

### Additional file 3. Alignment of *D. japonica* and *S. mediterranea* GGT1

*D. japonica* GGT1 [EST: Dj\_aH\_529\_E12.double]  
*S. mediterranea* GGT1 [GenBank: DN304849.1]

#### Protein Alignment

Identical rate of amino acids = 69.8%

Identical and homologous substitution rate of amino acids = 88.3%

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                20                40                60
GGT1_DUGJA  MGNETGI IYN DEMDDFSSP S KANIYNLPPS PSNYIRPYKR PMSSMSPFIM IDKNGQVELI 60
GGT1_SCHMD  MGTKTGIVYN DEMDDFSSPN KSN IYNLPPS PSNFIMPYKR PMSSMSPIII VDNEGNVDLV 60

                80                100               120
GGT1_DUGJA  LGASGGSRI I SSTLQVAVLA KLFNKSIKEA IDIPRVHHQL LPNIITVEMN FPDNIVKSLQ 120
GGT1_SCHMD  LGASGGSKIL SATTQVSILS KLLKKT I KEA IDIPRIHHQL IPDEVVAEMN FPDVLVESLR 120

                140               160
GGT1_DUGJA  KRGHEVQKTS DFAVCQGIKK SENSSF-WQC NADFRKMGLC DGS 162
GGT1_SCHMD  QKGHIVRKDP DYAVCQGI MK SLDSAYSWQC NADFRKMGLC DGF 163
    
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#### Nucleotide Alignment

Identical rate of nucleotides = 72.8%

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                20                40                60
GGT1_DUGJA-1 ATGGGAAATG AA ACTGGAAT CATTTACAAT GATGAAATGG ATGACTTTTC CTCACCAAGT 60
GGT1_SCHMD-1 ATGGGAAACCA AA ACTGGAAT AGTTTACAAC GACGAGATGG ACGATTTCTC TTCTCCGAAC 60

                80                100               120
GGT1_DUGJA-1 AAAGCAAATA TTTATAACTCT ACCGCCTTCT CCAAGTAACT ATATAAGACC GTATAAGCGA 120
GGT1_SCHMD-1 AAATCAAACA TTTACAACCT ACCACCATCT CCCAGTAACT TCATTATGCC ATATAAAGA 120

                140               160               180
GGT1_DUGJA-1 CCGATGTCGT CTATGTCTCC ATTTATTATG ATCGATAAAA ATGGACAAGT AGAATTAATT 180
GGT1_SCHMD-1 CCAATGTCAT CCATGTCTCC GATTATCATT GTTGATAAATG AAGGAAATGT TGATTTAGTT 180

                200               220               240
GGT1_DUGJA-1 CTTGGTGCTT CGGGAGGCAG TAGAATCATT TCAAGCACAT TACAAGTTGC AGTACTTGCT 240
GGT1_SCHMD-1 CTTGGAGCTT CTGGAGGCAG TAAAATACTT TCAGCTACAA CACAAGTTTC TATTTCTTCC 240

                260               280               300
GGT1_DUGJA-1 AAATTGTTCA AATAAAGCAT AAAAGAAGCG ATTGACATTC CACGAGTTCA TCATCAATTG 300
GGT1_SCHMD-1 AAATTGTTGA AAAAGACCAT TAAAGAGGCA ATAGACATTC CCCGAATTCA CCATCAATTA 300

                320               340               360
GGT1_DUGJA-1 TTGCCTAATA TAATCACTGT TGAAATGAAC TTTCTGATA ATATTGTTAA AAGTTTGCAG 360
GGT1_SCHMD-1 ATTCCAGATG AAGTTGTTGC GGAAATGAAT TTTCCGGATG TTCTAGTTGA AAGCTGAGG 360

                380               400               420
GGT1_DUGJA-1 AAAAGAGGTC ATGAAGTACA AAAGACGTCT GATTTTGC GG TTTGTCAAGG TATCAAAAAA 420
GGT1_SCHMD-1 CAAAAGGTC ATATTGTGAG AAAAGATCCT GATTATGCAG TATGTCAAGG CATAATGAAA 420

                440               460               480
GGT1_DUGJA-1 TCAGAAAATT CGTC - - - TTT CTGGCAATGT AATGCTGACT TTAGAAAAAT GGGACTATGT 477
GGT1_SCHMD-1 TCTTTGGATT CAGCATATTC ATGGCAGTGC AATGCTGACT TTAGAAAAAT GGGGTTATGT 480

GGT1_DUGJA-1 GATGGTTCAT AA 489
GGT1_SCHMD-1 GATGGATTTT GA 492
    
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