

C1

Consensus	-----HN--R-----m-----Wd--la--A--a--C--h-----GeNl-----	
SmVAL3	EEVQLILQVHNEHRA YRNLCGEKGI VPAE EILQPLEWDDLAAA AQRWSKKCNPFEE EEPIGNVGK--WN-SVGRNSVI-----QSELAEA	82
SmVAL23	EEVQLILQVHNEHRA YRNLCDDKDIVPAE EILQPLEWDDLAAA AQRWSKKCNPFEE EEPIGNVGK--WN-SVGRNSVI-----QSELAEA	82
SmVAL24	QEAQLMLRVHNEHRA YRKLCGEEDIVPAE EILQPLEWDDLAAA AQRWSKKCNPFDE EEPIGNVGK--WD-SVGRNSAI-----HSELAEA	82
SmVAL25	QEAQLMLRVHNEHRA YRKLCGEEDIVPAE EILQPLKWDDLAAA AQSWSVKCNPFDE EEPIGNVGK--WD-SVGRNSAI-----QSELAEA	82
SmVAL20	HEGRTLFNKHITDY RRLLLCKVPEQRP PYPYSEGELSWDDELE ELAAGQASV CNLSSE YKKTEIEKE-YRGQTIGINTAD-----NSDVINA	84
SmVAL10	STKELIFNFHNKIRE DVFKGVLSGQP KAKKMS--KLKWNKLLAKLAKGHVQK CILDSGDLGKLYVGK-FD-SVGOTVAE-----HTSIQNI	82
SmVAL18	KEVREYFQLHKY YRNSIRFCQMPKGPQAKYMS--PLQWNKHLAEKAQLTASRC DYSFSDSPDMRFEE-FS-SVAONLAD-----SPTIEKA	82
SmVAL4	EGQRAIYNFHKVKR KDVKNCRI PGQPPAKNLT--KLKWNKLLANKAKQQA KRCKYDSNDPNDFIIGD-FE-SIGONLAD-----YPTIEGA	82
SmVAL7	TQNSELLALHNAYR RNKIYGNVRDQ PQA MSML--KLTWSHKLAEMAQEWALQ CVPRRSNM TMRKGSK-WT-YVGQSI AF-----VPKVRQA	82
SmVAL19	OKLETIHR LHTYYRNS ILLCKVPTOPPAEDME-VLRWNDILANNAQQVANK C D LNF DLVNDKLL E H-FE-SIGONVAE-----SDTIKNA	82
SmVAL12	KDQDYLLKAHNRI RQYARSCNITGQPQAKRIL--NLWDDQLALKA TSKTCNFRFSNVTTYK----FK-DVGONIAG-----YANVQTA	79
SmVAL2	KNSEELLEHRKYRQ D LVDCKVDGQPPAKYMS--PLKWNHDLARQAQSLAINC TLQHDKRYSKQ----FI-WVGONIAL-----HPTIKSG	79
SmVAL1	AKSEELLNLHRKYRQ D LVDCKVDGQPPAKYMS--PLKWNHDLARQAQSLANKC ILRHDKRHSNQ----FS-WVGONIAL-----HPTIKSG	79
SmVAL21	KNSRELLEHRKYRQ D LVDCKVDGQPPAKYMS--PLKWNHDLARQAQSLANKC ILRHDKRHSNQ----FS-WVGONIAL-----HPTINSQ	79
SmVAL14	KNSRKLALHRKYRQ D LVDCKVNGQPPA YMS--KLKWNVDLAQQAQSLAS YC ILRQKGPRSKK----FT-WVGONIAF-----FSTINSA	79
SmVAL22	KNSRKLVLHRRFRQ D LVDCKVNGQPPAKYMS--KLKWNVDLAQQAQSLAN YC ILRQKGPHSKK----FI-LVGONMAF-----ASTIKSA	79
SmVAL8	AQLRKLLQYHNELRR NLTACKLEGQPPAKNLL--DLKWDNELASKAKDLANEC YFHNDVD-----LPEKWQ-YIGONIA G-----YQTIEQA	80
SmVAL9	TIREQLTMHNVVRE LAKFLG LIPROPEAVHMK--LLKWNMELEKRAQNLSDQCKSEHDEIEQRRIPE-FQ-NVGOTVWG-----TYTVERA	82
SmVAL5	ATREKLLKLHNNARV SVMHGRLEGQPIA KSIK--PLKWNMELEKKAQMLADT CYFGPDSA IERKVP G-FT-NVGONWAG-----ASTVDIG	82
SmVAL15	ATREKLLKLHNNARV SVMHGRLEGQPIA TSIK--PLKWNMELEKKAQMLADT CYFGPDSA IERKVP G-FT-NVGONWAG-----ASTVEIG	82
SmVAL27	TMRNELLTLHNKARQ SVRNGQLFGQ PRAVSIK--PLQWNVELERKAQNLSDRCQVGHDTNADR KIPK-FQ-YVGONWAG-----AKDIKTG	82
SmVAL26	AMRNELLTLHNEARQ AVRNGQLFGQPIA VSIK--PLKWNVELERKAQILSDQCRVGHDTNADRQIPE-FQ-YVGONWAG-----ATDIKTG	82
SmVAL28	AMRNELLTLHNEARQ AVRNGQLFGQPIA VSIK--PLKWNVELERKAQILSDQCRVGHDTNADRQIPE-FQ-YVGONWAG-----ATDIKTG	82

Group 1

SmVAL11_2nd	ESIHSVVLHNQYRS-----QHGSN-----PLVLDQNL SNMAQQWADHLLQOSHLSNSG YVYRGMK--VGENLGSRWSNGPM--ELNCKDL	77
SmVAL11_1st	DFREDCFRANNEKRL-----LHGVC-----ALRHSALD KTAQDWAE-ALLSEDIKNSPLSS-RG-EVGESISVRTSTGTHV--DMQGEHV	77
SmVAL6	RFNDQAIREHNRLRS-----LHGCP-----ELQLEDLMISAQKWAENLAAA EKLYHSN-----YN-DYGENLAFKMSASPC--QITGEEV	73
SmVAL13	QLNHDCALNEHNRLRA-----LHGCP-----PLKYDRRLAREAQAWAENLARLKIMEHSICDEY-----GENLASAQSTGKA--EMTGARA	73
SmVAL17	FEFNEECINEHNRLRA-----LHGCP-----ALILNLEYLAKDAQKYAEHLASVNELEHCTD TDS-----GENLAFFTAKIAQKDFTGADA	76
SmVAL16	KLNKEAIQAHNELRA-----LHGCP-----EISYDSKLASDSQKWA EHLASINCLQHSKGDDY-----GENLAFQMTAG A--SLNGREA	73

Group 2

	D1	I1
	C2 C3 C4 C5 C6	
Consensus	---W--E---y-----gHyTQ-vW-----GCa-----c-----vC-Y-p-gn---	
SmVAL3	VAYWMKEISNIYKHNTDFCSSTFGCNSYKQIVQAE TAYVCGGFT---RCR-QYEYPS SMLIACIYYSPK VKS--	148
SmVAL23	VAYWMKEISNIYKHNTDFCSSTFGCNSYKQIVQAE TAYVCGGFT---RCR-QYEYPS SMLIACIYYSPK VKS--	148
SmVAL24	VAYWMKEISNYDHNSDLCEP SHHCNTIYKQIVEAQTAYVCGGYT---RCE-EYEYPS NMLIACIYYSPK VMS--	148
SmVAL25	VAYWMKEISNYDHNSDLCEP SHHCNTIYKQIVQAE TAYVCGGYT---RCE-EYEYPS NMLVACIYYSPK MMS--	148
SmVAL20	VESWFNEBYQLDYDTNNKCEVPEDCLHYKRI VDCAKAEFIGCSVG---HCNTHTEVKSQIIVCYYS PMGDVKT	153
SmVAL10	LDTLBEKKNYDLDKNTCE-NE-CGNYKQLVWANTTDIGCASN---KCG-----NRYMVVCNYAPGADDE-	142
SmVAL18	VASWFIEYKKNYSFDDNTCK-DT-CMOYKQMVKGEE TEI GCGVQ---KCS-----NRFLVVCNYSPA A EED-	142
SmVAL4	MKDWLBEYKKNYNFEKNQCN-GD-CKNYKQMVWNTTEEI GCGYE---KCG-----KNYLIVCNYAPGD SED-	142
SmVAL7	ASVWFIEHKNYNFENNTCEANKTADYKQLAFADTTHI GCGYA---MCF-NLTGLDKVFFVVCNYGPGGKYAN	150
SmVAL19	MENWFREYHNNYNETDKCN-BS-CSNYRQMVWAKTKHIGCGLN---KCK-----KRKL MIVCNYSPSADK G	144
SmVAL12	MDEWFNEBYQYYDFDSENTCNSKS-CGNYLQIVWQKTTHI GCGVT---DCRKSQFPYGVFVVCNYAPGAKFD-	146
SmVAL2	VDAWFNEHKLNYNTNNCP--Q-CLHYTQMAWAKTTD I GCGVA---NCP-----RYGLSIVCNYGPGGNFNN	140
SmVAL1	VDAWFNEHKLNYNTNNCP--Q-CLHYTQMAWAKTTD I GCGVA---NCP-----RYGLSIVCNYGPGGNWNN	140
SmVAL21	VDAWFNEHKLNYNMNNCP--Q-CLHYTQMAWAKTTD I GCGVA---NCP-----RYGLSIVCNYGPGGNWNN	140
SmVAL14	VDAWFNEHKLNYSVNNCP--K-CVHYKQMVWAKTTD I GCGVA---NCQ-----RYGLSVVCYYPGPGGNWIN	140
SmVAL22	VDAWFNEHKLNYFVNNCP--Q-CLHYTQMVWAKTTD I GCGVA---NCS-----MYGLSIVCNYGPGGNWIN	140
SmVAL8	FDAAKDEYKQYNYYSKSCS-GV-CGHYTQLVWQNTTHVCGGIT---NCTGSYSFYPYGLSVVCNYGPGGNYEG	147
SmVAL9	VKLWFSAMYYNFNTNICSSAT-CGNYPQLVWENTTDVCGGVT---DCP---NFR TKLIVCNYGPGGNIPE	147
SmVAL5	FORWLNEYKNYDFFNRLCLVGR-CLHYTQIVWENTTD I GCGVA---TCP---HSPFKLSIVCNYGPGGGCPR	147
SmVAL15	FORWLNEYKNYDFFNRLCLVGR-CHSYTQIVWENTTD I GCGVA---TCP---HSPFKLSIVCNYGPGGGCPR	147
SmVAL27	FQSWLDEYKNYDFYTRTCRMGQ-CGHYTQLVWEDT TDVCGGVT---KCP---NFPYGLSIVCNYGPGGNYAG	147
SmVAL26	FQLWLDEYNNYDFYTRTCRMGQ-CGHYTQLVWEDT TDVCGGVT---DCP---NFPYGLSIVCNYGPGGNYPG	147
SmVAL28	FQLWLDEYKKNYDFYTRTCRMGQ-CGHYTQLVWEDT TDVCGGVT---DCP---NFPYGLSIVCNYGPGGNYPG	147

Group 1

SmVAL11_2nd	IEHWYQESGKYKFNSEPD SIQ-IGNFTQIVWTS S ERIGVGIAIQSYKSGEDLHKDSKMILVCLYHP PGNVIS	149
SmVAL11_1st	VNTWHSDAENYNYENGKGP-----AGNFTQLVWSSTREVFGKA-----CG-----PGKCVVVAHYRPPGNVLG	136
SmVAL6	SQTWYSEIDYHDF TQSYHP--N-SRHFTQMIWKSTTRAGFGLA-----FSQ---DQTKAYVVGRYLPVGNKGD	135
SmVAL13	TRNWDYIEIYHNFNFKQFS-Q-CGHFTQLIWKNTSKAGFGIQ-----HSV---DGHHVFI VGRYEPGNVNG	135
SmVAL17	TKTWYQESIEDYDFKRENQF--P-CGHFTQVVKSTITAGFGRA-----WSK-----DRHSIYVVG RYDP PGNFSD	138
SmVAL16	TRNWDYIEIIQHDFNGQNQP--G-TGHFTQVIWKSTIKAGFGSA-----LSK-----DGKVVYVGRYK PAGNIID	135

Group 2