

(A) Belongs to COG1213 - predicted sugar nucleotidyltransferases.

1. **MPG1_YEAST** [*Saccharomyces cerevisiae* (baker's yeast)]

Mannose-1-phosphate guanyltransferase (**EC 2.7.7.13**)

(ATP-mannose-1-phosphate guanylyltransferase) (GDP-mannose pyrophosphorylase) (NDP-hexose pyrophosphorylase).

FUNCTION: Involved in cell wall synthesis where it is required for glycosylation. Involved in cell cycle progression through cell-size checkpoint.

CATALYTIC ACTIVITY: GTP + alpha-D-mannose 1-phosphate = diphosphate + GDP-mannose.

SUBCELLULAR LOCATION: Cytoplasm

2. **RMLA_STRMU** [*Streptococcus mutans*]

3. **RMLA1_ECOLI** [*Escherichia coli*]

Glucose-1-phosphate thymidyltransferase

(dTDP-glucose synthase)(dTDP-glucose pyrophosphorylase) (**EC 2.7.7.24**)

FUNCTION: Catalyzes the formation of dTDP-glucose, from dTTP and glucose 1-phosphate, as well as its pyrophosphorolysis.

CATALYTIC ACTIVITY: dTTP + alpha-D-glucose 1-phosphate = diphosphate + dTDP-glucose.

4. **GLMU_ECOLI** [*Escherichia coli*] (N-terminal domain!)

UDP-N-acetylglucosamine pyrophosphorylase (**EC 2.7.7.23**)

N-acetylglucosamine-1-phosphate uridyltransferase)

FUNCTION: Catalyzes the last two sequential reactions in the de novo biosynthetic pathway for UDP-GlcNAc.

Responsible for the acetylation of Glc-N-1-P to give GlcNAc-1-P and for the uridyl transfer from UTP to GlcNAc-1-P which produces UDP-GlcNAc.

CATALYTIC ACTIVITY: UTP + N-acetyl-alpha-D-glucosamine 1-phosphate = diphosphate + UDP-N-acetyl-D-glucosamine.

5. **RFBF_SALTY** [*Salmonella typhimurium*]

Glucose-1-phosphate cytidyltransferase

CDP-glucose pyrophosphorylase) (**EC 2.7.7.33**)

FUNCTION: CDP-abequose biosynthesis within the O antigen biosynthesis pathway of lipopolysaccharide biosynthesis

CATALYTIC ACTIVITY: CTP + alpha-D-glucose 1-phosphate = diphosphate + CDP-glucose.

6. **ISPD_ECOLI** [*Escherichia coli*]

2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (**EC 2.7.7.60**)

(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidyltransferase)

FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2-C-methyl-D-erythritol from CTP and 2-C-methyl-D-erythritol 4-phosphate (MEP).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

(B) Multiple alignment of the predicted inositol-1-phosphate citydyltransferases (IMPCT) and other characterized proteins from the sugar nucleotidyltransferases family.

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RMLA_STRMU          MKGIILAGGSGTRLYPLTRAASKQLMPVYDKPMIYYPLSTLMLAGIKDILIIIST-----PQDLPRFKELLQDGSSEFG
RMLA1_ECOLI        MKMRKGIILAGGSGTRLYPVTMAVSKQLLPIYDKPMIYYPLSTLMLAGIRDILIIIST-----PQDTPRFQQLLGDGGSQWG
TM_IMP_CT          MREAIIVLASGAGKRLRSVTGDVPKVYRFDFGCELVKYPMISLMKNGVERFVLVVS-----EGYRDLGKVLNDLGLVEG
Tnea_IMP_CT        KEAVVLASGVGKRLRVTVTGELPKVYRFNGCELVKYPMISLMKNGVERFVLVVS-----EGYED-GRKVLKLDLGLVEG
PH1219             MKAVILAAAGYGTRMG----EKP KGLIKVAGRELIYRTIRNLIKLGITEFIIIVTN-----EKYREFYERFVKENKIN-
PAB2433            MKAVILAAAGYGTRMG----EKAKGLIKIAGREIYVRTIKNLMKQIGIEFVIIVTN-----ERYKDAYEELFKRYNIK-
PF1058             MNILGGEEVGVILAAAGYGRMG----EKPKGLLKIAGRELIYRTIKNLEKNKIEFIIIVTN-----ERYLQKFEFVKENNLQN
TK2279             MVPERAVILAAAGLGTTRMG----RKP KGLVRVAGREILYRTIRLLQENGVKKFIVVTN-----ERYAPLYQEFIERHGFD-
AF0263            MKAVILAAAGLGTTRLG----GVPKPLVRVVGCEIILRMTKLLSPH-VSEFIIIVA-----SRYADDIDAFLLKDKGFN-
aq_1367           MVETAVILAGGEGNRLKPLTTEVPKALLKLVAGRELLYRTIKQLQDVGKVFIVVN-----KKFEGKVKAFLEKHNF-
Saro3073           MDALIIAAGYGRSLADL-SPS-KPLTPVAGVPLIEIGVRQAMEAGVT-RVVVVT-----GHKADMVEAFPLADLSQRA
17H9-22           MALILAAAGFGSRLRPR-TKIPKPLTRVLGLTLAERVVCTLLDAGIR-RFLVAL-----GHEAETVRAHFSDIARRR
GZ13E1_32         MKCLIIAAGRGTRLSSR-GDS-KPLIPLLGLSLIERVILTAKKSGLS-DFYVVT-----GYNKEKVRQYLDRFQSQR
Rxy1021259       MPDERTTGREGVGAAVLAAAGFRGLREC-GRP-KPLARVAGLTLLETRVTLRAGGLEIVVVV-----GHNGEEVAG-----HCKAR
APE1514           MVVDVLAAGVLAAGFSRRFRG-LLGVKVAAGVVRGYPLLCYPTVSLALAGVDRVVFVAS-----QFNLNVLVVLGHCPFRV
RFBF_SALTY        MKAVILAGGLTRLSEETIVKPKPMVEIGGKPIILWHIMKMYSVHGIKDFIICCGYKGYVIKEYFANYFLHMSDVTFHM
MPG1_YEAST         MKGLILVGGYGTRLRPLTLTPKPLVVEFGNRPMLLHQIEALANAGVTDIVLAVN-----YRPEVMVETLKKYKEYEY
GLMU_ECOLI        MLNNAHSVILAAGKGTMRMS---DLPKVLHTLACKAMVQHVIDAANELGAAHVHLVYG-----HGGDLLKQALKDDNLN-
ISPD_ECOLI        ATTHLDVCAVVPAAAGFRRMQT---ECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAIS-----PGDSRFAQLPLAN
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RMLA_STRMU        --IKLSYAEQPSPDGLAQAFIIGEEFIG---DDHVALILGDNIYYGPLSRMLQKAAS-----KESGATVFGYQVKDPERFVGVEFD
RMLA1_ECOLI       --LNLQYKVPSPDGLAQAFIIGEEFIG---GDDCALVLGDNIIFYGHDLPKLMEAAVN-----KESGATVFAYHVNDDPERYGVVEFD
TM_IMP_CT         ----IVVENKQVLEGNAYSFFLSEPYVE---SEKFFLSCGDSLFPPEALKSAFSEDEFH-----IKLGVSK---RSDLIDPBEASKVLVN
Tnea_IMP_CT       ----VVIENSRVELGNAYSFFLLETPHVK---SERFFLSCGDSIFPPEALKNAIF-DDEFH-----IKLGVSK---RKDLIDPQEASKVLVD
PH1219           ----AKIIVNQNPBERGNFSLHVAKDYV---SGRFVLVMSDHVYEEKFLYELAINAFG-----LIADR---NPKYVDVEATKVKIE
PAB2433          ----GTVVVNPNERGNFSLHIAKDYV---SGKFVLVMSDHVYEEERFYEAVKGG-----LIADR---RPRYVDVDEATKVKVE
PF1058           ----VKLVNRFPEKGNYSLYVAKDFV---KGGKFLVMSDHIYEEKFYELALRGG-----LIVDR---NPKFVDIDEATKVKIE
TK2279           ----AEIINPEPEKGNHSLHLAKEV---SGKFALTMDSHVYSRDFIERAVRGRG-----LIADR---EPRWVDIGEATKQVK
AF0263           ----AKIVRHDRPEKGNYSLLVAKNKH---EDRFILTMGDHIVYSQQFIEKAVRGG-----VIADR---EPRFVDIGEATKIRVE
aq_1367          ----AEVIPNEHPEKENGYSLYLAKGRI---KGEFAVVMDSHIYEFKAFLEKAVEGK-----LIVDR---LGLYINKNEATKVKCE
Saro3073         GIEIVPVRLSDWSTPNGHSVMAGATRC---EGNYLLMMADHMFADILARLLLEDRPER---GVT-LAIDRRTDNP-LVDPDDATVWVKM
17H9-22         GVTIDFVEAEDWERGNGASALAAKGRGT---EAPFFLVLMIDHLFDS-KIARALADDPVP---GEMLAVDRDKDG--IFDLDVTRVKID
GZ13E1_32       NINITHITNEEWENGNGISVLKAKLL---DENFILLMGDHI FDESILVR-LKNERIAD--DEVMLAVDYNIE TNRLVVDVNDVTRVLVE
Rxy1021259     GLPVRVVENPDYPRNGT SVLAAMRFL---PERFVAMVDHIHTPE SVRLLRCEG-----DFVAAVDT---RPVYADPGEATRVRLE
APE1514         S---GVLISHSSTLNGNFSLEVLREAGLRGSRCLAVSMADHYPPS IARRLEIAGCN-----TLGVDS---RPRYIEVEGATHVSL
RFBF_SALTY      AENRMEVHHRKRVFEPNLTVDTGSSMTGGRLKRVAEYIWDDEAF LFTYGDGVADLDIKAT-IDFHKAHGSKATLTAFFPGRFGALDIR
MPG1_YEAST       G-VNITFSVETEP LGTAGPLKLAEDVLK---KDNSPFFVLNSDVICEYPPKELADPFKHAHG-----GKGTIVATKVDEPSKYGVI VHD
GLMU_ECOLI      -----WVLQAEQLGTGHAMQQAAPFFAD---DEDILMLYGDVPLISVETLQRLRDAKP-----QGGIGLLTVKLDDPTGYGRITRE
ISPD_ECOLI      -----HPQITVVDGGDERADSVLAGLKAAG---DAQVWLVDHAARPLCHQDLDARLLALS-----ETSRTGGIILAAPVRD TMKRAE

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RMLA_STRMU        ND--RNAISIEEKPE-HPKSHYAVTGLFYFDNSVVDIAKNIKPSRGELETIDVNKAYLDRGDLSEVMEERGFAWLDTGT HESL-59aa
RMLA1_ECOLI       KN--GTAISLEEKPL-EPKSNYAVTGLFYFDNDVVQMAKNLKPSARGELBITDINRIYLEQGRLSVAMMGRGYAWLDTGT HESL-58aa
TM_IMP_CT         E---DRIVKIGKR---IDEYNYFDTG VFMTKKVYSLKESFSWTEEISLYHVLQKAVDTGM-IVKVDFDG-NALWTEIDSPEDL-17aa
Tnea_IMP_CT       EN--DRIIRIGKK---IDEYNYFDTG VFMTKKVYQL-DVPSWSKEISLYHVLQKAVDLGM-IVKVDFDE-DAPWTEIDSPEDL-16aa
PH1219           G---MRVIEIGKK---LKEWNAVDTGFFILDDSI FETITRLV---QEKE-VVELRDVVKEA-KLKVTFVD-GLFWMVDVTPPEEL-213aa
PAB2433          K---DRIIEIGK---LKEWDALDTGFFILDDSI FVDVTSKLA---QEKE-VVELKDVVKEV-KLKVTFVD-GLFWMVDVTPPEE I-215aa
PF1058           N---DRVVDIGKE---IPSWDGVDTGFFILDDSI FSVIEDIL---KEKE-VVELKDVVKEA-RLKVSFVD-GLYWMVDVTPGDL-211aa
TK2279           D---EKVWKIGKR---LKEWDAIDTGFFVLDDEIFKVT EILE---NEKNGDYSLSEVMERA-KVSVTFVD-GLGWMVDVTPPEE I-218aa
AF0263           D---GRVAKIGKD---LREFDCVDTGFFVLDDEIF EHAEKLR---DREE--IPLSEIVKLA-RLPVTVYD-GLLWMDVDTKEDV-211aa
aq_1367          E---GRIKIYGN---LEKYDGFDTGFFVLDDEIF EFAEEAL---KEQK-KLTMSLAKRA-QIPCTEVS-GYFWMVDVTPPEE I-212aa
Saro3073         DE--GRITAIKGT---IAPYDAVDCGAF LATELVAIREAIAEAGKPGSLSDGMQRLADAG-RAGTMDIE-DAMWMDVDDPRAH-21aa
17H9-22         D---GRIEKIDKT---LVDWDAGDTGVMCLTSGLFEGLERAAASNKHG-LSDGLRELAGE-RARTVDVT-GLLWLDMDTPEAL-215aa
GZ13E1_32       D---NRILDIGKN---IKKYNAYDTGFLCSPAI FSAIEESLALNDSS--LSGGIRVLVASKG-KAKTFDIK-DDYWIDVDDEKTF-458aa
Rxy1021259     G---GRVVEFGKN---LPRYDGLDAGLFLCSR PALERLREASGGERLSWNLKRAWLASGG-EVVACDLA-GAPWTDVDT PQDL-233aa
APE1514         P---GQVRLGKD---VBE-CVDVIGIHTIEAGIASIGCIDLPPRGEASVQLITCAARKGYTFKLVLDVDE-GGPWMEVDSPEEL-21aa
RFBF_SALTY      A---GQVRSQKEP---KGDGAMINGGFFVNLNSVIDLIDNDATTWEQV---LMTLAQQG---ELMAFHEHGFQWPM DTLRDK-18aa
MPG1_YEAST       IATPNLIDRFVEKPK-EFVGNRINAGLYILNPEVIDLIEKMP TSIKET---FPILVBEK---QLYSFDLEGFWM DVGPKDF-135aa
GLMU_ECOLI       NGKVTGIVEHKDATDEQRQIQEINTGILIANGADMKRWLAKLTNNNAQGEYYITDI IALAYQEGREIVAVHPQRLSEVEGVNNR-227aa
ISPD_ECOLI       PGKNAIAHTVDRN---GLWHALTPQFFPRELLHDC LTRALN---EGATITDEASALEYCG--FHPQVLEGRADNIKVTRPEDL-16aa

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