

SEQUENCE LISTING

<110> CODEXIS, INC.
 ALVIZO, OSCAR
 ELGART, DAVID
 ORR, ROBERT KEVIN
 RIGGINS, JAMES NICHOLAS
 FRYSZKOWSKA, ANNA
 LEXA, KATRINA W.
 YI, XIANG
 DUAN, DA
 MOFFETT, COURTNEY DIANNE
 DELLAS, NIKKI
 MITCHELL, VESNA

<120> PENICILLIN-G ACYLASES

<130> CX2-161USP2

<140> TO BE ASSIGNED

<141> 2017-03-16

<160> 202

<210> 1

<211> 2541

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 1

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<210> 2

<211> 846

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 2

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Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala Asp
35           40           45
Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln Asp
50           55           60
Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr Val
65           70           75           80
Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile Arg
85           90           95
Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu Ser
100          105          110
Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn Ala
115          120          125
Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln Gln
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<210> 4

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 4

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ser Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
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<210> 5

<211> 2295

<212> DNA

<213> Artificial Sequence

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<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 6

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 6

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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				165				170					175		
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Thr	Gly	Ala	Tyr	195	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu
Val	Pro	Gly	Thr	210	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe
Leu	Asn	Pro	Lys	225	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn
Asn	Asn	Ser	Pro	245	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Val	Trp	Gly
Leu	Trp	Gly	Gly	260	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu
Lys	Gln	Pro	Arg	275	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg
Thr	Ser	Arg	Arg	290	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Lys
Asp	Ala	Thr	Ala	305	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Val
Asp	Lys	Leu	Ala	325	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Gly
Lys	Thr	Tyr	Gln	340	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Arg	Ala	Trp	Thr
Ser	Met	Leu	Lys	355	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Gly
Lys	Trp	Tyr	Ser	370	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Thr
Gly	Ser	Leu	Asn	385	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Leu
Gln	Gly	Asp	Lys	405	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly
Lys	Pro	Gln	Gln	420	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Gln
Thr	Leu	Ser	Lys	435	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Pro
Ala	Met	Ala	Leu	450	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Gln
Ala	Ala	Ala	Lys	465	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Gly
Thr	Glu	Asn	Asp	485	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Pro
Val	Leu	Ala	Trp	500	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ala
Pro	Asp	Gly	Lys	515	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Tyr
Glu	Ser	Phe	Gly	530	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Asp
Glu	His	Gln	Glu	545	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Thr
Glu	Val	Lys	Ile	565	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Ala
Asp	Asp	Thr	Tyr	580	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Gln
Asp	Arg	Leu	Phe		Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Thr

	595						600						605						
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile				
	610						615					620							
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu				
	625					630					635				640				
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn				
				645					650					655					
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln				
			660					665					670						
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp				
	675						680					685							
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser				
	690					695					700								
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys				
	705				710					715					720				
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu				
				725					730					735					
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr				
			740					745					750						
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala								
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<210> 7

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 7

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ggcaccattt catggggatc caccgccggg gggggtgata acgtcgatat ctttgccgaa 240
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgtaa 2295

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<210> 8

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 8

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20        25        30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35        40        45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50        55        60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65        70        75        80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85        90        95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100       105       110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115       120       125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130       135       140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145       150       155       160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165       170       175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180       185       190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195       200       205

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Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Arg	Ala	Trp	Leu	Thr	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Pro	370	375	380
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
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Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
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Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725					730						735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745						750	
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
		755					760								

<210> 9

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 9

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<210> 10

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 10

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Ser Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85      90      95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
      100     105     110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
      115     120     125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130     135     140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145     150     155     160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
      165     170     175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
      180     185     190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195     200     205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210     215     220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225     230     235     240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe

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				245					250				255				
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			260					265					270				
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		
		275					280					285					
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		
	290					295					300						
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val		
305				310					315						320		
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly		
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Arg	Ala	Trp	Leu	Thr		
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Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
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Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys		
705	710	715
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu		
725	730	735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr		
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala		
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<210> 11

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 11

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<210> 12
 <211> 764
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 12

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
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Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
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Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
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Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
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Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115						120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
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Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
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Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
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Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Thr	Pro
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Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
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Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
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Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
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Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
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Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
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Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
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Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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<210> 13
 <211> 2295
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 13

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<210> 14
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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50 55 60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Gly Phe
245 250 255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
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Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly

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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly																										
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln																										
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<210> 15

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 15

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<210> 16

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 16

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Ser	Val	Asp	Ile	Phe	Ala	Glu
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
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				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
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225					230					235					240
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				245					250					255	
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			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
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				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Arg	Ala	Trp	Leu	Thr
			340					345					350		
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$\langle 210 \rangle$	17
$\langle 211 \rangle$	2295

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 17

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<210> 18

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 18

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35				40					45				
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50				55				60						
Trp	Gly	Ser	Thr	Ala	Gly	Cys	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70				75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85				90						95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150				155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165				170						175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
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225					230					235				240	
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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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<400> 19

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<210> 20

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 20

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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10

15

Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
		50				55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
			115				120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
					135						140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
			195				200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
						215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
			275				280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
						295					300				
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305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
			355				360					365			
Lys	Trp	Tyr													

Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
450						455				460					
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
		530				535					540				
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600						605		
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Arg	Ile
		610				615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
		690				695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
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<210> 21

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 21

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gggccgcagt ttggttggtta tgtgccggcg tacacctac gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180

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ggcaccattt catggggatc caccgccggt ggggggatg atgtcgatat ctttgccgaa 240
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cgcgcttggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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gacggggcaa ccggctcgct gaacatcagc gtggggcgga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggcaa taacttcttc 1380
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tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 22

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 22

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser

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Lys	Leu	Ser	Ala	Glu 85	Lys	Pro	Gly	Tyr	Tyr 90	Gln	His	Asn	Gly	Glu 95	Trp
Val	Lys	Met	Leu	Ser 100	Arg	Lys	Glu	Thr	Ile 105	Ala	Val	Lys	Asp	Gly 110	Gln
Pro	Glu	Thr	Phe	Thr 115	Val	Trp	Arg	Thr	Leu 120	His	Gly	Asn	Val	Ile 125	Lys
Thr	Asp	Thr	Ala	Thr 130	Gln	Thr	Ala	Tyr	Ala 135	Lys	Ala	Arg	Ala	Trp 140	Asp
Gly 145	Lys	Glu	Val	Ala 150	Ser	Leu	Leu	Ala	Trp 155	Thr	His	Gln	Met	Lys 160	Ala
Lys	Asn	Trp	Pro	Glu 165	Trp	Thr	Gln	Gln	Ala 170	Ala	Lys	Gln	Ala	Leu 175	Thr
Ile	Asn	Trp	Tyr 180	Tyr	Ala	Asp	Val	Asn	Gly 185	Asn	Ile	Gly	Tyr 190	Val	His
Thr	Gly	Ala	Tyr 195	Pro	Asp	Arg	Gln	Pro	Gly 200	His	Asp	Pro	Arg 205	Leu	Pro
Val	Pro	Gly	Thr 210	Gly	Lys	Trp	Asp	Trp	Lys 215	Gly	Leu	Leu	Ser 220	Phe	Asp
Leu 225	Asn	Pro	Lys	Val 230	Tyr	Asn	Pro	Gln	Ser 235	Gly	Tyr	Ile	Ala	Asn 240	Trp
Asn	Asn	Ser	Pro	Gln 245	Lys	Asp	Tyr	Pro	Ala 250	Ser	Asp	Leu	Phe	Ala 255	Phe
Leu	Trp	Gly	Gly 260	Ala	Asp	Arg	Val	Thr	Glu 265	Ile	Asp	Thr	Ile 270	Leu	Asp
Lys	Gln	Pro	Arg 275	Phe	Thr	Ala	Asp	Gln	Ala 280	Trp	Asp	Val	Ile 285	Arg	Gln
Thr	Ser	Arg	Arg 290	Asp	Leu	Asn	Leu	Arg	Leu 295	Phe	Leu	Pro	Ala 300	Leu	Lys
Asp 305	Ala	Thr	Ala	Asn 310	Leu	Ala	Glu	Asn	Asp 315	Pro	Arg	Arg	Gln	Leu 320	Val
Asp	Lys	Leu	Ala	Ser 325	Trp	Asp	Gly	Glu	Asn 330	Leu	Val	Asn	Asp 335	Asp	Gly
Lys	Thr	Tyr	Gln 340	Gln	Pro	Gly	Ser	Ala	Ile 345	Leu	Asn	Ala	Trp 350	Leu	Thr
Ser	Met	Leu	Lys 355	Arg	Thr	Val	Val	Ala	Ala 360	Val	Pro	Ala	Pro 365	Phe	Gly
Lys	Trp	Tyr	Ser 370	Ala	Ser	Gly	Tyr	Glu	Thr 375	Thr	Gln	Asp	Gly 380	Pro	Thr
Gly 385	Ser	Leu	Asn	Ile 390	Ser	Val	Gly	Ala	Lys 395	Ile	Leu	Tyr	Glu	Ala 400	Leu
Gln	Gly	Asp	Lys 405	Ser	Pro	Ile	Pro	Gln	Ala 410	Val	Asp	Leu	Phe	Gly 415	Gly
Lys	Pro	Gln	Gln 420	Glu	Val	Ile	Leu	Ala	Ala 425	Leu	Asp	Asp	Ala 430	Trp	Gln
Thr	Leu	Ser	Lys 435	Arg	Tyr	Gly	Asn	Asp	Val 440	Thr	Gly	Trp	Lys 445	Thr	Pro
Ala	Met	Ala	Leu 450	Thr	Phe	Arg	Ala	Asn	Asn 455	Phe	Phe	Gly	Val 460	Pro	Gln
Ala 465	Ala	Ala	Lys	Glu 470	Ala	Arg	His	Gln	Ala 475	Glu	Tyr	Gln	Asn	Arg	Gly
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro

				485				490					495				
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala		
			500					505					510				
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr		
		515					520					525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
	530					535					540						
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr		
545					550				555						560		
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala		
			565					570					575				
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
		580						585				590					
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
	595					600					605						
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
610					615				620								
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625				630					635						640		
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650					655				
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
	660					665						670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
	675				680						685						
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
690					695				700								
Thr	Ser	Glu	Ile	Arg	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705				710				715							720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725					730				735					
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
	740					745						750					
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala						
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<210> 23

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 23

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ggcaccattt catggggatc caccgccggt atgggtgatg gggtcgatat ctttgccgaa 240
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agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480

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cccggccacg acccgctttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagct cgggctatat cgccaactgg 720
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acgcaaacgg cgtaa 2295

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<210> 24

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 24

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ser Thr Ala Gly Met Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95

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Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185				190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Arg
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305				310						315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385				390						395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro
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Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570						575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
	595					600						605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
610						615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650						655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665							670
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
			675				680								685
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730						735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
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<210> 25

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 25

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ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
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cccggccacg acccgcggtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttgcggttct gtggggcggt 780

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ccggcgctga aggacgccac cgcgaaactg gcggaacacg atccgcgccg ccaactgggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtgggt 1080
gccgcgggtc cagcgccggt tggttaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320
gacgtcacca actggaanaa ccctgccatg aaacttacct tccgggccaa caacttcttc 1380
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gatgtgggtg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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acgcaaacgg cgtaa 2295

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<210> 26
 <211> 764
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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	130					135					140				
Gly 145	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
Lys	Asn	Trp	Pro	Glu 165	Trp	Thr	Gln	Gln	Ala 170	Ala	Lys	Gln	Ala	Leu	Thr 160
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
Leu 225	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp 240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Val
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
Asp 305	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val 320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
Gly 385	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu 400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
Ala 465	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly 480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
Glu 545	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr 560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala

				565					570					575			
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
			580					585					590				
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
		595					600					605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625					630				635						640		
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
			660					665						670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
		675				680						685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
	690					695					700						
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705					710					715					720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725					730						735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
		740						745					750				
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala						
		755					760										

<210> 27

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 27

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggg cagggtgatg gggtcgatat ctttgccgaa 240
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccggttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttgcgcgtct gtggggcggt 780
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cagggtggtt 1080

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgtaa 2295

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<210> 28

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 28

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Lys Gln Ala Leu Thr
          165         170         175

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Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Arg
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
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Gly	Ser	Leu	Asn	Ile	Ala	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
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Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600						605		

Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
610						615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
	755						760								

<210> 29

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 29

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ggcaccatth catggggatc caccgccggg caccgtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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ctgtcgtttg atttgaatcc gaaagtgtat aaccgcaggt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttgcgcgtct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcggtgg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaactg gcggaacacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg caccgtggtt 1080
gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
gacgggcaa ccggctcgct gaacatcaga gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtgggtg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacia agagtctcag gaagtgtgtc aggtacagtt ggatcagacc 1680
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcgggtcttt aaccagctga aatggctggg taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 30

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 30

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20         25         30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35         40         45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50         55         60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65         70         75         80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85         90         95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100        105        110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115        120        125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130        135        140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145        150        155        160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165        170        175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
          180        185        190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
          195        200        205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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210	215	220
Leu Asn Pro Lys Val Tyr	Asn Pro Gln Ser Gly	Tyr Ile Ala Asn Trp
225	230	235
Asn Asn Ser Pro Gln Lys	Asp Tyr Pro Ala Ser	Asp Tyr Phe Ala Arg
245	250	255
Leu Trp Gly Gly Ala Asp	Arg Val Thr Glu Ile	Asp Thr Ile Leu Asp
260	265	270
Lys Gln Pro Arg Phe Thr	Ala Asp Gln Ala Trp	Asp Val Ile Arg Gln
275	280	285
Thr Ser Arg Arg Asp Leu	Asn Leu Arg Leu Phe	Leu Pro Ala Leu Lys
290	295	300
Asp Ala Thr Ala Asn Leu	Ala Glu Asn Asp Pro	Arg Arg Gln Leu Val
305	310	315
Asp Lys Leu Ala Ser Trp	Asp Gly Glu Asn Leu	Val Asn Asp Asp Gly
325	330	335
Lys Thr Tyr Gln Gln Pro	Gly Ser Ala Ile Leu	His Ala Trp Leu Lys
340	345	350
Ser Met Leu Lys Arg Thr	Val Val Ala Ala Val	Pro Ala Pro Phe Gly
355	360	365
Lys Trp Tyr Ser Arg Thr	Gly Tyr Glu Thr Thr	Gln Asp Gly Pro Thr
370	375	380
Gly Ser Leu Asn Ile Arg	Val Gly Ala Lys Ile	Leu Tyr Glu Ala Leu
385	390	395
Gln Gly Asp Lys Ser Pro	Ile Pro Gln Ala Val	Asp Leu Phe Gly Gly
405	410	415
Lys Pro Gln Gln Glu Val	Ile Leu Ala Ala Leu	Asp Asp Ala Trp Gln
420	425	430
Thr Leu Ser Lys Arg Tyr	Gly Asn Asp Val Thr	Asn Trp Lys Thr Pro
435	440	445
Ala Met Lys Leu Thr Phe	Arg Ala Asn Asn Phe	Phe Gly Val Pro Gln
450	455	460
Ala Ala Ala Lys Glu Ala	Arg His Gln Ala Glu	Tyr Gln Asn Arg Gly
465	470	475
Thr Glu Asn Asp Met Ile	Val Phe Ser Pro Thr	Ser Gly Asp Arg Pro
485	490	495
Val Leu Ala Trp Asp Val	Val Ala Pro Gly Gln	Ser Gly Phe Ile Ala
500	505	510
Pro Asp Gly Lys Ala Asp	Lys His Tyr Asp Asp	Gln Leu Lys Met Tyr
515	520	525
Glu Ser Phe Gly Arg Lys	Ser Leu Trp Leu Thr	Pro Gln Asp Val Asp
530	535	540
Glu His Lys Glu Ser Gln	Glu Val Leu Gln Val	Gln Leu Asp Gln Thr
545	550	555
Glu Val Lys Ile Val Arg	Asp Glu Tyr Gly Met	Pro His Ile Tyr Ala
565	570	575
Asp Asp Thr Tyr Arg Leu	Phe Tyr Gly Tyr Gly	Tyr Val Val Ala Gln
580	585	590
Asp Arg Leu Phe Gln Met	Glu Met Ala Arg Arg	Ser Thr Gln Gly Thr
595	600	605
Val Ser Glu Val Leu Gly	Lys Tyr Phe Val Ser	Phe Asp Lys Asp Ile
610	615	620
Arg Gln Asn Tyr Trp Pro	Asp Ser Ile Arg Ala	Gln Ile Ala Ser Leu
625	630	635
Ser Ala Glu Asp Lys Asp	Ile Leu Gln Gly Tyr	Ala Asp Gly Met Asn

				645					650					655					
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln				
			660					665						670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp				
		675					680							685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser				
	690					695					700								
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys				
705					710					715					720				
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu				
			725					730						735					
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr				
			740					745						750					
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala								
		755					760												

<210> 31

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 31

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcggtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
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gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
gacgggcca cggctcgt gaacatcaaa gtggggcgga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat ccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggcca caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggg tcttgccctgg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacia agagtctcag gaagtgtcgc aggtacagtt ggatcagacc 1680

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gaggtaaga tcgttcgca tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtcagtttt 1860
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggg taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 32

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 32

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20     25     30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35     40     45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50     55     60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85     90     95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100    105    110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu
245    250    255

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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	
		275					280					285				
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	
	290					295					300					
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	
305					310				315						320	
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	
			325					330					335			
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	
			340				345						350			
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	
		355				360						365				
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	
	370					375					380					
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	
385					390					395					400	
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	
			405					410						415		
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	
			420					425					430			
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro	
		435				440						445				
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	
	450				455					460						
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	
465					470				475						480	
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	
			485					490						495		
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	
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Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	
		515					520					525				
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	
	530					535					540					
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	
545					550					555					560	
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	
			565					570						575		
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	
		580						585					590			
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	
		595				600						605				
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile	
	610					615					620					
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	
625					630					635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
			645						650					655		
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	
		660						665					670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
		675					680					685				

Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
		755					760								

<210> 33

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 33

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aaactttccg	ccgagaagcc	gggctattac	cagcataacg	gcgagtgggt	gaagatgttg	300
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acgctgcacg	gcaacgtcat	taaaactgat	actgcgacgc	agaccgccta	tgccaaagcg	420
cgcgcctggg	atggcaaaga	ggtggcgtcc	ctgctggcgt	ggacgcacca	gatgaaggcc	480
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cccggccacg	acccgcgttt	gccggttccc	ggcactggaa	aatgggactg	gaaagggttg	660
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gcggatcgag	ttactgagat	cgacacgatc	ctcgataagc	aaccgcgctt	caccgccgat	840
caggcgtggg	atgtgatccg	ccaaaccagc	cgtcgggatc	tcaacctgcg	gttgttctta	900
ccggcgctga	aggacgccac	cgcgaaacctg	gcggaaaacg	atccgcgccg	ccaactgggtg	960
gataaactgg	cgagctggga	cggcgaaaac	cttgtcaacg	atgacggaaa	aacctatcag	1020
caaccgggat	cggcgattct	tcacgcctgg	ctgaaaagca	tgctcaagcg	cacgggtggtt	1080
gccgcggtcc	cagcgccgtt	tggttaagtgg	tacagccgta	ccggctatga	aaccaccag	1140
gacggggcaa	ccggctcgct	gaacatcaaa	gtgggggcca	aaatcctcta	cgaagctctg	1200
cagggtgata	agtcgccaat	cccgcaggcg	gtcgatctgt	ttggcgggaa	accgcagcag	1260
gaagtaatac	tggcggcgct	ggacgacgct	tggcagacgc	tgtcaaaacg	ctacggtaac	1320
gacgtcacca	actggaaaac	ccctgccatg	aaacttacct	tccggggcaa	caacttcttc	1380
ggcgtgccgc	aggcggcagc	aaaagaggcg	cgctcatcagg	cggagtacca	gaaccgcggt	1440
acggaaaacg	acatgattgt	cttctcaccg	acgtcgggtg	accgcccggt	tcttgccctgg	1500
gatgtggtgg	cgccggggca	aagcggtttt	atcgcgccgg	atggcaaagc	cgataagcac	1560
tatgacgatc	agctgaaaat	gtacgagagc	tttggccgta	aatcgctgtg	gttaacgcct	1620
caggacgttg	acgagcacia	agagtctcag	gaagtgtctg	aggtacagtt	ggatcagacc	1680
gaggtaaga	tcgttcgcga	tgaatacggc	atgccgcata	tttacgccga	tgataacctat	1740
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gcgcgccgca	gtactcaggg	gaccgtctcc	gaggtgctgg	gcaaatactt	cgtcagtttt	1860
gataaagata	ttcgccagaa	ctactggccg	gattctattc	gcgcgcagat	agcttccctc	1920
tccgctgagg	ataaagatat	tctgcagggc	tatgccgatg	gcatgaatgc	gtggatcgat	1980

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aaagtgaacg ccagccccga taagctgtta cccagcagct tctccacctt tggtttttaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggctctt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa 2295

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<210> 34

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 34

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1      5      10      15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20     25     30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35     40     45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50     55     60
Trp Gly Ser Thr Ala Gly Leu Gly Asp Gly Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85     90     95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100    105    110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Arg
245    250    255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260    265    270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275    280    285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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290	295	300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val		
305	310	315
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly		
	325	330
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys		
	340	345
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly		
	355	360
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr		
	370	375
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu		
385	390	395
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly		
	405	410
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln		
	420	425
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Asn Trp Lys Thr Pro		
	435	440
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln		
	450	455
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly		
465	470	475
Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro		
	485	490
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala		
	500	505
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr		
	515	520
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp		
	530	535
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr		
545	550	555
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala		
	565	570
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln		
	580	585
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr		
	595	600
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Ser Phe Asp Lys Asp Ile		
	610	615
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu		
625	630	635
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn		
	645	650
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln		
	660	665
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp		
	675	680
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser		
	690	695
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys		
705	710	715
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu		

				725						730					735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
				740											
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
				755											

<210> 35
 <211> 2295
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 35
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 gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
 ggaccatttt catggggatc caccgccggg caccgtgatg gggtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
 acgtgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
 cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
 tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
 cccggccacg acccgctgtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
 ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
 aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttgcgaaact gtggggcggt 780
 gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
 caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
 ccggcgctga aggacgccac cggaacctg gcggaacac atccgcgccg ccaactggtg 960
 gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
 caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg caccgtggtt 1080
 gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
 gacgggcaa ccggctcgtc gaacatcaaa gtggggcgga aaatcctcta cgaagctctg 1200
 cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
 gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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 gatgtggtgg cgccggggca aagcgggttt atcgcgccgg atggcaaagc cgataagcac 1560
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 ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
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<210> 36

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 36

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1      5      10      15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
      20      25      30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85      90      95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
      100     105     110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
      115     120     125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130     135     140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145     150     155     160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
      165     170     175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
      180     185     190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195     200     205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210     215     220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225     230     235     240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Lys
      245     250     255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
      260     265     270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
      275     280     285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
      290     295     300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305     310     315     320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
      325     330     335

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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	645	650	655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	660	665	670
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	675	680	685
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	690	695	700
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	705	710	715
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	725	730	735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	740	745	750
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala					755	760	

<210> 37
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 37
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 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
 ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
 acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
 cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
 tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
 cccggccacg acccgcgttt gccggttccc ggcaactgaa aatgggactg gaaagggttg 660
 ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
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 gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
 caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
 gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
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 gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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 gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
 acgcaaacgg cgcaccatca ccatcacat taa 2313

<210> 38
 <211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 38

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
		290				295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr

370		375		380
Gly Ser Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu				
385		390		395
Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly				400
		405		410
Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln				415
		420		425
Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Asp Asn Trp Lys Thr Pro				430
		435		440
Ala Met Lys Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln				445
		450		455
Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly				460
		465		470
Thr Ile Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asp Arg Pro				475
		485		490
Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala				495
		500		505
Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr				510
		515		520
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp				525
		530		535
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr				540
		545		550
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala				555
		565		570
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln				575
		580		585
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr				590
		595		600
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Trp Phe Asp Lys Asp Ile				605
		610		615
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu				620
		625		630
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn				635
		645		650
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln				655
		660		665
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp				670
		675		680
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser				685
		690		695
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys				700
		705		710
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu				715
		725		730
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr				735
		740		745
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His				750
		755		760
His His				765
770				

<211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 39
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 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
 ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
 acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
 cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
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<210> 40
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 40

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			20					25					30			
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	
		35					40					45				
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	
	50					55					60					
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu	
65					70					75					80	
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	
				85					90					95		
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	
			100					105					110			
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	
		115					120					125				
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	
	130					135						140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	
145					150					155					160	
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	
				165					170					175		
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	
			180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	
	195						200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	
	210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	
225					230					235					240	
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	
				245					250					255		
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	
		260						265					270			
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	
		275					280					285				
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	
	290					295					300					
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	
305					310					315					320	
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	
				325					330					335		
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	
			340					345					350			
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	
		355					360					365				
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	
	370					375					380					
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	
385					390					395					400	

<210> 41
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 41

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ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggttccc ggccactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaatggg tacagccgta ccggctatga aaccaccag 1140
gacgggcaa ccggctcgtc gaacatcaaa gtggggcgga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat ccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgacccatca ccaccacat taa 2313
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<210> 42

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 42

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Ala	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135						140			
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275				280						285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln

<400> 43

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aaagtgaacg ccagccccga taagctgtta cccagcagc tctccacctt tggttttaaa 2040
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acgcaaacgg cgcaccatca ccatcccat taa 2313
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<210> 44

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 44

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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5

10

15

Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr	20	25	30
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu	65	70	75
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	115	120	125
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	435	440	445

Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
450						455				460					
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Ala
			485						490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
		500						505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
	515					520						525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
530					535					540					
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
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Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600						605		
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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		660						665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675					680						685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
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Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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770															

<210> 45

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 45

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acgcaaacgg cgaccatca ccatcaccat taa 2313

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<210> 46

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 46

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70				75						80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
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Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165						170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200				205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
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Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
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Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
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Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
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Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
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Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390										

465					470					475				480	
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
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		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Gln	Asp	Gln	Thr
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
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Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
	595						600					605			
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675						680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 47

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 47

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<210> 48

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 48

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1           5           10          15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
        35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
       50          55          60

```

Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu	65	70	75	80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp		85	90	95
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln		100	105	110
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys		115	120	125
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp		130	135	140
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala		145	150	155
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr		160	165	170
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His		175	180	185
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro		190	195	200
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp		205	210	215
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp		220	225	230
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu		235	240	245
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp		250	255	260
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		265	270	275
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		280	285	290
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val		295	300	305
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly		310	315	320
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys		325	330	335
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly		340	345	350
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr		355	360	365
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu		370	375	380
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly		385	390	395
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln		400	405	410
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro		415	420	425
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln		430	435	440
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly		445	450	455
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro		460	465	470
																	475	480	485
																	490	495	

Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala		
			500					505					510				
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr		
		515					520					525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
		530				535					540						
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Ser	Asp	Gln	Thr		
545					550				555						560		
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala		
			565						570					575			
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
		580						585					590				
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
		595				600						605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625					630					635					640		
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645						650					655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
		660						665					670				
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
		675				680						685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
	690					695				700							
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705				710						715					720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725					730						735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
		740						745					750				
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His		
		755				760						765					
His	His																
	770																

<210> 49

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 49

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gggccgcagt tcggttgac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggtttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aacccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gccgcgggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
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gatgtggtgg cgccggggca aagcgggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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aaagtgaacg ccagccccga taagctgtta cccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttctctgacg ctaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcag ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgcaccatca ccataccat taa 2313

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<210> 50

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 50

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1           5           10          15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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				85				90					95		
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185				190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	

	515		520		525
Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp					
530		535		540	
Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr					
545		550		555	560
Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala					
	565		570		575
Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln					
	580		585		590
Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr					
	595		600		605
Val Ser Glu Val Leu Gly Lys Tyr Phe Val Trp Phe Asp Lys Asp Ile					
610		615		620	
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu					
625		630		635	640
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn					
	645		650		655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln					
	660		665		670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp					
	675		680		685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ala					
690		695		700	
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys					
705		710		715	720
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu					
	725		730		735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr					
	740		745		750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His					
	755		760		765
His His					
770					

<210> 51

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 51

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ggctatgacg tcaccggcaa tacgccgttt gccctaccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggg cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat gaagcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgcataccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataacc ggcctatcc ggatcgccag 600

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aacaactcgc cgcaaaaaga ctacccggcc tctgattact ttgcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgata ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaactg gcggaaaacg atccgcgccg ccaactgggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
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gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgacccatca ccatcaccat taa 2313

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<210> 52

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 52

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Leu Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110

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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	His	Thr	165	170	175
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Arg	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Gly	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Ser	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540

Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570						575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585						590	
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
	595						600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
610						615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740				745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
		755					760					765			
His	His														
	770														

<210> 53

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 53

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcggtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
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ccggcgctga aggacgccac cgcgaaactg gcggaaaacg atccgcgccg ccaactgggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtgggt 1080
gccgcgggtc cagcgccgtt tggtagaag tacagccgta ccggctatga aaccaccag 1140
gacgggcca cggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca actggaanaa ccctgccatg aaacttacct tccgggcca caacttcttc 1380
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgccctg 1500
gatgtgggtg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcaggcat ggcggtcttt aaccagctga aatggctggg taatccttcc 2220
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

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<210> 54

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 54

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20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115        120        125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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	130					135					140				
Gly 145	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
Lys 165	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
Ile 180	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
Thr 195	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
Val 210	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
Leu 225	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
Asn 245	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
Leu 260	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
Lys 275	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
Thr 290	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
Asp 305	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
Asp 325	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
Lys 340	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
Ser 355	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
Lys 370	Lys	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
Gly 385	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
Gln 400	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
Lys 420	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
Thr 435	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
Ala 450	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
Ala 465	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
Thr 485	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
Val 500	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
Pro 515	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
Glu 530	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
Glu 545	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
Glu 560	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala

				565					570					575			
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
			580					585					590				
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
		595					600					605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile		
		610				615					620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625					630				635						640		
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
			660					665						670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
		675				680						685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
	690					695					700						
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705					710					715					720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
				725				730						735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
		740						745					750				
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His		
		755				760						765					
His	His																
	770																

<210> 55

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 55

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catgggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactgttac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccggcc tctgattact ttgcgtgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcaaacctg gcggaacac atccgcgccg ccaactggtg 960

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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccggt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacggggccaa ccggcgggct gaacatcaaa gtggggggcga aaatcctcta cgaagctctg 1200
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

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<210> 56

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 56

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160

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Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590

Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
	770														

<210> 57

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 57

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ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720
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caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaactg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaac aacctatcag 1020
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acgcaaacgg cgcacatca ccatcaccat taa 2313

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<210> 58

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 58

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
           35           40           45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
           50           55           60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65           70           75           80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
           85           90           95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100          105          110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115          120          125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130          135          140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145          150          155          160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165          170          175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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			180								185								190				
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro								
		195					200					205											
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp								
	210					215					220												
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp								
225					230					235					240								
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu								
				245					250					255									
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp								
			260					265					270										
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln								
		275					280					285											
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys								
		290				295					300												
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val								
305				310					315						320								
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly								
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys								
			340				345						350										
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly								
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Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr								
		370				375					380												
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu								
385				390					395						400								
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly								
				405				410						415									
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln								
			420					425					430										
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro								
		435				440						445											
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln								
		450				455					460												
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly								
465				470																			

610	615	620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu		
625	630	635
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn		
645	650	655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln		
660	665	670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp		
675	680	685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser		
690	695	700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys		
705	710	715
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu		
725	730	735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr		
740	745	750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His		
755	760	765
His His		
770		

<210> 59

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 59

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcaactggaa aatgggactg gaaagggttg 660
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aacaactcgc cgcaaaaaga ctaccggcc tctgattact ttgcgctgct gtggggcggt 780
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gacgggcaa ccggcgggct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320

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<210> 60

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 60

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195         200         205

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Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Gly	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
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Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705				710						715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725					730						735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745						750	
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 61

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 61

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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaagcg ctacggtaac 1320
gacgtcgaca actggaanaa cctgccatg aaacttacct tccgggcca caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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caggacgttg acgagcacia agagtctcag gaagtgtgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 1860
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<210> 62

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 62

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1          5          10          15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180         185         190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195         200         205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210         215         220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp

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225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280				285				
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310				315					320	
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
	355						360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
	435						440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln


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gaggtaaga tcgttcgca tgaatacggc atgccgcata tttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 1860
gataaagata ttcgccaaaa ctactggccg gattctattc gcgcgcagat agcttccttc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta cccagcaggt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaaccg cgccaccatca ccatccacat taa 2313

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<210> 64

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 64

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
      20     25     30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35     40     45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
      50     55     60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85     90     95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
      100    105    110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
      115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
      165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
      180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu
      245    250    255

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Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310				315						320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			

Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
	770														

<210> 65

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 65

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
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caggacgttg acgagacca agagtctcag gaagtgtgc aggtacagtt ggatcagacc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata ttacgccga tgatacctat 1740
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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860

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aaagtgaacg ccagccccga taagctgtta cccagcagtg tctccacctt tggtttttaa 2040
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acgcaaacgg cgtaa                                     2295

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<210> 66

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 66

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
20         25         30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35         40         45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50         55         60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asn Val Asp Ile Phe Ala Glu
65         70         75         80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85         90         95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100        105        110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115        120        125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130        135        140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145        150        155        160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165        170        175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180        185        190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195        200        205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210        215        220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225        230        235        240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Val Trp Ala Phe
245        250        255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260        265        270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

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		275					280				285				
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Ile	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Lys	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu

705		710		715		720									
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
		755						760							

<210> 67
 <211> 2295
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 67

agcaatatgt	gggtgattgg	caaaaacaaa	gcccaggatg	cgaaggccat	tatggtcaat	60
gggccgcagt	ttggttgac	cgtgccggcg	tacacctacg	gtatcggcct	gcacggcgcg	120
ggctatgacg	tcaccggcaa	tacgccgttt	gcctatccgg	gcctcgtttt	tggtcacaac	180
ggcaccattt	catggggatc	caccgccggg	gggggtgatg	atgtcgatat	ctttgccgaa	240
aaactttccg	ccgagaagcc	gggctattac	cagcataacg	gcgagtgggt	gaagatgttg	300
agccgcaagg	agactattgc	ggtcaaagac	ggccagccgg	agacctttac	cgtttggcgc	360
acgtgcacg	gcaacgtcat	taaaaccgat	actgcgacgc	agaccgccta	tgccaaagcg	420
cgcgcctggg	atggcaaaga	ggtggcgtcc	ctgctggcgt	ggacgcacca	gatgaaggcc	480
aaaaactggc	cggagtggac	gcagcaggcg	gccaaacagg	cgctgaccat	taactggtac	540
tacgccgatg	tgaacggcaa	tatcggctat	gtgcataacc	gcgcctatcc	ggatcgccag	600
cccggccacg	acccgcgttt	gccggttccc	ggcactggaa	aatgggactg	gaaagggttg	660
ctgtcgtttg	atttgaatcc	gaaagtgtat	aaccgcagct	cgggctatat	cgccaactgg	720
aacaactcgc	cgcaaaaaga	ctaccgggcc	tctgatctgt	ggggcttcct	gtggggcggt	780
gcggatcgag	ttactgagat	cgacacgatc	ctcgataagc	aaccgcgctt	caccgccgat	840
caggcgtggg	atgtgatccg	ccaaaccagc	cgtcgggatc	tcaacctgcg	gttgttctta	900
ccggcgctga	aggacgccac	cgcgaaactg	gcggaaaacg	atccgcgccg	ccaactggtg	960
gataaactgg	cgagctggga	cggcgaaaac	cttgtcaacg	atgacggaaa	aacctatcag	1020
caaccgggat	cggcgattct	taacgcctgg	ctgaccagca	tgctcaagcg	cacggtggtt	1080
gccgcggtcc	cagcgcggtt	tggttaagatt	tacagcgcca	gtggctatga	aaccaccag	1140
gacgggcaa	ccggctcgct	gaacatcagc	gtggggcgga	aatcctcta	cgaagctctg	1200
cagggtgata	agtcgccaat	cccgcaggcg	gtcgatctgt	ttggcgggaa	accgcagcag	1260
gaagtaatac	tggcggcgct	ggacgacgct	tggcagacgc	tgtcaaaacg	ctacggtaac	1320
gacgtcaccg	gctggaaaac	ccctgccatg	gcgcttacct	tccgggcaa	taacttcttc	1380
ggcgtgccgc	aggcggcagc	aaaagaggcg	cgtcatcagg	cggagtacca	gaaccgcggt	1440
acggaaaacg	acatgattgt	cttctcaccg	acgtcgggta	accgcccggt	tcttgccctgg	1500
gatgtgggtg	cgccggggca	aagcggtttt	atcgcgccgg	atggcaaagc	cgataagcac	1560
tatgacgatc	agctgaaaat	gtacgagagc	tttggccgta	aatcgctgtg	gttaacgcct	1620
caggacgttg	acgagacca	agagtctcag	gaagtgtctg	aggtacagtt	ggatcagacc	1680
gaggttaaga	tcgttcgcga	tgaatacggc	atgccgcata	tttacgccga	tgatacctat	1740
cgactgtttt	acggctatgg	ctacgtgggtg	gcgcaggatc	gcctgtttcca	gatggaaatg	1800
gcgcgccgca	gtactcaggg	gaccgtctcc	gaggtgctgg	gcaaagcatt	cgtcagtttt	1860
gataaagata	ttcgccagaa	ctactggccg	gattctattc	gcgcgcagat	agcttccctc	1920
tccgtgagg	ataaatccat	tctgcagggc	tatgccgatg	gcatgaatgc	gtggatcgat	1980
aaagtgaacg	ccagccccga	taagctgtta	ccccagcagt	tctccacctt	tggtttttaa	2040
cccaagcatt	gggaaccgtt	tgatgtggcg	atgatttttg	tcggcaccat	ggcgaaccgt	2100
ttctctgaca	gcaccagcga	aattgataac	ctggcgctgc	tgacggcgct	aaaagacaaa	2160

tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
 gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
 acgcaaacgg cgtaa 2295

<210> 68
 <211> 764
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 68
 Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
 1 5 10 15
 Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Val Pro Ala Tyr Thr
 20 25 30
 Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
 35 40 45
 Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
 50 55 60
 Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
 65 70 75 80
 Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
 85 90 95
 Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
 100 105 110
 Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
 115 120 125
 Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
 130 135 140
 Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
 145 150 155 160
 Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
 165 170 175
 Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
 180 185 190
 Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
 195 200 205
 Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220
 Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
 225 230 235 240
 Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Trp Gly Phe
 245 250 255
 Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
 260 265 270
 Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
 275 280 285
 Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300
 Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320

Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Ile	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Thr	Pro
		435				440						445			
Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
		530				535					540				
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
		610				615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln</															

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 69
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 69
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gggccgcagt ttggttggtta tgtgccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgtgacag gcaacgtcat ttggaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggttccc ggcaactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagct cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcggtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaactg gcggaacacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacgaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag 1140
gacgggcca cggctcgt gaacatcagc gtggggcgga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat ccgcaggcg gtcatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggcca taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cgagtagcca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccgtt tcttgccctg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacca agagtctcag gaagtgtgc aggtacagtt ggatcagacc 1680
gaggtttaaga tcgttcgcga tgaatacggc atgccgcata ttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtcagtttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta cccagcagct tctccacctt tggtttttaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcaaacgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcag gccggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaac 2280
acgcaaacgg cgtaa 2295

<210> 70
 <211> 764
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 70

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala	1	5	10	15
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Tyr	Val	Pro	Ala	Tyr	Thr	20	25	30	
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45	
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60	
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu	65	70	75	80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110	
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp	115	120	125	
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140	
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155	160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr	340	345	350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly				

<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 71
agcaatatgt ggggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcttggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggtttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttgcgtgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaactg gcggaaaacg atccgcgccg ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
gacgggcaa ccggctcgtc gaacatcaaa gtggggggcg aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggcaa caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgccctg 1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcaca agagtctcag gaagtgtgc aggtacagtt ggatcagacc 1680
gaggtaaga tcgttcgcga tgaatacggc atgccgcata ttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtgggt gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaataactt cgtcagtttt 1860
gataaagata ttcgatgaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta cccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggccaaccgt 2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaaccg cgtaa 2295

<210> 72
<211> 764
<212> PRT
<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 72

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5					10					15	
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135						140			
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asp	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195						200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400

$\langle 220 \rangle$

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 73

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ggcaccatth catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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<210> 74

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 74

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			20					25					30				
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr		
		35					40					45					
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser		
	50				55						60						
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu		
65				70					75						80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp		
			85					90					95				
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln		
			100					105					110				
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys		
		115					120					125					
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp		
	130				135						140						
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala		
145				150					155						160		
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr		
			165					170						175			
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His		
			180					185				190					
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro		
	195				200						205						
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp		
	210				215					220							
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp		
225				230					235						240		
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu		
			245					250						255			
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp		
		260						265					270				
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		
	275						280					285					
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		
	290				295					300							
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val		
305				310					315						320		
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly		
			325					330					335				
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys		
		340					345						350				
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly		
	355					360						365					
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr		
	370				375						380						
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu		
385				390					395						400		
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly		
			405					410						415			
Lys	Pro	Gln	Gln	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln			
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Thr	Leu	Ser	Gly	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro		


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<210> 76

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 76

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45

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Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70				75						80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
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Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
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Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
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Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
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Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
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Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
		370				375					380				
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	
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Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	
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625					630					635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
			645						650					655		
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		660						665					670			
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	675						680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	
	690					695				700						
Thr	Ser	Lys	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	
705					710					715					720	
Tyr	Gly	Asp	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	
			725						730					735		
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	
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Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala					
		755					760									

<210> 77

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 77

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acgcaaacgg cgtaa 2295

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<210> 78

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 78

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp

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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
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Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
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			260					265					270		
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Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
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Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
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Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
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<210> 79

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 79

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<210> 80

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 80

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
           35           40           45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
           50           55           60
Trp Gly Ala Thr Ala Gly Met Gly Asp Gly Val Asp Ile Phe Ala Glu
65           70           75           80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
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Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
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<210> 81

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 81

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gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 1860
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<210> 82

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 82

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1           5           10          15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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				165				170				175			
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185				190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
	355						360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr


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acgcaaacgg cgtaa 2295

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<210> 84

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 84

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20        25        30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35        40        45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50        55        60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65        70        75        80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85        90        95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100       105       110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115       120       125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130       135       140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145       150       155       160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165       170       175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180       185       190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195       200       205

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Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
																		640

Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705				710						715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725					730						735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
		740					745						750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
	755					760									

<210> 85

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 85

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ggcaccattt	catggggatc	caccgccggt	cgtggtgatg	gtgtcgatat	ctttgccgaa	240
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agccgcaagg	agactattgc	ggtcaaagac	ggccagccgg	agacctttac	cgtttggcgc	360
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gatgtggtgg	cgccggggca	aagcggtttt	atcgcgccgg	atggcaaagc	cgataagcac	1560
tatgacgatc	agctgaaaat	gtacgagagc	tttggccgta	aatcgctgtg	gttaacgcct	1620

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<210> 86

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 86

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ser Thr Ala Gly Arg Gly Asp Gly Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85      90      95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
      100     105     110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
      115     120     125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130     135     140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145     150     155     160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
      165     170     175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
      180     185     190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195     200     205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210     215     220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225     230     235     240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe

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				245					250				255				
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp		
			260					265					270				
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		
		275					280					285					
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		
	290					295					300						
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val		
305				310					315						320		
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly		
			325					330						335			
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr		
		340				345							350				
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly		
	355					360						365					
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr		
	370				375						380						
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu		
385				390					395						400		
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly		
			405					410						415			
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln		
		420					425						430				
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Thr	Pro		
	435					440						445					
Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln		
	450				455						460						
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly		
465				470					475						480		
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro		
			485					490						495			
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala		
		500					505						510				
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr		
	515					520						525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
	530				535						540						
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		580						585					590				
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	595					600						605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625				630					635						640		
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
	660						665					670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		

675	680	685
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690	695	700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys		
705	710	715
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu		
725	730	735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr		
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala		
755	760	

<210> 87

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 87

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gataaactta ttcgccgaa ctactggccg gattctattc gcgcgcagat agcttccttc 1920

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<210> 88

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 88

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35        40        45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50        55        60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65        70        75        80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85        90        95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100       105       110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115       120       125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130       135       140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145       150       155       160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165       170       175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180       185       190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195       200       205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210       215       220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225       230       235       240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu
245       250       255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260       265       270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
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Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Ser	Phe	Gly
		355				360						365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
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Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Thr	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
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Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
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Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595				600						605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Leu	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Val	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720

Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 89

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 89

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<210> 90
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 90

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45	
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60	
Trp	Gly	Ser	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu	65	70	75	80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110	
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	115	120	125	
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140	
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155	160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val				

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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly			
					325						330						335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys			
					340						345						350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly			
					355						360						365	
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr			
					370						375						380	
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly			
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln			
					420						425						430	
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro			
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Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln			
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Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly			
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro			
					485						490						495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala			
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Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr			
					515						520						525	
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp			
					530						535						540	
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr			
545						550						555						560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala			
					565						570						575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln			
					580						585						590	
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr			
					595						600						605	
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile			
					610						615						620	
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu			
625						630						635						640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn			
					645						650						655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln			
					660						665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp			
					675						680						685	
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser			
					690						695						700	
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys			
705						710						715						720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu			
					725						730							

	740		745		750
Pro	Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr	Ala His His His His			
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His His					
770					

<210> 91
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 91
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 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
 ggccaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
 acgtgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
 cgcgcctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
 tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
 cccggccacg acccgctgtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
 ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720
 aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttggctctgt gtggggcggt 780
 gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
 caggcggtgg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
 ccggcgctga aggacgccac cggaacctg gcggaacac atccgcgccg ccaactggtg 960
 gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
 caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
 gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
 gacgggcca cggcggggt gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
 cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
 gaagtaatac tggcggcgct ggacgacgtc tggcagacgc tgtcaaaacg ctacggtaac 1320
 gacgtcgaca actggaanaa ccctgccatg aaacttacct tccgggcca caacttcttc 1380
 ggctgcccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcgtt 1440
 acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgccctg 1500
 gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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 caggacgttg acgagcaca agagtctcag gaagtgtgc aggtacagtt ggatcagacc 1680
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 gcgcgccgca gtactcaggg gaccgtctcc gaggtgtcgg gcaaataact cgtctggttt 1860
 gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
 tccgtgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
 aaagtgaacg ccagccccga taagctgtta cccagcagt tctccacctt tgggttttaa 2040
 cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
 ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
 tacggcaaac agcaggcat ggcggtcttt aaccagctga aatggctggt taatccttc 2220
 gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaa 2280

acgcaaacgg cgcaccatca ccatcaccat taa

2313

<210> 92

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 92

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
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Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Gly	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	

Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	645	650	655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	660	665	670
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	675	680	685
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	690	695	700
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	705	710	715
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	725	730	735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	740	745	750
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His	755	760	765

His His
770

<210> 93
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 93
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgtgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagct cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgattact tggcgctgct gtggggcggt 780
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caggcggtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaacct gcggaacacg atccgcgccg ccaactggtg 960
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caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacggggcaa ccggcgggct gaacatcaaa gtgggggcca aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat ccgcaggcg gtcatctgtt ttggcgggaa accgcagcag 1260
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ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcag ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaac 2280
acgcaaacgg cgaccatca ccatcaccat taa 2313

<210> 94
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 94

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
		130				135						140			
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Leu	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
		290				295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly

		355					360					365				
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	
	370					375					380					
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	
385					390					395					400	
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	
				405					410					415		
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	
			420					425					430			
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	
		435					440					445				
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	
	450					455					460					
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	
465				470						475					480	
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	
			485					490					495			
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	
			500				505						510			
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	
		515					520					525				
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	
	530					535					540					
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	
545				550						555					560	
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	
			565						570					575		
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	
			580					585					590			
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	
		595					600					605				
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile	
	610					615					620					
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	
625				630						635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
			645						650					655		
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	
			660					665					670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
		675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	
	690					695					700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	
705				710				</								

<210> 95
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 95
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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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<210> 96
<211> 770
<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 96

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
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Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
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Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
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Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
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Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
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Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
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Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
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						375						380			

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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln			
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Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro			
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	450					455					460							
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly			
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro			
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		515					520					525						
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr			
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln			
			580					585					590					
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr			
		595				600						605						
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile			
	610				615						620							
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu			
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn			
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Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln			
			660					665					670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp			
		675					680					685						
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser			
	690					695				700								
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys			
705					710					715					720			
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu			
				725					730					735				
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr			
			740					745					750					
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His			
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<210> 97

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 97

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<210> 98

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 98

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Leu Val His Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
      100      105      110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
      115      120      125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130      135      140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Lys Gln Ala Leu Thr
      165      170      175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
      180      185      190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195      200      205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210      215      220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225      230      235      240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu
      245      250      255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
      260      265      270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
      275      280      285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
      290      295      300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305      310      315      320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
      325      330      335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
      340      345      350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
      355      360      365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
      370      375      380
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<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 99

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<210> 100

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 100

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45	
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Cys	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60	
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu	65	70	75	80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110	
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	115	120	125	
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140	
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155	160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365	
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380	
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395	400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430	

Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
			485						490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
			645						650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675					680						685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
		740					745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
	770														

<210> 101

<211> 2298

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 101

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gcgggctatg acgtcaccgg caatacgccg tttgcctatc cgggcctcgt ttttggtcac 180
aacggcacca tttcatgggg atccaccgcc ggtgggggtg atgatgtcga tatctttgcc 240
gaaaaacttt ccgccgagaa gccgggctat taccagcata acggcgagtg ggtgaagatg 300
ttgagccgca aggagactat tgcggtcaaa gacggccagc cggagacctt taccgtttgg 360
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tactacgccg atgtgaacgg caatatcggc tatgtgcata ccggcgccta tccggatcgc 600
cagcccggcc acgaccgcg tttgccggtt cccggcactg gaaaatggga ctggaaaggg 660
ttgctgtcgt ttgatttgaa tccgaaagtg tataaccgc agtcgggcta tatcgccaac 720
tggaacaact cgccgcaaaa agactaccgc gcctctgatc tgcttcgcgtt cctgtggggc 780
ggtgcggatc gagttactga gatcgacacg atcctcgata agcaaccgcg cttaccgcc 840
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cagcaaccgg gatcggcgat tcttaacgcc tggctgacca gcatgctcaa gcgcacgggtg 1080
gttgccgcgg tcccagcgcc gtttggtgta tggtacagcg ccagtggcta tgaaaccacc 1140
caggacgggc caaccggctc gctgaacatc agcgtggggg cgaaaatcct ctacgaagct 1200
ctgcagggtg ataagtcgcc aatcccgcag gcggtcgatc tgtttggcgg gaaaccgcag 1260
caggaagtaa tactggcggc gctggacgac gcttggcaga cgctgtcaaa acgctacggt 1320
aacgacgtca ccggctggaa aaccctgcc atggcgctta ccttccgggc caataacttc 1380
ttcggcgtgc cgcaggcggc agcaaaagag gcgcgtcatc aggcggagta ccagaaccgc 1440
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tgggatgtgg tggcgccggg gcaaagcggg tttatcgcg cggatggcaa agccgataag 1560
cactatgacg atcagctgaa aatgtacgag agctttggcc gtaaatacgct gtggttaacg 1620
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tttgataaac gtattcgcca gaactactgg ccggattcta ttcgcgcgca gatagcttcc 1920
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gataaagtga acgccagccc cgataagctg ttaccccagc agttctccac ctttggtttt 2040
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cgtttctctg acagcaccag cgaaattgat aacctggcgc tgctgacggc gctaaaagac 2160
aaatacggca agcagcagg catggcggtc ttttaaccagc tgaaatggct ggttaatcct 2220
tccgcgcaa ccaccattgc ggcgcgggaa agcgcctatc cgctgaagtt tgatctgcaa 2280
aacacgcaaa cggcgtaa 2298
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<210> 102

<211> 765

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 102

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Thr	Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile
	50					55					60				
Ser	Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala
65					70					75					80
Glu	Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu
				85						90				95	
Trp	Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly
			100					105					110		
Gln	Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile
		115					120					125			
Lys	Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp
	130					135					140				
Asp	Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys
145					150					155					160
Ala	Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu
				165						170				175	
Thr	Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val
			180					185					190		
His	Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu
		195					200					205			
Pro	Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe
	210					215					220				
Asp	Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn
225					230					235					240
Trp	Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala
				245						250				255	
Phe	Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu
			260					265					270		
Asp	Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg
		275					280					285			
Gln	Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu
	290					295					300				
Lys	Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu
305					310					315					320
Val	Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp
				325					330					335	
Gly	Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu
			340					345					350		
Thr	Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe
		355					360					365			
Gly	Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro
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Gln Ala Ala Ala Lys	Glu Ala Arg His Gln	Ala Glu Tyr Gln Asn Arg		
465	470	475		480
Gly Thr Glu Asn Asp	Met Ile Val Phe Ser	Pro Thr Ser Gly Asn Arg		
	485	490		495
Pro Val Leu Ala Trp	Asp Val Val Ala Pro	Gly Gln Ser Gly Phe Ile		
	500	505		510
Ala Pro Asp Gly Lys	Ala Asp Lys His Tyr	Asp Asp Gln Leu Lys Met		
	515	520		525
Tyr Glu Ser Phe Gly	Arg Lys Ser Leu Trp	Leu Thr Pro Gln Asp Val		
	530	535		540
Asp Glu His Gln Glu	Ser Gln Glu Val Leu	Gln Val Gln Leu Asp Gln		
545	550	555		560
Thr Glu Val Lys Ile	Val Arg Asp Glu Tyr	Gly Met Pro His Ile Tyr		
	565	570		575
Ala Asp Asp Thr Tyr	Arg Leu Phe Tyr Gly	Tyr Gly Tyr Val Val Ala		
	580	585		590
Gln Asp Arg Leu Phe	Gln Met Glu Met Ala	Arg Arg Ser Thr Gln Gly		
	595	600		605
Thr Val Ser Glu Val	Leu Gly Lys Ala Phe	Val Ser Phe Asp Lys Arg		
	610	615		620
Ile Arg Gln Asn Tyr	Trp Pro Asp Ser Ile	Arg Ala Gln Ile Ala Ser		
625	630	635		640
Leu Ser Ala Glu Asp	Lys Ser Ile Leu Gln	Gly Tyr Ala Asp Gly Met		
	645	650		655
Asn Ala Trp Ile Asp	Lys Val Asn Ala Ser	Pro Asp Lys Leu Leu Pro		
	660	665		670
Gln Gln Phe Ser Thr	Phe Gly Phe Lys Pro	Lys His Trp Glu Pro Phe		
	675	680		685
Asp Val Ala Met Ile	Phe Val Gly Thr Met	Ala Asn Arg Phe Ser Asp		
	690	695		700
Ser Thr Ser Glu Ile	Asp Asn Leu Ala Leu	Leu Thr Ala Leu Lys Asp		
705	710	715		720
Lys Tyr Gly Lys Gln	Gln Gly Met Ala Val	Phe Asn Gln Leu Lys Trp		
	725	730		735
Leu Val Asn Pro Ser	Ala Pro Thr Thr Ile	Ala Ala Arg Glu Ser Ala		
	740	745		750
Tyr Pro Leu Lys Phe	Asp Leu Gln Asn Thr	Gln Thr Ala		
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<210> 103

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 103

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt ggggggtgatg atgtcgatat ctttgccgaa 240

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aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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tacggcaagc agcaggcgat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 104

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 104

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60

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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp		85	90	95
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln		100	105	110
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys		115	120	125
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp		130	135	140
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala		145	150	155
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr		165	170	175
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His		180	185	190
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro		195	200	205
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp		210	215	220
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp		225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Arg		245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp		260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val		305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly		325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr		340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly		355	360	365
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr		370	375	380
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu		385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly		405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln		420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Gly	Trp	Lys	Thr	Pro		435	440	445
Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln		450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly		465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro		485	490	495

Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala		
			500					505					510				
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr		
		515					520					525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
		530				535					540						
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr		
545					550				555						560		
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala		
			565						570					575			
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
		580						585					590				
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
		595				600						605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625				630					635						640		
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
		660					665							670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
		675				680						685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
	690					695				700							
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705				710					715						720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725				730							735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
		740					745						750				
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala						
		755				760											

<210> 105

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 105

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggg gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

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ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagtg cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg caccgtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccaccag 1140
gacgggcca ccggctcgct gaacatcagc gtggggcgga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat ccgcaggcg gtgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggcca taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
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gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
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gagggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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ttctctgaca gcaccagcga aattaaaaac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcag ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 106

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 106

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln

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Pro	Glu	Thr	100				105				110					
			Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	
Thr	Asp	Thr	115				120				125					
Gly	Lys	Glu	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	
145	Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
130																
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	160
145	Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
130																
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	175
145	Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
130																
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	220
145	Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225																
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Ala	Phe	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	270
145	Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
275																
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	365
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	380
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu									

530		535		540
Glu His Gln Glu Ser	Gln Glu Val Leu Gln Val	Gln Leu Asp Gln Thr		
545	550	555	560	
Glu Val Lys Ile Val	Arg Asp Glu Tyr Gly Met	Pro His Ile Tyr Ala		
	565	570	575	
Asp Asp Thr Tyr Arg	Leu Phe Tyr Gly Tyr Gly	Tyr Val Val Ala Gln		
	580	585	590	
Asp Arg Leu Phe Gln	Met Glu Met Ala Arg Arg	Ser Thr Gln Gly Thr		
	595	600	605	
Val Ser Glu Val Leu	Gly Lys Ala Phe Val Ser	Phe Asp Lys Asp Ile		
610	615	620		
Arg Gln Asn Tyr Trp	Pro Asp Ser Ile Arg Ala	Gln Ile Ala Ser Leu		
625	630	635	640	
Ser Ala Glu Asp Lys	Ser Ile Leu Gln Gly Tyr	Ala Asp Gly Met Asn		
	645	650	655	
Ala Trp Ile Asp Lys	Val Asn Ala Ser Pro Asp	Lys Leu Leu Pro Gln		
	660	665	670	
Gln Phe Ser Thr Phe	Gly Phe Lys Pro Lys His	Trp Glu Pro Phe Asp		
	675	680	685	
Val Ala Met Ile Phe	Val Gly Thr Met Ala Asn	Arg Phe Ser Asp Ser		
690	695	700		
Thr Ser Glu Ile Lys	Asn Leu Ala Leu Thr Ala	Leu Lys Asp Lys		
705	710	715	720	
Tyr Gly Lys Gln Gln	Gly Met Ala Val Phe Asn	Gln Leu Lys Trp Leu		
	725	730	735	
Val Asn Pro Ser Ala	Pro Thr Thr Ile Ala Ala	Arg Glu Ser Ala Tyr		
	740	745	750	
Pro Leu Lys Phe Asp	Leu Gln Asn Thr Gln Thr	Ala		
755	760			

<210> 107

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 107

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt cacggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgattact ttgcgcgtct gtggggcggt 780
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gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcacgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggcca ccggctcgct gaacatcaaa gtggggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320
gacgtcacca actggaaaac ccctgccatg aaacttacct tccgggcca caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgccctg 1500
gatgtggtgg cgccggggca aagcgggttt atcgcgccgg atggcaaagc cgataagcac 1560
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tacggcaagc agcaggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 108

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 108

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ser Thr Ala Gly His Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130         135         140

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Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Arg	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365	
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380	
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395	400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430	
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Asn	Trp	Lys	Thr	Pro	435	440	445	
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460	
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475	480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510	
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525	
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540	
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555	560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575	

Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	
			580					585					590			
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	
		595					600					605				
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile	
		610				615					620					
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	
625					630					635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
				645					650					655		
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	
			660					665					670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
		675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	
	690					695					700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	
705					710					715					720	
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	
				725					730					735		
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	
			740					745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala					
		755					760									

<210> 109

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 109

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tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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gccgcggtcc cagcgccgtt tggtaatggt tacagccgta ccggctatga aaccaccag 1140

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gacgggccaa ccggctcgct gaacatcaaa gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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<210> 110

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 110

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His

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			180					185					190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	
		195					200					205				
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	
	210					215					220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	
225					230					235				240		
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	
				245					250				255			
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	
			260					265					270			
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	
		275					280					285				
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	
	290					295					300					
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	
305				310					315					320		
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	
				325				330					335			
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	
			340				345					350				
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	
	355					360					365					
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	
	370					375					380					
Gly	Ser	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	
385				390					395					400		
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	
				405				410					415			
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	
			420					425					430			
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	
	435					440					445					
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	
	450					455				460						
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	
465				470						475				480		
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	
				485				490					495			
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	
			500				505						510			
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	
		515				520						525				
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	
	530															

610	615	620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu		
625	630	635
Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn		
645	650	655
Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln		
660	665	670
Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp		
675	680	685
Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser		
690	695	700
Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys		
705	710	715
Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu		
725	730	735
Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr		
740	745	750
Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His		
755	760	765
His His		
770		

<210> 111

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 111

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggg gggggatgat atgtcgatat ctttgccgaa 240
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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcggtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcattgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320

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acgcaaacgg cgtaa 2295

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<210> 112

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 112

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20         25         30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35         40         45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
50         55         60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65         70         75         80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85         90         95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100        105        110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115        120        125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130        135        140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145        150        155        160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165        170        175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180        185        190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195        200        205

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Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Pro	Phe	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr	370	375	380
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Thr	Ser	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
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Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725					730						735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745						750	
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
		755					760								

<210> 113

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 113

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aacaactcgc cgcaaaaaga ctaccgggcc tctgatctgt tcccgttcct gtggggcggt 780
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cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
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<210> 114

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 114

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1      5      10      15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
      20      25      30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85      90      95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
      100     105     110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
      115     120     125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130     135     140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145     150     155     160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
      165     170     175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
      180     185     190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195     200     205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210     215     220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225     230     235     240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Pro Phe

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				245					250				255				
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp		
			260					265					270				
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		
		275					280					285					
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		
	290					295					300						
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val		
305				310					315						320		
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly		
			325					330						335			
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr		
		340				345							350				
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly		
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Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr		
	370				375						380						
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu		
385				390					395						400		
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly		
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln		
		420					425						430				
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro		
	435					440						445					
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln		
	450				455					460							
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly		
465				470					475						480		
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro		
			485				490							495			
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala		
		500					505						510				
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr		
	515					520						525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
	530				535						540						
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly		
545				550					555						560		
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala		
			565				570							575			
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
		580					585						590				
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
	595				600							605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625				630					635						640		
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
	660						665					670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		

	675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
	755					760									

 $\langle 220 \rangle$

<400> 115

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cccaagcatt gggaaccggt tgatgtggcg atgatttttg tcggcaccat ggccaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcagggcat ggcgggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
acgcaaacgg cgtaa                                     2295

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<210> 116

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 116

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1           5           10           15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180         185         190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195         200         205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210         215         220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225         230         235         240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Pro Phe
245         250         255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260         265         270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275         280         285

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Thr 290	Ser 295	Arg 300	Arg 305	Asp 310	Leu 315	Asn 320	Leu 325	Arg 330	Leu 335	Phe 340	Leu 345	Pro 350	Ala 355	Leu 360	Lys 365
Asp 305	Ala 310	Thr 315	Ala 320	Asn 325	Leu 330	Ala 335	Glu 340	Asn 345	Asp 350	Pro 355	Arg 360	Ser 365	Gln 370	Leu 375	Val 380
Asp 310	Lys 315	Leu 320	Ala 325	Ser 330	Trp 335	Asp 340	Gly 345	Glu 350	Asn 355	Leu 360	Val 365	Asn 370	Asp 375	Asp 380	Gly 385
Lys 315	Thr 320	Tyr 325	Gln 330	Gln 335	Pro 340	Gly 345	Ser 350	Ala 355	Ile 360	Leu 365	Asn 370	Ala 375	Trp 380	Leu 385	Thr 390
Ser 320	Met 325	Leu 330	Lys 335	Arg 340	Thr 345	Val 350	Val 355	Ala 360	Ala 365	Val 370	Pro 375	Ala 380	Pro 385	Phe 390	Gly 395
Lys 325	Trp 330	Tyr 335	Ser 340	Ala 345	Ser 350	Gly 355	Tyr 360	Glu 365	Thr 370	Thr 375	Pro 380	Asp 385	Gly 390	Pro 395	Thr 400
Gly 330	Ser 335	Leu 340	Asn 345	Ile 350	Ser 355	Val 360	Gly 365	Ala 370	Lys 375	Ile 380	Leu 385	Tyr 390	Glu 395	Ala 400	Leu 405
Gln 335	Gly 340	Asp 345	Lys 350	Ser 355	Pro 360	Ile 365	Pro 370	Gln 375	Ala 380	Val 385	Asp 390	Leu 395	Phe 400	Gly 405	Gly 410
Lys 340	Pro 345	Gln 350	Gln 355	Glu 360	Val 365	Ile 370	Leu 375	Ala 380	Ala 385	Leu 390	Asp 395	Asp 400	Ala 405	Trp 410	Gln 415
Thr 345	Leu 350	Ser 355	Lys 360	Arg 365	Tyr 370	Gly 375	Asn 380	Asp 385	Val 390	Asp 395	Ser 400	Trp 405	Lys 410	Thr 415	Pro 420
Ala 350	Met 355	Ala 360	Leu 365	Thr 370	Trp 375	Arg 380	Ala 385	Asn 390	Asn 395	Phe 400	Phe 405	Gly 410	Val 415	Pro 420	Gln 425
Ala 355	Ala 360	Ala 365	Lys 370	Glu 375	Ala 380	Arg 385	Pro 390	Gln 395	Ala 400	Glu 405	Tyr 410	Gln 415	Asn 420	Arg 425	Gly 430
Thr 360	Glu 365	Asn 370	Asp 375	Met 380	Ile 385	Val 390	Phe 395	Ser 400	Pro 405	Thr 410	Ser 415	Gly 420	Asn 425	Arg 430	Pro 435
Val 365	Leu 370	Ala 375	Trp 380	Asp 385	Val 390	Val 395	Ala 400	Pro 405	Gly 410	Gln 415	Ser 420	Gly 425	Phe 430	Ile 435	Ala 440
Pro 370	Asp 375	Gly 380	Lys 385	Lys 390	Asp 395	Lys 400	His 405	Tyr 410	Asp 415	Asp 420	Gln 425	Leu 430	Lys 435	Met 440	Tyr 445
Glu 375	Ser 380	Phe 385	Gly 390	Arg 395	Lys 400	Ser 405	Leu 410	Trp 415	Leu 420	Thr 425	Pro 430	Gln 435	Asp 440	Val 445	Asp 450
Glu 380	His 385	Gln 390	Glu 395	Ser 400	Gln 405	Glu 410	Val 415	Leu 420	Gln 425	Val 430	Gln 435	Leu 440	Asp 445	Gln 450	Gly 455
Glu 385	Val 390	Lys 395	Ile 400	Val 405	Arg 410	Asp 415	Glu 420	Tyr 425	Gly 430	Met 435	Pro 440	His 445	Ile 450	Tyr 455	Ala 460
Asp 390	Asp 395	Thr 400	Tyr 405	Arg 410	Leu 415	Phe 420	Tyr 425	Gly 430	Tyr 435	Gly 440	Tyr 445	Val 450	Val 455	Ala 460	Gln 465
Asp 395	Arg 400	Leu 405	Phe 410	Gln 415	Met 420	Glu 425	Met 430	Ala 435	Arg 440	Arg 445	Ser 450	Thr 455	Gln 460	Gly 465	Thr 470
Val 400	Ser 405	Glu 410	Val 415	Leu 420	Gly 425	Lys 430	Ala 435	Phe 440	Val 445	Ser 450	Phe 455	Asp 460	Lys 465	Asp 470	Ile 475
Arg 405	Gln 410	Asn 415	Tyr 420	Trp 425	Pro 430	Asp 435	Ser 440	Ile 445	Arg 450	Ala 455	Gln 460	Ile 465	Ala 470	Ser 475	Leu 480
Ser 410	Ala 415	Glu 420	Asp 425	Lys 430	Ser 435	Ile 440	Leu 445	Gln 450	Gly 455	Tyr 460	Ala 465	Asp 470	Gly 475	Met 480	Asn 485
Ala 415	Trp 420	Ile 425	Asp 430	Lys 435	Val 440	Asn 445	Ala 450	Ser 455	Pro 460	Asp 465	Lys 470	Leu 475	Leu 480	Pro 485	Gln 490
Gln 420	Phe 425	Ser 4													

Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
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<210> 117

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 117

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggg gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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<210> 118

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 118

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45	
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60	
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu	65	70	75	80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110	
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp	115	120	125	
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140	
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155	160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Pro	Phe	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val	305	310	315	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly				

325														330														335													
Lys	Thr	Tyr	Gln		Gln	Pro	Gly	Ser	Ala		Ile	Leu	Asn	Ala	Trp	Leu		Thr																							
340														345														350													
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly																										
355														360														365													
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr																										
370														375														380													
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu																										
385														390														395													
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly																										
405														410														415													
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln																										
420														425														430													
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Gly	Trp	Lys	Thr	Pro																										
435														440														445													
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln																										
450														455														460													
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly																										
465														470														475													
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro																										
485														490														495													
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala																										
500														505														510													
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr																										
515														520														525													
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp																										
530														535														540													
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly																										
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<210> 119

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 119

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<210> 120

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 120

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Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	
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Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	
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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	
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Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	
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Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr	
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				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
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Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
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Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
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Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
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Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
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Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
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Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675				680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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<210> 121

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 121

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<210> 122

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 122

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      35      40      45
Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile Ser
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Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
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      195      200      205
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Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
      260      265      270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
      275      280      285
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290      295      300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Ser Gln Leu Val
305      310      315      320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
      325      330      335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
      340      345      350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
      355      360      365
Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Pro Asp Gly Pro Thr
      370      375      380
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<400> 123

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acgcaaacgg cgtaa 2295
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<210> 124

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 124

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

1

5

10

15

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
		50				55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
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Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp
			115				120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
					135						140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
			195				200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
						215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Leu	Phe	Pro	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
			275				280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
						295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
			355				360					365			
Lys	Trp	Tyr													

Ala	Met	Ala	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
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Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
		530				535					540				
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600						605		
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
		610				615					620				
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625					630					635					640
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
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			660					665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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<210> 125

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 125

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agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
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acgcaaacgg cgtaa 2295

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<210> 126
 <211> 764
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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<400> 126
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser

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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp
	115						120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
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	180							185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195						200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Phe	Pro	Phe
			245						250					255	
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		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
	275						280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val
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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
			325						330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
	340							345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly
			405						410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
	420							425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
	435						440					445			
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	Pro	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro

				485				490					495				
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		515					520					525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
		530				535					540						
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gly	Pro	Asp	Gln	Gly		
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala		
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
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Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625				630					635						640		
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
		660					665						670				
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
	675				680						685						
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser		
	690				695				700								
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705				710					715						720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725				730							735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
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Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala						
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<210> 127

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 127

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<210> 128

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 128

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1           5           10          15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95

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Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
			165						170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
		180						185				190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195						200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Phe	Pro	Phe
			245						250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
	275						280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val
305				310						315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
			325						330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Thr
		340						345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
	355						360					365			
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385				390						395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly
			405						410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
		420						425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
	435						440					445			

Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
530						535					540				
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
	595						600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
610						615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
			675				680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
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<210> 129

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 129

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggt gggggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat ttggaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcgttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgatagct tcccgttcct gtggggcggt 780

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ccggcgctga aggacgccac cgcgaaactg gcggaacacg atccgcgcag ccaactgggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tcatgcctgg ctgaccagca tgctcaagcg cacggtgggt 1080
gccgtgggtcc cagcgccggt tggttaagtgg tacagcgcca gtggctatga aaccaccccg 1140
gacgggcca cgggtcgcct gaacatcagc gtgggggcga aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaacg ctacggtaac 1320
gacgtcgata gctggaaaac ccctgccatg gcgcttacct ggcgggcca taacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtccgcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggt tcttgccctg 1500
gatgtgggtg cgccggggca aagcggtttt atcgcgccgg atggcaaaaa agataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata ttacgccga tgatacctat 1740
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aaagtgaacg ccagccccga taagctgtta cccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggccaaccgt 2100
tggtctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaaac agcagggcgt ggcggtcttt aaccagctga aatggctggg taatccttcc 2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgaaaaac 2280
acgcaaacgg cgtaa 2295

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<210> 130
 <211> 764
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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<400> 130
Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1          5          10          15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
20        25        30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35        40        45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50        55        60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65        70        75        80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85        90        95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100       105       110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115       120       125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

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130						135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170						175
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asp	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195						200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Phe	Pro	Phe
				245					250						255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
	275						280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
			325					330						335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Val	Val	Pro	Ala	Pro	Phe	Gly
	355					360						365			
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
			405						410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
	435					440						445			
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	Pro	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
			485						490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
	515						520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala

				565					570					575			
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
			580					585					590				
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
		595					600					605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile		
	610				615						620						
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625					630				635						640		
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650						655			
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
			660					665						670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
		675				680						685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser		
	690					695					700						
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705					710					715					720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725					730						735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
		740						745					750				
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala						
		755					760										

<210> 131

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 131

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcatcgtttt tggtcacaac 180
ggcaccattt catggggatc caccgccggg gggggatgat atgtcgatat ctttgccgaa 240
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acgctgcacg gcaacgtcat ttggaccgat actgcgacgc agaccgccta tgccaaagcg 420
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cccggccacg acccggttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
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gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttcacgggaa accgcagcag 1260
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caggacgttg acgagcacca agagtctcag gaagtgtcgc aggtaggggg cgatcagggc 1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcgaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgtaa 2295

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<210> 132

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 132

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165         170         175

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Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Glu	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Phe	Pro	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Ser	Gln	Leu	Val
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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	Pro	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525		</	

Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
610						615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Glu	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
	755						760								

<210> 133

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 133

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acgcaaacgg cgtaa 2295

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<210> 134

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 134

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20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Glu Gly Asn Ile Gly Tyr Val His
180         185         190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195         200         205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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210	215	220
Leu Asn Pro Lys Val Tyr	Asn Pro Gln Ser Gly	Tyr Ile Ala Asn Trp
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Asn Asn Ser Pro Gln Lys	Asp Tyr Pro Ala Ser	Asp Ser Phe Pro Phe
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Leu Trp Gly Gly Ala Asp	Arg Val Thr Glu Ile	Asp Thr Ile Leu Asp
260	265	270
Lys Gln Pro Arg Phe Thr	Ala Asp Gln Ala Trp	Asp Val Ile Arg Gln
275	280	285
Thr Ser Arg Arg Asp Leu	Asn Leu Arg Leu Phe	Leu Pro Ala Leu Lys
290	295	300
Asp Ala Thr Ala Asn Leu	Ala Glu Asn Asp Pro	Arg Arg Gln Leu Val
305	310	315
Asp Lys Leu Ala Ser Trp	Asp Gly Glu Asn Leu	Val Asn Asp Asp Gly
325	330	335
Lys Thr Tyr Gln Gln Pro	Gly Ser Ala Ile Leu	Asp Ala Trp Leu Thr
340	345	350
Ser Met Leu Lys Arg Thr	Val Val Ala Val Val	Pro Ala Pro Phe Gly
355	360	365
Lys Trp Tyr Ser Ala Ser	Gly Tyr Glu Thr Thr	Pro Asp Gly Pro Thr
370	375	380
Gly Ser Leu Asn Ile Ser	Val Gly Ala Lys Ile	Leu Tyr Glu Ala Leu
385	390	395
Gln Gly Asp Lys Ser Pro	Ile Pro Gln Ala Val	Asp Leu Phe Gly Gly
405	410	415
Lys Pro Gln Gln Glu Val	Ile Leu Ala Ala Leu	Asp Asp Ala Trp Gln
420	425	430
Thr Leu Ser Lys Arg Tyr	Gly Asn Asp Val Asp	Ser Trp Lys Thr Pro
435	440	445
Ala Met Ala Leu Thr Trp	Arg Ala Asn Asn Phe	Phe Gly Val Pro Gln
450	455	460
Ala Ala Ala Lys Glu Ala	Arg Pro Gln Ala Glu	Tyr Gln Asn Arg Gly
465	470	475
Thr Glu Asn Asp Met Ile	Val Phe Ser Pro Thr	Ser Gly Asn Arg Pro
485	490	495
Val Leu Ala Trp Asp Val	Val Ala Pro Gly Gln	Ser Gly Phe Ile Ala
500	505	510
Pro Asp Gly Lys Lys Asp	Lys His Tyr Asp Asp	Gln Leu Lys Met Tyr
515	520	525
Glu Ser Phe Gly Arg Lys	Ser Leu Trp Leu Thr	Pro Gln Asp Val Asp
530	535	540
Glu His Gln Glu Ser Gln	Glu Val Leu Gln Val	Gln Leu Asp Gln Gly
545	550	555
Glu Val Lys Ile Val Arg	Asp Glu Tyr Gly Met	Pro His Ile Tyr Ala
565	570	575
Asp Asp Thr Tyr Arg Leu	Phe Tyr Gly Tyr Gly	Tyr Val Val Ala Gln
580	585	590
Asp Arg Leu Phe Gln Met	Glu Met Ala Arg Arg	Ser Thr Gln Gly Thr
595	600	605
Val Ser Glu Val Leu Gly	Lys Ala Phe Val Ser	Phe Asp Lys Asp Ile
610	615	620
Arg Gln Asn Tyr Trp Pro	Asp Ser Ile Arg Ala	Gln Ile Ala Ser Leu
625	630	635
Ser Ala Glu Asp Lys Ser	Ile Leu Gln Gly Tyr	Ala Asp Gly Met Asn


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acgcaaacgg cgtaa 2295

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<210> 136

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 136

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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20     25     30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35     40     45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50     55     60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85     90     95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100    105    110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Ser Phe Pro Phe
245    250    255

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Leu 260	Trp 265	Gly 270	Gly 275	Ala 280	Asp 285	Arg 290	Val 295	Thr 300	Glu 305	Ile 310	Asp 315	Thr 320	Ile 325	Leu 330	Asp 335
Lys 340	Gln 345	Pro 350	Arg 355	Phe 360	Thr 365	Ala 370	Asp 375	Gln 380	Ala 385	Trp 390	Asp 395	Val 400	Ile 405	Arg 410	Gln 415
Thr 420	Ser 425	Arg 430	Arg 435	Asp 440	Leu 445	Asn 450	Leu 455	Arg 460	Leu 465	Phe 470	Leu 475	Pro 480	Ala 485	Leu 490	Lys 495
Asp 500	Ala 505	Thr 510	Ala 515	Asn 520	Leu 525	Ala 530	Glu 535	Asn 540	Asp 545	Pro 550	Arg 555	Arg 560	Gln 565	Leu 570	Val 575
Asp 580	Lys 585	Leu 590	Ala 595	Ser 600	Trp 605	Asp 610	Gly 615	Glu 620	Asn 625	Leu 630	Val 635	Val 640	Asn 645	Asp 650	Gly 655
Lys 660	Thr 665	Tyr 670	Gln 675	Gln 680	Pro 685	Gly 690	Ser 695	Ala 700	Ile 705	Leu 710	Asp 715	Ala 720	Trp 725	Leu 730	Thr 735
Ser 740	Met 745	Leu 750	Lys 755	Arg 760	Thr 765	Val 770	Val 775	Ala 780	Ala 785	Val 790	Pro 795	Ala 800	Pro 805	Phe 810	Gly 815
Lys 820	Trp 825	Tyr 830	Ser 835	Ala 840	Ser 845	Gly 850	Tyr 855	Glu 860	Thr 865	Thr 870	Pro 875	Asp 880	Gly 885	Pro 890	Thr 895
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Lys 1060	Pro 1065	Gln 1070	Gln 1075	Glu 1080	Val 1085	Ile 1090	Leu 1095	Ala 1100	Ala 1105	Leu 1110	Asp 1115	Asp 1120	Ala 1125	Trp 1130	Gln 1135
Thr 1140	Leu 1145	Ser 1150	Lys 1155	Arg 1160	Tyr 1165	Gly 1170	Asn 1175	Asp 1180	Val 1185	Asp 1190	Ser 1195	Trp 1200	Lys 1205	Thr 1210	Pro 1215
Ala 1220	Met 1225	Ala 1230	Leu 1235	Thr 1240	Trp 1245	Arg 1250	Ala 1255	Asn 1260	Asn 1265	Phe 1270	Phe 1275	Gly 1280	Val 1285	Pro 1290	Gln 1295
Ala 1300	Ala 1305	Ala 1310	Lys 1315	Glu 1320	Ala 1325	Arg 1330	Pro 1335	Gln 1340	Ala 1345	Glu 1350	Tyr 1355	Gln 1360	Asn 1365	Arg 1370	Gly 1375
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Glu 1780	Val 1785	Lys 1790	Ile 1795	Val 1800	Arg 1805	Asp 1810	Glu 1815	Tyr 1820	Gly 1825	Met 1830	Pro 1835	His 1840	Ile 1845	Tyr 1850	Ala 1855
Asp 1860	Asp 1865	Thr 1870	Tyr 1875	Arg 1880	Leu 1885	Phe 1890	Tyr 1895	Gly 1900	Tyr 1905	Gly 1910	Tyr 1915	Val 1920	Val 1925	Ala 1930	Gln 1935
Asp 1940	Arg 1945	Leu 1950	Phe 1955	Gln 1960	Met 1965	Glu 1970	Met 1975	Ala 1980	Arg 1985	Arg 1990	Ser 1995	Thr 2000	Gln 2005	Gly 2010	Thr 2015
Val 2020	Ser 2025	Glu 2030	Val 2035	Leu 2040	Gly 2045	Lys 2050	Ala 2055	Phe 2060	Val 2065	Ser 2070	Phe 2075	Asp 2080	Lys 2085	Asp	

Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala				
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<210> 137

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 137

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tccgctgagg	ataaatccat	tctgcagggc	tatgccgatg	gcatgaatgc	gtggatcgat	1980

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aaagtgaacg ccagccccga taagctgtta cccagcagct tctccacctt tggtttttaa 2040
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<210> 138

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 138

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Val Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35     40     45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50     55     60
Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85     90     95
Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100    105    110
Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Trp
115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Asp Gly Asn Ile Gly Tyr Val His
180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Ser Phe Pro Phe
245    250    255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260    265    270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275    280    285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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Lys 315	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Thr
Ser 320	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Val	Val	Pro	Ala	Pro	Phe	Gly
Lys 325	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr
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Gln 335	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	His	Gly
Lys 340	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
Thr 345	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
Ala 350	Met	Ala	Leu	Thr	Trp	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
Ala 355	Ala	Ala	Lys	Glu	Ala	Arg	Pro	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
Thr 360	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro
Val 365	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
Pro 370	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
Glu 375	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
Glu 380	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly
Glu 385	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
Asp 390	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
Asp 395	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
Val 400	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile
Arg 405	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
Ser 410	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
Ala 415	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
Gln 420	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
Val 425	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser
Thr 430	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
Thr 435	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu

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2313

<210> 140

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 140

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65				70						75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
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Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Phe	Pro	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	

Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr	370	375	380
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	Pro	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	Ser	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	645	650	655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	660	665	670
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	675	680	685
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Trp	Ser	Asp	Ser	690	695	700
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	705	710	715
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	725	730	735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	740	745	750
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His His
770

<210> 141
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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<210> 142
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 142

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ser	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Lys	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Trp	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Trp
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
		130				135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Phe	Pro	Phe
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
		290				295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly

		355					360					365				
Lys	Trp	Tyr	Ser	Ala	Ser	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr	
	370					375					380					
Gly	Ser	Leu	Asn	Ile	Ser	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	
385					390					395					400	
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	
				405					410					415		
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	
			420					425					430			
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro	
		435					440					445				
Ala	Met	Ala	Leu	Thr	Trp	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	
	450					455					460					
Ala	Ala	Ala	Lys	Glu	Ala	Arg	Pro	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	
465					470					475					480	
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asn	Arg	Pro	
				485					490					495		
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	
			500					505					510			
Pro	Asp	Gly	Lys	Lys	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	
		515					520					525				
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	
	530					535					540					
Glu	His	Gln	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	His	His	His	
545					550					555					560	
His	His	His	Asp	Gln	Gly	Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	
				565					570					575		
Met	Pro	His	Ile	Tyr	Ala	Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	
			580					585					590			
Gly	Tyr	Val	Val	Ala	Gln	Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	
		595					600					605				
Arg	Ser	Thr	Gln	Gly	Thr	Val	Ser	Glu	Val	Leu	Gly	Lys	Ala	Phe	Val	
	610					615					620					
Ser	Phe	Asp	Lys	Asp	Ile	Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	
625					630					635					640	
Ala	Gln	Ile	Ala	Ser	Leu	Ser	Ala	Glu	Asp	Lys	Ser	Ile	Leu	Gln	Gly	
				645					650					655		
Tyr	Ala	Asp	Gly	Met	Asn	Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	
			660					665					670			
Asp	Lys	Leu	Leu	Pro	Gln	Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	
		675					680					685				
His	Trp	Glu	Pro	Phe	Asp	Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	
	690					695					700					
Asn	Arg	Trp	Ser	Asp	Ser	Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	
705					710											

<210> 143
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 143
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 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
 ggccaccattt catggggagc gaccgccggt ggggggtgatg atgtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
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 cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
 tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
 cccggccacg acccgcgttt gccggttccc ggccactggaa aatgggactg gaaagggttg 660
 ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
 aacaactcgc cgcaaaaaga ctaccggcc tctgattatt ttgcgctgct gtggggcggt 780
 gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
 caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
 ccggcgcgtga aggacgccac cgcgaaactg gcggaaaacg atccgcgccg ccaactggtg 960
 gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
 caaccgggat cggcgattct tgatgcctgg ctgaaaagca tgctcaagcg cacggtggtt 1080
 gccgcggtcc cagcgccgtt tggttaagtgg tacagccgta ccggctatga aaccaccag 1140
 gacgggcca ccggcgggct gaacatcaaa gtggggcgca aaatcctcta cgaagctctg 1200
 cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
 gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
 gacgtcgaca gctggaaaac ccctgccatg aaacttacct tccgggcca caacttcttc 1380
 ggctgtccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
 acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgcttg 1500
 gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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 aaagtgaacg ccagccccga taagctgtta cccagcagc tctccacctt tggtttttaa 2040
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 ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
 tacggcaaac agcagggcgt ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
 gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
 acgcaaacgg cgcaccatca ccatcaccat taa 2313

<210> 144
 <211> 770
 <212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 144

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
		290				295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Lys
			340					345						350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
						375						380			

Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu			
385					390					395					400			
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly			
				405					410					415				
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln			
			420					425					430					
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro			
		435					440					445						
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln			
	450					455					460							
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly			
465					470					475					480			
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro			
				485					490					495				
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala			
			500					505					510					
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr			
		515					520					525						
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp			
	530					535					540							
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Gly			
545					550					555					560			
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala			
			565						570					575				
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln			
			580					585					590					
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr			
		595				600						605						
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile			
	610				615						620							
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu			
625					630					635					640			
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn			
			645						650					655				
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln			
		660					665						670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp			
		675					680					685						
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser			
	690					695				700								
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys			
705					710					715					720			
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu			
				725					730					735				
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr			
			740					745					750					
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His			
		755					760					765						
His	His																	
	770																	

<210> 145

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 145

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ggcaccattt catggggagc gaccgccggg ggggggtgat gtgtcgatat ctttgccgaa 240
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agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat ttggactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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acgcaaacgg cgcaccatca ccataccat taa 2313
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<210> 146

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 146

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ala Thr Ala Gly Gly Gly Asp Gly Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85      90      95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
      100      105      110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Trp
      115      120      125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130      135      140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145      150      155      160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Lys Gln Ala Leu Thr
      165      170      175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
      180      185      190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195      200      205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210      215      220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225      230      235      240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu
      245      250      255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
      260      265      270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
      275      280      285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290      295      300
Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305      310      315      320
Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
      325      330      335
Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu His Ala Trp Leu Lys
      340      345      350
Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
      355      360      365
Lys Trp Tyr Ser Arg Thr Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
      370      375      380
Gly Gly Leu Asn Ile Lys Val Gly Ala Lys Ile Leu Tyr Glu Ala Leu
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<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 147

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acgcaaacgg cgaccatca ccatccat taa 2313
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<210> 148

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 148

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45	
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60	
Trp	Gly	Ala	Thr	Ala	Gly	Gly	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu	65	70	75	80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110	
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	115	120	125	
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140	
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155	160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255	
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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365	
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380	
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395	400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430	

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	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
			485						490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
			565						570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
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625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675					680						685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740				745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
	770														

<210> 149

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 149

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<210> 150

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 150

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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	50					55					60						
Trp	Gly	Ala	Thr	Ala	Gly	Met	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu		
65					70					75					80		
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp		
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Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln		
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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala		
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Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His		
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			260					265					270				
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Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		
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Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln		

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Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
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Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
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Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Phe	Phe	Asp	Lys	Asp	Ile
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
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Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
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Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705				710							715				720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
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Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
		740		745								750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 151

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 151

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<210> 152

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 152

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45

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Trp	Gly	Ala	Thr	Ala	Gly	Met	Gly	Asp	Ser	Val	Asp	Ile	Phe	Ala	Glu	65	70	75
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	115	120	125
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr	370	375	380
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	
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Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	
		580						585					590			
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	
		595					600					605				
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile	
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Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	
				630						635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
			645						650					655		
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	
			660					665					670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
		675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	
		690				695					700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	
				710						715					720	
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	
			725						730					735		
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	
			740					745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His	
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His	His															
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<210> 153

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 153

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ggcaccattt catggggagc gaccgccggt tttggtgatg acgtcgatat ctttgccgaa 240
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<210> 154

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 154

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

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				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
			115					120				125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
			130				135				140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185				190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
			195				200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
			210			215				220					
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
			275				280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
						295				300					
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
			355					360				365			
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						375					380				
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385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420		</										


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<210> 156

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 156

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20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Ser Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95

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Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
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Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
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Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
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Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
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Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Val	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Leu	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
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		435					440					445			

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Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
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Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
610						615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
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Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665							670
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
			675				680								685
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730						735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745							750
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 157

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 157

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cccgccacg acccgcttt gccggttccc ggcactggaa aatgggactg gaaagggttg 660

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acgcaaacgg cgacccatca ccatccat taa 2313

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<210> 158
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys

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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
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Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Glu	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185				190			
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260				265					270			
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Leu	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
			405						410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
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		435					440					445			
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545					550					555				560	
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Arg	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740				745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 159

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 159

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<210> 160

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 160

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50          55          60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
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Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130         135         140

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Ile	Asn	Trp	Tyr 180	Tyr	Ala	Asp	Val	Glu 185	Gly	Asn	Ile	Gly	Tyr 190	Val	His
Thr	Gly	Ala 195	Tyr	Pro	Asp	Arg	Gln 200	Pro	Gly	His	Asp	Pro 205	Arg	Leu	Pro
Val	Pro 210	Gly	Thr	Gly	Lys	Trp 215	Asp	Trp	Lys	Gly	Leu 220	Leu	Ser	Phe	Asp
Leu 225	Asn	Pro	Lys	Val	Tyr 230	Asn	Pro	Gln	Ser	Gly 235	Tyr	Ile	Ala	Asn	Trp 240
Asn	Asn	Ser	Pro	Gln 245	Lys	Asp	Tyr	Pro	Ala 250	Ser	Asp	Tyr	Phe	Ala	Leu 255
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Lys	Gln 275	Pro	Arg	Phe	Thr	Ala	Asp 280	Gln	Ala	Trp	Asp	Val 285	Ile	Arg	Gln
Thr 290	Ser	Arg	Arg	Asp	Leu	Asn 295	Leu	Arg	Leu	Phe	Leu	Pro 300	Ala	Leu	Lys
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Asp	Lys	Leu	Ala	Ser 325	Trp	Asp	Gly	Glu	Asn 330	Leu	Val	Asn	Asp	Asp	Gly 335
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Gln	Gly	Asp	Lys 405	Ser	Pro	Ile	Pro	Gln	Ala 410	Val	Asp	Leu	Phe	Gly	Gly 415
Lys	Pro	Gln	Gln 420	Glu	Val	Ile	Leu	Ala 425	Ala	Leu	Asp	Asp	Ala	Trp	Gln 430
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Ala 450	Met	Lys	Leu	Thr	Phe	Arg 455	Ala	Asn	Asn	Phe	Phe	Gly 460	Val	Pro	Gln
Ala 465	Ala	Ala	Lys	Glu	Ala 470	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly 480
Thr	Glu	Asn	Asp	Met 485	Ile	Val	Phe	Ser	Pro 490	Thr	Ser	Gly	Asp	Arg	Pro 495
Val	Leu	Ala	Trp 500	Asp	Val	Val	Ala	Pro 505	Gly	Gln	Ser	Gly	Phe	Ile	Ala
Pro	Asp 515	Gly	Lys	Ala	Asp	Lys	His 520	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr 525
Glu 530	Ser	Phe	Gly	Arg	Lys	Ser 535	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp 540
Glu 545	His	Lys	Glu	Ser	Gln 550	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr 560
Glu	Val	Lys	Ile	Val 565	Arg	Asp	Glu	Tyr	Gly 570	Met	Pro	His	Ile	Tyr	Ala 575

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			580					585					590			
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	
		595					600					605				
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile	
		610				615					620					
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	
625					630					635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
				645					650					655		
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	
			660					665					670			
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
			675				680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	
	690					695					700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	
705					710					715					720	
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	
				725					730					735		
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	
			740					745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His	
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His	His															
	770															

<210> 161

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 161

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agccgcgaag	agactattgc	ggtcaaagac	ggccagccgg	agacctttac	cgtttatcgc	360
acgctgcacg	gcaacgtcat	taaaactgat	actgcgacgc	agaccgccta	tgccaaagcg	420
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ccggcgctga	aggacgccac	cgcgaacctg	gcggaaaacg	atccgcgccg	ccaactggtg	960
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gacggggccaa cgggcggcct gaacatcgca gtgggggcgaa aaatcctcta cgaagctctg 1200
caggggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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tacggcaaac agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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<210> 162

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 162

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr

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				165				170					175		
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Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Ser	Trp	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asn	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
						375					380				
Gly	Gly	Leu	Asn	Ile	Ala	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
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Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470						475				480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	

595					600					605					
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
610					615					620					
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
645					650					655					
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
660					665					670					
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
675					680					685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690					695					700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
725					730					735					
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
740					745					750					
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
755					760					765					
His	His														
770															

<210> 163

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 163

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ggcaccattt catggggagc gaccgccggt ggggggtgat acgtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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<210> 164

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 164

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100          105          110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115          120          125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130          135          140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145          150          155          160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165          170          175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
          180          185          190

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					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Trp	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
				310						315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Lys
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Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
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Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Pro
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
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Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
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Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
		530				535					540				
G															

Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665						670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730						735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 165

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 165

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agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
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cgcgctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
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cagggtgata agtcgccaat ccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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gacgtcgaca actggaaaac ccctgccatg aaacttacct tccgggcca caacttcttc 1380

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<210> 166
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

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<400> 166
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35         40         45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50         55         60
Trp Gly Ala Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65         70         75         80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85         90         95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100        105        110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115        120        125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130        135        140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145        150        155        160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165        170        175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180        185        190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195        200        205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp

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210	215	220
Leu Asn Pro Lys Val Tyr	Asn Pro Gln Ser Gly	Tyr Ile Ala Asn Trp
225	230	235
Asn Asn Ser Pro Gln Lys	Asp Tyr Pro Ala Ser	Asp Ser Phe Ala Leu
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Leu Trp Gly Gly Ala Asp	Arg Val Thr Glu Ile	Asp Thr Ile Leu Asp
260	265	270
Lys Gln Pro Arg Phe Thr	Ala Asp Gln Ala Trp	Asp Val Ile Arg Gln
275	280	285
Thr Ser Arg Arg Asp Leu	Asn Leu Arg Leu Phe	Leu Pro Ala Leu Lys
290	295	300
Asp Ala Thr Ala Asn Leu	Ala Glu Asn Asp Pro	Arg Arg Gln Leu Val
305	310	315
Asp Lys Leu Ala Ser Trp	Asp Gly Glu Asn Leu	Val Asn Asp Asp Gly
325	330	335
Lys Thr Tyr Gln Gln Pro	Gly Ser Ala Ile Leu	Asp Ala Trp Leu Thr
340	345	350
Ser Met Leu Lys Arg Thr	Val Val Ala Ala Val	Pro Ala Pro Phe Gly
355	360	365
Lys Trp Tyr Ser Arg Thr	Gly Tyr Glu Thr Thr	Gln Asp Gly Pro Pro
370	375	380
Gly Gly Leu Asn Ile Ala	Val Gly Ala Lys Ile	Leu Tyr Glu Ala Leu
385	390	395
Gln Gly Asp Lys Ser Pro	Ile Pro Gln Ala Val	Asp Leu Phe Gly Gly
405	410	415
Lys Pro Gln Gln Glu Val	Ile Leu Ala Ala Leu	Asp Asp Ala Trp Gln
420	425	430
Thr Leu Ser Lys Arg Tyr	Gly Asn Asp Val Asp	Asn Trp Lys Thr Pro
435	440	445
Ala Met Lys Leu Thr Phe	Arg Ala Asn Asn Phe	Phe Gly Val Pro Gln
450	455	460
Ala Ala Ala Lys Glu Ala	Arg His Gln Ala Glu	Tyr Gln Asn Arg Gly
465	470	475
Thr Glu Asn Asp Met Ile	Val Phe Ser Pro Thr	Ser Gly Asp Arg Pro
485	490	495
Val Leu Ala Trp Asp Val	Val Ala Pro Gly Gln	Ser Gly Phe Ile Ala
500	505	510
Pro Asp Gly Lys Ala Asp	Lys His Tyr Asp Asp	Gln Leu Lys Met Tyr
515	520	525
Glu Ser Phe Gly Arg Lys	Ser Leu Trp Leu Thr	Pro Gln Asp Val Asp
530	535	540
Glu His Lys Glu Ser Gln	Glu Val Leu Gln Val	Gln Leu Asp Gln Gly
545	550	555
Glu Val Lys Ile Val Arg	Asp Glu Tyr Gly Met	Pro His Ile Tyr Ala
565	570	575
Asp Asp Thr Tyr Arg Leu	Phe Tyr Gly Tyr Gly	Tyr Val Val Ala Gln
580	585	590
Asp Arg Leu Phe Gln Met	Glu Met Ala Arg Arg	Ser Thr Gln Gly Thr
595	600	605
Val Ser Glu Val Leu Gly	Lys Tyr Phe Val Trp	Phe Asp Lys Asp Ile
610	615	620
Arg Gln Asn Tyr Trp Pro	Asp Ser Ile Arg Ala	Gln Ile Ala Ser Leu
625	630	635
Ser Ala Glu Asp Lys Asp	Ile Leu Gln Gly Tyr	Ala Asp Gly Met Asn

				645				650					655				
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
			660					665					670				
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
		675					680					685					
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
	690					695					700						
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705					710					715					720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725					730						735			
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
			740					745						750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His		
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His	His																
	770																

<210> 167

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 167

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ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat ctttgccgaa 240
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cgcgctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccagacagg cgctgaccat taactggtac 540
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acgcaaacgg cgcaccatca ccatcacat taa 2313

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<210> 168

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 168

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1      5      10      15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
      20      25      30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
      35      40      45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
      50      55      60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65      70      75      80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
      85      90      95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
      100     105     110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
      115     120     125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
      130     135     140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145     150     155     160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Arg Gln Ala Leu Thr
      165     170     175
Ile Asn Trp Tyr Tyr Ala Asp Val Glu Gly Asn Ile Gly Tyr Val His
      180     185     190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
      195     200     205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
      210     215     220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225     230     235     240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu

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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
			275				280						285		
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
			290				295						300		
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
			305				310						315	320	
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
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Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
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Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
			435				440						445		
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Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
			465				470						475	480	
Thr	Glu	Asn	Thr	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
			485				490						495		
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
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Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
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			545				550						555	560	
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
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			580				585						590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
			595				600						605		
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
			610				615						620		
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
			625				630						635	640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly		

	675		680		685										
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690					695				700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
		740						745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 169

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 169

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acgcaaacgg cgcaccatca ccatcaccat taa 2313

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<210> 170

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 170

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20     25     30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35     40     45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50     55     60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85     90     95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100    105    110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Glu Gly Asn Ile Gly Tyr Val His
180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Thr Asp Tyr Phe Ala Leu
245    250    255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260    265    270

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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly	325	330	335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr	340	345	350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly	355	360	365
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380
Gly	Gly	Leu	Asn	Ile	Ala	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro	435	440	445
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile	610	615	620
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	645	650	655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	660	665	670
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	675	680	685
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	690	695	700

Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
			725						730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
		755					760					765			
His	His														
	770														

<210> 171

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 171

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aaactttccg	ccgagaagcc	gggctattac	cagcataacg	gcgagtgggt	gaagatgttg	300
agccgcgaag	agactattgc	ggtcaaagac	ggccagccgg	agacctttac	cgtttatcgc	360
acgtgcacg	gcaacgtcat	taaaactgat	actgcgacgc	agaccgccta	tgccaaagcg	420
cgcgcctggg	atggcaaaga	ggtggcgtcc	ctgctggcgt	ggacgcacca	gatgaaggcc	480
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

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<210> 172

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 172

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1      5      10      15
Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
20     25     30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35     40     45
Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
50     55     60
Trp Gly Ala Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
65     70     75     80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85     90     95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
100    105    110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
115    120    125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130    135    140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145    150    155    160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165    170    175
Ile Asn Trp Tyr Tyr Ala Asp Val Glu Gly Asn Ile Gly Tyr Val His
180    185    190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195    200    205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210    215    220
Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225    230    235    240
Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Phe Ala Leu
245    250    255
Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260    265    270
Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275    280    285
Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys

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Asp 305	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
Asp 310	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
Lys 315	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
Ser 320	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
Lys 325	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
Gly 330	Gly	Leu	Asn	Ile	Ala	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
Gln 335	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
Lys 340	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
Thr 345	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
Ala 350	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
Ala 355	Met	Ala	Lys	Glu	Thr	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
Thr 360	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
Val 365	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
Pro 370	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
Glu 375	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
Glu 380	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
Glu 385	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
Asp 390	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
Asp 395	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
Val 400	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
Arg 405	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
Ser 410	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
Ala 415	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
Gln 420	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
Val 425	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
Thr 430	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
Tyr 435	Gly	Glu	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu

				725					730					735					
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr				
			740					745					750						
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His				
		755					760					765							
His	His																		
	770																		

<210> 173

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 173

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acgcaaacgg cgcaccatca ccataccat taa                                     2313

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<210> 174
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 174

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Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr	35	40	45	
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser	50	55	60	
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp	85	90	95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln	100	105	110	
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys	115	120	125	
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp	130	135	140	
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala	145	150	155	160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr	165	170	175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asp	Gly	Asn	Ile	Gly	Tyr	Val	His	180	185	190	
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro	195	200	205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp	210	215	220	
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Pro	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315	320

Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Pro	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Ala	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Met	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
		530				535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
		610				615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln															

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
755 760 765
His His
770

<210> 175
<211> 2313
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 175
agcaatatgt ggggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgtgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggttccc ggcaactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctacccggcc tctgattatt gggcgctgct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840
caggcggtgg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
ccggcgctga aggacgccac cgcgaaactg gcggaacacg atccgcgcgc ccaactggtg 960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
caaccgggat cggcgattct tgacgcctgg ctgacaagca tgctcaagcg cagggtggtt 1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagccgta ccggctatga aaccacccag 1140
gacgggccaa cggcgccctt gaacatcgca gtggggcgca aaatcctcta cgaagctctg 1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
gacgtcgaca gctggaacac ccctgccatg aaacttacct tccgggcca caacttcttc 1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgccctg 1500
gatgtggtgg cgccggggca aagcgggttt atcgcgccgg atggcaaagc cgataagcac 1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
caggacgttg acgagcacia agagtctcag gaagtgtgc aggtacagtt ggatcagact 1680
gaggtaaga tcgttcgcga tgaatacggc atgccgata ttacgccga tgatacctat 1740
cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaataactt cgtctggttt 1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
aaagtgaacg ccagccccga taagctgtta cccagcagt tctccacctt tggttttaaa 2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaccgt 2100
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
tacggcaagc agcaggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
gcgccaacca ccattcggcg gcgggaaagc gcctatccgc tgaagtttga tctgcaaac 2280
acgcaaacgg cgacccatca ccatccatc taa 2313

<210> 176
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 176
 Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
 1 5 10 15
 Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
 20 25 30
 Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
 35 40 45
 Pro Phe Ala Tyr Pro Gly Ile Val Phe Gly His Asn Gly Thr Ile Ser
 50 55 60
 Trp Gly Ala Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala Glu
 65 70 75 80
 Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
 85 90 95
 Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
 100 105 110
 Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
 115 120 125
 Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
 130 135 140
 Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
 145 150 155 160
 Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
 165 170 175
 Ile Asn Trp Tyr Tyr Ala Asp Val Glu Gly Asn Ile Gly Tyr Val His
 180 185 190
 Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
 195 200 205
 Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220
 Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
 225 230 235 240
 Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Tyr Trp Ala Leu
 245 250 255
 Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
 260 265 270
 Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
 275 280 285
 Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300
 Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320
 Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
 325 330 335
 Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asp Ala Trp Leu Thr

			340					345				350			
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Ala	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
		515					520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
625					630					635					640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
		675					680					685			
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
	690														

<210> 177
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 177
 agcaatatgt ggggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
 gggccgcagt tcggttggac tgcgccggcg tatacctacg gtatcggcct gcacggcgcg 120
 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcattgtttt tggtcacaac 180
 ggcaccattt catggggagc gaccgccggt ttcggtgatg acgtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
 acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
 cgcgctgggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
 tacgccgatg tggagggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
 cccggccacg acccgcggtt gccggttccc ggcaactgaa aatgggactg gaaagggttg 660
 ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
 aacaactcgc cgcaaaaaga ctaccgggcc tctgattatg ctgcgctgct gtggggcggt 780
 gcggatcgag ttactgagat cgacacgacg ctcgataagc aaccgcgctt caccgccgat 840
 caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
 ccggcgctga aggacgccac cgcgaaactg gcggaaaacg atccgcgccg ccaactggtg 960
 gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacgaaa aacctatcag 1020
 caaccgggat cggcgattct tgacgcctgg ctgacaagca tgctcaagcg cacggtggtt 1080
 gccgcggtcc cagcgccgtt tggtaatggt tacagccgta ccggctatga aaccaccag 1140
 gacggggcaa cggcgccgtt gaacatcgca gtggggcgga aaatcctcta cgaagctctg 1200
 cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
 gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
 gacgtcgaca gctggaaaac ccctgccatg aaacttacct tccgggcaa caacttcttc 1380
 ggctgcccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt 1440
 acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccgtt tcttgccctg 1500
 gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
 tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct 1620
 caggacgttg acgagcaca agagtctcag gaagtgtgc aggtacagtt ggatcagact 1680
 gaggttaaga tcgttcgcga tgaatacggc atgccgcata ttacgccga tgatacctat 1740
 cgactgtttt acggctatgg ctacgtggtg gcgcaggatc gcctgttcca gatggaaatg 1800
 gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaatactt cgtctggttt 1860
 gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
 tccgctgagg ataaagatat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat 1980
 aaagtgaacg ccagccccga taagctgtta cccagcagc tctccacctt tggtttttaa 2040
 cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggccaaccgt 2100
 ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa 2160
 tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
 gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac 2280
 acgcaaacgg cgacaccatc ccatcaccat taa 2313

<210> 178

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 178

Ser	Asn	Met	Trp	Val	Ile	Gly	Lys	Asn	Lys	Ala	Gln	Asp	Ala	Lys	Ala
1				5				10						15	
Ile	Met	Val	Asn	Gly	Pro	Gln	Phe	Gly	Trp	Thr	Ala	Pro	Ala	Tyr	Thr
			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Phe	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105						110	
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120						125		
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135						140			
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Glu	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200						205		
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215						220			
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Ala	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280						285		
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
		290				295						300			
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
			355				360					365			

Lys 370	Trp 370	Tyr 370	Ser 370	Arg 370	Thr 370	Gly 375	Tyr 375	Glu 375	Thr 375	Thr 375	Gln 380	Asp 380	Gly 380	Pro 380	Thr 380
Gly 385	Gly 385	Leu 385	Asn 385	Ile 385	Ala 390	Val 390	Gly 390	Ala 390	Lys 395	Ile 395	Leu 395	Tyr 395	Glu 395	Ala 400	Leu 400
Gln 405	Gly 405	Asp 405	Lys 405	Ser 405	Pro 405	Ile 410	Pro 410	Gln 410	Ala 410	Val 410	Asp 410	Leu 415	Phe 415	Gly 415	Gly 415
Lys 420	Pro 420	Gln 420	Gln 420	Glu 420	Val 425	Ile 425	Leu 425	Ala 425	Ala 425	Leu 425	Asp 430	Asp 430	Ala 430	Trp 430	Gln 430
Thr 435	Leu 435	Ser 435	Lys 435	Arg 435	Tyr 440	Gly 440	Asn 440	Asp 440	Val 440	Asp 440	Ser 445	Trp 445	Lys 445	Thr 445	Pro 445
Ala 450	Met 450	Lys 450	Leu 450	Thr 450	Phe 455	Arg 455	Ala 455	Asn 455	Asn 455	Phe 455	Phe 460	Gly 460	Val 460	Pro 460	Gln 460
Ala 465	Ala 465	Ala 465	Lys 465	Glu 465	Ala 470	Arg 470	His 470	Gln 470	Ala 475	Glu 475	Tyr 475	Gln 475	Asn 475	Arg 475	Gly 480
Thr 485	Glu 485	Asn 485	Asp 485	Met 485	Ile 485	Val 485	Phe 485	Ser 490	Pro 490	Thr 490	Ser 490	Gly 495	Asp 495	Arg 495	Pro 495
Val 500	Leu 500	Ala 500	Trp 500	Asp 500	Val 500	Val 505	Ala 505	Pro 505	Gly 505	Gln 505	Ser 510	Gly 510	Phe 510	Ile 510	Ala 510
Pro 515	Asp 515	Gly 515	Lys 515	Ala 515	Asp 520	Lys 520	His 520	Tyr 520	Asp 520	Asp 520	Gln 525	Leu 525	Lys 525	Met 525	Tyr 525
Glu 530	Ser 530	Phe 530	Gly 530	Arg 530	Lys 535	Ser 535	Leu 535	Trp 535	Leu 540	Thr 540	Pro 540	Gln 540	Asp 540	Val 540	Asp 540
Glu 545	His 545	Lys 545	Glu 545	Ser 545	Gln 550	Glu 550	Val 550	Leu 550	Gln 555	Val 555	Gln 555	Leu 555	Asp 555	Gln 555	Thr 555
Glu 560	Val 560	Lys 560	Ile 560	Val 565	Arg 565	Asp 565	Glu 565	Tyr 565	Gly 570	Met 570	Pro 570	His 570	Ile 570	Tyr 575	Ala 575
Asp 580	Asp 580	Thr 580	Tyr 580	Arg 580	Leu 580	Phe 585	Tyr 585	Gly 585	Tyr 585	Gly 585	Tyr 585	Val 590	Val 590	Ala 590	Gln 590
Asp 595	Arg 595	Leu 595	Phe 595	Gln 595	Met 595	Glu 600	Met 600	Ala 600	Arg 600	Arg 600	Ser 605	Thr 605	Gln 605	Gly 605	Thr 605
Val 610	Ser 610	Glu 610	Val 610	Leu 610	Gly 615	Lys 615	Tyr 615	Phe 615	Val 615	Trp 615	Phe 620	Asp 620	Lys 620	Asp 620	Ile 620
Arg 625	Gln 625	Asn 625	Tyr 625	Trp 625	Pro 630	Asp 630	Ser 630	Ile 630	Arg 630	Ala 635	Gln 635	Ile 635	Ala 635	Ser 635	Leu 635
Ser 640	Ala 640	Glu 640	Asp 640	Lys 645	Asp 645	Ile 645	Leu 645	Gln 645	Gly 650	Tyr 650	Ala 650	Asp 650	Gly 650	Met 655	Asn 655
Ala 655	Trp 655	Ile 655	Asp 660	Lys 660	Val 660	Asn 665	Ala 665	Ser 665	Pro 665	Asp 665	Lys 665	Leu 665	Leu 665	Pro 665	Gln 665
Gln 670	Phe 670	Ser 675	Thr 675	Phe 675	Gly 680	Phe 680	Lys 680	Pro 680	Lys 680	His 680	Trp 685	Glu 685	Pro 685	Phe 685	Asp 685
Val 690	Ala 690	Met 690	Ile 690	Phe 690	Val 695	Gly 695	Thr 695	Met 695	Ala 695	Asn 695	Arg 700	Phe 700	Ser 700	Asp 700	Ser 700
Thr 705	Ser 705	Glu 705	Ile 705	Asp 710	Asn 710	Leu 710	Ala 710	Leu 710	Leu 715	Thr 715	Ala 715	Leu 715	Lys 715	Asp 715	Lys 715
Tyr 720	Gly 720	Lys 720	Gln 720	Gln 725	Gly 725	Met 725	Ala 725	Val 725	Phe 730	Asn 730	Gln 730	Leu 730	Lys 730	Trp 730	Leu 730
Val 735	Asn 735	Pro 735	Ser 740	Ala 740	Pro 740	Thr 740	Thr 745	Ile 745	Ala 745	Ala 745	Arg 745	Glu 745	Ser 745	Ala 745	Tyr 745
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<210> 179
 <211> 2313
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 179
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<210> 180
 <211> 770
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 180

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Ile	Val	Phe	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Phe	Gly	Asp	Asp	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135						140			
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Glu	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
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		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295						300			
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	Asp	Ala	Trp	Leu	Thr
			340					345						350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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385					390					395				400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly
				405					410					415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp
			420					425					430	Gln
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr
		435					440					445		Pro
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro
	450					455					460			Gln
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg
465					470					475				480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg
				485					490					495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile
			500					505					510	Ala
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met
		515					520					525		Tyr
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val
	530					535					540			Asp
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln
545					550					555				560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr
				565					570					575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala
			580					585					590	Gln
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly
	595						600						605	Thr
Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Asp
	610					615					620			Ile
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser
625					630					635				640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met
				645					650					655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro
			660					665					670	Gln
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe
	675						680					685		Asp
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp
	690					695				700				Ser
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp
705					710					715				Lys
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp
				725					730					735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala
			740					745					750	Tyr
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His
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His	His													
	770													

<210> 181

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 181

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgtg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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acgcaaacgg cgaccatca ccatcacat taa 2313
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<210> 182

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 182

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			20					25					30		
Tyr	Gly	Ile	Gly	Leu	His	Gly	Ala	Gly	Tyr	Asp	Val	Thr	Gly	Asn	Thr
		35					40					45			
Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	Cys	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135						140			
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195				200						205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Gly	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260						265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275				280						285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375						380			
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
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<210> 183
<211> 2313
<212> DNA
<213> Artificial Sequence
<220>
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<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 183

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<210> 184

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 184

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu		
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Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp		
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Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln		
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Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln		
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Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys		
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			325				330						335				
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys		
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Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly		
	355					360						365					
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr		
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<210> 186

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 186

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Pro	Phe	Ala	Tyr	Pro	Gly	Leu	Val	His	Gly	His	Asn	Gly	Thr	Ile	Ser
	50					55					60				
Trp	Gly	Ala	Thr	Ala	Gly	Gln	Gly	Asp	Gly	Val	Asp	Ile	Phe	Ala	Glu
65					70					75					80
Lys	Leu	Ser	Ala	Glu	Lys	Pro	Gly	Tyr	Tyr	Gln	His	Asn	Gly	Glu	Trp
				85					90					95	
Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
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Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
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Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
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		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
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Val	Ser	Glu	Val	Leu	Gly	Lys	Thr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile
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Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
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Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
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<210> 187

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 187

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<210> 188

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 188

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val His Gly His Asn Gly Thr Ile Ser

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Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
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Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
	115						120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
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Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
	180							185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195						200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Gly	Leu
			245						250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260					265					270			
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
	275						280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
		340					345						350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
	355						360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
			405						410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
		420						425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
	435					440						445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro

				485				490					495				
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala		
			500					505					510				
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr		
		515					520					525					
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp		
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Gly	Asp	Gln	Thr		
545					550				555						560		
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala		
			565					570					575				
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln		
		580						585				590					
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr		
	595					600					605						
Val	Ser	Glu	Val	Leu	Gly	Lys	Thr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile		
610					615				620								
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu		
625				630					635						640		
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn		
			645					650				655					
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln		
		660					665					670					
Gln	Phe	Glu	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp		
	675				680				685								
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser		
690					695				700								
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys		
705				710					715						720		
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu		
			725					730				735					
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr		
		740					745					750					
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His		
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His	His																
	770																

<210> 189

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 189

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ggctatgacg tcaccggcaa tacgccgtt gcctatccgg gcctcgtttg cggtcacaac 180
ggcaccattt catggggagc gaccgccgt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360

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aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat aaactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgctttt gccggtttcc ggactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagct cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccggcc tctgattact ttgcgctgct gtggggcggg 780
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cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag 1260
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acgcaaacgg cgcaccatca ccataccat taa 2313

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<210> 190

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 190

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Cys Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65           70           75           80

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Val	Lys	Met	Leu	Ser	Arg	Glu	Glu	Thr	Ile	Ala	Val	Lys	Asp	Gly	Gln
			100					105					110		
Pro	Glu	Thr	Phe	Thr	Val	Tyr	Arg	Thr	Leu	His	Gly	Asn	Val	Ile	Lys
		115					120					125			
Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
	130					135					140				
Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
		275					280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
		435					440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
 515 520 525
 Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
 530 535 540
 Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Val Asp Gln Thr
 545 550 555 560
 Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
 565 570 575
 Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
 580 585 590
 Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
 595 600 605
 Val Ser Glu Val Leu Gly Lys Tyr Phe Val Trp Phe Asp Lys Leu Ile
 610 615 620
 Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
 625 630 635 640
 Ser Ala Glu Asp Lys Asp Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
 645 650 655
 Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
 660 665 670
 Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
 675 680 685
 Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
 690 695 700
 Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
 705 710 715 720
 Tyr Gly Asp Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
 725 730 735
 Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
 740 745 750
 Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala His His His His
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<210> 191

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 191

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 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgttgt cggtcacaac 180
 ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
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 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540

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cccgccacg acccgctttt gccggtttcc ggactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagt cgggctatat cgccaactgg 720
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<210> 192

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 192

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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Val Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln

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

530		535		540	
Glu His Lys Glu Ser Gln	Glu Val Leu Gln Val	Gln Leu Asp Gln Thr			
545		550		555	560
Glu Val Lys Ile Val Arg Asp	Glu Tyr Gly Met Pro His Ile Tyr Ala				
	565		570		575
Asp Asp Thr Tyr Arg Leu Phe Tyr	Gly Tyr Gly Tyr Val Val Ala Gln				
	580		585		590
Asp Arg Leu Phe Gln Met Glu Met	Ala Arg Arg Ser Thr Gln Gly Thr				
	595		600		605
Val Ser Glu Val Leu Gly Lys Tyr Phe	Val Trp Phe Asp Lys Leu Ile				
	610		615		620
Arg Gln Asn Tyr Trp Pro Asp Ser Ile	Arg Ala Gln Ile Ala Ser Leu				
625		630		635	640
Ser Ala Glu Asp Lys Asp Ile Leu Gln	Gly Tyr Ala Asp Gly Met Asn				
	645		650		655
Ala Trp Ile Asp Lys Val Asn Ala Ser	Pro Asp Lys Leu Leu Pro Gln				
	660		665		670
Gln Phe Ser Thr Phe Gly Phe Lys Pro	Lys His Trp Glu Pro Phe Asp				
	675		680		685
Val Ala Met Ile Phe Val Gly Thr Met	Ala Asn Arg Phe Ser Asp Ser				
	690		695		700
Thr Ser Glu Ile Asp Asn Leu Ala Leu	Leu Thr Ala Leu Lys Asp Lys				
705		710		715	720
Tyr Gly Asp Gln Gln Gly Met Ala Val	Phe Asn Gln Leu Lys Trp Leu				
	725		730		735
Val Asn Pro Ser Ala Pro Thr Thr Ile	Ala Ala Arg Glu Ser Ala Tyr				
	740		745		750
Pro Leu Lys Phe Asp Leu Gln Asn Thr	Gln Thr Ala His His His His				
	755		760		765
His His					
770					

<210> 193

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 193

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtgtg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
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acgtgacag gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
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cccggccacg acccgcggtt gccggttccc ggcactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720

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caggcgtggg atgtgatccg ccaaaccagc cgtcgggacg tcaacctgcg gttgttctta 900
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gccgcggtcc cagcgcctgt tggtaaatgg tacagcagga ccggctatga aaccacccag 1140
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gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac 1320
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acggaaaacg acatgattgt cttctcaccg acgtcgggtg accgcccggt tcttgccctg 1500
gatgtgggtg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac 1560
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gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat 1740
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tacggcaaac agcagggcgt ggcggtcttt aaccagctga aatggctggt taatccttcc 2220
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acgcaaacgg cgcaccatca ccatcaccat taa 2313

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<210> 194

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 194

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Cys Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100          105          110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115          120          125

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Thr	Asp	Thr	Ala	Thr	Gln	Thr	Ala	Tyr	Ala	Lys	Ala	Arg	Ala	Trp	Asp
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Gly	Lys	Glu	Val	Ala	Ser	Leu	Leu	Ala	Trp	Thr	His	Gln	Met	Lys	Ala
145					150					155					160
Lys	Asn	Trp	Pro	Glu	Trp	Thr	Gln	Gln	Ala	Ala	Lys	Gln	Ala	Leu	Thr
				165					170					175	
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	Gly	Tyr	Val	His
			180					185					190		
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
	195						200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
	210					215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Gly	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
	275						280					285			
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
	290					295					300				
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
	355						360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
	370					375					380				
Gly	Gly	Leu	Asn	Ile	Gln	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
385					390					395					400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
				420				425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro
	435					440						445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Asn	Asn	Phe	Phe	Gly	Val	Pro	Gln
	450					455					460				
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
	515						520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
545					550					555					560

Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	
				565					570						575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	
			580					585						590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	
		595					600					605				
Val	Ser	Glu	Val	Leu	Gly	Lys	Thr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile	
	610					615					620					
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	
625					630					635					640	
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	
				645					650					655		
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln	
			660					665						670		
Gln	Phe	Glu	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp	
	675						680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser	
	690					695					700					
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys	
705					710					715					720	
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu	
				725					730					735		
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr	
			740					745					750			
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His	
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His	His															
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<210> 195

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 195

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ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcgtttg tggtcacaac 180
ggcaccattt catggggagc gaccgccggt cagggtgatg gggtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcgaag agactattgc ggtcaaagac ggccagccgg agacctttac cgtttatcgc 360
acgctgcacg gcaacgtcat taaaactgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgctc ctgctggcgt ggacgcacca gatgaaggcc 480
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ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagc cgggctatat cgccaactgg 720
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acgcaaacgg cgaccatca ccatcaccat taa 2313

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<210> 196

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 196

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Cys Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100          105          110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115          120          125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130          135          140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala

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145					150				155			160
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				165					170			175
Ile	Asn	Trp	Tyr	Tyr	Ala	Asp	Val	Asn	Gly	Asn	Ile	His
			180					185				190
Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro
		195					200				205	
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Ser
	210					215				220		Asp
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile
225					230					235		240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr
			245						250			255
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr
		260					265					270
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val
	275					280					285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro
	290					295					300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg
305					310					315		320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn
			325						330			335
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala
		340				345						350
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala
	355					360					365	
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp
	370				375						380	
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu
			405					410				415
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp
		420						425				430
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp
	435					440					445	
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Thr	Asn	Phe	Phe	Gly
	450				455					460		465
Ala	Met	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln
465					470				475			480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly
			485					490				495
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly
	500						505					510
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu
	515					520					525	
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln
	530				535					540		545
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu
545					550				555			560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His
			565					570				575
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val


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gataaactta ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc 1920
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<210> 198

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 198

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Cys Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100          105          110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115          120          125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130          135          140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
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Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Lys Gln Ala Leu Thr
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Thr	Gly	Ala	Tyr	Pro	Asp	Arg	Gln	Pro	Gly	His	Asp	Pro	Arg	Leu	Pro
		195					200					205			
Val	Pro	Gly	Thr	Gly	Lys	Trp	Asp	Trp	Lys	Gly	Leu	Leu	Ser	Phe	Asp
		210				215					220				
Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp
225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
			260					265					270		
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
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Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
305					310					315					320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Asn	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Val	Val	Pro	Ala	Pro	Phe	Gly
		355					360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
		435					440					445			
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	450					455					460				
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465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
			500					505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
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	530					535					540				
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
		595					600						605		

Val	Ser	Glu	Val	Leu	Gly	Lys	Tyr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile
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Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu
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Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn
				645					650					655	
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro	Gln
			660					665					670		
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe	Asp
	675					680					685				
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp	Ser
690						695					700				
Thr	Ser	Glu	Ile	Asp	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp	Lys
705					710					715					720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp	Leu
				725					730					735	
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala	Tyr
			740					745					750		
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His	His
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His	His														
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<210> 199

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 199

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<210> 200

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 200

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Ile Met Val Asn Gly Pro Gln Phe Gly Trp Thr Ala Pro Ala Tyr Thr
          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Cys Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
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Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

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225					230					235					240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu
				245					250					255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp
		260					265					270			
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln
	275					280					285				
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys
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Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val
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Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Ala	Asp	Asp	Gly
				325					330					335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys
			340					345					350		
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Ala	Val	Pro	Ala	Pro	Phe	Gly
	355						360					365			
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr
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Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu
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Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly
				405					410					415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln
			420					425					430		
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Ser	Trp	Lys	Thr	Pro
	435						440					445			
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln
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Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly
465					470					475					480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro
				485					490					495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala
		500						505					510		
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr
	515						520					525			
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp
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Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr
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Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala
				565					570					575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln
			580					585					590		
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr
	595						600					605			
Val	Ser	Glu	Val	Leu	Gly	Lys	Thr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile
	610					615					620				
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu

625					630					635				640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met Asn
				645					650					655
Ala	Trp	Ile	Asp	Lys	Val	Asn	Ala	Ser	Pro	Asp	Lys	Leu	Leu	Pro Gln
			660					665					670	
Gln	Phe	Ser	Thr	Phe	Gly	Phe	Lys	Pro	Lys	His	Trp	Glu	Pro	Phe Asp
		675					680					685		
Val	Ala	Met	Ile	Phe	Val	Gly	Thr	Met	Ala	Asn	Arg	Phe	Ser	Asp Ser
	690					695					700			
Thr	Ser	Glu	Ile	Glu	Asn	Leu	Ala	Leu	Leu	Thr	Ala	Leu	Lys	Asp Lys
705					710					715				720
Tyr	Gly	Lys	Gln	Gln	Gly	Met	Ala	Val	Phe	Asn	Gln	Leu	Lys	Trp Leu
			725					730						735
Val	Asn	Pro	Ser	Ala	Pro	Thr	Thr	Ile	Ala	Ala	Arg	Glu	Ser	Ala Tyr
			740					745						750
Pro	Leu	Lys	Phe	Asp	Leu	Gln	Asn	Thr	Gln	Thr	Ala	His	His	His His
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His	His													
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<210> 201

<211> 2313

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 201

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<210> 202

<211> 770

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant of Penicillin G Acylase From Kluyvera Citrophila

<400> 202

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
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          20          25          30
Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
          35          40          45
Pro Phe Ala Tyr Pro Gly Leu Val Cys Gly His Asn Gly Thr Ile Ser
          50          55          60
Trp Gly Ala Thr Ala Gly Gln Gly Asp Gly Val Asp Ile Phe Ala Glu
65          70          75          80
Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
          85          90          95
Val Lys Met Leu Ser Arg Glu Glu Thr Ile Ala Val Lys Asp Gly Gln
          100         105         110
Pro Glu Thr Phe Thr Val Tyr Arg Thr Leu His Gly Asn Val Ile Lys
          115         120         125
Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
          130         135         140
Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145         150         155         160
Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
          165         170         175
Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
          180         185         190
Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
          195         200         205
Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
          210         215         220

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Leu	Asn	Pro	Lys	Val	Tyr	Asn	Pro	Gln	Ser	Gly	Tyr	Ile	Ala	Asn	Trp	225	230	235	240
Asn	Asn	Ser	Pro	Gln	Lys	Asp	Tyr	Pro	Ala	Ser	Asp	Tyr	Phe	Ala	Leu	245	250	255	
Leu	Trp	Gly	Gly	Ala	Asp	Arg	Val	Thr	Glu	Ile	Asp	Thr	Ile	Leu	Asp	260	265	270	
Lys	Gln	Pro	Arg	Phe	Thr	Ala	Asp	Gln	Ala	Trp	Asp	Val	Ile	Arg	Gln	275	280	285	
Thr	Ser	Arg	Arg	Asp	Leu	Asn	Leu	Arg	Leu	Phe	Leu	Pro	Ala	Leu	Lys	290	295	300	
Asp	Ala	Thr	Ala	Asn	Leu	Ala	Glu	Asn	Asp	Pro	Arg	Arg	Gln	Leu	Val	305	310	315	320
Asp	Lys	Leu	Ala	Ser	Trp	Asp	Gly	Glu	Asn	Leu	Val	Ala	Asp	Asp	Gly	325	330	335	
Lys	Thr	Tyr	Gln	Gln	Pro	Gly	Ser	Ala	Ile	Leu	His	Ala	Trp	Leu	Lys	340	345	350	
Ser	Met	Leu	Lys	Arg	Thr	Val	Val	Ala	Val	Val	Pro	Ala	Pro	Phe	Gly	355	360	365	
Lys	Trp	Tyr	Ser	Arg	Thr	Gly	Tyr	Glu	Thr	Thr	Gln	Asp	Gly	Pro	Thr	370	375	380	
Gly	Gly	Leu	Asn	Ile	Lys	Val	Gly	Ala	Lys	Ile	Leu	Tyr	Glu	Ala	Leu	385	390	395	400
Gln	Gly	Asp	Lys	Ser	Pro	Ile	Pro	Gln	Ala	Val	Asp	Leu	Phe	Gly	Gly	405	410	415	
Lys	Pro	Gln	Gln	Glu	Val	Ile	Leu	Ala	Ala	Leu	Asp	Asp	Ala	Trp	Gln	420	425	430	
Thr	Leu	Ser	Lys	Arg	Tyr	Gly	Asn	Asp	Val	Asp	Asn	Trp	Lys	Thr	Pro	435	440	445	
Ala	Met	Lys	Leu	Thr	Phe	Arg	Ala	Thr	Asn	Phe	Phe	Gly	Val	Pro	Gln	450	455	460	
Ala	Ala	Ala	Lys	Glu	Ala	Arg	His	Gln	Ala	Glu	Tyr	Gln	Asn	Arg	Gly	465	470	475	480
Thr	Glu	Asn	Asp	Met	Ile	Val	Phe	Ser	Pro	Thr	Ser	Gly	Asp	Arg	Pro	485	490	495	
Val	Leu	Ala	Trp	Asp	Val	Val	Ala	Pro	Gly	Gln	Ser	Gly	Phe	Ile	Ala	500	505	510	
Pro	Asp	Gly	Lys	Ala	Asp	Lys	His	Tyr	Asp	Asp	Gln	Leu	Lys	Met	Tyr	515	520	525	
Glu	Ser	Phe	Gly	Arg	Lys	Ser	Leu	Trp	Leu	Thr	Pro	Gln	Asp	Val	Asp	530	535	540	
Glu	His	Lys	Glu	Ser	Gln	Glu	Val	Leu	Gln	Val	Gln	Leu	Asp	Gln	Thr	545	550	555	560
Glu	Val	Lys	Ile	Val	Arg	Asp	Glu	Tyr	Gly	Met	Pro	His	Ile	Tyr	Ala	565	570	575	
Asp	Asp	Thr	Tyr	Arg	Leu	Phe	Tyr	Gly	Tyr	Gly	Tyr	Val	Val	Ala	Gln	580	585	590	
Asp	Arg	Leu	Phe	Gln	Met	Glu	Met	Ala	Arg	Arg	Ser	Thr	Gln	Gly	Thr	595	600	605	
Val	Ser	Glu	Val	Leu	Gly	Lys	Thr	Phe	Val	Trp	Phe	Asp	Lys	Leu	Ile	610	615	620	
Arg	Gln	Asn	Tyr	Trp	Pro	Asp	Ser	Ile	Arg	Ala	Gln	Ile	Ala	Ser	Leu	625	630	635	640
Ser	Ala	Glu	Asp	Lys	Asp	Ile	Leu	Gln	Gly	Tyr	Ala	Asp	Gly	Met	Asn	645	650	655	

[illegible]