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26 VPGGTSRHLASRYVAHDCQRRRLRESLREEH-----A-VLDFASTIHKHASGGSGGATLAGAHSGGPATSVG-----P-AAGGAAGFMQPAAAGGM-----QAPPFGCGAGPFGQAAPLLHAP
27 -----GQLQQAALAAHERLAAGAAN-----PRQLTMAQAAAALEVLVQGLDSLAHEFHLLDFGLHSNVCGQFMAMINEAAPVFN-----FLEARRELRAAESGRLLS-----
28 YLRGLLGVRDSTPAIVVAETGQLPLPAYWTVQVARFVSNLQAMGGERARLAMDLSVALAADTCTCLPLARQPAWAQVSRPLAAAGAPCDLADDEGVAPELAEALLERHVASYTHASVKVQRYIEDVMGGISAEAYTPASFCDVPERFRRAASASASNEALAE
6 ATENSATNPEAEMRIVQVVASAW--LRSS-----VCIFQPLTLRLKGNLENTYSESESEQ-HHMEYIKFY-----TSPQCLAEAMDNLFHSNLL-----HGSFRABLDQTORECALGAQDQQ
29 -----AEGRVV-----EISKDPSFSTVDSATEAARQAQCLHV-----HFAPEQOE-----AMSLMLPH-----SSKNPSDNTVEGRQNMSSQAG
35 -----ARKKTAALMLQGSSPAA-----TLVDFMSGAGT-----TLVDFTLSGTGL-----LSTDDAAVDRGGQOS
36 -----QRKKTAALVLQGSSPVA-----TLIDFTLSGTGL-----LSTDDAAVDRGGQOS
30 -----RKSQV-----QQLADELSSDLSLESDQG-----STEVAAEDSAGDEEGGGGG
31 -----GVS-RVVRRLQEQY-----AQPTEG-----FARTGLKGD-----DSPPSDESTRGTSPIVA
37 -----ERQRGAKLVGVGQ-----QRSALHL-----FARTGLKGD-----DSPPSDESTRGTSPIVA
32 -----ERQRGAKLVGVGQ-----QRSALHL-----FARTGLKGD-----DSPPSDESTRGTSPIVA
3 YDSAAAAAASSSGPVARRDQMASFRNVLYR-----GVNEAAKCFVDTNVTKGFAPEPG-----HMLRVIOE-----HSPQCLADAAQLQSCQDW-----VRRYQCGQNMQAMSL
SAK1 AAAAAAATTPPAVVRQMGFLFRALVRY-----NLTNDEVCK-----FADTTLSCAAAAEPE-----HMLRVVAG-----GLSDROLGDCALHAYCTDW-----TGRHGERPAAGTDDQLTSGAGG
9 LIPAEAAQPK-SEAAARBAQLGREAMYIGSC-----AAGIPRHTR-TYCYKQESGPEHSRAPQAQWAA-TLH-----NLSPTORQRIIRRRKALTA-----VAPRRRRRAQSGSPATDNLNPGS
7 HPPGQALPPQVVARITSV-----TASMS-ELVHK-----A-ISPLNVK-RLATNMEVHAMVPV-PET-HMARVLLA-----GLSERORKDLLARERLTK-----FEAVQEEAAITSSSQAIPIRSRV
1 HGPS-----STQ-QARJERF-LERIF-VYMDQ-----VLSNCFV-QSMYNLETCQHERP-PDE-FWCA-GAS-----NLPCQLEEVLMARDHEMN-----VAPAEERVRITSELSASAA
25 LGPG-----SPH-AARIDRY-IGRMM-YMDR-----TILSPQCFV-QSMYNAMEMEPER-TDG-FWMA-GKYA-----NFSYEOLLEEIEENAKAHNAS-----APVQERARASESSHTT
13 RPNEMYIKRL-DEAFGR-KQAEH-----EG-----CAHPELVC-NRQNMETCEEVEP-PDS-FWTLVAGS-----RTPPAQVADCRITALTLRER-----EVVAAERESADQASCALHHA
17 RPNELYVKRV-EEAFAR-RAAAB-----YR-----CAKHELIC-NRQNMETCEEVEP-PDS-FWTLVAGS-----RTPPAQVADCRITALTLRER-----EVVAAERESADQASCALHHA
23 RPSELYLRKI-DAAFERCEEGARI-----WY-----PGLPDVIC-GAYQNVDTCTRPET-PDS-HAREVAEG-----GTCQOVSACRALALRER-----EVVAAERESADQASCALHHA
20 RPAAEFQRM-EAADFDR-KGRVV-----E-----GPHSELVS-NDQRNLDTCTAAAP-PYS-FARVVRER-----NCNTAOVSAACRALALRER-----EVVAAERESADQASCALHHA
22 RPRDHWLRQL-DVACTQ-KTRVV-----Q-----GKHPELIADD-PONLDTCTRLQEP-PEG-HARVVALA-----RTPPAQVADCRITALTLRER-----EVVAAERESADQASCALHHA
2 RPHD-----PGPQLKTAQ-YEQQLTPTFRA-----RQDYFFFLS-EQMYNLETCERGEPPDS-FWVVPVQG-----RFSPECIADAVADALALRER-----TAKAEERERLVAKDSVVAADRRL
24 RPQD-----PGP-ELKLR-RQQLM-PKMHA-----RQEYCLSK-AFMYNLETCEREGA-PVS-HAAVARS-----ALSPDOLAACALITALYRER-----AAPAAERERANEVAGRAVCGG
15 RPHD-----PRPAMKAAALRSTIPVCR-----RDYDGLLL-DYSRNLCTQPEDP-PRD-HAAVARS-----RSECORACALITALYRER-----VGPACERESAHQSAAGAAEQ
14 RPHD-----PTP-AMKIGQ-QDENW-PLLCA-----WRHYPSSLK-DCCRNMDCRLDPPG-HAAVVRG-----RTPPEORACALITALYRER-----VGPACERESAHQSAAGAAEQ
16 RPHD-----PTP-ALKMO-KDRNL-PLLRA-----WREQPSLLI-DARNLDTCTRLDPPG-HAAVVRG-----HTEACAAACALITALYRER-----VGPACERESAHQSAAGAAEQ
11 PPPE-----VVERMQEIVQR-ELLLL-YIRAA-----TNMSSVKRF-VANYKVE-MRMHLGDEGVG-MARTVALA-----OLSPESDSTTKLWRSRTK-----TAEFASQTCAGADSPSGVMG
10 AYAD-----DPS-SEGFR-EQLVR-GHONA-----LQLTRQDPK-HLTKTQ-LKKRTPKSKQE-LARKCVDV-----KDKCEKRRVLRLNELFR-----ESTTEORRLITHDA
33 -----QSEVLYGCAV-----OLSAQCLDRVALARANGLR-----LRAELRR-----TKVLEEREGGLAKQMVNIPDRML
34 -----QSEVLYGCAV-----OLSAQCLDRVALARANGLR-----LRAELRR-----TKVLEEREGGLAKQMVNIPDRML
5 CDPTNPVQVQVTAVERGHLLKHL-----VLNSPLMK-QLLNLENMQPAAE-AES-HADAIVAS-----QCAECORADILVLDLYGL-----IQVCAERERLFDRLQAIQVPTLR
12 CDSN-----NPI-VQKTA-VERMG-HMLKH-----VLNSQLMR-QLSNLETCOPAAP-PVG-HDVTVGS-----OLPQCAADITVVDLYRGL-----IDKPSAAAASTHRSSTSPAPAPA
4 NQOD-----ERA-AASLQ-AGEAT-HMLKHA-----SLAPDPTLM-VTQTHLETVLTAQ-DPS-HAAVVRT-----ELSPDQIRELRVFRVSDI-----SAVAAERANMRVAEGVHLHDSV
18 DFRD-----EAA-AAQAAA-AAQAA-YLIKGA-----SLAPDPTLA-TAMQHLESAPGAP-EFG-HALFVVRT-----ELSPQEAELRVWGLSGV-----RAVAAEREGGMATATATV-HGST
8 NPAD-----EAA-AHOKK-NAKIG-SLCRR-----SLAPDPTMI-AQSQTHLETDLTMAQ-DPG-FWAGVQAA-----RLDEEOLREMCVYELSGI-----GRVAAERANQAKSAGQTDPRS
21 NPAD-----EAA-AEAARA-LARLS-ALYRTA-----SLSPETVA-VLQTHMETREVVSA-PAG-HATAVLRQ-----DLSPQCAELGMMGLRGL-----DKITQERERDINARISQCAQEQK

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26 GGGSDAMNQ-----VGHTGHSGHLQLTTGSGSGAGPPGMSHLSAAGSGRAG-FCE-----AGSGQA-VSISNMASTANDA-----
27 SGGASLTFKEIKAPGEQEEEEEEELQAPAGAPAAVAGFS-----DRFAAEALV-REAVAGIRRDAAAPGTQAC-----
28 VHRMTEYQMANMWAASQTASRT-----PLEFVRSTTRLATGLMQTAS-AQHAAYCELLIAFYA-TPEV-----DRPOLVLS-TEVQLELGRAALELGLD-----
6 ADASRKM-----SGEGLTLVQQTALKKVRNLIQ-KTHLLYSSTIGVAAMR-IDRER-----ELEASSTIS-SSSSS-----
29 YLHVAKSSAELGLDKDKDNRRRQRAVMDLNCOISK-LIPI-----QGHYMKR-YPQHCDAALSNIAKHLGRE-----
35 LTGFAAHACRVESIRDRTNES-AEQQLNFTLVSEVDE-VLPI-----OTCIICAKV-GSGCPDMALATRAVQTMEL-----
36 LTGFAQHACKVEGINARQSG-AEQMLNFTLVSTVTK-VLPI-----OTCFVCASWSDSGCPDMALASRAVQSMKE-----
30 VQRPASNAKAQAQKDELDRQL-LEYWLKFTGCRK-LIPAO-----QQLCMVHS-PPYFDQKQEGAKAGPL-----
31 LVTNANSSELLTSHAGAQ-EBYVATMEFVAEQAL-ATPI-----QKAYINHAS-APPLPDIAADYNLLMDSQ-----
37 ETTQGEAFDTIAAEATRESIT-RELEKMRSHPTVLK-TIHR-----TSAIIVSS-YPYFDAAVAAVKTWRDDG-----
32 -----ILGES-----SMPPSSDSA-AAGTGNVVRASSAQ-----
3 AT-----YFESVGRYGTDRDRIKHANVM-RERILLVLTGEVFCCH-LIPI-----QARAVLKS-YPYFDVREVCNASQL-----
SAK1 LYGGRYGA-----RERTDGRYGTDRDRIHANVM-REKVVHVIVAEVCCY-LIPI-----QARAVVHS-OPVLDSSREVRAAHM-----
9 IAGLSTDYRTAVERQHNE-KHSLVRRFTGGVHQ-WIPI-----QARAVLQS-PPYFDPSIANCVEA-----
7 YADICSAARAAADRGRNLIQ-RHNINMEFVVFKG-VMDL-----OG-----PEKQLRKSRRR-----
1 SSDVIQTLSEVDIAERTRNVI-RHQAMDVGDFCMG-VLSEV-----QVARIMAAS-YPYFDGVALHCGVG-----
25 TAGPAATE-----SAHGISALTAVDADTDQIKRNL-REQQSHLDATDFCWS-VLPI-----QVRSIISAS-YPYFDGVALHMCAL-----
13 E-----AEGRAAPG-----SMQRELTAEAEAAAHANVT-AGHTTGLARDL-RSD-FIPI-----QCARGSVLS-YPYFDAAVAAVAVAN-----
17 E-----AEGRAAPG-----SMQRELTAEAEAAALDTNVA-AGHTTGLARDL-NST-LIPI-----QCARISVLS-YPYFDAAVAAVAVDI-----
23 AEAPCASPCELP-G-----SAHFQVGEAAAAAAEALNANVA-AEGRATRLAREFSN-LIPI-----QARCAALS-YPYFDAAVAAVAVASL-----
20 QG-----QEQQLR-S-----SHHLEKTSAAAAAABEDANVA-AEGHAMRLAREL-RSD-FIPI-----QARISVLS-YPYFDAAVAVATAGE-----
22 TE-----HEGWLQVA-----ASNVEKTSAAAAAAGCUDENVA-AEGRATKIADKLSSD-FIPI-----QCARGSVAS-YPYFDAAVAVATEVARI-----
2 SPWEEGPGANQGGSG-----PLKCCDVL-ELDYTAQLYRNVM-NOGGALEAVKDFGSN-FIPI-----QVVGSVLS-YPYFDAAVAVLNCSTM-----
4 GSAAAAAEPAA-----VEATPEAVRLCTGEVYSRNLG-AEQADIVKDF-SNG-VMSV-----QARIAVLS-YPYFDAAVAVLTTEEL-----
15 SGCSGAAAGTSGTATNAGGGAAGCVLRQGLP-----GSARPDVL-ELNQADSHRNVT-AEQALEIVKDF-SNG-VFV-----QMHCSVLS-HPYFDVLSLGADEL-----
14 RNAATAAAVGAETGQPTHQVLRGLGGVSDGVPAGDSASGCSSSSGGGKDVTFMSAAQSLQNVNVA-TEHCMGVVYDFGAG-VFV-----QMKRMSVLS-HPYFDILALTAEDM-----
16 RNAATAAAVGAETGQPTHQVLRGLGGVSDGVPAGDSASGCSSSSGGGKDVTFMSAAQSLQNVNVA-TEHCMGVVYDFGAG-VFV-----QMKRMSVLS-HPYFDILALTAEDM-----
11 QDFAV-----GSRSIDMTFMSAAESLQNVNVA-AGETVLGVIRDF-TNG-VFDE-----QMKRVAVLS-HPYFDILALTAEDM-----
10 -----QYLRACQMDTLKKNIR-QBVLIDHDFLSTFYTQ-TLPI-----QMARCVRS-PPYFDIPALITWAAQ-----
9 -----LQASDELKESIE-LPHKEVSQFVSASFHASD-LIPI-----QARSTEA-YPYMDVFGHETAAEEEGSQSGFSMALMGQRNNGSLMPVDSAFRMVSSVPPPL-----
3 A-----LQSVISITKVNCTSELKANIQ-EEHLAGMEFIGTKT-LIPI-----QARAVLQS-YPYFDVYQVATVALEKGGP-----
34 A-----MQQATASWQVHATADISANNI-QEHCVCMSFVRDAFGY-VLSPQARGASCKEAVAVRS-YPYFPEMYS-GTALQAGAGSL-----
5 L-----LAVGRQFAAEMETERTHSNVA-KESHAHTLLSCFFFGK-VLAP-----QARVAVVYS-YPYFDCAVAAVARS-----
12 TGCPLGSAASFLQQLQAGMAGGGGGGRPLVGGDARE-----GIERTDLAAMHIDKAAANN-KESARTLLCCFFFGK-VLAP-----QARVAVVYS-YPYFDCAVAAVARS-----
4 ADIRV-----AMKHLTVSPECEVQLQORSR-RKAAHLLLRGFGFR-TLSV-----QVRAAVVYS-YPYMDAAAIVATVEQ-----
18 QDIVR-----MMSQMTVSPECEVQLQORSR-RKSAHLLLRGYGH-TLTI-----QVRAAVVYS-YPYMDAAAIVATVEQ-----
8 -----MAVEMVPECEVLPILERSR-KESAAHLLLRGFGFR-TLSV-----QCRRAVLS-YPYFDNATGAAGV-----
21 EAQRAAANAASAAAAASGSGAAAAADGGFFRRQSSSSSGVGGGGGA-----VLHQLEVPPEAEVLPALSRNR-KESAAHLLLRGFGFR-TLSV-----QARVAVVYS-YPYFDNATGAAGV-----

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Figure 5-figure supplement 2 Multiple sequence alignment of SAK1 domains

The SAK1 domains of 37 chlorophyte proteins were aligned by MUSCLE (phylogeny.fr). Protein identities are as shown in Fig. 5-figure supplement 1. Star indicates a relatively conserved residue within the SAK1 domain that was predicted to be a possible phosphorylation site (Fig. 5-figure supplement 4).