



(86) Date de dépôt PCT/PCT Filing Date: 1998/10/23

(87) Date publication PCT/PCT Publication Date: 1999/04/29

(45) Date de délivrance/Issue Date: 2011/08/02

(85) Entrée phase nationale/National Entry: 2000/04/18

(86) N° demande PCT/PCT Application No.: US 1998/022500

(87) N° publication PCT/PCT Publication No.: 1999/020769

(30) Priorités/Priorities: 1997/10/23 (US08/956,564);
1997/10/23 (US08/956,324); 1997/10/23 (US08/956,323)

(51) Cl.Int./Int.Cl. *C12N 15/57* (2006.01),
A23K 1/165 (2006.01), *A61K 8/66* (2006.01),
A61Q 11/00 (2006.01), *C11D 3/386* (2006.01),
C12N 9/54 (2006.01), *C12N 9/58* (2006.01)

(72) Inventeurs/Inventors:
SCHELLENBERGER, VOLKER, US;
KELLIS, JAMES T., US;
PAECH, CHRISTIAN, US;
NADHERNY, JOANNE, US;
...

(73) Propriétaires/Owners:
GENENCOR INTERNATIONAL, INC., US;
THE PROCTER & GAMBLE COMPANY, US

(74) Agent: BERESKIN & PARR LLP/S.E.N.C.R.L., S.R.L.

(54) Titre : VARIANTES DE PROTEASE MULTISUBSTITUEES

(54) Title: MULTIPLY-SUBSTITUTED PROTEASE VARIANTS

(57) **Abrégé/Abstract:**

Novel protease variants derived from the DNA sequences of naturally-occurring or recombinant non-human proteases are disclosed. The variant proteases, in general, are obtained by in vitro modification of a precursor DNA sequence encoding the naturally-occurring or recombinant protease to generate the substitution of a plurality of amino acid residues in the amino acid sequence of a precursor protease. Such variant proteases have properties which are different from those of the precursor protease, such as altered wash performance. The substituted amino acid residue correspond to positions 62, 212, 230, 232, 252 and 257 of *Bacillus amyloliquefaciens subtilisin*.

(72) **Inventeurs(suite)/Inventors(continued):** NAKI, DONALD P., US; POULOSE, AYROOKARAN J., US;
COLLIER, KATHERINE D., US; CALDWELL, ROBERT M., US; BAECK, ANDRE C., BE

PCTWORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/57, 9/54, C11D 3/386, A23K 1/165	A2	(11) International Publication Number: WO 99/20769 (43) International Publication Date: 29 April 1999 (29.04.99)									
(21) International Application Number: PCT/US98/22500 (22) International Filing Date: 23 October 1998 (23.10.98) (30) Priority Data: <table border="0" style="width: 100%;"> <tr> <td style="width: 30%;">08/956,323</td> <td style="width: 30%;">23 October 1997 (23.10.97)</td> <td style="width: 40%;">US</td> </tr> <tr> <td>08/956,324</td> <td>23 October 1997 (23.10.97)</td> <td>US</td> </tr> <tr> <td>08/956,564</td> <td>23 October 1997 (23.10.97)</td> <td>US</td> </tr> </table> (71) Applicants: GENENCOR INTERNATIONAL, INC. [US/US]; 4 Cambridge Place, 1870 South Winton Road, Rochester, NY 14618 (US). THE PROCTER & GAMBLE COMPANY [US/US]; Procter & Gamble Plaza, Cincinnati, OH 45202 (US).		08/956,323	23 October 1997 (23.10.97)	US	08/956,324	23 October 1997 (23.10.97)	US	08/956,564	23 October 1997 (23.10.97)	US	(72) Inventors: SCHELLENBERGER, Volker; 1747 Sequoia Avenue, Burlingame, CA 94010 (US). KELLIS, James, T., Jr.; 111 Tan Oak Drive, Portola Valley, CA 94028 (US). PAECH, Christian; 914 Moreno Avenue, Palo Alto, CA 94303 (US). NADHERNY, Joanne; 681 Arguello No. 6, San Francisco, CA 94118 (US). NAKI, Donald, P.; 4815 - 25th Street, San Francisco, CA 94118 (US). POULOSE, Ayrookaran, J.; 2848 Wakefield Drive, Belmont, CA 94002 (US). COLLIER, Katherine, D.; 915 Wilmington Way, Redwood City, CA 94062 (US). CALDWELL, Robert, M.; 915 Wilmington Way, Redwood City, CA 94062 (US). BAECK, André, C.; Putsesteenweeg 273, B-2820 Bonheiden (BE). (74) Agent: ANDERSON, Kirsten, A.; Genencor International, Inc., 925 Page Mill Road, Palo Alto, CA 94304-1013 (US). (81) Designated States: AL, AM, AT, AT (Utility model), AU (Petty patent), AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ (Utility model), DE, DE (Utility model), DK, DK (Utility model), EE, EE (Utility model), ES, FI, FI (Utility model), GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (Utility model), SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
08/956,323	23 October 1997 (23.10.97)	US									
08/956,324	23 October 1997 (23.10.97)	US									
08/956,564	23 October 1997 (23.10.97)	US									
(54) Title: MULTIPLY-SUBSTITUTED PROTEASE VARIANTS (57) Abstract Novel protease variants derived from the DNA sequences of naturally-occurring or recombinant non-human proteases are disclosed. The variant proteases, in general, are obtained by <i>in vitro</i> modification of a precursor DNA sequence encoding the naturally-occurring or recombinant protease to generate the substitution of a plurality of amino acid residues in the amino acid sequence of a precursor protease. Such variant proteases have properties which are different from those of the precursor protease, such as altered wash performance. The substituted amino acid residue correspond to positions 62, 212, 230, 232, 252 and 257 of <i>Bacillus amyloliquefaciens</i> subtilisin.											

MULTIPLY-SUBSTITUTED PROTEASE VARIANTS10 Background of the Invention

Serine proteases are a subgroup of carbonyl hydrolases. They comprise a diverse class of enzymes having a wide range of specificities and biological functions. Stroud, R. Sci. Amer., 131:74-88. Despite their functional diversity, the catalytic machinery of serine proteases has been approached by at least two
15 genetically distinct families of enzymes: 1) the subtilisins and 2) the mammalian chymotrypsin-related and homologous bacterial serine proteases (e.g., trypsin and *S. gresius* trypsin). These two families of serine proteases show remarkably similar mechanisms of catalysis. Kraut, J. (1977), Annu. Rev. Biochem., 46:331-358. Furthermore, although the primary structure is unrelated, the tertiary structure of
20 these two enzyme families bring together a conserved catalytic triad of amino acids consisting of serine, histidine and aspartate.

Subtilisins are serine proteases (approx. MW 27,500) which are secreted in large amounts from a wide variety of *Bacillus* species and other microorganisms. The protein sequence of subtilisin has been determined from at least nine different
25 species of *Bacillus*. Markland, F.S., et al. (1983), Hoppe-Seyler's Z. Physiol. Chem., 364:1537-1540. The three-dimensional crystallographic structure of subtilisins from *Bacillus amyloliquefaciens*, *Bacillus licheniformis* and several natural variants of *B. lentus* have been reported. These studies indicate that although subtilisin is genetically unrelated to the mammalian serine proteases, it has a similar active site
30 structure. The x-ray crystal structures of subtilisin containing covalently bound peptide inhibitors (Robertus, J.D., et al. (1972), Biochemistry, 11:2439-2449) or product complexes (Robertus, J.D., et al. (1976), J. Biol. Chem., 251:1097-1103) have also provided information regarding the active site and putative substrate binding cleft of subtilisin. In addition, a large number of kinetic and chemical

-2-

modification studies have been reported for subtilisin ; Svendsen, B. (1976), Carlsberg Res. Commun., 41:237-291; Markland, F.S. Id.) as well as at least one report wherein the side chain of methionine at residue 222 of subtilisin was converted by hydrogen peroxide to methionine-sulfoxide (Stauffer, D.C., et al. (1965), J. Biol. Chem., 244:5333-5338) and extensive site-specific mutagenesis has been carried out (Wells and Estell (1988) TIBS 13:291-297)

Summary of the Invention

It is an object herein to provide a protease variant containing a substitution of an amino acid at one or more residue positions corresponding to residue positions selected from the group consisting of 62, 212, 230, 232, 252 and 257 of *Bacillus amyloliquefaciens* subtilisin.

While any combination of the above listed amino acid substitutions may be employed, the preferred protease variant enzymes of the present invention comprise the substitution of amino acid residues in the following combinations. All of the residue positions correspond to positions of *Bacillus amyloliquefaciens* subtilisin:

(1) a protease variant including substitutions of the amino acid residues at position 62 and at one or more of the following positions 103, 104, 109, 159, 213, 232, 236, 245, 248 and 252;

(2) a protease variant including substitutions of the amino acid residues at position 212 and at one or more of the following positions 12, 98, 102, 103, 104, 159, 232, 236, 245, 248 and 252;

(3) a protease variant including substitutions of the amino acid residues at position 230 and at one or more of the following positions 68, 103, 104, 159, 232, 236 and 245;

(4) a protease variant including substitutions of the amino acid residues at position 232 and at one or more of the following positions: 1, 9, 12, 61, 62, 68, 76, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 205, 209, 210, 212, 213, 217, 230, 236, 245, 248, 252, 257, 260, 270 and 275;

(5) a protease variant including substitutions of the amino acid residues at position 232 and at one or more of the following positions 103, 104, 236 and 245;

(6) a protease variant including substitutions of the amino acid residues at position 232 and 103 and at one or more of the following positions 1, 9, 12, 61, 62,

-3-

68, 76, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 205, 209, 210, 212, 213, 217, 230, 236, 245, 248, 252, 257, 260, 270 and 275;

(7) a protease variant including substitutions of the amino acid residues at position 232 and 104 and at one or more of the following positions 1, 9, 12, 61, 62,
5 68, 76, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 205, 209, 210, 212, 213, 217, 230, 236, 245, 248, 252, 257, 260, 270 and 275;

(8) a protease variant including substitutions of the amino acid residues at position 232 and 236 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 76, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 205, 209, 210, 212,
10 213, 217, 230, 236, 245, 248, 252, 257, 260, 270 and 275;

(9) a protease variant including substitutions of the amino acid residues at position 232 and 245 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 76, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 205, 209, 210, 212, 213, 217, 230, 236, 245, 248, 252, 257, 260, 270 and 275;

15 (10) a protease variant including substitutions of the amino acid residues at position 232, 103, 104, 236 and 245 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 76, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 205, 209, 210, 212, 213, 217, 230, 236, 245, 248, 252, 257, 260, 270 and 275;

(11) a protease variant including substitutions of the amino acid residues at
20 position 252 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 210, 212, 213, 217, 232, 236, 245, 248 and 270;

(12) a protease variant including substitutions of the amino acid residues at position 252 and at one or more of the following positions 103, 104, 236 and 245;

25 (13) a protease variant including substitutions of the amino acid residues at positions 252 and 103 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 210, 212, 213, 217, 232, 236, 245, 248 and 270;

(14) a protease variant including substitutions of the amino acid residues at
30 positions 252 and 104 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 210, 212, 213, 217, 232, 236, 245, 248 and 270;

(15) a protease variant including substitutions of the amino acid residues at positions 252 and 236 and at one or more of the following positions 1, 9, 12, 61, 62,

-4-

68, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 210, 212, 213, 217, 232, 236, 245, 248 and 270;

(16) a protease variant including substitutions of the amino acid residues at positions 252 and 245 and at one or more of the following positions 1, 9, 12, 61, 62,
5 68, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 210, 212, 213, 217, 232, 236, 245, 248 and 270;

(17) a protease variant including substitutions of the amino acid residues at positions 252, 103, 104, 236 and 245 and at one or more of the following positions 1, 9, 12, 61, 62, 68, 97, 98, 101, 102, 103, 104, 109, 130, 131, 159, 183, 185, 210, 212,
10 213, 217, 232, 236, 245, 248 and 270; and

(18) a protease variant including substitutions of the amino acid residues at position 257 and at one or more of the following positions 68, 103, 104, 205, 209, 210, 232, 236, 245 and 275. More preferred protease variants are substitution sets selected from the group consisting of residue positions corresponding to positions in
15 Table 1 of *Bacillus amyloliquefaciens* subtilisin:

74541-49

- 4a -

According to one aspect of the present invention, there is provided a protease variant comprising at least an amino acid substitution at residue position corresponding to residue position 212 of *Bacillus amyloliquefaciens* subtilisin as set forth in SEQ ID NO: 1, wherein the variant comprises: a substitution set selected from Table 1; a substitution set selected from Table 2; or a substitution set selected from Table 3, with the proviso that the substitution set does not comprise a substitution at residue position 232, 252 or 257 of *Bacillus amyloliquefaciens* subtilisin.

Table 1

[illegible]

43	68	103	104	159	232	236	245	252					
43	68	103	104	159	232	236	245						
43	68	103	104	159	232	236	245	252					
68	87	103	104	159	232	236	245	252	275				
68	103	104	159	232	236	245	257						
68	103	104	116	159	232	236	245						
68	103	104	159	232	236	245	248						
10	68	103	104	159	232	236	245						
68	103	104	159	203	232	236	245						
68	103	104	159	232	236	237	245						
68	76	79	103	104	159	232	236	245					
68	103	104	159	183	232	236	245						
68	103	104	159	174	206	232	236	245					
68	103	104	159	188	232	236	245						
68	103	104	159	230	232	236	245						
68	98	103	104	159	232	236	245						
68	103	104	159	215	232	236	245						
68	103	104	159	232	236	245	248						
68	76	103	104	159	232	236	245						

68	76	103	104	159	210	232	236	245					
68	76	103	104	159	232	236	245	257					
76	103	104	232	236	245	257							
68	103	104	159	232	236	245	257	275					
76	103	104	257	275									
68	103	104	159	224	232	236	245	257					
76	103	104	159	232	236	245	257						
68	76	103	104	159	209	232	236	245					
68	76	103	104	159	211	232	236	245					
12	68	76	103	104	159	214	232	236	245				
68	76	103	104	159	215	232	236	245					
12	68	76	103	104	159	232	236	245					
20	68	76	103	104	159	232	236	245	259				
68	87	76	103	104	159	232	236	245	260				
68	76	103	104	159	232	236	245	261					
76	103	104	232	236	242	245							
68	76	103	104	159	210	232	236	245					
12	48	68	76	103	104	159	232	236	245				
76	103	104	232	236	245				245				

76	103	104	159	192	232	236	245					
76	103	104	147	159	232	236	245	248	251			
12	68	76	103	104	159	232	236	245	272			
68	76	103	104	159	183	206	232	236	245			
68	76	103	104	159	232	236	245	256				
68	76	103	104	159	206	232	236	245				
27	68	76	103	104	159	232	236	245				
68	76	103	104	116	159	170	185	232	236	245		
61	68	103	104	159	232	236	245	248	252			
43	68	103	104	159	232	236	245	248	252			
68	103	104	159	212	232	236	245	248	252			
68	103	104	99	159	184	232	236	245	248	252		
103	104	159	232	236	245	248	252					
68	103	104	159	209	232	236	245	248	252			
68	103	104	109	159	232	236	245	248	252			
20	68	103	104	159	232	236	245	248	252			
68	103	104	159	209	232	236	245	248	252			
68	103	104	159	232	236	245	248	252	261			
68	103	104	159	185	232	236	245	248	252			

68	103	104	159	210	232	236	245	248	252			
68	103	104	159	185	210	232	236	245	248	252		
68	103	104	159	212	232	236	245	248	252			
68	103	104	159	213	232	236	245	248	252			
68	103	104	213	232	236	245	248	252				
68	103	104	159	215	232	236	245	248	252			
68	103	104	159	216	232	236	245	248	252			
20	68	103	104	159	232	236	245	248	252			
68	103	104	159	173	232	236	245	248	252			
68	103	104	159	232	236	245	248	251	252			
68	103	104	159	206	232	236	245	248	252			
68	103	104	159	232	236	245	248	252				
55	68	103	104	159	232	236	245	248	252			
68	103	104	159	232	236	245	248	252	255			
68	103	104	159	232	236	245	248	252	256			
68	103	104	159	232	236	245	248	252	260			
68	103	104	159	232	236	245	248	252	257			
68	103	104	159	232	236	245	248	252	258			
8	68	103	104	159	232	236	245	248	252	269		

68	103	104	116	159	232	236	245	248	252	260		
68	103	104	159	232	236	245	248	252	261			
68	103	104	159	232	236	245	248	252	261			
68	76	103	104	159	232	236	245	248	252			
68	103	104	232	236	245	248	252					
103	104	159	232	236	245	248	252					
68	103	104	159	232	236	245	248	252				
18	68	103	104	159	232	236	245	248	252			
68	103	104	159	232	236	245	248	252				
68	76	101	103	104	159	213	218	232	236	245	260	
68	103	104	159	228	232	236	245	248	252			
33	68	76	103	104	159	232	236	245	248	252		
68	76	89	103	104	159	210	213	232	236	245	260	
61	68	76	103	104	159	232	236	245	248	252		
103	104	159	205	210	232	236	245					
61	68	103	104	130	159	232	236	245	248	252		
61	68	103	104	133	137	159	232	236	245	248	252	
61	103	104	133	159	232	236	245	248	252			
68	103	104	159	232	236	245	248	252				

68	103	104	159	218	232	236	245	248	252			
61	68	103	104	159	160	232	236	245	248	252		
3	61	68	76	103	104	232	236	245	248	252		
61	68	103	104	159	167	232	236	245	248	252		
97	103	104	159	232	236	245	248	252				
98	103	104	159	232	236	245	248	252				
99	103	104	159	232	236	245	248	252				
101	103	104	159	232	236	245	248	252				
102	103	104	159	232	236	245	248	252				
103	104	106	159	232	236	245	248	252				
103	104	109	159	232	236	245	248	252				
103	104	159	232	236	245	248	252	261				
62	103	104	159	232	236	245	248	252				
103	104	159	184	232	236	245	248	252				
103	104	159	166	232	236	245	248	252				
103	104	159	217	232	236	245	248	252				
20	62	103	104	159	213	232	236	245	248	252		
62	103	104	159	213	232	236	245	248	252			
103	104	159	206	217	232	236	245	248	252			

62	103	104	159	206	232	236	245	248	252				
103	104	130	159	232	236	245	248	252					
103	104	131	159	232	236	245	248	252					
27	103	104	159	232	236	245	248	252					
38	103	104	159	232	236	245	248	252					
38	76	103	104	159	213	232	236	245	260				
68	76	103	104	159	213	232	236	245	260	271			
68	76	103	104	159	209	213	232	236	245	260			
68	76	103	104	159	210	213	232	236	245	260			
68	76	103	104	159	205	213	232	236	245	260			
68	76	103	104	159	210	232	236	245	260				
68	103	104	159	213	232	236	245	260					
76	103	104	159	213	232	236	245	260					
68	103	104	159	209	232	236	245						
68	103	104	159	210	232	236	245						
68	103	104	159	230	232	236	245						
68	103	104	159	126	232	236	245						
68	103	104	159	205	232	236	245						
68	103	104	159	210	232	236	245						

[illegible]

103	104	159	205	209	232	236	245	257				
68	103	104	159	205	209	210	232	236	245	260		
103	104	159	205	209	210	232	236	245				
103	104	159	209	210	232	236	245					
103	104	159	205	210	232	236	245					
68	103	104	128	159	232	236	245					
48	103	104	159	230	236	245						
48	68	103	104	159	209	232	236	245				
48	68	103	104	159	232	236	245	248	252			
48	68	103	104	159	232	236	245	257	261			
102	103	104	159	212	232	236	245	248	252			
12	102	103	104	159	212	232	236	245	248	252		
101	102	103	104	159	212	232	236	245	248	252		
98	102	103	104	159	212	232	236	245	248	252		
102	103	104	159	213	232	236	245	248	252			
103	104	131	159	232	236	245	248	252				
103	104	159	184	232	236	245	248	252				
103	104	159	232	236	244	245	248	252				
62	103	104	159	213	232	236	245	248	252	256		

12	62	103	104	159	213	232	236	245	248	252		
101	103	104	159	185	232	236	245	248	252			
101	103	104	159	206	232	236	245	248	252			
101	103	104	159	213	232	236	245	248	252			
98	102	103	104	159	232	236	245	248	252			
101	102	103	104	159	232	236	245	248	252			
98	102	103	104	159	212	232	236	245	248	252		
98	102	103	104	159	212	232	236	248	252			
62	103	104	109	159	213	232	236	245	248	252		
62	103	104	159	212	213	232	236	245	248	252		
62	101	103	104	159	212	213	232	236	245	248	252	
103	104	159	232	245	248	252						
103	104	159	230	245								
62	103	104	130	159	213	232	236	245	248	252		
101	103	104	130	159	232	236	245	248	252			
101	103	104	128	159	232	236	245	248	252			
62	101	103	104	159	213	232	236	245	248	252		
62	103	104	128	159	213	232	236	245	248	252		
62	103	104	128	159	213	232	236	245	248	252		

101	103	104	159	232	236	245	248	252	260			
101	103	104	131	159	232	236	245	248	252			
98	101	103	104	159	232	236	245	248	252			
99	101	103	104	159	232	236	245	248	252			
101	103	104	159	212	232	236	245	248	252			
101	103	104	159	209	232	236	245	248	252			
101	103	104	159	210	232	236	245	248	252			
101	103	104	159	205	232	236	245	248	252			
101	103	104	159	230	236	245						
101	103	104	159	194	232	236	245	248	252			
76	101	103	104	159	194	232	236	245	248	252		
101	103	104	159	230	232	236	245	248	252			
62	103	104	159	185	206	213	232	236	245	248	252	271

- 17 -

Most preferred protease variants are substitution sets selected from the group consisting of residue positions corresponding to positions in Table 2 of *Bacillus amyloliquefaciens* subtilisin:

Table 2

[illegible]

N43S	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K					
N43K	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R						
N43D	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K					
V68A	S87G	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K	R275S				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V						
V68A	S103A	V104I	N116D	G159D	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D						
R10C	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	V203E	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A232V	Q236H	K237E	Q245R						
V68A	N76D	I79N	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	N183D	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A174V	Q206L	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	S188C	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A230T	A232V	Q236H	Q245R						
V68A	A98T	S103A	V104I	G159D	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A215T	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248S						
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R						

V68A	N76D	S103A	V104I	G159D	P210R	A232V	Q236H	Q245R					
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V					
N76D	S103A	V104I	A232V	Q236H	Q245R	L257V							
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V	R275H					
N76D	S103A	V104I	L257V	R275H									
V68A	S103A	V104I	G159D	T224A	A232V	Q236H	Q245R	L257V					
N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V						
V68A	N76D	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R					
V68A	N76D	S103A	V104I	G159D	G211R	A232V	Q236H	Q245R					
V68A	N76D	S103A	V104I	G159D	G211V	A232V	Q236H	Q245R					
Q12R	V68A	N76D	S103A	V104I	G159D	Y214L	A232V	Q236H	Q245R				
V68A	N76D	S103A	V104I	G159D	A215R	A232V	Q236H	Q245R					
Q12R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R					
G20R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	S87R	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	S259G				
V68A	N76D	S103A	V104I	G159D	A232V	A232V	Q245R	Q245R	T260V				
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N261G					
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N261W					
N76D	S103A	V104I	A232V	Q236H	S242P	Q245R							
V68A	N76D	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R					

Q12R	A48V	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R				
N76D	S103A	V104I	A232V	Q236H	Q245R								
N76D	S103A	V104I	G159D	Y192F	A232V	Q236H	Q245R						
N76D	S103A	V104I	V147I	G159D	A232V	Q236H	Q245R	N248S	K251R				
Q12R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	A272S				
V68A	N76D	S103A	V104I	G159D	N183K	Q206L	A232V	Q236H	Q245R				
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	S256R					
V68A	N76D	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R					
K27R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	N76D	S103A	V104I	N116T	G159D	R170S	N185S	A232V	Q236H	Q245R			
G61E	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
N43D	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	G159D	S212P	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	S99N	G159D	N184D	A232V	Q236H	Q245R	N248D	N252K			
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			N252K			
V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	N248D	N252K				
G20R	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	G159D	Y209F	A232V	Q236H	Q245R	N248D	N252K				

V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261D			
V68A	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	P210R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	P210T	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	P210S	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	N185D	P210L	A232V	Q236H	Q245R	N248D	N252K		
V68A	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S212A	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S212E	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	T213E	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	T213S	A232V	Q236H	Q245R	N248D	N252K				
V68A	A103V	V104I	G159D	T213E	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	T213G	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A215V	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A215R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S216T	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S216V	A232V	Q236H	Q245R	N248D	N252K			

V68A	S103A	V104I	G159D	S216C	A232V	Q236H	Q245R	N248D	N252K				
G20A	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	G159D	N173D	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	K251V	N252K				
V68A	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252F					
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252L					
P55S	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252F				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	T255V				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	S256N				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	S256E				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	S256R				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	T260R				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	L257R				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	G258D				
I8V	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N269D			
V68A	S103A	V104I	N116S	G159D	A232V	Q236H	Q245R	N248D	N252K	T260E			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261D				

V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	A232S	Q236H	Q245R	N248D	N252K					
V68A	S103A	V104I	G159D	A232V	Q236R	Q245R	N248D	N252K				
N18S	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245V	N248D	N252K				
V68A	N76D	S101T	S103A	V104I	G159D	T213R	N218S	A232V	Q236H	Q245R	T260A	
V68A	S103A	V104I	G159D	A228V	A232V	Q236H	Q245R	N248D	N252K			
T33S	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K		
V68A	N76D	E89D	S103A	V104I	G159D	P210L	T213R	A232V	Q236H	Q245R	T260A	
G61E	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K		
S103A	V104I	G159D	V205I	P210I	A232V	Q236H	Q245R					
G61E	V68A	S103A	V104I	S130A	G159D	A232V	Q236H	Q245R	N248D	N252K		
G61E	V68A	S103A	V104I	A133S	Q137R	G159D	A232V	Q236H	Q245R	N248D	N252K	
G61E	S103A	V104I	A133V	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248G	N252K				
V68A	S103A	V104I	G159D	N218S	A232V	Q236H	Q245R	N248D	N252K			
G61E	V68A	S103A	V104I	G159D	S160V	A232V	Q236H	Q245R	N248D	N252K		
S3L	G61E	V68A	N76D	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K		

G61E	V68A	S103A	V104I	G159D	S167F	A232V	Q236H	Q245R	Q245R	Q245R	N252K		
G97E	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
A98D	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
S99E	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
S101E	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
S103A	V104I	S106E	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
S103A	V104I	Q109E	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K				
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R					
S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	Q245R	N252K					
N62D	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	N252K					
S103A	V104I	G159D	N184D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	S166D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	L217E	A232V	Q236H	Q245R	N248D	N252K					
G20R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	Q245R	N248D	N252K		
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N248D	N252K			
S103A	V104I	G159D	Q206R	L217E	A232V	Q236H	Q245R	N248D	N248D	N252K			
N62D	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R	N248D	N248D	N252K			

S103A	V104I	S130G	G159D	A232V	Q236H	Q245R	N248D	N252K				
S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K				
K27N	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
T38G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
T38A	N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A			
V68A	N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A	E271G		
V68A	N76D	S103A	V104I	G159D	Y209W	T213R	A232V	Q236H	Q245R	T260A		
V68A	N76D	S103A	V104I	G159D	P210I	T213R	A232V	Q236H	Q245R	T260A		
V68A	N76D	S103A	V104I	G159D	V205I	T213R	A232V	Q236H	Q245R	T260A		
V68A	N76D	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	T260A			
V68A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A				
N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A				
V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	A230V	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	L126F	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	V205I	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R					
S103A	V104I	G159D	A230V	Q236H	Q245R							

V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	T260A					
S103A	V104I	G159D	A232V	Q236H	Q245R							
V68A	S103A	V104I	G159D	A174V	A232V	Q236H	Q245R	L257V				
V68A	S103A	V104I	G159D	A194S	A232V	Q236H	Q245R	L257V				
V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	L257V				
S103A	V104I	G159D	A232V	Q236H	Q245R	L257V						
V68A	N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A	N261W		
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V	N261W				
S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A					
S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	N248D	N252K				
S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	L257V					
V68A	N76D	S103A	V104I	G159D	P210L	T213R	A232V	Q236H	Q245R	T260A		
Q12R	S103A	V104I	G159D	Y209W	T213R	A232V	Q236H	Q245R	T260A			
S103A	V104I	Y209W	A232V	Q236H	Q245R	L257V						
S103A	V104I	G159D	V205I	P210I	T213R	A232V	Q236H	Q245R	T260A			
S103A	V104I	G159D	V205I	Y209W	A232V	Q236H	Q245R	T260A				
V68A	S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R	Q245R		
S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R	L257V			
S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R	L257V			

V68A	S103A	V104I	G159D	V205I	Y209W	P210I	A232V	A232V	Q236H	Q236H	Q245R	T260A			
S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R	Q245R	Q245R					
S103A	V104I	G159D	Y209W	P210I	A232V	Q236H	Q245R	Q245R							
S103A	V104I	G159D	V205I	P210I	A232V	Q236H	Q245R	Q245R							
V68A	S103A	V104I	S128L	G159D	A232V	Q236H	Q245R	Q245R							
A48V	S103A	V104I	G159D	A230V	Q236H	Q245R									
A48V	V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	Q245R	Q245R					
A48V	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	Q245R	N248D	N252K				
A48V	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	Q245R	Q245R	L257V	N261W				
G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	Q245R	Q245R	N248D	N252K				
Q12R	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	Q236H	Q245R	N248D	N252K			
S101G	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	Q236H	Q245R	N248D	N252K			
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	Q236H	Q245R	N248D	N252K			
G102A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	Q245R	Q245R	N248D	N252K				
S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	Q245R	N248D	N252K						
S103A	V104I	G159D	N184S	A232V	Q236H	Q245R	Q245R	N248D	N252K						
S103A	V104I	G159D	N184G	A232V	Q236H	Q245R	Q245R	N248D	N252K						
S103A	V104I	G159D	A232V	Q236H	V244T	Q245R	Q245R	N248D	N252K						
S103A	V104I	G159D	A232V	Q236H	V244A	Q245R	Q245R	N248D	N252K						

N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K	S256R		
Q12R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	Q206E	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	T213Q	A232V	Q236H	Q245R	N248D	N252K			
A98L	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K		
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	N248D	N252K			
N62D	S103A	V104I	Q109R	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
N62D	S103A	V104I	G159D	S212G	T213R	A232V	Q236H	Q245R	N248D	N252K		
N62D	S101G	S103A	V104I	G159D	S212G	T213R	A232V	Q236H	Q245R	N248D	N252K	
S103A	V104I	G159D	A232V	Q245R	N248D	N252K				N248D	N252K	
S103A	V104I	G159D	A230V	Q245R								
N62D	S103A	V104I	S130G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	S130G	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	S128G	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	S128L	G159D	A232V	Q236H	Q245R	N248D	N252K			
N62D	S101G	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		

N62D	S103A	V104I	S128G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
N62D	S103A	V104I	S128L	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	T260A			
S101G	S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K			
A98V	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S99G	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	V205I	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	A230V	Q236H	Q245R						
S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K			
N76D	S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	G159D	A230V	A232V	Q236H	Q245R	N248D	N252K			
N62D	S103A	V104I	G159D	N185D	Q206E	T213R	A232V	Q236H	Q245R	N248D	N252K	E271Q

74541-49

- 31 -

It is a further object to provide DNA sequences encoding such protease variants, as well as expression vectors containing such variant DNA sequences.

Still further, another object of the invention is to provide host cells transformed with such vectors, as well as host cells which are capable of expressing
5 such DNA to produce protease variants either intracellularly or extracellularly.

There is further provided a cleaning composition comprising a protease variant of the present invention.

Additionally, there is provided an animal feed comprising a protease variant of the present invention.

10 Also provided is a composition for the treatment of a textile comprising a protease variant of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1 A-B depict the DNA and amino acid sequence for *Bacillus*
15 *amyloliquefaciens* subtilisin and a partial restriction map of this gene.

Fig. 2 depicts the conserved amino acid residues among subtilisins from *Bacillus amyloliquefaciens* (BPN)' and *Bacillus lentus* (wild-type).

Figs. 3A and 3B depict the amino acid sequence of four subtilisins. The top line represents the amino acid sequence of subtilisin from *Bacillus amyloliquefaciens* subtilisin (also sometimes referred to as subtilisin BPN'). The second line depicts the
20 amino acid sequence of subtilisin from *Bacillus subtilis*. The third line depicts the amino acid sequence of subtilisin from *B. licheniformis*. The fourth line depicts the amino acid sequence of subtilisin from *Bacillus lentus* (also referred to as subtilisin 309 in PCT WO89/06276). The symbol * denotes the absence of specific amino acid
25 residues as compared to subtilisin BPN'.

Detailed Description of the Invention

Proteases are carbonyl hydrolases which generally act to cleave peptide bonds of proteins or peptides. As used herein, "protease" means a naturally-
30 occurring protease or a recombinant protease. Naturally-occurring proteases include α -aminoacylpeptide hydrolase, peptidylamino acid hydrolase, acylamino hydrolase, serine carboxypeptidase, metallo-carboxypeptidase, thiol proteinase, carboxylproteinase and metalloproteinase. Serine, metallo, thiol and acid proteases are included, as well as endo and exo-proteases.

-32-

The present invention includes protease enzymes which are non-naturally occurring carbonyl hydrolase variants (protease variants) having a different proteolytic activity, stability, substrate specificity, pH profile and/or performance characteristic as compared to the precursor carbonyl hydrolase from which the amino acid sequence of the variant is derived. Specifically, such protease variants have an amino acid sequence not found in nature, which is derived by substitution of a plurality of amino acid residues of a precursor protease with different amino acids. The precursor protease may be a naturally-occurring protease or a recombinant protease.

The protease variants useful herein encompass the substitution of any of the nineteen naturally occurring L-amino acids at the designated amino acid residue positions. Such substitutions can be made in any precursor subtilisin (procaryotic, eucaryotic, mammalian, etc.). Throughout this application reference is made to various amino acids by way of common one - and three-letter codes. Such codes are identified in Dale, M.W. (1989), Molecular Genetics of Bacteria, John Wiley & Sons, Ltd., Appendix B.

The protease variants useful herein are preferably derived from a *Bacillus* subtilisin. More preferably, the protease variants are derived from *Bacillus lentus* subtilisin and/or subtilisin 309.

Subtilisins are bacterial or fungal proteases which generally act to cleave peptide bonds of proteins or peptides. As used herein, "subtilisin" means a naturally-occurring subtilisin or a recombinant subtilisin. A series of naturally-occurring subtilisins is known to be produced and often secreted by various microbial species. Amino acid sequences of the members of this series are not entirely homologous. However, the subtilisins in this series exhibit the same or similar type of proteolytic activity. This class of serine proteases shares a common amino acid sequence defining a catalytic triad which distinguishes them from the chymotrypsin related class of serine proteases. The subtilisins and chymotrypsin related serine proteases both have a catalytic triad comprising aspartate, histidine and serine. In the subtilisin related proteases the relative order of these amino acids, reading from the amino to carboxy terminus, is aspartate-histidine-serine. In the chymotrypsin related proteases, the relative order, however, is histidine-aspartate-serine. Thus, subtilisin herein refers to a serine protease having the catalytic triad of subtilisin related

74541-49

-33-

proteases. Examples include but are not limited to the subtilisins identified in Fig. 3 herein. Generally and for purposes of the present invention, numbering of the amino acids in proteases corresponds to the numbers assigned to the mature *Bacillus amyloliquefaciens* subtilisin sequence presented in Fig. 1.

5 "Recombinant subtilisin" or "recombinant protease" refer to a subtilisin or protease in which the DNA sequence encoding the subtilisin or protease is modified to produce a variant (or mutant) DNA sequence which encodes the substitution, deletion or insertion of one or more amino acids in the naturally-occurring amino acid sequence. Suitable methods to produce such modification, and which may be
10 combined with those disclosed herein, include those disclosed in US Patent RE 34,606, US Patent 5,204,015 and US Patent 5,185,258, U.S. Patent 5,700,676, U.S. Patent 5,801,038, and U.S. Patent 5,763,257.

"Non-human subtilisins" and the DNA encoding them may be obtained from many procaryotic and eucaryotic organisms. Suitable examples of procaryotic
15 organisms include gram negative organisms such as *E. coli* or *Pseudomonas* and gram positive bacteria such as *Micrococcus* or *Bacillus*. Examples of eucaryotic organisms from which subtilisin and their genes may be obtained include yeast such as *Saccharomyces cerevisiae*, fungi such as *Aspergillus* sp.

A "protease variant" has an amino acid sequence which is derived from the
20 amino acid sequence of a "precursor protease". The precursor proteases include naturally-occurring proteases and recombinant proteases. The amino acid sequence of the protease variant is "derived" from the precursor protease amino acid sequence by the substitution, deletion or insertion of one or more amino acids of the precursor amino acid sequence. Such modification is of the "precursor DNA sequence" which
25 encodes the amino acid sequence of the precursor protease rather than manipulation of the precursor protease enzyme *per se*. Suitable methods for such manipulation of the precursor DNA sequence include methods disclosed herein, as well as methods known to those skilled in the art (see, for example, EP 0 328299, WO89/06279 and the US patents already referenced herein).

30 Specific substitutions of amino acids at one or more residue positions corresponding to residue positions selected from the group consisting of 62, 212, 230, 232, 252 and 257 of *Bacillus amyloliquefaciens* subtilisin are identified herein.

-34-

Preferred variants are those having combinations of substitutions at residue positions corresponding to positions of *Bacillus amyloliquefaciens* subtilisin in Table 1.

5 More preferred variants are those having combinations of substitutions at residue positions corresponding to positions of *Bacillus amyloliquefaciens* subtilisin in Table 2.

Further preferred variants are those having combinations of substitutions at residue positions corresponding to positions of *Bacillus amyloliquefaciens* subtilisin in Table 3.

Table 3

68	103	104	159	232	236	245	252						
68	76	103	104	159	213	232	236	245	260				
68	103	104	159	232	236	245	248	252					
68	103	104	159	232	236	245							
68	103	104	140	159	232	236	245	252					
43	68	103	104	159	232	236	245	252					
43	68	103	104	159	232	236	245						
68	103	104	159	232	236	245	257						
68	76	103	104	159	210	232	236	245					
68	103	104	159	224	232	236	245	257					
76	103	104	159	232	236	245	257						
68	76	103	104	159	211	232	236	245					
12	68	76	103	104	159	214	232	236	245				
68	76	103	104	159	215	232	236	245					
12	68	76	103	104	159	232	236	245					
20	68	76	103	104	159	232	236	245	259				
68	76	87	103	104	159	232	236	245	260				

68	76	103	104	159	232	236	245	261				
12	48	68	76	103	104	159	232	236	245			
76	103	104	159	192	232	236	245					
76	103	104	147	159	232	236	245	248	251			
12	68	76	103	104	159	232	236	245	272			
68	76	103	104	159	183	206	232	236	245			
68	76	103	104	159	232	236	245	256				
68	76	103	104	159	206	232	236	245				
27	68	76	103	104	159	232	236	245				
68	103	104	159	212	232	236	245	248	252			
103	104	159	232	236	245	248	252					
68	103	104	159	209	232	236	245	248	252			
68	103	104	109	159	232	236	245	248	252			
20	68	103	104	159	232	236	245	248	252			
68	103	104	159	209	232	236	245	248	252			
68	103	104	159	210	232	236	245	248	252			
68	103	104	159	212	232	236	245	248	252			
68	103	104	159	213	232	236	245	248	252			

68	103	104	213	232	236	245	248	252					
68	103	104	159	215	232	236	245	248	252				
68	103	104	159	216	232	236	245	248	252				
20	68	103	104	159	232	236	245	248	252				
68	103	104	159	232	236	245	248	252	255				
68	103	104	159	232	236	245	248	252	256				
68	103	104	159	232	236	245	248	252	260				
68	103	104	159	228	232	236	245	248	252				
68	76	89	103	104	159	210	213	232	236	245	260		
68	103	104	159	218	232	236	245	248	252				

-38-

These amino acid position numbers refer to those assigned to the mature *Bacillus amyloliquefaciens* subtilisin sequence presented in Fig. 1. The invention, however, is not limited to the mutation of this particular subtilisin but extends to precursor proteases containing amino acid residues at positions which are

5 "equivalent" to the particular identified residues in *Bacillus amyloliquefaciens* subtilisin. In a preferred embodiment of the present invention, the precursor protease is *Bacillus lentus* subtilisin and the substitutions are made at the equivalent amino acid residue positions in *B. lentus* corresponding to those listed above.

A residue (amino acid) position of a precursor protease is equivalent to a

10 residue of *Bacillus amyloliquefaciens* subtilisin if it is either homologous (i.e., corresponding in position in either primary or tertiary structure) or analogous to a specific residue or portion of that residue in *Bacillus amyloliquefaciens* subtilisin (i.e., having the same or similar functional capacity to combine, react, or interact chemically).

15 In order to establish homology to primary structure, the amino acid sequence of a precursor protease is directly compared to the *Bacillus amyloliquefaciens* subtilisin primary sequence and particularly to a set of residues known to be invariant in subtilisins for which sequence is known. For example, Fig. 2 herein shows the conserved residues as between *B. amyloliquefaciens* subtilisin and *B. lentus*

20 subtilisin. After aligning the conserved residues, allowing for necessary insertions and deletions in order to maintain alignment (i.e., avoiding the elimination of conserved residues through arbitrary deletion and insertion), the residues equivalent to particular amino acids in the primary sequence of *Bacillus amyloliquefaciens* subtilisin are defined. Alignment of conserved residues preferably should conserve

25 100% of such residues. However, alignment of greater than 75% or as little as 50% of conserved residues is also adequate to define equivalent residues. Conservation of the catalytic triad, Asp32/His64/Ser221 should be maintained. Siezen et al. (1991) Protein Eng. 4(7):719-737 shows the alignment of a large number of serine proteases. Siezen et al. refer to the grouping as subtilases or subtilisin-like serine

30 proteases.

For example, in Fig. 3, the amino acid sequence of subtilisin from *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Bacillus licheniformis* (*carlsbergensis*) and *Bacillus lentus* are aligned to provide the maximum amount of homology between amino acid sequences. A comparison of these sequences shows that there are a

-39-

number of conserved residues contained in each sequence. These conserved residues (as between BPN' and *B. lentus*) are identified in Fig. 2.

These conserved residues, thus, may be used to define the corresponding equivalent amino acid residues of *Bacillus amyloliquefaciens* subtilisin in other
 5 subtilisins such as subtilisin from *Bacillus lentus* (PCT Publication No. W089/06279 published July 13, 1989), the preferred protease precursor enzyme herein, or the subtilisin referred to as PB92 (EP 0 328 299), which is highly homologous to the preferred *Bacillus lentus* subtilisin. The amino acid sequences of certain of these subtilisins are aligned in Figs. 3A and 3B with the sequence of *Bacillus*
 10 *amyloliquefaciens* subtilisin to produce the maximum homology of conserved residues. As can be seen, there are a number of deletions in the sequence of *Bacillus lentus* as compared to *Bacillus amyloliquefaciens* subtilisin. Thus, for example, the equivalent amino acid for Val165 in *Bacillus amyloliquefaciens* subtilisin in the other subtilisins is isoleucine for *B. lentus* and *B. licheniformis*.

15 "Equivalent residues" may also be defined by determining homology at the level of tertiary structure for a precursor protease whose tertiary structure has been determined by x-ray crystallography. Equivalent residues are defined as those for which the atomic coordinates of two or more of the main chain atoms of a particular amino acid residue of the precursor protease and *Bacillus amyloliquefaciens*
 20 subtilisin (N on N, CA on CA, C on C and O on O) are within 0.13nm and preferably 0.1nm after alignment. Alignment is achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the protease in question to the *Bacillus amyloliquefaciens* subtilisin. The best model is the crystallographic model giving the lowest R factor for
 25 experimental diffraction data at the highest resolution available.

$$R\ factor = \frac{\sum_h |Fo(h)| - |Fc(h)|}{\sum_h |Fo(h)|}$$

Equivalent residues which are functionally analogous to a specific residue of *Bacillus amyloliquefaciens* subtilisin are defined as those amino acids of the precursor protease which may adopt a conformation such that they either alter,
 30 modify or contribute to protein structure, substrate binding or catalysis in a manner

74541-49

-40-

defined and attributed to a specific residue of the *Bacillus amyloliquefaciens* subtilisin. Further, they are those residues of the precursor protease (for which a tertiary structure has been obtained by x-ray crystallography) which occupy an analogous position to the extent that, although the main chain atoms of the given
5 residue may not satisfy the criteria of equivalence on the basis of occupying a homologous position, the atomic coordinates of at least two of the side chain atoms of the residue lie within 0.13nm of the corresponding side chain atoms of *Bacillus amyloliquefaciens* subtilisin. The coordinates of the three dimensional structure of *Bacillus amyloliquefaciens* subtilisin are set forth in EPO Publication No. 0 251 446
10 (equivalent to US Patent 5,182,204)
and can be used as outlined above to determine equivalent residues on the level of tertiary structure.

Some of the residues identified for substitution are conserved residues whereas others are not. In the case of residues which are not conserved, the
15 substitution of one or more amino acids is limited to substitutions which produce a variant which has an amino acid sequence that does not correspond to one found in nature. In the case of conserved residues, such substitutions should not result in a naturally-occurring sequence. The protease variants of the present invention include the mature forms of protease variants, as well as the pro- and prepro-forms of such
20 protease variants. The prepro-forms are the preferred construction since this facilitates the expression, secretion and maturation of the protease variants.

"Prosequence" refers to a sequence of amino acids bound to the N-terminal portion of the mature form of a protease which when removed results in the appearance of the "mature" form of the protease. Many proteolytic enzymes are
25 found in nature as translational proenzyme products and, in the absence of post-translational processing, are expressed in this fashion. A preferred prosequence for producing protease variants is the putative prosequence of *Bacillus amyloliquefaciens* subtilisin, although other protease prosequences may be used.

A "signal sequence" or "presequence" refers to any sequence of amino acids
30 bound to the N-terminal portion of a protease or to the N-terminal portion of a proprotease which may participate in the secretion of the mature or pro forms of the protease. This definition of signal sequence is a functional one, meant to include all those amino acid sequences encoded by the N-terminal portion of the protease gene which participate in the effectuation of the secretion of protease under native

74541-49

-41-

conditions. The present invention utilizes such sequences to effect the secretion of the protease variants as defined herein. One possible signal sequence comprises the first seven amino acid residues of the signal sequence from *Bacillus subtilis* subtilisin fused to the remainder of the signal sequence of the subtilisin from *Bacillus*
5 *lentus* (ATCC 21536).

A "prepro" form of a protease variant consists of the mature form of the protease having a prosequence operably linked to the amino terminus of the protease and a "pre" or "signal" sequence operably linked to the amino terminus of the prosequence.

10 "Expression vector" refers to a DNA construct containing a DNA sequence which is operably linked to a suitable control sequence capable of effecting the expression of said DNA in a suitable host. Such control sequences include a promoter to effect transcription, an optional operator sequence to control such transcription, a sequence encoding suitable mRNA ribosome binding sites and
15 sequences which control termination of transcription and translation. The vector may be a plasmid, a phage particle, or simply a potential genomic insert. Once transformed into a suitable host, the vector may replicate and function independently of the host genome, or may, in some instances, integrate into the genome itself. In the present specification, "plasmid" and "vector" are sometimes used
20 interchangeably as the plasmid is the most commonly used form of vector at present. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which are, or become, known in the art.

The "host cells" used in the present invention generally are procaryotic or eucaryotic hosts which preferably have been manipulated by the methods disclosed
25 in US Patent RE 34,606 to render them incapable of secreting enzymatically active endoprotease. A preferred host cell for expressing protease is the *Bacillus* strain BG2036 which is deficient in enzymatically active neutral protease and alkaline protease (subtilisin). The construction of strain BG2036 is described in detail in US Patent 5,264,366. Other host cells for expressing protease include *Bacillus subtilis*
30 I168 (also described in US Patent RE 34,606 and US Patent 5,264,366) as well as any suitable

Bacillus strain such as *B. licheniformis*, *B. lentus*, etc.

Host cells are transformed or transfected with vectors constructed using recombinant DNA techniques. Such transformed host cells are capable of either

-42-

replicating vectors encoding the protease variants or expressing the desired protease variant. In the case of vectors which encode the pre- or prepro-form of the protease variant, such variants, when expressed, are typically secreted from the host cell into the host cell medium.

5 "Operably linked, " when describing the relationship between two DNA regions, simply means that they are functionally related to each other. For example, a presequence is operably linked to a peptide if it functions as a signal sequence, participating in the secretion of the mature form of the protein most probably involving cleavage of the signal sequence. A promoter is operably linked to a coding
10 sequence if it controls the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to permit translation.

The genes encoding the naturally-occurring precursor protease may be obtained in accord with the general methods known to those skilled in the art. The methods generally comprise synthesizing labeled probes having putative sequences
15 encoding regions of the protease of interest, preparing genomic libraries from organisms expressing the protease, and screening the libraries for the gene of interest by hybridization to the probes. Positively hybridizing clones are then mapped and sequenced.

The cloned protease is then used to transform a host cell in order to express
20 the protease. The protease gene is then ligated into a high copy number plasmid. This plasmid replicates in hosts in the sense that it contains the well-known elements necessary for plasmid replication: a promoter operably linked to the gene in question (which may be supplied as the gene's own homologous promoter if it is recognized, i.e., transcribed, by the host), a transcription termination and
25 polyadenylation region (necessary for stability of the mRNA transcribed by the host from the protease gene in certain eucaryotic host cells) which is exogenous or is supplied by the endogenous terminator region of the protease gene and, desirably, a selection gene such as an antibiotic resistance gene that enables continuous cultural maintenance of plasmid-infected host cells by growth in antibiotic-containing media.
30 High copy number plasmids also contain an origin of replication for the host, thereby enabling large numbers of plasmids to be generated in the cytoplasm without chromosomal limitations. However, it is within the scope herein to integrate multiple copies of the protease gene into host genome. This is facilitated by procaryotic and

74541-49

-43-

eucaryotic organisms which are particularly susceptible to homologous recombination.

The gene can be a natural *B. lentus* gene. Alternatively, a synthetic gene encoding a naturally-occurring or mutant precursor protease may be produced. In such an approach, the DNA and/or amino acid sequence of the precursor protease is determined. Multiple, overlapping synthetic single-stranded DNA fragments are thereafter synthesized, which upon hybridization and ligation produce a synthetic DNA encoding the precursor protease. An example of synthetic gene construction is set forth in Example 3 of US Patent 5,204,015.

Once the naturally-occurring or synthetic precursor protease gene has been cloned, a number of modifications are undertaken to enhance the use of the gene beyond synthesis of the naturally-occurring precursor protease. Such modifications include the production of recombinant proteases as disclosed in US Patent RE 34,606 and EPO Publication No. 0 251 446 and the production of protease variants described herein.

The following cassette mutagenesis method may be used to facilitate the construction of the protease variants of the present invention, although other methods may be used. First, the naturally-occurring gene encoding the protease is obtained and sequenced in whole or in part. Then the sequence is scanned for a point at which it is desired to make a mutation (deletion, insertion or substitution) of one or more amino acids in the encoded enzyme. The sequences flanking this point are evaluated for the presence of restriction sites for replacing a short segment of the gene with an oligonucleotide pool which when expressed will encode various mutants. Such restriction sites are preferably unique sites within the protease gene so as to facilitate the replacement of the gene segment. However, any convenient restriction site which is not overly redundant in the protease gene may be used, provided the gene fragments generated by restriction digestion can be reassembled in proper sequence. If restriction sites are not present at locations within a convenient distance from the selected point (from 10 to 15 nucleotides), such sites are generated by substituting nucleotides in the gene in such a fashion that neither the reading frame nor the amino acids encoded are changed in the final construction. Mutation of the gene in order to change its sequence to conform to the desired sequence is accomplished by M13 primer extension in accord with generally known

-44-

methods. The task of locating suitable flanking regions and evaluating the needed changes to arrive at two convenient restriction site sequences is made routine by the redundancy of the genetic code, a restriction enzyme map of the gene and the large number of different restriction enzymes. Note that if a convenient flanking restriction site is available, the above method need be used only in connection with the flanking region which does not contain a site.

Once the naturally-occurring DNA or synthetic DNA is cloned, the restriction sites flanking the positions to be mutated are digested with the cognate restriction enzymes and a plurality of end termini-complementary oligonucleotide cassettes are ligated into the gene. The mutagenesis is simplified by this method because all of the oligonucleotides can be synthesized so as to have the same restriction sites, and no synthetic linkers are necessary to create the restriction sites.

As used herein, proteolytic activity is defined as the rate of hydrolysis of peptide bonds per milligram of active enzyme. Many well known procedures exist for measuring proteolytic activity (K. M. Kalisz, "Microbial Proteinases," Advances in Biochemical Engineering/Biotechnology, A. Fiechter ed., 1988). In addition to or as an alternative to modified proteolytic activity, the variant enzymes of the present invention may have other modified properties such as K_m , k_{cat} , k_{cat}/K_m ratio and/or modified substrate specificity and/or modified pH activity profile. These enzymes can be tailored for the particular substrate which is anticipated to be present, for example, in the preparation of peptides or for hydrolytic processes such as laundry uses.

In one aspect of the invention, the objective is to secure a variant protease having altered, preferably improved wash performance as compared to a precursor protease in at least one detergent formulation and or under at least one set of wash conditions.

There is a variety of wash conditions including varying detergent formulations, wash water volume, wash water temperature and length of wash time that a protease variant might be exposed to. For example, detergent formulations used in different areas have different concentrations of their relevant components present in the wash water. For example, a European detergent typically has about 4500-5000 ppm of detergent components in the wash water while a Japanese detergent typically has approximately 667 ppm of detergent components in the wash

-45-

water. In North America, particularly the United States, a detergent typically has about 975 ppm of detergent components present in the wash water.

A low detergent concentration system includes detergents where less than about 800 ppm of detergent components are present in the wash water. Japanese
5 detergents are typically considered low detergent concentration system as they have approximately 667 ppm of detergent components present in the wash water.

A medium detergent concentration includes detergents where between about 800 ppm and about 2000ppm of detergent components are present in the wash water. North American detergents are generally considered to be medium detergent
10 concentration systems as they have approximately 975 ppm of detergent components present in the wash water. Brazil typically has approximately 1500 ppm of detergent components present in the wash water.

A high detergent concentration system includes detergents where greater than about 2000 ppm of detergent components are present in the wash water.
15 European detergents are generally considered to be high detergent concentration systems as they have approximately 4500-5000 ppm of detergent components in the wash water.

Latin American detergents are generally high suds phosphate builder detergents and the range of detergents used in Latin America can fall in both the
20 medium and high detergent concentrations as they range from 1500 ppm to 6000 ppm of detergent components in the wash water. As mentioned above, Brazil typically has approximately 1500 ppm of detergent components present in the wash water. However, other high suds phosphate builder detergent geographies, not limited to other Latin American countries, may have high detergent concentration
25 systems up to about 6000 ppm of detergent components present in the wash water.

In light of the foregoing, it is evident that concentrations of detergent compositions in typical wash solutions throughout the world varies from less than about 800 ppm of detergent composition ("low detergent concentration geographies"), for example about 667 ppm in Japan, to between about 800 ppm to
30 about 2000 ppm ("medium detergent concentration geographies"), for example about 975 ppm in U.S. and about 1500 ppm in Brazil, to greater than about 2000 ppm ("high detergent concentration geographies"), for example about 4500 ppm to about 5000 ppm in Europe and about 6000 ppm in high suds phosphate builder geographies.

74541-49

-46-

The concentrations of the typical wash solutions are determined empirically. For example, in the U.S., a typical washing machine holds a volume of about 64.4 L of wash solution. Accordingly, in order to obtain a concentration of about 975 ppm of detergent within the wash solution about 62.79 g of detergent composition must be added to the 64.4 L of wash solution. This amount is the typical amount measured into the wash water by the consumer using the measuring cup provided with the detergent.

As a further example, different geographies use different wash temperatures. The temperature of the wash water in Japan is typically less than that used in Europe.

Accordingly one aspect of the present invention includes a protease variant that shows improved wash performance in at least one set of wash conditions.

In another aspect of the invention, it has been determined that substitution of an amino acid at one or more residue positions corresponding to residue positions selected from the group consisting of 62, 212, 230, 232, 252 and 257 of *Bacillus amyloliquefaciens* subtilisin are important in improving the wash performance of the enzyme.

These substitutions are preferably made in *Bacillus lentus* (recombinant or native-type) subtilisin, although the substitutions may be made in any *Bacillus* protease.

Based on the screening results obtained with the variant proteases, the noted mutations in *Bacillus amyloliquefaciens* subtilisin are important to the proteolytic activity, performance and/or stability of these enzymes and the cleaning or wash performance of such variant enzymes.

Many of the protease variants of the invention are useful in formulating various detergent compositions or personal care formulations such as shampoos or lotions. A number of known compounds are suitable surfactants useful in compositions comprising the protease mutants of the invention. These include nonionic, anionic, cationic, or zwitterionic detergents, as disclosed in US 4,404,128 to Barry J. Anderson and US 4,261,868 to Jiri Flora, et al. A suitable detergent formulation is that described in Example 7 of US Patent 5,204,015,

The art is familiar with the different formulations which can be used as cleaning compositions. In addition to typical cleaning compositions, it is readily understood that the protease variants of the present invention may be

-47-

used for any purpose that native or wild-type proteases are used. Thus, these variants can be used, for example, in bar or liquid soap applications, dishcare formulations, contact lens cleaning solutions or products, peptide hydrolysis, waste treatment, textile applications, as fusion-cleavage enzymes in protein production, etc. The variants of the present invention may comprise enhanced performance in a detergent composition (as compared to the precursor). As used herein, enhanced performance in a detergent is defined as increasing cleaning of certain enzyme sensitive stains such as grass or blood, as determined by usual evaluation after a standard wash cycle.

Proteases of the invention can be formulated into known powdered and liquid detergents having pH between 6.5 and 12.0 at levels of about 0.01 to about 5% (preferably 0.1% to 0.5%) by weight. These detergent cleaning compositions can also include other enzymes such as known proteases, amylases, cellulases, lipases or endoglycosidases, as well as builders and stabilizers.

The addition of proteases of the invention to conventional cleaning compositions does not create any special use limitation. In other words, any temperature and pH suitable for the detergent is also suitable for the present compositions as long as the pH is within the above range, and the temperature is below the described protease's denaturing temperature. In addition, proteases of the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and stabilizers.

The present invention also relates to cleaning compositions containing the protease variants of the invention. The cleaning compositions may additionally contain additives which are commonly used in cleaning compositions. These can be selected from, but not limited to, bleaches, surfactants, builders, enzymes and bleach catalysts. It would be readily apparent to one of ordinary skill in the art what additives are suitable for inclusion into the compositions. The list provided herein is by no means exhaustive and should be only taken as examples of suitable additives. It will also be readily apparent to one of ordinary skill in the art to only use those additives which are compatible with the enzymes and other components in the composition, for example, surfactant.

When present, the amount of additive present in the cleaning composition is from about 0.01% to about 99.9%, preferably about 1% to about 95%, more preferably about 1% to about 80%.

74541-49

-48-

The variant proteases of the present invention can be included in animal feed such as part of animal feed additives as described in, for example, US 5,612,055; US 5,314,692; and US 5,147,642.

One aspect of the invention is a composition for the treatment of a textile that includes variant proteases of the present invention. The composition can be used to treat for example silk or wool as described in publications such as RD 216,034; EP 134,267; US 4,533,359; and EP 344,259.

The following is presented by way of example and is not to be construed as a limitation to the scope of the claims.

10

Example 1

A large number of protease variants were produced and purified using methods well known in the art. All mutations were made in *Bacillus lentus* GG36 subtilisin. The variants are shown in Table 4.

-
-
-

Table 4

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Q12R	N76D	S103A	I104T	S130T	A215V	M222S	Q245R						
Q12R	N76D	S103A	I104T	S130T	M222S	V227A	Q245R	L262S					
Q12R	N76D	S103A	I104T	S130T	A215T	M222S	Q245R						
Q12R	N76D	S103A	I104T	S130T	M222S	Q245R	N261D						
N76D	S103A	I104T	S130T	M222S	Q245R								
Q12R	N76D	S103A	I104T	S130T	N218D	M222S	Q245R	L262S	N269D				
Q12R	S57P	N76D	S103A	I104T	S130T	M222S	Q245R	K251Q					
Q12R	N76D	S103A	I104T	S130T	R170S	N185D	M222S	N243D	Q245R				
Q12R	N76D	S103A	I104T	S130T	M222S	Q245R	V268A						
Q12R	N76D	S103A	I104T	S130T	M222S	P210S	Q245R						
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V						
V68A	S103A	V104I	N116D	G159D	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D						
R10C	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	V203E	A232V	Q236H	Q245R						
V68A	S103A	V104I	G159D	A232V	Q236H	K237E	Q245R						
V68A	N76D	I79N	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	N183D	A232V	Q236H	Q245R						

V68A	S103A	V104I	G159D	A174V	Q206L	A232V	Q236H	Q245R				
V68A	S103A	V104I	G159D	S188C	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	A230T	A232V	Q236H	Q245R					
V68A	A98T	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	A215T	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248S					
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	N76D	S103A	V104I	G159D	P210R	A232V	Q236H	Q245R				
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V				
N76D	S103A	V104I	A232V	Q236H	Q245R	L257V						
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V	R275H				
N76D	S103A	V104I	L257V	R275H								
V68A	S103A	V104I	G159D	T224A	A232V	Q236H	Q245R	L257V				
N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V					
V68A	N76D	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R				
V68A	N76D	S103A	V104I	G159D	G211R	A232V	Q236H	Q245R				
V68A	N76D	S103A	V104I	G159D	G211V	A232V	Q236H	Q245R				
Q12R	V68A	N76D	S103A	V104I	G159D	Y214L	A232V	Q236H	Q245R			

V68A	N76D	S103A	V104I	G159D	A215R	A232V	Q236H	Q245R					
Q12R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R					
G20R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	S259G				
V68A	S87R	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	T260V				
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N261G					
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N261W					
N76D	S103A	V104I	A232V	Q236H	S242P	Q245R							
V68A	N76D	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R					
Q12R	A48V	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R				
N76D	S103A	V104I	A232V	Q236H	Q245R								
N76D	S103A	V104I	G159D	Y192F	A232V	Q236H	Q245R						
N76D	S103A	V104I	V147I	G159D	A232V	Q236H	Q245R	N248S	K251R				
Q12R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	A272S				
V68A	N76D	S103A	V104I	G159D	N183K	Q206L	A232V	Q236H	Q245R				
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	S256R					
V68A	N76D	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R					
K27R	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R					
V68A	N76D	S103A	V104I	N116T	G159D	R170S	N185S	A232V	Q236H	Q245R			

G61E	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
N43D	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S212P	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	S99N	G159D	N184D	A232V	Q236H	Q245R	N248D	N252K		
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	N248D	N252K			
G20R	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	Y209F	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261D			
V68A	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	P210R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	P210T	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	P210S	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	N185D	P210L	A232V	Q236H	Q245R	N248D	N252K		
V68A	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S212A	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			

V68A	S103A	V104I	G159D	S212E	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	T213E	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	T213S	A232V	Q236H	Q245R	N248D	N252K				
V68A	A103V	V104I	G159D	T213E	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	T213G	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A215V	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A215R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S216T	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S216V	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	S216C	A232V	Q236H	Q245R	N248D	N252K			
G20A	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	N173D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	K251V	N252K			
V68A	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252F				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252L				
P55S	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252F			

V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	T255V			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	S256N			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	S256E			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	S256R			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	T260R			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	L257R			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	G258D			
I8V	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N269D		
V68A	S103A	V104I	N116S	G159D	A232V	Q236H	Q245R	N248D	N252K	T260E		
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261D			
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	A232S	Q236H	Q245R	N248D	N252K					
V68A	S103A	V104I	G159D	A232V	Q236R	Q245R	N248D	N252K				
N18S	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	S103A	V104I	G159D	A232V	Q236H	Q245V	N248D	N252K				
V68A	N76D	S101T	S103A	V104I	G159D	T213R	N218S	A232V	Q236H	Q245R	T260A	

V68A	S103A	V104I	G159D	A228V	A232V	Q236H	Q245R	N248D	N252K				
T33S	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
V68A	N76D	E89D	S103A	V104I	G159D	P210L	T213R	A232V	Q236H	Q245R	T260A		
G61E	V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S103A	V104I	G159D	V205I	P210I	A232V	Q236H	Q245R						
G61E	V68A	S103A	V104I	S130A	G159D	A232V	Q236H	Q245R	N248D	N252K			
G61E	V68A	S103A	V104I	A133S	Q137R	G159D	A232V	Q236H	Q245R	N248D	N252K		
G61E	S103A	V104I	A133V	G159D	A232V	Q236H	Q245R	N248D	N252K				
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248G	N252K					
V68A	S103A	V104I	G159D	N218S	A232V	Q236H	Q245R	N248D	N252K				
G61E	V68A	S103A	V104I	G159D	S160V	A232V	Q236H	Q245R	N248D	N252K			
S3L	G61E	V68A	N76D	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K			
G61E	V68A	S103A	V104I	G159D	S167F	A232V	Q236H	Q245R	N248D	N252K			
G97E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
A98D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
S99E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
S101E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					

G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	S106E	G159D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	Q109E	G159D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R					
S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	N248D	N252K					
N62D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	N184D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	S166D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	L217E	A232V	Q236H	Q245R	N248D	N252K					
G20R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K			
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				
S103A	V104I	G159D	Q206R	L217E	A232V	Q236H	Q245R	N248D	N252K				
N62D	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R	N248D	N252K				
S103A	V104I	S130G	G159D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K					
K27N	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
T38G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					
T38A	N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A				

V68A	N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A	E271G		
V68A	N76D	S103A	V104I	G159D	Y209W	T213R	A232V	Q236H	Q245R	T260A		
V68A	N76D	S103A	V104I	G159D	P210I	T213R	A232V	Q236H	Q245R	T260A		
V68A	N76D	S103A	V104I	G159D	V205I	T213R	A232V	Q236H	Q245R	T260A		
V68A	N76D	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	T260A			
V68A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A				
N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A				
V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	A230V	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	L126F	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	V205I	A232V	Q236H	Q245R					
V68A	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R					
S103A	V104I	G159D	A230V	Q236H	Q245R							
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	T260A					
S103A	V104I	G159D	A232V	Q236H	Q245R							
V68A	S103A	V104I	G159D	A174V	A232V	Q236H	Q245R	L257V				
V68A	S103A	V104I	G159D	A194S	A232V	Q236H	Q245R	L257V				

V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	L257V				
S103A	V104I	G159D	A232V	Q236H	Q245R	L257V						
V68A	N76D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A	N261W		
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V	N261W				
S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	T260A					
S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	N248D	N252K				
S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	L257V					
V68A	N76D	S103A	V104I	G159D	P210L	T213R	A232V	Q236H	Q245R	T260A		
Q12R	S103A	V104I	G159D	Y209W	T213R	A232V	Q236H	Q245R	T260A			
S103A	V104I	Y209W	A232V	Q236H	Q245R	L257V						
S103A	V104I	G159D	V205I	P210I	T213R	A232V	Q236H	Q245R	T260A			
S103A	V104I	G159D	V205I	Y209W	A232V	Q236H	Q245R	T260A				
V68A	S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R			
S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R	L257V			
S103A	V104I	G159D	V205I	Y209W	A232V	Q236H	Q245R	L257V				
V68A	S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R	T260A		
S103A	V104I	G159D	V205I	Y209W	P210I	A232V	Q236H	Q245R				
S103A	V104I	G159D	Y209W	P210I	A232V	Q236H	Q245R					

S103A	V104I	G159D	V205I	P210I	A232V	Q236H	Q245R						
V68A	S103A	V104I	S128L	G159D	A232V	Q236H	Q245R						
A48V	S103A	V104I	G159D	A230V	Q236H	Q245R							
A48V	V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R					
A48V	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				
A48V	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V	N261W				
G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K				
Q12R	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			
S101G	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			
G102A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				
S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	N184S	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	N184G	A232V	Q236H	Q245R	N248D	N252K					
S103A	V104I	G159D	A232V	Q236H	V244T	Q245R	N248D	N252K					
S103A	V104I	G159D	A232V	Q236H	V244A	Q245R	N248D	N252K					
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K	S256R			
Q12R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K			

S101G	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	Q206E	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	T213Q	A232V	Q236H	Q245R	N248D	N252K			
A98L	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K		
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	N248D	N252K			
N62D	S103A	V104I	Q109R	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
N62D	S103A	V104I	G159D	S212G	T213R	A232V	Q236H	Q245R	N248D	N252K		
N62D	S101G	S103A	V104I	G159D	S212G	T213R	A232V	Q236H	Q245R	N248D	N252K	
S103A	V104I	G159D	A232V	Q245R	N248D	N252K						
S103A	V104I	G159D	A230V	Q245R								
N62D	S103A	V104I	S130G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	S130G	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	S128G	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	S128L	G159D	A232V	Q236H	Q245R	N248D	N252K			
N62D	S101G	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
N62D	S103A	V104I	S128G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		

N62D	S103A	V104I	S128L	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	T260A			
S101G	S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K			
A98V	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S99G	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	V205I	A232V	Q236H	Q245R	N248D	N252K			
S101G	S103A	V104I	G159D	A230V	Q236H	Q245R						
S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K			
N76D	S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K		
S101G	S103A	V104I	G159D	A230V	A232V	Q236H	Q245R	N248D	N252K			
N62D	S103A	V104I	G159D	N185D	Q206E	T213R	A232V	Q236H	Q245R	N248D	N252K	E271Q

Example 2

A large number of the protease variants produced in Example 1 were tested for performance in two types of detergent and wash conditions using a microswatch
5 assay described in "An improved method of assaying for a preferred enzyme and/or preferred detergent composition", U.S. Serial No. 60/068,796.

Table 5 lists the variant proteases assayed and the results of testing in two different detergents. For column A, the detergent was 0.67 g/l filtered Ariel Ultra (Procter & Gamble, Cincinnati, OH, USA), in a solution containing 3 grains per gallon
10 mixed $\text{Ca}^{2+}/\text{Mg}^{2+}$ hardness, and 0.3 ppm enzyme was used in each well at 20°C. For column B, the detergent was 3.38 g/l filtered Ariel Futur (Procter & Gamble, Cincinnati, OH, USA), in a solution containing 15 grains per gallon mixed $\text{Ca}^{2+}/\text{Mg}^{2+}$ hardness, and 0.3 ppm enzyme was used in each well at 40°C.

Table 5

														A	B
N76D	S103A	V104I												1	1
S103A	V104I	A228T												0.56	1.11
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K							1.41	1.85
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K							2.77	1.20
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R								2.26	1.67
V68A	S103A	V104I	N140D	G159D	A232V	Q236H	Q245R	N252K						2.96	1.42
N43S	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K						1.91	1.80
N43K	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R							2.05	1.78
N43D	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252K						2.00	1.34
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V							2.38	1.67
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D							2.83	0.53
V68A	S103A	V104I	G159D	A232V	Q236H	K237E	Q245R							2.87	0.20
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N252S							2.56	1.41
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V	R275H						3.97	0.47
V68A	S103A	V104I	G159D	T224A	A232V	Q236H	Q245R	L257V						3.35	1.28
G61E	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					3.77	0.09

[illegible]

[illegible]

[illegible]

[illegible]

V68A	N76D	S103A	V104I	G159D	Q236H	Q245R						3.00	0.61
V68A	N76D	S103A	V104I	G159D	L217I	Q236H	E271V					2.71	0.12
H17Q	V68A	N76D	S103A	V104I								2.46	0.38
V68A	N76D	S103A	V104I									2.46	0.61
V68A	N76D	S103A	V104I	G159D	Q236R							3.31	0.11
V68A	L75R	N76D	S103A	V104I	G159D	Q236H						3.06	0.14
V68A	N76D	S103A	V104I	A114V	V121I	G159D	Q236H	Q245R				3.11	0.40
Q12R	V68A	N76D	S103A	V104I	G159D	Q236H						3.12	0.34
V68A	N76D	S103A	V104I	G159D	Y209S	Q236H	T253K					3.18	0.03
V68A	N76D	S103A	V104I	N117K	G159D	N184S	Q236H					2.78	0.06
V68A	N76D	S103A	V104I	Q236H								2.49	0.57
V68A	N76D	S103A	V104I	G159D	Q236H	Q245L						3.37	0.03
V68A	N76D	S103A	V104I	N123S	G159D	Q236H	H249Y					3.11	0.03
V68A	N76D	S103A	V104I	G159D	Q236H	H249Q						3.15	0.04
V68A	N76D	S103A	V104I	G159D	Q236H	Q245R	N261D					3.31	0.03
V68A	N76D	S103A	V104I	S141N	G159D	Q236H	Q245R	T255S				3.26	0.62
V68A	N76D	S103A	V104I	G159D	Q236H	Q245R	R247H					2.78	0.03
V68A	N76D	S103A	V104I	G159D	A174V	N204D	Q236H	Q245R				3.28	0.02

V68A	N76D	S103A	V104I	G159D	N204D	Q236H	Q245R				3.34	0.02
V68A	N76D	S103A	V104I	A133V	G159D	N218D	Q245R				3.28	0.03
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R				2.91	0.58
V68A	N76D	S103A	V104I	G159D	A194I	V203A	Q245R				2.86	0.13
V68A	N76D	S103A	V104I	G159D	T213R	A232V	Q245R	T260A			1.30	1.73
T22K	V68A	N76D	S103A	V104I							1.83	1.13
V68A	N76D	S103A	V104I	G159D	P210R	A232V	Q245R				1.28	1.54
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V			3.72	0.8
N76D	S103A	V104I	A232V	Q236H	Q245R	L257V					0.6	1.5
N76D	S103A	V104I	L257V	R275H							1.91	0.15
N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	L257V				1.92	1.09
V68A	N76D	S103A	V104I	G159D	Y209W	A232V	Q245R				3.57	0.99
V68A	N76D	S103A	V104I	G159D	G211R	A232V	Q245R				1.74	1.76
V68A	N76D	S103A	V104I	G159D	G211V	A232V	Q245R				3.15	1.06
Q12R	V68A	N76D	S103A	V104I	G159D	Y214L	Q236H	Q245R	Q245R		2.33	1.92
V68A	N76D	S103A	V104I	G159D	A215R	A232V	Q245R				1.67	1.45
Q12R	V68A	N76D	S103A	V104I	G159D	A232V	Q245R				2.16	1.72
G20R	V68A	N76D	S103A	V104I	G159D	A232V	Q245R	S259G			2.77	1.59

[illegible]

Q12R	N76D	S103A	I104T	S130T	M222S	Q245R	V268A				0.77	1.60
Q12R	N76D	S103A	I104T	S130T	M222S	P210S	Q245R				0.73	1.66
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R				2.09	0.86

Example 3

Table 6 lists the variant proteases assayed from Example 1 and the results of testing in four different detergents. The same performance tests as in Example 2 were done on the noted variant proteases with the following detergents. For column A, the detergent was 0.67 g/l filtered Ariel Ultra (Procter & Gamble, Cincinnati, OH, USA), in a solution containing 3 grains per gallon mixed $\text{Ca}^{2+}/\text{Mg}^{2+}$ hardness, and 0.3 ppm enzyme was used in each well at 20°C. For column B, the detergent was 3.38 g/l filtered Ariel Futur (Procter & Gamble, Cincinnati, OH, USA), in a solution containing 15 grains per gallon mixed $\text{Ca}^{2+}/\text{Mg}^{2+}$ hardness, and 0.3 ppm enzyme was used in each well at 40°C. For column C, 3.5g/l HSP1 detergent (Procter & Gamble, Cincinnati, OH, USA), in a solution containing 8 grains per gallon mixed $\text{Ca}^{2+}/\text{Mg}^{2+}$ hardness, and 0.3 ppm enzyme was used in each well at 20°C. For column D, 1.5 ml/l Tide KT detergent (Procter & Gamble, Cincinnati, OH, USA), in a solution containing 3 grains per gallon mixed $\text{Ca}^{2+}/\text{Mg}^{2+}$ hardness, and 0.3 ppm enzyme was used in each well at 20°C.

Table 6

																	A	B	C	D
N76D	S103A	V104I															1	1	1	1
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K										1.44	1.41	1.39	1.26
V68A	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K								2.34	1.49	1.65	2.35
V68A	S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	N248D	N252K								1.05	1.41	1.20	1.19
G20R	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K								1.81	1.72	1.66	1.31
V68A	S103A	V104I	G159D	Y209F	A232V	Q236H	Q245R	N248D	N252K								2.19	1.38	1.60	2.02
V68A	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K								2.91	0.91	1.48	2.70
V68A	S103A	V104I	G159D	P210R	A232V	Q236H	Q245R	N248D	N252K								0.93	1.39	1.23	0.80
V68A	S103A	V104I	G159D	N185D	P210L	A232V	Q236H	Q245R	N248D	N252K	N252K						2.67	0.86	1.41	2.88
V68A	S103A	V104I	G159D	P210L	A232V	Q236H	Q245R	N248D	N252K								2.22	1.43	1.55	1.78
V68A	S103A	V104I	G159D	S212C	A232V	Q236H	Q245R	N248D	N252K								2.30	1.43	1.63	2.07
V68A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K								2.31	1.47	1.62	2.01
V68A	S103A	V104I	G159D	S212E	A232V	Q236H	Q245R	N248D	N252K								2.63	0.56	1.36	2.66
V68A	S103A	V104I	G159D	T213E	A232V	Q236H	Q245R	N248D	N252K								2.75	0.50	1.27	2.78
V68A	S103A	V104I	T213S	A232V	Q236H	Q245R	N248D	N252K									1.11	1.38	1.31	0.75

[illegible]

V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	G258D				2.56	0.59	1.30	2.64
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R				1.02	1.47	1.37	0.84
V68A	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K						1.04	1.50	1.32	0.73
V68A	S103A	V104I	G159D	A232V	Q236H	Q245V	N248D	N252K					2.60	0.93	1.41	2.67
V68A	S103A	V104I	G159D	A228V	A232V	Q236H	Q245R	N248D	N252K				2.31	1.38	1.53	1.57
G61E	V68A	S103A	V104I	S130A	G159D	A232V	Q236H	Q245R	N248D	N252K			2.83	0.25	1.33	2.44
G61E	S103A	V104I	A133V	G159D	A232V	Q236H	Q245R	N248D	N252K				2.10	0.97	1.36	2.29
V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248G	N252K					1.37	1.54	0.89	1.27
V68A	S103A	V104I	G159D	N218S	A232V	Q236H	Q245R	N248D	N252K				2.30	1.50	1.62	1.56
G20R	V68A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				1.72	1.72	1.67	1.15
V68A	N76D	E89D	S103A	V104I	G159D	P210L	T213R	A232V	Q236H	Q245R	T260A		1.32	1.30	1.11	1.28
V68A	N76D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				2.50	0.83	1.43	2.25
G61E	V68A	S103A	V104I	G159D	S160V	A232V	Q236H	Q245R	N248D	N252K			4.20	0.07	ND	1.28
S3L	G61E	V68A	N76D	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K			3.47	0.60	ND	1.45
G61E	V68A	S103A	V104I	G159D	Y167F	A232V	Q236H	Q245R	N248D	N252K			4.32	0.79	ND	1.55
G97E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					3.14	0.41	ND	1.40
A98D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					2.71	0.68	ND	1.72
S99E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					2.97	0.68	ND	1.71

S101E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K						3.50	0.27	ND	1.90
S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K						2.24	1.80	ND	1.33
G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K						3.35	1.33	ND	1.69
S103A	V104I	S106E	G159D	A232V	Q236H	Q245R	N248D	N252K						4.88	0.55	ND	2.71
S103A	V104I	Q109E	G159D	A232V	Q236H	Q245R	N248D	N252K						4.22	1.05	ND	2.40
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R						5.45	2.19	ND	2.58
S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	N248D	N252K						3.76	2.16	ND	1.82
N62D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K						7.42	0.13	ND	2.46
S103A	V104I	G159D	N184D	A232V	Q236H	Q245R	N248D	N252K						5.43	1.36	ND	2.84
S103A	V104I	G159D	S166D	A232V	Q236H	Q245R	N248D	N252K						5.12	1.21	ND	3.97
S103A	V104I	G159D	L217E	A232V	Q236H	Q245R	N248D	N252K						6.38	0.95	ND	3.09
G20R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				3.17	2.83	ND	2.60
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K					4.38	1.92	ND	2.54
S103A	V104I	G159D	Q206R	L217E	A232V	Q236H	Q245R	N248D	N252K					3.05	2.61	ND	1.10
N62D	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R	N248D	N252K					4.09	2.46	ND	2.55
S103A	V104I	G159D	N184G	A232V	Q236H	Q245R	N248D	N252K						2.32	2.08	ND	2.40
S103A	V104I	G159D	A232V	Q236H	V244T	Q245R	N248D	N252K						2.34	2.04	ND	1.86
S103A	V104I	G159D	A232V	Q236H	V244A	Q245R	N248D	N252K						2.24	2.11	ND	1.95

K27N	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K							2.81	1.56	ND	2.47
T38G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K							2.30	2.09	ND	1.82
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K	S256R					2.63	2.66	ND	1.44
Q12R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K					2.01	2.78	ND	1.99
N62D	S103A	V104I	G159D	N185D	Q206E	T213R	A232V	Q236H	Q245R	N248D	N252K	E271Q			7.74	0.94	ND	5.39
S101G	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K						5.14	1.41	ND	1.92
S101G	S103A	V104I	G159D	Q206E	A232V	Q236H	Q245R	N248D	N252K						4.97	0.57	ND	1.36
S101G	S103A	V104I	G159D	T213Q	A232V	Q236H	Q245R	N248D	N252K						2.41	1.86	ND	1.01
A98L	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K						4.42	0.50	ND	2.88
S101G	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K						5.86	1.20	ND	3.84
G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K						5.87	2.10	ND	3.19
Q12R	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K					2.98	2.67	ND	2.17
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K					4.02	0.41	ND	2.25
S101G	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K					6.63	2.07	ND	2.08
G102A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K						2.03	2.48	ND	2.25
N62D	S103A	V104I	Q109R	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K					2.96	2.76	ND	2.34
S103A	V104I	G159D	A232V	Q245R	N248D	N252K									2.74	2.10	ND	1.86
S103A	V104I	G159D	A230V	Q245R											2.11	2.35	ND	1.49

N62D	S103A	V104I	S130G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				3.42	0.71	ND	2.58
S101G	S103A	V104I	S130G	G159D	A232V	Q236H	Q245R	N248D	N252K					2.59	1.32	ND	1.61
S101G	S103A	V104I	S128G	G159D	A232V	Q236H	Q245R	N248D	N252K					1.30	1.23	ND	9.0
S101G	S103A	V104I	S128L	G159D	A232V	Q236H	Q245R	N248D	N252K					2.94	0.71	ND	1.08
N62D	S101G	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				3.17	0.83	ND	2.35
N62D	S103A	V104I	S128G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				2.15	1.38	ND	1.77
N62D	S103A	V104I	S128L	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				3.07	0.07	ND	1.45
S101G	S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K					2.26	1.16	ND	3.05
A98V	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					1.82	1.34	ND	1.08
S99G	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					2.16	1.47	ND	1.20
S101G	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K					1.79	1.38	ND	1.01
S101G	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K					1.15	1.18	ND	8.7
S101G	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	N248D	N252K					1.47	1.23	ND	1.03
S101G	S103A	V104I	G159D	V205I	A232V	Q236H	Q245R	N248D	N252K					1.90	1.38	ND	1.05
S101G	S103A	V104I	G159D	A230V	Q236H	Q245R								1.55	1.51	ND	1.23
S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K					1.96	1.30	ND	1.10
N76D	S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K				2.49	0.80	ND	1.25
G61E	V68A	S103A	V104I	G159D	S160V	A232V	Q236H	Q245R	N248D	N252K				420	7	128	ND

S3L	G61E	V68A	N76D	S103A	V104I	A232V	Q236H	Q245R	N248D	N252K			347	60	145	ND
G61E	V68A	S103A	V104I	G159D	Y167F	A232V	Q236H	Q245R	N248D	N252K			432	79	155	ND
G97E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					314	41	140	ND
A98D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					271	68	172	ND
S99E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					297	68	171	ND
S101E	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					350	27	190	ND
S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					224	180	133	ND
G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					335	133	169	ND
S103A	V104I	S106E	G159D	A232V	Q236H	Q245R	N248D	N252K					488	55	271	ND
S103A	V104I	Q109E	G159D	A232V	Q236H	Q245R	N248D	N252K					422	105	240	ND
S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K	N261R					545	219	258	ND
S103A	V104I	Q109R	G159D	A232V	Q236H	Q245R	N248D	N252K					376	216	182	ND
N62D	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					742	13	246	ND
S103A	V104I	G159D	N184D	A232V	Q236H	Q245R	N248D	N252K					543	136	284	ND
S103A	V104I	G159D	S166D	A232V	Q236H	Q245R	N248D	N252K					512	121	397	ND
S103A	V104I	G159D	L217E	A232V	Q236H	Q245R	N248D	N252K					638	95	309	ND
G20R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K			317	283	260	ND
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				438	192	254	ND

S103A	V104I	G159D	Q206R	L217E	A232V	Q236H	Q245R	N248D	N252K				305	261	110	ND
N62D	S103A	V104I	G159D	Q206R	A232V	Q236H	Q245R	N248D	N252K				409	246	255	ND
S103A	V104I	G159D	N184G	A232V	Q236H	Q245R	N248D	N252K					232	208	240	ND
S103A	V104I	G159D	A232V	Q236H	V244T	Q245R	N248D	N252K					234	204	186	ND
S103A	V104I	G159D	A232V	Q236H	V244A	Q245R	N248D	N252K					224	211	195	ND
K27N	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					281	156	247	ND
T38G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					230	209	182	ND
N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K	S256R			263	266	144	ND
Q12R	N62D	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K			201	278	199	
N62D	S103A	V104I	G159D	N185D	Q206E	T213R	A232V	Q236H	Q245R	N248D	N252K	E271Q	774	94	539	ND
S101G	S103A	V104I	G159D	N185D	A232V	Q236H	Q245R	N248D	N252K				514	141	192	ND
S101G	S103A	V104I	G159D	Q206E	A232V	Q236H	Q245R	N248D	N252K				497	57	136	ND
S101G	S103A	V104I	G159D	T213Q	A232V	Q236H	Q245R	N248D	N252K				241	186	101	ND
A98L	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				442	50	288	ND
S101G	G102A	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				586	120	384	ND
G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K				587	210	319	ND
Q12R	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K	N252K		298	267	217	ND
A98L	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K	N252K		402	41	225	ND

S101G	G102A	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K				663	207	208	ND
G102A	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K					203	248	225	ND
N62D	S103A	V104I	Q109R	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				296	276	234	ND
S103A	V104I	G159D	A232V	Q245R	N248D	N252K								274	210	186	ND
S103A	V104I	G159D	A230V	Q245R										211	235	149	ND
N62D	S103A	V104I	S130G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				342	71	258	ND
S101G	S103A	V104I	S130G	G159D	A232V	Q236H	Q245R	N248D	N252K					259	132	161	ND
S101G	S103A	V104I	S128G	G159D	A232V	Q236H	Q245R	N248D	N252K					130	123	90	ND
S101G	S103A	V104I	S128L	G159D	A232V	Q236H	Q245R	N248D	N252K					294	71	108	ND
N62D	S101G	S103A	V104I	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				317	83	235	ND
N62D	S103A	V104I	S128G	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				215	138	177	ND
N62D	S103A	V104I	S128L	G159D	T213R	A232V	Q236H	Q245R	N248D	N252K				307	7	145	ND
S101G	S103A	V104I	P131V	G159D	A232V	Q236H	Q245R	N248D	N252K					226	116	305	ND
A98V	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					182	134	108	ND
S99G	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K					216	147	120	ND
S101G	S103A	V104I	G159D	S212G	A232V	Q236H	Q245R	N248D	N252K					179	138	101	ND
S101G	S103A	V104I	G159D	Y209W	A232V	Q236H	Q245R	N248D	N252K					115	118	87	ND
S101G	S103A	V104I	G159D	P210I	A232V	Q236H	Q245R	N248D	N252K					147	123	103	ND

S101G	S103A	V104I	G159D	V205I	A232V	Q236H	Q245R	N248D	N252K				190	138	105	ND
S101G	S103A	V104I	G159D	A230V	Q236H	Q245R							155	151	123	ND
S101G	S103A	V104I	G159D	A194P	A232V	Q236H	Q245R	N248D	N252K				196	130	110	ND
N76D	S101G	S103A	V104I	G159D	A232V	Q236H	Q245R	N248D	N252K				249	80	125	ND

SEQUENCE LISTING

<110> Genencor International, Inc.

<120> Multiply-Substituted Protease Variants

<130> GC503-2-PCT

<140> PCT/US98/22500

<141> 1998-10-23

<160> 6

<170> FastSEQ for Windows Version 3.0

10 <210> 1

<211> 1497

<212> DNA

<213> B. amyloliquefaciens

<220>

<221> CDS

<222> (96)...(1245)

<400> 1

ggtctactaa aatattattc catactatac aattaataca cagaataatc tgtctattgg 60

20 ttattctgca aatgaaaaaa aggagaggat aaaga gtg aga ggc aaa aaa gta 113
 Val Arg Gly Lys Lys Val
 1 5

tgg atc agt ttg ctg ttt gct tta gcg tta atc ttt acg atg gcg ttc 161
 Trp Ile Ser Leu Leu Phe Ala Leu Ala Leu Ile Phe Thr Met Ala Phe
 10 15 20

ggc agc aca tcc tct gcc cag gcg gca ggg aaa tca aac ggg gaa aag 209
 Gly Ser Thr Ser Ser Ala Gln Ala Ala Gly Lys Ser Asn Gly Glu Lys
 25 30 35

30 aaa tat att gtc ggg ttt aaa cag aca atg agc acg atg agc gcc gct 257
 Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Thr Met Ser Ala Ala
 40 45 50

aag aag aaa gat gtc att tct gaa aaa ggc ggg aaa gtg caa aag caa 305
 Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly Lys Val Gln Lys Gln
 55 60 65 70

40 ttc aaa tat gta gac gca gct tca gtc aca tta aac gaa aaa gct gta 353
 Phe Lys Tyr Val Asp Ala Ala Ser Val Thr Leu Asn Glu Lys Ala Val
 75 80 85

	aaa gaa ttg aaa aaa gac ccg agc gtc gct tac gtt gaa gaa gat cac Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr Val Glu Glu Asp His 90 95 100	401
	gta gca cat gcg tac gcg cag tcc gtg cct tac ggc gta tca caa att Val Ala His Ala Tyr Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile 105 110 115	449
10	aaa gcc cct gct ctg cac tct caa ggc tac act gga tca aat gtt aaa Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys 120 125 130	497
	gta gcg gtt atc gac agc ggt atc gat tct tct cat cct gat tta aag Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys 135 140 145 150	545
20	gta gca agc gga gcc agc atg gtt cct tct gaa aca aat cct ttc caa Val Ala Ser Gly Ala Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln 155 160 165	593
	gac aac aac tct cac gga act cac gtt gcc ggc aca gtt gcg gct ctt Asp Asn Asn Ser His Gly Thr His Val Ala Gly Thr Val Ala Ala Leu 170 175 180	641
	aat aac tca atc ggt gta tta ggc gtt gcg cca agc gca tca ctt tac Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr 185 190 195	689
30	gct gta aaa gtt ctc ggt gct gac ggt tcc ggc caa tac agc tgg atc Ala Val Lys Val Leu Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile 200 205 210	737
	att aac gga atc gag tgg gcg atc gca aac aat atg gac gtt att aac Ile Asn Gly Ile Glu Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn 215 220 225 230	785
40	atg agc ctc ggc gga cct tct ggt tct gct gct tta aaa gcg gca gtt Met Ser Leu Gly Gly Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val 235 240 245	833
	gat aaa gcc gtt gca tcc ggc gtc gta gtc gtt gcg gca gcc ggt aac Asp Lys Ala Val Ala Ser Gly Val Val Val Val Ala Ala Ala Gly Asn 250 255 260	881
	gaa ggc act tcc ggc agc tca agc aca gtg ggc tac cct ggt aaa tac Glu Gly Thr Ser Gly Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr 265 270 275	929
50	cct tct gtc att gca gta ggc gct gtt gac agc agc aac caa aga gca Pro Ser Val Ile Ala Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala 280 285 290	977
	tct ttc tca agc gta gga cct gag ctt gat gtc atg gca cct ggc gta Ser Phe Ser Ser Val Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val 295 300 305 310	1025
60	tct atc caa agc acg ctt cct gga aac aaa tac ggg gcg tac aac ggt Ser Ile Gln Ser Thr Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly 315 320 325	1073

95

10 acg tca atg gca tct ccg cac gtt gcc gga gcg gct gct ttg att ctt 1121
 Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu
 330 335 340
 tct aag cac ccg aac tgg aca aac act caa gtc cgc agc agt tta gaa 1169
 Ser Lys His Pro Asn Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu
 345 350 355
 aac acc act aca aaa ctt ggt gat tct ttg tac tat gga aaa ggg ctg 1217
 Asn Thr Thr Thr Lys Leu Gly Asp Ser Leu Tyr Tyr Gly Lys Gly Leu
 360 365 370
 atc aac gta caa gcg gca gct cag taa a acataaaaaa ccggccttgg 1265
 Ile Asn Val Gln Ala Ala Ala Gln
 375 380
 ccccgccgggt tttttattat ttttcttcct ccgcatgttc aatccgctcc ataatcgacg 1325
 gatggctccc tctgaaaatt ttaacgagaa acggcggggtt gaccgggctc agtcccgtaa 1385
 20 cggccaactc ctgaaacgtc tcaatcgccg cttcccgggtt tccgggtcagc tcaatgccat 1445
 aacggtcggc ggcgttttcc tgataccggg agacggcatt cgtaatcgga tc 1497

<210> 2

<211> 1497

<212> PRT

<213> B. amyloliquefaciens

<400> 2

30 Gly Gly Thr Cys Thr Ala Cys Thr Ala Ala Ala Ala Thr Ala Thr Thr
 1 5 10 15
 Ala Thr Thr Cys Cys Ala Thr Ala Cys Thr Ala Thr Ala Cys Ala Ala
 20 25 30
 Thr Thr Ala Ala Thr Ala Cys Ala Cys Ala Gly Ala Ala Thr Ala Ala
 35 40 45
 Thr Cys Thr Gly Thr Cys Thr Ala Thr Thr Gly Gly Thr Thr Ala Thr
 50 55 60
 40 Thr Cys Thr Gly Cys Ala Ala Ala Thr Gly Ala Ala Ala Ala Ala Ala
 65 70 75 80
 Ala Gly Gly Ala Gly Ala Gly Gly Ala Thr Ala Ala Ala Gly Ala Gly
 85 90 95
 Thr Gly Ala Gly Ala Gly Gly Cys Ala Ala Ala Ala Ala Ala Gly Thr
 100 105 110
 50 Ala Thr Gly Gly Ala Thr Cys Ala Gly Thr Thr Thr Gly Cys Thr Gly
 115 120 125

96

Thr Thr Thr Gly Cys Thr Thr Thr Ala Gly Cys Gly Thr Thr Ala Ala
 130 135 140
 Thr Cys Thr Thr Thr Ala Cys Gly Ala Thr Gly Gly Cys Gly Thr Thr
 145 150 155 160
 Cys Gly Gly Cys Ala Gly Cys Ala Cys Ala Thr Cys Cys Thr Cys Thr
 165 170 175
 10 Gly Cys Cys Cys Ala Gly Gly Cys Gly Gly Cys Ala Gly Gly Gly Ala
 180 185 190
 Ala Ala Thr Cys Ala Ala Ala Cys Gly Gly Gly Gly Ala Ala Ala Ala
 195 200 205
 Gly Ala Ala Ala Thr Ala Thr Ala Thr Thr Gly Thr Cys Gly Gly Gly
 210 215 220
 20 Thr Thr Thr Ala Ala Ala Cys Ala Gly Ala Cys Ala Ala Thr Gly Ala
 225 230 235 240
 Gly Cys Ala Cys Gly Ala Thr Gly Ala Gly Cys Gly Cys Cys Gly Cys
 245 250 255
 Thr Ala Ala Gly Ala Ala Gly Ala Ala Ala Gly Ala Thr Gly Thr Cys
 260 265 270
 30 Ala Thr Thr Thr Cys Thr Gly Ala Ala Ala Ala Gly Gly Cys Gly
 275 280 285
 Gly Gly Ala Ala Ala Gly Thr Gly Cys Ala Ala Ala Gly Cys Ala
 290 295 300
 Ala Thr Thr Cys Ala Ala Ala Thr Ala Thr Gly Thr Ala Gly Ala Cys
 305 310 315 320
 Gly Cys Ala Gly Cys Thr Thr Cys Ala Gly Thr Cys Ala Cys Ala Thr
 325 330 335
 40 Thr Ala Ala Ala Cys Gly Ala Ala Ala Ala Gly Cys Thr Gly Thr
 340 345 350
 Ala Ala Ala Ala Gly Ala Ala Thr Thr Gly Ala Ala Ala Ala Ala
 355 360 365
 Gly Ala Cys Cys Cys Gly Ala Gly Cys Gly Thr Cys Gly Cys Thr Thr
 370 375 380
 50 Ala Cys Gly Thr Thr Gly Ala Ala Gly Ala Ala Gly Ala Thr Cys Ala
 385 390 395 400
 Cys Gly Thr Ala Gly Cys Ala Cys Ala Thr Gly Cys Gly Thr Ala Cys
 405 410 415
 Gly Cys Gly Cys Ala Gly Thr Cys Cys Gly Thr Gly Cys Cys Thr Thr
 420 425 430
 60 Ala Cys Gly Gly Cys Gly Thr Ala Thr Cys Ala Cys Ala Ala Ala Thr
 435 440 445

Thr Ala Ala Ala Gly Cys Cys Cys Cys Thr Gly Cys Thr Cys Thr Gly
 450 455 460
 Cys Ala Cys Thr Cys Thr Cys Ala Ala Gly Gly Cys Thr Ala Cys Ala
 465 470 475 480
 Cys Thr Gly Gly Ala Thr Cys Ala Ala Ala Thr Gly Thr Thr Ala Ala
 485 490 495
 10 Ala Gly Thr Ala Gly Cys Gly Gly Thr Thr Ala Thr Cys Gly Ala Cys
 500 505 510
 Ala Gly Cys Gly Gly Thr Ala Thr Cys Gly Ala Thr Thr Cys Thr Thr
 515 520 525
 Cys Thr Cys Ala Thr Cys Cys Thr Gly Ala Thr Thr Thr Ala Ala Ala
 530 535 540
 20 Gly Gly Thr Ala Gly Cys Ala Ala Gly Cys Gly Gly Ala Gly Cys Cys
 545 550 555 560
 Ala Gly Cys Ala Thr Gly Gly Thr Thr Cys Cys Thr Thr Cys Thr Gly
 565 570 575
 Ala Ala Ala Cys Ala Ala Ala Thr Cys Cys Thr Thr Thr Cys Cys Ala
 580 585 590
 30 Ala Gly Ala Cys Ala Ala Cys Ala Ala Cys Thr Cys Thr Cys Ala Cys
 595 600 605
 Gly Gly Ala Ala Cys Thr Cys Ala Cys Gly Thr Thr Gly Cys Cys Gly
 610 615 620
 Gly Cys Ala Cys Ala Gly Thr Thr Gly Cys Gly Gly Cys Thr Cys Thr
 625 630 635 640
 Thr Ala Ala Thr Ala Ala Cys Thr Cys Ala Ala Thr Cys Gly Gly Thr
 645 650 655
 40 Gly Thr Ala Thr Thr Ala Gly Gly Cys Gly Thr Thr Gly Cys Gly Cys
 660 665 670
 Cys Ala Ala Gly Cys Gly Cys Ala Thr Cys Ala Cys Thr Thr Thr Ala
 675 680 685
 Cys Gly Cys Thr Gly Thr Ala Ala Ala Ala Gly Thr Thr Cys Thr Cys
 690 695 700
 50 Gly Gly Thr Gly Cys Thr Gly Ala Cys Gly Gly Thr Thr Cys Cys Gly
 705 710 715 720
 Gly Cys Cys Ala Ala Thr Ala Cys Ala Gly Cys Thr Gly Gly Ala Thr
 725 730 735
 Cys Ala Thr Thr Ala Ala Cys Gly Gly Ala Ala Thr Cys Gly Ala Gly
 740 745 750
 60 Thr Gly Gly Gly Cys Gly Ala Thr Cys Gly Cys Ala Ala Ala Cys Ala
 755 760 765

Ala Thr Ala Thr Gly Gly Ala Cys Gly Thr Thr Ala Thr Thr Ala Ala
 770 775 780
 Cys Ala Thr Gly Ala Gly Cys Cys Thr Cys Gly Gly Cys Gly Gly Ala
 785 790 795 800
 10 Cys Cys Thr Thr Cys Thr Gly Gly Thr Thr Cys Thr Gly Cys Thr Gly
 805 810 815
 Cys Thr Thr Thr Ala Ala Ala Ala Gly Cys Gly Gly Cys Ala Gly Thr
 820 825 830
 Thr Gly Ala Thr Ala Ala Ala Gly Cys Cys Gly Thr Thr Gly Cys Ala
 835 840 845
 Thr Cys Cys Gly Gly Cys Gly Thr Cys Gly Thr Ala Gly Thr Cys Gly
 850 855 860
 20 Thr Thr Gly Cys Gly Gly Cys Ala Gly Cys Cys Gly Gly Thr Ala Ala
 865 870 875 880
 Cys Gly Ala Ala Gly Gly Cys Ala Cys Thr Thr Cys Cys Gly Gly Cys
 885 890 895
 Ala Gly Cys Thr Cys Ala Ala Gly Cys Ala Cys Ala Gly Thr Gly Gly
 900 905 910
 30 Gly Cys Thr Ala Cys Cys Cys Thr Gly Gly Thr Ala Ala Ala Thr Ala
 915 920 925
 Cys Cys Cys Thr Thr Cys Thr Gly Thr Cys Ala Thr Thr Gly Cys Ala
 930 935 940
 Gly Thr Ala Gly Gly Cys Gly Cys Thr Gly Thr Thr Gly Ala Cys Ala
 945 950 955 960
 40 Gly Cys Ala Gly Cys Ala Ala Cys Cys Ala Ala Ala Gly Ala Gly Cys
 965 970 975
 Ala Thr Cys Thr Thr Thr Cys Thr Cys Ala Ala Gly Cys Gly Thr Ala
 980 985 990
 Gly Gly Ala Cys Cys Thr Gly Ala Gly Cys Thr Thr Gly Ala Thr Gly
 995 1000 1005
 Thr Cys Ala Thr Gly Gly Cys Ala Cys Cys Thr Gly Gly Cys Gly Thr
 1010 1015 1020
 50 Ala Thr Cys Thr Ala Thr Cys Cys Ala Ala Ala Gly Cys Ala Cys Gly
 1025 1030 1035 104
 Cys Thr Thr Cys Cys Thr Gly Gly Ala Ala Ala Cys Ala Ala Thr
 1045 1050 1055
 Ala Cys Gly Gly Gly Gly Cys Gly Thr Ala Cys Ala Ala Cys Gly Gly
 1060 1065 1070
 60 Thr Ala Cys Gly Thr Cys Ala Ala Thr Gly Gly Cys Ala Thr Cys Thr
 1075 1080 1085

Cys Cys Gly Cys Ala Cys Gly Thr Thr Gly Cys Cys Gly Gly Ala Gly
 1090 1095 1100
 Cys Gly Gly Cys Thr Gly Cys Thr Thr Thr Gly Ala Thr Thr Cys Thr
 1105 1110 1115 112
 Thr Thr Cys Thr Ala Ala Gly Cys Ala Cys Cys Cys Gly Ala Ala Cys
 1125 1130 1135
 10 Thr Gly Gly Ala Cys Ala Ala Ala Cys Ala Cys Thr Cys Ala Ala Gly
 1140 1145 1150
 Thr Cys Cys Gly Cys Ala Gly Cys Ala Gly Thr Thr Thr Ala Gly Ala
 1155 1160 1165
 Ala Ala Ala Cys Ala Cys Cys Ala Cys Thr Ala Cys Ala Ala Ala Ala
 1170 1175 1180
 20 Cys Thr Thr Gly Gly Thr Gly Ala Thr Thr Cys Thr Thr Thr Gly Thr
 1185 1190 1195 120
 Ala Cys Thr Ala Thr Gly Gly Ala Ala Ala Ala Gly Gly Gly Cys Thr
 1205 1210 1215
 Gly Ala Thr Cys Ala Ala Cys Gly Thr Ala Cys Ala Ala Gly Cys Gly
 1220 1225 1230
 30 Gly Cys Ala Gly Cys Thr Cys Ala Gly Thr Ala Ala Ala Ala Cys Ala
 1235 1240 1245
 Thr Ala Ala Ala Ala Ala Ala Cys Cys Gly Gly Cys Cys Thr Thr Gly
 1250 1255 1260
 Gly Cys Cys Cys Cys Gly Cys Cys Gly Gly Thr Thr Thr Thr Thr Thr
 1265 1270 1275 128
 Ala Thr Thr Ala Thr Thr Thr Thr Thr Cys Thr Thr Cys Cys Thr Cys
 1285 1290 1295
 40 Cys Gly Cys Ala Thr Gly Thr Thr Cys Ala Ala Thr Cys Cys Gly Cys
 1300 1305 1310
 Thr Cys Cys Ala Thr Ala Ala Thr Cys Gly Ala Cys Gly Gly Ala Thr
 1315 1320 1325
 Gly Gly Cys Thr Cys Cys Cys Thr Cys Thr Gly Ala Ala Ala Ala Thr
 1330 1335 1340
 50 Thr Thr Thr Ala Ala Cys Gly Ala Gly Ala Ala Ala Cys Gly Gly Cys
 1345 1350 1355 136
 Gly Gly Gly Thr Thr Gly Ala Cys Cys Cys Gly Gly Cys Thr Cys Ala
 1365 1370 1375
 Gly Thr Cys Cys Cys Gly Thr Ala Ala Cys Gly Gly Cys Cys Ala Ala
 1380 1385 1390
 60 Cys Thr Cys Cys Thr Gly Ala Ala Ala Cys Gly Thr Cys Thr Cys Ala
 1395 1400 1405

100

Ala Thr Cys Gly Cys Cys Gly Cys Thr Thr Cys Cys Cys Gly Gly Thr
1410 1415 1420

Thr Thr Cys Cys Gly Gly Thr Cys Ala Gly Cys Thr Cys Ala Ala Thr
1425 1430 1435 144

10

Gly Cys Cys Ala Thr Ala Ala Cys Gly Gly Thr Cys Gly Gly Cys Gly
1445 1450 1455

Gly Cys Gly Thr Thr Thr Thr Cys Cys Thr Gly Ala Thr Ala Cys Cys
1460 1465 1470

Gly Gly Gly Ala Gly Ala Cys Gly Gly Cys Ala Thr Thr Cys Gly Thr
1475 1480 1485

Ala Ala Thr Cys Gly Gly Ala Thr Cys
1490 1495

20

<210> 3

<211> 275

<212> PRT

<213> B. amyloliquefaciens

<400> 3

Ala Gln Ser Val Pro Tyr Gly Val Ser Gln Ile Lys Ala Pro Ala Leu
1 5 10 15

30

His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
20 25 30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Lys Val Ala Gly Gly Ala
35 40 45

Ser Met Val Pro Ser Glu Thr Asn Pro Phe Gln Asp Asn Asn Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Val Ala Ala Leu Asn Asn Ser Ile Gly
65 70 75 80

40

Val Leu Gly Val Ala Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
85 90 95

Gly Ala Asp Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
100 105 110

Trp Ala Ile Ala Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

50

Pro Ser Gly Ser Ala Ala Leu Lys Ala Ala Val Asp Lys Ala Val Ala
130 135 140

Ser Gly Val Val Val Val Ala Ala Ala Gly Asn Glu Gly Thr Ser Gly
145 150 155 160

101

Ser Ser Ser Thr Val Gly Tyr Pro Gly Lys Tyr Pro Ser Val Ile Ala
165 170 175

Val Gly Ala Val Asp Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Val
180 185 190

Gly Pro Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
195 200 205

10 Leu Pro Gly Asn Lys Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Ser
210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn
225 230 235 240

Trp Thr Asn Thr Gln Val Arg Ser Ser Leu Glu Asn Thr Thr Thr Lys
245 250 255

20 Leu Gly Asp Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
260 265 270

Ala Ala Gln
275

<210> 4

<211> 275

<212> PRT

<213> B. subtilis

30 <400> 4

Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu
1 5 10 15

His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
20 25 30

Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly Gly Ala
35 40 45

40 Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser Ser His
50 55 60

Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly
65 70 75 80

Val Leu Gly Val Ser Pro Ser Ala Ser Leu Tyr Ala Val Lys Val Leu
85 90 95

50 Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
100 105 110

Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
115 120 125

Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
130 135 140

102

Ser Gly Ile Val Val Ala Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
145 150 155 160

Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
165 170 175

Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala
180 185 190

10 Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
195 200 205

Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr
210 215 220

Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
225 230 235 240

20 Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
245 250 255

Leu Gly Asn Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
260 265 270

Ala Ala Gln
275

<210> 5

30 <211> 274

<212> PRT

<213> B. licheniformis

<400> 5

Ala Gln Thr Val Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val
1 5 10 15

Gln Ala Gln Gly Phe Lys Gly Ala Asn Val Lys Val Ala Val Leu Asp
20 25 30

40 Thr Gly Ile Gln Ala Ser His Pro Asp Leu Asn Val Val Gly Gly Ala
35 40 45

Ser Phe Val Ala Gly Glu Ala Tyr Asn Thr Asp Gly Asn Gly His Gly
50 55 60

Thr His Val Ala Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val
65 70 75 80

50 Leu Gly Val Ala Pro Ser Val Ser Leu Tyr Ala Val Lys Val Leu Asn
85 90 95

Ser Ser Gly Ser Gly Ser Tyr Ser Gly Ile Val Ser Gly Ile Glu Trp
100 105 110

Ala Thr Thr Asn Gly Met Asp Val Ile Asn Met Ser Leu Gly Gly Ala
115 120 125

103

Ser Gly Ser Thr Ala Met Lys Gln Ala Val Asp Asn Ala Tyr Ala Arg
 130 135 140

Gly Val Val Val Val Ala Ala Ala Gly Asn Ser Gly Asn Ser Gly Ser
 145 150 155 160

Thr Asn Thr Ile Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val
 165 170 175

10 Gly Ala Val Asp Ser Asn Ser Asn Arg Ala Ser Phe Ser Ser Val Gly
 180 185 190

Ala Glu Leu Glu Val Met Ala Pro Gly Ala Gly Val Tyr Ser Thr Tyr
 195 200 205

Pro Thr Asn Thr Tyr Ala Thr Leu Asn Gly Thr Ser Met Ala Ser Pro
 210 215 220

20 His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Leu
 225 230 235 240

Ser Ala Ser Gln Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Tyr Leu
 245 250 255

Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala
 260 265 270

Ala Gln

30

<210> 6

<211> 269

<212> PRT

<213> B. lentus

<400> 6

Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
 1 5 10 15

40 His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
 20 25 30

Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
 35 40 45

Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
 50 55 60

His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
 65 70 75 80

50 Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
 85 90 95

Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
 100 105 110

104

Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
 115 120 125
 Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
 130 135 140
 Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
 145 150 155 160
 10 Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
 165 170 175
 Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
 180 185 190
 Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
 195 200 205
 20 Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
 210 215 220
 Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
 225 230 235 240
 Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
 245 250 255
 30 Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
 260 265

- 105 -

WHAT IS CLAIMED:

1. A protease variant comprising at least an amino acid substitution at residue position corresponding to residue position 212 of *Bacillus amyloliquefaciens* subtilisin as set forth in SEQ ID NO: 1, wherein the variant comprises proline at residue position 212,
with the proviso that the substitution set does not comprise a substitution at residue position 232, 252 or 257 of *Bacillus amyloliquefaciens* subtilisin.
2. The protease variant of claim 1 which comprises substitutions of the amino acid residues at one or both of positions 62 and 230.
3. The protease variant of claim 1 which comprises one or more amino acid substitution(s) at residue position corresponding to a residue position selected from 76, 87, 103, 104, 134, 141, 258, 268 and 271.
4. The protease variant of claim 1 which comprises a substitution set selected from:
N76D/S103A/V104I/S212P/E271V;
N76D/S103A/V104I/S212P/G258R;
N76D/S103A/V104I/S212P/V268F/E271V;
N76D/S87R/S103A/V104I/S212P/E271V;
N76D/S103A/V104I/S212P/Q245L/E271V;
N76D/S103A/V104I/T134S/S141N/S212P/E271V; and
N76D/S103A/V104I/S212P/Q236L/N243S/E271V.
5. The protease variant according to any one of claims 1 to 4 which is derived from a *Bacillus* subtilisin.

- 106 -

6. The protease variant according to claim 5 which is derived from *Bacillus lentus* subtilisin.

7. A DNA encoding the protease variant of any one of claims 1 to 6.

5

8. An expression vector comprising the DNA of claim 7.

9. A host cell transformed with the expression vector of claim 8.

10 10. A cleaning composition comprising the protease variant of any one of claims 1 to 6 and a cleaning acceptable diluent, surfactant or additive.

11. An animal feed comprising the protease variant of any one of claims 1 to 6.

15

12. A composition for treating a textile comprising the protease variant of any one of claims 1 to 6 and a cleaning acceptable diluent, surfactant or additive.

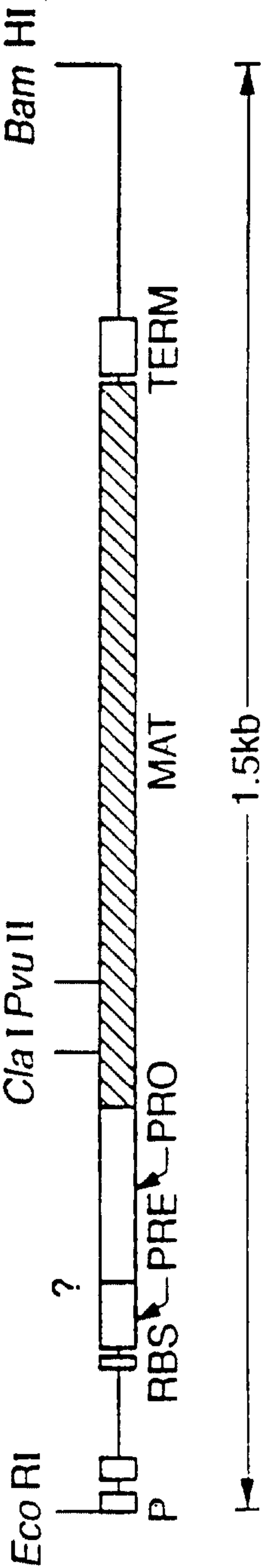
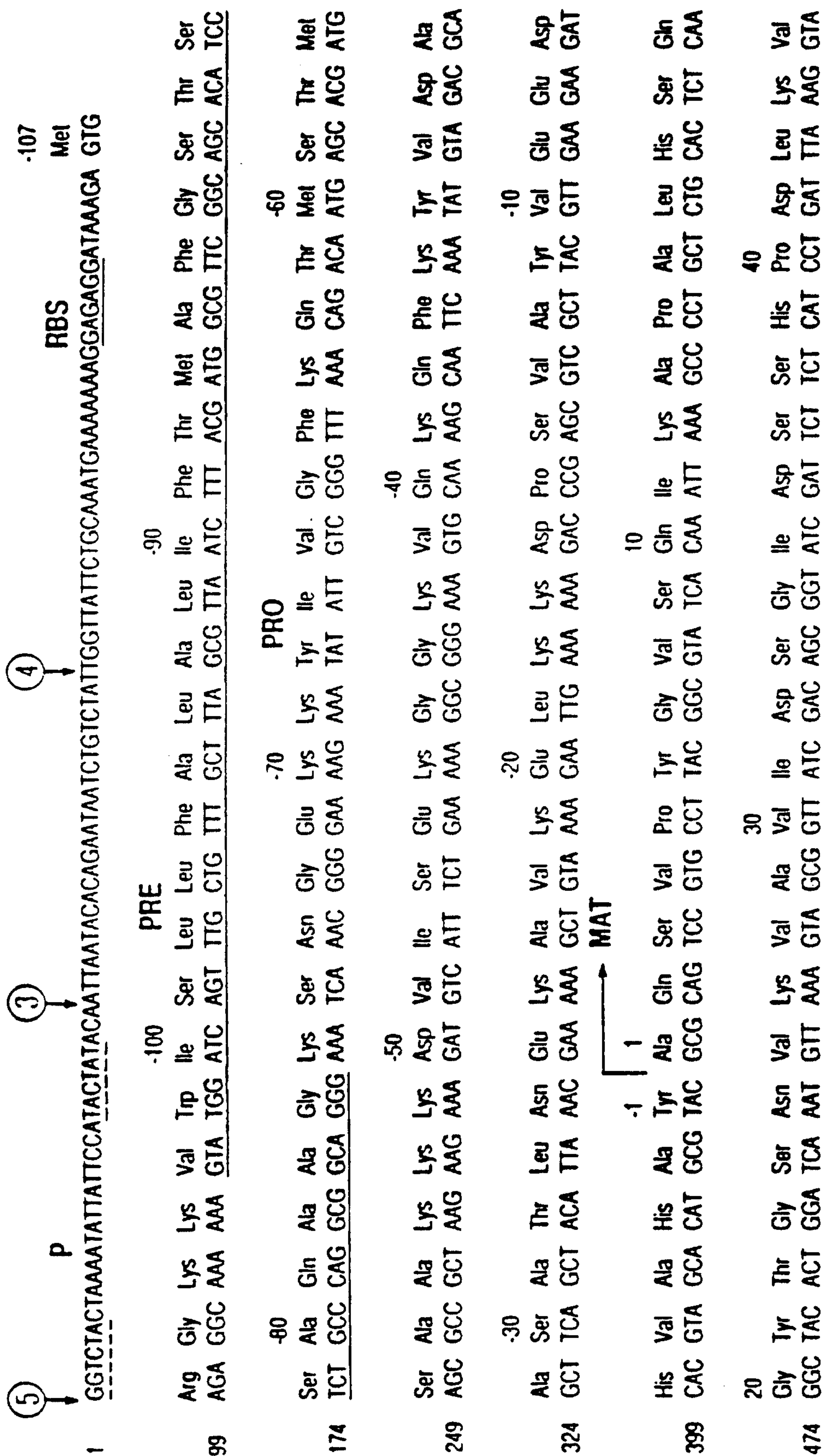


FIG. 1A



																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					</
--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

FIG. 1B - 2

[illegible]

	270		275			TERM
	Val	Gln	Ala	Ala	Gln	OC
1224	GTA	CAG	CGG	GCA	GCT	TAA
						<u>AACATAMAAACCGGCC</u> TTGGCCCGCGGTTTTTATTTTCTCCTCCGCATGTTCAATCCGCTCC

1316 ATAAATCGACGGATGGCTCCCTCTGAAATTTTAACGAGAAACGGCGGGTTGACCCGGCTCAGTCCCGTAACGGCCAGTCCCTGAAACGTCTCAATCGCCG

1416 CTCCCGGTTCCGGTCAGCTCAATGCCGTAACGGTCGGCGGGCTTTCCTGATACCGGGAGACGGCATTCGTAATCGGATC

FIG. 1B - 3

FIG. 1B

FIG. 1B-1

FIG.-1B-2

FIG. 1B-3

CONSERVED RESIDUES IN SUBTILISINS FROM
BACILLUS AMYLOLIQUEFACIENS

1	10	20
A Q S V P . G	A P A . H . .	G
21	30	40
. T G S . V K V A V . D . G	H P	
41	50	60
D L . . . G G A S . V P	Q D	
61	70	80
. N . H G T H V A G T . A A L N N S I G		
81	90	100
V L G V A P S A . L Y A V K V L G A . G		
101	110	120
S G . . S . L . . G . E W A . N		
121	130	140
V . N . S L G . P S . S	A . .	
141	150	160
. G V . V V A A . G N . G . . .		
161	170	180
. Y P . . Y	A V G A .	
181	190	200
D . . N . . A S F S . . G . . L D . . A		
201	210	220
P G V . . Q S T . P G . . Y	N G T	
221	230	240
S M A . P H V A G A A A L	K . . .	
241	250	260
W . . . Q . R . . L . N T	L G . .	
261	270	
. . Y G . G L . N . . A A . .		

FIG. 2

COMPARISON OF SUBTILISIN SEQUENCES FROM:

B.amyloliquefaciens
B.subtilis
B.licheniformis
B.lentus

01	A	Q	S	V	P	Y	G	V	S	Q	I	K	A	P	A	L	H	S	Q	G	Y	T	G	S	N	V	K	V	A	V	I	D	S	G	I	D	S	S	H	P	
	A	Q	S	V	P	Y	G	I	S	Q	I	K	A	P	A	L	H	S	Q	G	Y	T	G	S	N	V	K	V	A	V	I	D	S	G	I	D	S	S	H	P	
	A	Q	T	V	P	Y	G	I	P	L	I	K	A	D	K	V	Q	A	Q	G	F	K	G	A	N	V	K	V	A	V	L	D	T	G	I	Q	A	S	H	P	
	A	Q	S	V	P	W	G	I	S	R	V	Q	A	P	A	A	H	N	R	G	L	T	G	S	G	V	K	V	A	V	L	D	T	G	I	S	T	*	H	P	
41	D	L	K	V	A	G	G	A	S	M	V	P	S	E	T	N	P	F	Q	D	N	S	H	G	T	H	V	A	G	T	V	A	A	L	N	N	S	I	G		
	D	L	N	V	R	G	G	A	S	F	V	P	S	E	T	N	P	Y	Q	D	G	S	S	H	G	T	H	V	A	G	T	I	A	A	L	N	N	S	I	G	
	D	L	N	V	V	G	G	A	S	F	V	A	G	E	A	Y	N	*	T	D	G	N	G	H	G	T	H	V	A	G	T	V	A	A	L	D	N	T	G		
	D	L	N	I	R	G	G	A	S	F	V	P	G	E	*	P	S	T	Q	D	G	N	G	H	G	T	H	V	A	G	T	I	A	A	L	N	N	S	I	G	
81	V	L	G	V	A	P	S	A	S	L	Y	A	V	K	V	L	G	A	D	G	S	G	Q	Y	S	W	I	I	N	G	I	E	W	A	I	A	N	N	M	D	
	V	L	G	V	S	P	S	A	S	L	Y	A	V	K	V	L	D	S	T	G	S	G	Q	Y	S	W	I	I	N	G	I	E	W	A	I	S	N	N	M	D	
	V	L	G	V	A	P	S	V	S	L	Y	A	V	K	V	L	N	S	S	G	S	G	S	Y	S	G	I	V	S	G	I	E	W	A	T	N	G	M	D		
	V	L	G	V	A	P	S	A	E	L	Y	A	V	K	V	L	G	A	S	G	S	G	S	V	S	I	A	Q	G	L	E	W	A	G	N	N	G	M	H		
121	V	I	N	M	S	L	G	G	P	S	G	S	A	A	L	K	A	A	V	D	K	A	V	A	S	G	V	V	V	V	A	A	A	G	N	E	G	T	S	G	
	V	I	N	M	S	L	G	G	P	T	G	S	T	A	L	K	T	V	V	D	K	A	V	S	S	G	I	V	V	V	A	A	A	A	G	N	E	G	S	S	G
	V	I	N	M	S	L	G	G	A	S	G	S	T	A	M	K	Q	A	V	D	N	A	Y	A	R	G	V	V	V	V	A	A	A	A	G	N	S	G	N	S	G
	V	A	N	L	S	L	G	S	P	S	P	S	A	T	L	E	Q	A	V	N	S	A	T	S	R	G	V	L	V	V	A	A	A	S	G	N	S	G	A	G	S

FIG._3A

161 S S S T V G Y P G K Y P S V I A V G A V D S S N Q R A S F S S V G P E L D V M A
S T S T V G Y P A K Y P S T I A V G A V N S S N Q R A S F S S V G S E L D V M A
S T N T I G Y P A K Y P S V I A V G A V D S S N Q R A S F S S V G A E L D V M A
* * * I S Y P A R Y A N A M A V G A T D Q N N R A S F S S Q Y G A G L D I V A

201 P G V S I Q S S T L P G N K Y G A Y N G T S M A S P H V A G A A A L I L S K H P N
P G V S I Q S S T L P G N K Y G A Y N G T S M A S P H V A G A A A L I L S K H P T
P G A G V Y S S T Y P P T N T Y A T L N G T S M A S P H V A G A A A L I L S K H P N
P G V N V Q S S T Y P P G S T Y A S L N G T S M A S P H V A G A A A L V K Q K N P S

241 W T N T Q V R S S L E N T T K L G D S F Y Y G K G L I N V Q A A A Q
W T N A Q Q V R R D R L E S T A T Y L G N S F Y Y G K G L I N V Q A A A Q
L S A S Q Q V R R L S S T A T Y L G S S F Y Y G K G L I N V E A A A Q
W S N V Q I R R N H L K N T A T S L G S T N L Y G S G L V N A E A A T R

FIG._3B

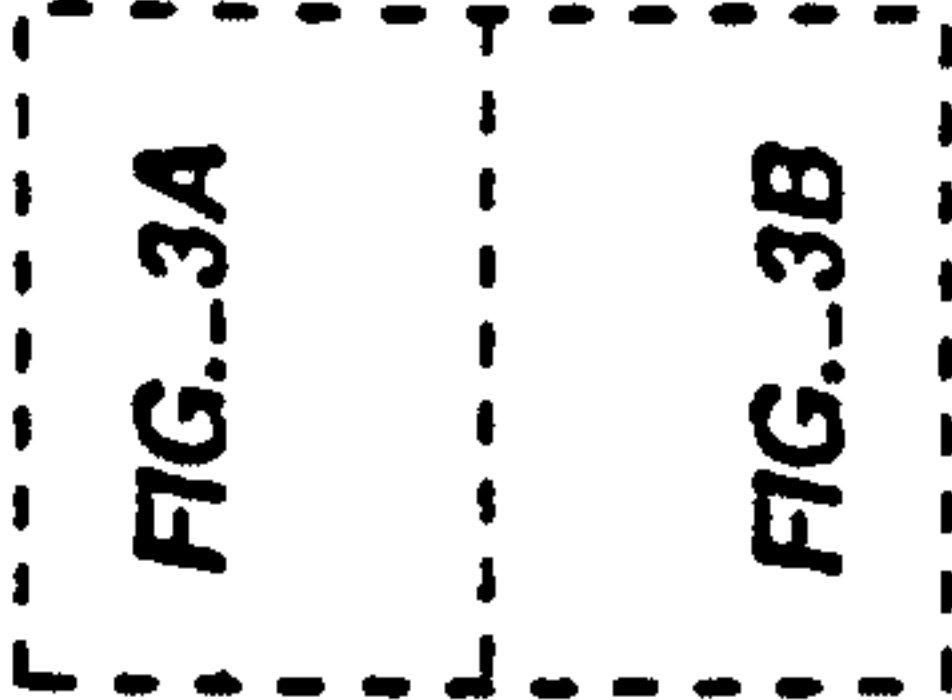


FIG._3