

KWS 0206 PCT

## SEQUENCE LISTING

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Universität Zürich

<120> HELMINTHOSPORIUM TURCICUM-RESISTENTE PFLANZE

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<151> 2013-09-04

<150> DE 10 2014 005 823.9

<151> 2014-04-24

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KWS 0206 PCT

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Val Glu Gly Ser Pro Thr Thr Trp Thr Pro Thr Ile Arg Leu Gly Gly  
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Gly Asp Tyr Thr Val Lys Asn Ile Ser Tyr Leu Tyr Asp Gln Gln Thr  
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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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Ile Arg Tyr Pro Phe Asn Leu Ala Asn Ala Thr Ala Asp Tyr Ser Gly  
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Asn Tyr Tyr Ser Cys Gly Tyr Thr Asp Leu Ser Val Ser Cys Glu Leu  
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Glu Val Glu Gly Ser Pro Thr Thr Trp Thr Pro Thr Ile Arg Leu Gly  
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Gly Asp Ile Tyr Thr Val Lys Asn Ile Ser Tyr Asp Tyr His Thr Ile  
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Ser Leu Ala Asp Asn Asp Val Leu Gly Gly Gly Glu Cys Pro Val Val  
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Arg His Asn Val Ser Phe Asn Glu Thr Trp Leu His Asn Ala Ser Ala  
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Phe Asp Asn Leu Thr Phe Phe Phe Gly Cys His Trp Gly Pro Arg Asn  
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Thr Pro Pro Glu Phe Ala Asp Tyr Asn Ile Ser Cys Ala Gly Phe Asn  
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Leu Asp Glu Gln Glu Glu Gln Glu Leu Ala Ser His Cys Asp Glu Val

KWS 0206 PCT

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Gly Gln Arg Ala Pro Glu Arg Ala Leu Ser Trp Pro Leu Arg Leu Ser	470	475
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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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 <213> Zea mays

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KWS 0206 PCT

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Ala	Thr	Glu	Thr	Pro	Val	Leu	Ile	Phe	Leu	Tyr	Phe	His	Lys	Ala	Ile
		35					40					45			
Arg	Ala	Glu	Leu	Glu	Ala	Leu	His	Gly	Ala	Ala	Val	Leu	Leu	Ala	Thr
	50					55					60				
Glu	Arg	Thr	Gly	Asp	Val	Glu	Met	Leu	Ala	Lys	Arg	Cys	Arg	Phe	Phe
65					70					75					80
Phe	Asn	Ile	Tyr	Lys	His	His	Cys	Asp	Ala	Glu	Asp	Ala	Val	Ile	Phe
				85					90					95	
Pro	Ala	Leu	Asp	Ile	Arg	Val	Lys	Asn	Val	Ala	Gly	Thr	Tyr	Ser	Leu
			100					105					110		
Glu	His	Lys	Gly	Glu	Ser	Asp	Leu	Phe	Ser	Gln	Leu	Phe	Asp	Leu	Leu
		115					120					125			
Gln	Leu	Asp	Ile	His	Asn	Asp	Asp	Gly	Leu	Arg	Arg	Glu	Leu	Ala	Ser
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Cys	Thr	Gly	Ala	Ile	Gln	Thr	Cys	Leu	Ser	Gln	His	Met	Ser	Lys	Glu
145					150					155					160
Glu	Glu	Gln	Val	Phe	Pro	Leu	Leu	Thr	Lys	Lys	Phe	Ser	Cys	Glu	Glu
				165					170					175	
Gln	Ala	Asp	Leu	Val	Trp	Gln	Phe	Leu	Cys	Asn	Ile	Pro	Val	Asn	Met
			180					185					190		
Val	Ala	Glu	Phe	Leu	Pro	Trp	Leu	Ser	Thr	Ser	Val	Thr	Ser	Asp	Glu
		195					200					205			
His	Gln	Asp	Ile	Arg	Asn	Cys	Leu	Cys	Lys	Val	Val	Pro	Asp	Glu	Lys
	210					215					220				
Leu	Leu	Gln	Gln	Val	Val	Phe	Thr	Trp	Met	Glu	Gly	Lys	Ala	Thr	Arg
225					230					235					240
Glu	Val	Ala	Glu	Ser	Ile	Ala	Ala	Gly	Ile	Ser	Ala	Arg	Asn	His	Ser
				245					250					255	
Val	Glu	Asp	Val	Pro	Asp	Gln	Gly	Lys	Ile	His	Ile	Cys	Leu	His	His
			260					265					270		
Asn	Ser	Lys	Leu	Gly	Ser	Lys	Asn	Cys	Gly	Glu	Ser	Asn	Gly	Pro	Gln
		275					280					285			
Ala	Asp	Lys	His	Pro	Ile	Asp	Asp	Ile	Leu	Tyr	Trp	His	Asn	Ala	Ile

KWS 0206 PCT

290	295	300
Arg Met Glu Leu Arg Asp Ile Lys Glu Glu Thr Arg Arg Val Gln Gln	310	315
305	325	330
Ser Gly Asp Phe Ser Asp Ile Ser Ala Phe Asn Glu Arg Leu Gln Phe	335	
Ile Ala Asp Val Cys Ile Tyr His Ser Ile Ala Glu Asp Gln Val Val	340	345
	345	350
Phe Pro Ala Val Asp Ser Glu Leu Ser Phe Val Gln Glu His Ala Glu	355	360
	365	
Glu Glu Cys Arg Phe Asn Asn Phe Arg Cys Leu Ile Gln Gln Ile Gln	370	375
	380	
Ile Ala Gly Ala Glu Ser Thr Ala Leu Asp Phe Tyr Ser Lys Leu Cys	385	390
	395	400
Ser His Ala Asp Lys Ile Leu Glu Ala Ile Glu Lys His Phe Cys Asn	405	410
	415	
Glu Glu Thr Lys Val Leu Pro Gln Ala Arg Met Leu Phe Ser Leu Glu	420	425
	430	
Lys Gln Arg Glu Leu Ser Tyr Lys Ser Leu Cys Val Met Pro Leu Lys	435	440
	445	
Leu Leu Glu Arg Val Leu Pro Trp Leu Val Ser Lys Leu Ser Asp Val	450	455
	460	
Gln Ala Thr Ser Phe Leu Gln Asn Ile Arg Leu Ala Ala Ser Pro Ser	465	470
	475	480
Glu Thr Ala Leu Val Thr Leu Ile Ser Gly Trp Ala Cys Lys Gly Arg	485	490
	495	
Asp Lys Ser Lys Asp Gly Glu Tyr Leu Cys Leu Thr Ser Gly Ala Ala	500	505
	510	
Arg Cys Leu Ser Asp Asp Val Asp Asp Leu Gly Lys Cys Arg Ser Phe	515	520
	525	
Cys Pro Cys Ala Ser Pro Asn Ser Ser Asp Leu Ser Leu Gln Leu His	530	535
	540	
Thr Glu Asn Asp Ser Arg Pro Gly Lys Arg Gly Lys Asp Ala Val Ser	545	550
	555	560
Phe Ser His Thr Asn Gly Ile Tyr Cys Ser Gln Thr Ala Asp Ile Glu		

KWS 0206 PCT

										565											570											575
Ala	Ile	Pro	Cys <sub>580</sub>	Ser	Lys	Lys	Pro	Cys <sub>585</sub>	Cys	Ile	Pro	Gly	Leu <sub>590</sub>	Arg	Val																	
Glu	Ser	Ser <sub>595</sub>	Asn	Leu	Gly	Ile	Gly <sub>600</sub>	Ser	Leu	Ala	Ser	Ala <sub>605</sub>	Lys	Ser	Phe																	
His	Ser <sub>610</sub>	Leu	Ser	Tyr	Asn	Ser <sub>615</sub>	Thr	Ala	Pro	Ser	Leu <sub>620</sub>	Tyr	Ser	Ser	Leu																	
Phe <sub>625</sub>	Ser	Trp	Glu	Thr	Asp <sub>630</sub>	Thr	Ser	Leu	Ser	Cys <sub>635</sub>	Ser	Asp	Ser	Ile	Ser <sub>640</sub>																	
Arg	Pro	Ile	Asp	Thr <sub>645</sub>	Ile	Phe	Lys	Phe	His <sub>650</sub>	Lys	Ala	Ile	Arg	Lys <sub>655</sub>	Asp																	
Leu	Glu	Tyr	Leu <sub>660</sub>	Asp	Val	Glu	Ser	Gly <sub>665</sub>	Lys	Leu	Ile	Asp	Gly <sub>670</sub>	Asn	Glu																	
Ser	Cys	Leu <sub>675</sub>	Arg	Gln	Phe	Ile	Gly <sub>680</sub>	Arg	Phe	Arg	Leu	Leu <sub>685</sub>	Trp	Gly	Leu																	
Tyr	Arg <sub>690</sub>	Ala	His	Ser	Asn	Ala <sub>695</sub>	Glu	Asp	Glu	Ile	Val <sub>700</sub>	Phe	Pro	Ala	Leu																	
Glu <sub>705</sub>	Ser	Arg	Glu	Thr	Leu <sub>710</sub>	His	Asn	Val	Ser	His <sub>715</sub>	Ser	Tyr	Thr	Leu	Asp <sub>720</sub>																	
His	Lys	Gln	Glu	Glu <sub>725</sub>	Gln	Leu	Phe	Glu	Asp <sub>730</sub>	Ile	Ser	Asn	Val	Leu <sub>735</sub>	Phe																	
Gln	Leu	Ser	Gln <sub>740</sub>	Leu	His	Asp	Ser	Gln <sub>745</sub>	Gly	His	Ala	Gln	Thr <sub>750</sub>	Glu	Val																	
Asn	Glu	Val <sub>755</sub>	Lys	Lys	Ser	Cys	Phe <sub>760</sub>	His	Ser	Ser	Asn	Asp <sub>765</sub>	Val	Asp	Phe																	
Ala	Arg <sub>770</sub>	Lys	Tyr	Asn	Glu	Leu <sub>775</sub>	Ala	Thr	Lys	Leu	Gln <sub>780</sub>	Gly	Met	Cys	Lys																	
Ser <sub>785</sub>	Ile	Arg	Val	Ala	Leu <sub>790</sub>	Thr	Asn	His	Val	His <sub>795</sub>	Arg	Glu	Glu	Leu	Glu <sub>800</sub>																	
Leu	Trp	Pro	Leu	Phe <sub>805</sub>	Asp	Lys	His	Phe	Ser <sub>810</sub>	Val	Glu	Glu	Gln	Asp <sub>815</sub>	Lys																	
Leu	Val	Gly	Arg <sub>820</sub>	Ile	Ile	Gly	Ser	Thr <sub>825</sub>	Gly	Ala	Glu	Val	Leu <sub>830</sub>	Gln	Ser																	
Met	Leu	Pro	Trp	Val	Thr	Ser	Val	Leu	Thr	Gln	Glu	Glu	Gln	Asn	Lys																	



KWS 0206 PCT

835					840					845					
Met	Leu	Asp	Met	Trp	Lys	Gln	Ala	Thr	Lys	Asn	Thr	Met	Phe	Gly	Glu
850						855					860				
Trp	Leu	Asn	Glu	Trp	Trp	Lys	Gly	Ala	Gly	Thr	Ala	Ser	Asp	Ser	Ser
865					870					875					880
Ala	Glu	Ala	Ser	Ser	Ala	Pro	Glu	Asp	Ser	His	Leu	Gln	Asp	Lys	Leu
				885					890					895	
Glu	Gln	Asn	Asp	Gln	Met	Phe	Lys	Pro	Gly	Trp	Lys	Asp	Ile	Phe	Arg
			900					905					910		
Met	Asn	Gln	Ser	Glu	Leu	Glu	Ala	Glu	Val	Arg	Lys	Val	Ser	Arg	Asp
		915					920					925			
Ser	Thr	Leu	Asp	Pro	Arg	Arg	Lys	Ala	Tyr	Leu	Ile	Gln	Asn	Leu	Met
	930					935					940				
Thr	Ser	Arg	Trp	Ile	Ala	Ala	Gln	Gln	Lys	Leu	Pro	Glu	Pro	Asn	Ser
945					950					955					960
Glu	Glu	Cys	Asn	His	Asp	Ala	Ser	Ile	Pro	Gly	Cys	Ala	Pro	Ser	Tyr
				965					970					975	
Arg	Asp	Gln	Glu	Lys	Gln	Ile	Tyr	Gly	Cys	Glu	His	Tyr	Lys	Arg	Asn
			980					985					990		
Cys	Lys	Leu	Val	Ala	Ala	Cys	Cys	Asn	Lys	Leu	Phe	Thr	Cys	Arg	Phe
		995					1000					1005			
Cys	His	Asp	Lys	Val	Ser	Asp	His	Thr	Met	Glu	Arg	Lys	Ala	Thr	
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Gln	Glu	Met	Met	Cys	Met	Val	Cys	Leu	Lys	Ile	Gln	Pro	Val	Gly	
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Ser	Phe	Cys	Gln	Thr	Pro	Ser	Cys	Asn	Arg	Leu	Ser	Met	Ala	Lys	
	1040					1045					1050				
Tyr	Tyr	Cys	Asn	Ile	Cys	Lys	Phe	Phe	Asp	Asp	Glu	Arg	Thr	Val	
	1055					1060					1065				
Tyr	His	Cys	Pro	Phe	Cys	Asn	Leu	Cys	Arg	Leu	Gly	Lys	Gly	Leu	
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Gly	Val	Asp	Phe	Phe	His	Cys	Met	Lys	Cys	Asn	Cys	Cys	Leu	Gly	
	1085					1090					1095				
Met	Lys	Leu	Thr	Glu	His	Lys	Cys	Arg	Glu	Lys	Gly	Leu	Glu	Thr	

KWS 0206 PCT

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Asn Cys Pro Ile Cys Cys	Asp Phe Leu Phe Thr	Ser Ser Ala Ala
1115	1120	1125
Val Arg Ala Leu Pro Cys	Gly His Phe Met His	Ser Ala Cys Phe
1130	1135	1140
Gln Ala Tyr Thr Cys Ser	His Tyr Thr Cys Pro	Ile Cys Cys Lys
1145	1150	1155
Ser Leu Gly Asp Met Ala	Val Tyr Phe Gly Met	Leu Asp Ala Leu
1160	1165	1170
Leu Ala Ala Glu Glu Leu	Pro Glu Glu Tyr Arg	Asp Arg Cys Gln
1175	1180	1185
Asp Ile Leu Cys Asn Asp	Cys Glu Arg Lys Gly	Arg Cys Arg Phe
1190	1195	1200
His Trp Leu Tyr His Lys	Cys Gly Ser Cys Gly	Ser Tyr Asn Thr
1205	1210	1215
Arg Val Ile Lys Thr Ala	Thr Ala Asp Cys Ser	Thr Pro Asn
1220	1225	1230

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KWS 0206 PCT

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35 40 45

Val Pro Tyr Ser Arg Ala Ser Met Ala Gln Leu Leu Gly Lys Met Pro  
50 55 60

Leu Gln Phe Thr Ser Lys Gln Ala Ala Glu Asp Met Ala Leu Ala Ala  
65 70 75 80

Tyr Asn Arg Ala Leu Lys Leu Ser Gly Pro Gly Leu Gln Val Met Gly  
85 90 95

Val Gly Phe Thr Gly Ser Leu Ala Ser Ser Arg Pro Lys His Gly Asp  
100 105 110

His Arg Phe Tyr Val Ser Thr Trp Thr His Asn Cys Leu Arg Thr Ser  
115 120 125

His Val Thr Leu Ser Lys Gly Leu Arg Ser Arg Glu Glu Glu Asp Lys  
130 135 140

Val Ser Ser Tyr Phe Leu Leu Lys Ala Ile Ala Asp Thr Cys Arg Val  
145 150 155 160

Ser Ala Thr Ile Gln Pro Asp Ile His Lys Ser Glu Ile Pro Glu Glu  
165 170 175

Ile Met Glu Gln Phe Asp Glu Asp Gln Glu Leu Gln Gln Val Ile Asn  
180 185 190

KWS 0206 PCT

Gly Gln Val Cys Met Lys Val Tyr Asn Phe Ala Ala Pro Ala Glu Ser  
195 200 205

Asn Leu Asn Arg Lys Ile Ile Leu Pro Gly Ser Phe Asn Pro Leu His  
210 215 220

Asp Gly His Leu Arg Leu Leu Glu Ala Ala Val Ser Met Cys Asp Asp  
225 230 235 240

Gly Leu Pro Phe Phe Glu Ile Ser Ala Ile Asn Ala Asp Lys Pro Pro  
245 250 255

Leu Ser Ile Ala Glu Ile Lys Arg Arg Val Glu Gln Phe Arg Lys Ala  
260 265 270

Gly Lys Asn Val Ile Ile Ser Asn Gln Pro Tyr Phe Tyr Lys Lys Ala  
275 280 285

Glu Leu Phe Pro Gly Ser Ala Phe Ile Ile Gly Ala Asp Thr Ala Ala  
290 295 300

Arg Leu Val Asn Pro Lys Tyr Tyr Gly Gly Asp Tyr Asn Arg Met Leu  
305 310 315 320

Glu Ile Leu Leu Glu Cys Lys Ser Ile Gly Thr Thr Phe Leu Val Gly  
325 330 335

Gly Arg Lys Ile Glu Gly Asp Phe Lys Val Leu Glu Asn Leu Asp Ile  
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Pro Glu Glu Leu Arg Glu Met Phe Ile Ser Ile Pro Glu Glu Lys Phe  
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atcccagaag tgatcatctc tgagcatgcc ttccgacaaa tagcacagat cgtccattac 360  
aaactggcac acaccgtgtc tgctctttat gacattgcat gcgggaagga tctgaagaaa 420

KWS 0206 PCT

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<213> Zea mays

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20          25          30

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Gly Gly Arg Ala Ala Asp Ile Leu Leu Trp Lys Asp Arg Asn Leu Ser
35          40          45

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Ala Gly Leu Leu Ala Gly Ala Thr Leu Val Trp Tyr Leu Phe Glu Val
50          55          60

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Val Glu Tyr Ser Ile Val Pro Leu Val Cys Gln Ile Ala Ile Leu Ala
65          70          75          80

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Met Leu Val Val Phe Ile Trp Ser Asn Ala Ala Pro Leu Leu Asn Ile
85          90          95

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Ala Pro Pro Arg Ile Pro Glu Val Ile Ile Ser Glu His Ala Phe Arg
100          105          110

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Gln Ile Ala Gln Ile Val His Tyr Lys Leu Ala His Thr Val Ser Ala
115          120          125

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Leu Tyr Asp Ile Ala Cys Gly Lys Asp Leu Lys Lys Phe Leu Leu Val
130          135          140

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Val Leu Ser Leu Leu Ile Val Ser Glu Val Gly Ser Ser Tyr Ser Phe
145          150          155          160

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Thr Ser Leu Leu Tyr Leu Gly Phe Leu Cys Ala His Thr Leu Pro Ala
165          170          175

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Leu Tyr Gln Arg Tyr Glu Thr Glu Val Asp His Leu Ala Ala Arg Gly
180          185          190

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Ser Glu Asp Ile Lys Arg Phe Tyr Lys Arg Ile Asp Ser Asn Leu Leu

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KWS 0206 PCT

195

200

205

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 gggaagccca ctgagtgtaa tacatatgca gacattgaag cagcatataa ctgcctcaag 480  
 gaaaaatatg gtgtagcaga tgaggatata atcttatatg gtcagtctgt tggaagtgg 540  
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 aagaacatcg ataaaattgg cttggtaa atgtccggtgc ttgtcattca tggtagatca 720  
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 aaacctcaag aggccaagaa gtgcccgcag atctcgcgaa agagcctgga cagccgattc 1020  
 gggaaatcca aaacagtgga tgttcctgat aaaccacgga tgagctcgga cgacatcgac 1080  
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Arg Leu Ala Ile Pro Glu Ile Ser Arg Ala Pro Ser Arg Arg Arg

KWS 0206 PCT

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Ala	Ala	Ala	Glu	Glu	Glu	Asp	Gly	Ala	Glu	Val	Val	Arg	Leu	Arg	Thr
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Ser	Ala	Thr	Val	Leu	Tyr	Ser	His	Gly	Asn	Ala	Ala	Asp	Leu	Gly	Gln
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Met	Tyr	Gly	Leu	Phe	Val	Glu	Leu	Ser	Arg	Arg	Leu	Arg	Val	Asn	Leu
		115					120					125			
Phe	Gly	Tyr	Asp	Tyr	Ser	Gly	Tyr	Gly	Arg	Ser	Thr	Gly	Lys	Pro	Thr
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Glu	Cys	Asn	Thr	Tyr	Ala	Asp	Ile	Glu	Ala	Ala	Tyr	Asn	Cys	Leu	Lys
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Glu	Lys	Tyr	Gly	Val	Ala	Asp	Glu	Asp	Ile	Ile	Leu	Tyr	Gly	Gln	Ser
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			180					185					190		
Arg	Ala	Val	Val	Leu	His	Ser	Pro	Ile	Leu	Ser	Gly	Leu	Arg	Val	Ile
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Lys	Ile	Gly	Leu	Val	Asn	Cys	Pro	Val	Leu	Val	Ile	His	Gly	Thr	Ser
225					230					235					240
Asp	Asp	Val	Val	Asp	Cys	Ser	His	Gly	Lys	Gln	Leu	Trp	Glu	His	Cys
				245					250					255	
Lys	Val	Lys	Tyr	Ser	Pro	Leu	Trp	Leu	Ser	Gly	Gly	Gly	His	Cys	Asn
			260					265					270		
Leu	Glu	Leu	Tyr	Pro	Asp	Tyr	Ile	Lys	His	Leu	Lys	Lys	Phe	Val	Ser
		275					280					285			
Ser	Val	Ser	Lys	Lys	Ala	Ser	Ser	Lys	Pro	Asp	Pro	Lys	Glu	Thr	Thr
	290					295					300				
Thr	Lys	Asp	Asp	Thr	Thr	Ser	Lys	Glu	Thr	Glu	Glu	Ala	Tyr	Pro	Glu

KWS 0206 PCT

305 310 315 320

Lys Pro Gln Glu Ala Lys Lys Cys Pro Gln Ile Ser Arg Lys Ser Leu  
 325 330 335

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Arg Met Ser Ser Asp Asp Ile Asp Lys Phe Arg Arg Ser Arg Cys Leu  
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Val Trp  
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<210> 19  
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<210> 21



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<400> 26

KWS 0206 PCT

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KWS 0206 PCT

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&lt;223&gt; PZE-108093748 Primer Allel X

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47

&lt;210&gt; 33

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PZE-108093748 Primer Allel Y

&lt;400&gt; 33

gaaggtcgga gtcaacggat tgatagagtt gcagctaata gcttcag

46

&lt;210&gt; 34

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PZE-108093748 gemeinsamer Primer

&lt;400&gt; 34

cctgcgcttt gtaaataagt taggcaaa

28

&lt;210&gt; 35

&lt;211&gt; 38

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PZE-108107671 Primer Allel X

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38

&lt;210&gt; 36

&lt;211&gt; 40

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&lt;220&gt;

&lt;223&gt; PZE-108107671 Primer Allel Y

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40

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21

&lt;210&gt; 38

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KWS 0206 PCT

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<210> 48  
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KWS 0206 PCT

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&lt;223&gt; MA0006 gemeinsamer Primer

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29

&lt;210&gt; 50

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; PZE-108097482 Primer Allel X

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43

&lt;210&gt; 51

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; PZE-108097482 Primer Allel Y

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42

&lt;210&gt; 52

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; PZE-108097482 gemeinsamer Primer

&lt;400&gt; 52

gactccagag agagacagaa aggaa

25

&lt;210&gt; 53

&lt;211&gt; 41

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; MA0002 Primer Allel X

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41

&lt;210&gt; 54

&lt;211&gt; 40

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&lt;213&gt; Artificial sequence

&lt;220&gt;

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KWS 0206 PCT

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KWS 0206 PCT

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## KWS 0206 PCT

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KWS 0206 PCT

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<210> 83  
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&lt;223&gt; MA0015 Primer Allel X

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44

&lt;210&gt; 84

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MA0015 Primer Allel Y

&lt;400&gt; 84

gaaggtcgga gtcaacggat tcacaggtat gccttgctca taaga

45

&lt;210&gt; 85

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MA0015 gemeinsamer Primer

&lt;400&gt; 85

catarccact gttctaggct ggtgaa

26

&lt;210&gt; 86

&lt;211&gt; 43

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MA0016 Primer Allel X

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43

&lt;210&gt; 87

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MA0016 Primer Allel Y

&lt;400&gt; 87

gaaggtcgga gtcaacggat tgagcaaccg gagataacca cg

42

&lt;210&gt; 88

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MA0016 gemeinsamer Primer

&lt;400&gt; 88

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30

&lt;210&gt; 89

## KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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22

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&lt;400&gt; 138

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KWS 0206 PCT

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&lt;223&gt; 579zmpm0\_216F Primer

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&lt;400&gt; 186

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&lt;400&gt; 187

gtcactatac ggagacggcg

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&lt;210&gt; 188

&lt;211&gt; 20

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KWS 0206 PCT

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KWS 0206 PCT

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21

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21

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KWS 0206 PCT

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KWS 0206 PCT

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KWS 0206 PCT

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