALLALLKKPWRRPPSTVKRILIAHNLLLGDTVMLTPLLAKLRRHYPQAEIVLLCKPAFVEVYRLNPYGVVPMPYQPASAASVAAIVNSGPYDLALIPGDNRYSWLALAAGSRWIIAHRPALHNAKSWPVNEYRDYPDEPMAWGDAVATLADGELPFPQRWAAPAYDFPPPASPFVVLHVGASNPVRFWSPEQWLALADWLAAQGYTPVWSGGGNERHIVDSIDPTRRYRSFVGELSLSQLLALLAGAKALICADTGVAHLAKWVDTPTMTLYGPGNPIAFGPGHFWRNNPIINVGFHPISCRDQHTLFGRELPWLERCNRNEANCQQFCNGQSACMQHITLSEIQTAFIHLLRKIQ  
  
>**gb|ACZ75059.1| lipopolysaccharide heptosyltransferase III [Dickeya dadantii Ech586]**MTSPHKVELRRILITKFRHHGDVLLTSPLFSILRQRYPDAQIDALVFADTAEMLSLHPAIDHLYTVDKKWKKLGVFGHLAKEWALLKTLRAQRYDTIIHLTESMRGLWIARFAGIPLGVTFRNSARDKLSFWKKTFQHRVPRISRRHTVESHLDTLRVLGIQPELEERRLQLVAGDAADQAVDQKLRDQQWQGQPFIVVHPTSRWLFKCWKSSAMAQAINTLCERGHTVVLSASPAESEMAMIADIKSQLTHPVLDLAGQLTLKQLSSLIGKAQLLLGVDSVPMHIASAMQTPVVALFGPSGETEWAPWMTINRVIVSDRHPCRPCGKDGCGGSKVSDCLQQISVQQVLLAVDSALLEAQA  
  
>**gb|ACZ75060.1| lipopolysaccharide heptosyltransferase I [Dickeya dadantii Ech586]**MRVLIVKTSSMGDVLHTLPALTDAMQVIHGIQFDWVVEEGFAQIPSWHPAVDRVIPVALRRWRKSWFSRETRAERAAFKTQLREKHYDAVIDAQGLLKSAVLVTRLAYGNKHGLDWKSAREPLASWFYQYRHPIARQQHAVERIRELFSFSLNYRKPTEQGDYAIAARFLSAQPADSQSYLVFLHATTRDEKHWPEAHWRKLIALAEARGLRIKLPWGAEHEHQRAQRLAAGFSHVEVLPRLSLEQVAGVLAGAKAVVSVDTGLSHLAAALDRPNITLYGPTDPGLIGGYGQNQHVCRPANSRNLADLQAADVWQHCASLLTE  
  
>**gb|ACZ75061.1| lipopolysaccharide heptosyltransferase II [Dickeya dadantii Ech586]**MKILVIGPSWVGDMMMSHSLYRTLKAEHPDAIIDVMAPAWCRPLLARMPEVRQALSMPLGHGMLALGERRRLGVSLREQQYDRAYVLPNSFKSALVPFFAAIPHRTGWRGEMRYGLLNDLRLLDKAAYPLMVQRYVALAYDRQRVHSAADLPQPLLWPQLTVDDAEIADIAAAFNLTDARPIIGFCPGAEFGPAKRWPHYHYGSLAQSLIDQGYQVVLFGSKNDHQAGDDIRQTLSDDAKDHCLNLAGQTTLDQAVVLIAACQAVVSNDSGLMHVAAALNRPLVALYGPSSPDFTPPLSHQADVIRLITGYHRVRKGDAEQGYHQSLIDIQPQQVLDALSCYLPVKGELA  
  
>**gb|ADN00527.1| ADP-heptose:LPS heptosyltransferase II [Dickeya dadantii 3937]**MKILVIGPSWVGDMMMSHSLYRTLKAEHPDAIIDVMAPAWCRPLLARMPEVHQALPMPLGHGMLALGERRRLGISLREQRYDRAYVLPNSFKSALVPFFAGIPHRTGWRGEMRYGLLNDLRILDKAAFPLMVQRYVALAYDRARIHTAADLPQPLLWPQLAVNDAEIADVTAAFNLTDNRPLIGFCPGAEFGPAKRWPHYHYGSLAQTLIEQGYQVVLFGSKNDHQAGEDIRQTLSADAREHCLNLAGQTALDQAVVLIAACQAIVSNDSGLMHVAAALNRPLVALYGPSSPDFTPPLSHQAEVIRLITGYHRVRKGDAEQGYHQSLIDIQPQQVLDALSRYLPAKGEPA  
  
>**gb|ADN00528.1| ADP-heptose:LPS heptosyl transferase I [Dickeya dadantii 3937]**MRVLIVKTSSMGDVLHTLPALTDAMQVIHGIQFDWVVEEGFAQIPGWHPAVDRVIPVAIRRWRKSWFSRETRAERAAFKKQLREKRYDAVIDAQGLLKSAVLVTRLALGNKHGLDWKSAREPLASWFYQYRHPIGRQQHAVERIRELFSVSLNYRKPTEQGDYAIAARFLAAQPADSQPYLVFLHATTRDEKHWPEAYWRELIALAEPRGLRIKLPWGAEHEHQRAQRLAAGFSHVDVLPRLTLAQVAGVLAGAQAVVSVDTGLSHLAAALDRPNITLYGPTDPGLIGGYGQNQHVCRPAGSRNLADLHAADVWQHCASLLTE  
  
>**gb|ADN00529.1| lipopolysaccharide core biosynthesis protein [Dickeya dadantii 3937]**MTSPRKVELRRILITKFRHHGDVLLTSPLFSILRQRYPDAQIDALVFADTAEMLSLHPAIDQLYTVDKKWKKLGTFGHLAKEWALLKTLRAQRYDAIIHLTESMRGLWIARLAGIPLGVTFRNNARDKLSFWKKTFQYRVPRVSRRHTVESHLDTLRILGIQPEPEERRLQLIAGEDADRAVDQKLRAQQWQGQPFIVVHPTSRWLFKCWKSSAMAEAINTLCERGHTIVLSASPAENEMAMIADIKSRLTHPVLDLAGQLTLKQLASLIGNAQLLLGVDSVPMHIASAMQTPVVALFGPSGETEWAPWMTVNRVIVSDRHPCRPCGKDGCGGGKVSDCLQQISVQQVLLAVDSALLEAQG  
  
>**gb|ADN00532.1| ADP-heptose--lipooligosaccharide heptosyltransferase II [Dickeya dadantii 3937]**MSKFSARLRIFPRGLLQLLKKPWRRAPTAVKRILVAHNLLLGDTVMLTPLLAKLRRNYPRAEIVLLCKPPFVEVYRLNPYGVVPMSYQPASAASVSAIVNSGPYDLALIPGDNRYSWLALAAGSRWIVAHRPALSNAKSWPVNGYRDYPVEPMAWGDAMAALTDGELPAPQRWSAPACDFPPPQSPFVVLHVGASNPVRFWPPERWLALADWLTTQGYTPVWSAGGNERHIVDAIDPERRYRSFAGELSLSQLLTLLADSKALICADTGVAHLAKWVNTPTMTLYGPGNPVAFGPGRFWQNNPIINLGFHPIPCRDQHTLFGRELSWLERCNRNETRCLQFCDGQSACMQQISLPEIQTAFTHLLRKI

GT19

>**gb|ACS86742.1| lipid-A-disaccharide synthase [Dickeya dadantii Ech703]**MPQRPLTIGLVAGETSGDILGAGLIQALKTAVPDARFVGVAGPRMQAAGCEAWYEMEELAVMGVVEVLGRLPRLLKIRRDLTRRFTELQPDVFVGIDAPDFNITLEERLKRSGIKTIHYVSPSVWAWRQKRVFKIARATHMVLAFLPFEKAFYDRFDVPCRFIGHTMADAMPLHPDKLAARRMLGLPEASRCLSLLPGSRSAEVDMLSADFLKTAALLRQTWPDMEVVVPLVNQRRREQFEHIKAAVAPNLAVRLLDGHAREAMIASDATLLASGTAALECMLAKSPMVVGYRMKPFTFWLAKRLVKTPWVSLPNLLAGRELVTELLQDDCTPENLAAALMPWLQGGEQVNVLQQTFLHLHEQIRCNADEQAAQAVLELSRS  
  
>**gb|ACT07974.1| lipid-A-disaccharide synthase [Dickeya zeae Ech1591]**MTQRPLTIGLVAGETSGDILGAGLIRALKAHVPDARFVGVAGPLMQAEGCEAWYEMEELAVMGVVEVLERLPRLLKIRRDLTQRFSALQPDVFVGIDAPDFNITLEGRLKRNGIKTIHYVSPSVWAWRQKRVFKIGKSTHLVLAFLPFEKAFYDRFNVPCRFIGHTMADAMPLHPDKAAARRTLGLPEDARCLAMLPGSRGAEVEMLSADFLKTAQLLRQTYPELEVIVPLVNQRRREQFEKIKAEVAPDMTVRLLDGQARDAMIASDAALLASGTAALECMLAKCPMVVGYRMKPFTYWLAKRLVKTPWVSLPNLLAGRELVSELLQDDCTPDKLSTALLPWLAGGDAAQQLQQTFLHLHEQIRCDADEQAAQAVLELCGYE  
  
>**gb|ACZ75828.1| lipid-A-disaccharide synthase [Dickeya dadantii Ech586]**MTQRPLTIGLVAGETSGDILGAGLIRALKAHMPDARFVGVAGPLMQAEGCEAWYEMEELAVMGVVEVLERLPRLLKIRRDLTQRFSELQPDVFVGIDAPDFNITLEGRLKRNGIKTIHYVSPSVWAWRQKRVFKIGKATHLVLAFLPFEKAFYDRFNVPCRFIGHTMADAMPLRPDKAAARRALGLPEQGRCLAILPGSRGAEVDMLSADFLKTAQMLRQTYPELEIVVPLVNSRRREQFEKIKVDVAPDMAVRLLDGQAREAMIACDATLLASGTAALECMLAKCPMVVGYRMKPFTYWLAKRLVKTPWVSLPNLLAGRELVRELLQDDCTPDKLSAALLPWLEGGDVAQHLQQTFLHLHEQIRCDADEQAAQAVLELWRS  
  
>**gb|ADM97292.1| tetraacyldisaccharide-1-P synthase [Dickeya dadantii 3937]**MAQRPLTIGLVAGETSGDILGAGLIRALKTHVPDARFVGVAGPRMQAEGCEAWYEMEELAVMGVVEVLGRLPRLLKIRRDLTQRFSELQPDVFVGIDAPDFNITLEGRLKRNGIKTIHYVSPSVWAWRQKRVFKIGKATDLVLAFLPFEKAFYDRFNVPCRFIGHTMADAMLLHPDKAAARRALGLAEDARCLAMLPGSRSAEVEMLSADFLKTAQLLRQTYPELEVVVPLVNQRRREQFERIKAEVAPEMDVHLLDGQAREAMTASDATLLASGTAALECMLAKSPMVVGYRMKPFTFWLAKRLVKTPWVSLPNLLAGRELVRELLQDDCTPDKLSAALQPWLAGGEAAQQLQQVFLHLHEQIRCDADEQAAQAVLELWRS

GT26

>**gb|ACS84029.1| glycosyl transferase, WecB/TagA/CpsF family [Dickeya dadantii Ech703]**MRETVPIYMLRGIAVSGFRDRDQCVAYLFPDGQPRPGMLVALNAEKVLTTERNDELRALMTVSCNYADGISVVCSIRRKYRAADVTRIAGVDLWEALMQRAGTLGTPVFLIGGRAQVLAETAERLRTRWRVNIVGMQDGYFDAEQQSTLLERINESGAQLVTVAMGSPRQELLIRDAYRRYPGALYMGVGGTYDVFTGHVRRAPAFWRRNGLEWCYRLLTQPSRIRRQWRLLRYLFYHFSGRL  
  
>**gb|ACT05060.1| glycosyl transferase, WecB/TagA/CpsF family [Dickeya zeae Ech1591]**MKDVPQYAIRGIPVQGFRDREQCVSTLFAGGSPPAGTLIAINAEKVLAAEHDATLRELMRQEEHCNYADGISVVCSIRRKYPGAQVERIAGADLWEALMQRAGQMGTPVFLLGGKPAVLAETERKLREQWQVNIVGVQDGYFAPEQRQSVLARVRDSGAQLVTVALGSPRQELLIRDCRQLYPDALYMGVGGTYDVFTGQVKRAPLTWQRYGVEWLYRLLTQPSRFRRQLKLLRYLAWHVGGRL  
  
>**gb|ACZ78720.1| glycosyl transferase, WecB/TagA/CpsF family [Dickeya dadantii Ech586]**MNDVPQYVIRGIPVHGFRDKAQCVSILFAGGSPQAGTLIAINAEKVLAADREAALRELMLQEGHCNYADGISVVRSIRRKYPGAQVERIAGADLWEALMQRAGELGTPVFLLGGKPSVLAATERKLREQWQVNIVGTQDGYFAPQQRQAVLERVRDSGAQLVTVALGSPRQELLIRDCRRLYPTALYMGVGGTYDVFTGLVKRAPLVWQRHGVEWLYRLLTQPSRFRRQLKLLRYLAWHISGRL  
  
>**gb|ADN00451.1| UDP-N-acetyl-D-mannosaminuronic acid (ManNAcA) transferase [Dickeya dadantii 3937]**MNDAQPQYRIRGIPVQGFRDMDQCVSALFAGGSPHPGTLIAINAEKVMAADRDASLRELMLQEGNCNYADGISVVCSIRRKYPGAQVQRIAGADLWEALMRRAGQLGTPVFLLGGKPAVLAETERKLREQWQVNIVGTQDGYFAPEQRQAVLERVRDSGAQLVTAALGSPRQELLMRDCRRLYPAALYMGVGGTYDVFTGQVKRAPPAWRRYGVEWLYRLLTQPSRFRRQFKLLRYLVWHFGGKL

GT28

>**gb|ACS84459.1| UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Dickeya dadantii Ech703]**MSGEGKRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIDIDFIRISGLRGKGLKALLLAPVRIFRAVCQARAIMRHYRPDVVLGMGGYVSGPGGLAAWLCGIPVVLHEQNGVAGLTNRGLSRIAKKVLQAFPGAFPHADVVGNPVRTDVLALPSPQERLADRQGPVRILVVGGSQGARILNQTMPDVAARLGDAVTIWHQTGKGAQGEVEAAYGRAGRPEHRITEFIDDMAAAYAWADVVVCRSGALTVSEIAAAGLPALFVPFQHKDRQQYWNALPLEKAGAARIVEQPQLSVETVSDILSGWDRGTLRDMAQKARAVAIPDATARVAAEVVAAADSRVAPAAQR  
  
>**gb|ACT05492.1| UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Dickeya zeae Ech1591]**MSGEGKRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIDIDFIRISGLRGKGLKALLLAPVRIFRAVRQAQAIMRRYQPDVVLGMGGYVSGPGGLAAWLCGIPVVLHEQNGIAGLTNRWLSRIAKKVLQAFPGAFPDADVVGNPVRTDVLALPSPTERLAERSGPVRVLVVGGSQGARVLNQTLPGVAARLHDAVTIWHQTGKGAQTEVQAAYEKAGEPQHRVTEFIDDMAAAYAWADVVVCRSGALTVSEIAAAGLPALFVPFQHKDRQQYWNALPLEQAGAAKIIEQAALSVEAISVVLSAWDRATLRDMAQRARTVAIPDATERVAAEVAAAAMQRAAQAVRN  
  
>**gb|ACZ78362.1| UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Dickeya dadantii Ech586]**MSGEGKRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIDIDFIRISGLRGKGLKALLLAPVRIFRAVRQAQAIMRRYQPDVVLGMGGYVSGPGGLAAWLCGIPVVLHEQNGIAGLTNRWLSRIAKKVLQAFPGAFPDADVVGNPVRTDVLALPSPTERLAERSGPVRVLVVGGSQGARVLNQTLPGVAARLHDAVTIWHQTGKGAQVEVQAAYVKAGEPQHRITEFIDDMAAAYAWADVVVCRSGALTVSEIAAAGLPALFVPFQHKDRQQYWNALPLEQAGAAKIIEQAELSVDAISDVLSSWDRTTLRDMAQKARTVAIPDATERVAAEVAAAAMQRTAQAVRN  
  
>**gb|ADN00043.1| UDP-N-acetylglucosamine:N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Dickeya dadantii 3937]**MSGEGKRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIDIDFIRISGLRGKGLTALLLAPVRIFRAVRQAQAIMRRYQPDVVLGMGGYVSGPGGLAAWLCGIPVVLHEQNGIAGLTNRWLSRIAKKVLQAFPGAFPHADVVGNPVRTDVLALPSPTERLADRSGPVRVLVVGGSQGARVLNQTLPGVAARLHDAVTIWHQTGKGAQAEVQAAYAQAGQPQHRITEFIDDMAAAYAWADVVVCRSGALTVSEIAAAGLPALFVPFQHKDRQQYWNALPLERAGAAKIIEQADLSVDTISEVLAAWERATLRDMAQKARTVAIPDATERVAAEVAAAAMQRAVHAVRN

GT30

>**gb|ACS83983.1| Three-deoxy-D-manno-octulosonic-acid transferase domain protein [Dickeya dadantii Ech703]**MIMLQTLYTLLFYMIQPLIWLRLWLRGRKIPAYRKRWGERYGFYKNQVKPEGILLHSVSVGETLAAVPLVRALRHRYPSLPITVTTMTPTGSERALSAFGKDVYHVYLPYDLPGAMSRFLNHIQPRLVIVMETELWPNMIQALHQRHIPLIIANARLSERSANGYRKLGGFMRALLRRITLIAVQNAEDGERFIDLGLKRSQLNVTGSLKFDISVTPELAARAVTLRRQWASQRPVWIAASTHEGEEKIIIDAHCELLRSFPTLLLILVPRHPDRFDDAKAIVKKAGLEYTLRSSGAIPPASSHVVIGDTMGELMLLYGIADLAFVGGSLIERGGHNPLEPAAHAIPVLMGPHIFNFKDICARLRESDGLITVTDTRSLVEQASNLLADEDYRRYYGRHAVEVLHKNQGALQSLLTLLEPYLPPRSQ  
  
>**gb|ACT08754.1| Three-deoxy-D-manno-octulosonic-acid transferase domain protein [Dickeya zeae Ech1591]**MIMLQTLYTFLFYMIQPLIWLRLWLRGRKIPAYRKRWGERYGFYRNQVKPEGILLHSVSVGETLAAVPLVRALRHRYPSLPITVTTMTPTGSERALSAFGKDVYHVYLPYDLPGAMTRFLDHVQPRLVIIMETELWPNLITALHQRNIPLIIANARLSERSANGYRKLGRFMRTLLRRITLIAVQNEEDGERFINLGLKRSQLNVTGSLKFDISVTPELAARAVTLRRQWAPQRPVWIAASTHDGEEKIIVDAHTELLKTFPTLLLILVPRHPDRFDDAKAIVRKAGLEYTLRSAGTVPPASSHVVIGDTMGELMLLYGIADLAFVGGSLIERGGHNPLEPAAHAIPVLMGPHTFNFKDICARLQESDGLITVRDTASLVGQITTLLSDDDYRRYHGHHAVDVLHKNQGALQSLLTLLEPYLPPRSQ  
  
>**gb|ACZ75054.1| Three-deoxy-D-manno-octulosonic-acid transferase domain protein [Dickeya dadantii Ech586]**MIMLQTLYTFLFYMIQPLIWLRLWLRGRKIPAYRKRWGERYGFYQSQVKPEGILLHSVSVGETLAAVPLVRALRHRYPSLPITVTTMTPTGSERALSAFGKDVYHVYLPYDLPGAMSRFLDHVKPRLVIIMETELWPNMITALHQREIPLIIANARLSERSANGYRKLGRFMRTLLRRITLIAVQNEEDGERFINLGLKRSQLNVTGSLKFDISVTPELAARAVTLRRQWAPQRPVWIAASTHEGEEKIIVDAHTELLKTFPTLLLILVPRHPDRFDDAKAIVRKAGLEYTLRSAGTVPPASSHVVIGDTMGELMLLYGIADLAFVGGSLIERGGHNPLEPAAHAIPVLMGPHTFNFKDICARLQQSDGLITVRDTASLVEQVTTLLSDDDYRRYHGHHAVDVLHKNQGALQSLLTLLEPYLPPRSQ  
  
>**gb|ADN00534.1| 3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase) [Dickeya dadantii 3937]**MLQTLYTFLFYMIQPLIWLRLWLRGRKIPAYRKRWGERYGFYKNQVKPEGILLHSVSVGETLAAVPLVRALRHRYPSLPITVTTMTPTGSERALSAFGKDVYHVYLPYDLPGAMARFLDHVQPRLVIIMETELWPNLITALHQRKIPLIIANARLSERSANGYRKLGRFMRTLLRRITLIAVQNAEDGERFINLGLKRSQLNVTGSLKFDISVTPELAARAVTLRRQWAPQRPVWIAASTHEGEEKIVVDAHTELLKTFPTLLLILVPRHPDRFDDAKAIVRKAGLEYTLRSAGTVPPASSHVVIGDSMGELMLLYGIADLAFVGGSLIERGGHNPLEPAAHAIPVLMGPHTFNFKDICARLQESDGLITVRDTASLVEQATTLLSDDDYRRYHGHHAVDVLHKNQGALQSLLSLLEPYLPPRSQ

GT35

>**gb|ACS84098.1| glycogen/starch/alpha-glucan phosphorylase [Dickeya dadantii Ech703]**MNSPFIYNSPTLSVDALKHSIAYKLMFTVGKDPSVASKHDWLNATVLAVRDRMVERWLRSNRAQLSQDVRQVYYLSMEFLLGRTLSNALLAMGMFDDLKLALDAMGLDLNELLEEEDDPGLGNGGLGRLAACFLDSLATMALPGRGYGIRYEYGMFKQNIVEGKQAESPDYWLEYGNPWEFARHSTRYKIRFGGRIQQEGSKTRWLETEEIVACAYDQIIPGFDTDATNTLRLWAAQASNEINLGKFNQGDYFAAVQDKNHSENVSRVLYPDDSTYSGRELRLRQEYFLVSATVQDILSRHWMMHKTYDNLAEKFAIHLNDTHPVLAIPELMRLLIDEHKFKWDAAWKVVTQVFSYTNHTLMGEALETWSVEMLGNILPRHLQLIFEINERFLEEVQARFPNERDLLKRVSVIDEDHGRKVRMAWLAVICSHKVNGVSQLHTDLMVQSLFADFARLYPERFCNKTNGVTPRRWLALANPWLSKVLDDAIGHNWRTDLSQLEDLKPNIDFPAFLQKVRNAKRENKKRLAIYIAQHLDVVVDPNALFDVQIKRIHEYKRQLLNVLHLITLYNRIKDDPSLDRVPRVAIFAGKAASAYYMAKHIIHLINDVAKVVNNDPAVKDKLKIVFIPNYGVSLAQIIIPAADLSEQISLAGTEASGTSNMKFALNGALTIGTLDGANVEMRERVGDDNIFIFGNTTEQVEELRRNGYNPRDFYNQDDELHRVLTQIATGVFSPDDPHRYADLFDSLVNFGDHYQLLADYRSYVDTHDKVDDIYRDEDEWTRRTLYNIANMGYFSADRTIQEYADEIWNIKPIRL  
  
>**gb|ACS84130.1| glycogen/starch/alpha-glucan phosphorylase [Dickeya dadantii Ech703]**MSSSFNLSQFSDSLFRKLNAYGRSSLRELTPRQCWQAVCAALSEQVDALAADSDARLAGAPVEYRHVNYLSMEFLPGRLTANNLINLGWYGVVAQVLERHGLALSDILEQETDPALGNGGLGRLAACYLDAMATAAQPAIGYGLHYQYGLFRQHFDAGEQHETADDWQRDSYPWSHPRPELAVEVGFGGDLIPQPDGGERWVPAQVVIGEATDIPVIGYHNGVMLPLRLWQATHPQPFDLAQFNAGHYLRAEQQGIAASSLTKVLYPNDNHPAGKRLRLMQQYFQCACAVADIFRRHLQAGRALETLPNLEVIQLNDTHPTLAIPETLRLLLDEHQLPWEQAWDITHRLFAYTNHTLMPEALECWDERLFRRLLPRHFSIIKIINARFRQQVEAHWPGNRRLWPRVAVLHRRQVRMANLCVVACFAVNGVAQLHSDLIIRDLFPEYHQLWPEKFHNVTNGITPRRWLLQCNPALSSLIDETLHTPWANRLTALETLADYADDAGFQARYRKIKQDNKADLARFIQREYGILIDPSAMFDVQIKRLHEYKRQHLNLLHILSLYRQLRDNPGLDIVPRIFLFGAKAAPGYVLAKNIIHAINGVAERINRDKRVNDRLKVVFLPDYRVSLAERIIPAADVSEQISTAGKEASGTGNMKLALNGALTVGTLDGANVEMAQQVGEENLFIFGHTVDQVKALQAKGYKPERYIAGHPLLASVLDELASGVFSHGDRTAFAPLLESLLKNGDPYLVLADFTPYCQAQQRVDALYRKPEEWTRRCILNTARMGMFSADRAIHDYQQRIWIVRR  
  
>**gb|ACT05120.1| glycogen/starch/alpha-glucan phosphorylase [Dickeya zeae Ech1591]**MNSPFIYNSPTLSVDALKHSIAYKLMFTIGKDPSIASKHDWLNAAVLAVRDRMVERWLRSSRAQLSQDVRQVYYLSMEFLLGRTLSNALLAMGMFDDLRDALEAMGLDLNELLEEEDDPALGNGGLGRLAACFLDSLATMALPGRGYGIRYEYGMFRQNIVDGKQAESPDYWLEYGNPWEFVRHSTRYKVRFGGRIQQEGSKTRWLETEEIIACAYDQIIPGFDTDATNTLRLWAAQASNEINLGKFNQGDYFAAVEDKNHSENVSRVLYPDDSTYSGRELRLRQEYFLVSATVQDILSRHWTMHKTYANLTEKFAIHLNDTHPVLAIPELMRLLIDEHKFKWDVAWDVVTKVFSYTNHTLMGEALETWPVDMMGKILPRHLQLIFEINDRFLDEVQERFPNEHDLFKRVSIIDEEHGRKVRMAWLAVICSHKVNGVSQLHTDLMVQSLFADFARIYPDRFCNKTNGVTPRRWLALANPSLSKVLDDTIGKTWRTDLSQLADLKPHIDFPAFLQKVRKAKQENKKRLALYIAQHLDIVVDPNALFDVQIKRIHEYKRQLLNVLHLITLYNRIKDDPDLDRVPRVAIFAGKAASAYYMAKHIIHLINDVASVVNNDPEVKDKLKIVFIPNYGVSLAQIIIPAADLSEQISLAGTEASGTSNMKFALNGALTIGTLDGANVEMRERVGEDNIFIFGNTTEEVEALRRSGYNPREFYNQDEELHRVLTQIATGVFSPDDPRRYADLFDSLVNFGDHYQLLADYRSYVDSHDKVDDVYRDEDEWTRRTLQNIANMGYFSADRTIQEYADEIWHIKPIRL  
  
>**gb|ACT05125.1| glycogen/starch/alpha-glucan phosphorylase [Dickeya zeae Ech1591]**MSPLFNSSQFAAALQHQLQACAQPSLQALSLRQCWQWVSAALTEQLDALTSAESAPPDAGPSGVRHVNYLSMEFLPGRLTGNNLLNLGWYNAVAEVLAQHGLALSDLLEQETDPALGNGGLGRLASCYLDAMATVGQPAIGYGLHYQYGLFRQHFDAGFQRETPDDWLRDSYPWARPRPELAVEVGFGGELVAQPGGGERWIPEQVVVGEATDIPVIGYHNGQVQPLRLWQATHSEPFDLEQFNAGHYLKAEQQGIAAASLTKVLYPNDNHAAGKKLRLMQQYFQCACAVADIFRRHERAGRPLATLPDYEVVQLNDTHPTLAIPETLRLLLDEYELSWEQAWQLTGRLFAYTNHTLMPEALECWDERLFGRLLPRHLSIIKTINEHLRRQVEARWPGERQVWARLAVVHRRQVRMANLCVVACFAVNGVAQMHSELVVRDLFPEYYQLWPTKFHNVTNGITPRRWLKQCNPALSALIDETLQTEWGNRLTLLEGLAPYAQDSAFRARYRQIKQDNKTQLAHFLRREYGIVVDPAAVFDVQIKRLHEYKRQHLNLLHILSLYKRLLIDPGLDIVPRLFLFGAKAAPGYVLAKNIIYAINCVAEHINRDKRVNDRLKVVFLPDYRVSLAERIIPAADVSEQISTAGKEASGTGNMKLALNGALTMGTLDGANVEMAQEVGAENLFIFGHTVDQVKTLIADGYKPARYIAANPLLKEILADLADGTFSHGDKTAFAPLLDSLLELGDPYLVLADFAPYCQAQQRVDALYREPDEWTRRCILNTARMGMFSADRAIQDYQKRIWTMRD  
  
>**gb|ACZ78658.1| glycogen/starch/alpha-glucan phosphorylase [Dickeya dadantii Ech586]**MSPLFNPSQFTAALQRQLQALAQPSLQALSLRQCWQLVSAALTEQLDVLIAAEPSPPDAATSISRHVNYLSMEFLPGRLTGNNLLNLGWYDAVAEVLAGHGLALSDVLEQETDPALGNGGLGRLASCYLDAMATVGQPAIGYGLHYQYGLFRQHFEAGFQRETPDDWLRDCYPWARPRPELAVEVGFGGELVIQPDGRERWIPDQVVIGEATDIPVIGYLNGRVQPLRLWQATHSEPFDLEQFNAGHYLKAEQRGIDAASLTKVLYPNDNHAAGKRLRLMQQYFQCACAVADIFRRHERAGRPLATLPDYEVVQLNDTHPTLAIPETLRVLLDDYELPWEQAWQLTGRLFAYTNHTLMPEALECWDERLFGRLLPRHLSIIKTINAHLRQQVEARWPGDKRVWARLAVVYRRQVRMANLCVVACFAVNGVAQMHSDLVVRDLFPEYHQLWPTKFHNVTNGITPRRWLKQCNPALSSLIDDTLRTEWGNRLTLLEGLAPYAQDSAFQARYRRIKQDNKTQLAQFLRRDYGIHIDPSALFDVQIKRLHEYKRQHLNLLHILSLYKRLLTDPGLDIVPRLFLFGAKAAPGYVLAKNIIYAINCVAEHINRDKRVNDRLKVVFLPDYRVSLAERIIPAADVSEQISTAGKEASGTGNMKLALNGALTVGTLDGANVEMAQEVGAENMFIFGHTVEQVKALIADGYKPTRYIAENPLLKEILTELGKGKFSHGDKTAFAPLLDSLLKLGDPYLVLADFAPYCQAQQRVDELYREPDEWTRRCILNTAHMGMFSADRAIHDYQKRIWTMRD  
  
>**gb|ACZ78667.1| glycogen/starch/alpha-glucan phosphorylase [Dickeya dadantii Ech586]**MNSPFIYNSPTLSVDALKHSIAYKLMFTVGKDPSIASKHDWLNAAVLAVRDRMVERWLRSNRAQLSQDVRQVYYLSMEFLLGRTLSNALLAMGMFDDLRDALEAMGLDLNELLEEEDDPALGNGGLGRLAACFLDSLATMALPGRGYGIRYEYGMFRQNIVDGKQAESPDYWLEYGNPWEFVRHSTRYKVRFGGRIQQEGSKTRWLETEEIIACAYDQIIPGFDTDATNTLRLWAAQASNEINLGKFNQGDYFAAVEDKNHSENVSRVLYPDDSTYSGRELRLRQEYFLVSATVQDILSRHWTMHKTYANLAEKFAIHLNDTHPVLAIPELMRLLIDEHKFKWDVAWDVVTKVFSYTNHTLMGEALETWPVDMMGKILPRHLQLIFEINDRFLDEVQERFPNDVDLLKRVSIIDEEHGRKVRMAWLAVICSHKVNGVSQLHTDLMVQSLFADFARVYPERFCNKTNGVTPRRWLALANRPLSKVLDETIGKTWRTDLSQLADLKPHIDYPAFLQKVRKAKQENKLRLAVYIAQHLDIVVDPNALFDVQIKRIHEYKRQLLNVLHLITLYNRIKDDPDLDRVPRVAIFAGKAASAYYMAKHIIHLINDVASVVNNDPAVKDKLKIVFIPNYGVSLAQIIIPAADLSEQISLAGTEASGTSNMKFALNGALTIGTLDGANVEMRERVGEENIFIFGNTTEQVEELRRNGYNPREFYNQDEELHRVLTQIATGVFSPDEPRRYADLFDSLVNFGDHYQLLADYRSYVDSQDRVDEVYCDEDEWTRRTLHNIANMGYFSSDRTIQEYADEIWHIKPIRL  
  
>**gb|ADN00381.1| Glycogen phosphorylase [Dickeya dadantii 3937]**MSPSFNPSRFAAALQRQLQACAQPSLQALSLRQCWQLVSAALTEQLDVLTSADPLPPDAAPAAARHVNYLSMEFLPGRLTGNNLLNLGWYDAVAEVLAQQGLALSDVLEQETDPALGNGGLGRLASCYLDAMATVGQPAIGYGLHYQYGLFRQHFDAGFQRETPDDWLRDSYPWARPRPELAVEVGFGGELVKQADGSERWIPEQMIVGEATDIPVIGYRNGRVQPLRLWQATHSDPFDLEQFNAGHYLKAEQQGITAASLTKVLYPNDNHTAGKKLRLMQQYFQCACAVADIFRRHERAGRPLETLPEYEVVQLNDTHPTLAIPETLRLLLDEHQMTWEQAWRLTGRLFAYTNHTLMPEALECWDERLFGRLLPRHLSIIKTINERLRQQVDARWPGDRQVWARLAVVHRRQVRMANLCVVACFAVNGVAQMHSDLVVRDLFPEYHQLWPTKFHNVTNGITPRRWLKQCNPALSSLIDDTLRTEWGNRLTLLDGLAPYAQDSAFRTRYRHIKQDNKTQLTQFLQREYGIRVDPTSLFDVQIKRLHEYKRQHLNLLHILSLYKRLLADPGLDIVPRLFLFGAKAAPGYVLAKNIIYAINCVAEHINRDKRVNDRLKVVFLPDYRVSLAERIIPAADVSEQISTAGKEASGTGNMKLALNGALTVGTLDGANVEMAQEVGAENLFIFGHTVEQVKTLTAGGYKPARYIAANPLLKEILAELADGTFSHGDKTAFAPLLDSLLKLGDPYLVLADFAPYCQAQQRVDELYREPDEWTRRCILNTARMGMFSADRAIHDYQKRIWTMRD  
  
>**gb|ADN00393.1| Glycogen phosphorylase [Dickeya dadantii 3937]**MNSPFIYNSPTLSVDALKHSIAYKLMFTVGKDPSIASKHDWLNAAVLAVRDRMVERWLRSNRAQLSQDVRQVYYLSMEFLLGRTLSNALLAMGMFDDLRDALEAMGLDLNELLEEEDDPALGNGGLGRLAACFLDSLATMALPGRGYGIRYEYGMFRQNIVDGRQAESPDYWLEYGNPWEFVRHSTRYKVRFGGRIQQEGSKTRWLETEEIIACAYDQIIPGFDTDATNTLRLWAAQASNEINLGKFNQGDYFAAVEDKNHSENVSRVLYPDDSTYSGRELRLRQEYFLVSATVQDILSRHWMMHKTYANLAEKFAIHLNDTHPVLAIPELMRLLIDEHKFKWDAAWGVVTKVFSYTNHTLMGEALETWPVDMMGKILPRHLQLIFEINDRFLEEVQERFPNEHDLLKRVSIIDEDHGRKVRMAWLAVICSHQVNGVSQLHTDLMVQSLFADFARIYPDRFCNKTNGVTPRRWLALANPSLSKVLDDTIGKTWRTDLSQLADLKPHIDFPVFLQKVRKAKQENKKRLAIYIAQHLDIVVDPNALFDVQIKRIHEYKRQLLNVLHLITLYNRIKDDPDLDRVPRVAIFAGKAASAYYMAKHIIHLINDVASVVNNDPEVKDKLKIVFIPNYGVSLAQIIIPAADLSEQISLAGTEASGTSNMKFALNGALTIGTLDGANVEMRERVGEENIFIFGNTTEQVEELRRNGYNPREFYNQDEELHRVLTQIATGVFSPDDPHRYADLFDSLVNFGDHYQLLADYRSYVDNHDKVDDVYRDEDEWTRRTLHNIANMGYFSADRTIQEYADDIWHIKPIRL

GT41

>**gb|ACT06436.1| Methyltransferase type 12 [Dickeya zeae Ech1591]**MTMPDAQPLANNADMAEDNDTTPLSSMSPPIPHTAPFHLHATAHLYGIKSAIPETARVFEIGCKDGGNLLPFALANPQAQAVGVDLDAEQIEKGNALIKQLELENIALFALDLESLLACDPGTFDYIIIHGLFSLIGGETRDALLRFCRDHLTAEGIICYCYNTYPGWKTGEILRDAIQLHSSLANDDKTSQASARAMLTYLSLGTSPDNPQNAALKAFIEQAEKQSDVDFALHYLQGLNQPCYFVDFYSQITKAGFAYVGDVRAYTELAEHYGDQVSSLHETICPENTTYLRQQYLDFAVNRSQRFSMLVSQTNAEDIFSGPDLARLADFSWAGDFQRIQLDSGTILNAHLSGTGETISTENSLVLGMLDILGEAWPNSLTFDELVFNTQLPDKPMPDHRDRVLDALKKLFIKGCSGLYFRLGDCFYRRSVCEKISILSGLAETGFGFNFWHQPVHLSDEEKAILKNLGNNEQYREPDFYVKLFELRNKGVLCGAPRTWLKLMQKAIIHLDADKIPSYIQSFFLIAFGTDNNGKFNAFLNFKNNQRTNSYLDRGVYEKIDYLVDKSEFEKARKRVQEIIASYPDTPSCWYPFINVYLKSNDYDGALKLIVKSIAAGMFSLDICADIVVCFRRQGILYYGLSLARKILLRDETQAKVWDSLGVMLNAVQSLESAFSCMKKALELAPDNLAYISNMGMTCFNLGHKDTLFYQRKVVELAPDAFNLHSNYLLGASHSDEMTPEELYKAHLFFGERVEMVSRRYNCRFNYSTNKVTERPLRIGFISGDFGEHPVTNFLEPIWNALDRREFSLYAYSSFQRKDEKAASLKQTAAGWHDVDKMGDLEVATLINKDEIDILIDLSGHTAYNRLPALAMKPAPIQMTWIGYPGTTGMRAMDYILLYKEFIGYAGKLDEFLTEKPIYLPAVKFFEPNKDSPDVNVLPALSNGYLTFASFNRPQKISDENLVLWGRVLVALPNSRLIIGYMTGQETIDYFRSKLIELGVRDEQLSFRMRTGLSEYLKMHHEVDILLDTYPYTGGTTIGHASWMGVPVLTREGDSLASKQSAVIMRVLGLDEFIAQSDDELIVKAQHWSHSLDKLNKIRSEMRGVMAARINSVDSPSIYFEKAMRRAWEIYCAGERPHSFTIDK  
  
>**gb|ACZ76412.1| Methyltransferase regulatory domain, predicted [Dickeya dadantii Ech586]**MTMPDTQPLANNTDLGEDTGKAPLSSMSPPIPHTAPFHLQATAHLYGIKSAAPEKARVLEIGCKDGGNLLPFALANPQAQAVGVDLDAEQIEKGNGLIQQLELENIALFALDLESLLACDPGTFDYIIIHGLFSLIGGETRDALLRFCHQHLTTEGIVCYCYNTYPGWKTGEILRDAIQLHSGLASDEQTANASARAMLTYMSLGTAPDNPQNAALKSFIEQAEKQSDVDFALLYLQGLNQPCYFVDFYSQITQAGFAYVGDVRAYTELAEHYGDQVSHLHETICPENTVYLRQQYLDFAVNRSQRFSILVPQERAGDILSGPDLAKLADFNWAGNFQRVRADGNRILNAHTSSTGETISTDNPVVLSILDALGESWPASLSLEQLVFNTRFPEKETDNHQQDVLDALRSLFAKGIDGVYVRIGNCPYRNSRHKTLTGLPGLATTDLAFNFWHEPVSLDSDERLFLQQLPPSLKDNDNAFYSQLWALRNKGVVWGTPRAWRDYLQEAIVKADATQVAVYIQSLVVYVSETNAGGFIEPEKPVTHKKNKLQDKNPLSRKVYEEMDRLTSLGHFAEVRTKAEEIISTYPDNLSVWYPFVNTYVRTGDFDGALGVITRAIALMPFNWDFYVDLSVCFWKKNEWHHGMALTRKVLRCDKRKGLAWDTLAVLLNITHNLDSAFICMEKALQIDPENPNFISHMGMVCHNLGRKDAIKYHRKTIELMPEAFHLYSNLLLGLSHDVDVTPQALYQEHVLFGNRVEAAAANYHQHFSYIQNKDSQRPLRIGFISGDFGDHPVTNFLEPIWNSLDRNLFSLYAYSSFQRNDAKAESLKQTAANWHNVDKMGDLELAMLINQDEIDILIDLSGHTAYNRLPVLALKPAPIQMTWIGYPGTTGMKTVDYILLDVHYRQGGALDPYLTEKIIYLPSVKYFEPVKDSPDVNELPALKNGYLTFASFNRPQKISDETLALWAKVLTTIPNSRLIMGYMTGQETIDYFRTRLLECGVNEEQLSFRMRTGLKEYLGMHREVDLLLDTYPYTGGTTVSHAAWMGVPVLTREGESIASRQGSVTMRILGLDDFISTSEDEFLQKALYWSQSLEKLSDVRAGIRGRIAARMNSVLSPSVYFEHAIRNAWQIYCEGKEPSSFSIDWESES

GT51

>**gb|ACS84147.1| penicillin-binding protein, 1A family [Dickeya dadantii Ech703]**MKFVKYLLILAVSCILLGTASLYGLYRYIEPQLPDVATLKDVRLQTPMQVYTADGELIAQFGEKRRIPLKLDQIPPVMVRAFIATEDSRFYEHHGIDPQGIIRATMIALTSGHASQGASTITQQLARNFFLSPEKTLLRKIKEVFLAVRIEQMMTKDEILELYLNKIYLGYRAYGVGAAAQVYFGRTIDQLTLGEMAMIAGLPKAPSTFNPLYSYDRAIARRNVVLARMLDENYITQAQYDQARNEKLNADYHAPEVAFSAPYMAEMVRQEMVKRYGEDAYNDGYKVYTTITRKLQQAADEAVRNNVMAYDMRHGYRGPDQELWKPRTAAWPQDKITEALKKLPTYGPLMPAAVLDATADKAHAMLPSGEKIELTLAGVRWARAYRSDTEQGPTPKRVMDVLDAGQQIWVRKVDKEWWLGQVPDVNSALVSVNPTNGAILALVGGFDFSQSKFNRATQALRQVGSNIKPFLYTAAMDKGLTLATILNDAPITRWDPGAGSDWSPKNSPPVYDGPIRLRQGLGQSKNVVMVRAMRAMGVDYAADYLERFGFPEQNIVHTESLALGAASFTPLQVVRGYAVMANGGYLIDPYFISKIENEAGATVFSASPKIVCDTCNLPVIYGETQRSAVLSDDSMENVATSQENPVQTAPQADPITPSEVARQANQSYAPHVISTPLAFLIKDALNSNVFGEPGWMGTGWRAGKVLQRHDIGGKTGTTNNSKDAWFSGYGPNIVASVWIGFDDHRRDLGRSSVSGVIRDQISGYEGGAKTAEPAWDDFMKVALAGLPEQKTPTPPGVVSVVIDRSSGKLSDGGGNSRQEYFIDGTQPTEKAVHDAGTTLFNTSSGQAEELF  
  
>**gb|ACS86592.1| penicillin-binding protein 1B [Dickeya dadantii Ech703]**MSRDDREPIGRKASASRRKPLRRPAARRRKDEDYDDEYEEYEDDYDDDDEEEEAMSRRPRKKRRLLGLMIRLFLIFVIVMSAYGVYLDSEIRGRIDGKVWQLPATVYGRMVNLEPGMAYSKKEMVNLLEGMQYREVNRITRPGEFTVQSNSIEILRRPFDFPDGKEGQIRAKMTFSSDRLQQIQNLENQRSFGFFRLDPKLITMLQSPNGEQRLFVQRSGFPDLLVQTLIATEDRHFYEHDGISFYSIARALVANLTAGRAVQGGSTLTQQLVKNLFLTNERSLWRKANEAYMALIMDYRYSKDRILELYLNEVYLGQSGNDQIRGFPLASLYYFGRPVNELSLDQQAMLVGMVKGASLYNPWRNPQVTLERRNLVLKLLQNQQIIDEDLYNMLSARPLGVQPKGGVISPQPAFMQMVRQELQQRLGDKVNDLSGVKIFTTLDPVSQDAAEKAVSDGIPALRAARNVQDLEAAMVVVDRFSGEVRAMVGGSDAQFAGFNRAMQARRPVGSLAKPPTYLTALSMPERFRLNTILADEPISLKQQNGTIWEPKNYDREFRGRVMLVDALANSLNVPTVNLGLAVGLDQISATLQRLGIPKEQIQTVPAMLLGAISLTPMEVAQEYQTIASGGNRATLSALRSVIAEDGKVLYQSFPQAEQAVPSQAAYLTLYGMQQVVERGTSRSLMVKFGNYHLAGKTGTTNDLRDSWFAGVDGKEVVISWVGRDNNGPAKLTGANGALTIYRRYLENETPLPLMLTPPEGISTMSVDGGGNFICNGSAGRALPVWTDNPQALCQSSQQPQPGTPDNQPGSQQQDSSVPDWIRQMFGK  
  
>**gb|ACS87387.1| monofunctional biosynthetic peptidoglycan transglycosylase [Dickeya dadantii Ech703]**MKSTPVLRRMIAVLKRLITCILLAAGACWLAGILLFAFLPVPFSAVMIDRQISAWASGDFSYVARSNWVSMDEIAAVMPLAVIAAEDQKFPQHWGFDFNAIQAALRHNERHGGSIRGASTLSQQTVKNLLLWDGRSWVRKGLEAGLTAIVELVWTKRRILTVYLNIAEFGPGIFGVEAASRHFFNKPASRLTSGEAAMLASVLPNPIRYRVDKPSIYVVRRQQWILRQMRQVGGEGFLIENHLR  
  
>**gb|ACT05145.1| penicillin-binding protein, 1A family [Dickeya zeae Ech1591]**MKFVKYLFILAVSCILLGVASLYGLYRYIEPQLPDVATLKDVRLQTPMQVYSADGELIAQFGEKRRIPLKLDQIPPTLVNAFIATEDSRFFEHHGVDPQGIIRAALIALTSGHASQGASTITQQLARNFFLSPERTLLRKIKEVFLAIRIEQTLTKEEILELYLNKIYLGYRAYGVGAAAQVYFGRPVDQLTLAQMAMIAGLPKAPSTFNPLYSYDRAVARRNVVLSRMLDENYITQVQYNQARSEKLVADYHAPEIAFSAPYLAEMVRQEMVKRYGEDAYNDGYQVYTTITRKLQLAAEDAVHNNVIAYDMRHGYRGPDQVLWKVGIPALTQDKIVEALKKLPVYGPLFPAVVTDAGADKAHAILASGDKIELPMVGVRWARAYRSDDQQGPTPKRVTDVLEAGQQIWVRKVDNDWWLAQVPDVNSALVSLNPKDGAILALVGGFDFNQSKFNRATQALRQVGSNIKPFLYTAAMDKGLTLATILNDAPITRWDPGAGSDWSPKNSPAVYDGPIRLRQGLGQSKNVVMVRAMRAMGVDYAANYLERFGFPEQNIVHTESLALGAASFTPLQVVRGYSVMANGGYLVDPYFITKIDNAAGNNLFTAMPKIVCDTCNLPVIYGDTQRSAVLSDDSMENVATSQENPVQAAPQVDPITPSEVARQAAMQPYAPHVISTPLAFLIKDALNSNVFGEPGWMGTGWRAGKVLQRHDIGGKTGTTNNSKDAWFSGYGPNVVASVWIGFDDHRRDLGRTSASGVIRDQISGYEGGAKSAEPAWDDFMKVALNGVPEQKTPPPQGVVTVTIDRSSGKLSDGGANSRQEYFIDGTQPNERAVHDAGTTLFNTSSGQAEELF  
  
>**gb|ACT05908.1| penicillin-binding protein 1B [Dickeya zeae Ech1591]**MSRDDREPIGRKRSASRHTPPRRQATRRRRDDDYDDDYEDEYENDYDDDEDDEEEVMSKRPRKKRRWLGWLIRLFLIFVVVMSVYGIYLDGEIRSRIDGKVWQLPAAVYGRMVNLEPGMAYSKKEMANLLEGMQYREVSRITRPGEFTVQANNIEILRRPFDFPDGKEGQIHAKMIFSNDRLSQIQNMDNQRNFGFFRLDPKLITMLQSPNGEQRLFVQRSGFPDLLVQTLIATEDRHFYEHDGISFYSIGRALVANLTAGRAVQGGSTLTQQLVKNLFLTNERSLWRKANEAYMALIMDYRYSKDRILELYLNEVYLGQSGNDQIRGFPLASLYYFGRPVNELSLDQQAMLVGMVKGASLYNPWRNPQVTLERRNLVLKLLQNQQVIDEDLYNMLSARPLGVQPKGGAISPQPAFMQMVRQELQQRLGDKANDLSGVKIFTTLDPVSQDAAEKAVEDGIPALRAARGVKDLESAMVIVDRFSGEIRAMVGGSDAQFAGFNRAMQARRSVGSLAKPPTYLTALSMPDRYRLNTILVDEPISLKQPNGTVWEPKNYDREFRGRVMLVDALANSLNVPTVNLGMAVGLDQVSDTLQKLGIPQNQIQAVPAMLLGAVSLTPMEVAQEYQTIASGGSRATLSALRSVIAEDGKVLYQSFPQAERAVPSQAAYLTLYGMQQVVERGTSRSLTVKFGNYHLAGKTGTTNDLRDSWFAGVDGKEVVITWVGRDNNGPAKLTGANGALTIYRRYLENQTPLPLVLTPPEGITTMSVDGSGNVICNGSAGRALPVWSDNPQALCQASQQAVQQPTNSPNGQPQQNQQEGGSVPDWIKQMFGQ  
  
>**gb|ACT08587.1| monofunctional biosynthetic peptidoglycan transglycosylase [Dickeya zeae Ech1591]**MRSVGRLRKGLSGGMIASVRRWILRIIFGVVAMWLVSLLLFAFLPVPFSAVMVDRQLSAWLNGDFSYVAHSDWVSMDEIAAVAPLAVIAAEDQKFSRHWGFDFDAISAAIAHNEQHENRIRGASTLSQQTVKNLLLWDGRSWLRKGLEAGLTAVVELVWTKRRILTVYLNIAEFGPGIFGIEAASRQFFNKPASRLTAAEAALLAAVLPNPIRYHVSKPTGYVMRRQQWILRQMGQLGGESFLKVNRLY  
  
>**gb|ACZ75210.1| monofunctional biosynthetic peptidoglycan transglycosylase [Dickeya dadantii Ech586]**MRQGRRPEKGGLARMAVSIRRWVWRILLGVVGIWLAAILLFAFLPVPFSAVMADRQLSAWLSGDFSYVAHSDWVSMDDIAAVAPLAVIAAEDQKFPQHWGFDFDAISAALKHNEQYENRIRGASTLSQQTVKNLLLWDGRSWLRKGLEAGLTVAVELVWTKRRILTVYLNIAEFGPGIFGIEAASRQFFNKPASRLTASEAALLAAVLPNPIRYRVNKPTGYVIRRQQWILRQMSQIGGEHFLEANRLY  
  
>**gb|ACZ77969.1| penicillin-binding protein 1B [Dickeya dadantii Ech586]**MSRDDREPIGRKRSASRHTPPRRQATRRRRDDDYDDDYEDEYEDDYDEDDEEEVMSKRPRKKRRWLGWLIRLFLIFVVVMSIYGVYLDGEIRSRIDGKVWQLPAAVYGRMVSLEPGMPYNKKDMIALLEGMQYREVSRITRPGEFTVQSNSIEILRRPFDFPDGKEGQIHAKMIFSSDRLSQIQNMDNQRNFGFFRLDPKLITMLQSPNGEQRLFVQRSGFPDLLVQTLIATEDRHFYEHDGISFYSIGRALIANLTAGRAVQGGSTLTQQLVKNLFLTNERSLWRKANEAYMALIMDYRYSKDRILELYLNEVYLGQSGNDQIRGFPLASLYYFGRPVDELSLDQQAMLVGMVKGASLYNPWRNPQVTLERRNLVLKLLQNQQVIDEDLYNMLSARPLGVQPKGGVISPQPAFMQMVRQELQQRLGDKANDLSGVKIFTTLDPVSQDAAEKAVEDGIPALRAARGVKDLESAMVIVDRFSGEVRAMVGGSDAQFAGFNRAMQARRSVGSLAKPPTYLTALSMPDRYRLNTILPDEPISLKQPNGTVWEPKNYDREFRGRVMLVDALANSLNVPTVNLGMAVGLDQISDTLQKLGIPQNQIQPVPAMLLGAISLTPMEVAQEYQTIASGGSRAPLSALRSVIAEDGKVLYQSFPQAERVVPSQAAYLTLYGMQQVVERGTSRSLMVKFGNYHLAGKTGTTNDLRDSWFAGVDGREVVITWVGRDNNGPAKLTGANGALTIYRRYLENQTPLPLMLTPPDGITTMTVDSSGNFICNGSAGRALPVWTDNPQALCQASQQQVVQSPAASSGSQSQPQPSQPGQPNQPNQPNQQQDGGSVPDWIKQMFGQ  
  
>**gb|ACZ78637.1| penicillin-binding protein, 1A family [Dickeya dadantii Ech586]**MKFVKYLFILAVSCILLGVASLYGLYRYIEPQLPDVATLKDVRLQTPMQVYSADGELIAQFGEKRRIPLKLDQIPPMMVNAFIATEDSRFFEHHGVDPQGIIRAAVIALTSGHASQGASTITQQLARNFFLSPERTLLRKIKEVFLAIRIEQTLTKDEILELYLNKIYLGYRAYGVGAAAQVYFGQPVDQLTLAQMAMIAGLPKAPSTFNPLYSYDRAVARRNVVLSRMLDENYITQAQYDQARNEKLVADYHAPEIAFSAPYMAEMVRQEMVKRYGEDAYSDGYQVYTTITRKLQLAAEDAVHNNVIAYDMRHGYRGPDQVLWKVGTPALTQDKIVEALKKLPVYGPLFPAVVTDTSADKAHAVMANGDKIELPMLGVRWARAYRSDDQQGPTPKRVTDVLAAGQQIWVRKVDNDWWLAQVPDVNSALVSLNPTDGAILALVGGFDFNQSKFNRATQALRQVGSNIKPFLYTAAMDKGLTLATILNDAPITRWDPGAGSDWSPKNSPPVYDGPIRLRQGLGQSKNVVMVRAMRAMGVDYAANYLERFGFPEQNIVHTESLALGAASFTPLQVVRGYSVMANGGYLVDPYFITKIDNAAGNTVFSATPKIVCDTCNLPVIYGDTQRSAVLSDDSMENVATSQENPVQAAPQVDPITPSEVARQAAAQPYAPHVISTPLAFLIKDALNSNVFGEPGWMGTGWRAGKVLQRHDIGGKTGTTNNSKDAWFSGYGANIVASVWIGFDDHRRDLGRTSASGVIRDQISGYEGGAKSAEPAWDDYMKVALAGVPEQPKTPPQGVVTVTIDRSTGKLSDGGGNSRQEYFIDGTQPTERAAHDAGTTLYNTSSGQAEELF  
  
>**gb|ADM96553.1| biosynthetic peptidoglycan transglycosylase [Dickeya dadantii 3937]**MRSAGLFGKGRLGRLAVCVRRWVLRIFIGVVAMWLAAILLFAFLPVPFSAVMIDRQLSAWLSGDFAYVAHSDWVSMDEIAAVAPLAVIAAEDQKFPQHWGFDFDAISAALRHNERHENRIRGASTLSQQTVKNLLLWDGRSWVRKGLEAGLTAVVELVWTKRRILTVYLNIAEFGPGIFGIEAASRQFFNKPASRLTASEAAMLAAVLPNPIRYRASKPSGYVMRRQQWILRQMSQIGGENFLEANRLY  
  
>**gb|ADM99610.1| penicillin-binding protein 1B (PBP1B) [Dickeya dadantii 3937]**MSRDDREPIGRKRSASRHTPPRKQATRRRRDDDYDDDYEEEYEEDYDDDEDDEEEVMSKRPRKKRRWLGLLIRLFLIFVVVMSIYGVYLDGEIRSRIDGKVWQLPAAVYGRMVNLEPGMAYSKKEMTNLLEGMQYREVSRITRPGEFTVQANGIEILRRPFDFPDGKEGQIHAKMIFSNDRLSQIQNMDNQRNFGFFRLDPKLITMLQSPNGEQRLFVQRSGFPDLLVQTLIATEDRHFYEHDGISFYSIGRAMLANLTAGRAVQGGSTLTQQLVKNLFLTNERSLWRKANEAYMALIMDYRYSKDRILELYLNEVYLGQSGNDQIRGFPLASLYYFGRPVNELSLDQQAMLVGMVKGASLYNPWRNPQVTLERRNLVLKLLQNQQVIDEDLYNMLSARPLGVQPKGGVISPQPAFMQMVRQELQQRLGDKANDLSGVKIFTTLDPVSQDAAEKAVEDGIPALRAARGVKDLESAMVIADRFSGEIRAMVGGSDAQFAGFNRAMQARRSVGSLAKPPTYLTALSMPDRYRLNTILADEPISLKQPNGTVWEPKNYDREFRGRVMLVDALANSLNVPTVNLGMAVGLDQVSDTLQKLGIPQNQIQAVPAMLLGAISLTPMEVAQEYQTIASGGNRASLSALRSVIAEDGKVLYQSFPQAERAVPSQAAYLTLYGMQQVVERGTSRSLMVKFGNYHLAGKTGTTNDLRDSWFAGVDGKEVVITWVGRDNNGPAKLTGANGALTIYRRYLENQTPLPLMLTPPEGITTMSVDSSGNFICNGSAGRALPVWTDNPQALCQASQQAVQQPANAPNGQPQQNQQEGGSVPDWIKQMFGQ  
  
>**gb|ADN00362.1| penicillin-binding protein 1A (PBP1A) [Dickeya dadantii 3937]**MKFVKYLFILAVSCILLGAASLYGLYRYIEPQLPDVATLKDVRLQTPMQVYSADGELIAQFGEKRRIPLKLDQVPPTLVNAFIATEDSRFFEHHGVDPQGIIRAAVIALTSGHASQGASTITQQLARNFFLSPERTLLRKIKEVFLAIRIEQTLTKEEILELYLNKIYLGYRAYGVGAAAQVYFGRPVDQLTLAQMAMIAGLPKAPSTFNPLYSYDRAVARRNVVLSRMLDENYITQAQYDQARSEKLVADYHAPEIAFSAPYLAEMVRQEMVKRYGEDAYNDGYQVYTTITRKLQLAAEDAVHNNVIAYDMRHGYRGPEQVLWKVGAPALTQDKIVEALKKLPVYGPLFPAVVTDASADKAHAMMASGDKIELPLAGVRWARAYRSDDQQGPTPKRVTDVLEAGQQIWVRKVDNDWWLAQVPDVNSALVSLNPQDGAVLALVGGFDFNQSKFNRATQALRQVGSNIKPFLYTAAMDKGLTLATILNDAPITRWDPGAGSDWSPKNSPPEYDGPIRLRQGLGQSKNVVMVRAMRAMGVDYAADYLERFGFPEQNIVHTESLSLGSASFTPLQVVRGYAVMTNGGYLVDPYFITKIDNASGSTVFTAIPKVVCDTCNLPVIYGDTQRSAVLSDDSMENVATSQENPVQAAPQADPATPSEVARQAATQPYAPHVISTPLSFLIKDALNSNVFGEPGWMGTGWRAGKVLQRRDIGGKTGTTNNSKDAWFSGYGPNIVASVWIGFDDHRRDLGRTSASGVIRDQISGYEGGAKSAEPAWDDFMKVALAGVPEQKTPPPQGIVTVTIDRSSGKLSDGGANSRQEYFIDGTQPTERAVHDAGTTLFNTSSGQAEELF

GT56

>**gb|ACS84027.1| 4-alpha-L-fucosyltransferase [Dickeya dadantii Ech703]**MNTLIHILGADIPHHNQTLLGFFNDNLTSEIPHHFMVAAQDAAALRRAFPALRIDAFGSKSALAMAVVRRAWADRSTRFFFHGQFNVWLWLALLARLILPTQVSWHIWGADLYETACGWQYRMFYLLRRRAFRQVGHVFATRGDLGVVQRFRPHLPASLLYFPTRMPPLSEPAANPGPSTPMTILVGNSGDRSNRHREALAAIHRQFGADVQVVLPMGYPAGNAAYVAQVVRQGTRLFGANFRVLHQPLAFDDYLALLRRCDLGYFIFQRQQGIGTLCLLIQLRVPFVISRSNPFWQDLAEQQLPVLFCEDQLDETCVWEARRQLARTDIRGITFFSPNYLPAWRQALVQATGGAA  
  
>**gb|ACT05058.1| 4-alpha-L-fucosyltransferase [Dickeya zeae Ech1591]**MTTLIHVLGADIPHHNHTVLRFFNDTLAPSLPLHQTRRFMVVSSAAFSESDYPMLHVTRFSSQKALARAVVAQAREDRSVRFFFHGQFNPWLWLALLCGGIRPTQAYWHIWGADLYEEARGWRYHWFYRLRRLAQRRVARVFATRGDIDYFRRRYPAAATSLLYFPTRMSQHAASPDEKTPDAPLTILVGNSGDRSNRHLAALDAIHRQFGTQVRVIVPMGYPAGNHAYVEQVSQHGLALFGAERCRVLRESLAFDDYLALLRTCDLGYFLFHRQQGIGTLCLLIQLGVPFVISRHNPFRQDLAEQRLPVLLGEEELNETMVRDAREQLRRVDTRQIAFFSPGYESGWRQALALAAGDGDD  
  
>**gb|ACZ78722.1| 4-alpha-L-fucosyltransferase [Dickeya dadantii Ech586]**MTTLIHVLGADIPHHNHTVLRFFNDTLAPSLPLYQTRRFMVVSAKAFSESDYPMLHVTRFSSQKALARAVVAQARADSSVRFFFHGQFNPWVWLALLFGAIRPVQAYWHIWGADVYEEAQGWRYRWFYRLRRLAQRRVARVFATRGDSDYFRQRYPAVPTSLLYFPTRMGQQVMGSNEKMPGTPLTILVGNSGDRSNRHLAALDAIHRQFGSQVRVIVPMGYPAGNHRWIEQVEQHGVALFGADRCRVLRESMAFDEYLALLKTCSLGYFLFHRQQGIGTLCLLIQLGVPFVISRHNPFRQDLAEQRLPVLLDDEPLSEARVREAREQLKRVDTRQIAFFSPGYEQGWRQALALAAGDSHD

GT81

>**gb|ACS85681.1| conserved hypothetical protein [Dickeya dadantii Ech703]**MSEFYQDGIITNFHNLTHRNVEELEYDLQVFSGQNSMGLILPSLFSELEGPALGKIIDELAQVPYLGEIVIGLDRADAEQFCFAHEFFSRLPQRHRILWNDGPRLTKLSQELVERELAPMEAGKGRNVWFCVGYTLASRRTSCIALHDCDIVTYDRNLLARLLYPIANPHFHYDFCKGYYARVADGKLNGRVGRLLVFPLLKSLQNVYGNSDYLEYMRSFRYPLSGEFAMRSHILRNLRIPSDWGLEIGVLSEIHRGTATSRICQVDIADNYDHKHQPMSESDPTSGLQRMAMDITKALYRKLAIQGVGITADSFRVLRATYYRTALDMIDSFEHDARMNGLHFDRHTEESAVELFADVITLSGQVYNDSPGDKPFVPSWNRVQSAFPDILERLYEAVEADNQEMSGGR  
  
>**gb|ACT06972.1| conserved hypothetical protein [Dickeya zeae Ech1591]**MSEFYQDGIITNFHNLTRRSVEELEYELQVFSGQSSMGLILPSLFSELEGPALDKIVDMLAQVPYLSEIVIGLDRADREQFLFARQFFSRLPQRHRILWNDGPRLTRLSQELTDKELAPMEQGKGRNVWFCVGYTLASRRTACIALHDCDIVTYDRAMLARLLYPIANPYFHYDFCKGYYARVAEGKLNGRVGRLLVFPLLKSLQSVYGNSDYLEYMRSFRYPLSGEFAMRSHVLRNLRIPSDWGLEIGMLSEIHRGTATSRICQVDIADNYDHKHQPMSENDPSSGLQRMAMDITKALYRKLAIQGVNITTDSFRVLRATYYRTALDMIDSFEHDARMNGLHFDRHTEESAVELFADVITQSGQVYSDSPGDKPFVPSWNRVQSAFPDILERLYDAVEADNQEMNDA  
  
>**gb|ACZ76929.1| conserved hypothetical protein [Dickeya dadantii Ech586]**MSEFYQDGMITNFHNLTRRSVEELEYELQVFSGQSSMGLILPSLYSELEGPALDKIVDMLSQVPYLSEIVIGLDRADREQFLFARQFFSRLPQRHRILWNDGPRLTRLSQELTDKELAPMEQGKGRNVWFCVGYTLASRRTACIALHDCDIVTYDRTMLARLLYPIANPYFHYDFCKGYYARVAEGKLNGRVGRLLVFPLLKSLQSVYGNSDYLEYMRSFRYPLSGEFAMRSHVLRNLRIPSDWGLEIGMLSEIHRGTATSRICQVDIADNYDHKHQPMSENDPSSGLQRMAMDITKALYRKLAIQGVNITTDSFRVLRATYYRTALDMIDSFEHDARMNGLHFDRHTEESAVELFADVITQSGQAYSDSPGDKPFVPSWNRVQSAFPDILERLYDAVEADNQEMSDA  
  
>**gb|ADM98478.1| Glycosyltransferase [Dickeya dadantii 3937]**MTKGERNMSEFYQDGIITNFHNLTRRSVEELEYELQVFSGQSSMGLILPSLFSELEGPALDKIVDMLAQVPYLSEIVIGLDRADRDQFLFARQFFSRLPQRHRILWNDGPRLTRLSQELADKELAPMEQGKGRNVWFCVGYTLASRRTACIALHDCDIVTYDRAMLARLLYPIANPYFHYDFCKGYYARVAEGKLNGRVGRLLVFPLLKSLQSVYGNSDYLDYMRSFRYPLSGEFAMRSHVLRNLRIPSDWGLEIGMLSEIHRGTATSRICQVDIADNYDHKHQPISENDPSSGLQRMAMDITKALYRKLAIQGVNITTDSFRVLRATYYRTALDMIDSFEHDARMNGLHFDRHTEESAVELFANVITQSGQAYSESPGDKPFVPSWNRVQSAFPDILERLYDAVEADNQEMNDA

GT83

>**gb|ACS87771.1| glycosyl transferase family 39 [Dickeya dadantii Ech703]**MKQTRQALLWLAVLLLYYIVPLSSRLLWQPDETRYAEISREMVAGGNWIAPHFLGIRYFEKPIAGYWINNIGQWLFGAKNAGVRAGSVISILLAAGLVYWLTLRLWQQRRTAWLAAVIYLSCLLVYGIGTYAVLDPMVTLWLAAAMCSFWGATQAVTRSGRLGGYLLLGVVCGMGFMTKGFLALAVPVIAVLPWVAFERRWKEVLLYGPLAIVSAVVVSLPWALAVAQQQPDYWHYFFWVEHVQRFADSANAQHKAPFWYYLPVLIAGTLPWLALLPASLWQGWKHRRQDSGAFYLLGWVVMPLIFFSIAKGKLPTYILPCFAPLAILMARYAVSLPTLRLLRVNGWLNLVFGLLCALVVVLALSPWGFAKKPLYQPDEGVKVLLAAGAFLCWALVGWLSLRRTEQRWHWAALCPLGVALAIGAAIPQRTMETKNPQWFLRQVEPQLSQSRYILADSVGVASAIAWEQKRSDIVMYSNRGELEYGLNYPDSAERFVGIGDFTGWLATHRREGNVSVVVTFSSAQQPIEHLPEADQVYRRGRMALLWYRQQ  
  
>**gb|ACT09021.1| glycosyl transferase family 39 [Dickeya zeae Ech1591]**MKYARQTTLWLALLLLYYFIPLNGRLLWQPDETRYAEISREMLAGGNWIAPHFLGIRYFEKPIAGYWVNNIGQWLLGDNNAGVRAGSVFSILLTAGLIYWLTQRLWQQRRTSLLAMAIYLSCLLVYGIGTYAVLDPIVTLWLAAAMCSFWGAAQATTRGSKIGGYLLLGVVCGMGFMTKGFLALAVPVIAVLPWVTLERRWKEVLLYGPLAIVSAVVVSLPWALAVARQQPDFWHYFFWVEHIQRFADSENAQHKAPFWYYLPVLIAGVLPWLALLPSSLLQGWRERRQDNSVFYLLGWVVMPLLFFSIAKGKLPTYILPCFAPLAILMARRATTLLNPRVLTINGWINLAFGVLCALIVALVLAPWGLSHRPLYQPQETVKVALGIAAFLFWGMIGWWTSRQAAARWHWAAVCPLGIALLIGMAIPQRVMESKHPQWFLRAPDVAAHLAQSRYILVNSVGIASAAAWEQKRSDILLYDNQGELEYGLSYPDSTDRMVPASAFADWLAAHRREGNVSLVLIFSSPTDPITGVPPADYTDRKGRVALLWYRQQ  
  
>**gb|ACZ79026.1| glycosyl transferase family 39 [Dickeya dadantii Ech586]**MKYARQTTLWLALLLLYYFIPLNGRLLWQPDETRYAEISREMLAGGNWIAPHFLGIRYFEKPIAGYWVNNIGQWLLGDNNAGVRAGSVFSILLTAGLIYWLTQRLWQQRRTSLLAMAIYLSCFLVYGIGTYAVLDPIVTLWLAAAMCSFWGAAQATTRSSKIGGYLLLGVVCGMGFMTKGFLALAVPVIAVLPWVTLERRWKEVLLYGPLAIISAVVVSLPWALAIARQEPDFWHYFFWIEHIQRFADSKNAQHKAPFWYYLPVLVAGVLPWLALLPSSLLQGWRERRQQSGAFYLLGWVVMPFLFFSIAKGKLPTYILPCFAPLAILMARRATTLLSPKMLTVNGWINLAFGVLCALIVVLVLAPWGLSHRPLYQPQEGAKVALGVIAFLFWGLIGWWTSRQAATRWHWAAVCPLGIALLVGMAIPQRVMESKHPQWFLRAPEVASHLAESRYILANSVGIASAAAWEQKRSDILMYDNQGELEYGLSYPDSADRMVSASEFADWLAAHRREGNVSLVLIFSSATDPITDLPPADYTDRKGRIALLWYRQQ  
  
>**gb|ADN00724.1| 4-amino-4-deoxy-L-arabinose transferase [Dickeya dadantii 3937]**MKYARQTTLWLVLLLLYYFIPLNGRLLWQPDETRYAEISREMLAGGNWIAPHFLGIRYFEKPIAGYWVNSIGQWLLGDNNAGVRAGVVFSILLTAALIYWLTQRLWQQRRTSLLAAAIYLSCLLVYGIGTYAVLDPIVTLWLAAAMCSFWGAAQATTRGSKIGGYLLLGVVCGMGFMTKGFLALAVPVIAVLPWVALERRWKEVLLYGPLAIVSAVAVSLPWALAVARQQPDFWHYFFWVEHIQRFADSANAQHKAPFWYYLPVLIGGVLPWLALLPSSLLQGWRERRQESGAFYLLGWVVMPFLFFSIAKGKLPTYILPCFAPLAILMARRATTLLNPRLLTINGWINLAFGLLCALIVVLVLAPWGLSHRPLYQPQETVKVALGVVAFLFWGLVGWWTLRHAAARWHWAAACPLGIALLIGMAIPQRVMESKHPQWFLRAPEVESRLSQSRYILANSVGVASAVAWEQKRGDILMYDNQGELEYGLSYPDSANRMVPADAFADWLATHRREGNVSLVLIFSSATDPITGVPPADYTDRKGRVALLWYRQQ

GT84

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