

SEQUENCE LISTING

<110> QITAN TECHNOLOGY LTD., CHENGDU

<120> MUTANT OF PORIN MONOMER, PROTEIN PORE, AND USE THEREOF

<130> PCT21092CN

<160> 30

<170> PatentIn version 3.5

<210> 1

<211> 283

<212> PRT

<213> Pseudomonas taeanensis

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Cys Ala Leu Arg Glu Pro Met Pro Ala Glu Leu Glu Asn Ala Thr Pro
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Thr Leu Thr Pro Arg Ala Ser Thr Tyr Tyr Asp Leu Leu Ala Leu Pro
35 40 45

Arg Pro Lys Gly Arg Leu Val Ala Ala Val Tyr Gly Phe Arg Asp Gln
50 55 60

Thr Gly Gln Tyr Lys Pro Thr Pro Ala Ser Ser Phe Ser Thr Ser Val
65 70 75 80

Thr Gln Gly Ala Ala Ser Met Leu Val Asp Ala Leu Gln Ala Ser Gly
85 90 95

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Glu Tyr Arg Val Asp Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280

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aaaaaaaaaca aaaaaaaaaa ataaaaaaaa aaaaagcaat acgtaactga acgaagtaca	120
ttaaaaaaaaaa aa	132
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<212> DNA
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gagattcaga gattcagaga tttttttttt tttt 94

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tttttttttt tttttttttt tttttttt 28

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<400> 22

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20 25 30

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

Lys Thr Thr Met Met Lys Phe Leu Val Ser Trp Leu Arg Asp Glu Gly
50 55 60

Ile Thr Gly Val Ala Leu Ala Ala Pro Thr His Ala Ala Lys Lys Val
65 70 75 80

Leu Ala Asn Ala Val Gly Glu Glu Val Ser Thr Ile His Ser Ile Leu
85 90 95

Lys Ile Asn Pro Thr Thr Tyr Glu Cys Lys Gln Phe Phe Glu Gln Ser
100 105 110

Ala Pro Pro Asp Leu Ser Lys Ile Arg Ile Leu Ile Cys Glu Glu Cys
115 120 125

Ser Phe Tyr Asp Ile Lys Leu Phe Glu Ile Leu Met Asn Ser Ile Gln
130 135 140

Pro Trp Thr Ile Ile Ile Gly Ile Gly Asp Arg Ala Gln Leu Arg Pro
145 150 155 160

Ala Asp Asp Lys Gly Ile Ser Arg Phe Phe Thr Asp Gln Arg Phe Glu
165 170 175

Gln Thr Tyr Leu Thr Glu Ile Lys Arg Ser Asn Met Pro Ile Ile Glu
180 185 190

Val Ala Thr Glu Ile Arg Asn Gly Gly Trp Ile Arg Glu Asn Ile Ile
195 200 205

Asp Asp Leu Gly Val Lys Gln Asp Lys Ser Val Ser Glu Phe Met Thr
210 215 220

Asn Tyr Phe Lys Val Val Lys Ser Ile Asp Asp Leu Tyr Glu Thr Arg
225 230 235 240

Met Tyr Ala Tyr Thr Asn Asn Ser Val Asp Thr Leu Asn Lys Ile Ile
245 250 255

Arg Lys Lys Leu Tyr Glu Thr Glu Gln Asp Phe Ile Val Gly Glu Pro
260 265 270

Ile Val Met Gln Glu Pro Leu Ile Arg Asp Ile Asn Tyr Glu Gly Lys
275 280 285

Arg Phe Gln Glu Ile Val Phe Asn Asn Gly Glu Tyr Leu Glu Val Ser
290 295 300

Glu Ile Lys Pro Met Glu Ser Val Leu Lys Cys Arg Asn Ile Asp Tyr
305 310 315 320

Gln Leu Val Leu His Tyr Tyr Gln Leu Lys Val Lys Ser Ile Asp Thr
325 330 335

Gly Glu Ser Gly Leu Ile Asn Thr Ile Ser Asp Lys Asn Glu Leu Asn
340 345 350

Lys Phe Tyr Met Phe Leu Gly Lys Val Cys Gln Asp Tyr Lys Ser Gly
355 360 365

Thr Ile Lys Ala Phe Trp Asp Asp Phe Trp Lys Ile Lys Asn Asn Tyr
370 375 380

His Arg Val Lys Pro Leu Pro Val Ser Thr Ile His Lys Gly Gln Gly
385 390 395 400

Ser Thr Val Asp Asn Ser Phe Leu Tyr Thr Pro Cys Ile Thr Lys Tyr
405 410 415

Ala Glu Pro Asp Leu Ala Ser Gln Leu Leu Tyr Val Gly Val Thr Arg
420 425 430

Ala Arg His Asn Val Asn Phe Val Gly
435 440

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<213> Artificial Sequence

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<223> helicase

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<400> 24

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Cys Ala Leu Arg Glu Pro Met Pro Ala Glu Leu Glu Asn Ala Thr Pro
20 25 30

Thr Leu Thr Pro Arg Ala Ser Thr Tyr Tyr Asp Leu Leu Ala Leu Pro
35 40 45

Arg Pro Lys Gly Arg Leu Val Ala Ala Val Tyr Gly Phe Arg Asp Gln
50 55 60

Thr Gly Gln Tyr Arg Pro Ser Pro Ala Ser Ala Gln Ser Thr Ser Val
65 70 75 80

Thr Gln Gly Ala Ala Ser Met Leu Val Asp Ala Leu Gln Ala Ser Gly
85 90 95

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Glu Tyr Arg Val Asp Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280

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<212> DNA
<213> Artificial Sequence

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tactacgacc tgctggctct cccgcgtccg aagggtcgcc tggtaggcggc ggtgtatggt 180
tttcgcgatc agactgggtca gtaccgtccg tccccggcgt cagcacaaaag caccagcgtc 240
accagggtg cagcgtctat gctggttgac gcattacaag cgtccggctg gttccgcgtg 300
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aacaaaccga ataccccagt taatatccaa gcggatctgc cttcgttgca ggaggcgaac 420
attctgctcg agggtagcgt gattgcatac gacaccaatg ttcgttctgg cggtagaggc 480

gctgcgtacc tgggtatcag cctgtcccaa gaatatcgcg ttgaccaggt tagcgtaa	540
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atttatagcg tgggtcgtaa tgccggcatt ttttaagttca tcgaattcaa agagttgttg	660
gaggcagaag cgggttatac cacaaacgag ccggcccaac tttgcgttct gagcgcaatc	720
gaggcggctg tggcccacct ggtcgcgcag ggcacgcagc gccgtctgtg gcaggctgcc	780
gatgagagct cctttgataa gagcagcttg ccgaagtaca tgagccaggc gagagccgac	840
ccgctgccg	849

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			20					25					30		

Thr	Leu	Thr	Pro	Arg	Ala	Ser	Thr	Tyr	Tyr	Asp	Leu	Leu	Ala	Leu	Pro
			35				40					45			

Arg	Pro	Lys	Gly	Arg	Leu	Val	Ala	Ala	Val	Tyr	Gly	Phe	Arg	Asp	Gln
			50			55					60				

Thr	Gly	Gln	Tyr	Lys	Pro	Gly	Pro	Ala	Ser	Thr	Lys	Ser	Thr	Ser	Val
65					70					75					80

Thr	Gln	Gly	Ala	Ala	Ser	Met	Leu	Val	Asp	Ala	Leu	Gln	Ala	Ser	Gly
			85						90					95	

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Glu Tyr Arg Val Asp Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280

<210> 27
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<220>
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<400> 27

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

Arg Pro Lys Gly Arg Leu Val Ala Ala Val Tyr Gly Phe Arg Asp Leu
50 55 60

Thr Gly Gln Tyr Arg Pro Ser Pro Ala Ser Ala Asn Ser Thr Ala Val
65 70 75 80

Thr Gln Gly Ala Ala Ser Met Leu Val Asp Ala Leu Gln Ala Ser Gly
85 90 95

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Glu Tyr Arg Val Asp Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280

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<212> PRT
<213> Artificial Sequence

<220>
<223> mutant 4

<400> 28

Met Asn Arg Leu Leu Ala Met Ala Met Leu Leu Ala Ala Leu Gln Gly
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Cys Ala Leu Arg Glu Pro Met Pro Ala Glu Leu Glu Asn Ala Thr Pro
20 25 30

Thr Leu Thr Pro Arg Ala Ser Thr Tyr Tyr Asp Leu Leu Ala Leu Pro
35 40 45

Arg Pro Lys Gly Arg Leu Val Ala Ala Val Tyr Gly Phe Arg Asp Leu
50 55 60

Thr Gly Gln Tyr Arg Pro Ser Pro Ala Ser Ala Leu Ser Thr Ala Val
65 70 75 80

Thr Gln Gly Ala Ala Ser Met Leu Val Asp Ala Leu Gln Ala Ser Gly
85 90 95

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Glu Tyr Arg Val Asp Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280

<210> 29
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<213> Artificial Sequence

<220>
<223> mutant 5

<400> 29

Met Asn Arg Leu Leu Ala Met Ala Met Leu Leu Ala Ala Leu Gln Gly
1 5 10 15

Cys Ala Leu Arg Glu Pro Met Pro Ala Glu Leu Glu Asn Ala Thr Pro
20 25 30

Thr Leu Thr Pro Arg Ala Ser Thr Tyr Tyr Asp Leu Leu Ala Leu Pro
35 40 45

Arg Pro Lys Gly Arg Leu Val Ala Ala Val Tyr Gly Phe Ser Val Gln
50 55 60

Thr Gly Gln Phe Arg Pro Ser Pro Ala Ser Ala Gln Ser Thr Ser Val
65 70 75 80

Thr Gln Gly Ala Ala Ser Met Leu Val Asp Ala Leu Gln Ala Ser Gly
85 90 95

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Glu Tyr Arg Val Asp Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280

<210> 30
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<213> Artificial Sequence

<220>
<223> mutant 6

<400> 30

Met Asn Arg Leu Leu Ala Met Ala Met Leu Leu Ala Ala Leu Gln Gly
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Cys Ala Leu Arg Glu Pro Met Pro Ala Glu Leu Glu Asn Ala Thr Pro
20 25 30

Thr Leu Thr Pro Arg Ala Ser Thr Tyr Tyr Asp Leu Leu Ala Leu Pro
35 40 45

Arg Pro Lys Gly Arg Leu Val Ala Ala Val Tyr Gly Phe Arg Asp Gln
50 55 60

Thr Gly Gln Phe Arg Pro Ser Pro Ala Ser Ala Gln Ser Thr Ser Val
65 70 75 80

Thr Gln Gly Ala Ala Ser Met Leu Val Asp Ala Leu Gln Ala Ser Gly
85 90 95

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

Arg Lys Ile Ile Arg Ala Ser Gln Asn Lys Pro Asn Thr Pro Val Asn
115 120 125

Ile Gln Ala Asp Leu Pro Ser Leu Gln Ala Ala Asn Ile Leu Leu Glu
130 135 140

Gly Gly Val Ile Ala Tyr Asp Thr Asn Val Arg Ser Gly Gly Glu Gly
145 150 155 160

Ala Ala Tyr Leu Gly Ile Ser Leu Ser Gln Asn Tyr Arg Val Asn Gln
165 170 175

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

Ala Asn Val Met Thr Ser Lys Thr Ile Tyr Ser Val Gly Arg Asn Ala
195 200 205

Gly Ile Phe Lys Phe Ile Glu Phe Lys Glu Leu Leu Glu Ala Glu Ala
210 215 220

Gly Tyr Thr Thr Asn Glu Pro Ala Gln Leu Cys Val Leu Ser Ala Ile
225 230 235 240

Glu Ala Ala Val Ala His Leu Val Ala Gln Gly Ile Glu Arg Arg Leu
245 250 255

Trp Gln Ala Ala Asp Glu Ser Ser Phe Asp Lys Ser Ser Leu Pro Lys
260 265 270

Tyr Met Ser Gln Ala Arg Ala Asp Pro Leu Pro
275 280