Figure 1

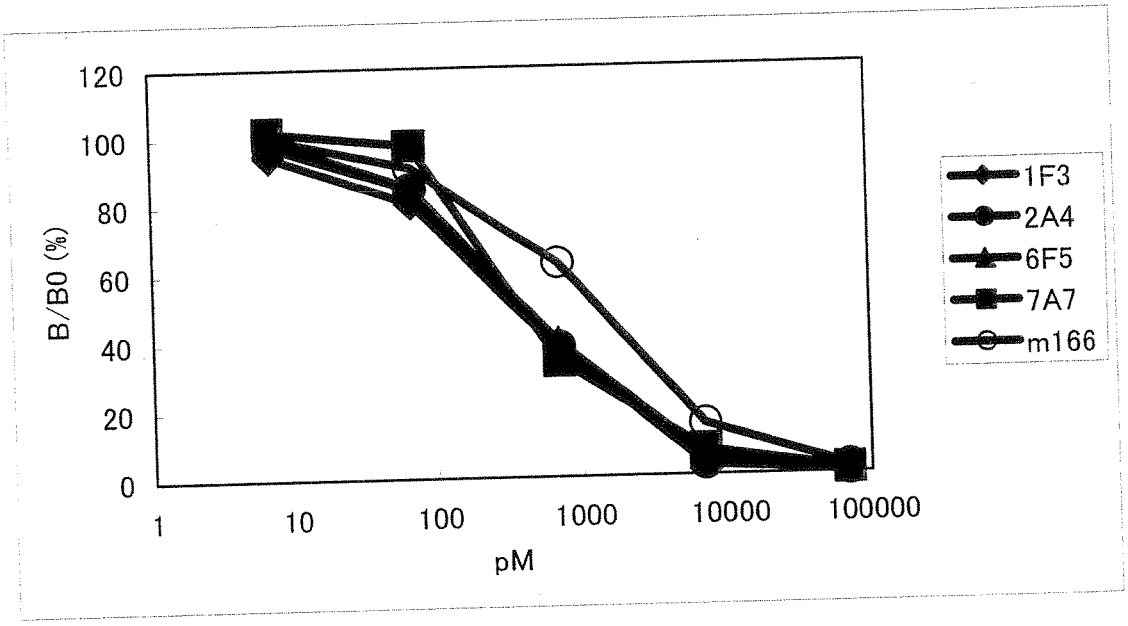


Figure 2

Clone	Kd (M)
m166	3.0×10^{-9}
1F3	3.7×10^{-10}
2A4	3.5×10^{-10}
6F5	1.1×10^{-10}
7A7	1.1×10^{-9}

Figure 3

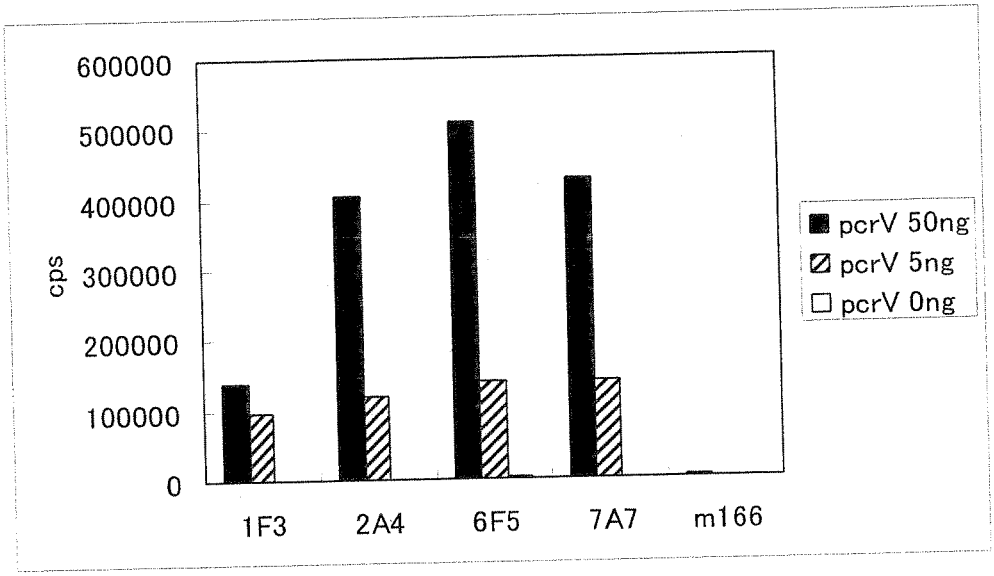


Figure 4

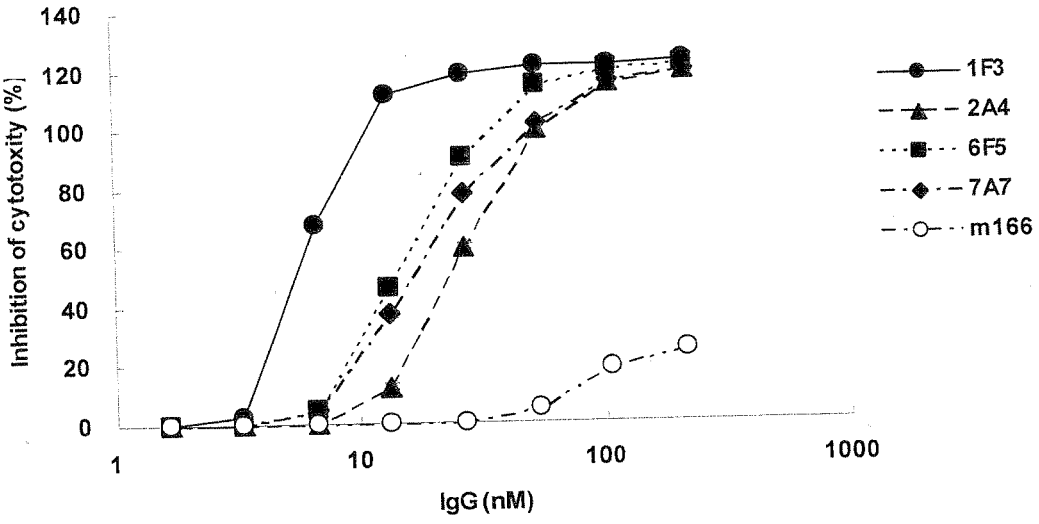


Figure 5

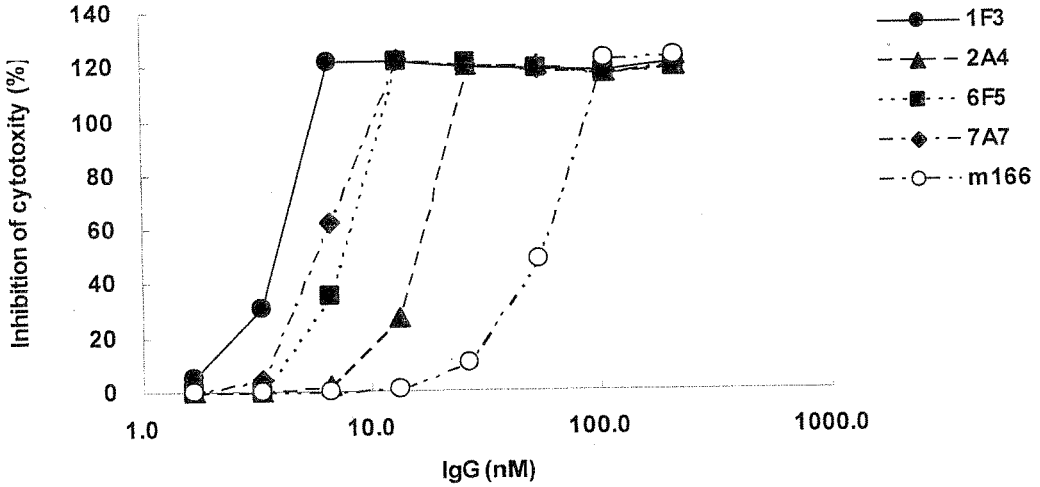
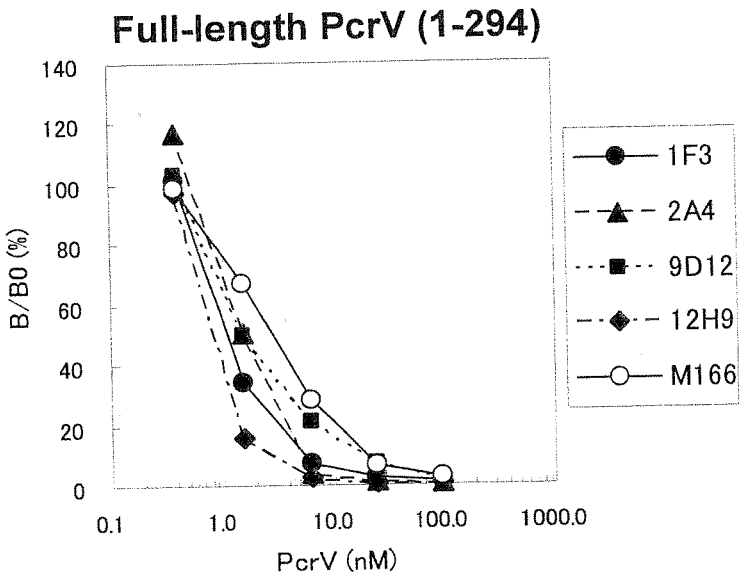

140
120
100
80
60
40
20
0
Inhibition of cytotoxity (%)
1.0
10.0
100.0
1000.0
IgG (nM)
1F3
2A4
6F5
7A7
m166

Figure 6


Full-length PcrV (1-294)
140
120
100
80
60
40
20
0
B/B0 (%)
0.1
1.0
10.0
100.0
1000.0
PcrV (nM)
1F3
2A4
9D12
12H9
M166

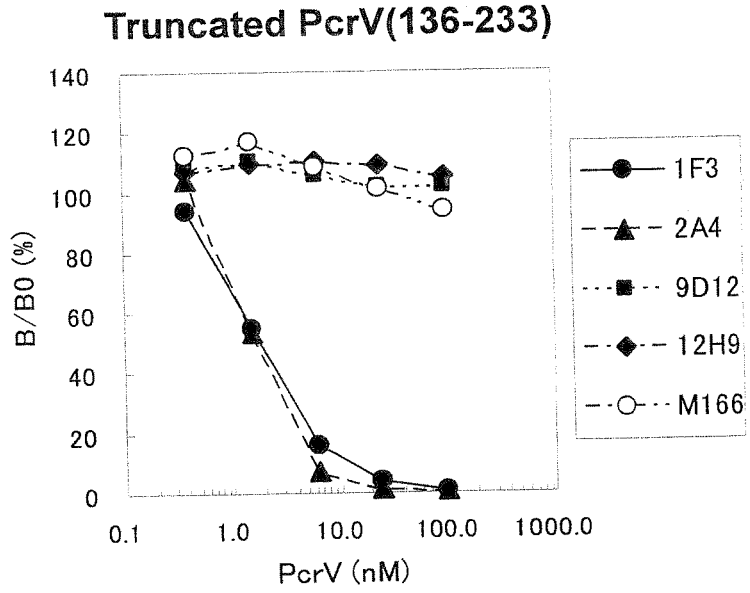

Truncated PcrV(136-233)
140
120
100
80
60
40
20
0
B/B0 (%)
0.1
1.0
10.0
100.0
1000.0
PcrV (nM)
1F3
2A4
9D12
12H9
M166

Figure 7

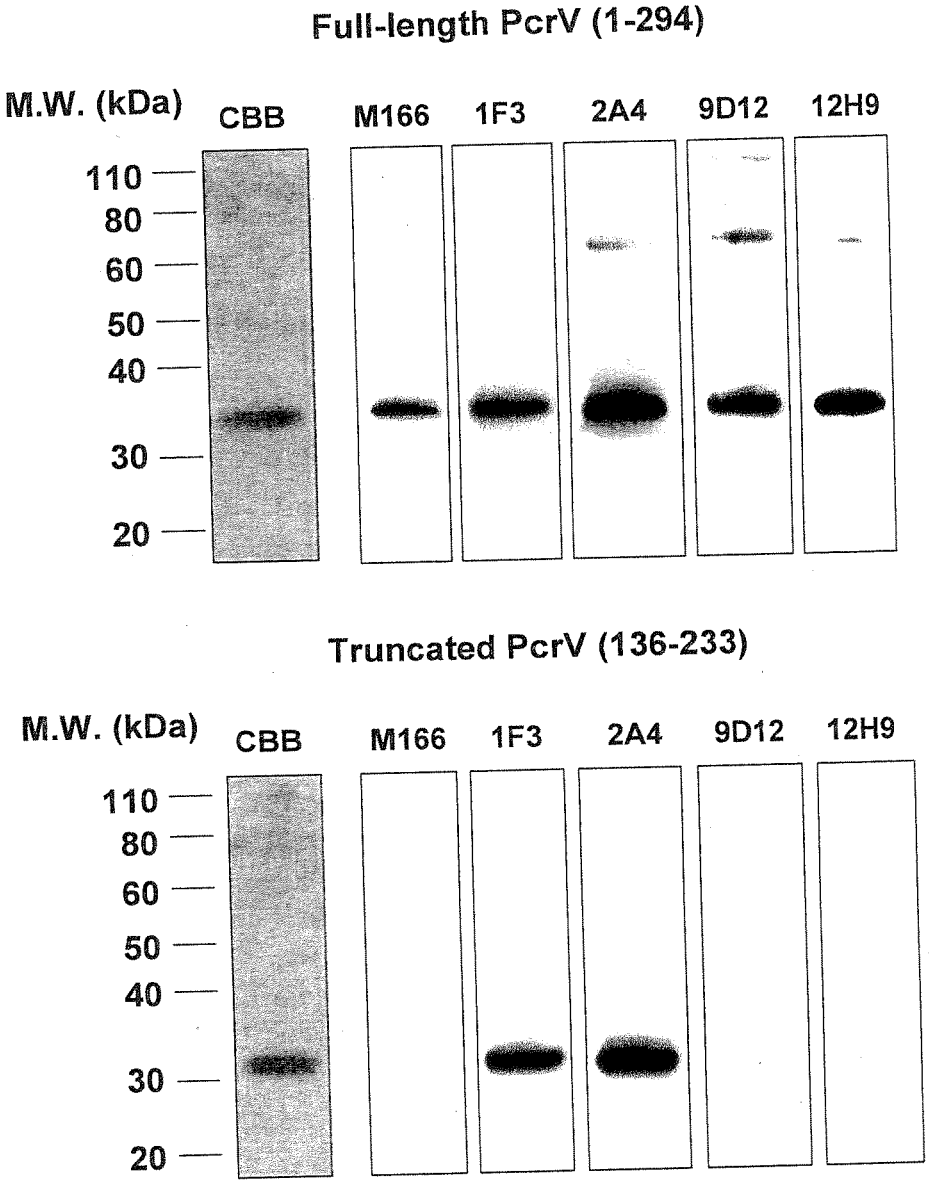
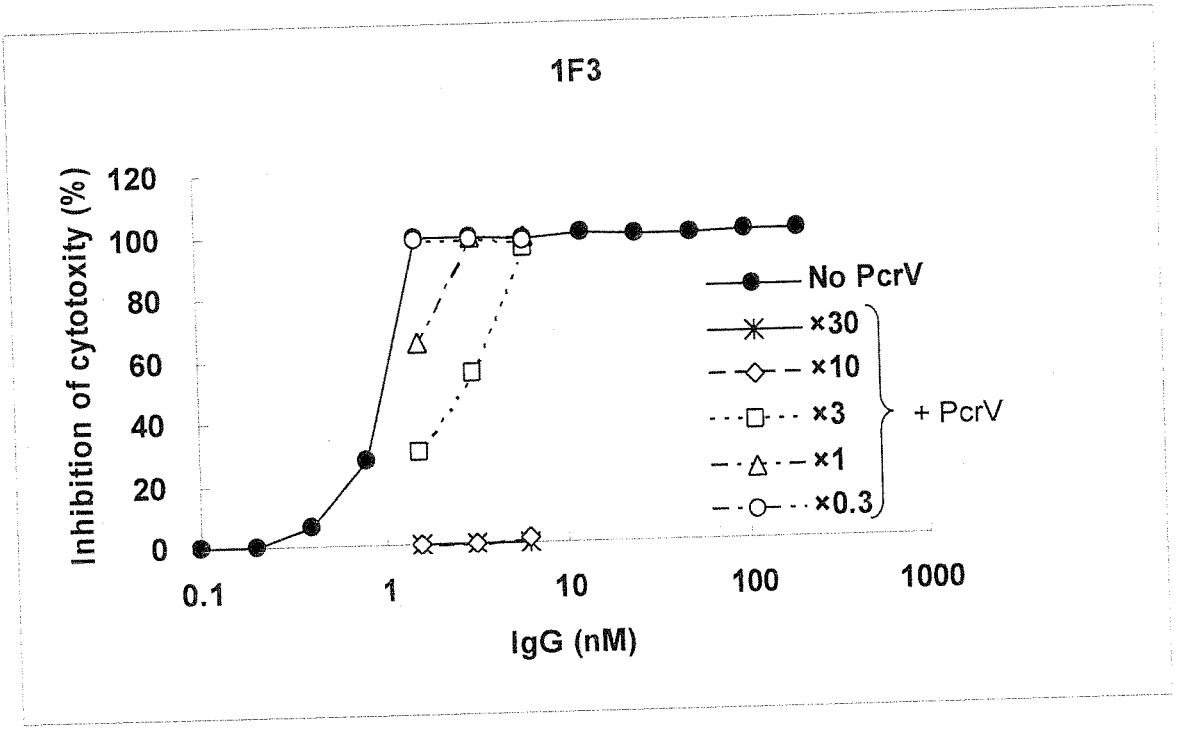
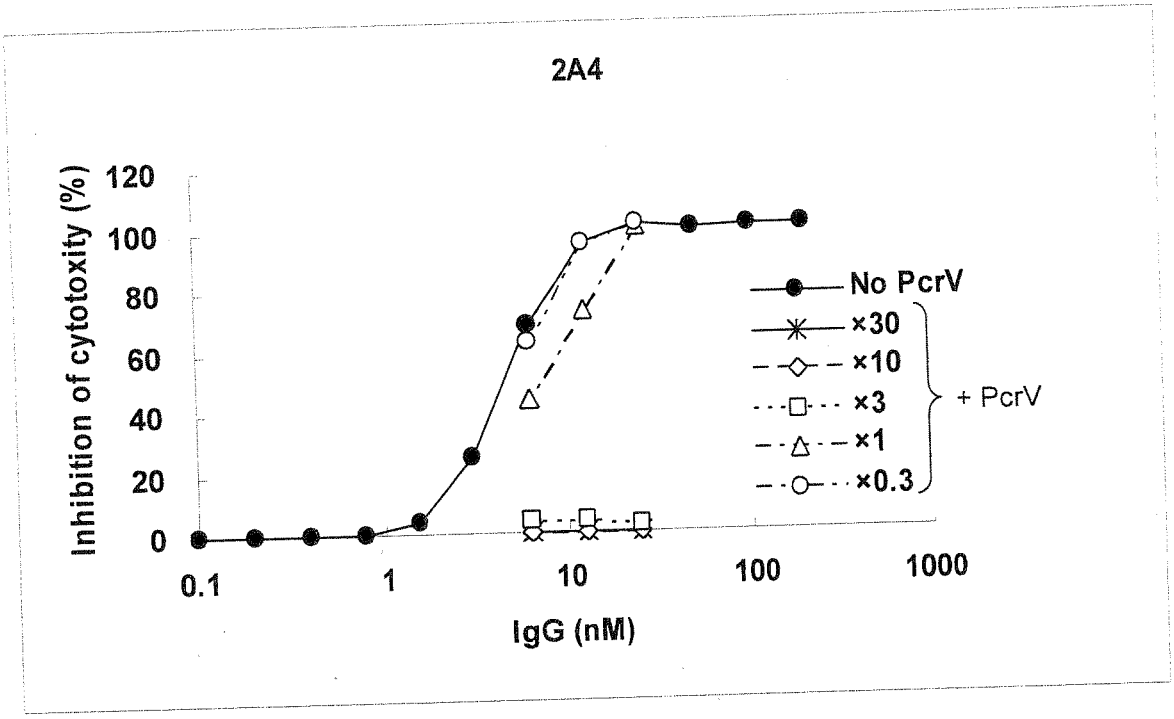

Full-length PcrV (1-294)
M.W. (kDa)
CBB
M166
1F3
2A4
9D12
12H9
110
80
60
50
40
30
20
Truncated PcrV (136-233)
M.W. (kDa)
CBB
M166
1F3
2A4
9D12
12H9
110
80
60
50
40
30
20

Figure 8

Suppression of neutralizing activity with full-length PcrV





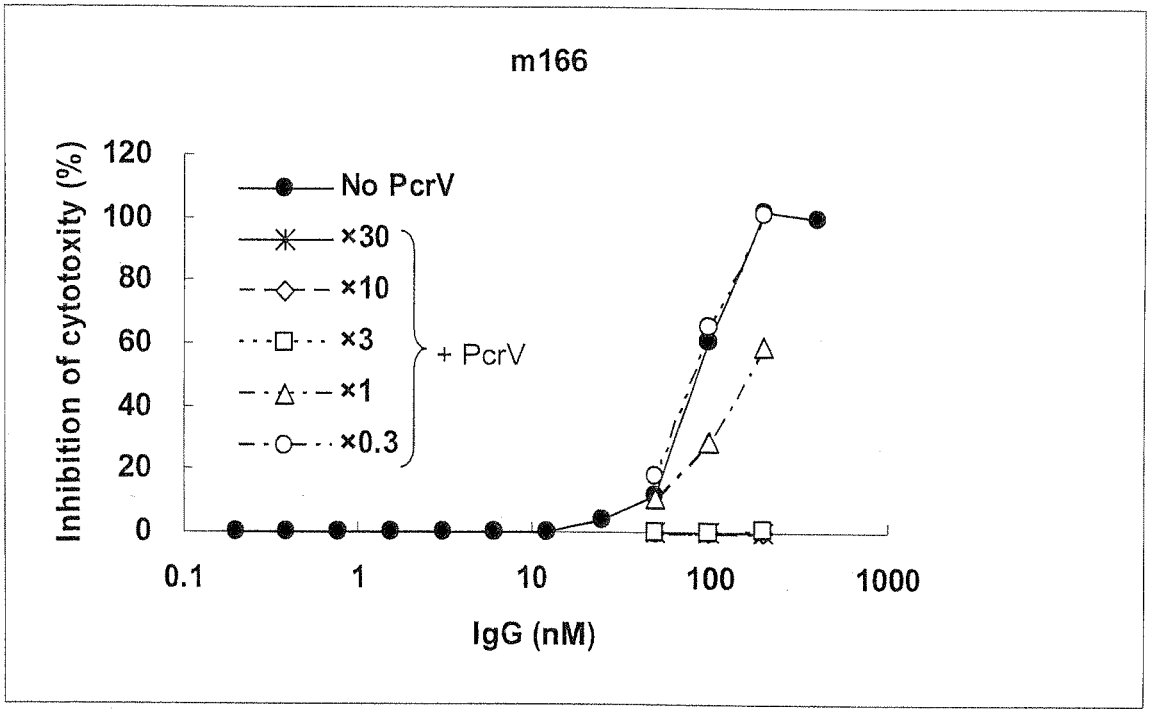
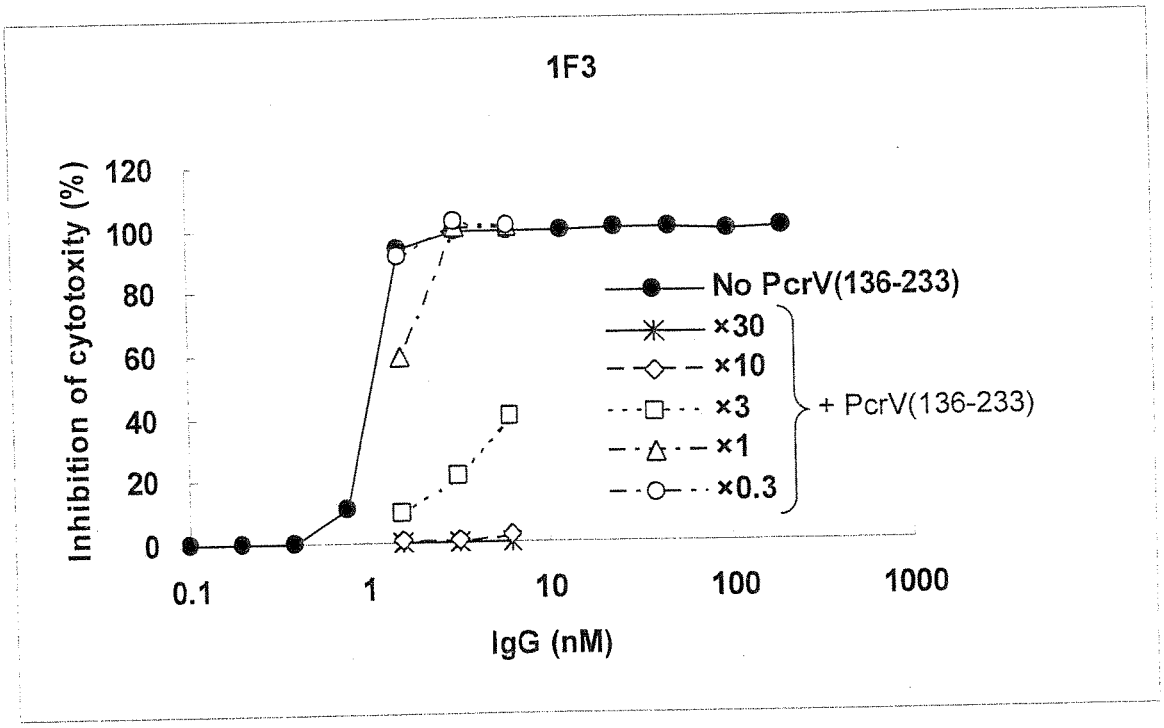
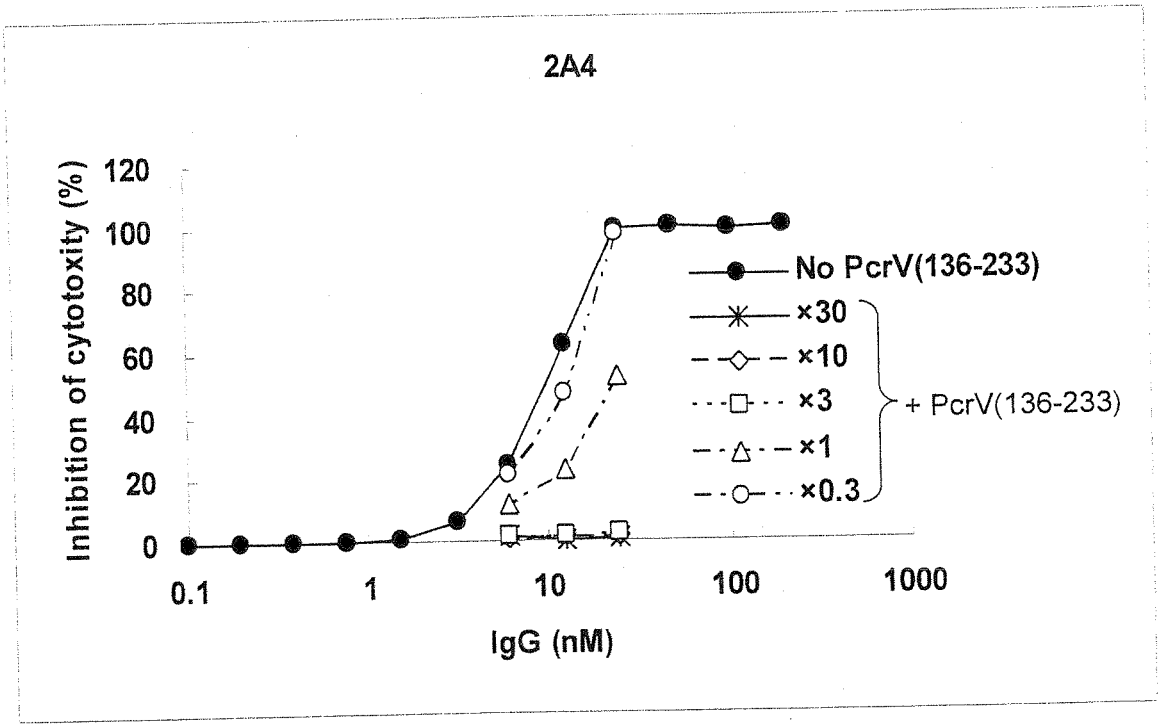

m166
Inhibition of cytotoxity (%)
120
100
80
60
40
20
0
No PcrV
×30
×10
×3
×1
×0.3
+ PcrV
0.1
1
10
100
1000
IgG (nM)

Figure 9

Suppression of neutralizing activity with truncated PcrV





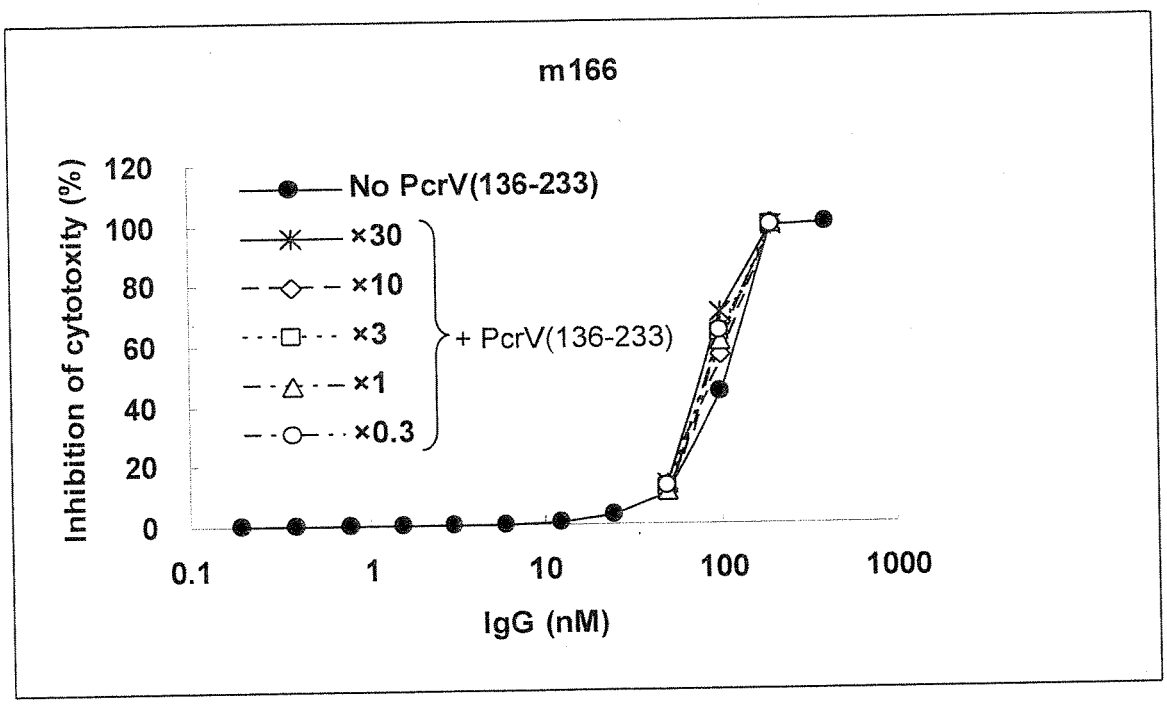

m166
Inhibition of cytotoxity (%)
120
100
80
60
40
20
0
No PcrV(136-233)
×30
×10
×3
×1
×0.3
+ PcrV(136-233)
0.1
1
10
100
1000
IgG (nM)

Figure 10

(SEQ ID NO: 11, 12)

Heavy Chain

QVQLQQPGAELVKPGASVKLSCKASGYSFTSYWMHWVKQRPGQGLEWIGEINPSN
GRTNYNEKFNTKATLTVDTSSSTAYMQLSSLTSEDSAVYYCVLYGNYVVYYTMDYW
GQGTSVTVSS

Light Chain

QIVLTQSPTIMSASLGEEITLTCSASTSVSYMEWYQQKSGTSPKILIYTTSKLASGVPS
RFSGSGSGTFYSLTISSVEAEDAADYYCHQWRNYPFTFGSGTKLEIKRAD

Figure 11

(SEQ ID NO: 13, 14)

Heavy Chain

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYNG
DTSYNPSLKSRISIARDTSKNQFFLQLNSVTTEDTATYSCAGSRNYYGAWFAYWGQG
TLVTVSA

Light Chain

DIVMTQSHKFMSTSIGDRVSINYKASQYVGTTVAWYQQKSGHSPKLLIYRASTRHTG
VPDRFTGSGSGTDFTLNISNVQSEDLADYFCQQYCSSPLTFGAGTYLEVKRAD

SEQ

SEQUENCE LISTING

<110> SHIONOGI&CO.,LTD.

<120> antibodies to PcrV

<130> 08P00114

<160> 26

<170> PatentIn version 3.1

<210> 1
<211> 294
<212> PRT
<213> Pseudomonas aeruginosa

<400> 1

Met Glu Val Arg Asn Leu Asn Ala Ala Arg Glu Leu Phe Leu Asp Glu
1 5 10 15

Leu Leu Ala Ala Ser Ala Ala Pro Ala Ser Ala Glu Gln Glu Glu Leu
20 25 30

Leu Ala Leu Leu Arg Ser Glu Arg Ile Val Leu Ala His Ala Gly Gln
35 40 45

Pro Leu Ser Glu Ala Gln Val Leu Lys Ala Leu Ala Trp Leu Leu Ala
50 55 60

Ala Asn Pro Ser Ala Pro Pro Gly Gln Gly Leu Glu Val Leu Arg Glu
65 70 75 80

Val Leu Gln Ala Arg Arg Gln Pro Gly Ala Gln Trp Asp Leu Arg Glu
85 90 95

Phe Leu Val Ser Ala Tyr Phe Ser Leu His Gly Arg Leu Asp Glu Asp
100 105 110

Val Ile Gly Val Tyr Lys Asp Val Leu Gln Thr Gln Asp Gly Lys Arg
115 120 125

Lys Ala Leu Leu Asp Glu Leu Lys Ala Leu Thr Ala Glu Leu Lys Val
130 135 140

Tyr Ser Val Ile Gln Ser Gln Ile Asn Ala Ala Leu Ser Ala Lys Gln
145 150 155 160

Gly Ile Arg Ile Asp Ala Gly Gly Ile Asp Leu Val Asp Pro Thr Leu
165 170 175

Tyr Gly Tyr Ala Val Gly Asp Pro Arg Trp Lys Asp Ser Pro Glu Tyr
180 185 190

Ala Leu Leu Ser Asn Leu Asp Thr Phe Ser Gly Lys Leu Ser Ile Lys
195 200 205

Asp Phe Leu Ser Gly Ser Pro Lys Gln Ser Gly Glu Leu Lys Gly Leu
210 215 220

SEQ

Ser Asp Glu Tyr Pro Phe Glu Lys Asp Asn Asn Pro Val Gly Asn Phe
225 230 235 240

Ala Thr Thr Val Ser Asp Arg Ser Arg Pro Leu Asn Asp Lys Val Asn
245 250 255

Glu Lys Thr Thr Leu Leu Asn Asp Thr Ser Ser Arg Tyr Asn Ser Ala
260 265 270

Val Glu Ala Leu Asn Arg Phe Ile Gln Lys Tyr Asp Ser Val Leu Arg
275 280 285

Asp Ile Leu Ser Ala Ile
290

<210> 2
<211> 885
<212> DNA
<213> Pseudomonas aeruginosa

<400> 2
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tcggcggcgc ctgccagtgc cgagcaggag gaactgctgg ccctgttgcg cagcgagcgg 120

atcgtgctgg cccacgccgg ccagccgctg agcgaggcgc aagtgctcaa ggcgctcgcc 180

tggttgctcg cggccaatcc gtccgcgcct ccggggcagg gcctcgaggt actccgcgaa 240

gtcctgcagg cacgtcggca gcccggtgcg cagtgggatc tgcgcgagtt cctggtgtcg 300

gcctatttca gcctgcacgg gcgtctcgac gaggatgtca tcggtgtcta caaggatgtc 360

ctgcagaccc aggacggcaa gcgcaaggcg ctgctcgacg agctcaaggc gctgaccgcg 420

gagttgaagg tctacagcgt gatccagtcg cagatcaacg ccgcgctgtc ggccaagcag 480

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gtcggcgatc ccaggtggaa ggacagcccc gagtatgcgc tgctgagcaa tctggatacc 600

ttcagcggca agctgtcgat caaggatttt ctcagcggct cgccgaagca gagcggggag 660

ctcaagggcc tcagcgatga gtaccccttc gagaaggaca acaacccggt cggcaatttc 720

gccaccacgg tgagcgaccg ctcgcgtccg ctgaacgaca aggtcaacga gaagaccacc 780

ctgctcaacg acaccagctc ccgctacaac tcggcggtcg aggcgctcaa ccgcttcatc 840

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<400> 3
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<211> 33
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<213> Artificial

<220>
<223> primer

<400> 4

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<400> 5
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<400> 6
gttaagcttc tcgaagggta ctc 23

<210> 7
<211> 24
<212> DNA
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<220>
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<400> 7
tagagtcacc gaggagccag ttgt 24

<210> 8
<211> 24
<212> DNA
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<220>
<223> primer

<400> 8
tccagagttc caagtcacag tcac 24

<210> 9
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<400> 9
aggggccagt ggatagaccg atggggctgt 30

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<220>
<223> primer

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<212> PRT
<213> Artificial

<220>
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<400> 11

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Asn Thr Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Val Leu Tyr Gly Asn Tyr Val Val Tyr Tyr Thr Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 12
<211> 109
<212> PRT
<213> Artificial

<220>
<223> VL of Antibody 1F3

<400> 12

Gln Ile Val Leu Thr Gln Ser Pro Thr Ile Met Ser Ala Ser Leu Gly
1 5 10 15

Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser Thr Ser Val Ser Tyr Met
20 25 30

Glu Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Ile Leu Ile Tyr
35 40 45

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

Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp Arg Asn Tyr Pro Phe Thr
85 90 95

SEQ

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg Ala Asp
100 105

<210> 13
<211> 120
<212> PRT
<213> Artificial

<220>
<223> VH of Antibody 2A4

<400> 13

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Thr Tyr Asn Gly Asp Thr Ser Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Ala Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Ser Cys
85 90 95

Ala Gly Ser Arg Asn Tyr Tyr Gly Ala Trp Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ala
115 120

<210> 14
<211> 110
<212> PRT
<213> Artificial

<220>
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<400> 14

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1 5 10 15

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

Val Ala Trp Tyr Gln Gln Lys Ser Gly His Ser Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile Ser Asn Val Gln Ser
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Cys Ser Ser Pro Leu
85 90 95

Thr Phe Gly Ala Gly Thr Tyr Leu Glu Val Lys Arg Ala Asp
100 105 110

<210> 15
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<212> PRT
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<220>
<223> CDR1 of 1F3 heavy chain

<400> 15

Ser Phe Thr Ser Tyr Trp Met His
1 5

<210> 16
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<220>
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<400> 16

Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe Asn Thr
1 5 10 15

<210> 17
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<400> 17

Tyr Gly Asn Tyr Val Val Tyr Tyr Thr Met Asp Tyr
1 5 10

<210> 18
<211> 10
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<220>
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<400> 18

Ser Ala Ser Thr Ser Val Ser Tyr Met Glu
1 5 10

<210> 19
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<400> 19

Thr Thr Ser Lys Leu Ala Ser
1 5

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His Gln Trp Arg Asn Tyr Pro Phe Thr
1 5

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<223> CDR1 of 2A4 heavy chain

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Ser Ile Thr Ser Asp Tyr Ala Trp Asn
1 5

<210> 22
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<400> 22

Tyr Ile Thr Tyr Asn Gly Asp Thr Ser Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

<210> 23
<211> 11
<212> PRT
<213> Artificial

<220>
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<400> 23

Ser Arg Asn Tyr Tyr Gly Ala Trp Phe Ala Tyr
1 5 10

<210> 24
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<212> PRT
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<220>
<223> CDR1 of 2A4 light chain

<400> 24

Lys Ala Ser Gln Tyr Val Gly Thr Thr Val Ala
1 5 10

<210> 25
<211> 7
<212> PRT
<213> Artificial

<220>
<223> CDR2 of 2A4 light chain

<400> 25

Arg Ala Ser Thr Arg His Thr
1 5

<210> 26
<211> 9
<212> PRT
<213> Artificial

<220>
<223> CDR3 of 2A4 light chain

<400> 26

Gln Gln Tyr Cys Ser Ser Pro Leu Thr
1 5