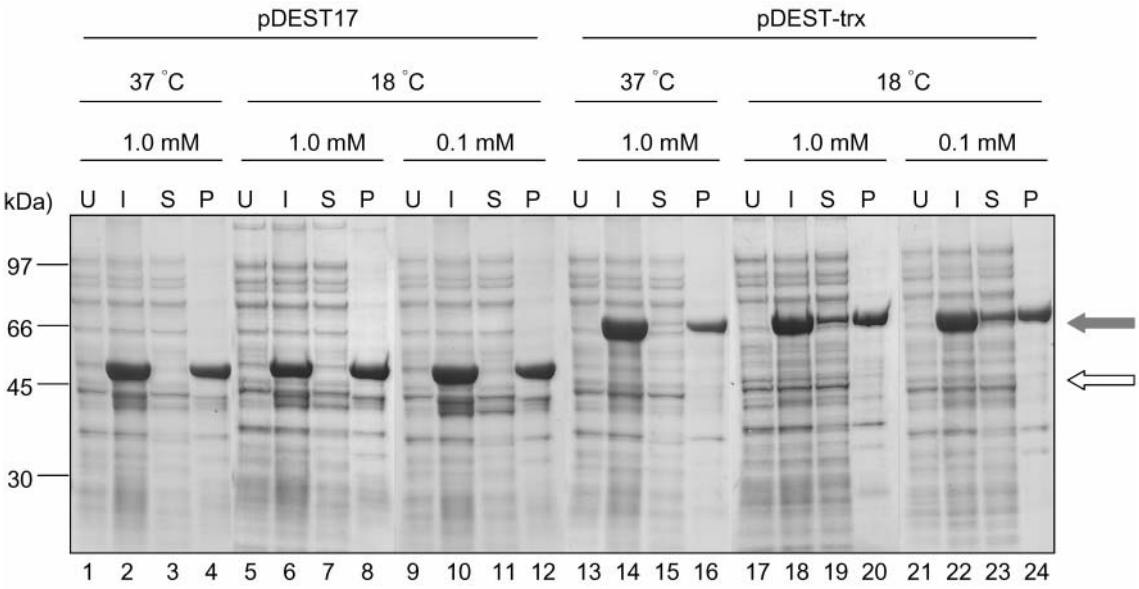
Supplementary materials

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.

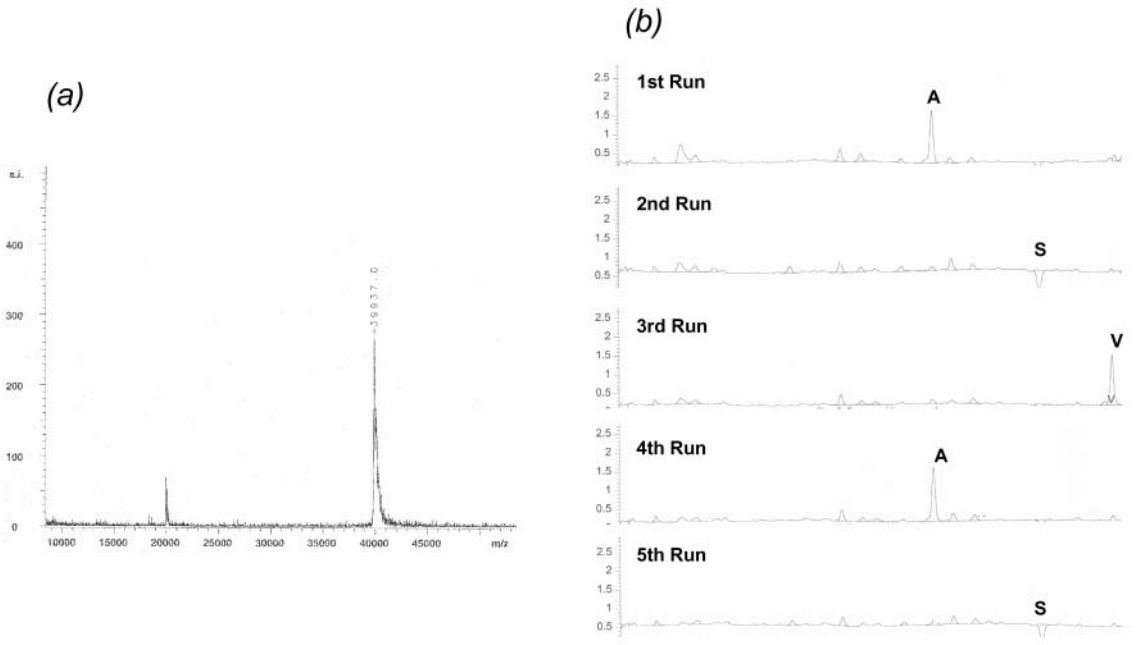
S2. CBB-stained SDS-PAGE gel (12.5% acrylamide) of expressed OsAGPR constructs. The $(His)_6$/OsAGPR position is marked by the open arrow and the Trx-$(His)_6$/OsAGPR position is marked by the gray arrow. U, I, S, and P denote the uninduced total fraction, the induced total fraction, the soluble fraction, 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).


(a)
a.i.
400
300
200
100
0
39937.0
10000
15000
20000
25000
30000
35000
40000
45000
m/z
(b)
1st Run
A
2nd Run
S
3rd Run
V
4th Run
A
5th Run
S
2.5
2
1.5
1
0.5