

AtRGA1 : -----MKRDHHQFQGRLSNHGTSSSSSSSSKDKMMVKKEEDGGGNMDELLAVLGKVRSSSEMAEVALKLEQ : 68
 OsSLR1 : -----MKREYQEAGG--SSGGSSADMGSCKDKVMAGAAGEED--VDELLAALGYKVRSSDMADVAQKLEQ : 63
 AtSCL9 : MITEPS-LTGISGMVNRNRLSGLPDQSSHSFT-PVTLYDGFNYNLSSDHINTVVA-----APENSVEIREEEED : 70
 OsGRAS23 : MLDS-----GSYDDVDYGDLESI PNPPAPHLNLF PLQFFPSNGFISSADDSHRS PAGMFGSTPSPTSTTTLENSED : 72
 AtSCL14 : MGSYPDGFPGSMDELDFNKDFDLP- PSSNQTLLGLANGFYLDLDFSSLDPPAYPSQNNNNNNINNKAVAG-DLLSS : 75
 AtLAS : ----- : -
 AtPAT1 : -----MYKQPRQELAYYFEENSVEKLRYLPVNNSSKKRFTLEPF : 40
 AtSHR : -----MDTLFRLVSLQQQQSSSIITNQSSLSRTSTTTTGSPTAYHYNFQNDVVVEECNFNFMDEEDL : 64

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AtRGA1 : LETMSN-----VQEDG-LSHLATDTVHYNPS-ELYSWLDNMLSELNP--PPLPASS----- : 116
 OsSLR1 : LEMAMGMGGVSAPGAADDGFVSHLATDTVHYNPS-DLSSWVESMLSELNAPLPPIPPAP----- : 121
 AtSCL9 : PADDPFDSDAVLGYISQMLNEEDMDKVCMLQESLDLEAAERSLYEALGKKYPPSPERN---LAFERNSEN--- : 139
 OsGRAS23 : LSESAD--DAVLAYINQFLL-DEDESCPG---TITSVEDSALLAVEKPFVDILTAS---QEACQENS-- : 132
 AtSCL14 : SSDDADFSDSVLYKISQVLMEEDEEEKPCMFHDALALQAAEKSLYEALGEKYSSSSSSASSVDHPERLASDSDGSCS : 152
 AtLAS : ----- : -
 AtPAT1 : P----- : 41
 AtSHR : SS----- : 66

AtRGA1 : -----NGLDPVLPS-----PEICG-----FPASD : 135
 OsSLR1 : -----PAARHASTS-----STVTGGGGSGFFELPAA : 148
 AtSCL9 : -----LDRVVPGNYTGGDCIGFNGGKIPKLSGGTLDPR---NPQSCSSILSVQPSNGLITTYGDI-DESSKNRE : 207
 OsGRAS23 : -----WIDSCCFTGNG-----GLLDTF-----TTTHAA : 156
 AtSCL14 : GGAFSDYASTTTTTSSDSHWSVDGLENRPSWLHTPMPSNFVFPQSTSRNSVTGGGGGNSAVYSGSGFDLLVSNMFK : 229
 AtLAS : ----- : -
 AtPAT1 : ----- : -
 AtSHR : ----- : -

AtRGA1 : YDLKVI PGNAIYQ-----FPAID--SSSSNNQNKRLKSCS----- : 169
 OsSLR1 : DSSSTYALRPI-----LPVATADPSAADSARDTKRMRTGG----- : 186
 AtSCL9 : NHQSVMLFRREIEEANRFNPEENELIVNFRENCVSKARKNSRDEICVEE----- : 259
 OsGRAS23 : CQPAPECFEKE-----KGECAVHKGRKNPHDDCLLFEES----- : 191
 AtSCL14 : DDELAMQFKKGVEEASKFLPKSSQLFIDVDSYIPMNSGSKENGSEVFKTEKKDTEHHHHHSYAPPNRLTGKSH : 306
 AtLAS : -----MLTSFKSSSSSEDATATTEN----- : 22
 AtPAT1 : -----DSPPYNALSTATYDDTCGSCVTDEN----- : 67
 AtSHR : -----SSSHNNHHNNNNNTYYSPFTTPT----- : 90

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AtRGA1 : -----SPDSMVTSTSTGQIGGVITTTTTTTT---AAGESTRSVILVD----- : 213
 OsSLR1 : -----GSTSSSSSSSSSLGGGASRGSVVEAAPATQGAANAAPVPPVVVD----- : 233
 AtSCL9 : -----RSSKLPAVFGEDILRSDDVVDKILVHVPG-GESEKFNALRDVLKKGVEKKKSAQGGKRRARG : 324
 OsGRAS23 : -----RRSKQLAVSEETVVR-EMFDKVLICN---GECELRAPLPABARNCGVYV-----GSGNKGRK : 246
 AtSCL14 : WRDEDEDFVEERSNKQSAVYVEESELSEMFDTIIVCGPGKPVCLNQNFPTESAKVVTQAQ-----NGAKIRGK : 376
 AtLAS : -----PPLCIASSSAATSASHHLRLRLFTAANFVSQSNFTAQNLSSILSLNSS----- : 72
 AtPAT1 : -----DFKHKIREIETVMGPDSDLIVDCTDSFDTASQEINGWRSTLEAISRR----- : 117
 AtSHR : -----QYHPATSSSTPSSIAAAALASPYSSSGHHNDPSAFSIPQTTPSFDFS----- : 137

LEUCINE HEPTAD I

AtRGA1 : -----SQENGVRIVHALMAABATQNNNTLEALVKQSCCLAVSQAGAMRKVATYEAARRIYR--- : 275
 OsSLR1 : -----TQEAGIRIVHALMAABAVQNNFAAALVKQETLAAASQCGAMRKVAAYGEAARRIYR--- : 295
 AtSCL9 : RGRGRGGGGGQNGKEVVDRSLLIHQAQAAADRRRCAGQLKQIRLHSTPFQGNQRLAHCPANGEARLAGTGS : 401
 OsGRAS23 : KGKS-----GASAEDDAVDTITLLHQAQAAADHHRNSNELKQIRQRSSAYSDAGORLAHCPANGEARLAGTGS : 318
 AtSCL14 : STSTS---HSNDSKKETADRTLLVLAQAVSVDRRTNEMLRQIREHSSPLENGSERLAHYEANSLEARLAGTGT : 450
 AtLAS : -----PHGDSTERLVHETRLASLRIN-RQQQDQTAETVATNTNEMTMSNSTVFTSSVCKEQELFR--- : 133
 AtPAT1 : -----DRADLVMSAKAMSENLMMAHSMHEKRLQMVSVSEPIQRLGAYLLEGVAGLASSGS : 176
 AtSHR : -----ANAKWADSVLEAARFSDKQTAQAQILWTNELSSPYEDTEOKLASYLQALFNEMTGSGE : 200

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AtRGA1 : --LSPPQ-NQIDH-----CLSDTLQMHYEYTCFYLKFAHFTANQAILDFEGKKR--VHVDFSSNQELQWELMQLA : 342
 OsSLR1 : --ERPADSTLLDA-----AFADLLHAHVEYSCFYLKFAHFTANQAILDFAGCHR--VHVDPGCKQEMQWELMQLA : 363
 AtSCL9 : QIKGIVSKPRSA-----AAVLKAHQELACCPERRLSYFITKTRDLVGNSSQR--VHVDFGLYEFQWETLTHR : 471
 OsGRAS23 : NIKRSLAAKRTSV-----YDILNAFKLVTAACPKKISNFFSIEAILNLSKGMTR--LHIVDGYQYEFQWETLTHR : 388
 AtSCL14 : QITALSSEKTS-----ADMLKAYQTMVSVCPKKAAIIFANHSMMRETANANT--IHIIDEGSYEFQWELTHR : 520
 AtLAS : -----TKNNNS-----DFESCYLWLNQLTPEIRFGHLTANQAILDETNDNGALHILDLDSQELQWELMQLA : 198
 AtPAT1 : SIKKALNRCPEPAS-----TELLSYMILYEVCPYFREGYSANGATAEAMKEENR--VHIIDFQNGQESQWETLQIA : 247
 AtSHR : RCMRTMVTAAATEKTCSESTRKTVLKEQEVSPWATEGHVAANGAILLEVDEGAK--IHIIDISSTFCTQWETLLEA : 275

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LEUCINE HEPTAD II

AtRGA1 : LALRE---GGPPTFRITGIGPPAP--DNSDH---DHEVGCKLAQLAEAIHVEFYRGFVANSLADLDASMLELR- : 408
 OsSLR1 : LALRP---GGPPTFRITGIGPPAP--DETDA---DQVVGKLAQEAHTIRVDFYRGLVAATLADLEPFMLQPEG : 430
 AtSCL9 : FSMY---GSPKVRITGIEFPQPGFRPAQR---VEETGQRLAAAKLFGVFFYK-ALAKKWDATQLBDDLDNR : 537
 OsGRAS23 : SKRP---GGPPTFRITGIGPPAP--DETDA---DQVVGKLAQEAHTIRVDFYRGLVAATLADLEPFMLQPEG : 456
 AtSCL14 : LSLSRP---GSPKVRITGIEFPQPGFRPAQR---VEETGQRLAAAKLFGVFFYK-ALAKKWDATQLBDDLDNR : 589
 AtLAS : LAERSSNPSSPESRITGCG---RDVTG---INRTGDLRTREADSLGQCFHF-TLVIVEEDTAGLLLOLRP : 264
 AtPAT1 : FAARP---GGPPTFRITGIGPPAP--DNSDH---DHEVGCKLAQLAEAIHVEFYRGFVANSLADLDASMLELR : 315
 AtSHR : LATES---DDTEHRLTLVVANKFVNDQTAASHRMKEIGNRMEKARLMGVVEEREN--LIHVGDSLSEFLLNELD : 346

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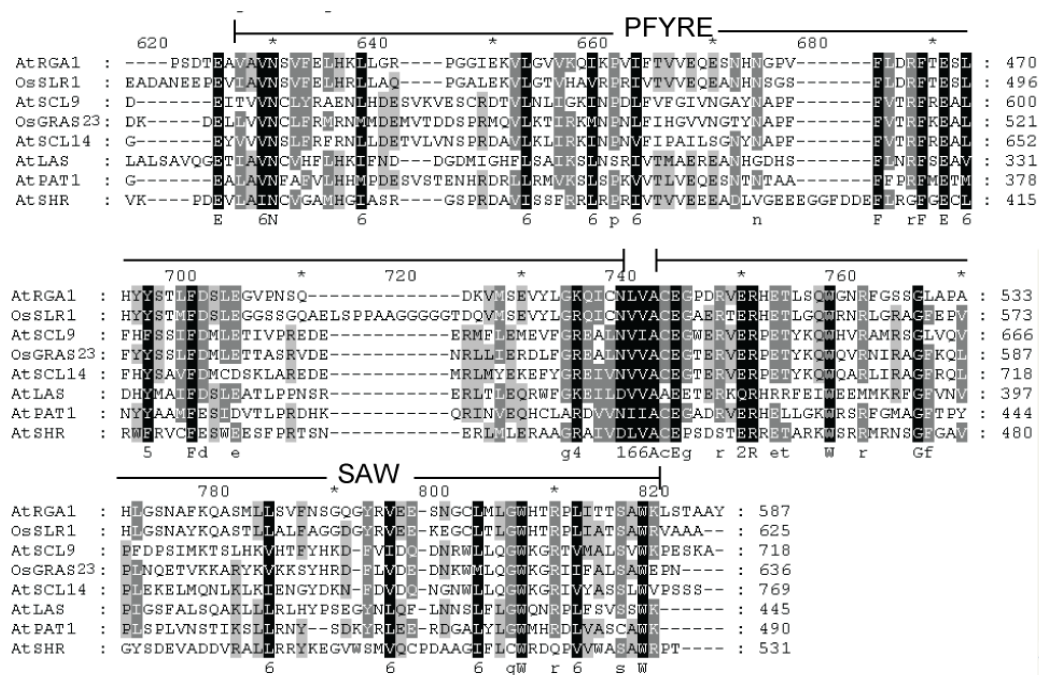


Figure S1. Alignment of deduced amino acids of OsGRAS23 with the well-characterized GRAS family proteins.