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SEQUENCE LISTING

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<120> Anti-tumor drug, medicament, composition, and use thereof

<130> BCT080084QT

<160> 23

<170> Patent In version 3.3

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Val Glu Leu Ala Ser Thr Trp Glu Val Gly Phe Pro Ala Glu Leu Tyr
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Hi s Leu Ala Leu Leu Trp Gl u Val Hi s Arg Gl y Pro Ala Arg Arg Ser
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Val Leu Ala Leu Thr Hi s Gl u Gl y Arg Phe Hi s Pro Gl y Leu Gl y Tyr
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Gl u Gl n Arg Tyr Hi s Ser Gl y Asp Val Arg Leu Asp Thr Val Gl y Ser
260 265 270

Asp Ala Tyr Arg Leu Ser Val Ser Arg Ala Leu Ser Ala Asp Gl n Gl y
275 280 285

Ser Tyr Arg Oys Ile Val Ser Gl u Trp Ile Ala Gl u Gl n Gl y Asn Trp
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Gl n Gl u Ile Gl n Gl u Lys Ala Val Gl u Val Ala Thr Val Val Ile Gl n
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Pro Ser Val Leu Arg Ala Ala Val Pro Lys Asn Val Ser Val Ala Gl u
325 330 335

Gl y Lys Gl u Leu Asp Leu Thr Oys Asn Ile Thr Thr Asp Arg Ala Asp
340 345 350

Asp Val Arg Pro Gl u Val Thr Trp Ser Phe Ser Arg Met Pro Asp Ser
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Thr Leu Pro Gl y Ser Arg Val Leu Ala Arg Leu Asp Arg Asp Ser Leu
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Val Hi s Ser Ser Pro Hi s Val Ala Leu Ser Hi s Val Asp Ala Arg Ser
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Tyr Hi s Leu Leu Val Arg Asp Val Ser Lys Gl u Asn Ser Gl y Tyr Tyr
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Tyr Oys Hi s Val Ser Leu Trp Ala Pro Gl y Hi s Asn Arg Ser Trp Hi s
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Lys Val Ala Gl u Ala Val Ser Ser Pro Ala Gl y Val Gl y Val Thr Trp
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Leu Gl u Pro Asp Tyr Gl n Val Tyr Leu Asn Ala Ser Lys Val Pro Gl y

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Asn Arg Arg Ser Asp Asn Val Val Thr Ser Gl u Leu Leu Al a Val Met
500 505 510

Asp Gl y Asp Trp Thr Leu Lys Tyr Gl y Gl u Arg Ser Lys Gl n Arg Al a
515 520 525

Gl n Asp Gl y Asp Phe Ile Phe Ser Lys Gl u His Thr Asp Thr Phe Asn
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Phe Arg Ile Gl n Arg Thr Thr Gl u Gl u Asp Arg Gl y Asn Tyr Tyr Cys
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Val Val Ser Al a Trp Thr Lys Gl n Arg Asn Asn Ser Trp Val Lys Ser
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Lys Asp Val Phe Ser Lys Pro Val Asn Ile Phe Trp Al a Leu Gl u Asp
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Ser Val Leu Val Val Lys Al a Arg Gl n Pro Lys Pro Phe Phe Al a Al a
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Gl y Asn Thr Phe Gl u Met Thr Cys Lys Val Ser Ser Lys Asn Ile Lys
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Ser Pro Arg Tyr Ser Val Leu Ile Met Al a Gl u Lys Pro Val Gl y Asp
625 630 635 640

Leu Ser Ser Pro Asn Gl u Thr Lys Tyr Ile Ile Ser Leu Asp Gl n Asp
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Ser Val Val Lys Leu Gl u Asn Trp Thr Asp Al a Ser Arg Val Asp Gl y
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Val Val Leu Gl u Lys Val Gl n Gl u Asp Gl u Phe Arg Tyr Arg Met Tyr
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Gl n Thr Gl n Val Ser Asp Al a Gl y Leu Tyr Arg Cys Met Val Thr Al a
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Trp Ser Pro Val Arg Gl y Ser Leu Trp Arg Gl u Al a Al a Thr Ser Leu
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Lys Leu Phe Cys Ile Ile Thr Val Glu Gly Ala Ala Leu Asp Pro Asp
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770 775 780

Asp Lys Ala Pro Val Leu Leu Ser Ser Leu Asp Arg Lys Gly Ile Val
785 790 795 800

Thr Thr Ser Arg Arg Asp Trp Lys Ser Asp Leu Ser Leu Glu Arg Val
805 810 815

Ser Val Leu Glu Phe Leu Leu Gln Val His Gly Ser Glu Asp Gln Asp
820 825 830

Phe Gly Asn Tyr Tyr Cys Ser Val Thr Pro Trp Val Lys Ser Pro Thr
835 840 845

Gly Ser Trp Gln Lys Glu Ala Glu Ile His Ser Lys Pro Val Phe Ile
850 855 860

Thr Val Lys Met Asp Val Leu Asn Ala Phe Lys Tyr Pro Leu Leu Ile
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Gly Val Gly Leu Ser Thr Val Ile Gly Leu Leu Ser Cys Leu Ile Gly
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Val Leu Glu Phe Leu Leu Gln Val His Gly Ser Glu Asp Gln Asp Phe
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Gly Asn Tyr Tyr Cys Ser Val Thr Pro Trp Val Lys Ser Pro Thr Gly
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g g n g a t g g t t c a c g t a n n g g n c a t c c c c t g a t a n n n g n t t t t c g c c t t t g a n n t g g a g n c 1020

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Ser	Pro	Asp	Leu	Gly	Thr	Asp	Asp	Asp	Asp	Lys	Met	Ala	Phe	Asp	Val
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Leu	Ser	Ser	Leu	Asp	Arg	Lys	Gly	Ile	Val	Thr	Thr	Ser	Arg	Arg	Asp
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Trp	Lys	Ser	Asp	Leu	Ser	Leu	Glu	Arg	Val	Ser	Val	Leu	Glu	Phe	Leu
				85					90					95	
Leu	Gln	Val	His	Gly	Ser	Glu	Asp	Gln	Asp	Phe	Gly	Asn	Tyr	Tyr	Cys
			100					105					110		
Ser	Val	Thr	Pro	Trp	Val	Lys	Ser	Pro	Thr	Gly	Ser	Trp	Gln	Lys	Glu
		115					120					125			
Ala	Glu	Ile	His	Ser	Lys	Pro	Val	Phe	Ile	Thr	Val	Lys	Met	Asp	Val
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145					150										

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			20					25					30		
Thr	Ser	Arg	Arg	Asp	Trp	Lys	Ser	Asp	Leu	Ser	Leu	Glu	Arg	Val	Ser
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Val	Leu	Glu	Phe	Leu	Leu	Gln	Val	His	Gly	Ser	Glu	Asp	Gln	Asp	Phe
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eof - seq1 . t x t

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Ser Trp Gln Lys Glu Ala Glu Ile His Ser
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Thr Ser Arg Arg Asp Trp Lys Ser Asp Leu Ser Leu Glu Arg Val Ser
35 40 45

Val Leu Glu Phe Leu Leu Gln Val His Gly Ser Glu Asp Gln Asp Phe
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Gly Asn Tyr Tyr Cys Ser Val Thr Pro Trp Val Lys Ser
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<211> 66
<212> PRT
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<400> 9

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Lys Ala Pro Val Leu Leu Ser Ser Leu Asp Arg Lys Gly Ile Val Thr
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Thr Ser Arg Arg Asp Trp Lys Ser Asp Leu Ser Leu Glu Arg Val Ser
35 40 45

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Gly Asn
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eof - seq1 . t x t

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Val Leu Glu
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Thr Ser Arg Arg Asp
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<211> 20

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<213> Homo sapi ens

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<211> 270

<212> DNA

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eol f - seq1 . t x t

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<210> 19
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<400> 19

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 gct cccgccg ggcgagcat g gggcgccct gg cct cgaggcc gct gct gct g gcgct cct gt 180
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eol f - seq1 . t xt

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eol f - seq1 . t x t

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eol f - seq l . t x t

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35 40 45

Ser Ser Phe Val Glu Leu Ala Ser Thr Trp Glu Val Gly Phe Pro Ala
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Gln Leu Tyr Gln Glu Arg Leu Gln Arg Gly Glu Ile Leu Leu Arg Arg
65 70 75 80

Thr Ala Asn Asp Ala Val Glu Leu His Ile Lys Asn Val Gln Pro Ser
85 90 95

Asp Gln Gly His Tyr Lys Cys Ser Thr Pro Ser Thr Asp Ala Thr Val
100 105 110

Gln Gly Asn Tyr Glu Asp Thr Val Gln Val Lys Val Leu Ala Asp Ser
115 120 125

Leu His Val Gly Pro Ser Ala Arg Pro Pro Pro Ser Leu Ser Leu Arg
130 135 140

Glu Gly Glu Pro Phe Glu Leu Arg Cys Thr Ala Ala Ser Ala Ser Pro
145 150 155 160

Leu His Thr His Leu Ala Leu Leu Trp Glu Val His Arg Gly Pro Ala
165 170 175

eol f - seq1 . t x t

Arg Arg Ser Val Leu Ala Leu Thr His Gly Arg Phe His Pro Gly
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195 200 205

Val Gly Ser Asp Ala Tyr Arg Leu Ser Val Ser Arg Ala Leu Ser Ala
210 215 220

Asp Gln Gly Ser Tyr Arg Cys Ile Val Ser Glu Trp Ile Ala Glu Gln
225 230 235 240

Gly Asn Trp Gln Glu Ile Gln Glu Lys Ala Val Glu Val Ala Thr Val
245 250 255

Val Ile Gln Pro Thr Val Leu Arg Ala Ala Val Pro Lys Asn Val Ser
260 265 270

Val Ala Glu Gly Lys Glu Leu Asp Leu Thr Cys Asn Ile Thr Thr Asp
275 280 285

Arg Ala Asp Asp Val Arg Pro Glu Val Thr Trp Ser Phe Ser Arg Met
290 295 300

Pro Asp Ser Thr Leu Pro Gly Ser Arg Val Leu Ala Arg Leu Asp Arg
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Asp Ser Leu Val His Ser Ser Pro His Val Ala Leu Ser His Val Asp
325 330 335

Ala Arg Ser Tyr His Leu Leu Val Arg Asp Val Ser Lys Glu Asn Ser
340 345 350

Gly Tyr Tyr Tyr Cys His Val Ser Leu Trp Ala Pro Gly His Asn Arg
355 360 365

Ser Trp His Lys Val Ala Glu Ala Val Ser Ser Pro Ala Gly Val Gly
370 375 380

Val Thr Trp Leu Glu Pro Asp Tyr Gln Val Tyr Leu Asn Ala Ser Lys
385 390 395 400

Val Pro Gly Phe Ala Asp Asp Pro Thr Glu Leu Ala Cys Gln Val Val
405 410 415

Asp Thr Lys Ser Gly Glu Ala Asn Val Arg Phe Thr Val Ser Trp Tyr
420 425 430

Tyr Arg Met Asn Arg Arg Ser Asp Asn Val Val Thr Ser Glu Leu Leu
435 440 445

Ala Val Met Asp Gly Asp Trp Thr Leu Lys Tyr Gly Glu Arg Ser Lys

eof - seq1 . t x t

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Thr Phe Asn Phe Arg Ile Gln Arg Thr Thr Glu Glu Asp Arg Gly Asn
485 490 495

Tyr Tyr Cys Val Val Ser Ala Trp Thr Lys Gln Arg Asn Asn Ser Trp
500 505 510

Val Lys Ser Lys Asp Val Phe Ser Lys Pro Val Asn Ile Phe Trp Ala
515 520 525

Leu Glu Asp Ser Val Leu Val Val Lys Ala Arg Gln Pro Lys Pro Phe
530 535 540

Phe Ala Ala Gly Asn Thr Phe Glu Met Thr Cys Lys Val Ser Ser Lys
545 550 555 560

Asn Ile Lys Ser Pro Arg Tyr Ser Val Leu Ile Met Ala Glu Lys Pro
565 570 575

Val Gly Asp Leu Ser Ser Pro Asn Glu Thr Lys Tyr Ile Ile Ser Leu
580 585 590

Asp Gln Asp Ser Val Val Lys Leu Glu Asn Trp Thr Asp Ala Ser Arg
595 600 605

Val Asp Gly Val Val Leu Glu Lys Val Gln Glu Asp Glu Phe Arg Tyr
610 615 620

Arg Met Tyr Gln Thr Gln Val Ser Asp Ala Gly Leu Tyr Arg Cys Met
625 630 635 640

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Thr Ser Leu Ser Asn Pro Ile Glu Ile Asp Phe Gln Thr Ser Gly Pro
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Ile Phe Asn Ala Ser Val His Ser Asp Thr Pro Ser Val Ile Arg Gly
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Asp Leu Ile Lys Leu Phe Cys Ile Ile Thr Val Glu Gly Ala Ala Leu
690 695 700

Asp Pro Asp Asp Met Ala Phe Asp Val Ser Trp Phe Ala Val His Ser
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Phe Gly Leu Asp Lys Ala Pro Val Leu Leu Ser Ser Leu Asp Arg Lys
725 730 735

eof - seq1 . t x t

Gly Ile Val Thr Thr Ser Arg Arg Asp Trp Lys Ser Asp Leu Ser Leu
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Glu Arg Val Ser Val Leu Glu Phe Leu Leu Gln Val His Gly Ser Glu
755 760 765

Asp Gln Asp Phe Gly Asn Tyr Tyr Cys Ser Val Thr Pro Trp Val Lys
770 775 780

Ser Pro Thr Gly Ser Trp Gln Lys Glu Ala Glu Ile His Ser Lys Pro
785 790 795 800

Val Phe Ile Thr Val Lys Met Asp Val Leu Asn Ala Phe Lys Tyr Pro
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Leu Leu Ile Gly Ile Gly Leu Ser Thr Val Ile Gly Leu Leu Ser Cys
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eol f - seq1 . t x t

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