

Supplementary Material

Figure S1. The deduced amino acid alignment of XsGAS with several germacrene A synthases from other plant species. AaGAS, germacrene A synthase (AFK93531) from *Artemisia annua*; HaGAS1, germacrene A synthase (Q4U3F7) from *Helianthus annuus*; LsGAS1, germacrene A synthase (AAM11626) from *Lactuca sativa*.

HaGAS1	MAAVGASAT-PLTNTKSTAEFVRPVANFPSPVWGDFLFSFSLDKSIMEEYAEAMEEPKEE
LsGAS1	MAAVEANGT-LQANTKTTTEPVRPLANFPSPVWGDRLFSFSLDNTELEGYAKAMEEPKEE
AaGAS	MAAVQANVTGIKENTKTSAPVRPLANFPSPVWGDRLFSFSLDRSELERYAIAMEKPKED
XsGAS	MAAVGANAT-LLTNTKSTVEPVRPLANFPSPVWGDMFLFSFSLDNSKMEEYAKAMEKPKQE
HaGAS1	VRRILIDPTMDSNKKLSLIYTVHRLGLTYMFLKEIEAQLDRLFKFENLEDYVELDLYTIS
LsGAS1	VRRLIVDPTMDSNKKLSLIYSVHRLGLTYLFLQEIEAQLDNIFKAFKLQDYDEVLDLYTTS
AaGAS	LRKLIVDPTMDSNEKLGLIYSVHRLGLTYMFLQEIESQLDKLFNKFSLQDYEEVDLYTIS
XsGAS	VRRILIDPTMDSNKKLSLIYVHRLGLTYMFLKEIEGQLDRLFEFENLEDYVDVDLHTIS
HaGAS1	INFQAFRHLGYKLPCDVFNKFKNDSTTFKESITGDVRGMLGLYESAQLRLKGENILDEA
LsGAS1	INFQVFRHLGHKLPCDVFNKFKDSSSGTFKESITNDVKGMLGLYECALRLRGESILDEA
AaGAS	INFQVFRHLGYKLPCDVFNKFKDVSSSGTFKASIMSDVRGMLGLYESAQLRIRGEKILDEA
XsGAS	INFQAFRHLGYKLPCDVFNKFKNNDSNAFKESIASDVRGLLGLYESAQLRVKGKILDDA
HaGAS1	SFAAETKLKSLVNTLEGSLAQQVKQSLRRPFHQGMMPMEARLYFSNYQEECSAHDSILKL
LsGAS1	SAFTVTQLKSVVNTLEGKLAQQVLQSLKRPFHQGMMPMEARFYFSNYDEECSTHESLVKL
AaGAS	SVFTEAKLKSVVNTLEGDLAQQVTQSLRRPFHQGMMPMEARLYFSNYEKECSTYDSLKL
XsGAS	SFAAETKLKSLVNTLEGSLAQQVKQALKRPFHQGMMPMEARLYFTNYQEEFSKYDSLKL
HaGAS1	AKLHFNYLQLQQKEELRIVSQWWKDMRFQETTPYIRDRVPEIYLWILGLYFEPYSLARI
LsGAS1	AKLHFNYLQLQQKEELRIVSKWWKDMRFQETTPYIRDRVPEIYLWILGLYFEPYSLARI
AaGAS	AKLHFKYELRQKEELRIVPKWWKDMRFHETTPYIRDRVPEIYLWILGLYFEPYSLARI
XsGAS	AKLHFNYLQLQQKEELRIVSKWWKDMRFQETTPYIRDRVPEIYLWILGLYFEPKYSLARI
HaGAS1	IATKITLFLVLDDTYDAYATIEEIRLLTDAINRWDISAMNQIPEYIRPFYKILLDEYAE
LsGAS1	IATKITLFLVLDDTYDAYATIEEIRLLTDAINRWDISAIEQIPEYIRPFYKILLDEYAE
AaGAS	IATKITLFLVLDDTYDAYATIEEIRPPTDAISKWDISAMEQIPEYIRPFYKILLDEYAE
XsGAS	IATKITLFLVLDDTYDAYGTLEELRLLTHAINRWDIMRAMSDIPEYIRPFYKILLDEYAE
HaGAS1	LEKQLAKEGRANSVIASKEAFQDIARGYLEEAETNSGYVASFPEYMKNGLITSAYNVIS
LsGAS1	LEKQLAKEGRAKSVIALKEAFQDIARGYLEEAETNSGYVASFPEYMKNGLVTSAYNVIS
AaGAS	IEKKMAKEGRANTVIASKEAFQDIARGYLEEAETNSGYVASFPEYMKNGLITSAYNVIS
XsGAS	LEKQLAKEGRKSVIASKEAFQDIARGYIEEAETNSGYVASFPEYMKNGLITSAYNVIS
HaGAS1	KSALVGMGEIVSEDALVWYESHQILQASELISRLQDDVMTYQFERERGSATGVDSYIK
LsGAS1	KSALVGMGEMVSEDALAWYESHKTLQASELISRLQDDVMTYQFERERGSATGVDSYIK
AaGAS	KSALVGMGEIVSEDALAWYESHKTLQASELISRLQDDVMTYQFERERGSATGVDAYIK
XsGAS	KSALVGMGEVVSADALAWYESHKILQASELISRLQDDVMTYQFERERGSATGVDSYIK
HaGAS1	TYGVSEKVAIDELKKMIENAWKEINEGCLKPREVSMDLLAPILNLARMIDVVYRYDDGFT
LsGAS1	TYGVSEKEAIDELNKMENAWKDINEGCLKPREVSMDLLAPILNLARMIDVVYRYDDGFT
AaGAS	TYGVSEKEAIDALKIMIENAWKDINEGCLKPRQVSMDLLAPILNLARMIDVVYRYDDGFT
XsGAS	TYGVSEKEAIEELKKMIENAWKDINEGCLKPREVSMDLLAPILNLARMIDVVYRYDDGFT
HaGAS1	FPGKTLKEYITLLFVGSSPM
LsGAS1	FPGKTMKEYITLLFVGSSPM
AaGAS	FPGKTLKEYINLLFVGSLPV
XsGAS	FPGKTLKEYITLLFVDSLPM