

Table 1. Accession numbers and characteristics of *Arabidopsis* SCRL proteins.

Gene name	Genomic sequence accession number	Coordinates of coding region (bp) <sup>a</sup>		intron size (bp)	Predicted cleavage site <sup>b</sup>	Protein size (Da) <sup>c</sup>	pI
SCRL1	AL049524.1	39538-39472	39379-39171	92	VEA/MK	7367	8.80
SCRL2	AC007230.2	8416-8478	8581-8786	102	VES/KT	7417	8.66
SCRL3	AC003981.1	67403-67337	67166-66982	170	VEG/AN	6854	8.70
SCRL4	AC018908.6	54157-54226	54330-54551	103	SQG/EE	7942	7.51
SCRL5	AC018908.6	55524-55602	55694-55914	91	SQG/EE	8451	5.05
SCRL6	AC018908.6	51899-51969	52070-52284	100	SQG/EK	7920	7.53
SCRL7	AC018908.6	57315-57384	57470-57645	85	HLS/QG	7987	8.13
SCRL8	AC018908.6	50405-50671		0	TIA/EK	7783	7.47
SCRL9	AC007018.6	12223-12154	12003-11808	150	IHA/HL	8377	6.30
SCRL10	AL161542.2	86784-86853	86985-87211	131	HLS/HE	9536	6.81
SCRL11	AL161542.2	87419-87488	87628-87815	139	NLA/KE	7035	7.88
SCRL12	AP000377.1	18885-18951	19166-19374	214	VKA/QR	7735	9.31
SCRL13	AP000377.1	10872-10938	11075-11292	136	VKA/QR	7770	9.04
SCRL14	AL161556.2	143120-143054	142889-142699	164	VEA/VL	6417	6.84
SCRL15	AC007018.6	115766-115835	116016-116248	180	VKC/EV	8811	7.59
SCRL16	AC005171.2	98657-98724	98892-99086	167	VKG/QV	7143	9.21
SCRL17	AC006053.2	57181-57115	57008-56781	106	VNG/GL	8206	6.84
SCRL18	AC006304.3	23232-23165	22993-22769	171	VQG/GL	8320	8.32
SCRL19	AB025626.1	15812-15746	15502-15172	243	VKG/RT	8372	8.69
SCRL20	AL161516.2	137791-137725	137561-137341	163	VKG/QG	8278	8.99
SCRL21	AF080119.1	16817-16751	16593-16334	157	GQA/KK	9458	8.35
SCRL22	AL161583.2	128853-128919	129097-129317	177	VEA/GA	8064	8.30
SCRL23	AL161540.2	5693-5759	5920-6137	160	SEA/GA	8007	8.10
SCRL24	AL161582.2	8095-8161	8397-8596	235	VEA/EK	7282	8.12
SCRL25	AL161582.2	6431-6498	6731-6924	232	VEA/KE	7209	8.31
SCRL26	AL161556.2	138561-138495	138367-138174	127	VEA/GL	6727	8.27
SCRL27	AB016870.1	26235-26169	25996-25784	172	VLS/HV	8630	8.97
SCRL28	AC007576.3	94125-94191	94379-94500	187	NEA/MN	4491	9.59

a: coordinates correspond to the genomic sequences whose accession numbers are given in the column to the left. b: the slash marks the predicted cleavage site according to signalP. c: predicted mass of mature, cleaved polypeptide in Daltons.