

Supplementary Figure 1: Purification of PCO_GH28-1 and -3 and heat-dependent fragmentation of PCO_GH28-1. A) SDS-PAGE and Coomassie staining of exemplary metal ion affinity purification of PCO_GH28-1 and -3 via the His₆ tags. Their expected sizes are indicated with an arrow (closed arrowhead). Medium (M), dialyzed medium (MD), precipitated protein (P), flow-though (FT), wash (W) and elution fractions (E0 – E3). Additional bands in the purification of PCO_GH28-1 (arrows with open arrowheads, 1 – 8) were analyzed by MS/MS (see Supplementary Table 2) and identified as fragments of PCO_GH28-1. B) PCO_GH-28-1 was treated with increasing temperatures during sample preparation for SDS-PAGE and detected on the western blot with an anti-V5 antibody.

		10		20		30		40	50		ဓ၀	70	5	30	_	90	100		_	110	
AaPGIP1	CNQN <mark>DK</mark> NTI	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	N – P	QTD	ccs	WYCLE	GDATVNH	VTA	TIFS-	GQISGQ <mark>I</mark>	PEVGD	PY	LKT	IFRKLSNLT	TIQPT	AKL	KNL	QILRLSW	104
AtPGIP1	CNQNDKNTI	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	D-F	QTD	ccs	WYCLE	GDATVNH	VTA	TIFS-	GQISGQ <mark>I</mark>	PAEVGD	PY	LET	VFRKLSNLT	TIQPT	AKL	KNL	RMLRLSW	104
CbPGIP1	CHKD <mark>DK</mark> NTI	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	D-F	QTD	ccs	WYCLE	GDATVNH	VTAS	STIFS-	GQISGQ <mark>I</mark>	PAEVGD	PY	ET	VFRKLSNLT	TIQPT	AKL	KDL	RMLRLSW	104
CrPGIP1	CNQDDKNTI	LLKI	KESLNNP	Y-HLA <mark>SW</mark>	H-F	ETD	ccs	WYCLE	GDATVNH	VTS	TIFS-	GQISGQI	PEVGD	PY	ET	VFRKLTNLT	QIQPTI	AKL	KNL	KYLRLSW	104
CsPGTP1	CNODDKST	ыкт	KKSLNNP	Y-HLASW	H – F	ETD	ccs	YCLE	GDATANH	VTS	TIFS-	GOISGOI	PEVGD	PY	ET	VFRKLSNLT	OTOPTI	AKI	ккі	KYLRLSW	104
CsPGTP2	CNKDDKNTI	LIKT	KKSLNNP	Y-HLASW	H - F	ETD	s	VCLE	GDATVNH	VTA	TTES-	GOTSGOT	PEVGD	PY	ET	VERKLSNLT	OTOPT	AKT	KKI	RYLRLSW	104
LaPGTP1	CNONDENT	ТКТ	KKSLNNP	Y-HLASW	D-F	отр	s	VCLE	GDATVNH	VTA	TTES-	GOTSGOT	PEVGD	TΥ	ET	VEBRITNIT	TOPT	AKT	KNI	RTIRISW	104
NoPGIP2	CNKNDKNT	лкт	KKSLNNP	Y-HLASW		отр	ccs	VCLE	GDATVNH	VTA	TTFS-	GKTSG0T	PEVGD	PY	ET	VERKLTNLT	TOPT	AKT	KNI	RTLRLSW	104
BoDGID2	CNODDETT		KKALNNP	V-HIASW				VCLE	CDATVNH	VTA	TTFS-	COISCOT	PEVCD	cv	OT	VERKLINLT	OTPRT	AKT	KVT	DGIDIGW	104
DEFECTED 2	CNODDKITT		KALNNE	I-HLASH				VOLD	GDAIVNH	VIA	MTD 0	GQI3GQI	PEVGD	0 V		WEDNE MNL	OT DDW	AKI		ROLFLOW	104
BIFGIFZ	CNODDKTT		KALNNP	I-HLASW		RTD		TCLE	GDATVNH	VIA	TIFS-	GQISGQI	PEVGD	51	QT	VFRKLINLI	QIPRI	AKL	KIL	RSLRLSW	104
BnPGIP5	CNQDDKTTI	LLKI	KKALNNP	Y-HLASW	D-F	QTD	ccs	WYCLE	GDATVNH	VTA.	TIFS-	GQISGQI	PPEVGDI	SY	QТ	VFRKLTNLT	QIPRTI	TKI	KYL	RSLRLSW	104
ESPGIPI	CNQDDKNTI	LLKI	KKSLNNP	Y-HLASW	D-F	QTD	ccs	WYCLE	GDATVNH	RVNA.	TIFS-	GQISGHI	PPEVGDI	PY.	ET	IFRKLSNLT	QIQPTI	ANI	KNL	RILRLSW	104
SirPGIP3	CNQDDKSTI	LLKI	K KSLNN P	Y-HLA <mark>SW</mark>	D-F	QTD	ccs	WYCLE	GDATVNH	RITA	TIFS-	GQISGQ <mark>I</mark>	PPAVGDI	PY	LQT I	VFRKLTNLT	EIQPTI	AKI	KNL	RTLRLSW	104
BsPGIP1	CNQD DKNTI	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	H – F	ETD	CCS	WYCLE	GDATVNH	RVTA I	TIFS-	GDISGQ <mark>I</mark>	PHEVGD	PY	DK	IFRKLTNLT	TIQPSI	AKI	KKL	RFLRLSW	104
NoPGIP1								(GDATVNH	VTS	VMQY-	GEISGHI	PELGD	SL	LNT	LILHKLPNLI	HIQPTI	AKI	KNL	TSLWISW	66
BnPGIP1	CHKD <mark>DK</mark> NTI	LLKI	K KAMNN P	Y-TII <mark>SW</mark>	D-F	KDD	CCT	WVSVE	GNAN	VTS	DISD-	DDVSAQI	PEVGD	ΡY	LQY	TLRKLPNLT	EIPPTI	AKL	KYL	KSLWLSW	101
BnPGIP11	CHKD <mark>DK</mark> NTI	LLKI	KKAMND P	Y-TII <mark>SW</mark>	D-F	KDD	CCT	WYSVE	GNAN	VTS	DLSD-	DDVSAQI	PEVGD	PY	LQY	TFRKLPNLT	EIPPTI	AKI	KYL	KSLWLSW	101
BrPGIP1	CHKDDKNTI	LLKI	KKAMND P	Y-TII <mark>SW</mark>	D-F	KDD	CCT	WYSVE	GNAN	VTS	DLSD-	DDVSAOI	PEVGD	PY	LOY	TFRKLPNLT	EIPPTI	AKI	KYL	KSLWLSW	101
BnPGTP7	CHKDDKNT	лкт	KKAMNDP	Y-TTTSW	D - F	KDD	CCT	VSVE	GNAN	VTS	DLSD-	DDVSAOT	PEVGD	PY	OY	TERKLONLT	ETPPT	AKT	KYL	KSLWLSW	101
BnPGTP14	CHKDDKNT	TKT	KKAMNDP	V-TTTSW		KDD	CCT	VSVE	GNAN	VTS	DISD-		PEVCD	DV	ñv.	TERKIONIT	FTDDTT	AKT	KYT	KSTWISW	101
PpDCTD17	CHEDDENT	TVT	KKA MND D	V-TTTOW		KDD		Veve	CNAN	UTC		DDVCAOT	DEVCD	DV	OV.	TERVI DNI T	FTDDTT	AVI	VVT	VCIWICW	101
Paper P10	CHEDDENT	TVT	KKAMND P	V-TTTOW		VED	CCT	UNVE	CNATTNH		DIGN-	DDVSAQT	DEVCD	DV	EV	TEUVIDNIT		AVT	VVT	DNTWTUW	104
Dapot p12	CUKDDKNU		KKAMNDE	V MTTOW		KED		WINNE C	CNATINH	VIE	DIG N	DDVSAQI	DEVCD	DV	EV	TEURI DNI M		AKI	K I I	DNIWIUW	104
BIIFGIFIS	CHKDDKNII		KAMNDP	1-1115		KED		WVAVE	GNATINH	VIF	DISN-	DDVSAQI	PPEVGDI	PI		TPHKLPNLI		AKL	KIL.	KNLWLHW	104
BrPGIP/	CHKDDKNTI		KRAMNDP	Y-TIISW	D-F	KKD	сст	WVAVE	GNATINH	VTF.	DISN-	DDVSAQI	PPEVGDI	PY.	EY.	IFHKLPNLT	EIPPT	AKL	KYL	KNLWLHW	104
BnPG1P3	CHKDDKNTI	TKI	KRAMNDP	Y-TIISW	D-F	KDD	CCT	WYAVE	GNASINH	WTS.	DISN-	DDVSTQ1	PPEVGDI	.PY	EY.	IFHKLPNLT	EIPPTI	TKL	KYL	RYLWLSW	104
BrPGIP3	CHKDDKNTI	LLKI	KKAMND P	Y-TII <mark>SW</mark>	D-F	KDD	CCT	WYAVE	GNASINH	VTS	DISN-	DDVSTQ <mark>I</mark>	PPEVGDI	PY	EY	IFHKLPNLT	EIPPTI	TKL	KYL	RYLWLSW	104
BnPGIP15	CHKDDENTI	LTKI	KKSLNNP	Y-TII <mark>SW</mark>	D-F	KDD	CCT	WVSVE	GDATVDH	RVIS	DISN-	DDVSAQI	PPEVGDI	PY	LQT I	IFRKLPNLT	EIQPTI	AKI	KYL	RFLWLSW	104
BrPGIP8	CHKDDENAI	LTK1	K KSLNN P	Y-TII <mark>SW</mark>	D-F	KDD	CCT	WVSVE	GDATVDH	VIS	DISN-	DDVSAQI	PEVGDI	SY	LQT	IFRKLPNLT	EIQPTI	AKI	KYL	RFLWLSW	104
EsPGIP2	CHKD <mark>DK</mark> KTI	LLKI	K KSLNN P	Y-TII <mark>SW</mark>	D-F	KDD	ccs	WVSIE	GDATVNH	VTS	DISN-	DELSAQI	PEVGD	ΡY	LQT	LIFRKLPNLT	EIQPTI	AKL	KYL	SFLWLSW	104
BnPGIP6	CNQNDKKTI	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	D-F	KSD	CCA	WNSLE	DDATVNR	vis	TIFS-	AQISGQ <mark>I</mark>	PEVGD	ΡY	QK	VFRKITNLT	QIPHT	TKL	KYL	RFLRLSW	104
BnPGIP8	CHKD <mark>DK</mark> NTI	LLKI	KKSLSNP	YNNII <mark>SW</mark>	D-F	KED	CCT	WFNVE	GDATVNH	VTS	HISY-	DOISAOI	PEVGD	ΡY	LOT	IFRKLSNLT	PIOPTI	AKI	KYL	RFLRLSW	105
BrPGIP6	CHKDDKNT	LLKI	KKSLSNP	YNNIISW	D-F	KED	CCT	FNVE	GDATVNH	VTS	HISY-	DQISAOT	PEVGD	PY	от	IFRKLSNLT	PIOPT	AKI	ку	RFLRLSW	105
BnPGIP9	CNONDENT	LLKT	KKSLNNP	Y-HJASW	н	ETD	CCS	YCLF	GDATVNH	VIS	TIFA-	GOISGOT	PEVGD	PY	Los	MFHRITNIT	OIPST	TKI	KYT	RSLRLSW	104
BrPGTP5	CNONDENT	TWT	KKSTNN	V-HI A CH	H-	ETD		VCIE	GDATIVNU	VTC	TTE>	GOTSCOT	PEVCD	DV.	20	MEHRITMIT	OTPOT	TYT	KV7	RSLPT CM	104
BrPGTP9	CNENDYN	TWT	KKSINN	Y-HI A CH	H	ETD		VCIE	GDATUNU	VTC	TTE	GOISCOI	PPEVCD	DV.	01	VEBRITNIT	OTPUC	TYT	KV7	TELWICH	104
BADCID12	CNONDER		VVCTNN	V-UT NOW	n	A L D		MNGTE	DD2 TUNE	VIC	TTE CAL	JOISC C	DEACD	DV		VEDVINNI	V PUP	TP	W V T	DEI DI CH	104
BNPGIPIZ	CNQNDKKT		KKSLNNP	I-HLASW	D-1	KSD	CCA	WNSLE	DDATVNR	VIS	TIFS-	AQISGQI	PPEVGDI	PI	QK	VERKITNLT	QIPHT	TKL	KYL	RFLRLSW	104
BNPGIPI6	CNQNDKKT	LKI	KKSLNNP	Y-HLASW	D-F	rsb	CCA	WNSLE	DDATVNR	VIS.	TIFS-	AQISGQI	PPEVGDI	PY	QK	VFREITNLT	QIPHTI	TKL	KYL	RELECSW	104
BrPGIP4	CNQNDKKTI	LLKI	K KSLNN P	Y-HLA <mark>SW</mark>	D-F	rsd	CCA	WNSLE	DDATVNR	VIS	TIFS-	AQISGQ <mark>I</mark>	PPEVGDI	PY	QK	VFRKITNLT	QIPHTI	TKL	KYL	RFLRLSW	104
LaPGIP3	CHKD <mark>DK</mark> TTI	LLKI	KKSLNNS	YV <mark>SW</mark>	D-P	KDD	ccs	WYAVE	GDVTVNH	VTS	AIYN-	DDGSGQ <mark>I</mark>	PPEVGDI	PY	LQT I	IFRKLPNLT	HIPPTI	AKI	KNL	TFLWLSW	102
LaPGIP2	CNQD <mark>D</mark> RNTI	LLKI	K KSLNN P	Y-HLA <mark>SW</mark>	D-F	QTD	ccs	WYCLE	GDATVNH	VIA	TIFS-	GDISGQ <mark>I</mark>	PLEVGE	ΡY	LQK I	VFRKLTNLT	HIPLTI	VNI	KNL	TFLRLSW	104
AtPGIP2	CHKD <mark>DK</mark> TTI	LLKI	K KSLNN P	Y-HLA <mark>SW</mark>	D-F	KTD	ccs	WYCLE	GDATVNH	VTS	IIQD-	GEISGQ <mark>I</mark>	PEVGD	PY	LTS	LIFRKLTNLT	HIQPTI	AKL	KNL	TFLRLSW	104
CrPGIP2	CHKD <mark>DK</mark> IT <mark>I</mark>	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	D-F	KTD	ccs	WYCLE	GDATVNH	VTS	FIQD-	GEISGQ <mark>I</mark>	PEVGD	ΡY	LKS	IFRKLTNLT	HIQPTI	AKI	KNL	TFLRLSW	104
CsPGIP3	CHKD <mark>DK</mark> ITI	LLKI	KKSLNNP	Y-HLA <mark>SW</mark>	D-I	KTD	ccs	WYCLE	GNATVNH	VTS	FIQD-	GEISG-QI	SEVGD	PY	LES	IFRKLTNLT	HIQPTI	AKL	KKL	TFLRLSW	104
SirPGIP3	CNED DKNTI	LLKI	KKSLNNP	H-HLA <mark>SW</mark>	N – E	ESD	ccs	WYCLD	GDATVNY	vis	GIFQ-	GTFSGQI	PAEVGD	ΡY	EE	VFRKIPNLT	QIPAT	TKL	KHL	RFLRLSW	104
SirPGIP2	CHPDDKRTI	LLKI	KKSLNNP	Y-TVIAW	D-F	KTD	ccs	WCCLE	GDASINH	ITT	DISN-	DPISAOI	PEVGD	PF	LOY	ILRKLPNLT	OIPPTI	TKL	KYL	RYLWLNW	104
AdPGTP1		LIRT	KOALNNP	Y-LLASW	N – F		CCD	YNVD	DLTTN	TTA	TIFS-	GNISGOT	PAAVGD	PY	от.	IFRKLSNLT	OTPSAT	SKL	SNL	KMVRLSW	102
EaPGIP1	CNRNDKKVI	TOT	KKSLNNP	Y-HLASW		KTD	CCD	WYVVE	DPTTN	TVOI	INLE-S-	GNISGOT	PATTGD	PF	ET	VERKLUNLT	TTPOST	TKI	TNL	KTLRLSY	102
CipDCID1	CNDNDKKA		KKO LNN	V-OT A CH		CTD			DITI N	TWO	NIFC-	ANTEC-OT	DAATAD	DE	E	VEDVITNIT	OTDEAT	CVI	TINT	VIIDRDUCY	102
G-DGID2	CNPNDKKA		KKSLNNP	I-QLASH		310			DDKM N			ANISGQI	PAATADI	P P		ODUUTENLI		SKI	T IN L	KELKESI	102
CAPGIPS	CNPKDKQVI		KEDLGNP	I-HLASW		NTD		I V V K	DRKTN	TNA	TVFQ-	ANISGQI	TGVGD	PI		OF HHITNLT	TIQPT	AKL	TNL	KMLRLSF	102
STPGIPI	CNPKDKKVI	PTŐT	KEDLGNP	Y-HLASW		NTD	CCY	WYVVK	DRKTN	INA	TVFQ-	ANISGQI	PAAVGDI	PY.	ET.	QFHHITNLT	TIQPAL	AKL	TNL	KMLKLSF	102
CCPGIP1	CNPQDKKVI	LLQI	KKALNNP	Y-LLA <mark>SW</mark>	D-F	KTD	CCD	WYCLE	DLKTH	RVIA1	TMFSD	DRLTGQI	PAQVGDI	PY	ET	LFRHLPNLN	TIQPSI	AKI	KNL	KTLRLSW	103
HuPGIP1	CNPHDKKVI	LLQI	KRALNNP	Y-LLA <mark>SW</mark>	D-F	KTD	CCD	WYCLE	DPTTH	rvvs	TMFSD	DRLTGQ <mark>I</mark>	PSEVGDI	PY	ET	LFRHLPNLN	TIQPSI	AKI	KNL	KTLRLSW	103
TcPGIP2	CNSH <mark>DK</mark> KVI	LLQI	KRALNNP	Y-LLA <mark>SW</mark>	D-F	KTD	CCD	WYCLE	DPTTH	RVVS	TMFSD	DRLTGQ <mark>I</mark>	PSEVGDI	PY	ET	LFRHLPNLN	TIQPSI	AKI	KNL	KTLRLSW	103
TcPGIP1	CNSH <mark>DK</mark> KVI	LLQI	K RALNN P	Y-LLA <mark>SW</mark>	D-F	KTD	CCD	WYCLE	DPTTH	rvvs	TMFSD	DRLTGQ <mark>I</mark>	PYEVGDI	PY	LET	LFRHLPNLN	TIQPSI	AKI	KNL	KTLRLSW	103
GrPGIP1	CNAQ <mark>DK</mark> KVI	LLKI	K KALGN P	Y-LLA <mark>SW</mark>	D-F	KTD	CCD	WYCLE	HPNTH	RVVS	TLFSD	DRLTGQ <mark>I</mark>	PEVGD	PY	LET	LFRHLPNLN	TIQPAI	AKI	KNL	KMLRLSW	103
MdPGIP1	CNPD <mark>DK</mark> KVI	ιīδτι	K KAFGD P	Y-VLT <mark>SW</mark>	K-S	DTD	CCD	WYCVT	DSTTN	INS	TIFA-	GQVSGQI	PALVGD	ΡY	ET	EFHKQPNLT	PIQPAI	AKL	KGL	KFLRLSW	102
PcPGIP1	CNPD <mark>DK</mark> KVI	LLQI	KKAFGD P	Y-VLA <mark>SW</mark>	K-S	DTD	CCD	WYCVT	DSTTN	INS	TIFA-	GQVSGQI	PALVGD	PY	ET	EFHKQPNLT	PIQPAI	AKL	KGL	KSLRLSW	102
PpPGIP1	CNPKDKKVI	LLOI	K KAFNN P	Y-VLS <mark>SW</mark>	N – F	ETD	CCD	WYSVT	DSTTN	VNS	TLFS-	GGLSGOI	TOVGD	PY	LET	EFHKOPNLT	PIOPSI	AKI	KRL	KELRLSW	102
MaPGIP1	CHPODKKAI	LLOI	KKGFNNP	H-VFSTW	D-F	NTD	CC-VN	GGAH	DEKNN	IET	EIYFGG-	GDLSGPI	PPEIGD	PY	RT	WWHKOPNLT	PIPOSI	TKL	ERL	SYLVITW	105
MnPGTP1	CHPODKKAI	LT.OT	KKGENNP	H-VESTW	D – P	NTD	CC-LH	RGVH	DEKNN	TET	EKYEGG-	GDLAGPT	PETGD	PY	RT	WWHKOPNLT	PTPOST	TKL	KRL	BYLVITW	105
AaPGTP=like1	ONTNOKNT	TOT	KKSLKNP		т – с	OTD	C-TK	SCIE	TN0	VTS	TTSS-	COLSCOT	NOTCO	DV	ON	DESVISNIT	NTPOT	TKI	NNT	DTLRLKK	101
FLOP1 /At PCTP-like1	CTENDENA	TOT	KKALCND		N - T			TOVE	TND	VTC	GVTC-	CEVECOT	EVOTOD	VD	DT	DEGVIDUIT	NTDDTT	TYT	WNIT		101
PROTE Like2	CCONDENA		KKALGNE		N - F			TGVE	mN C	V I G	3VI3-	GEV3GQI	B A OVCD	T D		DEGVIDUIT		myt	WW	DIIDIKA	101
BHPGIP=IIKes	SSSNDKNA		KALNNP	P-LLSSW	IN - F	QTD.		TGVE	G	VIA	1155-	GEISGQI	AQVGD	LE	RT	DESILIBLI	NIPHI	TKL	KIL.	DITERTKÖ	101
BrarLORI/BrPGIP-likel	SSSNDKNA	PTŐT	KKALNNP	P-LLSSW	N - F	QTD.	FC-TT	WTGVE	G	VTA	TISS-	GEISGQI	PAQVGD	TE.	RT.	DFSILTHLT	NIPHT	TKL	KYL	DTTKTKÖ	101
BsPGIP-likel	CTANDKNAI	LLQI	KKSLNNP	P-LLS <mark>SW</mark>	N-P	RTD	CC-TG	WIGVE	TDR	VTA	TISS-	GEISGQI	PYQIGDI	гD	RT	DFSYLTHLT	NIPRTI	TKL	KNL	DLLRLKQ	101
CrPGIP-likel	CTPNDKNAI	LLQI	KKSLNNP	P-LLS <mark>SW</mark>	N – F	RTD	CC-TS	WTGVE	BDH	LVTS	TISS-	GEISGQ <mark>I</mark>	PVQIGDI	LD	RT	DFSYLTHLT	NIPRSI	TKL	KNL	DLLRLKQ	101
CsPGIP-like1	CTPNDKNAI	LLQI	KKSLNNP	P-LLS <mark>SW</mark>	N – P	RTD	CC-TS	WTGVE	TDRI	IVTA	TISS-	GEISGQ <mark>I</mark>	PAQIGDI	SD.	RT	DFSYLTHLT	TIPRTI	TKL	KNL	DLLRLKQ	101
CsPGIP-like2	CTPNDKNAI	LLQI	K KSLNN P	P-LLS <mark>SW</mark>	N – F	RTD	CC-TS	WTGVE	TDG	VTA	TISS-	GEISGQ <mark>I</mark>	PVQIGDI	SD	RT	DFSYLTHLT	NIPRTI	TKL	KNL	DLLRLKQ	101
CsPGIP-like3	CTPN <mark>DK</mark> NAI	LLQI	KKSLNN P	P-LLS <mark>SW</mark>	N – I	RTD	CC-TS	WTGVE C	TDG	RVTA I	TISS-	GEISGQ <mark>I</mark>	PVQIGD	РҮ	RT	DFSYLTHLT	NIPRTI	TKL	KNL	DLLRLKQ	101
EsPGIP-like2	C TSN <mark>DK</mark> NAI	LLQI	K KSLNN P	H-LLS <mark>SW</mark>	N – F	RTD	CC-TS	WTGVE	TNS	VTA	TISS-	GEISGQ <mark>I</mark>	PNQIGD	ID	RT	DFSYLTHLT	NIPRTI	TKL	KNL	DLLRLKQ	101
CrPGIP-like3	CTAN <mark>DK</mark> NAI	LLEI	K KSLNNH	P-LLS <mark>SW</mark>	N – F	QTD	CC-TG	SGVE	TYG	VTY	TLSS-	кк				FS	NIPPAV	TKL	RSL	DTLFFKY	76
CsPGIP-like4	CTEN <mark>DK</mark> NAI	LLEI	K KSLNNH	P-LLS <mark>SW</mark>	N – F	QTD	CC-TG	SGVE	TYG	VTY	TLSS-	кк				FS	NIPPAI	TKL	KSL	DILFFKY	76
BnPGIP-like7	CNSVEKNAI	LLQI	KKSFNNP	R-KFS <mark>SW</mark>	N – F	QTD	CC-TT	SGVK	TNG	VTD	SLFS-	SKLYGQI	PDQIGD	LE	RS	FLTYLPHLT	NIPRTI	TKL	KNL	DSLILRH	101
BnPGIP-like9	CNSIEKNA	LLÕI	KKSFNNP	R-KFS <mark>SW</mark>	N - F	QTD	CC-TT	SGVK	TNG	VTD	SLFS-	SKRYGOT	PDQIGD	LE	RS	FLTYLPHLT	NIPRT	TKL	KNL	EYLILRH	101
BrPGIP-like5	CNSVEKNA	LLÕI	KKSFNNP	R-KFS <mark>SW</mark>	N - F	QTD	CC-TT	SGVK	TNG	VTD	SLFS-	SKLYG01	PDQIGD	LE	RS	FLTYLPHLT	NIPRT	TKI	KNL	DSLILRH	101
BnPGIP-like1	CNPKDKNT	LLOI	KKHFNNP	K-LLS <mark>SW</mark>	D-F	QTD	CC-TS	TGIE	TNG	VTL	SMASD	DSVVGOT	PDQIGD	PE	RT	EMSSI-NLT	NIPRT	TKI	кн	VLIFLSW	101
BnPGIP-like6	CNPKDKNT	LLOT	KKHFNND	K-LLSSW	D-	OTD	CC-TS	TGIE	TNC	VTT.	SMAND	DSVVG0	PDOIGD	PE	RT	EMSSI-NI.T	NIPRT	TKI	КН	VLIFI.SW	101
BrPGTP=like3	CNPKPKNT	LT.OT	KKHENND	K-LISCH	D-	OTD	C-TC	TGTP	TNC	VTT	SMA ND	DSVVCCT	PEOTOD	PF	BT	EMSSM-NT T	NTPPT	THI	KHT	VITETOW	101
BnDGTD=like2	CNSKDWM		KKHENN	E-FICON		2070	10-70	TCTP	ING	VTT 1	SMANV	BTLYCCT	PDOTOD	LP	D	EMSHM-VT M	NTPPT	TYT	KH7	VETETIM	101
DALGIF-IIKEZ	CNCKDKNT		VUPNNT	E-EICON	D.	210	-15 - mc	TOTE	G	V 1 11	CMA N	DTINC CT	POTOD	TP	D ^m	EMCUN VI	MIPRI	TAL	KIL I	VETETTW	101
DEGIFTIKES	NOKOKNTI		KRENNT	E-LTSSW	ы-1 N	210	TS TS	TGIE	G	V TL	CMC V	KILIGQI	DOTOD	т. 25	RT O	EMONN-KLT	MIPRI	TKT	NHL.	A E T E PTR	101
DEFGIF-IIK04	NOKDENT	TOT	REAL FUND	D LL CT	a-1	ATD	TS TS	TGIE	G	VTL	SMSKD	MNLVGHI	DOT GDI	ьE	QS 07	EMOVI NI	MTPRT	TKI	KHL.	DETETK	101
BRFGIP-11Ke8	NPKDKNTI	LQI	KHFNNP	U-LĹSTW	5-F	ATD	C-TS	TGIE	G	V'TL	SMSKD	KKLVGHI	DQIGDI	LE	QS	EMSYL-NLT	TIPRT	TKL	KHL	DLIFLTW	101
BIRGIP-11Ke4	NSKEENT	-rõi	KHFNNP	U-LĹSTW	5-P	ATD	C-TS	TGIE	TND	V'TL	SMSKD	KKLVGHI	LUG1GD	ьE	QS	EMSYL-NLT	TIPRTI	TKL	KHL	DLIFLTW	101
BrrGIP-like2	CNSNDKTTI	rki	KKSLNNP	Q-ILN <mark>SW</mark>	D-P	KTD	C-TN	TGVV	THR	ITG	TISA-	GDVVGQI	AEEIGD	TD	VI	DLSSLSRLR	TIPRSI	TKI	KNL	VYLRFRI	101
CrPGIP-like2	E <mark>DK</mark> TTI	LTK I	KISLNNP	Q-ILN <mark>SW</mark>	D-I	RTD	CC-ND	WIGVE C	THR	ITG	TVAA-	GDVVGH <mark>I</mark>	AEEIGD <mark>I</mark>	RD	VI	DWSSLYRLR	TIPRS	TKL	KNL	TYLRFRV	98
EsPGIP-like1	CKSNDKTTI	LLKI	KKSLNN P	R-ILD <mark>SW</mark>	D-F	LTD	CC-TY	WIGVV (G	ITG	TIAA-	GEVVGE	AEEIGD	RD	.VI	DWSSLYGLR	TIPRS	TKI	KNL	VYMRFRI	101
AFP	CNNNDKQA1	LLQI	K TALKN P	T-ITD <mark>SW</mark>	v-s	DDD	CCG	WDLVE <mark>(</mark>	DETSN	IIS	IIQDD	EALTGQI	P PQVGD I	PY	LQA .	WFRKLPNLF	KI PEE	SAL	KDL	KSLRLSS	103
GmPGIP1	CNPQ <mark>DK</mark> QT <mark>I</mark>	LLQI	K KELGN P	T-TLS <mark>SW</mark>	H-F	KTD	CCNNS	wvgvs	DTVTPTY	VDN	DLSE-	LNLRKPYPI	PSVGS	PC	KF	YITNNPNIV	TIPTT	TKL	TKL	RELNIRY	108
GmPGIP2	CNPL <mark>DK</mark> QAI	LLQI	KRELGNP	T-NLS <mark>SW</mark>	N – F	KTD	CCNNN	wvgvs	DTVTPTY	VDN	DLSE-	IYLTKPYP <mark>I</mark>	PSIGN	ΡY	KF	FITNSPNIV	TIPTT	TKL	TKL	RELYIRY	108
GmPGIP5	CNPRDKQVI	LLKI	KELGNP	T-TLS <mark>SW</mark>	L-F	TTD	CC-NN	vgvs	DTVTQTY	VHN	DLSD-	LNLPKPYSI	FSIGN	PY	EF	SITGTPNII	TIPPTI	TKL	TKL	RNLYIKY	107
GmPGIP7	CNPODKEAT	LLOI	KKEFGNP	T-TLS <mark>SW</mark>	L-F	TSD	CCNNN	VGVS	ANKTOSY	VNH	DLND-	LNLPKPYPT	PSVGN	ΡY	NF	SITNTNNLV	TIPPT	TKI	TML	RELOIRF	108
GmPGIP3	CNPODKOA	LLOT	KKDLGNP	T-TJ.SSW	L-T	TTD	CONRT	LGVS	DTDTOTY	VND	DLSD-	LNLPKPYST	PSTAN	PY	NF	SISRTPTIT	OIPSAT	AKT	TOL	RYLYTTH	108
PyPGTP1	CNPOPRON	TOT	KKDLOND	T-TISC	L	TTD	CONRT	LGVI		VNN	DLSC-	HNLPKDVD	SSLAN	pv	NF	YIGGINNI	PTPDAT	AKT	TOT	HYLVTTU	108
DypCTP2	CNROPHON		KEDICK	T-TT00W		110	CND	TGAT		V IN IN		INI DEPERT	DCCT N	E I DV	NE	VICCIMNLV	DIPDZ	AAL	124	UVIVIE	100
DypCTD3	CNROPHE		KKDI CNP			1 I D	C K D C	PGAC	DIDIQIY	VININ	DIN P	TCITVDVD	DCCUAN	r I DV	CT	VICDINNLV	DTPDC	ANI	- Q L	DELATU	100
PVFG1P3	NPODKEAL	-LQI	KULGNP	I-TLSSW	11 - F	NTD	CKPE	EGVS	DIDTKTY	VNS	DTND-	LSLIKPYPI	SSVAN	ΡY	SF	TISKINNLV	PPPSI	AKI	TKL	RFLIITH	108
rvrG1P4	NPODKQAI	-LQI	KULGNP	T-TLS SW	11 - F	NTD	CKPE	EGVS	DTDTKSY	VNI	DTWG-	LSLTKPYPI	SSVGN	ΡY	GS	TISKMNNLV	SIPPSI	AKI	TKL	GFIRISH	108
GmrG1P4	N-QDKQVI	LQΙ	KELGNP	T-KLSSW	1. – I	TTD	TCDTI	WEGVA	VTDSNNQTC	VDI	ILSH-	TWTAKBABI	PSIGN	РY	NY.	ILIDT-NFF	ALPSS	ANI	TNL	NYLNITY	T08
BargIP1	CHDDDFAAI	.VAI	DSALGSP	Y-HFASW	T – F	DSA	CCD	HDVD	DAATG	VVG	SVSQD	TNISGAI	PDAIGN	TΥ	QT	TLHHLPAIS	AIPDSE	AMI	TNL	SQLTISY	103
OsPGIP1	CNAG <mark>DK</mark> AAI	LLAI	KKALGD P	Y-HFA <mark>SW</mark>	T – F	DNL	CCE	WYDVT (DDTTD	RVVG	SVFQD	ANLTGTI	PDAVAG	TH	RT	TWHHLPQIS	PIPPAI	AKI	NRL	SLLIISW	103
ZmPGIP1	CHSG <mark>DK</mark> AAI	LLAI	K AALGN P	Y-HFA <mark>SW</mark>	T – F	DNP	CCD	WYDVD	DATTG	RVVG	AVFQD	ANLTGTI	PDAVSG	VH	QN	MLHHLPGIS	PIPPAI	GRI	SNL	SFLTISW	103
OsPGIP2	CHED DE AAI	LLAI	DDALGNP	Y-NLA <mark>SW</mark>	T-P	NTS	CCD	WYDVD <mark>(</mark>	DQDSG	rvvs	SVFQD	TNLTGAI	PDAIAN	ΤH	RT	LLHHLPSLS	PIPDSI	AAI	TDL	THLTISW	103
TaPGIP1	CHPS <mark>DK</mark> AAI	LLAV	KSAFGNO	S-HFA <mark>SW</mark>	T – F	STP	CCD	WHDIT	NDAG	VII	LFFED	VNLTGT <mark>I</mark>	DAISG	TE	LV	NLYYLPAIS	PIPKGI	AKI	SKL	TSLSISL	102
TaPGIP2	CHPSDKAAI	LLAI	KSAFGNO	S-HFASW	T - F	STP	CCE	HDDT	NDAG	vis	IFFVD	VNLTGTI	DAISG	TE	LV	NLYYLPAIS	PIPKGI	AKI	SKL	TSLTIAL	102
OsFOR1/OsPGIP-like1	CPPSDKOA	MRV	KOSLGN	A-TLST	SLA	SAD	CCF	DHVR	DEAG	VNNV	FIDGA	NDVRGOT	SAVAG	TA	MS	SLFRLPGLS	PIPACT	TAT	SNT	OFLTISH	103
							_		-	_											

Plant-specific LRRs*

 $^{\star}\ensuremath{\left(\text{as published for PvPGIP1 (marked in red) by Leckie et al 1999)}\right.}$

LxLxx----NxL-TGxIPxxLGxLxxLxxLxLxx-NxLTGxIPxxLGxLxxLxLxxLxxLxx LRR2 LRR3 LRR1

⊢

		120	130	140		150	160		170		180	190	20	0	210	220
AaPGIP1	TNLT	5PV	DFISQLKNLQFLDL	SYNDLSG	SIPAS	S <mark>L</mark> SLL <mark>P</mark> I	NLSLDLSR	NKLAGS	IPETFG	-LLI	PE-KV	PDLY-	LSHNQLSC	SI PKS	-LGNLDFNRIDE	SRNKLEGDASML 21
AtPGIP1	TNLT	PI	DFISQLKNLEFLEL	SFNDLSG	SIPSS		KILALELSR	NKLTGS	IPESFG	-SFI	PG-TV	PDLR-	LSHNQLSC	PIPKS	S-LGNIDFNRIDI	SRNKLQGDASML 21
CbPGIP1	TNLT	PI	DFISQLKNLEFLEL	FNDLSG	SIPSE		KILALELSR	NKLTGS	TPESFG	- 5-1	PG-TV	PDLR-	LSRNQLSC	PIPKS	S-LGNVDFNRIDI	SRNELQGDASML 21
CrPGIP1	TNLT	DT	DEISOLKNIEFIEL	FNDLSG	CT DCC		KIMALELSK	NKLTCS	TPESEG		PG-AV	PDLR-	LSHNQLSC	DIDKS	S-LGNLDFNRIDI	SRNKLEGDASML 21
CSPGIPI CSPGIPI	TNLT	PT	DFISOLKNLEFLEL	FNDLSG	STPS	SLSTLP	KIMALELSR	NKLTGS	TPESFG	-SFI	PG-TV	PDLR-	LSHNOLSO	PTPKS	-LGNLDFNRIDI	SRNKLEGDASME 21
LaPGIP1	TNLT	PI	DFISOLKNLOFLDL	FNNLSG	SIPSS	LSLLP	NILSLOLSR	NKLTGS	IPESFG	-SF	PV-KV	PDLY-	LSHNKLSC	SIPNS	-LGNLDFNRIDI	SRNKLEGDASML 21
NoPGIP2	TNLT	PI	DFISQLKNLQFLEL	SFNDLSG	si <mark>p</mark> ss	SLSMLP	NILSLQLSR	NKLTGS	IPESFG	-sFI	PG-QV	-PDLY-	LSHNQLS	SIPKS	-LGNLDFNRLDE	SR <mark>N</mark> KLE <mark>GD</mark> ASML 21
BnPGIP2	TNLT	SPV	GFLSELKNLQWVDL	SF <mark>N</mark> DLS <mark>G</mark>	SI <mark>P</mark> SS	S <mark>L</mark> SLL <mark>P</mark> I	N <mark>L</mark> VSLDLSR	NKLT <mark>G</mark> S	IPESF <mark>G</mark>	-SFI	PA-KV	-PDLY-	LSHNQLSC	YI <mark>P</mark> KI	-LGNLDFSKIDE	SRNKLG <mark>GD</mark> ASML 21
BrPGIP2	TNLT	PV	GFLSELKNLQWVDL	SFNDLSG	SIPSS	5LSLLP	NLVSLDLSR	NKLTGS	IPESFG	-SFI	PA-KV	PDLY-	LSHNQLSC	YIPKI	-LGNLDFSKIDE	SRNKLGGEASML 21
BnPGIP5	TNLT	PV	GFLSELKNLQFIDL	FNDLSG	SVPSS			NKLTGS	IPESFG	-SFI	PA-KV	PDLY-	LSHNQLSC	YIPKI	-LGNLDFNRIDE	SRNKLGGDASML 21
EsPGIP1	TNLT	PT	GFLSQLKNLQFLDL	FNGLTG	STPSS		NLSLDLSK	NKLTGP	TPESFG		QA-KV	PDLY-	LSHNELSC	SIPKS	-LGNLDFNRIDE	SRNKLQGDASML 21
SITPGIP3	TNLT	PT	DFLSOLKNLOFLDL	FNDLSG	STPS	SLSLLP	NIGALELSE	NKLTGS	TPESEG	-51	PG-TV	PDLI-	LSHNOLSO	STPKS	S-LGNLDFNRIDE	SRNKLEGDASML 21
NoPCIPI	TNLT	PV	EFLSOLKNLEYINL	SFNNLTG	SIPTS	LASLH	KLEFLELSR	NKLTGP	IPESFG	-SF	SG-KV	PDLF-	LSHNOLS	SIPKS	-LGNLDFNRIDI	SRNKLOGDASIL 17
BnPGIP1	NSLT	PV	EFLSQLKNLEYINL	FNKLSG	SI <mark>P</mark> GS	LSLLP	K <mark>L</mark> DFLELSR	NKLTGP	IPESFG	-SF	KR-AA	-YGIY-	LSHNQLSC	SIPKS	-LGNVDFNTIDI	SRNKLEGDASML 20
BnPGIP11	NSLT	5 PV	EFLSQLKNLEYINL	SF <mark>N</mark> KLS <mark>G</mark>	SI <mark>P</mark> GS	SLSLL P	K <mark>L</mark> DFLELSR	NKLT <mark>G</mark> P	IPESFG	-sF]	KR-TV	YGIY-	LSHNQLSC	SIPKS	-LGNIDFNTIDI	SRNKLE <mark>GD</mark> ASML 20.
BrPGIP1	NSLT	SPV	EFLSQLKNLEYINL	SFNKLSG	SI <mark>P</mark> GS	S <mark>L</mark> SLLP	K <mark>L</mark> DFLELSR	NKLTGP	IPESFG	-SFI	KR-XV	YGIY-	LSHNQLSC	SI PKS	S-LGNIDFNTIDI	SRNKLEGDASML 20
BnPGIP7	NSLT	SPV I	EFLSQLKNLQYIDL	SFNDLSG	SIPGS	5LSLLP	KLEILDLSR	NKLTGS	IPESFG	-SFI	KG-VM	YALF-	LSHNQLSC	SIPKS	S-LGNLDINQIDI	SRNKLEGDASML 20
BnPGIP14	NSLT	PV	EFLSQLKNLEYINL	SFNKLSG	SIPGS			NKLTGP	IPESFG	-SFI	KR-TV	YGIY-	LSHNQLSC	SIPKS	G-LGNLDINQIDI	SRNKLEGDASML 20
BnPGIP17	NNLT	PV	EFLSOLKNLOYIDL	FNDLSG	STPGS	SLSLLP	KLETLDLSR	NKLTGS	TPESEG	-51	KG-VM	YALF-	LSHNOLSO	STPKS	S-LGNIDFNIIDI	SRNKLEGDASML 20
BnPGIP13	NNLT	PV	EFLSQLKNLQYIDL	FNDLSG	SIPGS	SLSLLP	K <mark>L</mark> EILDLSR	NKLTGS	IPESFG	-SFI	KG-VM	YALF-	LSHNQLSC	SIPKS	-LGNLDINQIDI	SRNKLEGDASML 21
BrPGIP7	NNLT	5 PV	EFLSQLKNLQYIDL	SF <mark>N</mark> DLS <mark>G</mark>	SI <mark>P</mark> GS	SLSLL P	K <mark>L</mark> EILDLSR	NKLT <mark>G</mark> S	IPESF <mark>G</mark>	-sF]	KG-VM	YALF-	LSHNQLSC	SIPKS	-LGNLDINQIDI	SRNKLE <mark>GD</mark> ASML 21.
BnPGIP3	NNLS	5 PV	EFLSQLKNLEYINL	SF <mark>N</mark> KLSG	SI <mark>P</mark> GS	SLSLL P	K <mark>l</mark> eflelsr	NKLTGS	IPESFG	-SFI	KG-VV	YALY-	lshnqls0	SIPKS	S-LGNLDINQIDI	SRNKLEGDASML 21.
BrPGIP3	NNLS	SPV.	EFLSQLKNLEYINL	SFNKLSG	SIPGS	L SLLP	KLEFLELSR	NKLTGS	IPESFG	-SFI	KG-VV	YALY-	LSHNQLSC	SIPKS	S-LGNLDINQIDI	SRNKLEGDASML 21
BnPGIP15	THLT	PV	EFLSQLKDLEYINL	FNDLSG	SIPGS		KLGILELSK	NKLTGS	TPESFG		KG-VV	-PPELF-	LSHNQLSC	SIPKS	-LGNLDFHRIDE	SKNKLEGDASMM 21
BrPGIP8 FeDCID2	TNLT		AFLSOLKNLEYINL	FNDLSG	STPS	SLSLLP	KIGFLELSR	NKLTGP	TPESFG			-PDLF-	LSHNOLSO	STPKS	S-LGKLDIYRIDI	SRNKLOGDASMI. 21
BnPGIP6	TNLT	PV	EFLSQLMDLAYLNL	FNYFSG	SIPSS	LSLLP	KLEYLELSR	NKLTGP	IPELFR	-SF	PG-KA	PDLF-	LSHNQLNC	SIPKS	-LGKLDFYRIDI	SHNKLKGDASML 21
BnPGIP8	TNLT	S PI	DFFSQLKNLQYIDL	SY <mark>N</mark> DLS <mark>G</mark>	SI <mark>P</mark> TS	SLALL P	K <mark>l</mark> eylelsr	NKLT <mark>G</mark> P	IPELFR	t-s <mark>f</mark> l	PG-KA	PDLF-	LSHNQLNC	SIPKS	-LGKLDFYRIDI	SH <mark>N</mark> KLK <mark>GD</mark> ASML 21.
BrPGIP6	TNLT	G PI	DFFSQLKNLQYIDL	SY <mark>N</mark> DLS <mark>G</mark>	SI <mark>P</mark> TS	S <mark>L</mark> ALL P	K <mark>l</mark> eylelsri	NKLT <mark>G</mark> P	IPELFR	l-SFI	PG-KA	PDLF-	LSHNQLNG	SI PKS	-LGKLDFYRIDI	SHNKLKGDASML 21.
BnPGIP9	LNLT	SPV.	EFLSQLMNLEYLSL	FNQLSG	SIPSS	LALLP	KLSYVDLSR	NKLTGT	IPESFG	-SFI	PA-EL	AYLI-	LSHNQLSC	SIPKS	S-LGNLDFNRIDE	SRNKFTGDASML 21
BrPGIP5	LNLT	PV	EFLSQLMNLEYLSL	FNQLSG	SIPSS		KLSYVDLSR	NKLTGT	IPESFG	-SE	PA-EL	AYLI-	LSHNQLSC	SIPKS	G-LGNLDFNRIDE	SRNKFTGDASML 21
BrPGIP9 BrPGID12	TNLT	PV	EFLSOLMDIAYINT	SENTER	SIPSS	LSJ.T.PI	KLSYVDI.SP	NKLTCT	IPESFO	-SF	SG-EV	PDT.F-	LSHNOLS	SIPKS	-LGNLDFNRIDI	SRNRFIGDASMI 21
BnPGIP16	TNLT	PV	EFLSQLMDLAYLNL	FNYFSG	SIPSS	LSLLP	KLSYVDLSR	NKLTGT	IPESFG	-SF	SG-EV	PDLF-	LSHNOLSC	SIPKS	-LGNLDFNRIDE	SRNRFIGDASML 21
BrPGIP4	TNLT	PV	EFLSQLMDLAYLNL	FNYFSG	SIPSS	SLSLLP	K <mark>L</mark> SYVDLSR	NKLTGT	IPESFG	-SF	SG-EV	PDLF-	LSHNQLSC	SIPKS	-LGNLDFNRIDE	SRNRFIGDASML 21
LaPGIP3	TNLT	GPV	EFLSQLKNLEYINL	SF <mark>N</mark> KLS <mark>G</mark>	PI <mark>P</mark> SS	S <mark>L</mark> GSLH	K <mark>L</mark> GFLELSR	NKLT <mark>G</mark> P	IPESFG	-SF	IG-EV	PDLF-	LSHNQLSC	PI <mark>P</mark> KS	-LGNLDFNRIDI	SRNKLE <mark>GD</mark> ASIL 20.
LaPGIP2	TNLS	GPV	EFLSQLKNLEYMDL	FNDLSG	SIPSS	SLSSLP	K <mark>L</mark> GFLDLSR	NKLTGP	IPESFG	-SF	LG-ED	PYLL-	LSHNQLSC	SIPKS	-LGNLDFNKIDI	SRNKLQGDASML 21.
AtPGIP2	TNLT	PV	EFLSQLKNLEYIDL	SFNDLSG	SIPSS		KLEYLELSR	KLTGP	IPESFG	-TFS	SG-KV	PSLF-	LSHNQLSC	TIPKS	S-LGNPDFYRIDI	SRNKLQGDASIL 21
CrPGIP2	TNLT	PI	EFLSQLKNLEIIDL	FNDLSG	STREE		KLEYLELSK	NKLTGP	TPESEG	- 51	SG-KV	PSLF-	LSHNQLSC	TIPKS	-LGNSDFIRIDI	SRNKLOGDASIL 21
SirPGIP3	TNLT	PV	GFLSQLMNLAYLDL	FNQLSG	SIPSS	LSLLP	KLNYIDLSR	NKLTGT	IPESFG	-SF	PS-TG	PYLF-	LSHNQLTO	SIPRS	-LGNLDFYKIDE	SRNKLOGDASML 21
SirPGIP2	NNLT	PV	EFLSELKNLEYINL	FNNLSG	si <mark>p</mark> ss	SLSLLP	K <mark>l</mark> eyvdlgr	NKLTGS	IPESFG	-sFI	KVA	PYLL-	LSHNQLSC	SIPKS	-LGNLNYPKIDI	SRNKLEGDASVL 20
AdPGIP1	TNLS	GPV	SFFSQLKNLTFLDL	SF <mark>N</mark> DLT <mark>G</mark>	SI <mark>P</mark> SS	S <mark>L</mark> SKLTI	N <mark>L</mark> DAIHLDR	NKLT <mark>G</mark> P	IPNSFG	-EF	IG-QV	-PDLY-	LSHNQLTC	SIPKI	-LGDLNFTVIDV	SRNMLSGD I SFM 20
EgPGIP1	TNLS	GAI	SFLSQLENLTFLDL	SFNNLTG	EIPPS	SLSLLKI	NLDALHLDR	NKLTGK	IPDSIG	-KF	AG-KT	PDLY-	FSHNQLTO	AVPRS	-LGDLNFTVLDE	SRNKLEGDASFL 20
SinPGIP1	TNLS	PI	TFLSQLKNLTFLDL	SFNDLSG	SIPPS	SISNLP	NLDALHLDR	NKLTGS	IPDSLG	-KF	re-kv	PDLY-	LSHNHLTO	SVPRS	S-LGDLNFTVLDE	SRNQLEGDISFL 20
CaPGIP3	TNLT	PI	EFLSOLKNLTLLEL	NYNOLTG	TIPAS	SLSOLPI	NI.LATYLOR	NKLTGT	TPESFG	-RFI	KGPNI	PDII-	LSHNSLT	KVPTS	S-LGDLNFSTLDF	SRNKLEGDVSFL 20
CcPGIP1	TNLS	PV	DFLSQLKNLTFLDL	FNNLSG	SIPSS	SLSKLP	NLLALHLDR	NKLTGS	IPESLG	-RFI	KG-NV	PDLY-	LSHNKLT	TIPAS	-LGNLDFNTIDE	SRNLLEGDASML 20
HuPGIP1	TNLS	STV	DFLSQLKNLTYLDL	SFNNLSG	NIPSS	S <mark>L</mark> SSL <mark>P</mark> I	N <mark>LEALHLDR</mark>	NKFT <mark>G</mark> S	IPESF <mark>G</mark>	-MF	QG-KA	PDLF-	LSHNKLT	TI PAS	-LGNMDFNTIDI	SRNMLEGDASML 20.
TcPGIP2	TNLS	TV	DFLSQLKNLTYLDL	SFNNLSG	TIPSS		NLEALHLDR	NKFTGS	IPESLG	-MF	QG-KA	PDLF-	LSHNKLTO	TIPVS	S-LGNMDFNTIDI	SRNMLEGDASML 20
TCPGIP1	TNLS		DFLSQLKNLTYLDL	SFNNLSG	STRES		NLEALHLDR	NKETGS	TPESEG	-ME	QG-KA	PDLF-	LSHNKLTG	TIPVS	S-LGNMDFNTIDI	SRNMLEGDASML 20
MdPGIP1	TNLS	sv	DFLSQLKNLTFLDL	SFNNLTG	AIPSS	LSQLP	NLNALHLDR	NKLTGH	IPKSLG	-OF	IG-NV	PDLY-	LSHNQLSC	NIPTS	-FAOMDFTSIDI	SRNKLEGDASVI 20
PcPGIP1	TNLS	sv	DFLSQLKNLTFLDL	SFNNLTG	AI <mark>P</mark> SS	SLSELP	N <mark>L</mark> GALRLDR	NKLT <mark>G</mark> H	IPISF <mark>G</mark>	-QF	IG-NV	-PDLY-	LSHNQLSC	NIPTS	-FAQMDFTSIDI	. <mark>S</mark> RNKLE <mark>GD</mark> ASVI 20
PpPGIP1	TNIS	svi	DFLSQLKNLTFLEL	SFNNLTG	SI <mark>P</mark> SS	S <mark>L</mark> SQL <mark>P</mark> I	N <mark>LVALHLDR</mark>	NKLT <mark>G</mark> H	IPKSFG	-EFI	HG-SV	PDLY-	lshnqls0	TIPTS	-LAKLDFSTVDE	SRNKLE <mark>GD</mark> ASMI 20
MaPGIP1	ANLS	PI	DFLSEIKSLVSIEF	SFNNLTG	SIPSS		NLTGLALDR	NKLTGP		-EF(QG-FS	FYLK-	LSHNQLSC	KIPAS	S-LGKKDFTYVDI	SRNKLEGDASVL 21
MnPGIP1	TKLS	S T I	CFISOLKNUTFLDL	SENKETC			NLTGLVLDR	NKLTGP	TPASEG	-EF(UG-KV	FILK-	LENNOLS	KUPF	S-LGNKDENIVDI	SUNKLEGGAAVL 21
FLOR1/AtPGIP=like1	TSLS	PI	DYISELKSLTFLDL	FNOFTG	PIPGS	SLSOMP	KLEAIOIND	NKLTGS	IPNSFG	-SF	VG-NV	PNLY-	LSNNKLS	KIPES	-LSKYDFNAVDI	SGNGFEGDAFMF 20
BnPGIP-like3	TNLS	YI	DFISELKSVTFLDL	SF <mark>N</mark> QFT <mark>G</mark>	PI <mark>P</mark> GS	SLSQMP	K <mark>L</mark> GALQIND	NKLTGS	IPNSFG	-SF	VG-TV	PNLY-	LFNNKLSC	KVPES	-LSKYDFNAVDI	<mark>SGN</mark> SFI <mark>GD</mark> G <mark>S</mark> MF 20
BraFLOR1/BrPGIP-like1	TNLS	YI	DFISELKSVTFLDL	SFNQFTG	PI <mark>P</mark> GS	SLSQMP	K <mark>L</mark> DAIQIND	NKLTGS	IPNSFG	-SF	VG-KV	PNLY-	LFNNKLSC	KV PES	S-LSKYDFNAVDI	SGNSFTGDGSMF 20.
BsPGIP-likel	TNLS	SPI CT	DYISELKSVTFLDL	FNQFTG	PIPGS	LSQLP	KIQAIQINDI	NKLTGS	IPNSFG	-SF	VG-NV	PNLY-	LENNKLSC	RVPES	-LSKYDFNAVDI	SGNGFIGDGSMF 20
CrPGIP-likel	TNLS	PI	DYISELKTVTFLDL	SFNOFTG	PIPGS	LSOMP	KLOAIOVND	NKLTGS	IPNSFG	-SF	VG-NV	PNLY-	LFNNKLSC	KVPES	-LSKYDFNAVDI	SGNGFIGDGSMF 20
CsPGIP-like2	TNLS	PI	DYISELKTVTFLDL	FNQFTG	PIPGS	SLSQMP	KLQAIQVND	NKLTGS	IPNSFG	-SF	VG-NV	PNLY-	LFNNKLS	KVPES	-LSKYDFNAVDI	SGNGFIGDGSMF 20
CsPGIP-like3	TNLS	G PI	DYISELKTVTFLDL	S F <mark>N</mark> QFT <mark>G</mark>	PI <mark>P</mark> GS	SLSQMP	K <mark>L</mark> QAIQVND	NKLT <mark>G</mark> S	IPNSFG	-SF	VG-NV	PNLY-	LFNNKLSC	KVPES	-LSKYDFNAVDI	<mark>SGN</mark> GFI <mark>GD</mark> G <mark>S</mark> MF 20.
EsPGIP-like2	NNLS	G PI	EYISELKNVTFLDL	SF <mark>N</mark> QFT <mark>G</mark>	PI <mark>P</mark> GS	FSQMP	K <mark>L</mark> QAIQIND	NKLTGS	VPNSF G	-SF	VG-NV	PNLY-	LFNNKLSC	KI PES	S-LSKYDFNAVDI	SG <mark>N</mark> GFI <mark>GD</mark> G <mark>S</mark> MF 20
CrPGIP-like3	SNFS	PI	DNISDLKNLTYLGL	SENQLTG	PIPGS	SLSQMP	KLLAIHVND	NKLTGS	IPNSFG	-SF	VG-NV	PGLE-	LSNNRLSO	KIPES	B-LSKHDFNVVFI	SGNSFVGDGSMF 18
CsPGIP-like4	SNFS	PI	DNISDLKNLTYLGL	SENQLTG	PIPGI		KLEAIHVND	NKLTGS	UPNSFG	-SF	VG-NV	PGLD-		KIPES	-LSKHDFNSVFI	SGNSFVGDGSMF 18
BnPGIP=like/	NNLS	LI	DNIGELKRLSFLDL	SYNOFTG	PIPGS	SLSOMP	MLETIIVEH	NKLTGS	IPNSFG	-SF	VG-EV	PNLY-	LSNNKLSC	NIPES	S-LSKNDFNGVFI	SKNSFTGDGSMF 20
BrPGIP-like5	NNLS	PI	DNIGELKKLRFLDL	YNQFTG	PIPGS		MLETIIVEH	NKLTGS	IPNSFG	-SF	VG-EV	-PNLY-	LSNNKLS	NIPES	-LSKNDFNGVFI	SKNSFTGDGSMF 20
BnPGIP-like1	NKLS	GPI	DYISELKSVTFLDI	SF <mark>N</mark> KFT <mark>G</mark>	PI <mark>P</mark> GV	I TQMP	N <mark>L</mark> QTFQADN	NSLT <mark>G</mark> P	IPNSFG	-SF	VG-NV	PNLF-	LPYNKLS	KIPES	S-LSKIDFQAIVI	KG <mark>N</mark> GFT <mark>GD</mark> G <mark>S</mark> MF 20
BnPGIP-like6	NRLS	PI	DYISELKSVTFLDI	SFNKFTG	PIPGV	LTQMP	K <mark>L</mark> QTFQANN	NSLTGP	IPNSFG	-SF	VG-NA	-PNLF-	LPYNKLS	KIPES	-LSKIDFQAVVI	KGNGFTGDGSMF 20
BrPGIP-like3	NKLS	PI	DYVSELKSVTFLDI	SFNKFTG	PIPGV	TQMP	KLHTFQADN	NSLTGP	1 PNSFG	-SF	VG-NV	PNVF-	LPYNKLSC	KIPES	-LSKIDFQAIVI	KGNGFTGDGSMF 20
BnPGIP-like2	NKLS	PT1	DIISELKSVTFLDI	SENKETC	FIPGV PIPC ¹	TOMP	KLOTFOADN	SLTGP NSLTCP	VPNSFG	-SE	VG-SV		LKNNKLSC	KIDE 4	S-LSKMDFQAVVI	KGNGFTGDGSMF 20
BnPGIP=like4	NRLS	PI	DYISELKNVTFMDI.	YNKFTG	PVPGV	LTOMP	KLOTFOIDN	NSLTGP	IPNSFG	-SF	AD-SV	PNLF-	LKNNKLSC	KIPES	-LSKIDFOAVVI	AGNSFTGDGSMF 20
BnPGIP-like8	NRLS	PI	PEYISELKSVTFLDI	FNKFTG	PIPGV	LTQMP	NLQTFQADN	SLTGP	IPNSFG	-SF	VG-NV	-PNLF-	LPYNKLS	KIPES	-LSKIDFQAVVI	TGNSFTGDGSMF 20
BrPGIP-like4	NRLS	G PI	EYISELKSVTFLDI	SF <mark>N</mark> KFTG	PI <mark>P</mark> GW	ILTQMP	N <mark>L</mark> QTFQADN	NSLT <mark>G</mark> P	IPNSFG	-SF	VG-NV	PNLF-	LPYNKLSC	KI PES	S-LSKIDFQAVVI	TG <mark>N</mark> SFT <mark>GD</mark> G <mark>S</mark> MF 20
BrPGIP-like2	TELS	GPVI	DYISQLQNVTFLDL	SFNRFNG	SI <mark>P</mark> GS	SISQMH	R <mark>L</mark> ETIQLSH	NKLTGS	IPESFG	-SF	AG-KI	PKLY-	LGNNHLSC	EIPKS	-LSKTNFNTVSI	SG <mark>N</mark> NFS <mark>GDAS</mark> MF 20.
CrPGIP-like2	TELS	PI	EYISELQNVTFLDL	5 FNRFNG	SIPGS	SISLMP	KLEAVQLNR	NKLTGS	IPESFG	-SF	VG-KV	PDLY-		KIPKS	S-LSKSDFNTLSI	SGNKLSGDASMF 20
ESPGIP-likel	TSLS	PV	LFFPOLTKLTCLDL	SFNKLLG	VIPPO	LSTLP	NLKALHLER	NELTGE	IPDIFG	-NF	AG-S	PDLF-	LSHNOLTO	FVPKI	-ESKSDFN1LS1	SGNRESGDISFL 20
GmPGIP1	TNIS	QI	HFLSQIKALGFLDL	NNKLSG	NLPSV	LPSLP	DLYGISFDN	NYISCP	IPDLFA	-sv	SE-RF	GFIS-	LSGNRLIC	KIPAS	-LGKPDMKIVDI	SRNMLEGDASVL 21
GmPGIP2	TSVS	QI	HFLSQMKTLQFLEF	NCKLSG	NL <mark>P</mark> TV	ILPSL P	D <mark>L</mark> YGVAFDN	NRIS <mark>G</mark> A	IPDSFG	-FV	SK-RF	-GYMT-	LSGNRLS	KIPSS	-LGKLDLKTVDI	SRNKLE <mark>GD</mark> ASVL 21
GmPGIP5	TNVS	QI	RFLSQIKTLEFLDL	YNKLSG	NLPAV	ILPSLP1	NLVGISFDG	NRISGA	IPDSFG	-YFI	PK-SF	VMLS-		KIPAT	-LAKLDVKFVYI	SKNMLEGDASLL 21
GmPGIP7	TNVS	рт	DFLSOIKTLESIIF		KI Dy «	LSSI P	NUVGITED	NOTSCA	TPDSFG	- 51	SK-TE	KLMT-	TSBNDI	KID94	- FARLDFDFVDI	SENMLECDASVL 21
GMPG1P3 PyPGIP1	TNVS	GAT	DFLSQIKTLVTLDF	YNALSC	TLPPS	ISSI.P	NLGGITFDC	NRISCA	IPDSYC	-SF	SK-LF	-TAMT-	ISRNRLT	KIPP	-FANLNLAFVDI	SRNMLEGDASVI. 21
PvPGIP2	TNVS	AI	DFLSQIKTLVTLDF	YNALSG	TLPPS	ISSL	NLVGITFDG	NRISCA	IPDSYG	-SF	SK-LF		ISRNRLT	KIPPI	-FANLNLAFVDI	SRNMLEGDASVL 21
PvPGIP3	TNVS	QI	NFLSQMKTLITIDF	SYNALS G	TL <mark>P</mark> PS	SLSSLP	N <mark>L</mark> LGISLDG	NRIS <mark>G</mark> T	'IPGSF <mark>G</mark>	-SFI	PK-HF	-TVLT-	LSRNRLT	NI PAT	-LAKLELAFVDI	SENMLE <mark>GD</mark> ASVL 21
PvPGIP4	TNVS	QI	NFLSQMKSLITIDF	YNALS G	TLPPS	LSSLP	NLVGISLDG	NRISCT	IPGSFG	-SFI	PK-HF	TVLT-	LSRNRLT	NIPTI	-LAKLGLSFVDI	SENMLEGDASVL 21
GmPGIP4	TNVS	TI	OFLSHIKTLVSIDF	YNNLSG	NLPAS		NLGEMIFTG	NRISGA	TPUSEG	-SES	SE-EL		LSRNRLTO	KIPAT	-LAKLNLRFLDI	SKNMLEGDASVL 21
OspGIP1	TAVS	pv	SFLGGLKSLTLLDL	SFNSI.TC	AIPPO	LAAT.P	FLSGIDISP	NRLTOP	LPPAT.E	-SKI	LN-TTOOC.	-GAYIR-	LSRNNLSC	GIPAT	-YGGVAFE	10
ZmPGIP1	TGVS	PV	SFLGALTRLNQLDL	FNALTG	AVPAS	LAALP	SLYSIDISR	NRLTGS	LPPLLF	-SRI	LD-KAQQ-	-EAYLR-	LSHNNLT	SVPPF	-FSAVAFAQVDI	SRNAFAGDASGL 21
OsPGIP2	TAVS	5 PV	SFLANLTSLTMLDL	SFNSLTG	LI <mark>P</mark> PS	-	NLSAINLSR	NRLSGP	IPPGLF	-sn	LQ-LQDDDI	DEVYLR-	LSHNNLS	SVPAI	LLAAANLALVDI	SRNALT <mark>GD</mark> ASAV 21
TaPGIP1	TSVS	PI.	SFLGALTKLNDLTL	SSNSLTG	TIPAS	AGLR	TDTIDLRN	NRLT <mark>G</mark> T	IPPLFY	NSK	SP-II	PYLL-	LSNNHLS	SIPTE	-FAAVGFQFIDI	SHNALTGDASVF 20
TaPGIP2	TAVS	PI VT	DSLARIRSIDSVDI	SNSLSG	TTPAS	SESDIP	NURSIDIAC	NKLTCC	TPA	-SK	51-LL	FVLL- RSLT-	LSYNOL	SIPAI PT DPT	-FAAVGFLQVDI	SHNRLTGDASVF 20
GOLOWI' ORLEILEITKGI											~ **					ZU
Plant-specific LRRs	NxLTO	GxII	PxxLGxLxxLxxLxL	xxNxLTG	xIPx>	LGxLx	xLxxLxLxx1	NxLTGx	IPxxLG	-xL	xx-Lx	x-Lx-	LXXNXLTO	XIPXX	-LGxLxxLxLxI	XXNXLTGXIPXX
		1	BB3		T.RR/	1			T.B	285				LRR	5	I.BB7

		240	250	260	270	280	290	300	310	320	330	340
AaPGIP1	FGVN-	-TTWYID <mark>L</mark>	.SRNMFQFDL	SK <mark>V</mark> -ELPKTLGI	<mark>LD</mark> LNH <mark>N</mark> GIT	GNI <mark>P</mark> VQWTESP-	LQFF <mark>NVS</mark> Y	RLCGRIE	T <mark>GGNLQ</mark> KFDSY#	AYFH <mark>NRCLCG</mark> AP	LE-SCK	306
AtPGIP1	FGSN-F	-TTWSIDL	SRNMFQFDI	SKV-DIPKTLGI	LDLNHNGIT	GNIPVQWTEAP-	LQFFNVSYN	KLCGHI	TGGKLQTFDSYS	SYFHNKCLCGAP	LE-ICK	306
CrPGIP1 CrPGIP1	FGAN-F	-TSWSID	SRNMFQFDL	SKV-ELPKTLGI	LDLNHNGIT	GNIPVQWIEAF-	LQFFNVSY	RLCGHI	TGGKLQSFDSYS	SYSHNKCLCGAP	FD-NCK	306
CsPGIP1	FGAN-F	-TTWSID <mark>L</mark>	<mark>.S</mark> R <mark>N</mark> MFQ <mark>F</mark> DI	SK <mark>V</mark> -ELPKTLGV	<mark>LD</mark> LNH <mark>N</mark> GIT	GNI PVQWTETP-	LQFFNVSY	KLCGN I F	N <mark>GG</mark> K <mark>LQ</mark> TFDSYS	SYVH <mark>NKCLCG</mark> AP	LD-SCNL	307
CsPGIP2	FGAN-F	-TTWSIDL	SRNMFQFDI	SKV-ELPKTLGV	LDLNHNGIT	GNIPVQWTETP-	LQFFNVSYN	KLCGHI	NGGKLQTFDSYS	SYVHNKCLCGAP	LD-SCNL	307
LaPGIPI NoPGIP2	FGAN-F	-TTWSID	SRNMFQFDL	SKV-ELPKTLGV	LDLNHNGIT	GNIPVQWIEAF-	LQFFNVSY	KLCGHI	NGGKLQTFDSYS	SYFHNKCLCGAP	LE-TCK	306
BnPGIP2	FRAN-F	-TTWYID <mark>L</mark>	SRNMLQFDL	SR <mark>V</mark> -VIPKTLGI	<mark>ld</mark> lnh <mark>n</mark> git	GNI PVQWTEAP-	LQFFNVSY	RLCGHI	T <mark>GGTLQ</mark> EFDTYS	SYFH <mark>NKCLCG</mark> AP	LD-SCK	306
BrPGIP2	FGAN-F	C-TTWYIDL	SRNMLQFDL	SRV-VIPKTLGI	LDLNHNGIT	GNIPVQWTEAP-	LQFFNVSYN	RLCGHI	TGGTLQEFDTYS	SYFHNKCLCGAP	LD-SCK	306
EsPGIP5	FGAN-F	-TTWIID	SRNMFQFDL	SKV-VIFKILGI SKV-EISKTLGI	LDLNHNGII	GNIPVQWTEAP-	LQFFNVSY	QLCGHI	NGGKLQTFDSY	YFHNKCLCGAP	LD-SCK	306
SirPGIP3	FGAN-F	-TTWYID	.srnnyqfdl	SR <mark>V</mark> -EIPKTLGI	<mark>LD</mark> LNH <mark>N</mark> GIK	GNI PVQWTEAP-	LQFFNVSY	RLCGQIE	T <mark>GGKLQ</mark> TFDSYS	SYFH <mark>NKCLCG</mark> AP	LD-SCK	306
BsPGIP1	FGVN-F		SRNMFQFDL	SKV-EIPKTLGV	LDLNHNGIT	GNIPVQWTENP-	PQFLNVSY	KLCGHI	GKLQTFDSYS	SYFHNKCLCGAP	LG-NCK	304
NoPGIP1 BDBGTP1	FGAK-F	-TTWHIDI	SRNMFOFDI	SKV-EL-PRILGV	LDLNHNSLT	GSIPDOWTOLD-	LOTENVSY	IRLCGRIE	OGGDLORFDVY	YLHNKCLCDAP	LP-SCN	208
BnPGIP11	FGVK-	-TTWHID	<mark>.s</mark> r <mark>n</mark> mfQ <mark>f</mark> DI	SK <mark>V</mark> -KVAKTVNF	LDLNH <mark>N</mark> GLT	GSIPDQWTQLD-	LQTFNVSY	RLCGRIE	Q <mark>GGDLQ</mark> SFDAY	YLH <mark>NKCLCG</mark> AP	LP-S <mark>C</mark> N	303
BrPGIP1	FGVK-F	-TTWHIDL	SRNMFQFDI	SKV-KV-AKTVNF	LDLNHNGLT	GSIPDQWTQLD-	LQTFNVSYN	RLCGRIE	QGGDLQSFDAY	YLHNKCLCGAP	LP-SCN	303
BnPGIP7 BnPGTP14	FGAQ-F	-TTHNIDI	SRNMFOFNI	SMV-KVSKIVNF	LHLNHNGLT	GTIPIQWIQLD- GTIPIOWTOLD-	LOIFNVSY	RLCGRI	OGGELORFDAY	YLHNKCLCGAP	LO-SCK	303
BnPGIP17	FGVK-	-TTWHID	.SRNMFQFNI	SM <mark>V</mark> -KVSKTVNF	LHLNH <mark>N</mark> GLT	GTIPIQWTQLD-	LQIFNVSYN	IRLCGR I F	QGGELQRFDAY	YLH <mark>NKCLCG</mark> AP	LQ-SCK	303
BnPGIP10	FGAQ-F	-TTHNIDL	SRNMFQFNI	SMV-KVSKTVNF	LHLNHNGLT	GTIPIQWTQLD-	LQIFNVSYN	RLCGRIE	QGGELQRFDAY	YLHNKCLCGAP	LQ-SCK	306
BrPGIP13 BrPGIP7	FGAQ-F	-TTHNID	SRNMFOFNI	SMV-KVSKIVNF	LHLNHNGLT	GTIPIQWIQLD- GTIPIOWTOLD-	LOIFNVSY	RLCGRI	OGGELORFDAY	YLHNKCLCGAP	LQ-SCK	306
BnPGIP3	FGAK-	-TTQHID	.srnmfqfni	SK <mark>V</mark> -KVAKTVNF	LDLNH <mark>N</mark> SLT	GSI <mark>P</mark> VQWTQLD-	LQTFNVSY	RLCGRIE	Q <mark>GGDLQ</mark> RFDAYE	YLH <mark>NKCLC</mark> DAP	LQ-SCK	306
BrPGIP3	FGAK-F	C-TTQHIDL	SRNMFQFNI	SKV-KVAKTVNF	LDLNHNSLT	GSIPVQWTQLD-	LQTFNVSY	RLCGRI	QGGDLQRFDAY	YLHNKCLCDAP	LQ-SCK	306
BrPGIP15 BrPGIP8	FGAK-F	-TSWSVDL	SRNKLOFDI	SKV-KVATTVHN	LDLNHNRIT	GGIPVQWTELT- GSIPVOWTELT-	LOSFNVSY	RLCGRI	OGGDLOIFDAY	YLHNKCLCGAP	LO-SCN	307
EsPGIP2	FGAN-F	-TTWSID	.srnmfqfdl	sk <mark>v</mark> -kvaktvnq	<mark>LD</mark> LNH <mark>N</mark> GIT	GNIPVQWTELS-	LQSFNVSY	RLCGRIE	K <mark>GG</mark> DLQRFDSY	YLH <mark>NKCLCG</mark> AP	LQ-SCK	306
BnPGIP6	FGTN-F	-KTWTIDL	SRNMFQFDI	SKV-KV-AKTVNL	LDLNHNGIT	GSIPVQWTELS-	LQSFNVSYN	RLCGPI	KGGQLQRDGAY	YLHNKCLCGAP	LQ-RCK	306
BnPGIP8	FGTN-F	-KTWTIDI	SRNMFOFDI	SKV-KVAKTVNL	LDLNHNGIT	GSIPVQWTELS-	LOSENVSI	RLCGPII	KGGQLQRDGAI	YLHNKCLCGAP	LO-BCK	307
BnPGIP9	FGAN-F	-TTFSID	.SRNIFQFDL	SR <mark>V</mark> -VLHESLGV	LDLNHNGIT	GSIPVQWTEYS-	LQILNVSY	RLCGPIE	TGGSLQRFDSY1	YFH <mark>NKCLCG</mark> AP	LDSSCK	307
BrPGIP5	FGAN-F	C-TTFSIDL	SRNIFQFDL	SR <mark>V</mark> -VLHESLGV	LDLNHNGIT	GSIPVQWTEYS-	LQILNVSY	RLCGPII	TGGSLQRFDSY1	YFHNKCLCGAP	LDSSCK	307
BrPGIP9	FGAN-P	C-TTFSIDL	SRNMFQFDL	SRV-VLPESLGV	LDLNHNGIT	GSIPVQWTEYS-	LOLLNVSYN	RLCGPIE	TGGSLQRFDSY	YFHNKCLCGAP		306
BnPGIP12 BnPGIP16	FGAN-F	-TTFSID	SRNMFQFDL	SR <mark>V</mark> -EIPKTFGI	LDLNHNGIT	GSIPVQWTETP-	FQIFNVSY	RLCGRI	TGGKLQMFDSY	YFHNKCLCGAP	LDSSCK	307
BrPGIP4	FGAN-F	C-TTFSID	.SRNMFQFDL	SR <mark>V</mark> -EIPKTFGI	<mark>ld</mark> lnh <mark>n</mark> git	GSI <mark>P</mark> VQWTETP-	FQIF <mark>NVS</mark> Y	RLCGRIE	T <mark>GG</mark> K <mark>LQ</mark> MFDSY#	YFH <mark>NKCLCG</mark> AP	LD-SCK	306
LaPGIP3	FGTK-P	-TTWSINL	SRNKFQFDL	SKV-MLAKTINQ	LDLNHNDIT MDLNHNGIT	GTIPVQWTKSQ-	FQSFNVSY	RLCGPIE	QGGDLQRFDSYS	SYFHNKCLCGAP	LP-SCK	304
AtPGIP2	FGAK-	-TTWIVDI	SRNMFQFDL	SKV-KL-AKTLNN	LDMNHNGIT	GSIPAEWSKAY-	FQLLNVSY	RLCGRIE	KGEYIQRFDSYS	SFFHNKCLCGAP	LP-SCK	306
CrPGIP2	FG <mark>AK-</mark>	C-TTWILDI	SRNMFQFDL	SK <mark>V</mark> -KLAKTLNN	<mark>LD</mark> MNH <mark>N</mark> RIT	<mark>g</mark> gi <mark>p</mark> aewskay-	FQLL <mark>N</mark> V <mark>S</mark> Y	IRLCGRII	R <mark>G</mark> EYIQRFDSYS	SFLH <mark>NKCLCG</mark> AP	LP-S <mark>C</mark> K	306
CSPGIP3	FGAK-F	-TTWIVDI	SRNMFEFDL	SKV-KL-AKSLTR TEV-KI-SKTLSI	LDLNHNRIT VDLNHNGIT	GSIPAEWSKSE-	FQLLDVSY	IRLCGRI	KGENIORFDSTE SECTLOKIDSSS	SFYHNKCLCGAP	LP-SCK	306
SirPGIPS SirPGIP2	IGTN-	-TTPDIDL	SRNMLQFNL	SKV-NISRTLSH	LDLNHNKIT	GNIPAQWTEGS-	LRSLNVSY	RLCGRIE	TGENLORLDMYS	SYFH <mark>NKCLCG</mark> PP	LE-SCK	305
AdPGIP1	FGSN-F	-TIQIVDF	SRNKFQFDL	SK <mark>V</mark> -VFPQSLTS	<mark>LD</mark> LNH <mark>N</mark> KIY	<mark>G</mark> SL <mark>P</mark> VGLTKLD-	LQYL <mark>NVS</mark> Y	RLCGHI	T <mark>GG</mark> K <mark>LQ</mark> GFDQTS	SYFH <mark>NRCLCG</mark> AP	LP-DCK	304
EgPGIP1	FGEN-F	-TVQIVDI	SRNMLEFDL	TKV-EFPASLSS	LDVNHNRIT	GNLPDELTQLN-	MQYLNVSYN		PIGGDLQSFDSYS	SYFHNKCLCGSP	LP-SCN	304
CaPGIP1 CaPGIP3	FGKN-	-TIQTIDE	SRNALEFDL	SKV-ELPESLTS	LDLNHNRIF	GSLPQGLKDLQ-	LQFFNVSY	IRLCGQII	QGGTLQTFDMYS	SYLHNKCLCGSP	LP-DCK	304
StPGIP1	FGKN-F	C-TSQIID <mark>I</mark>	SRNSLEFDI.	SKS-EFAESLIS	<mark>LD</mark> LNH <mark>N</mark> RIF	<mark>G</mark> SL <mark>P</mark> QGLKDVP-	LQFF <mark>NVS</mark> Y	IR <mark>LCG</mark> QII	Q <mark>GGTLQ</mark> SFDVYS	SYLH <mark>NKCLCG</mark> SP	LP-DCK	305
CcPGIP1	FGSN-F	C-TTWQIDI	SRNMFQFNL	SKV-EIPKSLSR	LDLNHNKIF	GSLPQALTGAE -	LQFLNVSYN		VGGQLQSFDYS1	YFHNRCLCGAP	LE-SCK	305
TCPGIP1	FGSK-	-TTREID	SRNMFQFDL	SKV-EFPKSLAR	LDLNHNKIM	GSIPPGLTGVD-	LQFMNVSY	IRLCGQII	VGGRLQSFDYY	YFHNRCLCGAP	LE-SCK	305
TcPGIP1	FGSK-F	-TTREID <mark>L</mark>	.SRNMFQFDL	SK <mark>V</mark> -EFPKSLAR	LDLNH <mark>N</mark> KIM	GNI PPGLTGVD -	LQFMNVSY	IRLCGQ I I	<mark>PVGGRLQ</mark> SFDYY1	YFH <mark>NRCLCG</mark> AP	LE-SCK	305
GrPGIP1	FGPN-F	C-TTFEIDL	SRNVFQFDL	SKV-QFPKSLAR	LDLNHNKIT	GSIPAGLTDLE-	LQFMNVSYN	RLCGQIE	VGGRLQSFDYS1	YFHNRCLCGAP		306
PCPGIP1	FGLN-F	-TTQIVDI	SRNLLEFNL	SKV-EFPTSLTS	LDINHNKIY	GSIPVEFTQLN-	FQFLNVSY	RLCGQIE	VGGKLQSFDEYS	SYFHNRCLCGAP	LP-SCK	304
PpPGIP1	FGFN-F	C-TTQIVD <mark>L</mark>	SRNLLEFNL	SK <mark>V</mark> -EFSKSLTA	LDLNH <mark>N</mark> KIT	GSI <mark>P</mark> VGLTQVD-	LQFL <mark>NVS</mark> YN	RLCGQIE	PV <mark>GG</mark> KLQSFDSS1	YIH <mark>NQCLCG</mark> AP	LP-S	302
MaPGIP1	FGSNK	C-MTQQVYL	SRNSFEFDL	SEV-EFPKSLIE	LDLSHNKIT	GSIPVGLTAVDY	LQGLNVSYN	RLCGKI	VGGALQGFDYTV	YFHNRCLCGSP	LMESCK	310
MnPGIP1 AaPGIP-like1	FGRN-F	-TTIRID	SRNKFEFDL	SK <mark>V</mark> -KFARSIVS	LNLSHNRIF	GKIPRELNELH-	LEQFNVSY	RLCGHI	TGGLLQTFEGNA	AFSNNLCLCGNP	LK-AC	302
FLOR1/AtPGIP-like1	FGRN-F	C-TTVRVD <mark>L</mark>	.SRNMFNFDL	-K <mark>V</mark> -KFARSIVS	LDLSQ <mark>N</mark> HIY	<mark>G</mark> KI <mark>P</mark> PALTKLH-	LEHFNVSD1	HLCGKI	S <mark>GGLLQ</mark> TFEPS	AFAH <mark>NICLCG</mark> TP	LK-AC	301
BnPGIP-like3	FGRN-F	C-TTIRLDL	SRNMFEFDL	SKV-KFARSIVS	LDLSHNKIS	GKFPRELTKLR-	LEHFNVSYN	HLCCKI	SGGLLQTFEPS	AFSHNLCLCGTP	LK-AC	302
BrafLORI/BrPGIP-11Kel BsPGIP-likel	FGRN-F	-TTIRVDL	SRNRFQFDL	SKV-KFARTIVS	LDLSQNRIF	GKLPRELSKLR-	LEHFNVSY	HLCGKI	SGGLLQTFEPS	AFSHNLCLCGSP	LK-AC	302
CrPGIP-like1	FGRN-F	-TTIRVD <mark>L</mark>	SRNLFQFDL.	SK <mark>V</mark> -KFARSIVS	LDLSQ <mark>N</mark> RIF	<mark>G</mark> KF <mark>P</mark> RELSKLR-	LEHF <mark>NVS</mark> Y	HLCGKII	S <mark>GG</mark> L <mark>LQ</mark> TFEPS	AFSH <mark>NLCLCG</mark> TP	LK-AC	302
CsPGIP-likel	FGRN-F	C-TTVRVDL	SRNLFQFDL	SKV-KFARSIVS	LDLSHNRIF	GKFPRELSKLR-	LENFNVSYN	HLCCKI	SGGLLQTFEPS	FAHNLCLCGTP	LK-AC	302
CsPGIP-like3	FGRN-F	-TTVRVDL	SRNLFQFDL	SKV-KFARSIVS	LDLSHNRIF	GKFPRELSKLR-	LENFNVSY	HLCGKI	SGGLLQTFEPS	FAHNLCLCGTP	LK-AC	302
EsPGIP-like2	FGRN-F	C-TTVRVD <mark>L</mark>	SRNMFQFDL	SK <mark>V</mark> -KFARSIVS	<mark>ld</mark> lsk <mark>n</mark> rif	<mark>G</mark> KF <mark>P</mark> RELSKLR-	LEHF <mark>NVS</mark> YN	RLCGKI	R <mark>GGLLQ</mark> TFEPS#	AFSH <mark>NLCLCG</mark> TP	LK-AC	302
CrPGIP-like3	FGRN-F	C-TTIQVDL	SRNKFQFDL	SKV-KFARSILT	LDLSQNQIF	GKIPQQLTNLR-	LERFNVSYN	RLCGKI	RGGFLQTSEPS	AFSHNLCLCGIP		278
CSPGIP-like4 BnPGIP-like7	FGRN-F	-STVSLDL	SRNMFEFDL	SKV-QFARGIVD	LDLSUNRIF	GSLPRELIELRG	LKLFNVSH	RLCGKI	RGGLLQSFKSYV	FAHNRCLCGAP	LK-AC	303
BnPGIP-like9	FGRN-F	C-STVSLD	SRNMFEFDL	SK <mark>V</mark> -QFARGIVD	<mark>LD</mark> LSH <mark>N</mark> RIF	<mark>GNLP</mark> RELIELRG	LKLFNVSH	RLCGKII	R <mark>GGLLQ</mark> SFKSYV	FAHNRCLCGTP	LK-AC	303
BrPGIP-like5	FGRN-F	-STVSLDL	SRNMFEFDL	SKV-QFARGIVD	LDLSHNRIF	GNLPRELIELRG	LEBENTSYN	RLCGKI	RGGLLQSFKSY	FAENRCLCGTP	LKKAC	303
BnPGIP-like6	FGGN-F	-RTVQLD	SRNLFEFDL	SK <mark>V</mark> -KFGKSMAL	LDLSHNRIF	GTLPRELTELR-	LERFNISY	RLCGKI	R <mark>GGQLQ</mark> TFKSYP	FAENRCLCGSP	LKKAC	303
BrPGIP-like3	FGGN-F	-RTVQLD	SRNLFEFDL	SKV-KFGKSMAL	LDLSNNRIF	GTLPRELTELR-	LERFNISY	RLCGKI	R <mark>GG</mark> Q <mark>LQ</mark> TFKSYE	FAENRCLCGSP	LKKAC	303
BnPGIP-like2	FGGN-F	-RTVQVDL	SRNLFEFDL	SKI-KFGKSLAM	LDLSHNRIF	GTLPRELTQLH-	LERFNISY	RLCGKI	RGGOLOTFKSYF	FAENRCLCGSP	LKKAC	303
BnPGIP-like4	FGGN-F	-RTVQVD	SRNKFEFDL	SKV-KFGKSMAL	LDLSHNRIF	GKLPRELTELP-	LQRFNISY	RLCGKI	R <mark>GG</mark> K <mark>LQ</mark> TFKSYF	FAHNRCLCGSP	LKKAC	303
BnPGIP-like8	FGGN-F	-RTVQVD	SRNKFEFDL	SKV-KFGKSMAL	LDLSHNRIF	GKLPRELTELH-	LQRFNISY	RLCGKII	RGGKLQTFKSYF	FAHNRCLCGSP	LKKAC	303
BrPGIP-like4	FGHN-F	C-RTVQVDL C-TTVRLDL	SRNKFEFDL	SKV-KFGKSMAL	LDLSHNRIF	GKLPRELTELH-	LNOFNIST	RLCGKI	OGGLIONFGVYF	FAHNRCLCGSP FSNNLCLCGAP	LKKAC	303
CrPGIP-like2	FGRN-	-TTVTLD	SRNNFHFNL	SKV-KLAKSLVS	LDLSHNRIF	GELPLELTNLR-	LDHFNVSF	RLCGST	Q <mark>GG</mark> R <mark>LQ</mark> SFEVYE	FSNNLCLCG TP	LE-RC	299
EsPGIP-like1	FGHN-F	R-TTVRLDL	SRNNFHFDL	SKV-KLAKSLVS	LDLSHNRVF	GELPLELTKLR-	LDHFNISFN	RLCGTI	20 <mark>GGLLQ</mark> NFEVYE	FSNNLCLCGAP	LQ-RC	302
AFP GmPGTP1	FGPR-F	-HTERIYL	ANNLFAFDL	GKV-RLSKTLGL	LDVGHNLIY	GTLPKGLTSLKD	LYYLDVSY	INLCGRI	RGGKLOEFDASI	YANNKCLCGSP	LP-SCKRF	304
GmPGIP2	FGSE-F	-RTEMIY <mark>L</mark>	AHNLFAFDF	GK <mark>V</mark> -RVPKVLDS	<mark>LD</mark> VGH <mark>N</mark> RLY	<mark>G</mark> TL <mark>P</mark> KGLTSLKN	LYRFDV <mark>S</mark> Y	KLCGEIF	R <mark>GG</mark> K <mark>LQ</mark> EIDESH	YAN <mark>NKCLCG</mark> SP	LP-S <mark>C</mark> KRF	313
GmPGIP5	FGSE-F	-HTRHMYL	GNNSFAFDL	GKL-GLSKTLEG	LDLSHNRLY	GTLPKGLTSLKD	LYYLDVSY	INLCGKIE	RGGKLQEFDAST	YAHNKCLCGSP	LP-SCKRF	312
GmPGIP/ GmPGIP3	FGTE-F	-NTQKILL	AKNMLAFDL	GKV-GLSKNLNG	LDLRNNRIY	GTLPQGLTALKF	LHSFNVSF	DLCGEI	QGGNMQRFDVSS	YANNKCLCGSP	LP-PCT	- 313
PvPGIP1	FGSD-	-NTKKIH <mark>L</mark>	AKNSLAFDL	GK <mark>V</mark> -GLSKNLNG	LD LRNNRIY	<mark>gtlp</mark> qgltqlkf	LQSLNVSF	NLCGEII	Q <mark>GGNL</mark> KRFDVSS	YANNKCLCGSP	LP-S <mark>C</mark> T	311
PvPGIP2	FGSD-F	-NTQKIHL	AKNSLAFDL	GKN-GLSKNLNG	LDLRNNRIY	GTL PQGLTQLKF	LHSLNVSF		QGGNLORFDVSI	YANNKCLCGSP	LP-ACT	311
PVPGIP3 PVPGIP4	FGAN-F	-NLRKIDL	AKNLLAFDL	GKI-SL-RSKNLEG	LDLRKNRIY	GTLPKVLTSLKY	LRTLNVSY	NLCGQII	QGGKLQRFSEY	YAHNKCLCGSP	LP-PCT	312
GmPGIP4	FGSE-	-DTVQIN <mark>I</mark>	GKNNLAFDL	GK <mark>V</mark> -EFSEILAI	LD LRHNRIY	<mark>gtlp</mark> qgltalkh	LTKLNVSN	NLCGEI	Q <mark>GGNLQ</mark> RIKVNS	SYAHNK <mark>CLCG</mark> SP	LP-ACTLV	-N 314
BdPGIP1	FGAV-F	-PLQYLDV	SRNAVNENM	SSV-EFPVQLSY	VDLSHNAIR	GSVPMQVASLTG	LODENVSEN	RLCGTV	TGGNMAKFDRYS	SYLHNKCLCGTP	LT-ACRORPIN	NRN 313
ZmPGIP1	FGRA-	-PVQQMDL	SRNAFSFNL	SAV-ELPEQLNS	LDLSHNAIY	GGI PGQVVNLTN	LQLFKVSY	RLWGAVI	PGGNMGSFDAYS	SFQHNRCLCGPP	LADPCK	310
OsPGIP2	FRRA-F	RYVDI	SRNGFVFNM	SG <mark>V</mark> -EFAEETYY	VD VSH <mark>N</mark> AIR	GGI PAQAANLTN	LQTFNV <mark>S</mark> YI	KMCGAV	AMPRFDAYC	YQH <mark>NKCLCG</mark> AP	LATACRRR	309
TaPGIP1	FGRT-F	-ELESINL	SHIALSFDL	SSV-EFPEEMQA	MDASYNAIR	GGI PAQVANVTN	LRQFNVSYN		AALARLDVYN	FOR A CLCGAP	PDPCKK	306
OsFOR1/OsPGIP=like1	FAAG-H	R-PIGKVDL	SWNDLDFDL	SKL-VFPPELTY	LDLSHNRIR	GTVPRSLAALST	LQTLDLSY	RLCGPLI	RLHGVIRHGCKI	YEHNOCAGGAP	LG-GCHQS	306
Plant-specific LPPs	LGYL-		XXNXITCHT	Par-LG	LYLYNNT	GYTPYYLCYL	LXXLXLX	IXI.TCYT	YYLGYL VYL VY			
Franc Sheering RWVS	~~~~~	· • • • • • • • • • • • • • • • • • • •		X D X D X		CUTE VURGETXX				4		
	LRF	۲7 .		LRR8		LRR9		LF	RR10			

Supplementary Figure 2: Alignment of PGIPs and PGIP-like proteins. Conserved amino acid residues above 80% identity are highlighted in blue. Leucine-rich repeats (LRRs) were displayed below as reported by Leckie *et al.* (1999) for PvPGIP2 from *Phaseolus vulgaris* (highlighted in red). For full sequences, see Supplementary Table 3.



Supplementary Figure 3: Predicted functional classes from *B. rapa* ssp. *pekinensis* cell wall proteins (CWPs). The annotation of proteins is based on the presence of functional domains predicted by InterPro, GO Term and BLAST bioinformatics analysis. Analysis includes only proteins that possess a signal peptide for the secretory pathway according to SignalP and were predicted to be localized extracellularly by DeepLoc analysis. For a full list of identified proteins, see Supplementary Table 4.



Supplementary Figure 4: Binding of *P. cochleariae* PG family members PCO_GH28-1 and -3 to pectic substrates. Culture medium containing PCO_GH28-1 and -3 (M) was incubated with cross-linked pectin (CLP) and methylated CLP (mCLP), respectively. Centrifugation separated the pectin pellet and associated proteins (P) from the supernatant (S). Unbound proteins were removed from the pellet by washing (W). The volumes applied to the western blot were chosen in such a way that the cumulative signals of S, W and P correspond to the initially used amount of M. The PG family members were detected in a western blot with an anti-V5 antibody. The additional bands below the PCO_GH28-1 signal in the western blot were analyzed by LC-MS/MS and assigned to fragments of the PG, which occur as an artefact of the sample boiling for SDS-PAGE (Supplementary Figure 1, Supplementary Table 2).



Supplementary Figure 5: SDS-PAGE of pull-down assay of *B. rapa* ssp. *pekinensis* CWPs with an empty column (negative control). Non-treated (nt) CWP extracts were pre-treated (pt) with column resin to reduce unspecific binding to the column and then passed over columns without immobilized protein. Proteins not interacting with the column material were in the flow-through (ft), while interacting proteins were eluted from the column analogous to the PG family member columns. Elution fraction E1 was analyzed by LC-MS/MS. For detailed information on interacting LRR and total proteins, see Supplementary Table 6. E0 - 4: elution fractions 1 - 4.

Α

BrPGIP1_BRA_Chifu-401-42 BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop BrPGIP3_BRA_Chifu-401-42 BrPGIP7_BRA_Chifu-401-42 BnPGIP14_BNA

BrPGIP1_BRA_Chifu-401-42 BrPGIP_FGIP1.1_BRA_Cantonner_Witkrop BrPGIP3_BRA_Chifu-401-42 BrPGIP7_BRA_Chifu-401-42 BnPGIP14_BNA

BrPGIP1_BRA_Chifu-401-42 BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop BrPGIP3_BRA_Chifu-401-42 BrPGIP7_BRA_Chifu-401-42 BnPGIP14_14_BNA

BrPGIP1_BRA_Chitu-401-42 BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop BrPGIP3_BRA_Chifu-401-42 BrPGIP7_BRA_Chifu-401-42 BnPGIP14_BNA

BrPGIP1_BRA_Chifu-401-42 BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop BrPGIP3_BRA_Chifu-401-42 BrPGIP7_BRA_Chifu-401-42 BnPGIP14_BNA

BrPGIP1_BRA_Chifu-401-42 BrPGIP_PGIP1.1_BRA_Cantonner_Witkrop BrPGIP3_BRA_Chifu-401-42 BrPGIP7_BRA_Chifu-401-42 BnPGIP14_BNA

	10	20	30	40	50	6(
MG-KTT MG-KTT MEGKTT MD-KTT	ILLLLFA) ILLLLFA) ILLLLFA) ILLLLFA)	LLLTTSLSKD: LLLTTSLSKD: LLLTTSLSKD: LLLTTSLSKD:	LCHKDDKNTL LCHKDDKNTL LCHKDDKNTL LCHKDDKNTL	LKIKKAMNDP LKIKKAMNDP LKIKKAMNDP LKIKKAMNDP	YTIISWDPKD Y SWDPKD YTIISWDPKD YTIISWDPK <mark>K</mark>	DCCTWY DCCTWY DCCTWY DCCTWY
MG KTT	LUTTTELEA	LLLTTSLSKD.	LCHKDDKNTL	LKIKKAMNDP	YTIISWDPKD	DCCTWY
	70	80	90	100	110	12
SVECGN SVECGN AVECGN AVECGN SVECGN	ANRVTS ANRVTS ASINHRVTS ATINHRVTS ANRVTS	SLDLSDDDVS SLDLSDDDVS SLDI SNDDVS SLDI SNDDVS SLDLSDDDVS	AQIPPEVGDL AQIPPEVGDL QIPPEVGDL AQIPPEVGDL AQIPPEVGDL	PYLQYLTFRK PYLQYLTFRK PYLDYLIFHK PYLDYLIFHK PYLQYLTFRK	LPNLTGEIPP LPNLTGEIPP LPNLTGEIPP LPNLTGEIPP LPNLTGEIPP	TIAKLY TIAKLY TI <mark>T</mark> KLY TIAKLY TIAKLY
	130	140	150	160	170	18
YLKSLW YLKSLW YL <mark>RY</mark> LW YL <mark>RN</mark> LW YLKSLW	LSWNSLIGI LSWNSLTGI LSWNNLSGI LHWNNLTGI LSWNSLTGI	PVPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI	nleyinlsfn nleyinlsfn nleyinlsfn nl <mark>g</mark> yi <mark>ð</mark> lsfn nleyinlsfn	KLSGSIPGSL KLSGSIPGSL LSGSIPGSL KLSGSIPGSL	SLLPKLDFLE SLLPKL <mark>E</mark> FLE SLLPKL <mark>ET</mark> LD SLLPKLDFLE	LSRNKI LSRNKI LSRNKI LSRNKI
YLKSLW YLKSLW YL <mark>RY</mark> LW YL <mark>RN</mark> LW YLKSLW	LSWNSLTGJ LSWNSLTGJ LSWN <mark>NLS</mark> GJ LHWNNLTGJ LSWNSLTGJ	PVPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI	NLEYINLSFN NLEYINLSFN NLQYIDLSFN NLQYIDLSFN NLEYINLSFN	KLSGSIPGSL KLSGSIPGSL DLSGSIPGSL KLSGSIPGSL	SLLPKLDFLE SLLPKL <mark>E</mark> FLE SLLPKL <mark>EI</mark> LD SLLPKLDFLE	LSRNKI LSRNKI LSRNKI LSRNKI
YLKSLW YLKSLW YLRYLW YIRNLW YLKSLW TGPIPE TGSIPE TGSIPE	LSWNSLIG LSWNSLIG LSWNNLIG LSWNSLIG LSWNSLIG SFGSFKRI SFGSFKRI SFGSFKRI SFGSFKGV	VPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI 200 VYGIYLSHNQ VYGIYLSHNQ YYAIYLSINQ YALFLSHNQ	NLEYINLSFN NLEYINLSFN NLEYINLSFN NLEYINLSFN LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG LSGSIPK <mark>SLG</mark>	KLSGSIPGSL KLSGSIPGSL LSGSIPGSL 220 NIDENTIDLS NIDENTIDLS NLDINQIDLS NLDINQIDLS	SLIPKLDFLE SLIPKLDFLE SLIPKLDFLE 230 RNKLEGDASM RNKLEGDASM RNKLEGDASM	LSRNKI LSRNKI LSRNKI 24 LFGVKK LFGTKK LFGTKK LFGAKK
YLKSLW YLKSLW YLRNLW YLRNLW YLKSLW TGPIPE TGPIPE TGSIPE TGSIPE	LSWNSLIG LSWNSLIG LSWNNLG LSWNSLIG LSWNSLIG SFGSFKRA SFGSFKRA SFGSFKRA SFGSFKRA SFGSFKRA	VPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI PVPEFLSQLKI 200 VYGIYLSHNQ: VYGIYLSHNQ: VYGIYLSHNQ: VYGIYLSHNQ:	NLEYINLSFN NLEYINLSFN NLEYINLSFN NLEYINLSFN LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG	KLSGSIPGSL KLSGSIPGSL LSGSIPGSL 220 NIDENTIDLS NIDENTIDLS NIDINQIDLS NIDINQIDLS	SLLPKLDFLE SLLPKLDFLE SLLPKLDFLE 230 RNKLEGDASM RNKLEGDASM RNKLEGDASM	LSRNKI LSRNKI LSRNKI LSRNKI LFGVKK LFGRKK LFGRKK LFGACK
YLKSLW YLKSLW YLRYLW YIRNLW YLKSLW TGPIPE TGPIPE TGSIPE TGSIPE	LSWNSLIG LSWNSLIG LSWNNLG LSWNNLIG LSWNSLIG SFGSFKR SFGSFKR SFGSFKR SFGSFKR SFGSFKR SFGSFKR SFGSFKR	200 200 200 200 200 200 200 200 200 200	NLEYINLSFN NLEYINLSFN NLEYINLSFN NLEYINLSFN 210 LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG	KLSGSIPGSL KLSGSIPGSL LSGSIPGSL 220 NIDENTIDLS NIDENTIDLS NIDENTIDLS NIDENTIDLS NIDENTIDLS NIDENTIDLS	230 RNKLEGDASM RNKLEGDASM RNKLEGDASM RNKLEGDASM	LSRNKI LSRNKI LSRNKI LSRNKI 24 LFGVKI LFGQKI LFGAQI LFGAQI LFGAQI
YLKSLW YLKSLW YLRYLW YIRYLW YLRNLW YLKSLW TGPIPE TGSIPE TGSIPE TGSIPE TGSIPE TTWHID TTWHID TTOHID TTOHID TTHNID	LSWNSLTG LSWNSLTG LSWNNLGJ LSWNNLTGJ LSWNSLTGJ SFGSFKR SFGSFKR SFGSFKR 250 LSRNMFQF LSRNMFQF LSRNMFQFT LSRNMFQFT	VPEFLSQLKI VPEFLSQLKI VPEFLSQLKI 200 VYGIYLSHNQ: VYGIYLSHNQ: VYGIYLSHNQ: VYGIYLSHNQ: VYGIYLSHNQ: ISKVKVAKT ISKVKVAKT ISKVKVAKT ISVKVSKT ISVKVSKT	NLEYINLSFN NLEYINLSFN NLEYINLSFN NLEYINLSFN 210 250 LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG LSGSIPKSLG UNFLDLNHNG VNFLDLNHNS VNFLDLNHNS VNFLLLNHNG VNFLLLNHNG	KLSGSIPGSL KLSGSIPGSL KLSGSIPGSL LSGSIPGSL LSGSIPGSL LSGSIPGSL LSGSIPGSL LSGSIPGSL LSGSIPGUT LSGSIPGUT LSGSIPGUT LSGIPGUT LSGIPGUT LSGIPGUT	230 RNKLEGDASM RNKLEGDASM RNKLEGDASM RNKLEGDASM RNKLEGDASM RNKLEGDASM QLDLQTFNVS QLDLQTFNVS QLDLQTFNVS QLDLQTFNVS QLDLQTFNVS	LSRNK: LSRNK: LSRNK: LSRNK: LSRNK: LFGVKI LFGQKI LFGAGI LFGAGI LFGAGI SG YNRLCC YNRLCC YNRLCC YNRLCC

RIPQGGDLQ<mark>I</mark>FDAYAYLHNKCLCGAPL<mark>E</mark>SC<mark>NVKIQATDLYLNLPSE</mark> RIPQGGDLQRFDAYAYLHNKCLC<mark>D</mark>APLQSCK RIPQGG<mark>E</mark>LQRFDAYAYLHNKCLCGAPLQSCK RIPQGG<mark>E</mark>LQRFDAYAYLHNKCLCGAPLQSCK

В	10	20	30	40	50	60
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42 BrPGIP_like1_BRA_Cantonner_Witkrop	MKLLLHLSIFFTIL MKLLLHLSIFFTIL	FISLPSSHSS FISLPSSHSS	SSNDKNALLQ SSNDKNALLQ	IKKALNNPPL IKKALNNPPL	LSSWNPQTDF	CTTWTG CTTWTG
PREDICTED:PG_inhibitor_1-like_BOL	MILLLHLSIFFTIL	FISLPSSHSS	SSNDKNALLQ	IKKALNNPPL	LSSWNPQT <mark>N</mark> F	CTTWTG
	70	80	90	100	110	120
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42	VECTNGRVTALTIS	SGEISGQIPA	QVGDLLELRT	LDFSYLTHLT	GNIPHTITKL	KYLDLL
PREDICTED:PG_inhibitor_1-like_BOL	VECTNGRVIALTIS	SGEISGQIPA	QVGDLLELRI QVGDLLELRI	LDFSYLTHLT	GNIPHTITKL	KYLDLL
	130	140	150	160	170	180
BrFGIP-like1/Bra-FLOR1_BRA_Chifu-401-42 BrFGIP_like1_BRA_Cantonner_Witkrop PREDICTED:PG_inhibitor_1-like_BOL	RLKQTNLSCYIPDF RLKQTNLSGYIPDF RLKQTNLSGYIPDF	ISELKSVTFL ISELKSVTFL ISELKSVTFL	DLSFNQFTCP DLSFNQFTGP DLSFNQFTGP	IPCSLSQMPK IPGSLSQMPK IPGSLSQMPK	LDAIQINDNK LDAIQINDNK L <mark>G</mark> A <mark>I</mark> QINDNK	LTCSIP LTGSIP LTGSIP
	190	200	210	220	230	240
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42	NSFGSFVGKVPNLY	LFNNKLSGKV	PESLSKYDFN	AVDLSGNSFT	GDGSMFFGRN	KTTIRV
BrPGIP_like1_BRA_Cantonner_Witkrop PREDICTED:PG_inhibitor_1-like_BOL	NSFGSFVGKVPNLY NSFGSFVG <mark>T</mark> VPNLY	LFNNKLSGKV LFNNKLSGKV	PESLSKYDFN PESLSKYDFN	AVDLSGNSFT AVDLSGNSF <mark>T</mark>	GDGSMFFGRN. GDGS <mark>V</mark> FFGRN:	KTTIRV KTTIRV
	250	260	270	280	290	300
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42 BrPGIP_like1_BRA_Cantonner_Witkrop	DLSRNMFEFDLSKV DLSRNMFEFDLSKV	KFARSIVSLD KFARSIVSLD	LSHNKIFGKF LSHNKIFGKF	PRELNKLRLE PRELNKLRLE	HFNVSYNHLC HFNVSYNHLC	GKIPSG GKIPSG
PREDICTED:PG_inhibitor_1-like_BOL	DLSRNMFEFDLSKV	KFARSIVSLD	lshnki <mark>s</mark> gkf	PREL <mark>T</mark> KLRLE	HFNVSYNHLC	GKIPSG
	310	320	_			
BrPGIP-like1/Bra-FLOR1_BRA_Chifu-401-42	GLLQTFEPSAFSHN	LCLCGTPLKA	С			

GLLQTFEPSAFSHNLCLCGTPLKAC GLLQTFEPSAFSHNLCLCGTPLKAC

BrPGIP-likel/Bra-FLOR1_BRA_Chifu-401-4 BrPGIP_likel_BRA_Cantonner_Witkrop PREDICTED:PG_inhibitor_1-like_BOL

C	10	20	30	40	50	60
BrPGIP-like5/FLOR1_BRA_Chifu-401-42 BrPGIP_like5_BRA_Cantonner_Witkrop unnamed_protein_product_BRA_Z1	MKLLLHLSIFFAIL MKLLLHLSIFFAIL MKLLLHLSIFFAIL	FISLPSSYSC FISLPSSYSC FISLPSSYSC	NSVEKNALLQ NSVEKNALLQ NSVEKNALLQ	IKKSFNNPRKI IKKSFNNPRKI IKKSFNNPRKI	FSSWNPQTDCC FSSWNPQTDCC FSSWNPQTDCC	CTTWSG CTTWSG CTTWSG
BrPGIP-like5/FLOR1_BRA_Chifu-401-42 BrPGIP_like5_BRA_Cantonner_Witkrop unnamed_protein_product_BRA_Z1	70 VKCTNGRVTDLSLF VKCTNGRVTDLSLF VKCTNGRVTDLSLF	80 I SSKLYGQIPD SSKLYGQIPD SSKLYGQIPD	90 J QIGDLLELRS QIGDLLELRS QIGDLLELRS	100 I LFLTYLPHLTO LFLTYLPHLTO LFLTYLPHLTO	110 GNIPRTITKLE GNIPRTITKLE GNIPRTITKLE	120 KNL <mark>DS</mark> L KNLEYL KNLEYL
BrPGIP-like5/FLOR1_BRA_Chifu-401-42 BrPGIP_like5_Cantonner_Witkrop unnamed_protein_product_BRA_Z1	130 ILRHNNLSGPIPDN ILRHNNLSGPIPDN ILRHNNLSGPIPDN	140 IGELKKLRFL IGELKKLRFL IGELKKLRFL	150 J DLSYNQFTGP DLSYNQFTGP DLSYNOFTGP	160 IPGSLSQMPMI IPGSLSQMPMI IPGSLSOMPMI	170 LETIIVEHNKI LETIIVEHNKI LETIIVEHNKI	180 LTGSIP LTGSIP LTGSIP
BrPGIP-like5/FLOR1_BRA_Chifu-401-42 BrPGIP_like5_BRA_Cantonner_Witkrop unnamed_protein_product_BRA_Z1	190 NSFGSFVGEVPNLY NSFGSFVGEVPNLY NSFGSFVGEVPNLY	200 I LSNNKLSGNI LSNNKLSGNI LSNNKLSGNI	210 PESLSKNDFN PESLSKNDFN PESLSKNDFN	220 GVFLSKNSFT GVFLSKNSFT GVFLSKNSFT	230 GDGSMFFGRNI GDGSMFFGRNI GDGSMFFGRNI	240 KSTVSL KSTISL KSTVSL
BrPGIP-like5/FLOR1_BRA_Chifu-401-42 BrPGIP_like5_BRA_Cantonner_Witkrop unnamed_protein_product_BRA_Z1	250 DLSRNMFEFDLSKV DLSRNMFEFDLSKV DLSRNMFEFDLSKV	260 QFARGIVDLD QFARGIVDLD QFARGIVDLD	270 LSHNRIFGNL LSHNRIFGNL LSHNRIFGNL	280 PRELIELRGLJ PRELIELRGLJ	290 KLFNVSHNRLO KLFNVSHNRLO KLFNVSHNRLO	300 CGKIPR CGKIPR CGKIPR
BrPGIP-like5/FLOR1_BRA_Chifu-401-42 BrPGIP_like5_BRA_Cantonner_Witkrop unnamed_protein_product_BRA_Z1	310 GGLLQSFKSYVFAH GGLLQSFKSYVFAH GGLLQSFKSYVFAH	320 I NRCLCGTPLK NRCLCGTPLK NRCLCGTPLK	AC AC AC			

Supplementary Figure 6: Alignment of BrPGIPs and BrPGIP-like proteins with homologs from different B. rapa ssp. pekinensis cultivars and Brassica species. CWPs for the pulldown assay were obtained from the B. rapa ssp. pekinensis (BRA) cultivar "Cantonner Witkrop," while sequences for mass spectrometry and bioinformatic analyses were obtained from the NCBI database and originate from the "Chifu-401-42" cultivar. If the Mascot analyses resulted in hits other than from the "Chifu-401-42" sequences, we aligned those together with the sequences from "Cantonner Witkrop." Matching peptides from the Mascot analyses were marked in blue, amino acid differences were highlighted in black. A) For the hit BnPGIP14 (ABX46560.1) from B. napus (BNA), one peptide matched to BrPGIP1 and -1.1, while the second matched BrPGIP3 and -7. B) One amino acid difference between the detected peptide and the BrPGIP-like1 sequences resulted in the identification of the homologous "Predicted: polygalacturonase inhibitor-like1" (XP 013617122.1) from B. oleraceae var. oleracea (BOL). C) All peptides match perfectly with the hit "unnamed protein product" (VDC72802.1) from the B. rapa cultivar "Z1" and BrPGIP-like5 from "Cantonner Witkrop," but differ in one amino acid from the BrPGIP-like5/FLOR1 sequence (XP 009146639) from "Chifu-401-42." Altogether, we are confident that discrepancies resulted from cultivar-dependent or even individual-dependent amino acid differences and that the proteins we identified were BrPGIP1.1 and -3 as well as BrPGIP-like1 and -like5.



Supplementary Figure 7: Expression of *BrPGIPs* and *BrPGIP-like proteins* in untreated *B. rapa* ssp. *pekinensis.* The expression levels of the *BrPGIPs* and *BrPGIP-like proteins* were quantified by RT-qPCR, and transcript abundance was expressed as RNA molecules of the gene of interest (GOI) per 1000 RNA molecules of the reference gene *UBIQUITIN-CONJUGATING ENZYME 21 (UBC21).* Error bars indicate the standard error of the mean (SEM).



Supplementary Figure 8: Interaction assay of PCO_GH28-1, -2, -4, -5, -6, -8, -9 with BrPGIP-like1-containing culture medium. Culture medium from BrPGIP-like1-expressing (P-L1) as well as wild-type (WT) yeast was incubated with various *P. cochleariae* PG family members and cross-linked with formaldehyde. The PG family members were detected in a western blot with an anti-V5 antibody. Arrows indicate the expected size of PG family members (open arrowhead) and PG-PGIP complex (closed arrowhead).