SEQUENCE LISTING

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Cheng, Man
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<120> Methods and Compositions for Improving Efficiency of Nucleic Acids Amplification Reactions

<130> 002558-088710PC

<140> WO PCT/US10/20371
<141> 2010-01-07

<150> US 61/143,350
<151> 2009-01-08

<160> 47

<170> FastSEQ for Windows Version 4.0

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Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Lys Ile
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Ile Val Asp Ala Glu Lys Val Glu Lys Lys Phe Leu Gly Arg Pro Ile
65   70   75   80
Thr Val Trp Arg Leu Tyr Phe Glu His Pro Gln Asp Val Pro Thr Ile
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Arg Glu Lys Ile Arg Glu His Ser Ala Val Val Asp Ile Phe Glu Tyr
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Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
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Met Glu Gly Asp Glu Glu Leu Lys Leu Leu Ala Phe Ala Ile Ala Thr
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145   150   155   160
Ser Tyr Ala Asp Glu Glu Glu Ala Lys Val Ile Thr Trp Lys Lys Ile
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Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
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Arg Phe Leu Lys Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Ile Thr
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Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
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His Phe Asp Leu Tyr His Val Ile Arg Arg Thr Ile Asn Leu Pro Thr
260 265 270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
275 280 285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Thr Gly Glu Gly
290 295 300
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305 310 315 320
Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365
Pro Asn Lys Pro Asp Glu Arg Glu Tyr Glu Arg Arg Leu Arg Glu Ser
370 375 380
Tyr Ala Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385 390 395 400
Ile Val Ser Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
405 410 415
His Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Arg Asn Tyr
420 425 430
Asp Val Ala Pro Glu Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly
435 440 445
Phe Ile Pro Ser Leu Leu Lys Arg Leu Leu Asp Glu Arg Gln Lys Ile
450 455 460
Lys Thr Lys Met Lys Ala Ser Gln Asp Pro Ile Glu Lys Ile Met Leu
465 470 475 480
Asp Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Tyr Tyr Gly
485 490 495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
500 505 510
Ser Val Thr Ala Trp Gly Arg Glu Tyr Ile Glu Phe Val Trp Lys Glu
515 520 525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
530 535 540
Leu Tyr Ala Thr Ile Pro Gly Gly Lys Ser Glu Glu Ile Lys Lys Lys
545 550 555 560
Ala Leu Glu Phe Val Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu
565 570 575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
580 585 590
Lys Lys Tyr Ala Leu Ile Asp Glu Glu Gly Lys Ile Ile Thr Arg Gly
595 600 605
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
610 615 620
Ala Arg Val Leu Glu Ala Ile Leu Lys His Gly Asn Val Glu Glu Ala
625 630 635 640
Val Arg Ile Val Lys Glu Val Thr Gln Lys Leu Ser Lys Tyr Glu Ile
645 650 655
Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
660 665 670
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Arg Leu Ala
675 680 685
Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
690 695 700
Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705 710 715 720

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        755                 760                 765
Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
    770                 775                 780
Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785                 790                 795                 800
Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805                 810                 815
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binding domain

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polymerase with polymerase domain and heterologous
DNA binding domain and two point mutations E141A
and D143A to abolish 3'-5' exonuclease activity

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ggccgtggtg cggtaagcga aaaggacgcg ccgaaggagc tgctgcagat gctggagaag 180
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<220>
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<210> 6
<211> 397
<212> DNA
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<223> synthetic monoclonal antibody M13-vh heavy-chain
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aatggagagt tcaaggctag ggccacactg actgcagaca gatcctccag cacagcctac 240
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<210> 7
<211> 391
<212> DNA
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      variable region

<400> 7
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<210> 8
<211> 388
<212> DNA
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<220>
<223> synthetic monoclonal antibody M22-vh heavy-chain
      variable region

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<210> 9
<211> 388
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic monoclonal antibody M28-vh heavy-chain
variable region

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<212> DNA
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<220>
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variable region

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<210> 13
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variable region

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20 25 30
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35 40 45
Gly Gln Ile Tyr Pro Gly Asp Gly Gly Val Asn Tyr Asn Gly Glu Phe
50 55 60
Lys Ala Arg Ala Thr Leu Thr Ala Asp Arg Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Ser Ser Ser Tyr Tyr Gly Gly Ser Ser Val Ser Trp Leu Ala Tyr
100 105 110
Trp Gly Gln Gly Thr Leu Val Ser Val Ser Ala Ala Lys Thr Thr Pro
115 120 125
Pro Ser Val Tyr
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<211> 130
<212> PRT
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variable region

<400> 15
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1 5 10 15
Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Tyr Pro Gly Asp Gly Glu Thr Trp His Thr Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Glu Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Glu Arg Asp Arg Phe Asp Gly Ser Trp Phe Ala Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Pro Pro Ser
115 120 125
Val Tyr
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<211> 129
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35 40 45
Gly Arg Ile Asp Pro Tyr Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60
Ser Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
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100 105 110
Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
115 120 125
Tyr

<210> 17
<211> 129
<212> PRT
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35 40 45
Gly Arg Ile Asp Pro Tyr Asp Ser Asp Thr His Tyr Asn Gln Lys Phe
50 55 60
Ser Asp Lys Ala Ile Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
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100 105 110
Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
115 120 125
Tyr

<210> 18
<211> 121
<212> PRT
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20 25 30
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35 40 45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys Phe Gln Gly
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Ser His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110
Arg Ala Asp Ala Ala Pro Thr Val Ser
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variable region

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20 25 30
Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45
Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
50 55 60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Asn Ile His
65 70 75 80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr His Cys Gln Gln Ser Asn
85 90 95
Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110
Ala Asp Ala Ala Pro Thr Val Ser
115 120

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variable region

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20 25 30
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35 40 45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys Ser Gln Ser
85 90 95
Thr His Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110
Arg Ala Asp Ala Ala Pro Thr Val Ser
115 120

<210> 21
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<220>
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variable region

<400> 21
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20 25 30
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35 40 45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Phe Cys Ser Gln Ser
85 90 95
Thr His Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110
Arg Ala Asp Ala Ala Pro Thr Val Ser
115 120

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polyhistidine tag, six adjacent histidines

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His His His His His His
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