

SEQUENCE LISTING

<110> SUMITOMO CHEMICAL COMPANY, LIMITED
Kataoka Bio Laboratory Co., LTD.

<120> Protein having peptidoglycan degrading activity, DNA encoding same, preparation and method for decomposing microorganisms

<130> S44521W001

<150> JP2020-056455

<151> 2020-03-26

<160> 26

<170> PatentIn version 3.5

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<212> DNA

<213> Tumebacillus sp. NITE BP-02779

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<221> CDS

<222> (1)..(696)

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<222> (205)..(696)

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Lys	Asp	Gly	Ser	Val	Arg	Leu	Asp	Val	Ala	Glu	Arg	Pro	Ser	Asn	Gly	
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Ile	Arg	Ala	Asn	Asn	Asn	Thr	Ala	Asn	Pro	Ile	Gly	Ser	Val	Ser	Val		
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Gly	Ser	Trp	Pro	Ala	Gln	Ser	Leu	Asn	Ala	Gly	Ala	Ile	Ala	Val	Lys		
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Lys	Ser	Gly	Val	Met	Phe	Glu	Thr	Gln	Tyr	Arg	Ala	Gly	Ser	Tyr	Asp		
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Ser	Ser	Ile	Pro	Gly	Thr	Asn	Ile	Met	Ser	Gln	Asn	Gly	Thr	His	Tyr		
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t	gc	ga	ca	gg	aa	ac	tg	tc	tg	at	ac	aa	ta	ta	ta		672
Tyr	Ala	Asp	Gln	Gly	Lys	Thr	Trp	Ser	Trp	Met	Thr	Asn	Tyr	Tyr	Tyr		
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-20 -15 -10 -5

Val Thr Ala Ala Ala Ala Tyr Thr Lys Pro Ser Thr Ile Arg Val Gly
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Ile Arg Ala Asn Asn Asn Thr Ala Asn Pro Ile Gly Ser Val Ser Val
15 20 25

Val Pro Trp Tyr Asp Tyr Asn Ile Asp Val Leu Pro Asn Glu Trp Ile
30 35 40

Gly Ser Trp Pro Ala Gln Ser Leu Asn Ala Gly Ala Ile Ala Val Lys
45 50 55 60

Met Tyr Ala Trp Tyr His Ile Leu His Pro Lys Tyr Ser Thr Cys Asp
65 70 75

Val Asp Asn Thr Val Asn Ser Gln Val Tyr Lys Ala Gly Ser Arg Tyr
80 85 90

Ser Asn Thr Thr Thr Ala Val Asp Asn Met Ser Gly Ile Gly Ile Leu
95 100 105

Lys Ser Gly Val Met Phe Glu Thr Gln Tyr Arg Ala Gly Ser Tyr Asp
110 115 120

Ser Ser Ile Pro Gly Thr Asn Ile Met Ser Gln Asn Gly Thr His Tyr
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Pro Gly Ser Ala Gln Phe Thr Tyr
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Ser Val Gly Ser Val Tyr Ala Gln Pro Ala His Ala Glu Gln Ser Thr
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Lys Gln Ser Val Ala Thr Ala Pro Val Leu Glu Ser Ala Phe Thr Ser
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gct gcg aag gaa ttt ggc gtt ccg aag gac ctg ctg atg gcg atc tcc 192
Ala Ala Lys Glu Phe Gly Val Pro Lys Asp Leu Leu Met Ala Ile Ser
25 30 35

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Tyr Ser Glu Ser Arg Trp Gln Ile Ala Pro Glu Glu Ala Arg Thr Ser
40 45 50

tcg gag ccg gat aaa aac aac ggc aag ggt ctg atg cac ctc cag gac 288
Ser Glu Pro Asp Lys Asn Asn Gly Lys Gly Leu Met His Leu Gln Asp
55 60 65

aac tcc ttc aaa aaa ggt ctg agc gaa gca gca aaa gcg ctc ggc gtt 336

Asn	Ser	Phe	Lys	Lys	Gly	Leu	Ser	Glu	Ala	Ala	Lys	Ala	Leu	Gly	Val	
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Ser	Lys	Lys	Gln	Met	Glu	Asp	Asp	Ile	Gln	Leu	Asn	Ile	Arg	Gly	Gly	
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Ala	Tyr	Leu	Leu	Ser	Lys	Ala	Gln	Lys	Asp	Leu	Gly	Lys	Thr	Leu	Thr	
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gcc	aac	gcg	aac	gat	tgg	tac	gaa	gcg	gtc	gct	tcc	ttc	gaa	gga	gcc	480
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Lys	Asp	Lys	Asp	Leu	Gly	Ala	Leu	Phe	Ala	Asp	Glu	Val	Tyr	Arg	Val	
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Leu	Lys	Glu	Gly	Thr	Ala	Leu	Ala	Ile	Ser	Gly	Gly	Thr	Leu	Thr	Leu	
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atc	tgg	aac	ccg	gcc	agc	tcg	tcg	aac	tat	gcg	gtt	gcc	tcc	cgc	ccc	720
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Tyr	Ser	Gly	Ser	Ile	Asn	Trp	Phe	Lys	Asp	Pro	Ala	Ala	Gln	Val	Ser	
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Ala	His	Tyr	Ile	Val	Arg	Ser	Ser	Asp	Gly	Gln	Ile	Thr	Gln	Leu	Val	
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caa	gac	aag	gac	atc	gcg	tgg	cat	gcg	cgc	acc	ttc	aac	acc	aac	ggc	912
Gln	Asp	Lys	Asp	Ile	Ala	Trp	His	Ala	Arg	Thr	Phe	Asn	Thr	Asn	Gly	
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acc tac acg atg ggc aat ggc acc aac ccg atc tcc aac tac gcg acg Thr Tyr Thr Met Gly Asn Gly Thr Asn Pro Ile Ser Asn Tyr Ala Thr 390 395 400	1296
tgg aga ccg acg atc acg acc tcg ggc aac tac caa gtg aaa gtc ttc Trp Arg Pro Thr Ile Thr Ser Gly Asn Tyr Gln Val Lys Val Phe 405 410 415 420	1344
atc ccg tcc aac ttc gcc gcg acc acc aac gcg aag tac gag atc cat Ile Pro Ser Asn Phe Ala Ala Thr Thr Asn Ala Lys Tyr Glu Ile His 425 430 435	1392
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aac caa tgg gtg agc ctc ggc acc tac agt ttt gca gcc ggc acc acc Asn Gln Trp Val Ser Leu Gly Thr Tyr Ser Phe Ala Ala Gly Thr Thr 455 460 465	1488
ggc tac gtc atg ttg ggt gac aac acc ggc gac aaa gcg tac gtc ggc	1536

Gly Tyr Val Met Leu Gly Asp Asn Thr Gly Asp Lys Ala Tyr Val Gly
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 Ile Asp Gly Met Arg Phe Leu Ala Gln
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1566

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 <213> Tumebacillus sp. NITE BP-02779

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 -10 -5 -1 1

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 5 10 15 20

Ala Ala Lys Glu Phe Gly Val Pro Lys Asp Leu Leu Met Ala Ile Ser
 25 30 35

Tyr Ser Glu Ser Arg Trp Gln Ile Ala Pro Glu Glu Ala Arg Thr Ser
 40 45 50

Ser Glu Pro Asp Lys Asn Asn Gly Lys Gly Leu Met His Leu Gln Asp
 55 60 65

Asn Ser Phe Lys Lys Gly Leu Ser Glu Ala Ala Lys Ala Leu Gly Val
 70 75 80

Ser Lys Lys Gln Met Glu Asp Asp Ile Gln Leu Asn Ile Arg Gly Gly
 85 90 95 100

Ala Tyr Leu Leu Ser Lys Ala Gln Lys Asp Leu Gly Lys Thr Leu Thr
 105 110 115

Ala Asn Ala Asn Asp Trp Tyr Glu Ala Val Ala Ser Phe Glu Gly Ala
120 125 130

Lys Asp Lys Asp Leu Gly Ala Leu Phe Ala Asp Glu Val Tyr Arg Val
135 140 145

Leu Lys Glu Gly Thr Ala Leu Ala Ile Ser Gly Gly Thr Leu Thr Leu
150 155 160

Asp Pro Asn Lys Ser Ile Ala Pro Ala Lys Gly Ser Tyr Ala Gly Leu
165 170 175 180

Ile Pro Gly Gly Thr Asn Tyr Gly Leu Thr Pro Asp Tyr Ser Gly Ala
185 190 195

Ile Trp Asn Pro Ala Ser Ser Ser Asn Tyr Ala Val Ala Ser Arg Pro
200 205 210

Thr Ser Asn Ala Ile Thr Ser Val Ile Ile His Asp Thr Glu Gly Ser
215 220 225

Tyr Ser Gly Ser Ile Asn Trp Phe Lys Asp Pro Ala Ala Gln Val Ser
230 235 240

Ala His Tyr Ile Val Arg Ser Ser Asp Gly Gln Ile Thr Gln Leu Val
245 250 255 260

Gln Asp Lys Asp Ile Ala Trp His Ala Arg Thr Phe Asn Thr Asn Gly
265 270 275

Ile Gly Ile Glu His Glu Gly Tyr Ala Ala Gln Thr Gly Trp Tyr Thr
280 285 290

Asp Ala Met Tyr Thr Ala Ser Ala Ala Leu Thr Arg Ala Val Cys Leu
295 300 305

Lys Tyr Asn Ile Pro Met Asp Arg Glu His Ile Met Ala His Ser Glu

310

315

320

Leu Trp Gly Asn Asp His Thr Asp Pro Gly Val Asn Trp Asp Trp Asn
 325 330 335 340

Lys Tyr Met Ser Lys Val Thr Gly Val Thr Lys Asn Tyr Asp Ala Val
 345 350 355

Leu Val Asp Asn Thr Asp Ala Ser Ser Gly Phe Ser Leu Gly Gly Pro
 360 365 370

Ser Gln Tyr Trp His Pro Thr Ala Gly Tyr Gly Ile His Asn Gln Met
 375 380 385

Thr Tyr Thr Met Gly Asn Gly Thr Asn Pro Ile Ser Asn Tyr Ala Thr
 390 395 400

Trp Arg Pro Thr Ile Thr Thr Ser Gly Asn Tyr Gln Val Lys Val Phe
 405 410 415 420

Ile Pro Ser Asn Phe Ala Ala Thr Thr Asn Ala Lys Tyr Glu Ile His
 425 430 435

Tyr Asn Gly Gly Val Ile Thr Lys Thr Ile Ser Gln Ala Ala Tyr Ser
 440 445 450

Asn Gln Trp Val Ser Leu Gly Thr Tyr Ser Phe Ala Ala Gly Thr Thr
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Ile Asp Gly Met Arg Phe Leu Ala Gln
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<212> DNA

<213> Artificial Sequence

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<223> 27F, primer for 16S rRNA cloning

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<223> 339F, primer for 16S rRNA sequencing

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<223> 536R, primer for 16S rRNA sequencing

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acgcttggaac acgagtgcta ataccggata atctcttgga tcgcatgggtc tgagagtaaa 180

aggagctttt gcttcactgc yagatggacc cgcggcgcat tagctagttg gtgaggtaat 240

ggctcaccaa ggcgacgatg cgtagccgac ctgagagggt gaccggccac actgggactg 300

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cctgacggag caacgccgcg tgagtgatga aggccttcgg gttgtaaaac tctgtcttct 420

gtgaagaacc atcctgtgca gagaaagctc aggacctgac ggtaacagag gaggaagccc 480

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<213> Tumebacillus sp. NITE BP-02779

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Trp Pro Ala Gln Ser Leu Asn Ala Gly Ala Ile Ala Val Lys
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Met Tyr Ala Trp Tyr His Ile Leu His Pro Lys
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<210> 13
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<210> 14

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Leu Lys

<210> 15

<211> 10

<212> PRT

<213> Tumebacillus sp. NITE BP-02779

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1 5 10

<210> 16

<211> 27

<212> PRT

<213> Tumebacillus sp. NITE BP-02779

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20 25

<210> 17

<211> 18

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<213> Tumebacillus sp. NITE BP-02779

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Thr Tyr

<210> 18

<211> 10

<212> PRT

<213> Tumebacillus sp. NITE BP-02779

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<223> F primer for ID2839 cloning

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<210> 20

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> R primer for ID2839 cloning

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<213> Artificial Sequence

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<223> His_Tb restriction site

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1 5 10 15

Arg Gly Ser His
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<211> 33

<212> DNA

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<223> F primer for ID1644 cloning

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<211> 27

<212> DNA

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<223> R primer for ID1644 cloning

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