

Table S1. Peptide sequences of 3-5 kDa peptide fraction ultrafiltrated from bromelain-hydrolyzed CGM with 4 h hydrolysis.

	RP-HPLC peak retention time	4.0 min	5.55 min	6.5 min	8.1 min	12.3 min	13.1 min	14.5 min	15.6 min	19.1 min	23.03 min	24.9 min	41.9 min	
Zein-16	Area%	21.1%	48.6%	10.6%	9.6%	80.2%	11.2%	23.3%	6.4%	45.0%	4.1%	8.5%	45.8	
	Coverage%	15.8%	16.4%	8.7%	8.2%	14.2%	19.1%	15.3%	12.6%	71.0%	69.9%	43.2%	22.4	
	Sequences	VALAL	GC	KVLIVALAL	MKVLII	RH	KVLIVALAL	VALAL	QQCC	MKVLII	KVLIVALAL	IVALAL	ASAASS	
		LALAASA	TP	FYLPP	QQ	CS	LALAA	QQF	ATY	SGGCGC	LALAASAASS	LALAASAASS	TS	
		FYM	VGSVGS		QP	LQ	GGCGC	GSCGVGSVGS	GVVL	TP	TSGGCGC	TSGGCGC	LPP	
		PPPFYL	RH		GELAA	QPQGELA	TP	PFLG	QQCC	PFHLPPPFYM	TP	PFHLPPPFYM	HRY	
		CH	CS			AQQLTA	QQCC	IR	QP	PPPFY	PFH	PPPFY	LTA	
		IR	GVVL				ATY		GELAA	SPC	YM	SVGS	PCNAAAG	
			GELA				GVVL			GSCGVGSVGS	PPPFYLPP	PFLG		
										PFLG	PW	CSPAATP		
										CVEFL	YP	YGSP		
										RH	PP	GL		
										PAATP	LSPC	PG		
								YGSP	GSCGVG	PCPCNA				
								CCH	IR					
								EPLHRY	EPLHRY					
								ATY	ATY					
								GVVL	GVVL					
								SFL	SFL					
								VA	ALM					
								LTA	AA					
								MCGL	VA					
								CPCNAAAGG	LTA					
								VYY						
Zein-19	Area%	26.3%	27.6%	17.8%	21.5%	75.2%	24.3%	56.6%	16.2%	35.4%	5.4%	5.9%	14.2	
	Coverage%	23.3%	8.8%	16.2%	26.7%	22.1%	13.1%	30.8%	12.5%	61.2%	76.5%	39.6%	10	
	Sequences	LLM	KIFSLLM	KIFSLLM	MATKIFSLLM	RLQQ	KIFSLLM	KIFSLL	KIFSLLM	CVAN	KVLIVALAL	IFSLLM	MATKIFSLL	
		LLM	LLALSTC	LLALSTC	LLALSTC	ASNIPLS	LLALSTC	LLALSTCVAN	LLALSTC	ATIFPQCSQA	LALAASAASS	LLALSTC	LLALSTC	
		LLPPYL	HIIGGAL	IFPQCS	PIASLLPP	AL	QLVL	ATIFPQC	AIAASNIPL	PIASLLPPY	TSGGCGCQTP	ATIFPQCSQA	PIASLLPP	
		PSII		QLVL	SIASI	SLVQ	LLPFY	AIAASNIPLS	ALAN	SIACICEN	PFH	PIASLLPPY		
		QQ		PL	IAASNIPL	RAQQL	HIIGGAL	AL	LSP	PALQPYR	YM	PSIIA		
AIAASNIP			FL	ALAN	NQVALAN		SLVQ		AIAASNIPLS	PPPFYLPPQ	LVQTI			

FNQLSTLN	TQQQ	LLPFN	QQILL	LSPYS	PL	QPQPWQYP	RAQQLQQLV
AYS	HIIGGAL	LAALNPAA	LAAANR	QQILL	LVQTI	PPQLSPCQQF	AAYLQQQLL
QQQQLLP		LPFVQ	LL	LLPFY	RAQQL	GSCGVGVS	PFSQLATA
SFL			QLQQLL	TLL	NQVALAN	PFLGQCV	PAAYL
TQQLP				QLQQLLP	LSPYSQQQQF	IRQV	QQQILLP
				HIIGGAL	LPFNQLSTLN	EPLHRYQATY	PAASY
					PAAYLQQQLL	GVVLSFLQQ	QQQHIIGGAL
					PFSQLATAYS	QP	
					QQQQLLPFNQ	ALM	
					LAAANRASFL	AAQVAQQLTA	
					TQQ	MCGLQLQQPG	
					TLL	PCPCNAAAGG	
					QLQQLLPFVQ	VY	

Glutenin	Area%	52.9%	46.6%	5.3%	20.2%	100.0%	11.2%	42.1%	5.9%	29.0%	5.8%	7.1%	12.1%
	Coverage%	39.9%	8.5%	4.0%	15.2%	24.2%	12.1%	20.2%	15.7%	63.2%	68.6%	29.6%	12.6%
	Sequences	VALAL	GVG	VLLVALAK	AL	HP	LAL	VLLVALA	HVPPP	LAASATS	LVALAL	AL	SATST
		LALAASATST	STPILG		LALAASATST	PH	LALAA	GTCGVG	QCC	HTSGGCG	LALAASATST	LALAASATST	HVPPP
		HTSG	QVA		PHP	CQQPH	QPP	STPILG	QL	PPVHLPPP	HTSGGCG	HTSGGCGC	SG
		PILG	GLLAA		CP	GVG	RP	PTA	SG	HVPPPVHLPP	CPC	VHLPPP	VA
		LRH			GLLAA	STPILG	QQCCQQL	TPYCSP	VA	PPCH	PHPS	HVPPPVHLPP	GLL
		CSPTA			GLLAA	RH	TPCPYAA	IFG	GLL	RP	GTCGVG	PPCHYP	IA
		PYCSP			TP	CS		VA	TAQ	PHP	STPILG	SP	LTA
		LRH				QS		GLLAA	LTA	CPC	CVE	GTCG	
		HRY				LR			TPCPYAA	PHPS	FIRH	VL	
		GLVL				QQQPQSG				GTCGVG	CSPT	SIL	
		VALAL				VA				STPILG	YA	SG	
		GLLAA				GLLAA				PTA	LTAMCGL		
		IA				LTA				TPYCSP	TPCPYAAAG		
		MCGL								LR			
		TPCPYAAAG								CC			
										IFGLVL			
										SIL			
										LLAA			
										IA			
										LTAMCGL			
										TPCPYAA			

Table S2. Peptide sequences of <1 kDa peptide fraction ultrafiltrated from ficin-hydrolyzed CGM with 4 h hydrolysis

	RP-HPLC peak retention time	4.1 min	6.4 min	12.9 min	14.2 min	15.9 min	17.5 min	19.3 min	19.9 min	21.7 min	23.03 min	41.9 min	51.3 min	
Zein-16	Area%	23.5%	44.5%	6.0%	9.2%	11.8%	3.9%	19.9%	20.7%	18.0%	13.4%	2.0%	14.0%	
	Coverage%	43.7%	18.6%	8.7%	51.9%	23.0%	67.2%	79.8%	65.0%	30.1%	31.7%	13.1%	60.7%	
	Sequences	KVLIVALAL	GCQTP	LTA	MKVLV	VLIVALAL	MKVLIVALAL	MKVLIVALAL	KVLIVALAL	KVLIVALAL	KVLIVALAL	AASAASS	SVGS	ALAASAASS
		LALAA	GQCVEF	MCGL	LPPPFYM	AASS	LALAASAASS	LALAAS	LALAASAASS	LALAASAASS	LALAASAASS	TS	PFLG	TSGGCGC
		GGCGCQTP	RHQCS	PG	PPPFYLPP	TSGGCGC	TSGGCG	TSGGCGCQTP	TSGGCGCQTP	TSG	GCQTP	QCSPAATP	LPPPFYM	
		PF	HQIRQ	PCP	GSCGVGVS	CQF	PFYM	PFHLPPPFYM	PFH	QPQPWQYPTQ	LPPQ	YGSPQC	CGVGSVGS	
		PPFYM	GVVLQS		PFLG	GSCGVGSCGS	PPF	PPF	FYM	PPQLS	PW		PFLGQCVEFL	
		PPFYM	QPQGELA		FL	PAATP	LPPQ	QLSPCQF	PPPFYLPP	GSPQCQ	YPTQ		RH	
		LPPQ			PHQCSPA	YG	QPQPWQYPTQ	GSCGVGSCGS	PW	HRY	PP		CSPAATP	
		GSCGVGVS			YGSP		PPQLSPCQF	PFLGQCVEFL	YPT	PCNAAAG	VGSVGS		YGSP	
		GQCVEF			AL		GSCGVGVS	RHQCSAATP	VGSVGS		HRYQ		AL	
		LQ			QCCHQIRQV		PFLGQCV	YGSPQCQ	PFLG		GVVL		QCCH	
		QQCC			EPLHRYQATY		GSPQCQAL	QQCCHQTRQV	CVE		PCNAAAG		PLHRY	
		QV			GVVLQSFLQ		QQCCHQIR	EPLHRYQATY	GSP				GELAA	
		EPLH			ALM		QSFLQ	GVVLQSFLQ	AL				AQQLTA	
		QATY			AA		QPQGELAA	QPQG	QQC				MCG	
		GVVLQSF			PCPCNA		CGLQLQQPG	TA	QV				PCNAAAG	
		LM					PCPCNAA	MCGLQLQQPG	EPLHRYQATY				VY	
		AAQV						PCPCNAAAGG	GVVL					
								VYY	SF					
								LAALM						
								QVA						
								QLTA						
								AA						
Zein-19	Area%	22.8%	52.0%	23.6%	9.6%	2.3%	2.8%	4.0%	3.2%	2.6%	8.6%	11.2%	12.2%	
	Coverage%	21.7%	20.0%	28.8%	55.8%	7.9%	61.7%	67.1%	52.9%	69.2%	20.0%	10.8%	29.6%	
	Sequences	MATKIFSLM	KIFSLLM	MATKIFSLM	KIFSLLM	KIFSLLM	IFSLLM	FSLLM	SLPPYL	TKIFSLLM	QSPAL	MATKIFSLM	SLLM	
		LLALSTC	LLALSTC	LLALSTC	LLALSTCVAN	LLALS	LLALSTCVAN	LLALSTCVAN	PSIIASICEN	LLALSTCV	ALAN	LLALSTC	LLALS	
		IFPQCS	AL	TIFPQC	ATIFPQC	AAANRAS	ATIFPQCSQA	ATIFPQCSQA	PALQP	PPYL	LSPYSQQQF	ATIFPQCSQA	ATIFPQCSQA	
		PIASLLPP	SLVQ	PIASLLPP	SIASI		PIASLLPPYL	PIASLLPPYL	SNIPLS	PSIIASICEN	FNQLSTLN		YRLQQ	
		QLVL	QLVL	QLVL	AIAASNIPLS		PSIIASICEN	PSIIASI	PLLFQQSPQL	PALQPYRLQQ	PAAAYLLQQ		AIAASNIPL	
		PLLN	PL	QQQL	PLLQQSPAL		PALQPYRLQQ	AIAASNIPLS	SLVQSLVQTI	AIAASNIPLS	QQQL		ALAN	
		LLPFYQ	QQILLPF	QQQL	SLVQS		AIAASNIPLS	PL	RAQQLQLVL	PLLQQSPAL	TQQQL		LSPYSQQ	
		HIIGAL	LLALSTC	LAALNP	NQLSTLN		PLLQQSPAL	PAL	PLINQVALAN	SLVQSLVQTI			FNQ	

QLQQLL	QQQLLP	PAAYL	SLVQSLV	SLVQSLVQTI	LSPYSQQQF	RAQQLQ	LAALNPA
HIIGGAL	HIIGGAL	PFSQLATAYS	PLINQVALAN	RAQQL	LPFNQLST	LVL	QILLPFSQ
		QQ	LSPYSQQQF	QF	QQQILLPFSQ	PLINQVALAN	ASFL
		LLPEN	LPPQQ	LPFNQLSTLN	LAAANR	LSPYSQQQF	TQQQ
		ALNPAAYL	PFSQLATAYS	PAAYLQQQLL	LQQLLPFVQ	LPFNQLST	
		QILLPFSQ	QQQQLLPEN	PFSQLATAYS	LALTDPAASY	QQQQLLPENQ	
		RASFL	NPATLL	QQQQLLPFNQ	QQHIIG	LAAL	
		TQQQLLPFYQ	QLQ	LAALNPAAYL		QILLPFSQ	
		QFAA	PFVQ	QQQILLPFSQ		LAAANRA	
		TLL	LALTDPAASY	AANPATLL		ATLL	
		QLQQLLPFVQ		QLQQLLPFVQ		QLQQLLPFVQ	
				LALTDPAAY		LALTDPAASY	
						QQHIIG	

Glutenin	Area%	35.4%	25.0%	28.2%	5.2%	3.0%	3.8%	24.8%	26.6%	7.0%	18.0%	10.0%	23.0%
	Coverage%	27.8%	5.8%	19.3%	19.3%	12.6%	71.3%	67.3%	84.8%	65.0%	27.4%	9.4%	28.3%
	Sequences	ALAL	PILGQC	AASATST	SATST	VLLVALAL	VLLVALAL	VLLVALAL	LLVALAL	MRVLLALAL	MRVLLALAL	VHLPPP	MRVLLV
		LALAA	QVA	HTSGGCGCQP	HTSGGCGCQP	LA	LA	LALAASATST	LALAASATST	LALAASATST	LAASATST	HVPPPVHL	VHLPPP
		QPP	GLLAA	PILGQC	PTA	TST	HLPPV	HTSGGCG	HTSGGCGCQP	HTSGGCGCQP	HTSGG	VCVE	HVPPPVHLPP
		QRPQ		IL	TPYCSPQCQS	HTSGG	HLPPVHLPP	PPVHLPPP	PPVHLPPP	PPVHLPPP	CHYPT	FLR	PPCH
		PQPHP		QVA	LR	QP	PVHLPPPVHL	HVPPPVHLPP	HLPPVHLPP	HLPPVHLPP	RP		SP
		CPC		GLLAA	QLR	PPPVHLPP	PPPVHLPPP	PSP	PVHLPPPVHL	PVHLPPPVHL	PHP		GTCGVG
		PILGQCVE		LTAMCGL	QVEP		VHLPP	CQLQGTGCVG	PPPVHLPPP	PPPVHLPPP	QGTGCVG		ST
		PYCSPQ			QVEPQHRY		PPCHYPTQPP	STPILGQCVE	HVPPVHLPP	ILGQCVE	STP		CVE
		QCCQQL					PC	FLRHQCSPTA	PPCHYPTQPP	FLR	QHRY		FLR
		QVA					QPHSP	TPYCSPQCQS	PQPHPQPHP	CSPQCQS	PYAAAGG		GLLAA
		GLLAA					GTCGVG	LRQQCCQLR	CPCQQPHSP	LRQQCC	VP		IA
		QPP					STPILG	QVEPQH	CQLQGTGCVG	QHRYQA			LTAMCG
		TPCPYAAA					CVE	QA	STPILGQCVE	IFGLVL			
							FLRHQCSPTA	IFGLVLQSIL	FLR	AQIAQQ			
							TPYCSPQCQS	QQQPQSGQVA	PTA	LTAMC			
							QQLR	GLLAAQIAQQ	TPYCSPQCQS	TPCPYAAAGG			
							QVEPQ	LTAMCGLQQP	LRQQCCQLR	VP			
							QA	TPCPYAA	QQQPQSGQVA				
							IFGLVLQSIL		GLLAAQIAQQ				
							QQQPQSG			LTAM			
							AQIAQQ			GLQQP			
							LTAMCGLQQP			TPCPY			
							TPCP			AAAG			

Table S3. Peptide sequences of 5-10 kDa peptide fraction ultrafiltrated from papain-hydrolyzed CGM wth 3 h hydrolysis

Compared peptides	RP-HPLC peak retention time	5.05 min	6.8 min	13.3 min	16.5 min	18.3 min	19.5 min	21.5 min	24.5 min	42.7 min	52.9 min	
Zein-16	Area%	11.1%	8.9%	17.6%	20.7%	2.3%	8.3%	37.1%	19.0%	20.5%	34.0%	
	Coverage%	47.5%	62.3%	43.2%	89.1%	42.6%	92.9%	98.4%	84.2%	18.6%	84.2%	
	Sequences	MKVLIVA	VALAL	KVLIVALAL	MKVLIVALAL	MKVLIVALAL	MKVLIVALAL	VLIVALAL	MKVLIVALAL	KVLIVALAL	VEFL	KVLIVALAL
		PPFYM	LALA	LALAASAA	LALAASAASS	HLPPFYM	LALAASAASS	LAL	LALAASAASS	PLHRY	PLHRY	LALAASAASS
		PPPFYLPQQ	GGCGCQTP	TSGGCGCQ	TSGGCGCQTP	PPPFYLPQQ	TSGGCGCQTP	SAASS	TSGGCGCQTP	FLQQ	FLQQ	TSGGCGCQTP
		QP	PF	PPPFYLPQQ	PF	QPQPW	PFHLPPFYM	TSGGCGCQTP	PFHLP	QPQGEA	QPQGEA	PFHLPPFYM
		PPQLSPCQF	PPPFYM	FLGQCVEFL	PPPFYLPQQ	PTQ	PPPFYLPQQ	PFHLPPFYM	QPWQYPTQ	QVAQQL	QVAQQL	PQQ
		GSCG	PPP	RYQATY	QYPTQ	PPQLSPCQF	QPQPWQYPTQ	PPPFYLPQQ	PPQLSPCQF	GLLQQL	GLLQQL	QPQPW
		PFLGQCVEFL	YLPPQQ	GVV	PPQLSPCQF	GSCG	PPQLSPCQF	PPQLSPCQF	QPQPWQYPTQ	GSCG	GSCG	LSPCQF
		RHQC	PQLSPCQF	QPQGEAALM	GSCG	PFLGQCVE	GSCG	PPQLSPCQF	PPQLSPCQF	PFLGQCVEFL	PFLGQCVEFL	GSCG
		EPLHRYQATY	GSCG	QLTA	PFLGQCVEF	TY	GQCVEFL	GSCG	GSCG	RHQC	RHQC	PFL
		GVVLSQFL	CSPAATP	LQQPG	HQCSPA	GVVLSQFL	RHQCSPAATP	PFLGQCVEFL	YGSPQCQALQ	YGSPQCQALQ	YGSPQCQALQ	CVEFL
		QLTA	YGSPQCQALQ	PCPCN	YGSPQCQALQ	PCPCNA	YGSPQCQALQ	RHQCSPAATP	QCCHQI	QCCHQI	QCCHQI	CSPAATP
		MCGLQLQPPG	QCCHQIRQV	QCC	QCC	PG	QCCHQIRQV	YGSPQCQALQ	HRYQATY	HRYQATY	HRYQATY	YGSPQCQALQ
		TQ	EPLHRYQATY	EPLHRYQATY	EPLHRYQATY	EPLHRYQATY	EPLHRYQATY	QCCHQIRQV	QCCHQIRQV	GVVLSQFLQ	GVVLSQFLQ	QCCHQIRQV
			AQVAQQLTA	GVVLSQFLQ	GVVLSQFLQ	GVVLSQFLQ	GVVLSQFLQ	EPLHRYQATY	EPLHRYQATY	QPQGEAALM	QPQGEAALM	EPLHRYQATY
			MCGLQLQPPG	QPQGEAALM	QPQGEAALM	QPQGEAALM	QPQGEAALM	GVVLSQFLQ	GVVLSQFLQ	AAQVAQQLTA	AAQVAQQLTA	GVVLSQFLQ
			PCN	AAQVAQQLTA	AAQVAQQLTA	AAQVAQQLTA	AAQVAQQLTA	QPQGEAALM	QPQGEAALM	MCGLQLQPPG	MCGLQLQPPG	QPQGEAALM
				MCGLQLQPPG	MCGLQLQPPG	MCGLQLQPPG	MCGLQLQPPG	AAQVAQQLTA	AAQVAQQLTA	PCPCNAAAG	PCPCNAAAG	AAQVAQQL
				PCPCNAAAG	PCPCNAAAG	PCPCNAAAG	PCPCNAAAG	MCGLQLQPPG	MCGLQLQPPG			GLLQQL
			QV	QV	QV	QV	PCPCNAAAG	PCPCNAAAG			PCPCNAAAG	
			VY	VY	VY	VY	VY	VY			VY	
Zein-19	Area%	11.3%	13.0%	25.5%	17.7%	1.2%	4.8%	13.6%	3.5%	31.3%	15.3%	
	Coverage%	27.9%	44.2%	34.6%	67.5%	11.2%	67.9%	93.3%	87.1%	17.5%	44.6%	
	Sequences	ATIFPQCSQA	KIFSLLM	KIFSLLM	MATKIFSLLM	IPLS	LLALSTCVAN	MATKIFSLLM	ATIFPQCSQA	MATKIFSLLM	MATKIFSLLM	LLALSTCVAN
		PIAS	LLALSTC	LLALSTC	LLALSTCVAN	PLL	ATIFPQCSQA	LLALSTCVAN	PIASLLPPYL	IAASNIPL	IAASNIPL	ATIFPQCSQA
		CEN	IASLLPPYL	PIASLLPPYL	ATIFP	LLPFYQ	PIASLLPPYL	ATIFPQCSQA	PSIIASICEN	ALAN	ALAN	PIASL
		PALQPYRLQ	PSTTA	PSIIAS	PIASLLPPYL	QFA	PSIIASICEN	PIASLLPPYL	PALQPYRLQ	LSP	LSP	RLQ
		NQLSTLN	LS	AL	PSIIASICEN	PATLL	PALQPYRLQ	PSIIASICEN	AIAASNIPLS	QQQF	QQQF	AIAA
		PAAYLQ	PLLFQ	SLVQSLVQTI	PALQPYRLQ	QLQQL	AIAASNIPLS	PALQPYRLQ	PLLFQSPAL	FNQ	FNQ	NIPLS
		LLPFYQ	SLVQSLVQTI	RAQQL	AIAASNIPLS		PLLFQ	AIAASNIPLS	SLVQSLVQTI	LAA	LAA	PLL
		QFAANPATLL	PLINQVA	QLVL	VQTI		RAQQLQQLVL	RAQQLQQLVL	PLLFQSPAL	RAQQLQQLVL	LAAANRA	VQSLVQTI
		QLQQL	QQQLL	QQILLPF	RAQQLQ		PLINQ	SLVQSLVQTI	PLINQVALAN	PLINQVALAN		RA
		LALT	PFSQL	LLPFYQ	QVALAN		SPYSQQQF	RAQQLQQLVL	LSPYSQQQF	LSPYSQQQF		PLINOVA
		FYQ	QQQLLQ	QQQLL	LSPYSQQQ		LPFNQLSTLN	PLINQVALAN	LPFNQLSTLN	LPFNQLSTLN		QQQF
			LAAL	HIIGGAL	LQQQLL		PAAYLQQQLL	LSP	PA	PA		QLLPENQ
			QQILLPFSQ	PL	FPSQLATA		QQQLLPENQ	QQQF	PFSQLATAYS	PFSQLATAYS		QQQILL
		QQQLLPFYQ	QF	AYL		LAALNPAAYL	LPFNQLSTLN	QQQLLPENQ	QQQLLPENQ		AANRASFL	
		QFAA	LL	QQILLPFS		ANRASFL	PAAYLQQQLL	PAAYL	PAAYL		TQQ	

QLLPF	NRASFL	TQQQLLP	FPSQLATAYS	QQQILLPFSQ	LLPFVQ
VL	TQQQLLPFYQ	ALLTDPAAASY	QQQQLLPENQ	LAALNPAAYL	LALTD
	QFAANP	QQHIIG	LAALNPAAYL	TQQQLLPFYQ	LAA
	QQLLPFVQ		QQQILLPFSQ	QFAANPATLL	LVL
	LALTDPAASY		LAALNPAAYL	QLQQLLPFVQ	YL
	QQHIIG		TQ	LALTDPAASY	
			LPFYQ	QQHIIGGALF	
			QFAANPATLL		
			QLQQL		
			LALTDPAASY		
			QQ		

Glutenin	Area%	23.4%	7.9%	27.4%	34.3%	10.9%	15.1%	32.2%	20.4%	10.5%	31.7%
	Coverage%	51.6%	89.2%	34.1%	80.0%	47.5%	69.1%	96.9%	76.7%	5.4%	77.1%
	Sequences	MRVLLVA	RVLLVALAL	MRVLLVALAL	MAAKIFSILM	AASATST	RVLLVALAL	RVLLVALAL	MAAKIFSILM	VE	VLLVALAL
		HTSGGCGCQP	LALAASATST	LALAA	LLALSACVLD	HTSGGCGCQP	LALAASATST	LALAASATST	LLALSACVLD	FLRH	LALAASATST
		PPPVHL	HTSG	TSGGCGCQ	ATIFPQYSQA	PP	HTSGGCGCQP	HTSGGCGCQP	HTSGGCGCQP	PQSGQVA	HTSGGCGCQP
		HP	CQP	HVPPP	PIAALL	VHLPPP	PPPVHLPPP	PPPVHLPPP	PPPVHLPPP		PP
		CPCQQPHSP	PPPVHLPPP	TQPP	PSMTASV	HLPPP	CHYPTQPP	HLPPP	HLPPP		VHLPPP
		CQLQGTGCVG	HLPPP	RPQHPQPHP	EN	PVHLPPP	RPQHPQPHP	PVHLPPP	VPPP		HLPPP
		STPILGQCVE	PVHLPPP	PILGQC	PTLQPYRLQQ	PPPVHLPPP	CPCQQPHSP	PPPVHLPPP	PPCHYPTQPP		PVHLPPP
		FLRHQCSPTA	HVPPP	VLQSIL	NLPLS	HVPPP	TCGCVG	HVPPP	RPQHPQPHP		PPPVHLPPP
		TPYSCPQCQC	PPCHYPT	QQQ	PLLQQSPAL	PCHYPTQPP	STPILGQCVE	PPCHYPTQPP	CPCQQPHSP		HVPPP
		LRQCCQQLR	RPQHPQPHP	VA	SLVQ	CQPHSP	FLRHQCSPTA	RPQHPQPHP	CQLQGTGCVG		PPCHYPTQPP
		QQQPQSGQ	CPCQQPHSP	GLLAAQIAQQ	VQTI	CSPTA	TPYCSPQCQS	CPCQQPHSP	STPILGQCVE		RPQHPQPHP
		GLQQP	STPILGQCVE	LTAMC	RAQQLQQLVL	TPYCSP	LRQCCQQLR	CQLQGTGCVG	TPYCSPQCQS		HPSP
		TPCPYAAAGG	FLRHQCSPTA		QVALAN	QQQPQSGQ	QVEPQHRYQA	STPILGQCVE	LRQCCQQLR		CQLQGTGCVG
		IL	LRQCCQQLR		LSPYSQQQ	RP	IFGLVLQ	FLRHQCSPTA	HRYQA		CVE
			QVEPQHRYOA		LQQQLL	CQ	GLLAAQTAQQ	TPYCSPQCQS	GLVLQSI		TPYCSPQCQS
			IFGLVLQSIL		PFSQLATA	IL	LTAMCGLQQP	LRQCCQQLR	QQQPQSGQVA		LRQCCQQL
			QQQPQSGQV		FLPENQ		TPCP	QVEPQHRYQA	LTAMCGLQQP		PQSGQVA
			LAAQIAQQ		LAALNPAAYL			IFGLVLQSIL			GLLAAQIAQQ
			LTAMCGLQQP		QQQILLPFGQ			QQQPQSGQVA			LTAMCGLQQP
			TPC		LATTNRASFL			GLLAAQIAQQ			TPCPYAAA
			TPYC		TQQQLLPFYQ			LTAMCGLQQP			ST
					PATLL			TPCPYAA			PLR
					QLQQLL						
					NPAAFY						
					QQHIIGGAI						
					QF						