

ATGAPC1.SEQ	MADKKIRIGINGFGRIGRLVAFVVLQRDDVELVAVNDPFTTTEYMTYMEKYDSVHGQWKHEHLKIKDETLLEGEKFPVTVEGIRNPEELIPWAEAGADYVV	100
ATGAPC2.SEQ	MADKKIRIGINGFGRIGRLVAFVVLQRDDVELVAVNDPFTTTEYMTYMEKYDSVHGQWKHEHLKIKDDTLLEGEKFPVTVEGIRNPEELIPWGEAGADFVV	100
HSGAPDH.SEQ	..MGKVKVGVNGFGRIGRLVIRAAFNSGKVDIVAINDPFDLNYMYMEQYDSTHGKF.HGTVKAENGKLVINGN.PITIEQERDFSKIRWGDAGAEYVV	96
OSGAPC1.SEQ	..MGKIKIGINGFGRIGRLVAFVALQSEDVELVAVNDPFTTDTYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
OSGAPC2.SEQ	..MAKIKIGINGFGRIGRLVAFVALQSDDELVAVNDPFTTDTYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
OSGAPC3.SEQ	..MGKIKIGINGFGRIGRLVAFVALQSEDVELVAVNDPFTTTEYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
ZMGAPC1.SEQ	..MGKIKIGINGFGRIGRLVAFVALQSEDVELVAVNDPFTTDTYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
ZMGAPC2.SEQ	..MGKIKIGINGFGRIGRLVAFVALQSEDVELVAVNDPFTTDTYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
ZMGAPC3.SEQ	..MAKIKIGINGFGRIGRLVAFVALQSDDELVAVNDPFTTDTYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
ZMGAPC4.SEQ	..MAKIKIGINGFGRIGRLVAFVALQSDDELVAVNDPFTTDTYMTYMEKYDTVHGQWKHEVVKIKDSKTLLEGEKFPVTVEGIRNPEELIPWAEAGAEYVV	98
ATGAPC1.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	200
ATGAPC2.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	200
HSGAPDH.SEQ	ESTGVFTTMEKGAHLQGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	196
OSGAPC1.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
OSGAPC2.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
OSGAPC3.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
ZMGAPC1.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
ZMGAPC2.SEQ	ESTGVFTDKIKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
ZMGAPC3.SEQ	ESTGVFTDQEKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
ZMGAPC4.SEQ	ESTGVFTDQEKAAAHKGGARKVVISAPSKDAPMFVGVNEHEVYKSDLDIVSNASCTTNCLAPLAKVINRFGIVEGLMTTVHSLITATQKTVDGPSMKDW	198
ATGAPC1.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	300
ATGAPC2.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	300
HSGAPDH.SEQ	RDGRGLQNIIFASTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	296
OSGAPC1.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
OSGAPC2.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
OSGAPC3.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
ZMGAPC1.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
ZMGAPC2.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
ZMGAPC3.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
ZMGAPC4.SEQ	RGGRAPSFNIIISSTGAAKAVGKVLFDLNGKLTGMSFRVETVIVSVVLLTVRLKPSATYDEIRKAAAESEGLKGIIGYVEEDIVSTDQGGSRSSIFD	298
ATGAPC1.SEQ	AKAGIALSDKFKVLVSWYDNEGYSSRVVDLIVHMSKA.	338
ATGAPC2.SEQ	AKAGIALSDKFKVLVSWYDNEGYSSRVVDLIVHMSKA.	338
HSGAPDH.SEQ	AGAGIALNDHFVKLISWYDNEGYSSRVVDIMAHMASKE	335
OSGAPC1.SEQ	AKAGIALNDNFVKLVAWYDNEGYSSRVVDLIRHMAKTO	337
OSGAPC2.SEQ	AKAGIALNDNFVKLISWYDNEGYSSRVVDLIRHMAKTO	337
OSGAPC3.SEQ	AKAGIALNDNFVKLISWYDNEGYSSRVVDLIRHMAKTO	337
ZMGAPC1.SEQ	AKAGIALNDNFVKLISWYDNEGYSSRVVDLIRHMAKTO	337
ZMGAPC2.SEQ	AKAGIALNDNFVKLISWYDNEGYSSRVVDLIRHMAKTO	337
ZMGAPC3.SEQ	AKAGIALNDNFVKLISWYDNEGYSSRVVDLIRHMAKTO	337
ZMGAPC4.SEQ	AKAGIALNDNFVKLISWYDNEGYSSRVVDLIRHMAKTO	337

Fig. 1 Suppl. Partial sequences alignment of cytosolic GAPDH isoforms from three plants (*Arabidopsis thaliana*, *Oryza sativa*, *Zea mays*) and *Homo sapiens*. The alignment is focused on the highly conserved Cys residues and its neighbouring residues in GAPDH three-dimensional structure among plants and *H. sapiens*. The proton-relay residues in human GAPDH are completely conserved in plants. These residues in human proton-relay, including Cys152, Cys156, Thr153, His178 and Tyr314 (corresponding to Cys154, Cys158, Thr155, His181 and Tyr316 in *Oryza sativa*) are marked in red. Abbreviation and accession numbers: *Arabidopsis thaliana* GAPC: AtGAPC1, NP_172801.1; AtGAPC2, NP_187062.1; *Homo sapiens* GAPDH, HsGAPDH, P04406.3. *Oryza sativa* GAPC: OsGAPC1, Q0J8A4.1; OsGAPC2, Q7FAH2.1; OsGAPC3, Q6K5G8.1; *Zea mays* GAPC, ZmGAPC1, NP_001105413.1; ZmGAPC2, AAA87578.1; ZmGAPC3, AAA87579.1; ZmGAPC1, AAA87580.1