

## Supplementary Information

**Figure S1.** Alignment between different ADP-Glc PPases and UDP-Glc PPases Schematic, used in Panel A of Figure 1. (Ref: *Solanum*: ADP-Glc PPase small subunit from potato; *AtuGlgC*, *A. tumefaciens* ADP-Glc PPase; *EcoGlgC*, *E. coli* ADP-Glc PPase; Chimera, chimeric *SmuGalU*- $\Delta$ 294*EcoGlgC*; *SmuGalU*, *S. mutans* UDP-Glc PPase; *HpyGalU*, *H. pylori* UDP-Glc PPase; *CglGalU*, *C. glutamicum* UDP-Glc PPase). The amino acidic residue P<sup>295</sup> indicating the beginning of the *E. coli* ADP-Glc PPase C-term domain is over-marked.

		..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		10      20      30      40      50      60
<i>Solanum</i>	(1)	-----QTCLDPDASRSVLSGIIILGGGAGTRLYPLTKKRAKPAVPLGANYRLLDIPVSN
<i>AtuGlgC</i>	(1)	--MSEK-----RVQPLARDAMAYVLAGGRGSRLLKELTDRRAKPAVYFGGKARIIDFALSN
<i>EcoGlgC</i>	(1)	MVSLKNDHMLLARQPLKSVALLIAGGRGTRLKDLTNKRAKPAVHFGGKFRILDFALSN
<b>CHIMERA</b>	(1)	-----MPSKKVRKAVI PAAGLGTRFLPATKALAKEMLPITV-DKPTIQFIVEE
<i>SmuGalU</i>	(1)	-----MPSKKVRKAVI PAAGLGTRFLPATKALAKEMLPITV-DKPTIQFIVEE
<i>HpyGalU</i>	(1)	-----MIKKCLFPAAGYGRFLPITKTIPKEMLPITV-DKPLIQYAVEE
<i>CglGalU</i>	(1)	-----MSLPIDEHVNNAVKTVVVPAAGLGTRFLPATKTVPKELLPVV-DTEGIELIAAE
		..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		70      80      90      100      110      120
<i>Solanum</i>	(53)	CLNSNTISKIYVLTQFN SASLNRHLSRAYASNMGGYKNEG-----
<i>AtuGlgC</i>	(54)	ALNSGIRRIQVATQYKAHSLIRHLQRGWDFFRPERNE-----
<i>EcoGlgC</i>	(61)	CLNSGIRRMGVITQYQSHLTVQHIQRGWSFFNEEMNE-----
<b>CHIMERA</b>	(47)	ALKSGIEDILLVVTGKSKRSIEDHFD-----SNFELEYNLEQKGTDLKLV
<i>SmuGalU</i>	(47)	ALKSGIEDILLVVTGKSKRSIEDHFD-----SNFELEYNLEQKGTDLKLV
<i>HpyGalU</i>	(43)	AMEAGCEVMAIVTGRNKRSLEDYFD-----TSYEIEHQIQGTNKENALKSI
<i>CglGalU</i>	(53)	AAELGATRLAIIITAPNKAGVLAHFE-----RSSELEETLMERGKTDQVEII
		..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		130      140      150      160      170      180
<i>Solanum</i>	(92)	-----FMEVLAQQSPENPHWFQG-----TADAVRQYLWLFEEHTVLE-----
<i>AtuGlgC</i>	(91)	-----SFDILPASQQRVSETQWYEG-----TADAVYQNLDIIEPYAPEY-----
<i>EcoGlgC</i>	(98)	-----FVDLLPAQQRMKGENWYRG-----TADAVTQNLDTIRRYKAEDLAGDH-----
<b>CHIMERA</b>	(93)	NDTTAIN-LHFIRQS-----HPRGLGDAVLQAK-----AFVGN-----
<i>SmuGalU</i>	(93)	NDTTAIN-LHFIRQS-----HPRGLGDAVLQAK-----AFVGN-----
<i>HpyGalU</i>	(89)	RNIIEKCCFSYVRQK-----QMKGLGHAILTGE-----ALIGNE-----
<i>CglGalU</i>	(99)	RRAADLIKAVPVTQD-----KPLGLGHAVGLAE-----SVLD--DD
		..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		190      200      210      220      230      240
<i>Solanum</i>	(130)	---YLILAGDHLIY-RMDYE-----KFIQAHRETDADITVAALPMDEKRATAFGLM
<i>AtuGlgC</i>	(129)	---MVLILAGDHIY-KMDYE-----YMLQOHVDSGADVTIGCLEVPRMEATGFGVM
<i>EcoGlgC</i>	(136)	---VVILAGDHIY-KQDYS-----RMLIDHVEKGARCTVACMPVPIEEASAFGVM
<b>CHIMERA</b>	(126)	--PFVVMLGDDLMD-----ITDDKAIPLTRQLMNDYEETHA-STIAVMEVPHEDVSAYGV
<i>SmuGalU</i>	(126)	--PFVVMLGDDLMD-----ITDDKAIPLTRQLMNDYEETHA-STIAVMEVPHEDVSAYGV
<i>HpyGalU</i>	(123)	--PFAVILADDLC-----ISHDHPSVLK-QMSTLYQKYQC-SIVAIEEVALEEVSKYGV
<i>CglGalU</i>	(133)	EDVVAVMLPDDLVL-----LPT---GVME-RMAQVRAEFGG-SVLCAVEVSEADVSKYGI
		..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		250      260      270      280      290      300
<i>Solanum</i>	(176)	KIDEE-----GRITIEFAEKFOGEQLQAMKVDTTILGLDDKRAKEM-----
<i>AtuGlgC</i>	(175)	HVNEK-----DEIDDFIEKF-----ADPPGIPGN
<i>EcoGlgC</i>	(182)	AVDEN-----DKITIEFVEKF-----ANPPSPMPND
<b>CHIMERA</b>	(178)	IAP--QGEQVS---GLYSVDTFVEKF-----AP-----
<i>SmuGalU</i>	(178)	IAP--QGEQVS---GLYSVDTFVEKF-----AP-----
<i>HpyGalU</i>	(173)	IRG---EWLEE---GVYEIKDMVEKF-----NQ-----
<i>CglGalU</i>	(182)	FEI---EAD---TKSDSVKVKGMVEKF-----AI-----
		..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		310      320      330      340      350      360
<i>Solanum</i>	(216)	--P-----FIASMEIYVVISKDVMLNLLRDKF-PGANDFGSEV-----IPGAT

Figure S1. Cont.

<i>AtuGlgC</i>	(199)	EGF-----ALASMGIIYVFHTK-FLMEAVRRDAA---DPTS--SRDFGK-----DIIPYIV
<i>EcoGlgC</i>	(206)	PSK-----SLASMGIIYVFDAD-PLYELLEEDDR---DENS--SHDFGK-----DLIPKIT
<b>CHIMERA</b>	(201)	---KEAPSNLAIIGRYLLT--PEIFTILET-----QEP-GAGNEVQLTDAIDTL
<i>SmuGalU</i>	(201)	---KEAPSNLAIIGRYLLT--PEIFTILET-----QEP-GAGNEVQLTDAIDTL
<i>HpyGalU</i>	(195)	---EDAPSNLAVIGRYILT--PDIFEILSE-----TKP-GKNNEIQITDALRTO
<i>CglGalU</i>	(206)	---EDAPSRLAATGRYLLD--RKIFDALRR-----ITP-GAGGELQLTDAIDL
		..... ..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		370                  380                  390                  400                  410                  420
<i>Solanum</i>	(251)	SLGMRVQAYLY---DG--YWEDIGTIEAFYNANLGITK---KPV-----
<i>AtuGlgC</i>	(243)	EHG-KAVAHRFADSCVRSDFEHE-P--YWRDVGTIDAYWQANIDLTD---V-V-----
<i>EcoGlgC</i>	(250)	EAG-LAYAHPPPLSCVQSDPAE-P--YWRDVGTLEAYWKANLDLAS---V-V-----
<b>CHIMERA</b>	(244)	NKTQ-RVFAREF-----KGKRYDVGDKFGFMKTSIDYALK-----
<i>SmuGalU</i>	(244)	NKTQ-RVFAREF-----KGKRYDVGDKFGFMKTSIDYALK-----
<i>HpyGalU</i>	(238)	AKRK-RIIAYQF-----KGKRYDCGSVEGYIEASNAYYKKRL-----
<i>CglGalU</i>	(249)	IDEGHPVHIVH-----QGKRHDLGNPPGGYIPACVDFGLS-----HPVYGAQ
		..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		430                  440                  450                  460                  470                  480
<i>Solanum</i>	(291)	-----PDFSFYDRSAPIYTPRYLP
<i>AtuGlgC</i>	(288)	-----PDLDIYDKSWPIWTYAEITP
<i>EcoGlgC</i>	(295)	-----PELDMYDRNWPIRTYNESLP
<b>CHIMERA</b>	(280)	-----QVKEDLKAYIIELGKKLDQKSTQKNSDPELDMYDRNWPIRTYNESLP
<i>SmuGalU</i>	(280)	-----QVKEDLKAYIIELGKKLDQKSTQKNSD-----
<i>HpyGalU</i>	(274)	-----
<i>CglGalU</i>	(291)	LKDAIKQILAEHEAA-----
		..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		490                  500                  510                  520                  530                  540
<i>Solanum</i>	(311)	SSKML-----DADVTDSVIGEGCVIKNCKIHHSVVGRLRSCISEGAIEDSLLMG-ADY
<i>AtuGlgC</i>	(308)	PAKfVHDDEDRRG-SAVSSVVSGDCIISGAA LNRSLLFTGVRANSYSRLENAVVLPVSV---
<i>EcoGlgC</i>	(315)	PAKfVQDRSGSHG-MTLNSLVSGGCVISGSVVVQSVLFSRVRVNSFCNIDSAVLLPEV---
<b>CHIMERA</b>	(327)	PAKfVQDRSGSHG-MTLNSLVSGGCVISGSVVVQSVLFSRVRVNSFCNIDSAVLLPEV---
<i>SmuGalU</i>	(307)	-----
<i>HpyGalU</i>	(274)	-----
<i>CglGalU</i>	(305)	-----
		..... ..... ..... ..... ..... ..... ..... ..... ..... .....
		550                  560                  570                  580                  590                  600
<i>Solanum</i>	(363)	YETDADRKLLAAKGSVPIGIGKNCHIKRAIIDKNARIGDNVKII-----EAARETD
<i>AtuGlgC</i>	(365)	-----KIGRHAQLSNVVIDHGVVPEGLIVGEDPELDAKRFRRTESGI
<i>EcoGlgC</i>	(372)	-----WVGRSCLRRRCVIDRACVPEGMVIGENAEEDARRFYRSEEGI
<b>CHIMERA</b>	(383)	-----WVGRSCLRRRCVIDRACVPEGMVIGENAEEDARRFYRSEEGI
<i>SmuGalU</i>	(307)	-----
<i>HpyGalU</i>	(274)	-----
<i>CglGalU</i>	(305)	-----
		..... ..... ..... .....
		610                  620
<i>Solanum</i>	(420)	GYFIKSGIVTVIKDALIPSGIVI
<i>AtuGlgC</i>	(365)	CLITQSMIDKLDL-----
<i>EcoGlgC</i>	(415)	VLVTREMLRKLGHKQER-----
<b>CHIMERA</b>	(427)	VLVTREMLRKLGHKQER-----
<i>SmuGalU</i>	(307)	-----
<i>HpyGalU</i>	(274)	-----
<i>CglGalU</i>	(305)	-----

**Figure S2.** Alignment of chimeric enzyme sequence and templates used for homology modeling. (Ref.: 2pa4a, chain A of *C. glutamicum* UDP-Glc PPase; 3juja, chain A of *H. pylori* UDP-Glc PPase; 3BRK, *A. tumefaciens* ADP-Glc PPase; 1yp3a, chain A of potato tuber ADP-Glc PPase).

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.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          10      20      30      40      50      60
2pa4a    ----- VKTVVVPAAAG LGTRFLPATK TVPKELLPVV -DTPGIELIA AEAAELGATR
3juja    -----M IKKCLFPAAG YGTRFLPITK TIPKEMPLIV -DKPLIQYAV EEAMEAGCEV
3BRK     -----QPLAR DAMAYVLGG RGSRLKELTD RRAKPAVYFG GKARIIDFAL SNALNSGIRR
1yp3a    QTCLDPDASR SVLGII LGGG AGTRLYPLTK KRAKPAVPLG ANYRLIDIPV SNCLNSNISK
Chimeric -----MPSKK VRKAVIPAAAG LGTRFLPATK ALAKEMPLIV -DKPTIQFIV EEALKSGIED

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          70      80      90      100     110     120
2pa4a    LAIITAPNKA GVLAHFE--- -----R SSELEETLME RGKTDQVEII RRAADLIKAV
3juja    MAIVTGRNKR SLEDYFD--- -----T SYEIEHQIQG TNKENALKSI RNIEKCCFS
3BRK     IGVATQYKAH SLIRHLQRGW DFFRPERNE- -----SFD
1yp3a    IYVLTQFNSA SLNRHLSRAY -----EG- -----FVE
Chimeric ILVVTGKSKR SIEDHFD--- -----S NFELEYNLEQ KGKTDLLKLV NDTTAIN-LH

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          130     140     150     160     170     180
2pa4a    PVTQD----- KPLG LGHAVGLAE- -----SVLD--DD EDVVAVMLPD
3juja    YVRQK----- QMKG LGHAILTGE- -----ALIGNE-- --PFAVILAD
3BRK     ILPAS----- -WYEG----- -TADAVYQ NIDIIEPYAP EY----- --MVI LAGD
1yp3a    VLAAQQSPEN PDWFQG----- -TADAVRQ YLWLFEEHTV LE----- --YLI LAGD
Chimeric FIRQS----- HPRG LGDAVLQAK- -----AFVGN-- --PFVVMLGD

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          190     200     210     220     230     240
2pa4a    DLV-----L PT---GVME- RMAQVRAEFG G-SVLCAVEV SEADVSKYGI FEI----EAD
3juja    DLC-----I SHDHPSVLK- QMTSLYQKYQ C-SIVAIEEV ALEEVSKEYGV IRG----EWL
3BRK     HIY-KMDYE- -----YMLQQHVD SG ADVTIGCLEV PRMEATGFGV MHVNEK----
1yp3a    HLY-RMDYE- -----KFIQAHRETD ADITVAALPM DEKRATAFGL MKIDEE----
Chimeric DLMD-----I TDDKAIPLTR QLMNDYEETH A-STIAVMEV PHEDVSAYGV IAP---QGE

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          250     260     270     280     290     300
2pa4a    --TKDSVVKK VKGMVEKP-- -----AI-----EDAPS
3juja    EE---GVYE IKDMVEKP-- -----NQ-----EDAPS
3BRK     -----DE IIDFIEKP-- -----ADPPGIP GNEGF-----
1yp3a    -----GR IIEFAEKPQG EQLQAMKVDT TILGLDDKRA KEM-----P-----
Chimeric VS---GLYS VDTFVEKP-- -----AP-----KEAPS

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          310     320     330     340     350     360
2pa4a    RLAATGRYLL D--RKIFDAL RR-----ITPGA GGELQLTDAI DLLIDEGHPV
3juja    NLAVIGRYLL T--PDIFEIL SE-----TKPGK NNEIQITDAL RTQAKRK-RI
3BRK     ALASMGIVYF HTK-FLMEAV RRDA-----DI-----I PYIVEHG-KA
1yp3a    FIASMGIVVI SKD-VMLNLL RDKF-PGAND FGSEV-----I PGATSLGMRV
Chimeric NLAIIGRYLL T--PEIFTIL ET-----QEPGA GNEVQLTDAI DTLNKTO-RV

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
          370     380     390     400     410     420
2pa4a    HIVIH----- Q GKRHDLGNPG GYIPACVDFG LS-----HPV YGAQLKDAIK
3juja    IAYQF----- K GKRYDCGSVE GYIEASNAAY KKRL-----
3BRK     VAHREFADSCV RSDFEHE-P- -YWRDVGTD AYWQANIDL T D---V-V---
1yp3a    QAYLY----- DG- -YWEDIGTIE AFYNANLGIT K---KPV---
Chimeric FAREF----- K GKRYDVGDKF GFMKTSIDYA LKHP-----
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

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Figure S2. Cont.

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                430      440      450      460      470      480
2pa4a      QILAEHEAA- -----
3juja      -----
3BRK      -----PDLI IYDKSWPIWT YAEITPPAKF
1yp3a      -----PDFS FYDRSAPIYT QPRYLPPSKM
Chimeric   -----Q VKEDLKAYII ELGKKLDQKS TQKNSDPELD MYDRNWPIRT YNESLPPAKF

                .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
                490      500      510      520      530      540
2pa4a      -----
3juja      -----
3BRK      VHDDDDRGG- -SAVSSVVG DCIISGAALN RSLLEFTGVRA NSYSRLENVA VLPSV-----
1yp3a      L-----D ADVTDSVIGE GCVIKNCKIH HSVVGLRSCI SEGAIIEDSL LMG--ADYYE
Chimeric   VQDRSGSHG- -MTLNSLVSG GCVISGSVVV QSVLFSRVRV NSFCNIDSAV LLPEV-----

                .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
                550      560      570      580      590      600
2pa4a      -----
3juja      -----
3BRK      -----KIGR HAQLSNVVID HGVVIPEGLI VGEDPELDAK RFRRTESGIC
1yp3a      TDADRKLLAA KGSVPIGIGK NCHIKRAIID KNARIGDNVK II-----
Chimeric   -----WVGR SCRLRRCVID RACVIPEGMV IGENAEEDAR RFYRSEEGIV

                .....|.....| .....|.....| .....|.....| .....|.....| .....|.....|
                610      620      630      640      650
2pa4a      -----
3juja      -----
3BRK      LITQSMIDKL -----
1yp3a      -----NKDN VQEAARETDG YFIKSGIVTV IKDALIPSGI II
Chimeric   LVTREMLRKL GHKQER-----

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