

Supplemental Figure S3. Amino acid sequence alignment of AtGPRAT2, AtGPRAT3 and GPRATs from *B. subtilis* and *E. coli*. Sequences were aligned using CLUSTALW. The GPRAT residues conserved in all four sequences are shaded black and those conserved in AtGPRAT2 and one or two of the other sequences are shaded gray. The green bar denotes the chloroplast transit peptide of AtGPRAT2 predicted by ChloroP (Emanuelsson et al., 1999, Protein Sci. 8: 978-994). For heterologous expression in *E. coli*, AtGPRAT2 was truncated by 75 residues and Asn76 converted into the starting methionine residue marked with |. The N-terminal cys residue revealed after autoprocessing is marked with +. Mutations in AtGPRAT2 that confer resistance to DAS734 are shown above the sequence and the resistance levels in seedling assays for the lines carrying the mutation are in parentheses.

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AtGPRAT2 (1) MAATSSISSLSLNAPNKLNNNNNNKPHRFLRNPFLNPSSSSFSPLPASISSSSSPSFLRVSNPLTLAADDNDYDEKPRE|CGVGIYEDSEASR
AtGPRAT3 (1) ----MAFSVEEISSILPNSLSANPRN-VSQNTISPSEFKK---SLKEYASKTLISLSCRRSLSPVFSAG--TYVTNVEDDKLHEE|CGVGIYEDPEASR
BsubGPRAT (1) -----MLAEIKGLNEE|CGVFGIWHHEEAPQ
EcoligPRAT (1) -----MCGIVGIAVMPVNPQ

AtGPRAT2 (101) LQYLLALHALQHRGQEGAGIVTVSKDKVLQITITGVGLVSDVVFSESKLDQLPGDIAIGHVRYSTAGSSMLKNVOPFVAG-YRFGSVGV|AHNGNLVNYTKLRA
AtGPRAT3 (91) LSKLALHALQHRGQEGAGIVAANQN-GLESITGVGLVSDVVFESKLNLPDIAIGHVRYSTAGSMLKNVOPRIAS-CKLGS|LVAHNCNFMVNYKQKLT
BsubGPRAT (26) ITMYGLHSLQHRGQEGAGIVATDGE-KLTAHKGQGLITVDFVQNGELSKVKKGKGAIGHVRYRFS---YENVOP|LLFRSQNNGSLA|AHNGNLVNYATQKQ
EcoligPRAT (16) STYDALTVLQHRGQDAGLITIDANNCFRLRKANGLVSDVVFEARHMQR|LQGNMCGIGHVRYRSTAGSSSASEAOPHYVN--SPYGIT|LAHNGNLVNAHELK

AtGPRAT2 (200) DEEENGSL-IFN|SSDTEVVLHLIA-----ISKARPFMRIVDACEK|LQAYSMVVFTEDK-LVAVRDPHCFRPLVMCRRSN---GAVVBASETQA
AtGPRAT3 (189) KLEENGSL-IFN|SSDTEVVLHLIA-----KSKAKTELLRVIDACEK|LQAYSMVVFTEDK-LIAVRDPHCFRPLVMCRRSN---GAVVBASETQA
BsubGPRAT (121) QLENGQS-IFQ|SSDTEVLAHLIK-----RSGHFTLKDQIKNSLSMLK|GAYAF|IMTETE-MIVALDENGLRPLSIEMMG---DAYVBASETQA
EcoligPRAT (114) KLEEEKRRHINT|SDSE|LLNIFASELDNFRHYPLE|DNIFAAL|AATNRLIRGAYACVAMIIGHGMVAFR|DENGLRPLVLCR|RIDENRTEYMVASEVLA

AtGPRAT2 (285) LDLEATYER|EVV|PGEVLVVDK-DGVK|CQCLMPHEPKO|CFE|H|HYE|SL|ENS|IVFGRS|VY|E|SR|HVF|CE|L|ATE|SP|----VDCD|VV|IA|V|ED|SG|VVA|ALGY
AtGPRAT3 (274) LDLDATYER|EVV|PGEVLVVDK-DGVK|CQCLMPHEPKO|CFE|H|HYE|SL|ENS|IVFGRS|VY|E|SR|HVF|CE|L|ATE|SP|----VDCD|VV|IA|V|ED|SG|VVA|ALGY
BsubGPRAT (205) FDVVGATYER|EVV|PGEVLIIND-EGMK|SERFSMNINRS|CS|MY|Y|F|SR|PDS|NID|GIN|V|S|AR|K|N|K|ML|A|Q|E|S|A|----VEAD|VV|T|G|V|ED|SS|I|S|A|I|GY
EcoligPRAT (214) LDPLGFDFL|D|V|P|G|E|A|I|Y|T|E|G|L|F|T|Q|C|A|D|N|E|V|S|N|P|L|E|Y|V|Y|E|A|E|D|S|F|I|D|K|I|S|V|Y|S|A|R|V|N|M|K|K|G|E|K|I|A|E|W|E|D|L|D|I|D|V|V|I|P|I|P|E|T|S|C|D|I|A|E|I

AtGPRAT2 (379) AAKACVAFQ|GLIRSHYVGRTF|E|E|S|K|I|R|D|F|G|V|K|L|K|L|S|P|V|R|G|V|E|K|R|V|V|V|D|D|S|I|V|R|G|T|S|S|K|I|V|R|L|R|E|A|G|A|K|E|V|H|M|R|I|A|S|P|P|I|A|S|C|Y|G|V|D|I|P|S|S
AtGPRAT3 (369) AAKAGVFP|Q|ICLLRSHYAKRTF|E|E|T|C|E|I|R|D|F|A|V|K|V|K|L|S|P|V|R|A|V|L|E|C|K|R|V|V|V|D|D|S|I|V|R|G|T|S|L|K|I|V|R|L|R|D|A|G|A|K|E|V|H|M|R|I|A|D|P|M|I|A|S|C|Y|G|V|D|I|P|S|S
BsubGPRAT (299) AEATGHPYEL|GLIKRNVVGRTF|I|Q|S|C|A|L|E|Q|G|V|R|K|L|S|A|V|R|G|V|E|K|R|V|V|V|D|D|S|I|V|R|G|T|S|R|R|I|V|M|L|R|E|A|G|A|T|E|V|H|K|I|S|S|E|P|I|A|H|P|C|F|Y|G|I|D|T|S|T|H
EcoligPRAT (314) ARILCKPYRQ|CFVKNRNVGRTF|I|E|C|Q|L|R|K|S|V|R|K|L|N|A|N|A|E|F|R|D|K|N|L|V|D|D|S|I|V|R|G|T|S|E|Q|I|E|M|A|R|E|A|G|A|K|V|Y|L|A|S|A|E|I|R|F|P|N|V|Y|G|I|D|I|P|S|A

AtGPRAT2 (479) NELISNRMSVDE|RDY|H|C|D|S|L|A|F|L|S|P|E|T|K|K|H|L|G|----EDSR|S|F|C|Y|A|C|F|T|C|D|Y|P|V|K|P|T|E|D|K|V|K|R|G|C|F|I|D|D|G|L|V|G|G|I|H|N|I|E|G|W|V|R|----
AtGPRAT3 (469) QELISKMSVEA|QKH|N|C|D|S|L|A|F|L|S|P|L|S|K|G|V|Y|G|P|---VES|H|R|Y|C|Y|A|C|F|T|C|K|P|V|K|T|E|S|E|A|D|A|S|----
BsubGPRAT (399) EELIASSHSVE|TRQEL|GAD|I|S|F|L|S|V|E|G|L|K|G|I|G|R|K|Y|D|D|S|N|C|G|Q|L|A|C|F|T|C|K|Y|P|T|E|I|Y|Q|D|I|V|L|P|H|V|K|E|A|V|L|T|K|----
EcoligPRAT (414) TELIAGHREVE|E|RQI|E|G|A|D|C|L|E|F|Q|D|L|N|D|I|D|A|V|R|A|E|N|P|D|I|Q|Q|E|C|S|V|E|N|G|V|V|T|K|D|V|D|Q|Y|L|D|P|L|D|L|R|N|D|D|A|K|A|V|R|Q|R|E|N|E|V|N|E|L|M|H|N|E|G

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