SEQUENCE LISTING

<110> Abbott Biotechnology Ltd. et al.

<120> Improved High Concentration Anti-TNF-alpha Antibody Liquid Formulation

<130> 117813-01020

<140> Concurrently filed herewith
<141> 2011-11-11

<150> US 61/412728
<151> 2010-11-11

<150> US 61/413960
<151> 2010-11-15

<160> 53

<170> PatentIn Ver. 2.0

<210> 1
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<212> PRT
<213> Artificial Sequence

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

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<223> human antibody

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20   25   30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

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

<210> 3
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<223> human antibody

<220>
<221> VARIANT
<222> (9)
<223> Xaa = Thr or Ala

<400> 3
Gln Arg Tyr Asn Arg Ala Pro Tyr Xaa
1 5

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<220>
<221> VARIANT
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<210> 5
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Ala Ala Ser Thr Leu Gln Ser
1 5

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<400> 6
Ala Ile Thr Trp Asn Ser Gly His Ile Asp Tyr Ala Asp Ser Val Glu
 1   5   10   15
Gly

<210> 7
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<223> human antibody

<400> 7
Arg Ala Ser Gln Gly Ile Arg Asn Tyr Leu Ala
 1   5   10

<210> 8
<211> 5
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<400> 8
Asp Tyr Ala Met His
 1   5

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<220>
<223> 2SD4 light chain variable region

<400> 9
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1   5   10   15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Tyr
                85   90   95
Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105

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

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Gln Lys Tyr Asn Ser Ala Pro Tyr Ala
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<223> EP B12 light chain variable region CDR3

<400> 12
Gln Lys Tyr Asn Arg Ala Pro Tyr Ala
 1   5

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<400> 13

Gln Lys Tyr Gln Arg Ala Pro Tyr Thr
1 5

<210> 14
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<220>
<223> VL100A9 light chain variable region CDR3

<400> 14
Gln Lys Tyr Ser Ser Ala Pro Tyr Thr
1 5

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<400> 15
Gln Lys Tyr Asn Ser Ala Pro Tyr Thr
1 5

<210> 16
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<220>
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<400> 16
Gln Lys Tyr Asn Arg Ala Pro Tyr Thr
1 5

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<400> 17
Gln Lys Tyr Asn Ser Ala Pro Tyr Tyr
1 5

<210> 18
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<223> VLLOG7 light chain variable region CDR3

<400> 18
Gln Lys Tyr Asn Ser Ala Pro Tyr Asn
1 5

<210> 19
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<223> VLLOG9 light chain variable region CDR3

<400> 19
Gln Lys Tyr Thr Ser Ala Pro Tyr Thr
1 5

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<400> 20
Gln Lys Tyr Asn Arg Ala Pro Tyr Asn
1 5

<210> 21
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<223> VLLOH10 light chain variable region CDR3

<400> 21
Gln Lys Tyr Asn Ser Ala Ala Tyr Ser
1 5

<210> 22
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<400> 22
Gln Gln Tyr Asn Ser Ala Pro Asp Thr
1 5

<210> 23
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<223> VL1C1 light chain variable region CDR3

<400> 23
Gln Lys Tyr Asn Ser Asp Pro Tyr Thr
 1   5

<210> 24
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<223> VL0.1F4 light chain variable region CDR3

<400> 24
Gln Lys Tyr Ile Ser Ala Pro Tyr Thr
 1   5

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<400> 25
Gln Lys Tyr Asn Arg Pro Pro Tyr Thr
 1   5

<210> 26
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<223> LOE7.A light chain variable region CDR3

<400> 26
Gln Arg Tyr Asn Arg Ala Pro Tyr Ala
 1   5

<210> 27
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<400> 27
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asn
 1   5   10

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<400> 28
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Lys
 1   5   10

<210> 29
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<400> 29
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Tyr
 1   5   10

<210> 30
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<400> 30
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu Asp Asp
 1   5   10

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<223> VH1B12 heavy chain variable region CDR3

<400> 31
Ala Ser Tyr Leu Ser Thr Ser Phe Ser Leu Asp Tyr
 1   5   10

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<400> 32
Ala Ser Tyr Leu Ser Thr Ser Ser Ser Leu His Tyr
 1   5   10

<210> 33
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<400> 33
Ala Ser Phe Leu Ser Thr Ser Ser Ser Leu Glu Tyr
 1   5   10

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<400> 34
Ala Ser Tyr Leu Ser Thr Ala Ser Ser Leu Glu Tyr
 1   5   10

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<400> 35
Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Asn
 1   5   10

<210> 36
<211> 321
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<400> 36
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atcacttgtc gggcaagtca gggcatcaga aattacttag cctggtatca gcaaaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 180
cggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctacagcct 240
gaagatgttg caacttatta ctgtcaaagg tataaccgtg caccgtatac ttttggccag 300
gggaccaagg tggaaatcaa a   321

<210> 37
<211> 363
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<400> 37
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ccggcaggtc cctgagactc 60
tcctgtgcgg cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggaatg ggtctcagct atcacttgga atagtggtca catagactat 180
gcggactctg tggagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggat acggccgtat attactgtgc gaaagtctcg 300
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agt 363

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<400> 38
His Gly Ser His Asp Asn
1 5

<210> 39
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<400> 39
Gln Ser Tyr Asp Arg Tyr Thr His Pro Ala Leu Leu
1 5 10

<210> 40
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<400> 40
Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 41
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<400> 41
Tyr Asn Asp Gln Arg Pro Ser
1 5

<210> 42
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<400> 42
Phe Thr Phe Ser Ser Tyr Gly Met His
1 5

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<400> 43
Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn Thr Val Lys
1 5 10

<210> 44
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<400> 44
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ala Phe Ile Arg Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Lys Thr His Gly Ser His Asp Asn Trp Gly Gln Gly Thr Met Val Thr
100 105 110

Val Ser Ser
115

<210> 45
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<400> 45
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ser Asn
20 25 30

Thr Val Lys Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Tyr Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

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Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Tyr Thr
                 85                  90                  95

His Pro Ala Leu Leu Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110


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<400> 46
Ser Ile His Asn Arg Gly Thr Ile Phe Tyr Leu Asp Ser Val Lys Gly
 1               5                  10                  15


<210> 47
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<212> PRT
<213> Homo Sapiens

<400> 47
Gly Arg Ser Asn Ser Tyr Ala Met Asp Tyr
 1               5                  10


<210> 48
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<400> 48
Arg Ser Thr Gln Thr Leu Val His Arg Asn Gly Asp Thr Tyr Leu Glu
 1               5                  10                  15


<210> 49
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<400> 49
Lys Val Ser Asn Arg Phe Ser
 1               5


<210> 50
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<400> 50
Phe Gln Gly Ser His Val Pro Tyr Thr
 1               5


<210> 51
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1 5 10 15 20

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
25 30

<210> 52
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Trp Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 53
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<400> 53
Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu
1 5 10 15 20

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
25 30