

SEQUENCE LISTING

<110> Henkel KGaA

<120> Neue Alkalische Protease aus *Bacillus gibsonii* und Wasch- und Reinigungsmittel enthaltend diese neue Alkalische Protease

<130> H07394 PCT

<160> 2

<170> PatentIn version 3.3

<210> 1

<211> 1152

<212> DNA

<213> *Bacillus gibsonii*

<220>

<221> CDS

<222> (1)..(1152)

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gct	cta	gta	aca	gtg	aca	gat	tct	gca	tct	gca	gca	gaa	gaa	aag	gta	96
Ala	Leu	Val	Thr	Val	Thr	Asp	Ser	Ala	Ser	Ala	Ala	Glu	Glu	Lys	Val	
			20					25					30			

aag	tac	tta	ata	gga	ttt	gaa	gaa	gaa	gca	gag	ctt	gaa	gcc	ttc	acg	144
Lys	Tyr	Leu	Ile	Gly	Phe	Glu	Glu	Glu	Ala	Glu	Leu	Glu	Ala	Phe	Thr	
		35					40					45				

gag	gaa	gtt	gac	caa	att	ggg	gta	ttt	tct	gta	gag	gaa	caa	agt	gta	192
Glu	Glu	Val	Asp	Gln	Ile	Gly	Val	Phe	Ser	Val	Glu	Glu	Gln	Ser	Val	
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gta	gag	gat	acg	tta	gat	att	gat	gta	gac	att	att	gat	gaa	tat	gaa	240
Val	Glu	Asp	Thr	Leu	Asp	Ile	Asp	Val	Asp	Ile	Ile	Asp	Glu	Tyr	Glu	
65				70				75						80		

tat	att	gat	gta	cta	tct	gta	gaa	tta	gat	cct	gaa	gat	gta	gac	gca	288
Tyr	Ile	Asp	Val	Leu	Ser	Val	Glu	Leu	Asp	Pro	Glu	Asp	Val	Asp	Ala	
			85					90						95		

tta	agc	gat	gaa	gaa	ggg	att	tct	ttt	att	gaa	gaa	gac	ttt	gag	atg	336
Leu	Ser	Asp	Glu	Glu	Gly	Ile	Ser	Phe	Ile	Glu	Glu	Asp	Phe	Glu	Met	
			100					105					110			

tct	atc	caa	caa	act	gtt	cca	tgg	gga	att	act	cgt	gta	caa	gct	cca	384
Ser	Ile	Gln	Gln	Thr	Val	Pro	Trp	Gly	Ile	Thr	Arg	Val	Gln	Ala	Pro	
		115					120					125				

gct	gtt	cat	aat	cgt	gga	gta	aca	ggg	tcg	gga	gta	aga	gta	gct	atc	432
Ala	Val	His	Asn	Arg	Gly	Val	Thr	Gly	Ser	Gly	Val	Arg	Val	Ala	Ile	
	130					135					140					

ctt gat tca ggt att tct caa cat agt gac tta acc att cgt ggg gga Leu Asp Ser Gly Ile Ser Gln His Ser Asp Leu Thr Ile Arg Gly Gly 145 150 155 160	480
gca agc ttt gtg cct gga gag cca aca acg gaa gat cta aat ggt cat Ala Ser Phe Val Pro Gly Glu Pro Thr Thr Glu Asp Leu Asn Gly His 165 170 175	528
ggt act cat gtt gcg ggt acg gta gcc gca ctt aac aat tcg ttt ggt Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Phe Gly 180 185 190	576
gta atc ggt gtt gcg cca agt gcg gac tta tac gca gtc aaa gta ctc Val Ile Gly Val Ala Pro Ser Ala Asp Leu Tyr Ala Val Lys Val Leu 195 200 205	624
ggt gca ggt gga aga ggt agt gtt agt gga atc gct caa ggt cta gag Gly Ala Gly Gly Arg Gly Ser Val Ser Gly Ile Ala Gln Gly Leu Glu 210 215 220	672
tgg gct gca gcg aat aac atg cat att gcc aac atg agt ctc ggc gca Trp Ala Ala Ala Asn Asn Met His Ile Ala Asn Met Ser Leu Gly Ala 225 230 235 240	720
gat gca cct agc tca acg ctt gag cgt gca gtt aac tat gcg aca agc Asp Ala Pro Ser Ser Thr Leu Glu Arg Ala Val Asn Tyr Ala Thr Ser 245 250 255	768
cgt ggt gta ttg gtc att gca gcg aca ggt aac aat ggc tca ggt tca Arg Gly Val Leu Val Ile Ala Ala Thr Gly Asn Asn Gly Ser Gly Ser 260 265 270	816
gtt ggc tat cct gct cgt tac gca aac gca atg gct gta gga gca acg Val Gly Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr 275 280 285	864
gac cag aac aac aga cgt gca aac ttt tct caa tat ggt aca ggc att Asp Gln Asn Asn Arg Arg Ala Asn Phe Ser Gln Tyr Gly Thr Gly Ile 290 295 300	912
gac atc gta gct cct ggg gtt aat gta caa agt acg tat cca gga aat Asp Ile Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Asn 305 310 315 320	960
cgg tat gcg agc ctg aat ggt aca tct atg gca act cca cac gtg gct Arg Tyr Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala 325 330 335	1008
ggt gtc gct gcg ctt gta aag caa cgt aac cca tct tgg aat gca act Gly Val Ala Ala Leu Val Lys Gln Arg Asn Pro Ser Trp Asn Ala Thr 340 345 350	1056
caa att cgt aat cat ttg aag aat act gca aca aat cta gga aac tca Gln Ile Arg Asn His Leu Lys Asn Thr Ala Thr Asn Leu Gly Asn Ser 355 360 365	1104
tcg caa ttt ggt agt ggt cta gtt aat gca gaa gca gca ata cgc taa Ser Gln Phe Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Ile Arg 370 375 380	1152

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 <213> *Bacillus gibsonii*

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Lys Tyr Leu Ile Gly Phe Glu Glu Glu Ala Glu Leu Glu Ala Phe Thr
 35 40 45

Glu Glu Val Asp Gln Ile Gly Val Phe Ser Val Glu Glu Gln Ser Val
 50 55 60

Val Glu Asp Thr Leu Asp Ile Asp Val Asp Ile Ile Asp Glu Tyr Glu
 65 70 75 80

Tyr Ile Asp Val Leu Ser Val Glu Leu Asp Pro Glu Asp Val Asp Ala
 85 90 95

Leu Ser Asp Glu Glu Gly Ile Ser Phe Ile Glu Glu Asp Phe Glu Met
 100 105 110

Ser Ile Gln Gln Thr Val Pro Trp Gly Ile Thr Arg Val Gln Ala Pro
 115 120 125

Ala Val His Asn Arg Gly Val Thr Gly Ser Gly Val Arg Val Ala Ile
 130 135 140

Leu Asp Ser Gly Ile Ser Gln His Ser Asp Leu Thr Ile Arg Gly Gly
 145 150 155 160

Ala Ser Phe Val Pro Gly Glu Pro Thr Thr Glu Asp Leu Asn Gly His
 165 170 175

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Phe Gly
 180 185 190

Val Ile Gly Val Ala Pro Ser Ala Asp Leu Tyr Ala Val Lys Val Leu
 195 200 205

Gly Ala Gly Gly Arg Gly Ser Val Ser Gly Ile Ala Gln Gly Leu Glu
210 215 220

Trp Ala Ala Ala Asn Asn Met His Ile Ala Asn Met Ser Leu Gly Ala
225 230 235 240

Asp Ala Pro Ser Ser Thr Leu Glu Arg Ala Val Asn Tyr Ala Thr Ser
245 250 255

Arg Gly Val Leu Val Ile Ala Ala Thr Gly Asn Asn Gly Ser Gly Ser
260 265 270

Val Gly Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr
275 280 285

Asp Gln Asn Asn Arg Arg Ala Asn Phe Ser Gln Tyr Gly Thr Gly Ile
290 295 300

Asp Ile Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Asn
305 310 315 320

Arg Tyr Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala
325 330 335

Gly Val Ala Ala Leu Val Lys Gln Arg Asn Pro Ser Trp Asn Ala Thr
340 345 350

Gln Ile Arg Asn His Leu Lys Asn Thr Ala Thr Asn Leu Gly Asn Ser
355 360 365

Ser Gln Phe Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Ile Arg
370 375 380