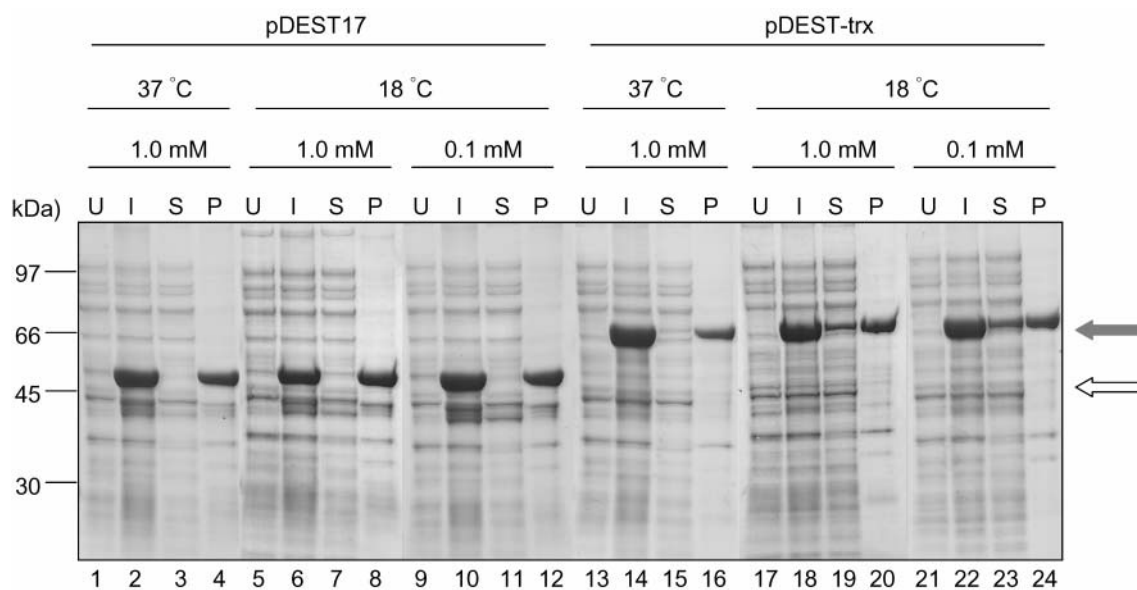


Supplementary materials

S1. Amino acid sequence alignment of *Oryza sativa* OsAGPR, *Arabidopsis thaliana* AtAGPR, and *Thermotoga maritima* TmAGPR. Residues that are conserved or conservatively exchanged with respect to OsAGPR are colored blue and green, respectively. The arrow marks the first residue of the purified OsAGPR domain.

OsAGPR (AK071544)	1:MGSTALGGGAPARLGLAPKDGVFGSNLKQCGGFMLKTTTPKVGSSSVRVRASVASSPQKQH	60
AtAGPR	1:M-----SFRVSASSSVKPEK--	15
TmAGPR	1:M-----	1
OsAGPR (AK071544)	61:SPKTSGVKSGEEVRIAVLGASGYTGAEIVRLLANHPQFRIKVMTADRKAGEQFGSVFPHL	120
AtAGPR	16:-----DIRIGLLGASGYTGAEIVRLLANHPHFQVTLMTADRKAGQSMESVFPHL	64
TmAGPR	2:-----IRAGIIGATGYTGLELVRLKNHPKAITYLSSRTYAGKKLEEIPFEST	49
OsAGPR (AK071544)	121:ITQD-LPNLVAVKDADFSNVDVFCCLPHGTTQEI IKGLPQELKIVDLSADFRLRDINEY	179
AtAGPR	65:RAQK-LPTLVSVKDADFSTVDVFCCLPHGTTQEI IKELPTALKIVDLSADFRLRNIAEY	123
TmAGPR	50:LENSILSEEDPEKVSKNCDV--LFTALEAGASYDLVRELKG-VKIIDLGADFREDDPGVY	106
OsAGPR (AK071544)	180:AEWYGHSHRAPELQQEAVYGLTEVLRNEIRNARLVANPGCYPTS IQLPVPLIKAKLIKV	239
AtAGPR	124:EEWYGOPHKAVELQKEVVYGLTEILREDIKKARLVANPGCYPTTIQLPLVPLIKANLIKH	183
TmAGPR	107:REWYGKELSCYENIKR-VYGLPELHREEIKNAQVVGNGPCYPTSVIILALAPALKHNLVDP	165
OsAGPR (AK071544)	240:SNIIIDAKSGVSGAGRGAKEANLYTEIAEGIHAYGIKGRHVPEIEQGLSEAAESKVTIS	299
AtAGPR	184:ENIIIDAKSGVSGAGRGAKEANLYSEIAEGISSYGVTRHRHVPEIEQGLSDVAQSKVTIS	243
TmAGPR	166:ETILVDAKSGVSGAGRKEKVDYLESEVNESLRPNVAKHRHVPEMEQELGKISGKKVNVV	225
OsAGPR (AK071544)	300:FTPNLICMKRGMQSTMFVEMAPGVTANDLYQHLKSTYEGEEFVKLLNGSSVPHTRHVVGS	359
AtAGPR	244:FTPPLMPMIRGMQSTIYVEMAPGVRTEDLHQQLKTSYEDEEFVKVLDEGVVPRTHNVGS	303
TmAGPR	226:FTPPLVPMTRGILSTIYVVKTDKSEEEIHEAY-LEF-YKNEPFVHVLPMGIYESTKWCYGS	283
OsAGPR (AK071544)	360:NYCFMNVFED-RIPGRAIIISVIDNLVKGASGQAVQNLMMLGPENTGLQYQPLFP	415
AtAGPR	304:NYCHMSVFPD-RIPGRAIIISVIDNLVKGASGQALQNLNIMLGYPETIGLLHQPLFP	359
TmAGPR	284:NHVFIMGQMEERTNTL-ILMSAIDNLVKGASGQAVQNMNIMFGLDETKGLEETPIYF	339

S2. CBB-stained SDS-PAGE gel (12.5% acrylamide) of expressed OsAGPR constructs. The (His)₆/OsAGPR position is marked by the open arrow and the Trx-(His)₆/OsAGPR position is marked by the gray arrow. U, I, S, and P denote the uninduced total fraction, the induced total fraction, the soluble fraction, and the insoluble fraction, respectively.



S3. Structural features of purified OsAGPR(Ala50-Pro366).

(a) MALDI-TOF MS spectrum. All MS spectra were obtained using a Biflex III MALDI-TOF MS spectrometer (Bruker) operating in the linear and positive mode and with a mass accuracy of 0.2%. Sample solutions were prepared in water with 0.1% trifluoroacetic acid (TFA). All samples were prepared using the dried droplet method, which involves first mixing the analyte (intact protein) with an equal volume of matrix solution (a saturated solution of sinapinic acid in 33% acetonitrile/water containing 0.1% TFA (v/v)) and then depositing the mixture onto a stainless steel target plate.

(b) Sequencing chromatograms of the first five N-terminal amino acids. SDS-PAGE-separated proteins were transferred by electroblotting them onto an Immobilon-P transfer membrane (0.45 mm pore size; MILLIPORE) soaked in 48 mM Tris-base, 39 mM glycine, and 20% methanol (v/v). After transfer, the membrane was stained with Bio-Safe Coomassie (Bio-Rad Laboratories, Inc.). Visible protein bands were excised and the first five N-terminal amino acids sequenced using a HP241 protein sequencer (Agilent Technologies).

