

```

      *      20      *      40      *      60
AtTPT  : MESRVLLRATANVVGIPKLRPIGAIHRQFSTASSSSFSVKPIGGIGEGANLISGRQLRPILLLD : 65
Gs39C12 : --MDMDFRKTLLKHSLN-----HFVFISSHSIWKSTNECVFKDKYALRRWSCPMRKF DWTITRQYLV : 58
AtPPT1  : --MQSSAVFSLSPSLPLLPKRRSLRHHPIITTAASSSDLNVSFPMVWVSIPLSRRSWRLASSDSPL : 63
Gs16F5  : --MIAFATPLGNTSWKLGYSRLKSVIYFQSTTSSHPKLTIRPSIQPWLFPVQ---NOKTVDHPS : 60
AtGPT1  : --MVLSVKQTLSP-----KIGLFRNP-----SSSLGRSPVSLSFSTELPKRTVLAVS--- : 47
Gs14H8  : --MIEAAFVPLSCLFSK-QHRWTVVSRNKNKNSISSHMEGSKKLLGTPRFTLSRSQFLNVSYLRL : 62
      m

      *      80      *      100      *      120      *
AtTPT  : SSAINGGEKREILKPVKAAAEEGGDTAGDAKVG-----FLAKYPWLVLTGFFFMWYFLNVIIF : 122
Gs39C12 : AKARRLPQFYCLANTSLDEPSKESIKVTEASQ-----PSQNTASUKRQLKVASVYFFLWYAFNIVY : 118
AtPPT1  : RAWSGVPSPIHSLDTNRFRTAATAVPESAEE-----GDNSGKLTKEVLELGLLEFAMWYLFNVIYF : 122
Gs16F5  : HLTSSFSPPMMLTLDG----AESSTGTSSSNV-----RQPVSQSLQKLIALTFFYIGCWYAAVNIIF : 115
AtGPT1  : -KPLHLSSSLRAKSPVVRCEAYEADRSEPHPIGDAAAETKSEAAKKLLKIGIYFATWVALNVIIF : 111
Gs14H8  : TKYNNVAASSKGEKDIIRAAVDKSE-SGGSPQ---KSSVGVSPVLVHTLKVGFYFFLWYFFNVIIF : 123
      6 f W5 N 5

      140      *      160      *      180      *
AtTPT  : NILNKKIYNYFPYPYFVSVIHLFVGVYCLISWSVGLPKRAPIDSNLLKVLIPVAVCHALGHVTS : 187
Gs39C12 : NISNKKLLNAYFPFPWTVAWVQLAVGVFVYVPLWLLHLRKAPHIPLEDIKRLLPVAAAHTIGHIST : 183
AtPPT1  : NIYNKQVLKALHAFMTVTLVQFAVGSVLITIMWVNLNLYKRPKISGAQLAAIPLAVVHTLGMVFT : 187
Gs16F5  : NIYNKRVLKVFPLFATVTLVQFLMGSVGLALWISGLHRFQKASLEDLKKIYPLALSHLIGMVLTI : 180
AtGPT1  : NIYNKKVINAYPYPWLTSTLSLAAGSMLMMLISWAVGIVETPKTDFDFWKTLPVAVVAHTIGHVAA : 176
Gs14H8  : NIANKRTLNMMWKYPWVLSLTIQLGVGALYCTFLWVGLRTPKPNVSKKLIKALIWPSLGHVLAAT : 188
      NI NK l p 6 G W 6 k 6 p a H 6G

      200      *      220      *      240      *      260
AtTPT  : NVSFAAVVVSFTHTIKALEPFFNAASQFIM-CQSIPITLWLSLAPVVLGVAMASLTELSTFNMVLG : 251
Gs39C12 : VVSLGAVVVISFTHVVKALEPFFVNVLASAVIL-RSVFPIPVYLSLLPVVGGVVIASVTELSTFTWTG : 247
AtPPT1  : NMSLGKVSVSFTHTIKALEPFFSVLLSAMFL-CEKPTPWVVGAVPIVGGVALASISEVVSFNMVAG : 251
Gs16F5  : NVSLRQVVSFTHTIKALEPFFSVALSCLFIPGTAYTIWVYLSLPIVGGVTLASISEVVSFNMVIG : 245
AtGPT1  : TVSMKVVVSFTHTIKSGEPAFSVLVSRLFIL-GETFPTSVMYLSLPIIIGGCALSALTELMFNMVIG : 240
Gs14H8  : CMSFSLVVISFTHVVKSAEPVFGAVGSAVL-GEFFHPLTYLTLVPIVSGVALSAAATELIFTWTG : 252
      6S Va6SFTH 6K EP f S 6 g l 6 P66 Gv 6 3E6 F w G

      *      280      *      300      *      320
AtTPT  : FISAMISNLSFTYRSIFSKKAMTD-----MDSTWVYAYISIIALFVCIPPAIIVEG---PKGLN : 307
Gs39C12 : FMAAMLNFAFTSRNIFSKISMNDQTSYKHMSPANLFAVLTILSTFILLPVALLILEG---PKLYQ : 309
AtPPT1  : FSSAMASNLTNQSRRVLSKKVMVKK--DDSLDNITLFSIITLMSLVLMAPVTFTEG-----IKF : 309
Gs16F5  : FLTAMASNVAFQSRVLSKKFMKG---VQFDNLNLFAYISILSFVTMLPFTLLLEAGRUREMAS : 306
AtGPT1  : FMGAMISNLAFFVRNIFSKKGMK---GKSVSGMNYAACLSMSSLILTPFAIIVEG---PQMWV : 298
Gs14H8  : FITAMISNVAFVTRNITSKFTMVDFKNEKTLIAQNTYALITIIISFFMELPFALLHEG---FPPLV : 314
      F AM SN f Rn6 SK M n 5a 6366s P Eg

      *      340      *      360      *      380      *
AtTPT  : HGFADAIAKVGMTKFIISDLFVWGMFYHLYNQLATNTLERVAPLTHAVGNVLRVVFVIGFSIVVIFG : 372
Gs39C12 : GWILATSGKTTSMQLITGLLTSGLFFLYNEVAFYALDSVHPITHSVGNMTRKRVVITITSLLVFK : 374
AtPPT1  : TPSYIQSAGVNVKQIYTKSLIAALCFHAYQVSYMHILARVSPVTHSVGNMCKRVVIVSVVIFFK : 374
Gs16F5  : VATHIGSEGCTIPVLLLRIAIAGFLHFLYMQFSYVWLKRVNVPVTHSVGNMTRKRVVIVSVVIFFK : 371
AtGPT1  : DGWQATALATVG-PQFVWVVAQSVFYHLYNQVSYMSLDQISPLTFVGNMTRKRVVIVSVVIFFR : 362
Gs14H8  : S----AIAGVSKAKLFGSIFMCSLFYHLYNEVSYLCLDNVSPVSVSIGMTIKRVVIVVIFG : 375
      1Yn2 L 6 P63 s6GN 6KR6 6I S66 F

      400      *      420
AtTPT  : NKISTQTGIGTGIAIAGVAMYSIIKAKIEEEKRQGKKA : 410
Gs39C12 : NPIIPANAIGSAIAISGVLLYSLTRKYYSQKIK----- : 407
AtPPT1  : TPVSPVNAFGTGIAGVFLYSRVKGIKPKPKTA---- : 408
Gs16F5  : NQVTLNKGITAIAGVAIYSQVKNISTKKKEKIE-- : 407
AtGPT1  : TPVQPVNAGAAIAILGTFLYSQAKL----- : 388
Gs14H8  : TPVIRLNFISTIAIIGTMLYSLAKAKLPSKREKQ--- : 410
      6 n G IA6 G 6YS K

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## Supplemental Figure S1

**Supplemental Figure S1: Protein alignment of plastidic phosphate transporters (pPT) from *Arabidopsis thaliana* (At) and *Galdieria sulphuraria* (Gs).** Multiple sequence alignment program ClustalW2 (Larkin et al., 2007) at EMBL-EBI lined up the sequence similarities and the tool GeneDoc (<http://www.nrbsc.org/gfx/genedoc/index.html>) visualized and edited the higher plant pPT proteins and their red algal homologues Gs39C12 (GsTPT), Gs16F5 (GsPPT) and Gs14H8 (GsGPT). AtTPT, Triose-Phosphate-Translocator, AGI genome code At5g46110; AtGPT1, Glucose-6-Phosphate-Translocator, At5g54800; AtPPT1, Phosphoenolpyruvate-Translocator, At5g33320;