

AtGGH1 MWRYICLPFFLLWNDIGLAKESBSILPSESGFVGSR-----SPVCSPPDNLNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 AtGGH2 MWSYVWLPLVALSLFKDSIIMAKAAIILPSSQIGFVISR-----SPVCSAPPDNLNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 AtGGH3 MWRFCEFFLSLLFFDVSAVKSABSIFFPSQIGVDSRVFESLSLSPVCSAPPDNLNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Pt1 MWNYLWIPFLLSLSEKELTLARSAATTSSPILPSSQLAD--SPS-----APKCEAPPDNLNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Pt2 MWSYLVIPFLMSLSKELTLARAATATSSPILPSSQLAD--DPS-----VPRCSAPPDNLNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Gm1 MPNDSVLSLFFVTLFTCLLSATSDDHDIILPSSQLAD--DVS-----CIATDPSLNYKPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Gm2 SSDAVVWLFHLAFFSQCLPSAWAHSAILPSSQLAR--SPQS-----CFAPDNLNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 LeGGH1 MGNYSISIFFLLCGITTABEQLFNYSYLLPSS-----SCPAPDPALNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 LeGGH2 MQMETNFLIPFFTFIQLMSTHVKEQLPSSQLNFP-----SCFATDPAALNRPVIGILSHPGDG-----ASGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 LeGGH3 MSNYFLISLLTSLFLVVTIIESAELFVPA-----CCPLDNLNRPVIGILSHPGDG-----DSGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Os MGSPPHRLLLLAVALHRSAAAAGVRLPRGR-----ACAAPTDPAAVDRPVIGILSHPGDG-----AGGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Hv MASLPQHLLPVLVLLALLGPPSSAGAGVRLPRAG-----ACAAPTDPAAVDRPVIGILSHPGDG-----AGGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 Zm MDSRCPHLLLLPLVLLAALLPSSSGVPEVWLPTSGG---AGPLSCAPDPAVDRPVIGILSHPGDG-----AGGRLENDPSSYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL
 RnGGH MASLGRLLCAVLLLCGLASPLSGSYERGSRRP IGLIMQBCYC-----NMTKLGFRFYIAASYVKFAEACGARVIPLIYNENPEILFQKLEL

AtGGH1 VNGVLF TGGWA--KKGYDFEIKKIFKALEKNDAGEHFPVYICLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 AtGGH2 VNGVLF TGGWA--KEGHYDFEIKKIFNKVLEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFMDARNSASLQFVENVNTQGTIFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 AtGGH3 VNGVLF TGGWA--KKGHYDFEIKKIFNKVLEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFNSVNYASLQFENVNIETVFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Pt1 VNGVLF TGGWA--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Pt2 VNGVLF TGGWA--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Gm1 VNGVLF TGGWA--VKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Gm2 VNGVLF TGGWA--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 LeGGH1 VNGVLF TGGWA--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 LeGGH2 VNGVLF TGGWS--KKGYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 LeGGH3 VNGVLF TGGWA--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Os VNGVLF TGGSV--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Hv VNGVLF TGGSV--KKGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 Zm VNGVLF TGGSE--KEGHYDFEIKKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT
 RnGGH VNGVLF TGGC--ANLTHSGYSRVAKIFKALEKNDAGEHFPVYIACLGFELLSMIISQNRDILEFEDAENASSLQFVENVNDGTFORFPPHLLKKLSTDCLVMQNHRYGISPOFQNEHLSFFFEILT

AtGGH1 TCIDENSKTYVSTVRAKRYPIITCFQWHPEKNAFEWGSSA--IPHSEDAIQVTQHAANYLSEARAKSLN--RPESQKVLNLIYNYKPTYCGYAGIGYDEVYIFQQRSRF
 AtGGH2 TCVD--NGKVYVSTVQSTKRYPIITCFQWHPEKNAFEWGSSK--IPHSEDAIQVTQHAANYLSEARAKSLN--RPESQKVLNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 AtGGH3 TSADKDKSTVSTVRSKRYPIITCFQWHPEKNAFEWGSSA--IPHSEDAIQVTQHAANYLSEARAKSMN--RPSSEKVLNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Pt1 NSADEDNQVYVSTVQARNYPITCFQWHPEKNAFEWGSSM--IPHSEDAIQVTQHAANYLSEARAKSLN--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Pt2 TSTDENQVYVSTVQACGYPITCFQWHPEKNAFEWGSSM--IPHSEDAIQVTQHAANYLSEARAKSLN--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Gm1 TSGDRDCKTVSTAR--RKYPIITCFQWHPEKNAFEWGLSILKAPHEDAIQVTQSTANFSEARAKSTN--TPDAQKVRD--SLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Gm2 TCTDEDDKVYVSTVRSQNYPIITCFQWHPEKNAFEWGSSR--IPHSEDAIQVTQHAANYLSEARAKSLN--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 LeGGH1 TSTDENKQVYVSTVQARNYPITCFQWHPEKNAFEWGSSR--IPHSEDAIQVTQHAANYLSEARAKSSN--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 LeGGH2 TSVDKKNKVYVSTVQARNYPITCFQWHPEKNAFEWGSSQ--IPHSEDAIQVTQHAANYLSEARAKSSN--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 LeGGH3 TSTDTRNKVYVSTVQARNYPITCFQWHPEKNAFEWGSSA--IPHSEDAIQVTQHAANYLSEARAKSSN--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Os TSPDENGEVYVSTVQARNYPITCFQWHPEKNAFEWGLSILKAPHEDAIQVTQSTANFSEARAKSON--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Hv TSPDENGEVYVSTVQARNYPITCFQWHPEKNAFEWGLSILKAPHEDAIQVTQSTANFSEARAKSON--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 Zm TSPDENKQVYVSTVQARNYPITCFQWHPEKNAFEWGLSILKAPHEDAIQVTQSTANFSEARAKSON--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL
 RnGGH VNTDG--KTE--LSSMEYKYPYIYVQWHPEKNAFEWGLSILKAPHEDAIQVTQSTANFSEARAKSON--RPPARKVLDNLIYNYKPTYCGYAGIGYDEVYIFQQRSL

Supplemental Figure S1

Legend on following page

Supplemental Figure S1. Alignment of GGH amino acid sequences. Representative GGH amino acid sequences for eudicots and dicots are illustrated and compared with rat GGH. Identical residues are shaded in black, similar residues are in gray, the predicted signal peptide regions are in blue, and potential *N*-glycosylation motifs (NXS/TX, where *X* is any residue except Pro) are in green. Based on human GGH, red arrows indicate catalytically essential residues and the regions that form the dimer interface are underlined with dots. Sequences for tomato (Le), Arabidopsis (At), soybean (Gm), *Populus trichocarpa* (Pt), rice (Os), barley (Hv), maize (Zm), and rat (Rn) were compiled from EST and genome databases.