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| **Protein function** | | **Gene code** | **Gene name** | **Protein sequences** |
| **Nucleotide sugarbiosynthesis** | **Dtdp**  **rhamnose** | [fig|6666666.596377.peg.1088](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.1088) | Glucokinase | MRPALIGDIGGTNARLALVTPGDITPHDIINLPCADYPGVIEAIQDYLTRVGAAGDNAPREACLAFACPVHAERVKMTNNHWDFRKSEVRETLNLSLFKVINDFTAQALGVPHVTADDLVAVQAGDGQAHSTRLVIGPGTGLGVAGVFPGQHAWIPLPTEGGHVTFAPTDDTERALLDVFLQHHKRVSVERILCGQGLLELYQAHCALDDQAPRCTSPAEVTQAANQGDPIATATLLRFLKILGDVCGDATLTMGARGGVYLCGGILPRLLDWLPKSQLRDGFVNKGRMGAYNADIPVWVVTHPWTGLLGAAEALHNEEVF |
| [fig|6666666.596377.peg.1957](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.1957) | Phosphoglucomutase | MTTPTIPASIFRAYDIRGIVDDTLTEDTVEWIGRAIGSAAATRGESTVVVARDGRLSGPRLQAALMRGLNAAGRDVIDIGMVPTPVLYFATHILDGTRSGVMVTGSHNPPDYNGFKIVLDGDTLSGDAITALYERLQSGDLTQGEGRIRQEDVRDAYLTRILGDVTINRPIKAVVDCGNG  VAGELGPQLIERLGVDTIPLFDEIDGTFPNHHPDPGKPENLQDLIRTVQETGADIGLAFDGDGDRLGVITPRGRLIYPDHLLMAFATDMLSRNPGAKVIFDVKCTGNLVKVISDAGGEPEMWRTGHSLIKARMKETGAQLAGEMSGHIFFKERWYGFDDGLYAAARLVEILANYAGDADAYFDSFPQDIGTPEINITVTDSNKFNLVDKLAREGDFGDGIKTTLDGIRVDYPDGWGLCRASNTTPVLVLRFEGKNDAALARIKAQFANALKDVDPALTLPQA |

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|  |  | [fig|6666666.596377.peg.568](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.568) | Glucose-1-phosphate thymidylytransferase | MKGIILAGGSGTRLYPITRGISKQLLPVYDKPMIYYPLSVLMLAGIRDILVITTPEDQDGFQRLLSNGSQWGINLTYAAQPSPDGLAQAFIIGEKFIGGDSVCLVLGDNIYYGQGLSRMLQAAATRDKGATVFGYQVNDPERFGVVEFDDNLRAISIEEKPANPKSDYAVTGLYFYDNDV  VDIAKQVEPSERGELEITSINQAYLERGDLNVELLGRGFAWLDTGTFDSLHDAASFIETLEKRQGLKIACLEEVAYRMGFIGEKELLAEAEKLKKNSYGTYLKKLAKTANKRAL |
| [fig|6666666.596377.peg.570](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.570) | dTDP glucose 4.6 dehydratase | MKLLITGGAGFIGSAVIRHIIRNTEDSVVNVDKLTYAGNLESLAAASDNERYIFEQVDINNRVDLDRVFREQQPDAVMHLAAESHVDRSIDGPADFIETNIVGTYTLLEAARYYWQGLGHERQQVFRFHHISTDEVYGDLPHPADTTNSAHYLFTETTPYAPSSPYSASKASSDHLVRAW  RRTYGLPTLITNCSNNYGPYHFPEKLIPLMILNALEGKPLPVYGKGDQIRDWLYVEDHARALYKVITEGKVGETYNIGGNNEKQNIEVVLSLCDILQELYPQSTPYRELINYVPDRPGHDMRYAIDASKIQKELGWQPQETFDTGIRKTVQWYLDHLDWCKRVQDGSYQRERMGFNK |
| [fig|6666666.596377.peg.567](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.567) | dTDP 4 dehydrorhamnose 3,5 epimerase | MKIIETRIPDVKIIEPKVFGDERGFFMETWNEKAFREAGINATFVQDNHSRSVKNTLRGLHYQVKQPQGKLVRVTRGEVLDVVVDLRLESPTFGRWVGEYLSEDNNLMLWVPPRFAHGFLVVSDEADFQYKCTDFYAPEYERSIVWDDPDISIEWGVSEVDKLRLSAKDMMGQSFDAAKTELLISS |

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|  |  | [fig|6666666.596377.peg.569](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.569) | dTDP 4 dehydrorhamnose reductase | MKILLLGKTGQVGFELHRSLSSLGTVIAPGRAELDLHKEHAVANYLAYTKPSMIVNAAAWTAVDAAEGKKNEAERLNTGLPAQLAQYAAANSARLFHYSSDYVYPGNGEMPWKENSDTGPLSHYGKTKLKGDEAIEQSSADYVIFRTSWVYSARGSNFMKTMLRLAKSKSELSIVADQIGAPTPARLIAQVTTLAIHRQLRKGLYHLVPKGETSWYGFAQEIFLLAQKNGEQLTISPDNVYPIPTSDYPTPATRPLNSRMEATKLETALSIQLPDWQSQLELTLCEYLEK |
| **Dtdp**  **fructose** | fig|6666666.596377.peg.1269 | Glucose-6-phosphate isomerase (EC 5.3.1.9) | MAASSRTPPDSLPAWQTLKQHAQALKHVHLKNLFGNDPGRWTHFTRQVAGLTLDLSKQRWDDDTLEHLLALAEEAGVPGAIEALLSGKRVNVSENRPALHTALRLPPGASLDVEGEDVAAAVHESLTQMERLVARLHAGQWRGATGKPIRHVVNLGVGGSDLGPQMVTHALADYRPDDIHPVEVHFASTMDGSQLADYLTRFNPETTLFVLSSKSFTTIDTLSNANTARDWLIGRLSKHGELPSANPVSEELIIRQHFIGVSASPDKMSEWGITPDHQLMFWEWVGGRYSLWGTIGLPIALVVGMENFRELLAGAHAMDRHFQEAPLAENLPVLLGLAGIWNVNFLDIRAHSILPYDGRLEYFAAYLEQLEMESNGKSVTGQGQAVNYSTCPVLWGQLGPNAQHAFYQLLHQGTQPVVCDFIAPLKRYDEVEDPDTRRHLKSQHRLALANCFAQSRVLMLGDDAIDDDGPRPAHKRYRGN  QPSTTVLLDKLTPATLGSLIALYEHKVFVQAVIWDINPFDQWGVELGKQIATDTRKIIDHQGDLARLDASSRGLIEAFWAAEQE |
| **Regulationof biosynthesis** | | fig 6666666.596377.peg.1974 | Protein-PII uridylyltransferase | MLLHHYRFEPDTTLFDLELFRTELAGSRSPIAPFKAALGEIQTRLDERFRAGADIRDLVRGRAWYLDQLLAIAWEQHDWPDDGVALVAVGGYGRGELHPHSDIDLLLLLEHDDDTPYREPLTAFITFLWDIGLEIGHSVRSLNDCEREAAADVTVITNLLESRLIAGPEALRERMRERLN  ADHVWPADRFFEAKWQEQIARHYRYNNSEYHLEPNLKSSPGGLRDIQMIGWVAKRHFGTEEYTDIVANGFMNDAELRILSQGQAFLWQVRYALHMLTGRAEDRLLFDHQRTIAEMFGFRDTPEGLAVEQFMKRYYRHVTALAGLNDMLLQHFDEVILRGKEALETVKLNERFETKGGYIQVRSRNLFREQPSAMLELFLLMAKHPEIEGVRADTIRLIRDHRHQIDDHYREDPHHQRLFMAIMRAPGNVPRQLRRMNRYGILGKYLPEFGRAVGLMQHDLFHIYTVDAHTLRLLKFLHGFRKPEAKDDFPVAATLMQQLPKLDLLWIAGLFHDIGKGRGGDHSEIGARDVEQFCQRHHVPQHDTNLVSWLVEHHLLMSMTAQKRDISDPDVIRDFAMEVRNETRLDYLYVLTVADINATNPTLWNGWRASLLRQLHAETKRALRRGLKNPPDRDDWVRETRTEARSLLQTIGVDETDIDRLWDSLGEDYFLQYAPSEIVWQTQGILAHQPSPLPLVLISAPTADMTEGGTKVFIHTRSVDDLFAATAAAMEQLGLSIHDARIATSNNDWTLNTFIVLDNQGQPIRDPARIEEMRQHLVEELDDPDDYPDIVTRHTPRQLKHFRVATEVLIEQDPANDRTLLELSAPDRPGLLARVGRIFMEQDIALSAAKIATLGERVEDVFFITTKAGEPLTDPDRQQQLRERLIEVLGV |
| [fig|6666666.596377.peg.704](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.704) | Ntrc | MTEPARNDVARVVIVDDDRAIRWVLERALAQPDLEVECIERADTALSRLLESPPDVLVTDIRMPGIDGLDLMARVREAHPDLPVIVMTAHSDLDSAVASYQGGAFEYLPKPFDVDEALALVRRAIAHARERQRPVTVPEGLNAEIIGEAPAMQEVFRAIGRLSHSHITVLINGESGTGKERVAEALHQHSPRQGKPFIALNMAAIPRDLIESELFGHEKGAFTGATSQRQGRFEQANGGTLFLDEIGDMPAETQTRLLRVLADGEFYRVGGHTPTKVDVRIIAATHQNLESLVDDGRFREDLFHRLNVIRIHLPKLAERREDIPRLTSHFLAEAAKELSTDVKVLTPEAEAHLTRLPWPGNVRQLENICRWLTVMASGREVLVEDLPAELRSPSASESSAHGDWRSAFRDWADHALAEGHTHLLEEAVPDFERILIETALKHTGGRKGEAAELLGWGRNTLTRKLKTLLPALADE |
| [fig|6666666.596377.peg.705](https://rast.nmpdr.org/seedviewer.cgi?page=Annotation&feature=fig|6666666.596377.peg.705) | NtrB | MQDTTMHQRLLEHLTTAVLLLDGRLNVRWMNPAAEALFAVSLSRVKGMSLDGMLGGDESIDEVLAKARDAFHPFTQREARITPLNSDPLTVDYTVTPLSDMELLLEVEPRDRLMQISREEALTTRQETIKVLARGLAHEVKNPLGGIRGAAQLLERDLDNPALREFTHIIVQEVDRLRDMVDSMLGPNYIVKHEPVNIHKVLERVRSLLIAEHPWVDIQRDYDPSLPELFGDEAQMIQAVLNVARNAVQAMGDAETPTPTLVLRTRARRQFTLGAERHRLVSEVGIIDNGPGIPGTLQETLFYPMVSGRAEGSGLGLSIAQSILHQHQGLIECDSRPGRTEFRLLIPLVINVTGEAS |
| fig|370767.3.peg.587 | Exopolysaccharide synthesis, ExoD | MDDRREGSTLMDLIASLERMEQDAQRVSVDDVVHAVGRRSFGPLLLVTGLITLAPIIGDIPGMPTLMALLVLLVSVQLLVGRETFWLPGWMLKRSISRDKFDKGIYYLKKPARWIDGLLRVRLPWLTGYIGIRVTAVVCLMIALAMPPMEFIPFSANGAGLALSLLGLGLVARDGAALLLGVALFGVTCTLILVGLL |
| **Regulation of the EPS excretion** | | fig|6666666.596377.peg.2793 | PilZ | MATQKALSLTVPDVPTLLSAYMPFLDRGGMFIPTRGYYDLGQTVYLLLTLPGESERLSLSGEVIWVSPDGVTGRRMPGIGIHFNAQDYRVRDRIETLLAGQLDKAAPSFTL |
| fig|6666666.596377.peg.598 | Tetratricopeptide | MLLPKRSTIVATLAGLTLTALMIPSAWALDDEAQAAKKEEGMRLWGIHQWEKMQPPLETAAESGDVEAMYYLGEANRLLSRGLSQAALDWYHQAAQHGDPYAMLRLFDGGACELGDVCPENGDDWPQAALELTLPKAEAGDPEAMAALYDIYFYVKDPDEDEAMKWLRRAAEAGQVESMNLLGKIARNDEESYANDTERLEAAEVWFRKAAEAGYAPAMNNLAAVLSNLERNEEAWEWMATASEAGHINGRRWVAACNIVHEEQGRDLCRSAAKPDPAKGWAIVLATKQEVPNTYSTATLERYRDKISPEQRKEGEEIVDEWLNREPPLSYFPEKFGP |
| fig|6666666.596377.peg.3383 | beta-barrel BamB | MTPLFSTSMFSRSTFSKRTFSTPVMRVALGAAALALLAGCASKSEPAYTPKELKSFEATSTLETLWQEDVGDGLGRARYPIAPAREGDNVFAADAQGVVMSFSADDGEERWEVDLDTPISSALTAIAGQVYLGTRNGEVISLDQSDGSVNWRSRVSSEVLAAPQANPELLVVQSIDGQVTALDRASGDERWVFSSSLPSLTLRGTGTPMVIEPVSFVGLANGRLTTIDNRNGQPLWDMQIATPQGRSEVERLVDLAGQPVLSREGRLFVTSYNGQLVALEATRGNVIWERELSSRHTPLLVGDLLFVVTDDSHVVAIDSTNGQEVWRNDALEDRWLTAPAFADGRVVVGDFEGYVHLIDAREGELVGRTEVDSSGISVPAVTEGDVIHVLANDGHFETLEVSP |
| fig|6666666.596377.peg.890 | beta-barrel BamD | MRVFSAANRFGVFALSFALLAGCASNGNNDTAYDEDEYAGVAERELYERARDALDANRFNIAVERLEALDTRYPFGEHAEQAQLELIYAYYENGNWEEARAAASRFIRLHPDHPQVDYAYYLRGLSAWQAGRFSLERLRLIDISKRDLGATRDAYSDFRELIQRYPQSEYAPDAQQRIVYLRELLARHELHVADYYLRRGAYLAAVERGRWVVEKYPESNATHDALATMVEGYLGLEMDDRANEVLAVLRDNAPNHDQLEGNRFVPKHID |
|  | | fig|6666666.596377.peg.654 | beta-barrel BamE | MQKLTRIITLSVSIAVISGCSYVGVYKRDIPQGNLVTEEMVDQLQP  GMTQEQVTYVMGRPLLEAPFDASEWDYVFRLDKAYAGVEQRR  VTLTFDDQGRLANIDQEGDFSKDIPLEADSTGGPAPDTTDPTEAI  PNEPRQNTTPSTTN |

**Figure 1**: (A) Glucose standard curve (B) glucuronic acid standard curve and (C) Potassium sulfate standard curve plotted to estimate total carbohydrate, uronic acid and sulfate contents in CS-EPS, respectively