

CRD

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AtGEX1 MDRFSRKCLLFLLLIILLDSPL--TCHSWGWFSSSSSSAEDPYSSS----FSRSRKSNDPFSMEVFSDQKAVQVLE---NKLVLGLTSCWQNAYSYLLAGCKETIATEEKR 101
BrGEX1 MDHFKRRLYLLFL-LITLIDSPI--TCHSWGWFSSSGENTN----PS----SSRSIKSNTEFSIEVFSDDKAVQVLEDAKNKLAGPNSCWQNAYGYLLSGCKGMVATEEQR 99
OsGEX1 MRRHAGTIILLLLILACLWLCPGRSSGFSWNIFFSSSSSSSPPTAGESRAAPMLELDGAVADFLMDGADDPRAVKLLENARSKLAGPSNCWQEAYRRLFASCGDIMADKEMQ 110

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211

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AtGEX1 KRFAYLSDCFIKDSGRPAFPTCKDESVMMSCLKKLDDHEHKIYLDFLLETNTICQQLQSNAFKNEIERLVNELKNTAQYTEDKLDILESKSDALIQTSSMIHDSLGSLD 211
BrGEX1 KRFAYLSDCFQKESGRPDFPTCNDKQTMMSCLLKKLDDHEHKIYLEFMLETNTICQQLQSHALKNEIERLVNDLKRSAQNTEEKLDILESKSDDILQGTSKIHESVGLID 209
OsGEX1 SRLAWHLSSCFQEDSGRPPFPRCGEVSDMVHCRKRLGVSEDQVLEFFLETNLCHQLQAEAFKHNTERLVNDLTRTSKSAEKELVIEERSDQIIQESRKVQETISIE 220

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321

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AtGEX1 VRVQNVASVTNTLETSSVSGLSQQTVEISQEKNIAESQLALRDGQVKMKETLKDGMDFLDAYTNIQEGVDKLSKDTEQIEVEISVLGNNLSTKMIDLQSTTDDIGTKTR 321
BrGEX1 VVVNNVAHKTNTIGTQMSGLSQQTRDIYQEQKSITESQLALKEGQEMGEAMKVGMEMFNDSVTDVKDGVDRLKNDTKQIGGKINQLGEKMSEKMTALENQTSIIIGTMTN 319
OsGEX1 MQADHLAEASKNVGDQIDDVLAHSKAIFEQSKEIADSQAKLREGQTEMRETIDAGMTHIQESYESLGNGMDKLKEEAVDIQREIKTVGDSMSTKMQDLQSTANDIGSVAG 330

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431

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AtGEX1 SSLDKQQKLLDGQTVALDGIQFLTRFQSEALQESRNTLQRLKEFSQEQQEDLAKRQEKLQEVHDHFLFENSKSMLEAQVAFEAKQANMFVALDKLFALHNAMLLESRVIKA 431
BrGEX1 STLDNQQKLLEGQSVAIDSIQSLNQFQSEALQESRSTLQRFAEFSQEQQEDLAKRQEQLQVHDHFLFENSKSMLAQEAFEAKQASMFVALDKLFALHNAMLLESRVIKA 429
OsGEX1 KSLENQMQLLDGQSKAMDGLNNLYSFQAQALEESRETVQLAQFGQRQEELSRQEEIRQAHEHLIHNSHILEAQEEFRAKQANIFAALDKLYILHNAILAESRFIKA 440

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533

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AtGEX1 FVIYFLSIFVIYMTSTKQTYIIRPRLYIGLCVTLALEVASLRYVN-DTERQAWMIN---LIRSLFALLASAQLLHAALSYRDYEVLNHQILLRLVDKVNDMQSKK---- 533
BrGEX1 FFIYFLSIFVIYMTSTKQTYIIRPRLYIGLCVTLALEVASLRYVN-DEEHRAWVIN---VLRSFAVLASAQLLHSAFTYRDYEVLNHNILLRLVDKVNSMQSKR---- 531
OsGEX1 FFFYCCIVFLIYMLTSAKQTFSIRGHLYFGLCITLLLEIGLIKLGADDIDKQFWISKVFLVRSVFLALATVQMLHAIFTFRDYELLNHHLLLQTLVEKVRALEETAAAGE 550

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593

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AtGEX1 -ELSYDE---DTESEVDWTSWVDTLDTDDDDNLADPDYKIPLLIKDNPVTT-----SSLTRRLYNFRPR----- 593
BrGEX1 -EILWDE---DTDSEVDWNSWIDTDITDDDSLGDPDYRIPEIKDNVGFT-----SSMTKRLYNLRPR----- 591
OsGEX1 KMLPYGGGGAESERSLMDYSWFDELADEVDSNADPSYALPGDEQRQVAVVAPRRRHCASPEEVVGENSITTSAGRRYNLRPRSSYRQT 639

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	% identity	
	BrGEX1	OsGEX1
AtGEX1	73.81	43.84
BrGEX1		42.13

**Figure S1.** Sequence alignment of AtGEX1 (At5g55490), BrGEX1 (XP\_009120059) and OsGEX1 (XP\_015611623). Alignment was performed using Clustal Omega (<https://www.ebi.ac.uk/Tools/msa/clustalo/>). Amino acid residues that do not match with AtGEX1 are highlighted in pink. CRD is shown as a box. Percent identities between each sequence are shown below the alignment

**Table S1.** PCR Primers Used for Plasmid Construction.

<b>Name</b>	<b>sequence (5'-3')</b>
BrGEX1F1	GCCGCCCCCTTCACCATGGATCATTTTAAAAGAAG
BrGEX1R1	GGCGCGCCCAACCCTTTTATCGTGGACGGAGATTGT
OsGEX1F2	GCCGCCCCCTTCACCATGAGGAGACACGCAG
OsGEX1R2	GGCGCGCCCAACCCTTTCACGTCTGCCTGTA ACTACTCCG

**Table S2.** PCR Primers Used for Quantitative Real-Time PCR.

<b>Gene name</b>	<b>Direction</b>	<b>Sequence (5'-3')</b>
<i>AtGEX1</i> (At5g55490)	Forward	GGCTTTACATTGGTTTGTGCG
	Reverse	ACTTCATAGTCCCTGTATGACAAAG
<i>UBQ10</i> (At4g05320)	Forward	GGCCTTGTATAATCCCTGATGAATAAG
	Reverse	AAAGAGATAACAGGAACGGAAACATAGT
<i>BrGEX1</i>	Forward	TCTGTCACTGACGTCAAGGTAGG
	Reverse	TCTCCAACGCAGTCATCTTCTC
<i>OsGEX1</i>	Forward	GAGAGCCTTGGCAATGGGAT
	Reverse	ATGGCCTTGCTCTGTCCATC