

# SEQUENCE LISTING

<110> Süd-Chemie

<120> Thermostable xylanase for the selective hydrolysis of pentose-containing polysaccharides

<130> HE 143 784 n17

<160> 8

<170> PatentIn version 3.4

<210> 1

<211> 307

<212> PRT

<213> Unknown

<220>

<223> Originating from a metagenomic clone library without identification of the source organism.

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Leu Ser Asn Glu Glu Gln Tyr Gln Leu Val Val Val Arg Glu Phe Asn  
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Ser Val Thr Pro Glu Asn Val Met Lys Trp Asp Thr Ile Glu Pro Ile  
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Arg Gly Gln Leu Asn Phe Glu Pro Ala Asp Gln Leu Val Asp Phe Ala  
35 40 45

Arg Arg His Gly Gln Ile Val Arg Glu His Thr Leu Val Trp His Asn  
50 55 60

Gln Leu Pro Ser Trp Leu Thr Asn Gly Asn Phe Thr Asn Gln Glu Leu  
65 70 75 80

Glu Glu Ile Leu Arg Gln His Ile Tyr Asp Val Val Arg His Phe Lys  
85 90 95

Gly Lys Val Tyr Ser Trp Asp Val Val Asn Glu Pro Leu Asn Glu Asp  
100 105 110

Gly Thr Leu Arg Asp Ser Ile Trp Leu Arg Ala Ile Gly Pro Asp Tyr  
115 120 125

Ile Ala Lys Ala Phe Gln Trp Ala His Glu Ala Asp Pro His Ala Lys  
130 135 140

Leu Tyr Ile Asn Asp Tyr Asn Ile Glu Trp Ile Gly Pro Lys Ser Asn  
145 150 155 160

Gly Met Tyr Glu Leu Val Lys Ser Leu Lys Glu Ala Gly Val Pro Ile

165					170					175					
Asp	Gly	Val	Gly	Phe	Gln	Gly	His	Leu	Gly	Ile	Gln	Tyr	Gly	Phe	Pro
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Gly	Asp	Ile	Gln	Gln	Asn	Ile	Gln	Arg	Phe	Ala	Asp	Leu	Gly	Leu	Asp
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Val	Ala	Leu	Ser	Glu	Val	Asp	Val	Arg	Met	Ile	Leu	Pro	Val	Thr	Gln
	210					215					220				
Glu	Lys	Leu	Ala	Thr	Gln	Ala	Glu	Tyr	Tyr	Arg	Arg	Leu	Met	Asp	Ala
225					230					235					240
Cys	Leu	Asn	Val	Arg	Arg	Cys	Val	Ser	Phe	Thr	Val	Trp	Gly	Phe	Thr
				245					250					255	
Asp	Ala	His	Ser	Trp	Val	Pro	Gly	Phe	Phe	Gln	Gly	Gln	Gly	Ala	Ala
			260					265					270		
Thr	Ile	Phe	Asp	Glu	Asn	Tyr	Gln	Pro	Lys	Pro	Ala	Tyr	Phe	Ala	Leu
	275						280					285			
Lys	Asp	Glu	Leu	Thr	Glu	Arg	Ser	Gly	Arg	Pro	Gln	Gly	Lys	His	Tyr
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Arg	Asn	Glu													
305															

<210> 2  
 <211> 330  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Originating from a metagenomic clone library without  
 identification of the source organism.

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Thr	Ala	Val	Asp	Val	Asn	Ala	Leu	Ser	Asn	Glu	Glu	Gln	Tyr	Gln	Leu
			20					25					30		
Val	Val	Val	Arg	Glu	Phe	Asn	Ser	Val	Thr	Pro	Glu	Asn	Val	Met	Lys
		35					40					45			
Trp	Asp	Thr	Ile	Glu	Pro	Ile	Arg	Gly	Gln	Leu	Asn	Phe	Glu	Pro	Ala
	50					55					60				

Asp	Gln	Leu	Val	Asp	Phe	Ala	Arg	Arg	His	Gly	Gln	Ile	Val	Arg	Glu	65	70	75	80
His	Thr	Leu	Val	Trp	His	Asn	Gln	Leu	Pro	Ser	Trp	Leu	Thr	Asn	Gly	85	90	95	
Asn	Phe	Thr	Asn	Gln	Glu	Leu	Glu	Glu	Ile	Leu	Arg	Gln	His	Ile	Tyr	100	105	110	
Asp	Val	Val	Arg	His	Phe	Lys	Gly	Lys	Val	Tyr	Ser	Trp	Asp	Val	Val	115	120	125	
Asn	Glu	Pro	Leu	Asn	Glu	Asp	Gly	Thr	Leu	Arg	Asp	Ser	Ile	Trp	Leu	130	135	140	
Arg	Ala	Ile	Gly	Pro	Asp	Tyr	Ile	Ala	Lys	Ala	Phe	Gln	Trp	Ala	His	145	150	155	160
Glu	Ala	Asp	Pro	His	Ala	Lys	Leu	Tyr	Ile	Asn	Asp	Tyr	Asn	Ile	Glu	165	170	175	
Trp	Ile	Gly	Pro	Lys	Ser	Asn	Gly	Met	Tyr	Glu	Leu	Val	Lys	Ser	Leu	180	185	190	
Lys	Glu	Ala	Gly	Val	Pro	Ile	Asp	Gly	Val	Gly	Phe	Gln	Gly	His	Leu	195	200	205	
Gly	Ile	Gln	Tyr	Gly	Phe	Pro	Gly	Asp	Ile	Gln	Gln	Asn	Ile	Gln	Arg	210	215	220	
Phe	Ala	Asp	Leu	Gly	Leu	Asp	Val	Ala	Leu	Ser	Glu	Val	Asp	Val	Arg	225	230	235	240
Met	Ile	Leu	Pro	Val	Thr	Gln	Glu	Lys	Leu	Ala	Thr	Gln	Ala	Glu	Tyr	245	250	255	
Tyr	Arg	Arg	Leu	Met	Asp	Ala	Cys	Leu	Asn	Val	Arg	Arg	Cys	Val	Ser	260	265	270	
Phe	Thr	Val	Trp	Gly	Phe	Thr	Asp	Ala	His	Ser	Trp	Val	Pro	Gly	Phe	275	280	285	
Phe	Gln	Gly	Gln	Gly	Ala	Ala	Thr	Ile	Phe	Asp	Glu	Asn	Tyr	Gln	Pro	290	295	300	
Lys	Pro	Ala	Tyr	Phe	Ala	Leu	Lys	Asp	Glu	Leu	Thr	Glu	Arg	Ser	Gly	305	310	315	320

Arg Pro Gln Gly Lys His Tyr Arg Asn Glu  
325 330

<210> 3  
<211> 331  
<212> PRT  
<213> Unknown

<220>  
<223> Originating from a metagenomic clone library without  
identification of the source organism.

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Gly Thr Ala Val Asp Val Asn Ala Leu Ser Asn Glu Glu Gln Tyr Gln  
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Leu Val Val Val Arg Glu Phe Asn Ser Val Thr Pro Glu Asn Val Met  
35 40 45

Lys Trp Asp Thr Ile Glu Pro Ile Arg Gly Gln Leu Asn Phe Glu Pro  
50 55 60

Ala Asp Gln Leu Val Asp Phe Ala Arg Arg His Gly Gln Ile Val Arg  
65 70 75 80

Glu His Thr Leu Val Trp His Asn Gln Leu Pro Ser Trp Leu Thr Asn  
85 90 95

Gly Asn Phe Thr Asn Gln Glu Leu Glu Glu Ile Leu Arg Gln His Ile  
100 105 110

Tyr Asp Val Val Arg His Phe Lys Gly Lys Val Tyr Ser Trp Asp Val  
115 120 125

Val Asn Glu Pro Leu Asn Glu Asp Gly Thr Leu Arg Asp Ser Ile Trp  
130 135 140

Leu Arg Ala Ile Gly Pro Asp Tyr Ile Ala Lys Ala Phe Gln Trp Ala  
145 150 155 160

His Glu Ala Asp Pro His Ala Lys Leu Tyr Ile Asn Asp Tyr Asn Ile  
165 170 175

Glu Trp Ile Gly Pro Lys Ser Asn Gly Met Tyr Glu Leu Val Lys Ser  
180 185 190

Leu Lys Glu Ala Gly Val Pro Ile Asp Gly Val Gly Phe Gln Gly His  
195 200 205

Leu Gly Ile Gln Tyr Gly Phe Pro Gly Asp Ile Gln Gln Asn Ile Gln  
210 215 220

Arg Phe Ala Asp Leu Gly Leu Asp Val Ala Leu Ser Glu Val Asp Val  
225 230 235 240

Arg Met Ile Leu Pro Val Thr Gln Glu Lys Leu Ala Thr Gln Ala Glu  
245 250 255

Tyr Tyr Arg Arg Leu Met Asp Ala Cys Leu Asn Val Arg Arg Cys Val  
260 265 270

Ser Phe Thr Val Trp Gly Phe Thr Asp Ala His Ser Trp Val Pro Gly  
275 280 285

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

Pro Lys Pro Ala Tyr Phe Ala Leu Lys Asp Glu Leu Thr Glu Arg Ser  
305 310 315 320

Gly Arg Pro Gln Gly Lys His Tyr Arg Asn Glu  
325 330

<210> 4

<211> 414

<212> PRT

<213> Unknown

<220>

<223> Originating from a metagenomic clone library without  
identification of the source organism.

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Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser  
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln  
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe  
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu  
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val  
65 70 75 80

Ser	Leu	Asp	Lys	Arg	Leu	Gly	Leu	Arg	Asp	Tyr	Ala	Ala	Arg	Thr	His	85	90	95
Leu	Ser	Ile	Gly	Thr	Ala	Val	Asp	Val	Asn	Ala	Leu	Ser	Asn	Glu	Glu	100	105	110
Gln	Tyr	Gln	Leu	Val	Val	Val	Arg	Glu	Phe	Asn	Ser	Val	Thr	Pro	Glu	115	120	125
Asn	Val	Met	Lys	Trp	Asp	Thr	Ile	Glu	Pro	Ile	Arg	Gly	Gln	Leu	Asn	130	135	140
Phe	Glu	Pro	Ala	Asp	Gln	Leu	Val	Asp	Phe	Ala	Arg	Arg	His	Gly	Gln	145	150	155
Ile	Val	Arg	Glu	His	Thr	Leu	Val	Trp	His	Asn	Gln	Leu	Pro	Ser	Trp	165	170	175
Leu	Thr	Asn	Gly	Asn	Phe	Thr	Asn	Gln	Glu	Leu	Glu	Glu	Ile	Leu	Arg	180	185	190
Gln	His	Ile	Tyr	Asp	Val	Val	Arg	His	Phe	Lys	Gly	Lys	Val	Tyr	Ser	195	200	205
Trp	Asp	Val	Val	Asn	Glu	Pro	Leu	Asn	Glu	Asp	Gly	Thr	Leu	Arg	Asp	210	215	220
Ser	Ile	Trp	Leu	Arg	Ala	Ile	Gly	Pro	Asp	Tyr	Ile	Ala	Lys	Ala	Phe	225	230	235
Gln	Trp	Ala	His	Glu	Ala	Asp	Pro	His	Ala	Lys	Leu	Tyr	Ile	Asn	Asp	245	250	255
Tyr	Asn	Ile	Glu	Trp	Ile	Gly	Pro	Lys	Ser	Asn	Gly	Met	Tyr	Glu	Leu	260	265	270
Val	Lys	Ser	Leu	Lys	Glu	Ala	Gly	Val	Pro	Ile	Asp	Gly	Val	Gly	Phe	275	280	285
Gln	Gly	His	Leu	Gly	Ile	Gln	Tyr	Gly	Phe	Pro	Gly	Asp	Ile	Gln	Gln	290	295	300
Asn	Ile	Gln	Arg	Phe	Ala	Asp	Leu	Gly	Leu	Asp	Val	Ala	Leu	Ser	Glu	305	310	315
Val	Asp	Val	Arg	Met	Ile	Leu	Pro	Val	Thr	Gln	Glu	Lys	Leu	Ala	Thr	325	330	335
Gln	Ala	Glu	Tyr	Tyr	Arg	Arg	Leu	Met	Asp	Ala	Cys	Leu	Asn	Val	Arg			

340	345	350
Arg Cys Val Ser Phe Thr Val Trp Gly Phe Thr Asp Ala His Ser Trp		
355	360	365
Val Pro Gly Phe Phe Gln Gly Gln Gly Ala Ala Thr Ile Phe Asp Glu		
370	375	380
Asn Tyr Gln Pro Lys Pro Ala Tyr Phe Ala Leu Lys Asp Glu Leu Thr		
385	390	395
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Glu Arg Ser Gly Arg Pro Gln Gly Lys His Tyr Arg Asn Glu		
405	410	

<210> 5  
 <211> 924  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Originating from a metagenomic clone library without  
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 gcagatcagc tcgtagattt tgcacggcgg catggtcaga tagtgagaga gcacacactc 180  
 gtctggcata accaactgcc cagctggttg acaaattgga actttaccaa ccaggagctg 240  
 gaggaaatac tgcgacagca catctatgat gttgtaaggc atttcaaggg caagggtgat 300  
 tcttgggacg tagtgaacga gccctgaat gaagatggtg ccctaaggga tagcatatgg 360  
 cttagggcta ttggtccgga ttacatagcc aaagctttcc aatgggcgca cgaggctgat 420  
 ccacatgcca aactctacat caatgactac aacattgagt ggatcgggcc taagagcaat 480  
 ggaatgtacg agctggtgaa gagtctcaag gaagcaggtg tgcctatcga tggcgtggga 540  
 tttcaaggac atctcggcat acagtatgga tttcctgggg atattcaaca gaatattcag 600  
 agatttgctg atctgggatt ggatgtggct ctgtctgagg tggatgtgcg catgattcta 660  
 cctgttacc c aagagaaact tgctacacag gctgagtatt accgtcgact tatggatgct 720  
 tgtctgaatg tacgacgatg cgtatctttc acagtgtggg gattcaccga tgctcactca 780  
 tgggtaccgc gattcttcca aggacaaggc gggccacta tatttgatga gaattatcag 840  
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<210> 6  
 <211> 993  
 <212> DNA

<213> Unknown

<220>

<223> Originating from a metagenomic clone library without identification of the source organism.

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gttaccacag aaaatgtcat gaaatgggat actattgagc ccatacgtgg tcagctaaat	180
tttgagccag cagatcagct cgtagatttt gcacggcggc atggtcagat agtgagagag	240
cacacactcg tctggcataa ccaactgcc agctgggtga caaatggtaa ctttaccaac	300
caggagctgg aggaataact gcgacagcac atctatgatg ttgtaaggca tttcaagggc	360
aaggtgtatt cttgggacgt agtgaacgag cccctgaatg aagatgggtac cctaagggat	420
agcatatggc ttagggctat tggccggat tacatagcca aagctttcca atgggcgcac	480
gaggctgatc cacatgccaa actctacatc aatgactaca acattgagtg gatcgggcct	540
aagagcaatg gaatgtacga gctggtgaag agtctcaagg aagcaggtgt gcctatcgat	600
ggcgtgggat ttcaaggaca tctcggcata cagtatggat ttcttgggga tattcaacag	660
aatattcaga gatttgctga tctgggattg gatgtggctc tgtctgaggt ggatgtgcgc	720
atgattctac ctgttaccca agagaaactt gctacacagg ctgagtatta ccgtcgactt	780
atggatgctt gtctgaatgt acgacgatgc gtatctttca cagtgtgggg attcaccgat	840
gctcactcat gggtagccgg attcttccaa ggacaagggt cggccactat atttgatgag	900
aattatcagc cgaaaccagc gtattttgct ttgaaggatg aacttactga gcgttcaggt	960
cgacctcagg gcaaacatta taggaacgaa taa	993

<210> 7

<211> 996

<212> DNA

<213> Unknown

<220>

<223> Originating from a metagenomic clone library without identification of the source organism.

<400> 7

aagagattgg gactgagaga ttacgctgct agaaccact tgtctatcgg aaccgccgtt	60
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tctgttacc cagagaacgt gatgaagtgg gacaccatcg agccaattag aggacagctg	180
aactttgagc cagctgacca gttggttgac ttcgctagaa gacacggaca gattgtgaga	240
gagcacaccc ttgtttggca caaccagctg ccattcttgg tgaccaacgg caacttcacc	300
aaccaggaac tggaagagat tctgagacag cacatctacg acgttgtag acacttcaag	360
ggcaagggtg actcttggga cgttggttaac gagccattga acgaggacgg tactctgaga	420



gactctatct ggctgagagc tatcggtcca gactacatcg ctaaggcttt tcagtgggct	480
cacgaagctg atccacacgc caagctgtac atcaacgact acaacatcga gtggatcggt	540
ccaaagtcta acggaatgta cgagctggtg aagtctttga aagaggccgg cgttcctatt	600
gatgggtgttg gtttccaggg tcacctgggt attcagtacg gtttcccagg tgacatccag	660
cagaacatcc agagatttgc tgacctggga ctggatgttg ctttgtctga agtggatgtg	720
agaatgatcc tgccagtgc ccaggaaaag ttggctactc aggccgagta ctatagaaga	780
ttgatggacg cctgcctgaa tgttagaaga tgcgtgtctt tcaactgtgtg gggttttact	840
gacgctcact cttgggttcc aggattcttt cagggtcaag gtgccgctac tatcttcgac	900
gagaactacc agccaaagcc agcttacttt gccttgaagg acgagttgac cgagagatct	960
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<210> 8  
 <211> 1245  
 <212> DNA  
 <213> Unknown

<220>  
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ccagtcaaca ctacaacaga agatgaaacg gcacaaattc cggctgaagc tgtcatcggt	120
tactcagatt tagaagggga ttctgatgtt gctgttttgc cattttccaa cagcacaaat	180
aacgggttat tgtttataaa tactactatt gccagcattg ctgctaaaga agaaggggta	240
agcttgata agagattggg actgagagat tacgctgcta gaaccactt gtctatcgga	300
accgccgttg acgttaacgc tctgtctaac gaggaacagt accagctggg tgttgtgaga	360
gagttcaact ctgttacctt agagaacgtg atgaagtggg acaccatcga gccaataga	420
ggacagctga actttgagcc agctgaccag ttgggtgact tcgctagaag acacggacag	480
attgtgagag agcacaccct tgtttggcac aaccagctgc catcttggtt gaccaacggc	540
aacttcacca accaggaact ggaagagatt ctgagacagc acatctacga cgttgtgaga	600
cacttcaagg gcaaggtgta ctcttgggac gttgttaacg agccattgaa cgaggacggt	660
actctgagag actctatctg gctgagagct atcggtccag actacatcgc taaggctttt	720
cagtgggctc acgaagctga tccacacgcc aagctgtaca tcaacgacta caacatcgag	780
tggatcggtc caaagtctaa cggaatgtac gagctggtga agtctttgaa agaggccggc	840
gttcctattg atggtgttgg tttccagggg cacctgggta ttcagtacgg tttcccaggt	900
gacatccagc agaacatcca gagatttgcg gacctgggac tggatgttgc tttgtctgaa	960
gtggatgtga gaatgatcct gccagtgacc caggaaaagt tggctactca ggccgagtac	1020

tatagaagat	tgatggacgc	ctgcctgaat	gttagaagat	gcgtgtcttt	cactgtgtgg	1080
ggttttactg	acgctcactc	ttgggttcca	ggattctttc	agggtcaagg	tgccgctact	1140
atcttcgacg	agaactacca	gccaaagcca	gcttactttg	ccttgaagga	cgagttgacc	1200
gagagatctg	gtagaccaca	gggaaagcac	tacagaaacg	agtaa		1245