Supplemental Figure 1: Sequence alignment based on the structural superimposition of PcGSTO1 and GSTs representative of different classes found by DALI (46) to be the closest structural neighbors of PcGSTO1.

CgGSTO : GST from *Corynebacterium glutamicum* (PDB ID 3M1G, UniProKB ref. Q8NR03, Midwest Center for Structural Genomics, unpublished results); gmGSTT : a tau class GST from *glycine max* (PDB ID 2VO4 (58), UniProKB ref. O49235); DmGSTD: a delta class GST from *Drosophila melanogaster* (PDB ID 3F6F, UniProKB ref. Q9VGA1, Wongsantichon and coworkers, unpublished results); ScGST, a GST from *Saccharomyces cerevisiae* (PDB ID 3ERF (59), UniProKB ref. Q12390); PmGSTB, a beta class GST from *Proteus mirabilis* (PDB ID 2PMT (60), UniProKB ref. P15214); hGSTO, a omega class GST from human (PDB ID 1EEM (10), UniProKB ref. P78417). The sequence alignment was generated with the programs STRAP (61) and ESPript (62). PcGSTO1 and hGSTO secondary structure elements are shown above and below the sequence alignment, respectively.

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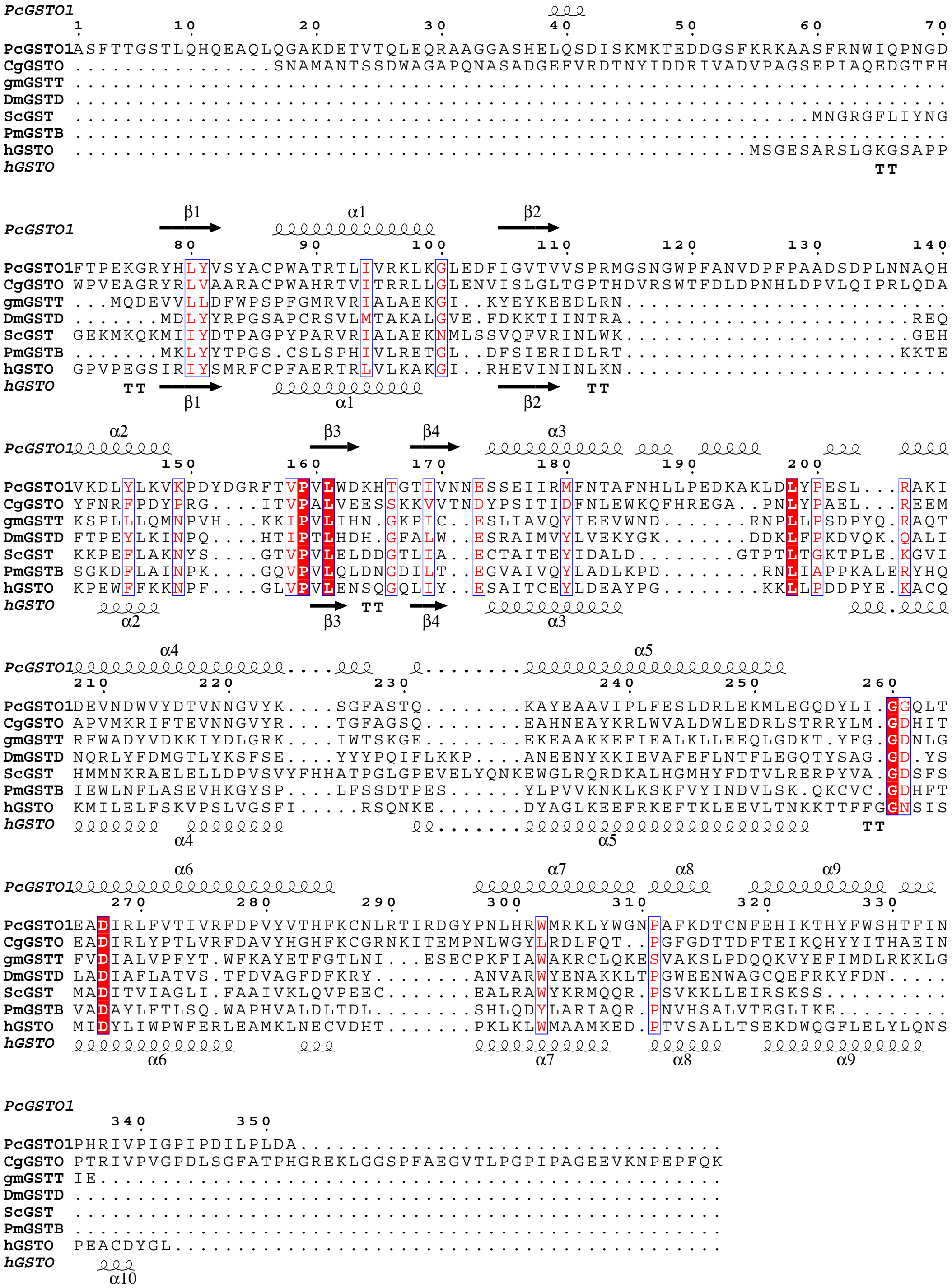

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       1       10        20        30        40        50        60        70
PcGSTO1ASFTTGSTLQHQEAQLQGAKDETVTQLEQRAAGGASHELQSDISKMKTEDDGSFKRKAASFRNWIQPNGD
CgGSTO ................SNAMANTSSDWAGAPQNASADGEFVRDTNYIDDRIVADVPAGSEPIAQEDGTFH
gmGSTT ......................................................................
DmGSTD ......................................................................
ScGST  ...........................................................MNGRGFLIYNG
PmGSTB ......................................................................
hGSTO  ......................................................MSGESARSLGKGSAPP

               80        90       100       110       120       130       140
PcGSTO1FTPEKGRYHLYVSYACPWATRTLIVRKLKGLEDFIGVTVVSPRMGSNGWPFANVDPFPAADSDPLNNAQH
CgGSTO WPVEAGRYRLVAARACPWAHRTVITRRLLGLENVISLGLTGPTHDVRSWTFDLDPNHLDPVLQIPRLQDA
gmGSTT ...MQDEVVLLDFWPSPFGMRVRIALAEKGI..KYEYKEEDLRN..........................
DmGSTD .......MDLYYRPGSAPCRSVLMTAKALGVE.FDKKTIINTRA.......................REQ
ScGST  GEKMKQKMIIYDTPAGPYPARVRIALAEKNMLSSVQFVRINLWK.......................GEH
PmGSTB .......MKLYYTPGS.CSLSPHIVLRETGL..DFSIERIDLRT......................KKTE
hGSTO  GPVPEGSIRIYSMRFCPFAERTRLVLKAKGI..RHEVININLKN..........................

              150       160       170       180       190       200
PcGSTO1VKDLYLKVKPDYDGRFTVPVLWDKHTGTIVNNESSEIIRMFNTAFNHLLPEDKAKLDLYPESL...RAKI
CgGSTO YFNRFPDYPRG....ITVPALVEESSKKVVTNDYPSITIDFNLEWKQFHREGA..PNLYPAEL...REEM
gmGSTT KSPLLLQMNPVH...KKIPVLIHN.GKPIC..ESLIAVQYIEEVWND.......RNPLLPSDPYQ.RAQT
DmGSTD FTPEYLKINPQ....HTIPTLHDH.GFALW..ESRAIMVYLVEKYGK.......DDKLFPKDVQK.QALI
ScGST  KKPEFLAKNYS....GTVPVLELDDGTLIA..ECTAITEYIDALD........GTPTLTGKTPLE.KGVI
PmGSTB SGKDFLAINPK....GQVPVLQLDNGDILT..EGVAIVQYLADLKPD........RNLIAPPKALERYHQ
hGSTO  KPEWFFKKNPF....GLVPVLENSQGQLIY..ESAITCEYLDEAYPG........KKLLPDDPYE.KACQ

       210       220           230               240       250        260
PcGSTO1DEVNDWVYDTVNNGVYK....SGFASTQ........KAYEAAVIPLFESLDRLEKMLEGQDYLI.GGQLT
CgGSTO APVMKRIFTEVNNGVYR....TGFAGSQ........EAHNEAYKRLWVALDWLEDRLSTRRYLM.GDHIT
gmGSTT RFWADYVDKKIYDLGRK....IWTSKGE........EKEAAKKEFIEALKLLEEQLGDKT.YFG.GDNLG
DmGSTD NQRLYFDMGTLYKSFSE....YYYPQIFLKKP....ANEENYKKIEVAFEFLNTFLEGQTYSAG.GD.YS
ScGST  HMMNKRAELELLDPVSVYFHHATPGLGPEVELYQNKEWGLRQRDKALHGMHYFDTVLRERPYVA.GDSFS
PmGSTB IEWLNFLASEVHKGYSP....LFSSDTPES......YLPVVKNKLKSKFVYINDVLSK.QKCVC.GDHFT
hGSTO  KMILELFSKVPSLVGSFI.....RSQNKE.......DYAGLKEEFRKEFTKLEEVLTNKKTTFFGGNSIS

          270       280       290       300       310       320       330
PcGSTO1EADIRLFVTIVRFDPVYVTHFKCNLRTIRDGYPNLHRWMRKLYWGNPAFKDTCNFEHIKTHYFWSHTFIN
CgGSTO EADIRLYPTLVRFDAVYHGHFKCGRNKITEMPNLWGYLRDLFQT..PGFGDTTDFTEIKQHYYITHAEIN
gmGSTT FVDIALVPFYT.WFKAYETFGTLNI...ESECPKFIAWAKRCLQKESVAKSLPDQQKVYEFIMDLRKKLG
DmGSTD LADIAFLATVS.TFDVAGFDFKRY........ANVARWYENAKKLTPGWEENWAGCQEFRKYFDN.....
ScGST  MADITVIAGLI.FAAIVKLQVPEEC.......EALRAWYKRMQQR.PSVKKLLEIRSKSS..........
PmGSTB VADAYLFTLSQ.WAPHVALDLTDL........SHLQDYLARIAQR.PNVHSALVTEGLIKE.........
hGSTO  MIDYLIWPWFERLEAMKLNECVDHT.......PKLKLWMAAMKED.PTVSALLTSEKDWQGFLELYLQNS

          340       350
PcGSTO1PHRIVPIGPIPDILPLDA..................................
CgGSTO PTRIVPVGPDLSGFATPHGREKLGGSPFAEGVTLPGPIPAGEEVKNPEPFQK
gmGSTT IE..................................................
DmGSTD ....................................................
ScGST  ....................................................
PmGSTB ....................................................
hGSTO  PEACDYGL............................................
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Supplemental Table 1 : Primers used in this study.
The *Nco*I and *Bam*HI cloning restriction sites are underlined in the primers. The mutagenic codons are in bold.

Name	Sequence
GSTO1 full length for	5’CCCCCATGGCTACCACCATCTGCCTGCGA 3’
GSTO1 truncated for	5’CCCCCATGGCTAGCTTCACAACCGGCAGC 3’
GSTO1 rev	5’CCCCGGATCCTCAGGCGTCGAGAGGGAG 3’
GSTO3 for	5’CCCCCATGGCTCCCATCCCCGACGAG 3’
GSTO3 rev	5’CCCCGGATCCCTACGGGATATCACGGCC 3’
GSTO1 C86S for	5’TACGTCTCGTACGCGTCCCCTTGGGCCACCCGC 3’
GSTO1 C86S rev	5’GCGGGTGGCCCAAGGGGACGCGTACGAGACGTA 3’
GSTO3 C37S for	5’TACGCTGGCTGGTTCAGTCCGTTTGTCCAGAGG 3’
GSTO3 C37S rev	5’CCTCTGGACAAACGGACTGAACCAGCCAGCGTA 3’