

-continued

Val Val Thr Val Thr Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
 215 220 225

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
 230 235 240

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
 245 250 255

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 260 265 270

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 275 280 285

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
 290 295 300

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 305 310 315

Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
 320 325 330

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 335 340 345

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 350 355 360

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 365 370 375

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 380 385 390

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 395 400 405

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
 410 415 420

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 425 430 435

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 440 445 450

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 455 460 465

Ser Pro Gly Lys
 469

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 214 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Asp Val Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu
 1 5 10 15

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

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

Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser
 50 55 60

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

-continued

Ser Asn Leu Asp Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln
 80 85 90

Gly Asn Thr Leu Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu
 95 1 00 1 05

Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 140 145 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
 155 160 165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
 170 175 180

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
 185 190 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
 200 205 210

Arg Gly Glu Cys
 214

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr
 1 5 10 15

Gly Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
 20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45

Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
 50 55 60

Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser
 65 70 75

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
 80 85 90

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
 95 1 00 1 05

Tyr Cys Gln Gln Gly Asn Thr Leu Pro Pro Thr Phe Gly Gln Gly
 110 115 120

Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
 125 130 135

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 140 145 150

Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
 155 160 165

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 170 175 180

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 185 190 195

-continued

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 200 205 210
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
 215 220 225
 Lys Ser Phe Asn Arg Gly Glu Cys
 230 233

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Thr
 20 25 30
 Gly Tyr Thr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 35 40 45
 Glu Trp Val Ala Leu Ile Asn Pro Tyr Lys Gly Val Thr Thr Tyr
 50 55 60
 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser
 65 70 75
 Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 80 85 90
 Thr Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser
 95 1 00 1 05
 Asp Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val
 110 115 120
 Ser Ser
 122

We claim:

1. A humanized antibody variable domain comprising non-human Complementarity Determining Region (CDR) amino acid residues which bind an antigen incorporated into a human antibody variable domain, and further comprising a Framework Region (FR) amino acid substitution at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 36H, 39H, 43H, 45H, 69H, 70H, 74H, and 92H, utilizing the numbering system set forth in Kabat.
2. The humanized variable domain of claim 1 wherein the substituted residue is the residue found at the corresponding location of the non-human antibody from which the non-human CDR amino acid residues are obtained.
3. The humanized variable domain of claim 1 wherein no human Framework Region (FR) residue other than those set forth in the group has been substituted.
4. The humanized variable domain of claim 1 wherein the human antibody variable domain is a consensus human variable domain.
5. The humanized variable domain of claim 1 wherein the residue at site 4L has been substituted.
6. The humanized variable domain of claim 1 wherein the residue at site 38L has been substituted.
7. The humanized variable domain of claim 1 wherein the residue at site 43L has been substituted.

8. The humanized variable domain of claim 1 wherein the residue at site 44L has been substituted.
9. The humanized variable domain of claim 1 wherein the residue at site 58L has been substituted.
10. The humanized variable domain of claim 1 wherein the residue at site 62L has been substituted.
11. The humanized variable domain of claim 1 wherein the residue at site 65L has been substituted.
12. The humanized variable domain of claim 1 wherein the residue at site 66L has been substituted.
13. The humanized variable domain of claim 1 wherein the residue at site 67L has been substituted.
14. The humanized variable domain of claim 1 wherein the residue at site 68L has been substituted.
15. The humanized variable domain of claim 1 wherein the residue at site 69L has been substituted.
16. The humanized variable domain of claim 1 wherein the residue at site 73L has been substituted.
17. The humanized variable domain of claim 1 wherein the residue at site 85L has been substituted.
18. The humanized variable domain of claim 1 wherein the residue at site 98L has been substituted.
19. The humanized variable domain of claim 1 wherein the residue at site 2H has been substituted.
20. The humanized variable domain of claim 1 wherein the residue at site 4H has been substituted.

21. The humanized variable domain of claim 1 wherein the residue at site 36H has been substituted.
22. The humanized variable domain of claim 1 wherein the residue at site 39H has been substituted.
23. The humanized variable domain of claim 1 wherein the residue at site 43H has been substituted.
24. The humanized variable domain of claim 1 wherein the residue at site 45H has been substituted.
25. The humanized variable domain of claim 1 wherein the residue at site 69H has been substituted.
26. The humanized variable domain of claim 1 wherein the residue at site 70H has been substituted.
27. The humanized variable domain of claim 1 wherein the residue at site 74H has been substituted.
28. The humanized variable domain of claim 1 wherein the residue at site 92H has been substituted.
29. An antibody comprising the humanized variable domain of claim 1.
30. An antibody which binds p185^{HER2} and comprises a humanized antibody variable domain, wherein the humanized antibody variable domain comprises non-human Complementarity Determining Region (CDR) amino acid residues which bind p185^{HER2} incorporated into a human antibody variable domain, and further comprises a Framework Region (FR) amino acid substitution at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 46L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 36H, 39H, 43H, 45H, 69H, 70H, 74H, 75H, 76H, 78H and 92H, utilizing the numbering system set forth in Kabat.
31. The antibody of claim 30 wherein the substituted residue is the residue found at the corresponding location of the non-human antibody from which the non-human CDR amino acid residues are obtained.
32. The antibody of claim 30 wherein no human Framework Region (FR) residue other than those set forth in the group has been substituted.
33. The antibody of claim 30 wherein the human antibody variable domain is a consensus human variable domain.
34. The antibody of claim 30 wherein the residue at site 4L has been substituted.
35. The antibody of claim 30 wherein the residue at site 38L has been substituted.
36. The antibody of claim 30 wherein the residue at site 43L has been substituted.
37. The antibody of claim 30 wherein the residue at site 44L has been substituted.
38. The antibody of claim 30 wherein the residue at site 46L has been substituted.
39. The antibody of claim 30 wherein the residue at site 58L has been substituted.
40. The antibody of claim 30 wherein the residue at site 62L has been substituted.
41. The antibody of claim 30 wherein the residue at site 65L has been substituted.
42. The antibody of claim 30 wherein the residue at site 66L has been substituted.
43. The antibody of claim 30 wherein the residue at site 67L has been substituted.
44. The antibody of claim 30 wherein the residue at site 68L has been substituted.
45. The antibody of claim 30 wherein the residue at site 69L has been substituted.
46. The antibody of claim 30 wherein the residue at site 73L has been substituted.
47. The antibody of claim 30 wherein the residue at site 85L has been substituted.
48. The antibody of claim 30 wherein the residue at site 98L has been substituted.

49. The antibody of claim 30 wherein the residue at site 2H has been substituted.
50. The antibody of claim 30 wherein the residue at site 4H has been substituted.
51. The antibody of claim 30 wherein the residue at site 36H has been substituted.
52. The antibody of claim 30 wherein the residue at site 39H has been substituted.
53. The antibody of claim 30 wherein the residue at site 43H has been substituted.
54. The antibody of claim 30 wherein the residue at site 45H has been substituted.
55. The antibody of claim 30 wherein the residue at site 69H has been substituted.
56. The antibody of claim 30 wherein the residue at site 70H has been substituted.
57. The antibody of claim 30 wherein the residue at site 74H has been substituted.
58. The antibody of claim 30 wherein the residue at site 75H has been substituted.
59. The antibody of claim 30 wherein the residue at site 76H has been substituted.
60. The antibody of claim 30 wherein the residue at site 78H has been substituted.
61. The antibody of claim 30 wherein the residue at site 92H has been substituted.
62. A humanized antibody variable domain comprising non-human Complementarity Determining Region (CDR) amino acid residues which bind an antigen incorporated into a consensus human variable domain, and further comprising an amino acid substitution at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 46L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 36H, 39H, 43H, 45H, 69H, 70H, 74H, 75H, 76H, 78H and 92H, utilizing the numbering system set forth in Kabat.
63. A humanized antibody which lacks immunogenicity compared to a non-human parent antibody upon repeated administration to a human patient in order to treat a chronic disease in that patient, wherein the humanized antibody comprises non-human Complementarity Determining Region (CDR) amino acid residues which bind an antigen incorporated into a human antibody variable domain, and further comprises an amino acid substitution at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 46L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 36H, 39H, 43H, 45H, 69H, 70H, 74H, 75H, 76H, 78H and 92H, utilizing the numbering system set forth in Kabat.
64. A humanized variant of a non-human parent antibody which binds an antigen and comprises a human variable domain comprising the most frequently occurring amino acid residues at each location in all human immunoglobulins of a human heavy chain immunoglobulin subgroup wherein amino acid residues forming Complementarity Determining Regions (CDRs) thereof comprise non-human antibody amino acid residues, and further comprises a Framework Region (FR) substitution where the substituted FR residue: (a) noncovalently binds antigen directly; (b) interacts with a CDR; (c) introduces a glycosylation site which affects the antigen binding or affinity of the antibody; or (d) participates in the V_L-V_H interface by affecting the proximity or orientation of the V_L and V_H regions with respect to one another.
65. The humanized variant of claim 63 which binds the antigen up to 3-fold more in the binding affinity than the parent antibody binds antigen.
66. A humanized antibody heavy chain variable domain comprising non-human Complementarity Determining

Region (CDR) amino acid residues which bind antigen incorporated into a human antibody variable domain, and further comprising a Framework Region (FR) amino acid substitution at a site selected from the group consisting of: 24H, 73H, 76H, 78H, and 93H, utilizing the numbering system set forth in Kabat.

67. The humanized variable domain of claim 66 wherein the substituted residue is the residue found at the corresponding location of the non-human antibody from which the non-human CDR amino acid residues are obtained.

68. The humanized variable domain of claim 66 wherein no human Framework Region (FR) residue other than those set forth in the group has been substituted.

69. The humanized variable domain of claim 66 wherein the human antibody variable domain is a consensus human variable domain.

70. The humanized variable domain of claim 66 wherein the residue at site 24H has been substituted.

71. The humanized variable domain of claim 66 wherein the residue at site 73H has been substituted.

72. The humanized variable domain of claim 66 wherein the residue at site 76H has been substituted.

73. The humanized variable domain of claim 66 wherein the residue at site 78H has been substituted.

74. The humanized variable domain of claim 66 wherein the residue at site 93H has been substituted.

75. The humanized variable domain of claim 66 which further comprises an amino acid substitution at site 71H.

76. The humanized variable domain of claim 66 which further comprises amino acid substitutions at sites 71H and 73H.

77. The humanized variable domain of claim 66 which further comprises amino acid substitutions at sites 71H, 73H and 78H.

78. An antibody comprising the humanized variable domain of claim 66.

79. A humanized variant of a non-human parent antibody which binds an antigen, wherein the humanized variant comprises Complementarity Determining Region (CDR) amino acid residues of the non-human parent antibody incorporated into a human antibody variable domain, and further comprises Framework Region (FR) substitutions at heavy chain positions 71H, 73H, 78H and 93H, utilizing the numbering system set forth in Kabat.

80. A humanized antibody variable domain comprising non-human Complementarity Determining Region (CDR) amino acid residues which bind an antigen incorporated into a human antibody variable domain, and further comprising a Framework Region (FR) amino acid substitution where the substituted FR residue:

(a) noncovalently binds antigen directly;

(b) interacts with a CDR; or

(c) participates in the V_L - V_H interface by affecting the proximity or orientation of the V_L and V_H regions with respect to one another, and wherein the substituted FR residue is at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 24H, 36H, 39H, 43H, 45H, 69H, 70H, 73H, 74H, 76H, 78H, 92H and 93H, utilizing the numbering system set forth in Kabat.

81. The humanized variable domain of claim 80 wherein the substituted residue is the residue found at the corresponding location of the non-human antibody from which the non-human CDR amino acid residues are obtained.

82. The humanized variable domain of claim 80 wherein no human Framework Region (FR) residue other than those set forth in the group has been substituted.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 6,407,213 B1
DATED : June 18, 2002
INVENTOR(S) : Carter et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 88,

Line 63, please delete "63" and insert therefor -- 79 --.

Signed and Sealed this

Third Day of December, 2002



JAMES E. ROGAN
Director of the United States Patent and Trademark Office

14042 U.S. PTO
112105

Approved for use through 07/31/2006. OMB 0651-0032
U.S. Patent and Trademark Office, U.S. DEPARTMENT OF COMMERCE

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UTILITY PATENT APPLICATION TRANSMITTAL <small>(Only for new nonprovisional applications under 37 C.F.R. 1.53(b))</small>	Attorney Docket No.	CARP0001-112
	First Inventor	John R. Adair et al.
	Title	HUMANISED ANTIBODIES
	Express Mail Label No.	EY146 601 565US

112105 U.S. PTO
 11/28/02
 112105

EVL46601565US

<p style="text-align: center;">APPLICATION ELEMENTS</p> <p><i>See MPEP chapter 600 concerning utility patent application contents.</i></p> <ol style="list-style-type: none"> <input checked="" type="checkbox"/> Fee Transmittal Form (e.g., PTO/SB/17) <i>(Submit an original and a duplicate for fee processing)</i> <input type="checkbox"/> Applicant claims small entity status. <i>See 37 CFR 1.27.</i> <input checked="" type="checkbox"/> Specification [Total Pages <u>70</u>] <i>Both the claims and abstract must start on a new page (For information on the preferred arrangement, see MPEP 608.01(a))</i> <input checked="" type="checkbox"/> Drawing(s) (35 U.S.C. 113) [Total Sheets <u>18</u>] Oath or Declaration [Total Sheets <u>03</u>] <ol style="list-style-type: none"> <input type="checkbox"/> Newly executed (original or copy) <input checked="" type="checkbox"/> Copy from a prior application (37 CFR 1.63 (d)) <i>(for a continuation/divisional with Box 18 completed)</i> <ol style="list-style-type: none"> <input type="checkbox"/> DELETION OF INVENTOR(S) <i>Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).</i> <input checked="" type="checkbox"/> Application Data Sheet. See 37 CFR 1.75 <input type="checkbox"/> CD-ROM or CD-R in duplicate, large table or Computer Program (Appendix) <ul style="list-style-type: none"> <input type="checkbox"/> Landscape Table on CD Nucleotide and/or Amino Acid Sequence Submission <i>(if applicable, items a.-c. are required)</i> <ol style="list-style-type: none"> Computer Readable Form (CRF) <ol style="list-style-type: none"> <input type="checkbox"/> Computer Readable Form (CRF) <input checked="" type="checkbox"/> Transfer Request (37 CFR 1.821(e)) Specification Sequence Listing on: <ol style="list-style-type: none"> <input type="checkbox"/> CD-ROM or CD-R (2 copies); or <input checked="" type="checkbox"/> Paper Copy <input checked="" type="checkbox"/> Statements verifying identity of above copies 	<p>ADDRESS TO: Commissioner for Patents P.O. Box 1450 Alexandria VA 22313-1450</p> <p style="text-align: center;">ACCOMPANYING APPLICATIONS PARTS</p> <ol style="list-style-type: none"> <input type="checkbox"/> Assignment Papers (cover sheet & document(s)) Name of Assignee _____ <input type="checkbox"/> 37 C.F.R. 3.73(b) Statement <input checked="" type="checkbox"/> Copy of Power of Attorney <i>(when there is an assignee)</i> <input type="checkbox"/> English Translation Document (if applicable) <input type="checkbox"/> Information Disclosure Statement (PTO/SB/08 or PTO-1449) <input type="checkbox"/> Copies of foreign patent documents, publications & other information <input checked="" type="checkbox"/> Preliminary Amendment and Request for Interference under 37 C.F.R. § 42.202 <input checked="" type="checkbox"/> Return Receipt Postcard (MPEP 503) <i>(Should be specifically itemized)</i> <input checked="" type="checkbox"/> Certified Copy of Priority Document Was Received in Parent Application Serial No. 07743,329, Filed September 17, 1991 (if foreign priority is claimed) <input type="checkbox"/> Nonpublication Request under 35 U.S.C. 122(b)(2)(B)(i). Applicant must attach form PTO/SB/35 or equivalent. <input checked="" type="checkbox"/> Other: Copy of Change of Correspondence Address - Application dated December 23, 2002, from Application Serial No. 08/846,658, Filed May 1, 1997.
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18. If a CONTINUING APPLICATION, check appropriate box, and supply the requisite information below and in the first sentence of the specification following the title, or in an Application Data Sheet under 37 CFR 1.76:

Continuation Divisional Continuation-in-part (CIP) of prior Application No. Serial No. 08/846,658, Filed May 1, 1997, which is a Continuation of Application Serial No. 08/293,589, Filed September 7, 1994, now U.S. Patent No. 5,859,205, Issued January 12, 1999, which is a File Wrapper Continuation of Application Serial No. 07743,329, Filed September 17, 1991, Abandoned, which is a 35 U.S.C. 371 National Stage Application of International Application No. PCT/GB90/02017, International Filing Date of December 21, 1990, which claims priority to Great Britain Application No. 8928874.0, Filed December 21, 1989, all applications incorporated by reference herein in their entireties.

Prior application information: Examiner Minh Tam B. Davis Art Unit: 1642

19. CORRESPONDENCE ADDRESS

The address associated with Customer Number **34132** OR Correspondence address below

Name			
Address			
City	State	Zip Code	
Country	Telephone	Email address	

Signature	<i>Doreen Yatro Trujillo</i>	Date	November 21, 2005
Name (Print/Type)	Doreen Yatro Trujillo	Registration No. (Attorney/Agent)	35,719

This collection of information is required by 37 CFR 1.53(b). The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.11 and 1.14. This collection is estimated to take 12 minutes to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Mail Stop Patent Application, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.
If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

112105

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

Effective on 12/08/2004.

Fees pursuant to the Consolidated Appropriations Act, 2005 (H.R. 4818).

FEE TRANSMITTAL for FY 2005

Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT (\$) **1,000.00**

Complete if Known

Application Number	Not Yet Assigned
Filing Date	November 21, 2005
First Named Inventor	John R. Adair et al.
Examiner Name	Not Yet Assigned
Art Unit	Not Yet Assigned
Attorney Docket No.	CARP0001-112

METHOD OF PAYMENT (check all that apply)

Check Credit Card Money Order None Other (please identify) : _____
 Deposit Account Deposit Account Number: **50-1275** Deposit Account Name: **Cozen O'Connor, P.C.**

For the above-identified deposit account, the Director is hereby authorized to: (check all that apply)

Charge fee(s) indicated below Charge fee(s) indicated below, except for the filing fee
 Charge any additional fee(s) or underpayments of fee(s) Credit any overpayments

Under 37 CFR 1.16 and 1.17
WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

FEE CALCULATION

1. BASIC FILING, SEARCH, AND EXAMINATION FEES

Application Type	FILING FEES		SEARCH FEES		EXAMINATION FEES		Fees Paid (\$)
	Fee (\$)	Small Entity Fee(\$)	Fee(\$)	Small Entity Fee(\$)	Fee(\$)	Small Entity Fee(\$)	
Utility	300	150	500	250	200	100	<u>\$1,000.00</u>
Design	200	100	100	50	130	65	—
Plant	200	100	300	150	160	80	—
Reissue	300	150	500	250	600	300	—
Provisional	200	100	0	0	0	0	—

2. EXCESS CLAIM FEES

Fee Description	Fee (\$)	Small Entity Fee (\$)
Each claim over 20 (including Reissues)	50	25
Each independent claim over 3 (including Reissues)	200	100
Multiple dependent claims	360	180
Total Claims	Extra Claims	Fee(\$)
<u>02</u> - <u>20</u> or HP= <u>00</u> x _____ = _____		
HP = highest number of total claims paid for, if greater than 20.		
Indep. Claims	Extra Claims	Fee(\$)
<u>01</u> - <u>03</u> or HP= <u>00</u> x _____ = _____		
HP = highest number of independent claims paid for, if greater than 3.		

3. APPLICATION SIZE FEE

If the specification and drawings exceed 100 sheets of paper (excluding electronically filed sequence or computer listings under 37 CFR 1.52(e)), the application size fee due is \$250 (\$125 for small entity) for each additional 50 sheets or fraction thereof. See 35 U.S.C. 41(a)(1)(G) and 37 CFR 1.16(s).

Total Sheets	Extra Sheets	Number of each additional 50 or fraction thereof	Fee (\$)	Fee Paid (\$)
_____	_____	_____ / 50 = _____ (round up to a whole number) x _____ = _____		

4. OTHER FEE(S)

Non-English Specification, \$130 fee (no small entity discount) _____
 Other (e.g., late filing surcharge): _____

SUBMITTED BY

Signature		Registration No. (Attorney/Agent)	35,719	Telephone	(215) 655-5593
Name (Print/Type)	Doreen Yatko Trujillo	Date	November 21, 2005		

This collection of information is required by 37 CFR 1.136. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 30 minutes to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

If you need assistance in completing this form, call 1-800-PTO-9199 (1-800-786-9199) and select option 2.

HUMANISED ANTIBODIESField of the Invention

The present invention relates to humanised antibody molecules, to processes for their production using recombinant DNA technology, and to their therapeutic uses.

The term "humanised antibody molecule" is used to describe a molecule having an antigen binding site derived from an immunoglobulin from a non-human species, and remaining immunoglobulin-derived parts of the molecule being derived from a human immunoglobulin. The antigen binding site typically comprises complementarity determining regions (CDRs) which determine the binding specificity of the antibody molecule and which are carried on appropriate framework regions in the variable domains. There are 3 CDRs (CDR1, CDR2 and CDR3) in each of the heavy and light chain variable domains.

In the description, reference is made to a number of publications by number. The publications are listed in numerical order at the end of the description.

Background of the Invention

Natural immunoglobulins have been known for many years, as have the various fragments thereof, such as the Fab, (Fab')₂ and Fc fragments, which can be derived by enzymatic cleavage. Natural immunoglobulins comprise a generally Y-shaped molecule having an antigen-binding site towards the end of each upper arm. The remainder of the structure, and particularly the stem of the Y, mediates the effector functions associated with immunoglobulins.

Natural immunoglobulins have been used in assay, diagnosis and, to a more limited extent, therapy. However, such uses, especially in therapy, were hindered until recently by the polyclonal nature of natural immunoglobulins. A significant step towards the realisation of the potential

- 2 -

of immunoglobulins as therapeutic agents was the discovery of procedures for the production of monoclonal antibodies (MAbs) of defined specificity (1).

However, most MAbs are produced by hybridomas which are fusions of rodent spleen cells with rodent myeloma cells. They are therefore essentially rodent proteins. There are very few reports of the production of human MAbs.

Since most available MAbs are of rodent origin, they are naturally antigenic in humans and thus can give rise to an undesirable immune response termed the HAMA (Human Anti-Mouse Antibody) response. Therefore, the use of rodent MAbs as therapeutic agents in humans is inherently limited by the fact that the human subject will mount an immunological response to the MAb and will either remove it entirely or at least reduce its effectiveness. In practice, MAbs of rodent origin may not be used in patients for more than one or a few treatments as a HAMA response soon develops rendering the MAb ineffective as well as giving rise to undesirable reactions. For instance, OKT3 a mouse IgG2a/k MAb which recognises an antigen in the T-cell receptor-CD3 complex has been approved for use in many countries throughout the world as an immunosuppressant in the treatment of acute allograft rejection [Chatenoud et al (2) and Jeffers et al (3)]. However, in view of the rodent nature of this and other such MAbs, a significant HAMA response which may include a major anti-idiotypic component, may build up on use. Clearly, it would be highly desirable to diminish or abolish this undesirable HAMA response and thus enlarge the areas of use of these very useful antibodies.

Proposals have therefore been made to render non-human MAbs less antigenic in humans. Such techniques can be generically termed "humanisation" techniques. These

- 3 -

techniques typically involve the use of recombinant DNA technology to manipulate DNA sequences encoding the polypeptide chains of the antibody molecule.

Early methods for humanising MABs involved production of chimeric antibodies in which an antigen binding site comprising the complete variable domains of one antibody is linked to constant domains derived from another antibody. Methods for carrying out such chimerisation procedures are described in EP0120694 (Celltech Limited), EP0125023 (Genentech Inc. and City of Hope), EP-A-0 171496 (Res. Dev. Corp. Japan), EP-A-0 173 494 (Stanford University), and WO 86/01533 (Celltech Limited). This latter Celltech application (WO 86/01533) discloses a process for preparing an antibody molecule having the variable domains from a mouse MAB and the constant domains from a human immunoglobulin. Such humanised chimeric antibodies, however, still contain a significant proportion of non-human amino acid sequence, i.e. the complete non-human variable domains, and thus may still elicit some HAMA response, particularly if administered over a prolonged period [Begent et al (ref. 4)].

In an alternative approach, described in EP-A-0239400 (Winter), the complementarity determining regions (CDRs) of a mouse MAB have been grafted onto the framework regions of the variable domains of a human immunoglobulin by site directed mutagenesis using long oligonucleotides. The present invention relates to humanised antibody molecules prepared according to this alternative approach, i.e. CDR-grafted humanised antibody molecules. Such CDR-grafted humanised antibodies are much less likely to give rise to a HAMA response than humanised chimeric antibodies in view of the much lower proportion of non-human amino acid sequence which they contain.

- 4 -

The earliest work on humanising MABs by CDR-grafting was carried out on MABs recognising synthetic antigens, such as the NP or NIP antigens. However, examples in which a mouse MAB recognising lysozyme and a rat MAB recognising an antigen on human T-cells were humanised by CDR-grafting have been described by Verhoeven et al (5) and Riechmann et al (6) respectively. The preparation of CDR-grafted antibody to the antigen on human T cells is also described in WO 89/07452 (Medical Research Council).

In Riechmann et al/Medical Research Council it was found that transfer of the CDR regions alone [as defined by Kabat refs. (7) and (8)] was not sufficient to provide satisfactory antigen binding activity in the CDR-grafted product. Riechmann et al found that it was necessary to convert a serine residue at position 27 of the human sequence to the corresponding rat phenylalanine residue to obtain a CDR-grafted product having improved antigen binding activity. This residue at position 27 of the heavy chain is within the structural loop adjacent to CDRI. A further construct which additionally contained a human serine to rat tyrosine change at position 30 of the heavy chain did not have a significantly altered binding activity over the humanised antibody with the serine to phenylalanine change at position 27 alone. These results indicate that changes to residues of the human sequence outside the CDR regions, in particular in the structural loop adjacent to CDRI, may be necessary to obtain effective antigen binding activity for CDR-grafted antibodies which recognise more complex antigens. Even so the binding affinity of the best CDR-grafted antibodies obtained was still significantly less than the original MAB.

Very recently Queen et al (9) have described the preparation of a humanised antibody that binds to the

- 5 -

interleukin 2 receptor, by combining the CDRs of a murine MAb (anti-Tac) with human immunoglobulin framework and constant regions. The human framework regions were chosen to maximise homology with the anti-Tac MAb sequence. In addition computer modelling was used to identify framework amino acid residues which were likely to interact with the CDRs or antigen, and mouse amino acids were used at these positions in the humanised antibody.

In WO 90/07861 Queen et al propose four criteria for designing humanised immunoglobulins. The first criterion is to use as the human acceptor the framework from a particular human immunoglobulin that is unusually homologous to the non-human donor immunoglobulin to be humanised, or to use a consensus framework from many human antibodies. The second criterion is to use the donor amino acid rather than the acceptor if the human acceptor residue is unusual and the donor residue is typical for human sequences at a specific residue of the framework. The third criterion is to use the donor framework amino acid residue rather than the acceptor at positions immediately adjacent to the CDRs. The fourth criterion is to use the donor amino acid residue at framework positions at which the amino acid is predicted to have a side chain atom within about 3 Å of the CDRs in a three-dimensional immunoglobulin model and to be capable of interacting with the antigen or with the CDRs of the humanised immunoglobulin. It is proposed that criteria two, three or four may be applied in addition or alternatively to criterion one, and may be applied singly or in any combination.

WO 90/07861 describes in detail the preparation of a single CDR-grafted humanised antibody, a humanised antibody having specificity for the p55 Tac protein of the

- 6 -

IL-2 receptor. The combination of all four criteria, as above, were employed in designing this humanised antibody, the variable region frameworks of the human antibody Eu (7) being used as acceptor. In the resultant humanised antibody the donor CDRs were as defined by Kabat et al (7 and 8) and in addition the mouse donor residues were used in place of the human acceptor residues, at positions 27, 30, 48, 66, 67, 89, 91, 94, 103, 104, 105 and 107 in the heavy chain and at positions 48, 60 and 63 in the light chain, of the variable region frameworks. The humanised anti-Tac antibody obtained is reported to have an affinity for p55 of $3 \times 10^9 \text{ M}^{-1}$, about one-third of that of the murine MAb.

We have further investigated the preparation of CDR-grafted humanised antibody molecules and have identified a hierarchy of positions within the framework of the variable regions (i.e. outside both the Kabat CDRs and structural loops of the variable regions) at which the amino acid identities of the residues are important for obtaining CDR-grafted products with satisfactory binding affinity. This has enabled us to establish a protocol for obtaining satisfactory CDR-grafted products which may be applied very widely irrespective of the level of homology between the donor immunoglobulin and acceptor framework. The set of residues which we have identified as being of critical importance does not coincide with the residues identified by Queen et al (9).

Summary of the Invention

Accordingly, in a first aspect the invention provides a CDR-grafted antibody heavy chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 6, 23 and/or 24, 48 and/or 49, 71 and/or 73, 75 and/or 76 and/or 78 and 88 and/or 91.

- 7 -

In preferred embodiments, the heavy chain framework comprises donor residues at positions 23, 24, 49, 71, 73 and 78 or at positions 23, 24 and 49. The residues at positions 71, 73 and 78 of the heavy chain framework are preferably either all acceptor or all donor residues.

In particularly preferred embodiments the heavy chain framework additionally comprises donor residues at one, some or all of positions 6, 37, 48 and 94. Also it is particularly preferred that residues at positions of the heavy chain framework which are commonly conserved across species, i.e. positions 2, 4, 25, 36, 39, 47, 93, 103, 104, 106 and 107, if not conserved between donor and acceptor, additionally comprise donor residues. Most preferably the heavy chain framework additionally comprises donor residues at positions 2, 4, 6, 25, 36, 37, 39, 47, 48, 93, 94, 103, 104, 106 and 107.

In addition the heavy chain framework optionally comprises donor residues at one, some or all of positions:

1 and 3,
72 and 76,
69 (if 48 is different between donor and acceptor),
38 and 46 (if 48 is the donor residue),
80 and 20 (if 69 is the donor residue),
67,
82 and 18 (if 67 is the donor residue),
91,
88, and
any one or more of 9, 11, 41, 87, 108, 110 and 112.

In the first and other aspects of the present invention reference is made to CDR-grafted antibody products comprising acceptor framework and donor antigen binding regions. It will be appreciated that the invention is widely applicable to the CDR-grafting of antibodies in

- 8 -

general. Thus, the donor and acceptor antibodies may be derived from animals of the same species and even same antibody class or sub-class. More usually, however, the donor and acceptor antibodies are derived from animals of different species. Typically the donor antibody is a non-human antibody, such as a rodent MAb, and the acceptor antibody is a human antibody.

In the first and other aspects of the present invention, the donor antigen binding region typically comprises at least one CDR from the donor antibody. Usually the donor antigen binding region comprises at least two and preferably all three CDRs of each of the heavy chain and/or light chain variable regions. The CDRs may comprise the Kabat CDRs, the structural loop CDRs or a composite of the Kabat and structural loop CDRs and any combination of any of these. Preferably, the antigen binding regions of the CDR-grafted heavy chain variable domain comprise CDRs corresponding to the Kabat CDRs at CDR2 (residues 50-65) and CDR3 (residues 95-100) and a composite of the Kabat and structural loop CDRs at CDR1 (residues 26-35).

The residue designations given above and elsewhere in the present application are numbered according to the Kabat numbering [refs. (7) and (8)]. Thus the residue designations do not always correspond directly with the linear numbering of the amino acid residues. The actual linear amino acid sequence may contain fewer or additional amino acids than in the strict Kabat numbering corresponding to a shortening of, or insertion into, a structural component, whether framework or CDR, of the basic variable domain structure. For example, the heavy chain variable region of the anti-Tac antibody described by Queen *et al* (9) contains a single amino acid insert (residue 52a) after residue 52 of CDR2 and a three amino

- 9 -

acid insert (residues 82a, 82b and 82c) after framework residue 82, in the Kabat numbering. The correct Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

The invention also provides in a second aspect a CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 1 and/or 3 and 46 and/or 47. Preferably the CDR grafted light chain of the second aspect comprises donor residues at positions 46 and/or 47.

The invention also provides in a third aspect a CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 46, 48, 58 and 71.

In a preferred embodiment of the third aspect, the framework comprises donor residues at all of positions 46, 48, 58 and 71.

In particularly preferred embodiments of the second and third aspects, the framework additionally comprises donor residues at positions 36, 44, 47, 85 and 87. Similarly positions of the light chain framework which are commonly conserved across species, i.e. positions 2, 4, 6, 35, 49, 62, 64-69, 98, 99, 101 and 102, if not conserved between donor and acceptor, additionally comprise donor residues. Most preferably the light chain framework additionally comprises donor residues at positions 2, 4, 6, 35, 36, 38, 44, 47, 49, 62, 64-69, 85, 87, 98, 99, 101 and 102.

- 10 -

In addition the framework of the second or third aspects optionally comprises donor residues at one, some or all of positions:

1 and 3,

63,

60 (if 60 and 54 are able to form a potential saltbridge),

70 (if 70 and 24 are able to form a potential saltbridge),

73 and 21 (if 47 is different between donor and acceptor),

37 and 45 (if 47 is different between donor and acceptor),

and

any one or more of 10, 12, 40, 80, 103 and 105.

Preferably, the antigen binding regions of the CDR-grafted light chain variable domain comprise CDRs corresponding to the Kabat CDRs at CDR1 (residue 24-34), CDR2 (residues 50-56) and CDR3 (residues 89-97).

The invention further provides in a fourth aspect a CDR-grafted antibody molecule comprising at least one CDR-grafted heavy chain and at least one CDR-grafted light chain according to the first and second or first and third aspects of the invention.

The humanised antibody molecules and chains of the present invention may comprise: a complete antibody molecule, having full length heavy and light chains; a fragment thereof, such as a Fab, (Fab')₂ or FV fragment; a light chain or heavy chain monomer or dimer; or a single chain antibody, e.g. a single chain FV in which heavy and light chain variable regions are joined by a peptide linker; or any other CDR-grafted molecule with the same specificity as the original donor antibody. Similarly the CDR-grafted heavy and light chain variable region may be combined with other antibody domains as appropriate.

- 11 -

Also the heavy or light chains or humanised antibody molecules of the present invention may have attached to them an effector or reporter molecule. For instance, it may have a macrocycle, for chelating a heavy metal atom, or a toxin, such as ricin, attached to it by a covalent bridging structure. Alternatively, the procedures of recombinant DNA technology may be used to produce an immunoglobulin molecule in which the Fc fragment or CH3 domain of a complete immunoglobulin molecule has been replaced by, or has attached thereto by peptide linkage, a functional non-immunoglobulin protein, such as an enzyme or toxin molecule.

Any appropriate acceptor variable region framework sequences may be used having regard to class/type of the donor antibody from which the antigen binding regions are derived. Preferably, the type of acceptor framework used is of the same/similar class/type as the donor antibody. Conveniently, the framework may be chosen to maximise/optimize homology with the donor antibody sequence particularly at positions close or adjacent to the CDRs. However, a high level of homology between donor and acceptor sequences is not important for application of the present invention. The present invention identifies a hierarchy of framework residue positions at which donor residues may be important or desirable for obtaining a CDR-grafted antibody product having satisfactory binding properties. The CDR-grafted products usually have binding affinities of at least 10^5 M^{-1} , preferably at least about 10^8 M^{-1} , or especially in the range 10^8 - 10^{12} M^{-1} . In principle, the present invention is applicable to any combination of donor and acceptor antibodies irrespective of the level of homology between their sequences. A protocol for applying the invention to any particular donor-acceptor antibody pair is given hereinafter. Examples of human frameworks which may be

- 12 -

used are KOL, NEWM, REI, EU, LAY and POM (refs. 4 and 5) and the like; for instance KOL and NEWM for the heavy chain and REI for the light chain and EU, LAY and POM for both the heavy chain and the light chain.

Also the constant region domains of the products of the invention may be selected having regard to the proposed function of the antibody in particular the effector functions which may be required. For example, the constant region domains may be human IgA, IgE, IgG or IgM domains. In particular, IgG human constant region domains may be used, especially of the IgG1 and IgG3 isotypes, when the humanised antibody molecule is intended for therapeutic uses, and antibody effector functions are required. Alternatively, IgG2 and IgG4 isotypes may be used when the humanised antibody molecule is intended for therapeutic purposes and antibody effector functions are not required, e.g. for simple blocking of lymphokine activity.

However, the remainder of the antibody molecules need not comprise only protein sequences from immunoglobulins. For instance, a gene may be constructed in which a DNA sequence encoding part of a human immunoglobulin chain is fused to a DNA sequence encoding the amino acid sequence of a functional polypeptide such as an effector or reporter molecule.

Preferably the CDR-grafted antibody heavy and light chain and antibody molecule products are produced by recombinant DNA technology.

Thus in further aspects the invention also includes DNA sequences coding for the CDR-grafted heavy and light chains, cloning and expression vectors containing the DNA sequences, host cells transformed with the DNA sequences

- 13 -

and processes for producing the CDR-grafted chains and antibody molecules comprising expressing the DNA sequences in the transformed host cells.

The general methods by which the vectors may be constructed, transfection methods and culture methods are well known per se and form no part of the invention. Such methods are shown, for instance, in references 10 and 11.

The DNA sequences which encode the donor amino acid sequence may be obtained by methods well known in the art. For example the donor coding sequences may be obtained by genomic cloning, or cDNA cloning from suitable hybridoma cell lines. Positive clones may be screened using appropriate probes for the heavy and light chain genes in question. Also PCR cloning may be used.

DNA coding for acceptor, e.g. human acceptor, sequences may be obtained in any appropriate way. For example DNA sequences coding for preferred human acceptor frameworks such as KOL, REI, EU and NEWM, are widely available to workers in the art.

The standard techniques of molecular biology may be used to prepare DNA sequences coding for the CDR-grafted products. Desired DNA sequences may be synthesised completely or in part using oligonucleotide synthesis techniques. Site-directed mutagenesis and polymerase chain reaction (PCR) techniques may be used as appropriate. For example oligonucleotide directed synthesis as described by Jones et al (ref. 20) may be used. Also oligonucleotide directed mutagenesis of a pre-existing variable region as, for example, described by Verhoeven et al (ref. 5) or Riechmann et al (ref. 6) may be used. Also enzymatic filling in of gapped

- 14 -

oligonucleotides using T₄ DNA polymerase as, for example, described by Queen et al (ref. 9) may be used.

Any suitable host cell/vector system may be used for expression of the DNA sequences coding for the CDR-grafted heavy and light chains. Bacterial e.g. E. coli, and other microbial systems may be used, in particular for expression of antibody fragments such as Fab and (Fab')₂ fragments, and especially FV fragments and single chain antibody fragments e.g. single chain FVs. Eucaryotic e.g. mammalian host cell expression systems may be used for production of larger CDR-grafted antibody products, including complete antibody molecules. Suitable mammalian host cells include CHO cells and myeloma or hybridoma cell lines.

Thus, in a further aspect the present invention provides a process for producing a CDR-grafted antibody product comprising:

- (a) producing in an expression vector an operon having a DNA sequence which encodes an antibody heavy chain according to the first aspect of the invention;

and/or

- (b) producing in an expression vector an operon having a DNA sequence which encodes a complementary antibody light chain according to the second or third aspect of the invention;
- (c) transfecting a host cell with the or each vector; and
- (d) culturing the transfected cell line to produce the CDR-grafted antibody product.

- 15 -

The CDR-grafted product may comprise only heavy or light chain derived polypeptide, in which case only a heavy chain or light chain polypeptide coding sequence is used to transfect the host cells.

For production of products comprising both heavy and light chains, the cell line may be transfected with two vectors, the first vector may contain an operon encoding a light chain-derived polypeptide and the second vector containing an operon encoding a heavy chain-derived polypeptide. Preferably, the vectors are identical, except in so far as the coding sequences and selectable markers are concerned, so as to ensure as far as possible that each polypeptide chain is equally expressed. Alternatively, a single vector may be used, the vector including the sequences encoding both light chain- and heavy chain-derived polypeptides.

The DNA in the coding sequences for the light and heavy chains may comprise cDNA or genomic DNA or both. However, it is preferred that the DNA sequence encoding the heavy or light chain comprises at least partially, genomic DNA, preferably a fusion of cDNA and genomic DNA.

The present invention is applicable to antibodies of any appropriate specificity. Advantageously, however, the invention may be applied to the humanisation of non-human antibodies which are used for in vivo therapy or diagnosis. Thus the antibodies may be site-specific antibodies such as tumour-specific or cell surface-specific antibodies, suitable for use in in vivo therapy or diagnosis, e.g. tumour imaging. Examples of cell surface-specific antibodies are anti-T cell antibodies, such as anti-CD3, and CD4 and adhesion molecules, such as CR3, ICAM and ELAM. The antibodies may have specificity for interleukins (including lymphokines, growth factors and stimulating factors), hormones and other biologically active compounds, and receptors for any of these. For

- 16 -

example, the antibodies may have specificity for any of the following: Interferons α , β , γ or δ , IL1, IL2, IL3, or IL4, etc., TNF, GCSF, GMCSF, EPO, hGH, or insulin, etc.

The the present invention also includes therapeutic and diagnostic compositions comprising the CDR-grafted products of the invention and uses of such compositions in therapy and diagnosis.

Accordingly in a further aspect the invention provides a therapeutic or diagnostic composition comprising a CDR-grafted antibody heavy or light chain or molecule according to previous aspects of the invention in combination with a pharmaceutically acceptable carrier, diluent or excipient.

Accordingly also the invention provides a method of therapy or diagnosis comprising administering an effective amount of a CDR-grafted antibody heavy or light chain or molecule according to previous aspects of the invention to a human or animal subject.

A preferred protocol for obtaining CDR-grafted antibody heavy and light chains in accordance with the present invention is set out below together with the rationale by which we have derived this protocol. This protocol and rationale are given without prejudice to the generality of the invention as hereinbefore described and defined.

Protocol

It is first of all necessary to sequence the DNA coding for the heavy and light chain variable regions of the donor antibody, to determine their amino acid sequences. It is also necessary to choose appropriate acceptor heavy and light chain variable regions, of known amino acid sequence. The CDR-grafted chain is then designed

- 17 -

starting from the basis of the acceptor sequence. It will be appreciated that in some cases the donor and acceptor amino acid residues may be identical at a particular position and thus no change of acceptor framework residue is required.

1. As a first step donor residues are substituted for acceptor residues in the CDRs. For this purpose the CDRs are preferably defined as follows:

Heavy chain - CDR1: residues 26-35
 - CDR2: residues 50-65
 - CDR3: residues 95-102
Light chain - CDR1: residues 24-34
 - CDR2: residues 50-56
 - CDR3: residues 89-97

The positions at which donor residues are to be substituted for acceptor in the framework are then chosen as follows, first of all with respect to the heavy chain and subsequently with respect to the light chain.

2. Heavy Chain

- 2.1 Choose donor residues at all of positions 23, 24, 49, 71, 73 and 78 of the heavy chain or all of positions 23, 24 and 49 (71, 73 and 78 are always either all donor or all acceptor).
- 2.2 Check that the following have the same amino acid in donor and acceptor sequences, and if not preferably choose the donor: 2, 4, 6, 25, 36, 37, 39, 47, 48, 93, 94, 103, 104, 106 and 107.

- 18 -

2.3 To further optimise affinity consider choosing donor residues at one, some or any of:

- i. 1, 3
- ii. 72, 76
- iii. If 48 is different between donor and acceptor sequences, consider 69
- iv. If at 48 the donor residue is chosen, consider 38 and 46
- v. If at 69 the donor residue is chosen, consider 80 and then 20
- vi. 67
- vii. If at 67 the donor residue is chosen, consider 82 and then 18
- viii. 91
- ix. 88
- x. 9, 11, 41, 87, 108, 110, 112

3. Light Chain

3.1 Choose donor at 46, 48, 58 and 71

3.2 Check that the following have the same amino acid in donor and acceptor sequences, if not preferably choose donor:

2, 4, 6, 35, 38, 44, 47, 49, 62, 64-69 inclusive, 85, 87, 98, 99, 101 and 102

3.3 To further optimise affinity consider choosing donor residues at one, some or any of:

- i. 1, 3
- ii. 63

- 19 -

- iii. 60, if 60 and 54 are able to form potential saltbridge
- iv. 70, if 70 and 24 are able to form potential saltbridge
- v. 73, and 21 if 47 is different between donor and acceptor
- vi. 37, and 45 if 47 is different between donor and acceptor
- vii. 10, 12, 40, 80, 103, 105

Rationale

In order to transfer the binding site of an antibody into a different acceptor framework, a number of factors need to be considered.

1. The extent of the CDRs
The CDRs (Complementary Determining Regions) were defined by Wu and Kabat (refs. 4 and 5) on the basis of an analysis of the variability of different regions of antibody variable regions. Three regions per domain were recognised. In the light chain the sequences are 24-34, 50-56, 89-97 (numbering according to Kabat (ref. 4), Eu Index) inclusive and in the heavy chain the sequences are 31-35, 50-65 and 95-102 inclusive.

When antibody structures became available it became apparent that these CDR regions corresponded in the main to loop regions which extended from the β barrel framework of the light and heavy variable domains. For H1 there was a discrepancy in that the loop was from 26 to 32 inclusive and for H2 the loop was 52 to 56 and for L2 from 50 to 53. However, with the exception of H1 the CDR regions encompassed the loop regions and extended into the β strand

- 20 -

frameworks. In H1 residue 26 tends to be a serine and 27 a phenylalanine or tyrosine, residue 29 is a phenylalanine in most cases. Residues 28 and 30 which are surface residues exposed to solvent might be involved in antigen-binding. A prudent definition of the H1 CDR therefore would include residues 26-35 to include both the loop region and the hypervariable residues 33-35.

It is of interest to note the example of Riechmann et al (ref. 3), who used the residue 31-35 choice for CDR-H1. In order to produce efficient antigen binding, residue 27 also needed to be recruited from the donor (rat) antibody.

2. Non-CDR residues which contribute to antigen binding

By examination of available X-ray structures we have identified a number of residues which may have an effect on net antigen binding and which can be demonstrated by experiment. These residues can be sub-divided into a number of groups.

2.1 Surface residues near CDR [all numbering as in Kabat et al (ref. 7)].

2.1.1. Heavy Chain - Key residues are 23, 71 and 73. Other residues which may contribute to a lesser extent are 1, 3 and 76. Finally 25 is usually conserved but the murine residue should be used if there is a difference.

2.1.2 Light Chain - Many residues close to the CDRs, e.g. 63, 65, 67 and 69 are conserved. If conserved none of the surface residues in the light chain are likely to have a major effect. However, if the murine residue at these positions

- 21 -

is unusual, then it would be of benefit to analyse the likely contribution more closely. Other residues which may also contribute to binding are 1 and 3, and also 60 and 70 if the residues at these positions and at 54 and 24 respectively are potentially able to form a salt bridge i.e. 60 + 54; 70 + 24.

2.2 Packing residues near the CDRs.

2.2.1. Heavy Chain - Key residues are 24, 49 and 78. Other key residues would be 36 if not a tryptophan, 94 if not an arginine, 104 and 106 if not glycines and 107 if not a threonine. Residues which may make a further contribution to stable packing of the heavy chain and hence improved affinity are 2, 4, 6, 38, 46, 67 and 69. 67 packs against the CDR residue 63 and this pair could be either both mouse or both human. Finally, residues which contribute to packing in this region but from a longer range are 18, 20, 80, 82 and 86. 82 packs against 67 and in turn 18 packs against 82. 80 packs against 69 and in turn 20 packs against 80. 86 forms an H bond network with 38 and 46. Many of the mouse-human differences appear minor e.g. Leu-Ile, but could have an minor impact on correct packing which could translate into altered positioning of the CDRs.

2.2.2. Light Chain - Key residues are 48, 58 and 71. Other key residues would be 6 if not glutamine, 35 if not tryptophan, 62 if not phenylalanine or tryosine, 64, 66, 68, 99 and 101 if not glycines and 102 if not a threonine. Residues which make a further contribution are 2, 4, 37, 45 and 47. Finally residues 73 and 21 and 19 may make long distance packing contributions of a minor nature.

- 22 -

- 2.3. Residues at the variable domain interface between heavy and light chains - In both the light and heavy chains most of the non-CDR interface residues are conserved. If a conserved residue is replaced by a residue of different character, e.g. size or charge, it should be considered for retention as the murine residue.
- 2.3.1. Heavy Chain - Residues which need to be considered are 37 if the residue is not a valine but is of larger side chain volume or has a charge or polarity. Other residues are 39 if not a glutamine, 45 if not a leucine, 47 if not a tryptophan, 91 if not a phenylalanine or tyrosine, 93 if not an alanine and 103 if not a tryptophan. Residue 89 is also at the interface but is not in a position where the side chain could be of great impact.
- 2.3.2. Light Chain - Residues which need to be considered are 36, if not a tyrosine, 38 if not a glutamine, 44 if not a proline, 46, 49 if not a tyrosine, residue 85, residue 87 if not a tyrosine and 98 if not a phenylalanine.
- 2.4. Variable-Constant region interface - The elbow angle between variable and constant regions may be affected by alterations in packing of key residues in the variable region against the constant region which may affect the position of V_L and V_H with respect to one another. Therefore it is worth noting the residues likely to be in contact with the constant region. In the heavy chain the surface residues potentially in contact with the variable region are conserved between mouse and human antibodies therefore the variable region contact residues may influence the V-C interaction. In the light chain the amino acids found at a number of the constant

- 23 -

region contact points vary, and the V & C regions are not in such close proximity as the heavy chain. Therefore the influences of the light chain V-C interface may be minor.

- 2.4.1. Heavy Chain - Contact residues are 7, 11, 41, 87, 108, 110, 112.
- 2.4.2. Light Chain - In the light chain potentially contacting residues are 10, 12, 40, 80, 83, 103 and 105.

The above analysis coupled with our considerable practical experimental experience in the CDR-grafting of a number of different antibodies have lead us to the protocol given above.

The present invention is now described, by way of example only, with reference to the accompanying Figures 1 - 13.

Brief Description of the Figures

- Figure 1 shows DNA and amino acid sequences of the OKT3 light chain;
- Figure 2 shows DNA and amino acid sequences of the OKT3 heavy chain;
- Figure 3 shows the alignment of the OKT3 light variable region amino acid sequence with that of the light variable region of the human antibody REI;
- Figure 4 shows the alignment of the OKT3 heavy variable region amino acid sequence with that of the heavy variable region of the human antibody KOL;
- Figure 5 shows the heavy variable region amino acid sequences of OKT3, KOL and various corresponding CDR grafts;
- Figure 6 shows the light variable region amino acid sequences of OKT3, REI and various corresponding CDR grafts;

- 24 -

- Figure 7 shows a graph of binding assay results for various grafted OKT3 antibodies'
- Figure 8 shows a graph of blocking assay results for various grafted OKT3 antibodies;
- Figure 9 shows a similar graph of blocking assay results;
- Figure 10 shows similar graphs for both binding assay and blocking assay results;
- Figure 11 shows further similar graphs for both binding assay and blocking assay results;
- Figure 12 shows a graph of competition assay results for a minimally grafted OKT3 antibody compared with the OKT3 murine reference standard, and
- Figure 13 shows a similar graph of competition assay results comparing a fully grafted OKT3 antibody with the murine reference standard.

- 25 -

DETAILED DESCRIPTION OF EMBODIMENTS OF THE INVENTIONEXAMPLE 1CDR-GRAFTING OF OKT3MATERIAL AND METHODS1. INCOMING CELLS

Hybridoma cells producing antibody OKT3 were provided by Ortho (seedlot 4882.1) and were grown up in antibiotic free Dulbecco's Modified Eagles Medium (DMEM) supplemented with glutamine and 5% foetal calf serum, and divided to provide both an overgrown supernatant for evaluation and cells for extraction of RNA. The overgrown supernatant was shown to contain 250 ug/mL murine IgG2a/kappa antibody. The supernatant was negative for murine lambda light chain and IgG1, IgG2b, IgG3, IgA and IgM heavy chain. 20mL of supernatant was assayed to confirm that the antibody present was OKT3.

2. MOLECULAR BIOLOGY PROCEDURES

Basic molecular biology procedures were as described in Maniatis *et al* (ref. 9) with, in some cases, minor modifications. DNA sequencing was performed as described in Sanger *et al* (ref. 11) and the Amersham International Plc sequencing handbook. Site directed mutagenesis was as described in Kramer *et al* (ref. 12) and the Anglian Biotechnology Ltd. handbook. COS cell expression and metabolic labelling studies were as described in Whittle *et al* (ref. 13)

- 26 -

3. RESEARCH ASSAYS**3.1. ASSEMBLY ASSAYS**

Assembly assays were performed on supernatants from transfected COS cells to determine the amount of intact IgG present.

3.1.1. COS CELLS TRANSFECTED WITH MOUSE OKT3 GENES

The assembly assay for intact mouse IgG in COS cell supernatants was an ELISA with the following format:

96 well microtitre plates were coated with F(ab')₂ goat anti-mouse IgG Fc. The plates were washed in water and samples added for 1 hour at room temperature. The plates were washed and F(ab')₂ goat anti-mouse IgG F(ab')₂ (HRPO conjugated) was then added. Substrate was added to reveal the reaction. UPC10, a mouse IgG2a myeloma, was used as a standard.

3.1.2. COS AND CHO CELLS TRANSFECTED WITH CHIMERIC OR CDR-GRAFTED OKT3 GENES

The assembly assay for chimeric or CDR-grafted antibody in COS cell supernatants was an ELISA with the following format:

96 well microtitre plates were coated with F(ab')₂ goat anti-human IgG Fc. The plates were washed and samples added and incubated for 1 hour at room temperature. The plates were washed and monoclonal mouse anti-human kappa chain was added for 1 hour at room temperature.

The plates were washed and F(ab')₂ goat anti-mouse IgG Fc (HRPO conjugated) was added. Enzyme substrate was added to reveal the reaction. Chimeric B72.3 (IgG4) (ref. 13) was used as a standard. The use of a monoclonal anti-kappa chain in this assay allows grafted antibodies to be read from the chimeric standard.

- 27 -

3.2. ASSAY FOR ANTIGEN BINDING ACTIVITY

Material from COS cell supernatants was assayed for OKT3 antigen binding activity onto CD3 positive cells in a direct assay. The procedure was as follows:

HUT 78 cells (human T cell line, CD3 positive) were maintained in culture. Monolayers of HUT 78 cells were prepared onto 96 well ELISA plates using poly-L-lysine and glutaraldehyde. Samples were added to the monolayers for 1 hour at room temperature.

The plates were washed gently using PBS. F(ab')₂ goat anti-human IgG Fc (HRPO conjugated) or F(ab')₂ goat anti-mouse IgG Fc (HRPO conjugated) was added as appropriate for humanised or mouse samples. Substrate was added to reveal the reaction.

The negative control for the cell-based assay was chimeric B72.3. The positive control was mouse Orthomune OKT3 or chimeric OKT3, when available. This cell-based assay was difficult to perform, and an alternative assay was developed for CDR-grafted OKT3 which was more sensitive and easier to carry out.

In this system CDR-grafted OKT3 produced by COS cells was tested for its ability to bind to the CD3-positive HPB-ALL (human peripheral blood acute lymphocytic leukemia) cell line. It was also tested for its ability to block the binding of murine OKT3 to these cells. Binding was measured by the following procedure: HPB-ALL cells were harvested from tissue culture. Cells were incubated at 4°C for 1 hour with various dilutions of test antibody, positive control antibody, or negative control antibody. The cells were washed once and incubated at 4°C for 1 hour with an FITC-labelled goat anti-human IgG (Fc-

- 28 -

specific, mouse absorbed). The cells were washed twice and analysed by cytofluorography. Chimeric OKT3 was used as a positive control for direct binding. Cells incubated with mock-transfected COS cell supernatant, followed by the FITC-labelled goat anti-human IgG, provided the negative control. To test the ability of CDR-grafted OKT3 to block murine OKT3 binding, the HPB-ALL cells were incubated at 4°C for 1 hour with various dilutions of test antibody or control antibody. A fixed saturating amount of FITC OKT3 was added. The samples were incubated for 1 hour at 4°C, washed twice and analysed by cytofluorography. FITC-labelled OKT3 was used as a positive control to determine maximum binding. Unlabelled murine OKT3 served as a reference standard for blocking. Negative controls were unstained cells with or without mock-transfected cell supernatant. The ability of the CDR-grafted OKT3 light chain to bind CD3-positive cells and block the binding of murine OKT3 was initially tested in combination with the chimeric OKT3 heavy chain. The chimeric OKT3 heavy chain is composed of the murine OKT3 variable region and the human IgG4 constant region. The chimeric heavy chain gene is expressed in the same expression vector used for the CDR-grafted genes. The CDR-grafted light chain expression vector and the chimeric heavy chain expression vector were co-transfected into COS cells. The fully chimeric OKT3 antibody (chimeric light chain and chimeric heavy chain) was found to be fully capable of binding to CD3 positive cells and blocking the binding of murine OKT3 to these cells.

3.3 DETERMINATION OF RELATIVE BINDING AFFINITY

The relative binding affinities of CDR-grafted

- 29 -

anti-CD3 monoclonal antibodies were determined by competition binding (ref. 6) using the HPB-ALL human T cell line as a source of CD3 antigen, and fluorescein-conjugated murine OKT3 (F1-OKT3) of known binding affinity as a tracer antibody. The binding affinity of F1-OKT3 tracer antibody was determined by a direct binding assay in which increasing amounts of F1-OKT3 were incubated with HPB-ALL (5×10^5) in PBS with 5% foetal calf serum for 60 min. at 4°C. Cells were washed, and the fluorescence intensity was determined on a FACScan flow cytometer calibrated with quantitative microbead standards (Flow Cytometry Standards, Research Triangle Park, NC). Fluorescence intensity per antibody molecule (F/P ratio) was determined by using microbeads which have a predetermined number of mouse IgG antibody binding sites (Simply Cellular beads, Flow Cytometry Standards). F/P equals the fluorescence intensity of beads saturated with F1-OKT3 divided by the number of binding sites per bead. The amount of bound and free F1-OKT3 was calculated from the mean fluorescence intensity per cell, and the ratio of bound/free was plotted against the number of moles of antibody bound. A linear fit was used to determine the affinity of binding (absolute value of the slope).

For competitive binding, increasing amounts of competitor antibody were added to a sub-saturating dose of F1-OKT3 and incubated with 5×10^5 HPB-ALL in 200 ml of PBS with 5% foetal calf serum, for 60 min at 4°C. The fluorescence intensities of the cells were measured on a FACScan flow cytometer calibrated with quantitative microbead standards. The concentrations of bound and free F1-OKT3 were calculated. The affinities of competing anti-

- 30 -

bodies were calculated from the equation $[X]-[OKT3] = (1/Kx) - (1/Ka)$, where Ka is the affinity of murine OKT3, Kx is the affinity of competitor X , $[]$ is the concentration of competitor antibody at which bound/free binding is $R/2$, and R is the maximal bound/free binding.

4. CDNA LIBRARY CONSTRUCTION

4.1. mRNA PREPARATION AND CDNA SYNTHESIS

OKT3 producing cells were grown as described above and 1.2×10^9 cells harvested and mRNA extracted using the guanidinium/LiCl extraction procedure. cDNA was prepared by priming from Oligo-dT to generate full length cDNA. The cDNA was methylated and EcoRI linkers added for cloning.

4.2. LIBRARY CONSTRUCTION

The cDNA library was ligated to pSP65 vector DNA which had been EcoRI cut and the 5' phosphate groups removed by calf intestinal phosphatase (EcoRI/CIP). The ligation was used to transform high transformation efficiency Escherichia coli (E.coli) HB101. A cDNA library was prepared. 3600 colonies were screened for the light chain and 10000 colonies were screened for the heavy chain.

5. SCREENING

E.coli colonies positive for either heavy or light chain probes were identified by oligonucleotide screening using the oligonucleotides:

5' TCCAGATGTAACTGCTCAC for the light chain, which is complementary to a sequence in the mouse kappa constant region, and 5' CAGGGGCCAGTGGATGGATAGAC for the heavy chain which is complementary to a sequence in the mouse IgG2a constant CH1 domain region. 12 light chain and 9 heavy chain clones

- 31 -

were identified and taken for second round screening. Positive clones from the second round of screening were grown up and DNA prepared. The sizes of the gene inserts were estimated by gel electrophoresis and inserts of a size capable of containing a full length cDNA were subcloned into M13 for DNA sequencing.

6. DNA SEQUENCING

Clones representing four size classes for both heavy and light chains were obtained in M13. DNA sequence for the 5' untranslated regions, signal sequences, variable regions and 3' untranslated regions of full length cDNAs [Figures 1(a) and 2(a)] were obtained and the corresponding amino acid sequences predicted [(Figures 1(b) and 2(b)]. In Figure 1(a) the untranslated DNA regions are shown in uppercase, and in both Figures 1 and 2 the signal sequences are underlined.

7. CONSTRUCTION OF cDNA EXPRESSION VECTORS

Celltech expression vectors are based on the plasmid pEE6hCMV (ref. 14). A polylinker for the insertion of genes to be expressed has been introduced after the major immediate early promoter/enhancer of the human Cytomegalovirus (hCMV). Marker genes for selection of the plasmid in transfected eukaryotic cells can be inserted as BamH1 cassettes in the unique BamH1 site of pEE6 hCMV; for instance, the neo marker to provide pEE6 hCMV neo. It is usual practice to insert the neo and gpt markers prior to insertion of the gene of interest, whereas the GS marker is inserted last because of the presence of internal EcoR1 sites in the cassette.

- 32 -

The selectable markers are expressed from the SV40 late promoter which also provides an origin of replication so that the vectors can be used for expression in the COS cell transient expression system.

The mouse sequences were excised from the M13 based vectors described above as EcoRI fragments and cloned into either pEE6-hCMV-neo for the heavy chain and into EE6-hCMV-gpt for the light chain to yield vectors pJA136 and pJA135 respectively.

8. EXPRESSION OF cDNAS IN COS CELLS

Plasmids pJA135 and pJA136 were co-transfected into COS cells and supernatant from the transient expression experiment was shown to contain assembled antibody which bound to T-cell enriched lymphocytes. Metabolic labelling experiments using ³⁵S methionine showed expression and assembly of heavy and light chains.

9. CONSTRUCTION OF CHIMERIC GENES

Construction of chimeric genes followed a previously described strategy [Whittle *et al* (ref. 13)]. A restriction site near the 3' end of the variable domain sequence is identified and used to attach an oligonucleotide adapter coding for the remainder of the mouse variable region and a suitable restriction site for attachment to the constant region of choice.

9.1. LIGHT CHAIN GENE CONSTRUCTION

The mouse light chain cDNA sequence contains an Aval site near the 3' end of the variable region [Fig. 1(a)]. The majority of the sequence of the variable region was isolated as a 396 bp. EcoRI-Aval fragment. An oligonucleotide adapter was designed to replace the remainder of the 3'

- 34 -

An internal HindIII site was not included in this adapter, to differentiate the two chimeric light chain genes.

The variable region fragment was isolated as a 376 bp EcoRI-AvaI fragment. The oligonucleotide linker was ligated to NruI cut pNW361 and then the adapted 396bp constant region was isolated after recutting the modified pNW361 with EcoRI. The variable region fragment and the modified constant region fragment were ligated directly into EcoRI/CIP treated pEB6hCMVneo to yield pJA137. Initially all clones examined had the insert in the incorrect orientation. Therefore, the insert was re-isolated and recloned to turn the insert round and yield plasmid pJA141. Several clones with the insert in the correct orientation were obtained and the adapter sequence of one was confirmed by DNA sequencing

9.3. HEAVY CHAIN GENE CONSTRUCTION

9.3.1. CHOICE OF HEAVY CHAIN GENE ISOTYPE

The constant region isotype chosen for the heavy chain was human IgG4.

9.3.2. GENE CONSTRUCTION

The heavy chain cDNA sequence showed a BstI site near the 3' end of the variable region [Fig. 2(a)]. The majority of the sequence of the variable region was isolated as a 426bp. EcoRI/CIP/BstI fragment. An oligonucleotide adapter was designated to replace the remainder of the 3' region of the variable region from the BstI site up to and including a unique HindIII site which had been previously engineered into the first two amino acids of the constant region.

The linker was ligated to the V_H fragment and the EcoRI-HindIII adapted fragment was purified from the ligation mixture.

- 35 -

The variable region was ligated to the constant region by cutting pJA91 with EcoRI and HindIII removing the intron fragment and replacing it with the V_H to yield pJA142. Clones were isolated after transformation into E.coli JM101 and the linker and junction sequences were confirmed by DNA sequencing. (N.B. The HindIII site is lost on cloning).

10. CONSTRUCTION OF CHIMERIC EXPRESSION VECTORS

10.1. neo AND gpt VECTORS

The chimeric light chain (version 1) was removed from pJA143 as an EcoRI fragment and cloned into EcoRI/CIP treated pEE6hCMVneo expression vector to yield pJA145. Clones with the insert in the correct orientation were identified by restriction mapping.

The chimeric light chain (version 2) was constructed as described above.

The chimeric heavy chain gene was isolated from pJA142 as a 2.5Kbp EcoRI/BamHI fragment and cloned into the EcoRI/BclI/CIP treated vector fragment of a derivative of pEE6hCMVgpt to yield plasmid pJA144.

10.2. GS SEPARATE VECTORS

GS versions of pJA141 and pJA144 were constructed by replacing the neo and gpt cassettes by a BamHI/SalI/CIP treatment of the plasmids, isolation of the vector fragment and ligation to a GS-containing fragment from the plasmid pRO49 to yield the light chain vector pJA179 and the heavy chain vector pJA180.

10.3. GS SINGLE VECTOR CONSTRUCTION

Single vector constructions containing the cL (chimeric light), cH (chimeric heavy) and GS genes on one plasmid in the order cL-cH-GS, or cH-cL-GS

- 36 -

and with transcription of the genes being head to tail e.g. cL>cH>GS were constructed. These plasmids were made by treating pJA179 or pJA180 with BamHI/CIP and ligating in a BglII/HindIII hCMV promoter cassette along with either the HindIII/BamHI fragment from pJA141 into pJA180 to give the cH-cL-GS plasmid pJA182 or the HindIII/BamHI fragment from pJA144 into pJA179 to give the cL-cH-GS plasmid pJA181.

11. EXPRESSION OF CHIMERIC GENES

11.1. EXPRESSION IN COS CELLS

The chimeric antibody plasmid pJA145 (cL) and pJA144 (cH) were co-transfected into COS cells and supernatant from the transient expression experiment was shown to contain assembled antibody which bound to the HUT 78 human T-cell line. Metabolic labelling experiments using ³⁵S methionine showed expression and assembly of heavy and light chains. However the light chain mobility seen on reduced gels suggested that the potential glycosylation site was being glycosylated. Expression in COS cells in the presence of tunicamycin showed a reduction in size of the light chain to that shown for control chimeric antibodies and the OKT3 mouse light chain. Therefore JA141 was constructed and expressed. In this case the light chain did not show an aberrant mobility or a size shift in the presence or absence of tunicamycin. This second version of the chimeric light chain, when expressed in association with chimeric heavy (cH) chain, produced antibody which showed good binding to HUT 78 cells. In both cases antigen binding was equivalent to that of the mouse antibody.

- 37 -

- 11.2 **EXPRESSION IN CHINESE HAMSTER OVARY (CHO) CELLS**
Stable cell lines have been prepared from plasmids PJA141/pJA144 and from pJA179/pJA180, pJA181 and pJA182 by transfection into CHO cells.

12. **CDR-GRAFTING**

The approach taken was to try to introduce sufficient mouse residues into a human variable region framework to generate antigen binding activity comparable to the mouse and chimeric antibodies.

12.1. **VARIABLE REGION ANALYSIS**

From an examination of a small database of structures of antibodies and antigen-antibody complexes it is clear that only a small number of antibody residues make direct contact with antigen. Other residues may contribute to antigen binding by positioning the contact residues in favourable configurations and also by inducing a stable packing of the individual variable domains and stable interaction of the light and heavy chain variable domains. The residues chosen for transfer can be identified in a number of ways:

- (a) By examination of antibody X-ray crystal structures the antigen binding surface can be predominantly located on a series of loops, three per domain, which extend from the B-barrel framework.
- (b) By analysis of antibody variable domain sequences regions of hypervariability [termed the Complementarity Determining Regions (CDRs) by Wu and Kabat (ref. 5)] can be identified. In the most but not all cases these CDRs correspond to, but extend a short way beyond, the loop regions noted above.

- 38 -

- (c) Residues not identified by (a) and (b) may contribute to antigen binding directly or indirectly by affecting antigen binding site topology, or by inducing a stable packing of the individual variable domains and stabilising the inter-variable domain interaction. These residues may be identified either by superimposing the sequences for a given antibody on a known structure and looking at key residues for their contribution, or by sequence alignment analysis and noting "idiosyncratic" residues followed by examination of their structural location and likely effects.

12.1.1. LIGHT CHAIN

Figure 3 shows an alignment of sequences for the human framework region RE1 and the OKT3 light variable region. The structural loops (LOOP) and CDRs (KARAT) believed to correspond to the antigen binding region are marked. Also marked are a number of other residues which may also contribute to antigen binding as described in 13.1(c). Above the sequence in Figure 3 the residue type indicates the spatial location of each residue side chain, derived by examination of resolved structures from X-ray crystallography analysis. The key to this residue type designation is as follows:

N - near to CDR (From X-ray Structures)	
P - Packing	B - Buried Non-Packing
S - Surface	E - Exposed
I - Interface	* - Interface
- Packing/Part Exposed	
? - Non-CDR Residues which may require to be left as Mouse sequence.	

- 39 -

Residues underlined in Figure 3 are amino acids. RE1 was chosen as the human framework because the light chain is a kappa chain and the kappa variable regions show higher homology with the mouse sequences than a lambda light variable region, e.g. KOL (see below). RE1 was chosen in preference to another kappa light chain because the X-ray structure of the light chain has been determined so that a structural examination of individual residues could be made.

12.1.2. HEAVY CHAIN

Similarly Figure 4 shows an alignment of sequences for the human framework region KOL and the OKT3 heavy variable region. The structural loops and CDRs believed to correspond to the antigen binding region are marked. Also marked are a number of other residues which may also contribute to antigen binding as described in 12.1(c). The residue type key and other indicators used in Figure 4 are the same as those used in Figure 3. KOL was chosen as the heavy chain framework because the X-ray structure has been determined to a better resolution than, for example, NEWM and also the sequence alignment of OKT3 heavy variable region showed a slightly better homology to KOL than to NEWM.

12.2. DESIGN OF VARIABLE GENES

The variable region domains were designed with mouse variable region optimal codon usage [Grantham and Perrin (ref. 15)] and used the B72.3 signal sequences [Whittle *et al* (ref. 13)]. The sequences were designed to be attached to the constant region in the same way as for the chimeric genes described above. Some constructs contained the "Kozak consensus sequence" [Kozak (ref. 16)] directly linked to the 5' of the signal

- 40 -

sequence in the gene. This sequence motif is believed to have a beneficial role in translation initiation in eukaryotes.

12.3. GENE CONSTRUCTION

To build the variable regions, various strategies are available. The sequence may be assembled by using oligonucleotides in a manner similar to Jones *et al* (ref. 17) or by simultaneously replacing all of the CDRs or loop regions by oligonucleotide directed site specific mutagenesis in a manner similar to Verhoeyen *et al* (ref. 2). Both strategies were used and a list of constructions is set out in Tables 1 and 2 and Figures 4 and 5. It was noted in several cases that the mutagenesis approach led to deletions and rearrangements in the gene being remodelled, while the success of the assembly approach was very sensitive to the quality of the oligonucleotides.

13. CONSTRUCTION OF EXPRESSION VECTORS

Genes were isolated from M13 or SP65 based intermediate vectors and cloned into pEE6hCMVneo for the light chains and pEE6hCMVgpt for the heavy chains in a manner similar to that for the chimeric genes as described above.

TABLE 1 CDR-GRAFTED GENE CONSTRUCTS

CODE	MOUSE SEQUENCE CONTENT	METHOD OF CONSTRUCTION	KOZAK SEQUENCE - +	
LIGHT CHAIN ALL HUMAN FRAMEWORK RE1				
121	26-32, 50-56, 91-96 inclusive	SDM and gene assembly	+	n.d.
121A	26-32, 50-56, 91-96 inclusive +1, 3, 46, 47	Partial gene assembly	n.d.	+
121B	26-32, 50-56, 91-96 inclusive + 46, 47	Partial gene assembly	n.d.	+
221	24-24, 50-56, 91-96 inclusive	Partial gene assembly	+	+
221A	24-34, 50-56, 91-96 inclusive +1, 3, 46, 47	Partial gene assembly	+	+
221B	24-34, 50-56, 91-96 inclusive +1, 3	Partial gene assembly	+	+
221C	24-34, 50-56, 91-96 inclusive	Partial gene assembly	+	+
HEAVY CHAIN ALL HUMAN FRAMEWORK KOL				
121	26-32, 50-56, 95-100B inclusive	Gene assembly	n.d.	+
131	26-32, 50-58, 95-100B inclusive	Gene assembly	n.d.	+
141	26-32, 50-65, 95-100B inclusive	Partial gene assembly	+	n.d.
321	26-35, 50-56, 95-100B inclusive	Partial gene assembly	+	n.d.
331	26-35, 50-58, 95-100B inclusive	Partial gene assembly	+	
		Gene assembly		+
341	26-35, 50-65, 95-100B inclusive	SDM	+	
		Partial gene assembly		+
341A	26-35, 50-65, 95-100B inclusive +6, 23, 24, 48, 49, 71, 73, 76, 78, 88, 91 (+63 = human)	Gene assembly	n.d.	+
341B	26-35, 50-65, 95-100B inclusive + 48, 49, 71, 73, 76, 78, 88, 91 (+63 + human)	Gene assembly	n.d.	+

KEY

n.d.	not done
SDM	Site directed mutagenesis
Gene assembly	Variable region assembled entirely from oligonucleotides
Partial gene assembly	Variable region assembled by combination of restriction fragments either from other genes originally created by SDM and gene assembly or by oligonucleotide assembly of part of the variable region and reconstruction with restriction fragments from other genes originally created by SDM and gene assembly

- 42 -

14. EXPRESSION OF CDR-GRAFTED GENES

14.1. PRODUCTION OF ANTIBODY CONSISTING OF GRAFTED LIGHT (gL) CHAINS WITH MOUSE HEAVY (mH) OR CHIMERIC HEAVY (cH) CHAINS

All gL chains, in association with mH or cH produced reasonable amounts of antibody.

Insertion of the Kozak consensus sequence at a position 5' to the ATG (kgL constructs) however, led to a 2-5 fold improvement in net expression. Over an extended series of experiments expression levels were raised from approximately 200ng/ml to approximately 500 ng/ml for kgL/cH or kgL/mH combinations.

When direct binding to antigen on HUT 78 cells was measured, a construct designed to include mouse sequence based on loop length (gL121) did not lead to active antibody in association with mH or cH. A construct designed to include mouse sequence based on Kabat CDRs (gL221) demonstrated some weak binding in association with mH or cH. However, when framework residues 1, 3, 46, 47 were changed from the human to the murine OKT3 equivalents based on the arguments outlined in Section 12.1 antigen binding was demonstrated when both of the new constructs, which were termed 121A and 221A were co-expressed with cH. When the effects of these residues were examined in more detail, it appears that residues 1 and 3 are not major contributing residues as the product of the gL221B gene shows little detectable binding activity in association with cH. The light chain product of gL221C, in which mouse sequences are present at 46 and 47, shows good binding activity in association with cH.

- 43 -

14.2 PRODUCTION OF ANTIBODY CONSISTING OF GRAFTED HEAVY (gH) CHAINS WITH MOUSE LIGHT (mL) OR CHIMERIC LIGHT (cL) CHAINS

Expression of the gH genes proved to be more difficult to achieve than for gL. First, inclusion of the Kozak sequence appeared to have no marked effect on expression of gH genes. Expression appears to be slightly improved but not to the same degree as seen for the grafted light chain.

Also, it proved difficult to demonstrate production of expected quantities of material when the loop choice (amino acid 26-32) for CDR1 is used, e.g. gH121, 131, 141 and no conclusions can be drawn about these constructs.

Moreover, co-expression of the gH341 gene with cL or mL has been variable and has tended to produce lower amounts of antibody than the cH/cL or mH/mL combinations. The alterations to gH341 to produce gH341A and gH341B lead to improved levels of expression.

This may be due either to a general increase in the fraction of mouse sequence in the variable region, or to the alteration at position 63 where the residue is returned to the human amino acid Valine (Val) from Phenylalanine (Phe) to avoid possible internal packing problems with the rest of the human framework. This arrangement also occurs in gH331 and gH321.

When gH321 or gH331 were expressed in association with cL, antibody was produced but antibody binding activity was not detected.

When the more conservative gH341 gene was used antigen binding could be detected in association with cL or mL, but the activity was only marginally above the background level.

- 44 -

When further mouse residues were substituted based on the arguments in 12.1, antigen binding could be clearly demonstrated for the antibody produced when kgH341A and kgH341B were expressed in association with cL.

14.3 PRODUCTION OF FULLY CDR-GRAFTED ANTIBODY

The kgL221A gene was co-expressed with kgH341, kgH341A or kgH341B. For the combination kgH221A/kgH341 very little material was produced in a normal COS cell expression.

For the combinations kgL221A/kgH341A or kgH221A/kgH341B amounts of antibody similar to gL/cH was produced.

In several experiments no antigen binding activity could be detected with kgH221A/gH341 or kgH221A/kgH341 combinations, although expression levels were very low.

Antigen binding was detected when kgL221A/kgH341A or kgH221A/kgH341B combinations were expressed. In the case of the antibody produced from the kgL221A/kgH341A combination the antigen binding was very similar to that of the chimeric antibody.

An analysis of the above results is given below.

15. DISCUSSION OF CDR-GRAFTING RESULTS

In the design of the fully humanised antibody the aim was to transfer the minimum number of mouse amino acids that would confer antigen binding onto a human antibody framework.

15.1. LIGHT CHAIN

15.1.1. EXTENT OF THE CDRs

For the light chain the regions defining the loops known from structural studies of other antibodies to contain the antigen contacting residues, and

- 45 -

those hypervariable sequences defined by Kabat et al (refs. 4 and 5) as Complementarity Determining Regions (CDRs) are equivalent for CDR2. For CDR1 the hypervariable region extends from residues 24-34 inclusive while the structural loop extends from 26-32 inclusive. In the case of OKT3 there is only one amino acid difference between the two options, at amino acid 24, where the mouse sequence is a serine and the human framework RE1 has glutamine. For CDR3 the loop extends from residues 91-96 inclusive while the Kabat hypervariability extends from residues 89-97 inclusive. For OKT3 amino acids 89, 90 and 97 are the same between OKT3 and RE1 (Fig. 3). When constructs based on the loop choice for CDR1 (gL121) and the Kabat choice (gL221) were made and co-expressed with mH or cH no evidence for antigen binding activity could be found for gL121, but trace activity could be detected for the gL221, suggesting that a single extra mouse residue in the grafted variable region could have some detectable effect. Both gene constructs were reasonably well expressed in the transient expression system.

15.1.2. FRAMEWORK RESIDUES

The remaining framework residues were then further examined, in particular amino acids known from X-ray analysis of other antibodies to be close to the CDRs and also those amino acids which in OKT3 showed differences from the consensus framework for the mouse subgroup (subgroup VI) to which OKT3 shows most homology. Four positions 1, 3, 46 and 47 were identified and their possible contribution was examined by substituting the mouse amino acid for the human amino acid at each position. Therefore gL221A (gL221 + D1Q, Q3V, L46R, L47W,

- 46 -

see Figure 3 and Table 1) was made, cloned in EE6hCMVneo and co-expressed with cH (pJA144). The resultant antibody was well expressed and showed good binding activity. When the related genes gL221B (gL221 + D1Q, Q3V) and gL221C (gL221 + L46R, L47W) were made and similarly tested, while both genes produced antibody when co-expressed with cH, only the gL221C/cH combination showed good antigen binding. When the gL121A (gL121 + D1Q, Q3V, L46R, L47W) gene was made and co-expressed with cH, antibody was produced which also bound to antigen.

15.2. HEAVY CHAIN

15.2.1. EXTENT OF THE CDRs

For the heavy chain the loop and hypervariability analyses agree only in CDR3. For CDR1 the loop region extends from residues 26-32 inclusive whereas the Kabat CDR extends from residues 31-35 inclusive. For CDR2 the loop region is from 50-58 inclusive while the hypervariable region covers amino acids 50-65 inclusive. Therefore humanised heavy chains were constructed using the framework from antibody KOL and with various combinations of these CDR choices, including a shorter choice for CDR2 of 50-56 inclusive as there was some uncertainty as to the definition of the end point for the CDR2 loop around residues 56 to 58. The genes were co-expressed with mL or cL initially. In the case of the gH genes with loop choices for CDR1 e.g. gH121, gH131, gH141 very little antibody was produced in the culture supernatants. As no free light chain was detected it was presumed that the antibody was being made and assembled inside the cell but that the heavy chain was aberrant in some way, possibly incorrectly folded, and therefore the antibody was

- 47 -

being degraded internally. In some experiments trace amounts of antibody could be detected in ^{35}S labelling studies.

As no net antibody was produced, analysis of these constructs was not pursued further.

When, however, a combination of the loop choice and the Kabat choice for CDR1 was tested (mouse amino acids 26-35 inclusive) and in which residues 31 (Ser to Arg), 33 (Ala to Thr), and 35 (Tyr to His) were changed from the human residues to the mouse residue and compared to the first series, antibody was produced for gH321, kgH331 and kgH341 when co-expressed with cL. Expression was generally low and could not be markedly improved by the insertion of the Kozak consensus sequence 5' to the ATG of the signal sequence of the gene, as distinct from the case of the gL genes where such insertion led to a 2-5 fold increase in net antibody production. However, only in the case of gH341/mL or kgH341/cL could marginal antigen binding activity be demonstrated. When the kgH341 gene was co-expressed with kgL221A, the net yield of antibody was too low to give a signal above the background level in the antigen binding assay.

15.2.2. FRAMEWORK RESIDUES

As in the case of the light chain the heavy chain frameworks were re-examined. Possibly because of the lower initial homology between the mouse and human heavy variable domains compared to the light chains, more amino acid positions proved to be of interest. Two genes kgH341A and kgH341B were constructed, with 11 or 8 human residues respectively substituted by mouse residues compared to gH341, and with the CDR2 residue 63 returned to the human amino acid potentially to

- 48 -

improve domain packing. Both showed antigen binding when combined with cL or kgL221A, the kgH341A gene with all 11 changes appearing to be the superior choice.

15.3

INTERIM CONCLUSIONS

It has been demonstrated, therefore, for OKT3 that to transfer antigen binding ability to the humanised antibody, mouse residues outside the CDR regions defined by the Kabat hypervariability or structural loop choices are required for both the light and heavy chains. Fewer extra residues are needed for the light chain, possibly due to the higher initial homology between the mouse and human kappa variable regions.

Of the changes seven (1 and 3 from the light chain and 6, 23, 71, 73 and 76 from the heavy chain) are predicted from a knowledge of other antibody structures to be either partly exposed or on the antibody surface. It has been shown here that residues 1 and 3 in the light chain are not absolutely required to be the mouse sequence; and for the heavy chain the gh341B heavy chain in combination with the 221A light chain generated only weak binding activity. Therefore the presence of the 6, 23 and 24 changes are important to maintain a binding affinity similar to that of the murine antibody. It was important, therefore, to further study the individual contribution of the other 8 mouse residues of the kgH341A gene compared to kgH341.

16.

FURTHER CDR-GRAFTING EXPERIMENTS

Additional CDR-grafted heavy chain genes were prepared substantially as described above. With reference to Table 2 the further heavy chain genes were based upon the gh341 (plasmid pJA178) and

- 49 -

gH341A (plasmid pJA185) with either mouse OKT3 or human KOL residues at 6, 23, 24, 48, 49, 63, 71, 73, 76, 78, 88 and 91, as indicated. The CDR-grafted light chain genes used in these further experiments were gL221, gL221A, gL221B and gL221C as described above.

- 50 -

TABLE 2OKT3 HEAVY CHAIN CDR GRAFTS1. gH341 and derivatives

RES NUM	6	23	24	48	49	63	71	73	76	78	88	91
OKT3vh	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>F</u>	<u>T</u>	<u>K</u>	<u>S</u>	<u>A</u>	<u>A</u>	<u>Y</u>
gH341	E	S	S	V	A	F	R	N	N	L	G	F JA178
gH341A	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>S</u>	<u>A</u>	<u>A</u>	<u>Y</u> JA185
gH341E	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>S</u>	<u>A</u>	<u>G</u>	<u>G</u> JA198
gH341*	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>N</u>	<u>A</u>	<u>G</u>	<u>F</u> JA207
gH341*	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>R</u>	<u>N</u>	<u>N</u>	<u>A</u>	<u>G</u>	<u>F</u> JA209
gH341D	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>N</u>	<u>L</u>	<u>G</u>	<u>F</u> JA197
gH341*	<u>Q</u>	<u>K</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>R</u>	<u>N</u>	<u>N</u>	<u>L</u>	<u>G</u>	<u>F</u> JA199
gH341C	<u>Q</u>	<u>K</u>	<u>A</u>	<u>V</u>	<u>A</u>	<u>F</u>	<u>R</u>	<u>N</u>	<u>N</u>	<u>L</u>	<u>G</u>	<u>F</u> JA184
gH341*	<u>Q</u>	<u>S</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>S</u>	<u>A</u>	<u>A</u>	<u>Y</u> JA203
gH341*	E	S	A	I	G	V	T	K	S	A	A	Y JA205
gH341B	E	S	S	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>S</u>	<u>A</u>	<u>A</u>	<u>Y</u> JA183
gH341*	<u>Q</u>	<u>S</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>S</u>	<u>A</u>	<u>G</u>	<u>F</u> JA204
gH341*	E	S	A	I	G	V	T	K	S	A	G	F JA206
gH341*	<u>Q</u>	<u>S</u>	<u>A</u>	<u>I</u>	<u>G</u>	<u>V</u>	<u>T</u>	<u>K</u>	<u>N</u>	<u>A</u>	<u>G</u>	<u>F</u> JA208
KOL	E	S	S	V	A		R	N	N	L	G	F

OKT3 LIGHT CHAIN CDR GRAFTS2. gL221 and derivatives

RES NUM	1	3	46	47
OKT3v1	<u>Q</u>	<u>V</u>	<u>R</u>	<u>W</u>
GL221	D	Q	L	L DA221
gL221A	<u>Q</u>	<u>V</u>	<u>R</u>	<u>W</u> DA221A
gL221B	<u>Q</u>	<u>V</u>	L	L DA221B
GL221C	D	Q	<u>R</u>	<u>W</u> DA221C
RE1	D	Q	L	L

MURINE RESIDUES ARE UNDERLINED

- 51 -

The CDR-grafted heavy and light chain genes were co-expressed in COS cells either with one another in various combinations but also with the corresponding murine and chimeric heavy and light chain genes substantially as described above. The resultant antibody products were then assayed in binding and blocking assays with HPB-ALL cells as described above.

The results of the assays for various grafted heavy chains co-expressed with the gL221C light chain are given in Figures 7 and 8 (for the JA184, JA185, JA197 and JA198 constructs - see Table 2), in Figure 9 (for the JA183, JA184, JA185 and JA197 constructs) in Figure 10 (for the chimeric, JA185, JA199, JA204, JA205, JA207, JA208 and JA209 constructs) and in Figure 11 (for the JA183, JA184, JA185, JA198, JA203, JA205 and JA206 constructs).

The basic grafted product without any human to murine changes in the variable frameworks, i.e. gL221 co-expressed with gh341 (JA178), and also the "fully grafted" product, having most human to murine changes in the grafted heavy chain framework, i.e. gL221C co-expressed with gh341A (JA185), were assayed for relative binding affinity in a competition assay against murine OKT3 reference standard, using HPB-ALL cells. The assay used was as described above in section 3.3. The results obtained are given in Figure 12 for the basic grafted product and in Figure 13 for the fully grafted product. These results indicate that the basic grafted product has negligible binding ability as compared with the OKT3 murine reference standard; whereas the "fully grafted" product has a binding ability very similar to that of the OKT3 murine reference standard.

The binding and blocking assay results indicate the following:

- 52 -

The JA198 and JA207 constructs appear to have the best binding characteristics and similar binding abilities, both substantially the same as the chimeric and fully grafted gH341A products. This indicates that positions 88 and 91 and position 76 are not highly critical for maintaining the OKT3 binding ability; whereas at least some of positions 6, 23, 24, 48, 49, 71, 73 and 78 are more important.

This is borne out by the finding that the JA209 and JA199, although of similar binding ability to one another, are of lower binding ability than the JA198 and JA207 constructs. This indicates the importance of having mouse residues at positions 71, 73 and 78, which are either completely or partially human in the JA199 and JA209 constructs respectively.

Moreover, on comparing the results obtained for the JA205 and JA183 constructs it is seen that there is a decrease in binding going from the JA205 to the JA183 constructs. This indicates the importance of retaining a mouse residue at position 23, the only position changed between JA205 and JA183.

These and other results lead us to the conclusion that of the 11 mouse framework residues used in the gH341A (JA185) construct, it is important to retain mouse residues at all of positions 6, 23, 24, 48 and 49, and possibly for maximum binding affinity at 71, 73 and 78.

Similar Experiments were carried out to CDR-graft a number of the rodent antibodies including antibodies having specificity for CD4 (OKT4), ICAM-1 (R6-5), TAG72 (B72.3), and TNF α (61E71, 101.4, hTNF1, hTNF2 and hTNF3).

- 53 -

EXAMPLE 2CDR-GRAFTING OF A MURINE ANTI-CD4 T CELL
RECEPTOR ANTIBODY, OKT4A

Anti OKT4A CDR-grafted heavy and light chain genes were prepared, expressed and tested substantially as described above in Example 1 for CDR-grafted OKT3. The CDR grafting of OKT4A is described in detail in Ortho patent application PCT/GB 90..... of even date herewith entitled "Humanised Antibodies". The disclosure of this Ortho patent application PCT/GB 90 is incorporated herein by reference. A number of CDR-grafted OKT4 antibodies have been prepared. Presently the CDR-grafted OKT4A of choice is the combination of the grafted light chain LCDR2 and the grafted heavy chain HCDR10.

THE LIGHT CHAIN

The human acceptor framework used for the grafted light chains was RE1. The preferred LCDR2 light chain has human to mouse changes at positions 33, 34, 38, 49 and 89 in addition to the structural loop CDRs. Of these changed positions, positions 33, 34 and 89 fall within the preferred extended CDRs of the present invention (positions 33 and 34 in CDR1 and position 89 in CDR3). The human to murine changes at positions 38 and 49 corresponds to positions at which the amino acid residues are preferably donor murine amino acid residues in accordance with the present invention.

A comparison of the amino acid sequences of the donor murine light chain variable domain and the RE1 human acceptor light chain variable further reveals that the murine and human residues are identical at all of positions 46, 48 and 71 and at all of positions 2, 4, 6, 35, 36, 44, 47, 62, 64-69, 85, 87, 98, 99 and 101 and 102. However the amino acid residue at position 58 in LCDR2 is

- 54 -

the human RE1 framework residue not the mouse OKT4 residue as would be preferred in accordance with the present invention.

THE HEAVY CHAIN

The human acceptor framework used for the grafted heavy chains was KOL.

The preferred CDR graft HCDR10 heavy chain has human to mouse changes at positions 24, 35, 57, 58, 60, 88 and 91 in addition to the structural loop CDRs.

Of these positions, positions 35 (CDR1) and positions 57, 58 and 60 (CDR2) fall within the preferred extended CDRs of the present invention. Also the human to mouse change at position 24 corresponds to a position at which the amino acid residue is a donor murine residue in accordance with the present invention. Moreover, the human to mouse changes at positions 88 and 91 correspond to positions at which the amino acid residues are optionally donor murine residues.

Moreover, a comparison of the murine OKT4A and human KOL heavy chain variable amino acid sequences reveals that the murine and human residues are identical at all of positions 23, 49, 71, 73 and 78 and at all of positions 2, 4, 6, 25, 36, 37, 39, 47, 48, 93, 94, 103, 104, 106 and 107.

Thus the OKT4A CDR-grafted heavy chain HCDR10 corresponds to a particularly preferred embodiment according to the present invention.

EXAMPLE 3CDR-GRAFTING OF AN ANTI-MUCIN SPECIFIC MURINE ANTIBODY, B72.3

The cloning of the genes coding for the anti-mucin specific murine monoclonal antibody B72.3 and the preparation of B72.3 mouse-human chimeric antibodies has been described previously (ref. 13 and WO 89/01783). CDR-grafted versions of B72.3 were prepared as follows.

(a) B72.3 Light Chain

CDR-grafting of this light chain was accomplished by direct transfer of the murine CDRs into the framework of the human light chain RE1.

The regions transferred were:

<u>CDR Number</u>	<u>Residues</u>
1	24-34
2	50-56
3	90-96

The activity of the resulting grafted light chain was assessed by co-expression in COS cells, of genes for the combinations:

B72.3 cH/B72.3 cL

and B72.3 cH/B72.3 gL

Supernatants were assayed for antibody concentration and for the ability to bind to microtitre plates coated with mucin. The results obtained indicated that, in combination with the B72.3 cH chain, B72.3 cL and B72.3 gL had similar binding properties.

Comparison of the murine B72.3 and RE1 light chain amino acid sequences reveals that the residues are identical at positions 46, 58 and 71 but are different at position 48.

- 56 -

Thus changing the human residue to the donor mouse residue at position 48 may further improve the binding characteristics of the CDR-grafted light chain, (B72.3 gL) in accordance with the present invention.

(b) B72.3 heavy chain

i. Choice of framework

At the outset it was necessary to make a choice of human framework. Simply put, the question was as follows: Was it necessary to use the framework regions from an antibody whose crystal structure was known or could the choice be made on some other criteria?

For B72.3 heavy chain, it was reasoned that, while knowledge of structure was important, transfer of the CDRs from mouse to human frameworks might be facilitated if the overall homology between the donor and receptor frameworks was maximised.

Comparison of the B72.3 heavy chain sequence with those in Kabat (ref. 4) for human heavy chains showed clearly that B72.3 had poor homology for KOL and NEWM (for which crystal structures are available) but was very homologous to the heavy chain for EU.

On this basis, EU was chosen for the CDR-grafting and the following residues transferred as CDRs.

<u>CDR Number</u>	<u>Residues</u>
1	27-36
2	50-63
3	93-102

- 57 -

Also it was noticed that the FR4 region of EU was unlike that of any other human (or mouse) antibody. Consequently, in the grafted heavy chain genes this was also changed to produce a "consensus" human sequence. (Preliminary experiments showed that grafted heavy chain genes containing the EU FR4 sequence expressed very poorly in transient expression systems.)

ii. Results with grafted heavy chain genes

Expression of grafted heavy chain genes containing all human framework regions with either gL or cL genes produced a grafted antibody with little ability to bind to mucin. The grafted antibody had about 1% the activity of the chimeric antibody.

In these experiments, however, it was noted that the activity of the grafted antibody could be increased to ~ 10% of B72.3 by exposure to pHs of 2-3.5.

This observation provided a clue as to how the activity of the grafted antibody could be improved without acid treatment. It was postulated that acid exposure brought about the protonation of an acidic residue (pKa of aspartic acid = 3.86 and of glutamine acid = 4.25) which in turn caused a change in structure of the CDR loops, or allowed better access of antigen.

From comparison of the sequences of B72.3 (ref. 13) and EU (refs. 4 and 5), it was clear that, in going from the mouse to human frameworks, only two positions had been changed in such a way that acidic residues had been introduced. These

- 58 -

positions are at residues 73 and 81, where K to E and Q to E changes had been made, respectively.

Which of these positions might be important was determined by examining the crystal structure of the KOL antibody. In KOL heavy chain, position 81 is far removed from either of the CDR loops.

Position 73, however, is close to both CDRs 1 and 3 of the heavy chain and, in this position it was possible to envisage that a K to E change in this region could have a detrimental effect on antigen binding.

iii. Framework changes in B72.3 gH gene

On the basis of the above analysis, E73 was mutated to a lysine (K). It was found that this change had a dramatic effect on the ability of the grafted Ab to bind to mucin. Further the ability of the grafted B72.3 produced by the mutated gH/gL combination to bind to mucin was similar to that of the B72.3 chimeric antibody.

iv. Other framework changes

In the course of the above experiments, other changes were made in the heavy chain framework regions. Within the accuracy of the assays used, none of the changes, either alone or together, appeared beneficial.

v. Other

All assays used measured the ability of the grafted Ab to bind to mucin and, as a whole, indicated that the single framework change at position 73 is sufficient to generate an antibody with similar binding properties to B72.3.

- 59 -

Comparison of the B72.3 murine and EU heavy chain sequences reveals that the mouse and human residues are identical at positions 23, 24, 71 and 78.

Thus the mutated CDR-grafted B72.3 heavy chain corresponds to a preferred embodiment of the present invention.

EXAMPLE 4**CDR-GRAFTING OF A MURINE ANTI-ICAM-1 MONOCLONAL ANTIBODY**

A murine antibody, R6-5-D6 (EP 0314863) having specificity for Intercellular Adhesion Molecule 1 (ICAM-1) was CDR-grafted substantially as described above in previous examples. This work is described in greater detail in co-pending application, British Patent Application No. 9009549.8, the disclosure of which is incorporated herein by reference.

The human EU framework was used as the acceptor framework for both heavy and light chains. The CDR-grafted antibody currently of choice is provided by co-expression of grafted light chain gL221A and grafted heavy chain gH341D which has a binding affinity for ICAM 1 of about 75% of that of the corresponding mouse-human chimeric antibody.

LIGHT CHAIN

gL221A has murine CDRs at positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3). In addition several framework residues are also the murine amino acid. These residues were chosen after consideration of the possible contribution of these residues to domain packing and stability of the conformation of the antigen binding region. The residues which have been retained as mouse are at positions 2, 3, 48 (?), 60, 84, 85 and 87.

Comparison of the murine anti-ICAM 1 and human EU light chain amino acid sequences reveals that the murine and human residues are identical at positions 46, 58 and 71.

HEAVY CHAIN

gH341D has murine CDRs at positions 26-35 (CDR1), 50-56 (CDR2) and 94-100B (CDR3). In addition murine residues were used in gH341D at positions 24, 48, 69, 71, 73, 80, 88 and 91. Comparison of the murine anti-ICAM 1 and human EU heavy chain amino acid sequences are identical at positions 23, 49 and 78.

- 61 -

EXAMPLE 5CDR-Grafting of murine anti-TNF α antibodies

A number of murine anti-TNF α monoclonal antibodies were CDR-grafted substantially as described above in previous examples. These antibodies include the murine monoclonal antibodies designated 61 E71, hTNF1, hTNF3 and 101.4. A brief summary of the CDR-grafting of each of these antibodies is given below.

61E71

A similar analysis as described above (Example 1, Section 12.1.) was done for 61E71 and for the heavy chain 10 residues were identified at 23, 24, 48, 49, 68, 69, 71, 73, 75 and 88 as residues to potentially retain as murine. The human frameworks chosen for CDR-grafting of this antibody, and the hTNF3 and 101.4 antibodies were RE1 for the light chain and KOL for the heavy chain. Three genes were built, the first of which contained 23, 24, 48, 49, 71 and 73 [gH341(6)] as murine residues. The second gene also had 75 and 88 as murine residues [gH341(8)] while the third gene additionally had 68, 69, 75 and 88 as murine residues [gH341(10)]. Each was co-expressed with gL221, the minimum grafted light chain (CDRs only). The gL221/gH341(6) and gL221/gH341(8) antibodies both bound as well to TNF as murine 61E71. The gL221/gH341(10) antibody did not express and this combination was not taken further. Subsequently the gL221/gH341(6) antibody was assessed in an L929 cell competition assay in which the antibody competes against the TNF receptor on L929 cells for binding to TNF in solution. In this assay the gL221/gH341(6) antibody was approximately 10% as active as murine 61E71.

- 62 -

hTNF1

hTNF1 is a monoclonal antibody which recognises an epitope on human TNF- . The EU human framework was used for CDR-grafting of both the heavy and light variable domains.

Heavy Chain

In the CDR-grafted heavy chain (ghTNF1) mouse CDRs were used at positions 26-35 (CDR1), 50-65 (CDR2) and 95-102 (CDR3). Mouse residues were also used in the frameworks at positions 48, 67, 69, 71, 73, 76, 89, 91, 94 and 108. Comparison of the TNF1 mouse and EU human heavy chain residues reveals that these are identical at positions 23, 24, 29 and 78.

Light Chain

In the CDR-grafted light chain (gLhTNF1) mouse CDRs were used at positions 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3). In addition mouse residues were used in the frameworks at positions 3, 42, 48, 49, 83, 106 and 108. Comparison of the hTNF1 mouse and EU human light chain residues reveals that these are identical at positions 46, 58 and 71.

The grafted hTNF1 heavy chain was co-expressed with the chimeric light chain and the binding ability of the product compared with that of the chimeric light chain/chimeric heavy chain product in a TNF binding assay. The grafted heavy chain product appeared to have binding ability for TNF slightly better than the fully chimeric product.

Similarly, a grafted heavy chain/grafted light chain product was co-expressed and compared with the fully chimeric product and found to have closely similar binding properties to the latter product.

- 63 -

hTNF3

hTNF3 recognises an epitope on human TNF- α . The sequence of hTNF3 shows only 21 differences compared to 61E71 in the light and heavy chain variable regions, 10 in the light chain (2 in the CDRs at positions 50, 96 and 8 in the framework at 1, 19, 40, 45, 46, 76, 103 and 106) and 11 in the heavy chain (3 in the CDR regions at positions 52, 60 and 95 and 8 in the framework at 1, 10, 38, 40, 67, 73, 87 and 105). The light and heavy chains of the 61E71 and hTNF3 chimeric antibodies can be exchanged without loss of activity in the direct binding assay. However 61E71 is an order of magnitude less able to compete with the TNF receptor on L929 cells for TNF- α compared to hTNF3. Based on the 61E71 CDR grafting data gL221 and gH341(+23, 24, 48, 49 71 and 73 as mouse) genes have been built for hTNF3 and tested and the resultant grafted antibody binds well to TNF- α , but competes very poorly in the L929 assay. It is possible that in this case also the framework residues identified for OKT3 programme may improve the competitive binding ability of this antibody.

101.4

101.4 is a further murine monoclonal antibody able to recognise human TNF- α . The heavy chain of this antibody shows good homology to KOL and so the CDR-grafting has been based on RE1 for the light chain and KOL for the heavy chain. Several grafted heavy chain genes have been constructed with conservative choices for the CDR's (gH341) and which have one or a small number of non-CDR residues at positions 73, 78 or 77-79 inclusive, as the mouse amino acids. These have been co-expressed with cL or gL221. In all cases binding to TNF equivalent to the chimeric antibody is seen and when co-expressed with cL the resultant antibodies are able to compete well in the L929 assay. However, with gL221 the resultant antibodies

- 64 -

are at least an order of magnitude less able to compete for TNF against the TNF receptor on L929 cells.

Mouse residues at other positions in the heavy chain, for example, at 23 and 24 together or at 76 have been demonstrated to provide no improvement to the competitive ability of the grafted antibody in the L929 assay.

A number of other antibodies including antibodies having specificity for interleukins e.g. IL1 and cancer markers such as carcinoembryonic antigen (CEA) e.g. the monoclonal antibody A5B7 (ref. 21), have been successfully CDR-grafted according to the present invention.

It will be appreciated that the foregoing examples are given by way of illustration only and are not intended to limit the scope of the claimed invention. Changes and modifications may be made to the methods described whilst still falling within the spirit and scope of the invention.

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- 67 -

CLAIMS

1. A CDR-grafted antibody heavy chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 6, 23 and/or 24, 48 and/or 49, 71 and/or 73, 75 and/or 76 and/or 78 and 88 and/or 91.
2. A CDR-grafted heavy chain according to Claim 1 comprising donor residues at positions 23, 24, 49, 71, 73 and 78, or at positions 23, 24 and 49.
3. A CDR-grafted heavy chain according to Claim 2 comprising donor residues at positions 2, 4, 6, 25, 36, 37, 39, 47, 48, 93, 94, 103, 104, 106 and 107.
4. A CDR-grafted heavy chain according to Claim 2 or 3, comprising donor residues at one, some or all of positions:
1 and 3,
69 (if 48 is different between donor and acceptor),
38 and 46 (if 48 is the donor residue),
67,
82 and 18 (if 67 is the donor residue),
91, and
any one or more of 9, 11, 41, 87, 108, 110 and 112.
5. A CDR-grafted heavy chain according to any of the preceding comprising donor CDRs at positions 26-35, 50-65 and 95-100.
6. A CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 1 and/or 3 and 46 and/or 47.

- 68 -

7. A CDR-grafted light chain according to Claim 6 comprising donor residues at positions 46 and 47.
8. A CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 46, 48, 58 and 71.
9. A CDR-grafted light chain according to Claim 8 comprising donor residues at positions 46, 48, 58 and 71.
10. A CDR-grafted light chain according to Claim 8 or 9, comprising donor residues at positions 2, 4, 6, 35, 36, 38, 44, 47, 49, 62, 64-69, 85, 87, 98, 99, 101 and 102.
11. A CDR-grafted light chain according to Claim 9 or 10, comprising donor residues at one, some or all of positions:
1 and 3,
63,
60 (if 60 and 54 are able to form a potential saltbridge),
70 (if 70 and 24 are able to form a potential saltbridge),
73 and 21 (if 47 is different between donor and acceptor),
37 and 45 (if 47 is different between donor and acceptor), and
any one or more of 10, 12, 40, 83, 103 and 105.
12. A CDR-grafted light chain according to any one of Claims 6-11, comprising donor CDRs at positions 24-34, 50-56 and 89-97.

- 69 -

13. A CDR-grafted antibody molecule comprising at least one CDR-grafted heavy chain according to any one of Claims 1-5 and at least one CDR-grafted light chain according to any one of Claims 6-12.
14. A CDR-grafted antibody molecule according to Claim 13, which is a site-specific antibody molecule.
15. A CDR-grafted antibody molecule according to Claim 13 which has specificity for an interleukin, hormone or other biologically active compound or a receptor therefor.
16. A CDR-grafted antibody heavy or light chain or molecule according to any one of the preceding claims comprising human acceptor residues and non-human donor residues.
17. A DNA sequence which codes for a CDR-grafted heavy chain according to Claim 1 or a CDR-grafted light chain according to Claim 6 or Claim 8.
18. A cloning or expression vector containing a DNA sequence according to Claim 17.
19. A host cell transformed with a DNA sequence according to Claim 17.
20. A process for the production of a CDR-grafted antibody sequence according to Claim 17 in a transformed host cell.
21. A process for producing a CDR-grafted antibody product comprising:

- 70 -

- (a) producing in an expression vector an operon having a DNA sequence which encodes an antibody heavy chain according to Claim 1;
 - and/or
 - (b) producing in an expression vector an operon having a DNA sequence which encodes a complementary antibody light chain according to Claim 6 or Claim 8;
 - (c) transfecting a host cell with the or each vector;
 - and
 - (d) culturing the transfected cell line to produce the CDR-grafted antibody product.
22. A therapeutic or diagnostic composition comprising a CDR-grafted antibody heavy chain according to Claim 1, or a CDR-grafted light chain according to Claim 6 or Claim 8, or a CDR-grafted antibody molecule according to Claim 13 in combination with a pharmaceutically acceptable carrier, diluent or excipient.
23. A method of therapy or diagnosis comprising administering an effective amount of a CDR-grafted heavy chain according to Claim 1, or a CDR-grafted light chain according to Claim 6 or Claim 8, or a CDR-grafted antibody molecule according to Claim 13 to a human or animal subject.



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<p>(21) International Application Number: PCT/GB90/02017 (22) International Filing Date: 21 December 1990 (21.12.90) (30) Priority data: 8928874.0 21 December 1989 (21.12.89) GB (71) Applicant (for all designated States except US): CELLTECH LIMITED (GB/GB); 216 Bath Road, Slough, Berkshire SL1 4EN (GB). (72) Inventors; and (75) Inventors/Applicants (for US only): ADAIR, John, Robert (GB/GB); 23 George Road, Stokenchurch, High Wycombe, Buckinghamshire HP14 3RN (GB). ATHWAL, Diljjet, Singh (GB/GB); Flat 35, Knollys House, Tavistock Square, London WC1 (GB). EMTAGE, John, Spencer (GB/GB); 49 Temple Mill Island, Temple, Marlow, Buckinghamshire SL7 1SQ (GB).</p>	<p>(74) Agent: MERCER, Christopher, Paul; Carpmaels & Ransford, 43 Bloomsbury Square, London WC1A 2RA (GB). (81) Designated States: AT, AT (European patent), AU, BB, BE (European patent), BF (OAPI patent), BG, BJ (OAPI patent), BR, CF (OAPI patent), CG (OAPI patent), CH, CH (European patent), CM (OAPI patent), DE, DE (European patent), DK, FI, FR (European patent), GA (OAPI patent), GB, GB (European patent), GR, HU, IT (European patent), JP, KP, KR, LK, LU, LU (European patent), MC, MG, ML (OAPI patent), MR (OAPI patent), MW, NL, NL (European patent), NO, RO, SD, SE, SE (European patent), SN (OAPI patent), SU, TD (OAPI patent), TG (OAPI patent), US. Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments. With a request for rectification under Rule 91.1(f).</i></p>	
<p>(54) Title: HUMANISED ANTIBODIES</p> <p>(57) Abstract</p> <p>CDR-grafted antibody heavy and light chains comprise acceptor framework and donor antigen binding regions, the heavy chains comprising donor residues at at least one of positions (6, 23) and/or (24, 48) and/or (49, 71) and/or (73, 75) and/or (76) and/or (78) and (88) and/or (91). The CDR-grafted light chains comprise donor residues at at least one of positions (1) and/or (3) and (46) and/or (47) or at at least one of positions (46, 48, 58) and (71). The CDR-grafted antibodies are preferably humanised antibodies, having non human, e.g. rodent, donor and human acceptor frameworks, and may be used for <i>in vivo</i> therapy and diagnosis. A generally applicable protocol is disclosed for obtaining CDR-grafted antibodies.</p>		

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1/18

```
1 GAATTCCCAA AGACAAAatg gattttcaag tgcagatttt cagcttcctg
51 ctaatcagtg cctcagtcat aatataccaga ggacaaattg ttctcaccca
101 gtctccagca atcatgtctg catctccagg ggagaaggtc accatgacct
151 gcagtgccag ctcaagtgtg agttacatga actggtagca gcagaagtca
201 ggcacctccc ccaaaagatg gatttatgac acatccaaac tggcttctgg
251 agtccctgct cacttcaggg gcagtgggtc tgggacctct tactcttca
301 caatcagcgg catggaggct gaagatgctg ccacttatta ctgccagcag
351 tggagtagta accattcac gttcggctcg gggacaaagt tggaaataaa
401 ccgggctgat actgcaccaa ctgtatccat cttcccacca tccagtgagc
451 agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac
501 cccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa
551 tggcgtcctg aacagttgga ctgatacagga cagcaaagac agcacctaca
601 gcatgagcag caccctcacg ttgaccaagg acgagtatga acgacataac
651 agctatacct gtgaggccac tcacaagaca tcaacttcac ccattgtcaa
701 gagcttcaac aggaatgagt gtTAGAGACA AAGGTCCTGA GACGCCACCA
751 CCAGCTCCCA GCTCCATCCT ATCTTCCCTT CTAAGGTCTT GGAGGCTTCC
801 CCACAAGCGC tTACCACTGT TGCGGTGCTC TAAACCTCCT CCCACCTCCT
851 TCTCCTCCTC CTCCCTTTCC TTGGCTTTTA TCATGCTAAT ATTTGCAGAA
901 AATATTCAAT AAAGTGAGTC TTTGCCTTGA AAAAAAAAAA AAA
(SEQ ID NO:4)
```

FIG. 1a

```
1 MDFQVQIFSF LLISASVIIS RGOQIVLTQSP AIMSASPGEK VTMTCSASSS
51 VSYMNWYQQK SGTSPKRWIY DTSKLAGSVP AHFRGSGSGT SYSLTISGME
101 AEDAATYYCQ QWSSNPFTFG SGTKLEINRA DTAPTVSIFP PSSEQLTSGG
151 ASVVCFLNNF YPKDINVKWK IDGSERQNGV LNSWTDQDSK DSTYSMSSTL
201 TLTKDEYERH NSYTCEATHK TSTSPIVKSF NRNEC* (SEQ ID NO:5)
```

FIG. 1b

```

1 GAATTCCCCT CTCCACAGAC ACTGAAAAC CTGACTCAAC ATGGAAAGGC
51 ACTGGATCTT TCTACTCCTG TTGTCAGTAA CTGCAGGTGT CCACTCCCAG
101 GTCCAGCTGC AGCAGTCTGG GGCTGAACTG GCAAGACCTG GGGCCTCAGT
151 GAAGATGTCC TGCAAGGCTT CTGGCTACAC CTTTACTAGG TACACGATGC
201 ACTGGGTAAG ACAGAGGCCT GGACAGGGTC TGGAAATGGAT TGGATACATT
251 ATTCCTAGCC GTGGTTATAC TAATTACAAT CAGAAGTTCA AGGACAAGGC
301 CACATTGACT ACAGACAAAT CCTCCAGCAC AGCCTACATG CAACTGAGCA
351 GCCTGACATC TGAGGACTCT GCAGTCTATT ACTGTGCAAG ATATTATGAT
401 GATCATTACT GCCTTGACTA CTGGGGCCAA GGCACCACTC TCACAGTCTC
451 CTCAGCCAAA ACAACAGCCC CATCGGTCTA TCCACTGGCC CCTGTGTGTG
501 GAGATACAAC TGGCTCCTCG GTGACTCTAG GATGCCTGGT CAAGGGTTAT
551 TTCCCTGAGC CAGTGACCTT GACCTGGAAC TCTGGATCCC TGTCCAGTGG
601 TGTGCACACC TTCCCAGCTG TCCTGCAGTC TGACCTCTAC ACCCTCAGCA
651 GCTCAGTGAC TGTAACCTCG AGCACCTGGC CCAGCCAGTC CATCACCTGC
701 AATGTGGCCC ACCCGGCAAG CAGCACCAAG GTGGACAAGA AAATTGAGCC
801 ACCTCTTGGG TGGACCATCC GTCTTCATCT TCCCTCCAAA GATCAAGGAT
851 GTAICTCATGA TCTCCCTGAG CCCCATAGTC ACATGTGTGG TGGTGGATGT
901 GAGCGAGGAT GACCCAGATG TCCAGATCAG CTGGTTTGTG AACAACTGG
951 AAGTACACAC AGCTCAGACA CAAACCCATA GAGAGGATTA CAACAGTACT
1001 CTCCGGGTGG TCAGTGCCCT CCCCATCCAG CACCAGGACT GGATGAGTGG
1051 CAAGGAGTTC AAATGCAAGG TCAACAACAA AGACCTCCCA GCGCCCATCG
1101 AGAGAACCAT CTCAAACCC AAAGGGTCAG TAAGAGCTCC ACAGGTATAT
1151 GTCTTGCCCT CACCAGAAGA AGAGATGACT AAGAAACAGG TCACTCTGAC
1201 CTGCATGGTC ACAGACTTCA TGCCTGAAGA CATTTACGTG GAGTGGACCA
1251 ACAACGGGAA AACAGAGCTA AACTACAAGA AACTGAACC AGTCTGGAC
1301 TCTGATGGTT CTTACTTCAT GTACAGCAAG CTGAGAGTGG AAAAGAAGAA
1351 CTGGGTGGAA AGAAATAGCT ACTCCTGTTC AGTGGTCCAC GAGGGTCTGC
1401 ACAATACCA CACGACTAAG AGCTTCTCCC GGACTCCGGG TAAATGAGCT
1451 CAGCACCCAC AAAACTCTCA GGTCCAAAGA GAGACCCACA CTCATCTCCA
1501 TGCTTCCCTT GTATAAATAA AGCACCCAGC AATGCCTGGG ACCATGTAAA
1551 AAAAAAAAAA AAAGGAATTC (SEQ ID NO:6)

```

FIG. 2a

DKT 3 HEAVY CHAIN PROTEIN SEQUENCE DEDUCED FROM DNA SEQUENCE

1	<u>MERHWIFLLL</u>	<u>LSVTAGVHSQ</u>	VQLQQSGAEL	ARPGASVKMS	CKASGYTFTR
51	YTMHWVKQRP	GQGLEWIGYI	NPSRGYTNYN	QKFKDKATLT	TDKSSSTAYM
101	QLSSLTSEDS	AVYYCARYYD	DHYCLDYWGQ	GTTLTVSSAK	TTAPSVYPLA
151	PVCGDTTGSS	VTLGCLVKGY	FPEPVTLTWN	SGSLSSGVHT	FPAVLQSDLY
201	TLSSSVTVTS	STWPSQSITC	NVAHPASSTK	VDKKIEPRGP	TIKPCPPCKC
251	PAPNLLGGPS	VFIFPPKIKD	VLMISSLPIV	TCVVVDVSED	DPDVQISWFV
301	NNVEVHTAQT	QTHREDYNST	LRVVSALPIQ	HQDWMSGKEF	KCKVNNKDLP
351	APIERTISKP	KGSVRAPQVY	VLPPPEEEMT	KKQVTLTCMV	TDFMPEDIYV
401	EWTNNGKTEL	NYKNTEPVL	SDGSYFMYSK	LRVEKKNWVE	RNSYSCSVVH
451	EGLHNHHTTK	SFSRTPGK*	(SEQ ID NO: 7)		

FIG. 2b

4/18

```

1                23                42
NN      N                N      N      N
RES TYPE  SBspSPESsSsBSbSsSsSsPSPSPsPSsse*s*s*p*Pi^ISsSe
Dkt3vl    QIVLTQSPAIMSASPGEKVTMTCSASS.SVSYMNWYQQKSGT
REI       DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQIPPGK
? ?
      CDR1 (LOOP)      *****
      CDR1 (KABAT)    *****

                    56                85
N  NN
RES TYPE  *IsiPpIeesesssSBEsePsPSBSSEsPspSpsseesSPePb
Dkt3vl    SPKRWIYDTSKLAGVPAHFRGSGSGTSYSLTISGMEAEDAAT
REI       APKLLIYEASNLQAGVPSRFSGSGSGTDYTETISSLQPEDIAT (SEQ
ID NO:8)  ? ??                ? ?
      ***** CDR2 (LOOP/KABAT)

                    102  108
RES TYPE  PiPIPIes**iPIIsPPSPSPSS
Dkt3vl    YYCQQWSSNPFTFGSGTKLEINR (SEQ ID NO:29)
REIvl     YYCQQYQSLPYTFGGTKLQITR (SEQ ID NO:9)
          ? ?
          ***** CDR3 (LOOP)
          ***** CRD3(KABAT)

```

FIG. 3

```

NN N                23 26    32 35  N39  43
RES TYPE  SESPs^SBssSsSSssSpSpSPsPSEbSBssBePi^PIpiesss
Dkt3h     QVQLQQSGAELARPGASVKMSCKASGYTFTRYTMNHWVKQRPGQ
KDL       QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGK
           ?                ??

*****          CDR1 (LOOP)
*****          CDR1 (KABAT)

           52a   60     65     NN  N   82abc   89
RES TYPE  IIeIppp^sssssss^ps^pSSsbSpseSsSseSp^pSpSssS^ePb
Dkt3vh    GLEWIGYINPSRGYTNTNQKFKRKATLTTDKSSSTAYMQLSSLTSEDSAV
KDL       GLEWVAIIWDDGSDQHYADSVKGRFTISRDNskNTLELQMDSLPPEDTGV
           ??                ? ? ? ? ?

*****          CDR2 (LOOP)
*****          CDR2 (KABAT)

           92 N                107    113
RES TYPE  PiPIEissssiisssbibi*EIPIP*spSBSS
Dkt3vh    YYCARYYDDHY.....CLDYWGQGTTLTVSS (SEQ ID NO:30)
KDL       YFCARDGGHGFcssASCFGPDYWGQGTpVTVSS (SEQ ID NO:10)
           *****          CRD4 (KABAT/LOOP)

```

FIG. 4

6/18

DKT 3 HEAVY CHAIN CDR GRAFTS

1. gh341 and derivatives

	1	26	35	39	43	
DKt3vh	QVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRPGQ					
gh341	QVQLVESGGGVVQDGRSLRLSCSSSGYTFTRYTMHWVRQAPGK					JA178
gh341A	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA185
gh341E	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA198
gh341*	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA207
gh341*	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA209
gh341D	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA197
gh341*	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA199
gh341C	QVQLVQSGGGVVQPGRSLRLSCKASGYTFTRYTMHWVRQAPGK					JA184
gh341*	QVQLVQSGGGVVQPGRSLRLSCSASGYTFTRYTMHWVRQAPGK					JA203
gh341*	QVQLVESGGGVVQPGRSLRLSCSASGYTFTRYTMHWVRQAPGK					JA205
gh341B	QVQLVESGGGVVQPGRSLRLSCSSSGYTFTRYTMHWVRQAPGK					JA183
gh341*	QVQLVQSGGGVVQPGRSLRLSCSASGYTFTRYTMHWVRQAPGK					JA204
gh341*	QVQLVESGGGVVQPGRSLRLSCSASGYTFTRYTMHWVRQAPGK					JA206
gh341*	QVQLVQSGGGVVQPGRSLRLSCSASGYTFTRYTMHWVRQAPGK					JA208
KDL	QVQLVESGGGVVQPGRSLRLSCSSSGIFSSYAMYWVRQAPGK					

FIG. 5a

7/18

	44	50	65	83	
Dkt3vh	GLEWIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLT				
gH341	GLEWVAYINPSRGYTNYNQKFKDRFTISRDNKNTLFLQMDSLR				JA178
gH341A	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA185
gH341E	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA198
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKNTAFQMDSLR				JA207
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISRDNKNTAFQMDSLR				JA209
gH341D	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKNTLFLQMDSLR				JA197
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISRDNKNTLFLQMDSLR				JA199
gH341C	GLEWVAYINPSRGYTNYNQKFKDRFTISRDNKNTLFLQMDSLR				JA184
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA207
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA205
gH341B	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA183
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA204
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKSTAFQMDSLR				JA206
gH341*	GLEWIGYINPSRGYTNYNQKVKDRFTISIDKSKNTAFQMDSLR				JA208
KDL	GLEWVAI I WDDGSDQHYADSVKGRFTISRDNKNTLFLQMDSLR				

FIG. 5b

8/18

	84	95	102	113		SEQ ID NO:
Okt3vh	SEDSAVYYCARYYDDHY.....		CLDYWGQGTTLTVSS			30
gH341	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA178	11
gH341A	PEDTAVYYCARYYDDHY.....		CLDYWGQGTTLTVSS		JA185	12
gH341E	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA198	13
gH341*	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA207	14
gH341D	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA197	15
gH341*	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA209	16
gH341*	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA199	17
gH341C	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA184	18
gH341*	PEDTAVYYCARYYDDHY.....		CLDYWGQGTTLTVSS		JA203	19
gH341*	PEDTAVYYCARYYDDHY.....		CLDYWGQGTTLTVSS		JA205	20
gH341B	PEDTAVYYCARYYDDHY.....		CLDYWGQGTTLTVSS		JA183	21
gH341*	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA204	22
gH341*	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA206	23
gH341*	PEDTGVYFCARYYDDHY.....		CLDYWGQGTTLTVSS		JA208	24
KOL	PEDTGVYFCARDGGHGFCSASCFGPDYWGQGPVTVSS					10

FIG. 5c

9/18

OKT3 LIGHT CHAIN CDR GRAFTING

1. gL221 and derivatives

	1	24	34	42	
Okt3v1	<u>QIVLTQSPAOMSASPGEKVTMTCSASS</u> .SVSYMNWYQQKSGT				
gL221	<u>DIQMTQSPSSLSASVGDRVITITCSASS</u> .SVSYMNWYQQTPGK				
gL221A	<u>QIVMTQSPSSLSASVGDRVITITCSASS</u> .SVSYMNWYQQTPGK				
gL221B	<u>QIVMTQSPSSLSASVGDRVITITCSASS</u> .SVSYMNWYQQTPGK				
gL221C	<u>DIQMTQSPSSLSASVGDRVITITCSASS</u> .SVSYMNWYQQTPGK				
REI	<u>DIQMTQSPSSLSASVGDRVITITCSASS</u> QDIKYLWYQQTPGK				
	43	50	56	85	
Okt3v1	<u>SPKRWIYDTSKLAGVPAHFRGSGSGT</u> SYSLTISGMEAEDAAT				
gL221	<u>APKLLIYDTSKLAGVPSRFGSGSGT</u> DYFTFTISSLQPEDIAT				
gL221A	<u>APKRWIYDTSKLAGVPSRFGSGSGT</u> DYFTFTISSLQPEDIAT				
gL221B	<u>APKLLIYDTSKLAGVPSRFGSGSGT</u> DYFTFTISSLQPEDIAT				
gL221C	<u>APKRWIYDTSKLAGVPSRFGSGSGT</u> DYFTFTISSLQPEDIAT				
REI	<u>APKLLIYEASNLOAGVPSRFGSGSGT</u> DYFTFTISSLQPEDIAT (SEQ ID NO:8)				
	86	91	96	108	
Okt3v1	<u>YYCQOWSSNP</u> FTFGSGTKLEINR (SEQ ID NO:29)				
gL221	<u>YYCQOWSSNP</u> PETFGQGTKLQITR (SEQ ID NO:25)				
gL221A	<u>YYCQOWSSNP</u> PETFGQGTKLQITR (SEQ ID NO:26)				
gL221B	<u>YYCQOWSSNP</u> PETFGQGTKLQITR (SEQ ID NO:27)				
gL221C	<u>YYCQOWSSNP</u> PETFGQGTKLQITR (SEQ ID NO:28)				
REI	<u>YYCQOYQSLPY</u> TFGQGTKLQITR (SEQ ID NO:9)				

CDR'S ARE UNDERLINED

FRAMEWORK RESIDUES INCLUDED IN THE GENE ARE DOUBLE UNDERLINED

FIG. 6

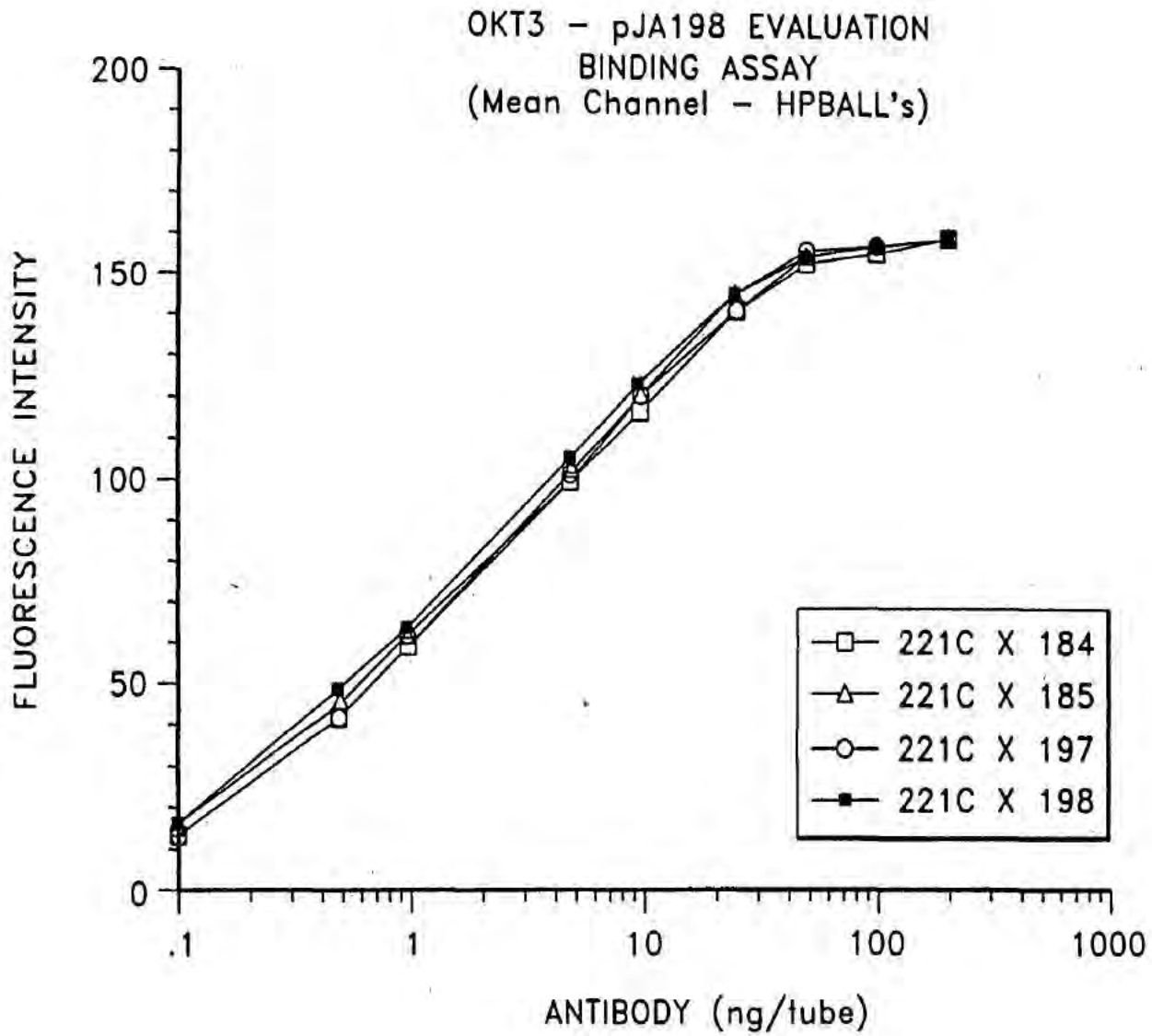


FIG. 7

OKT3 - pJA198 EVALUATION
BLOCKING ASSAY
(Mean Channel - HPBALL's)

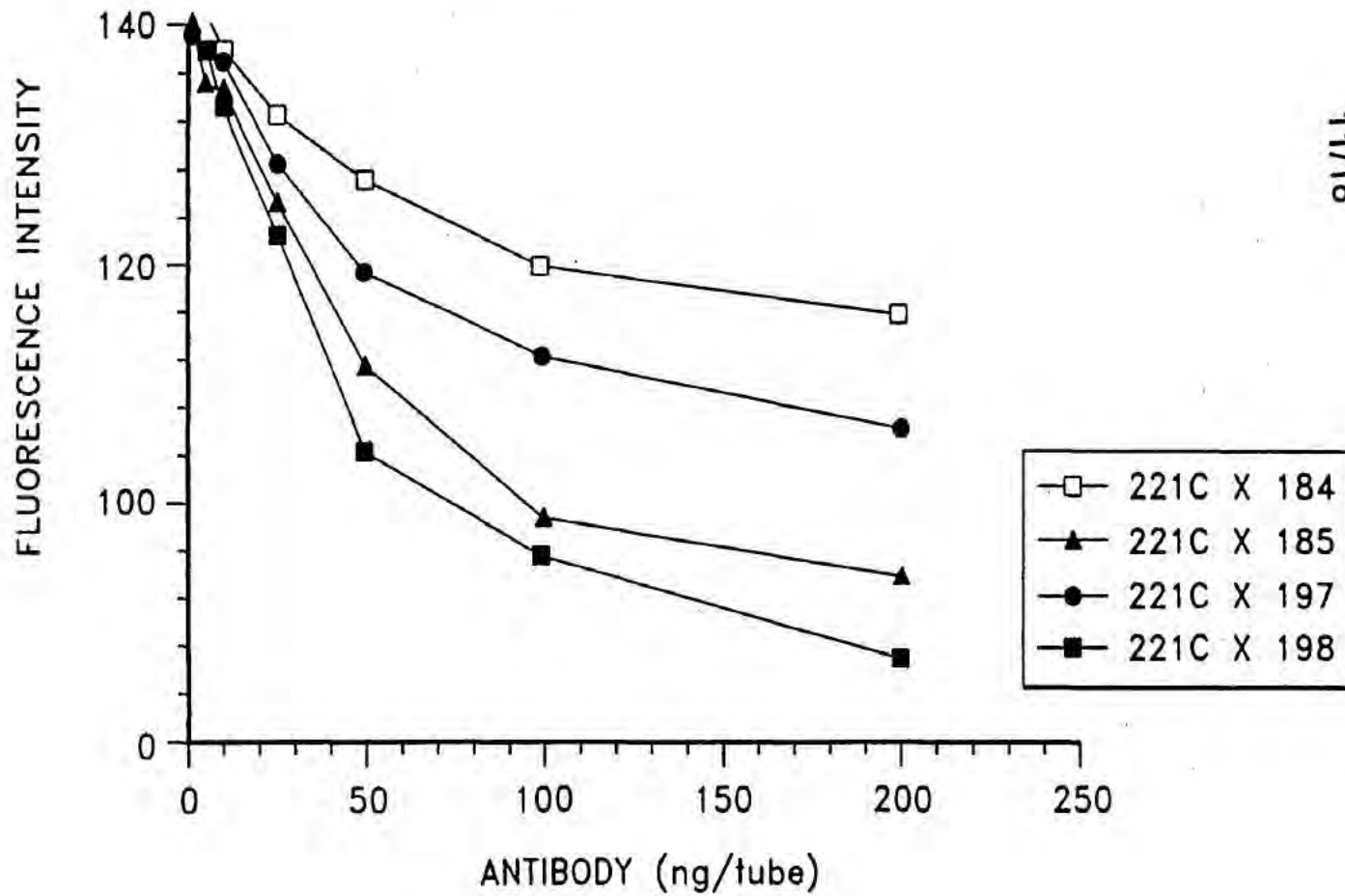


FIG. 8

BLOCKING ASSAY
(Mean Channel - HPBALL's)

12/18

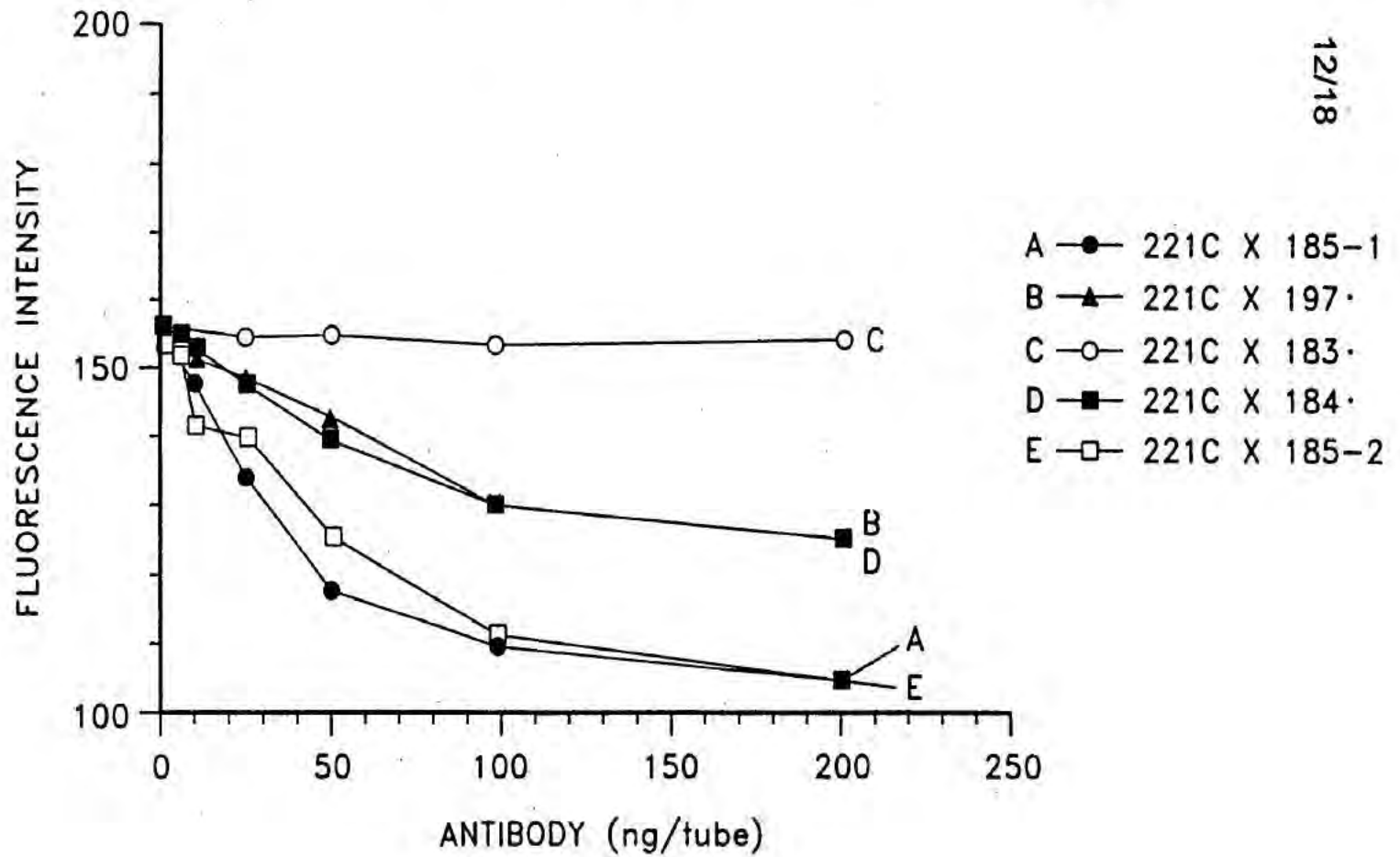
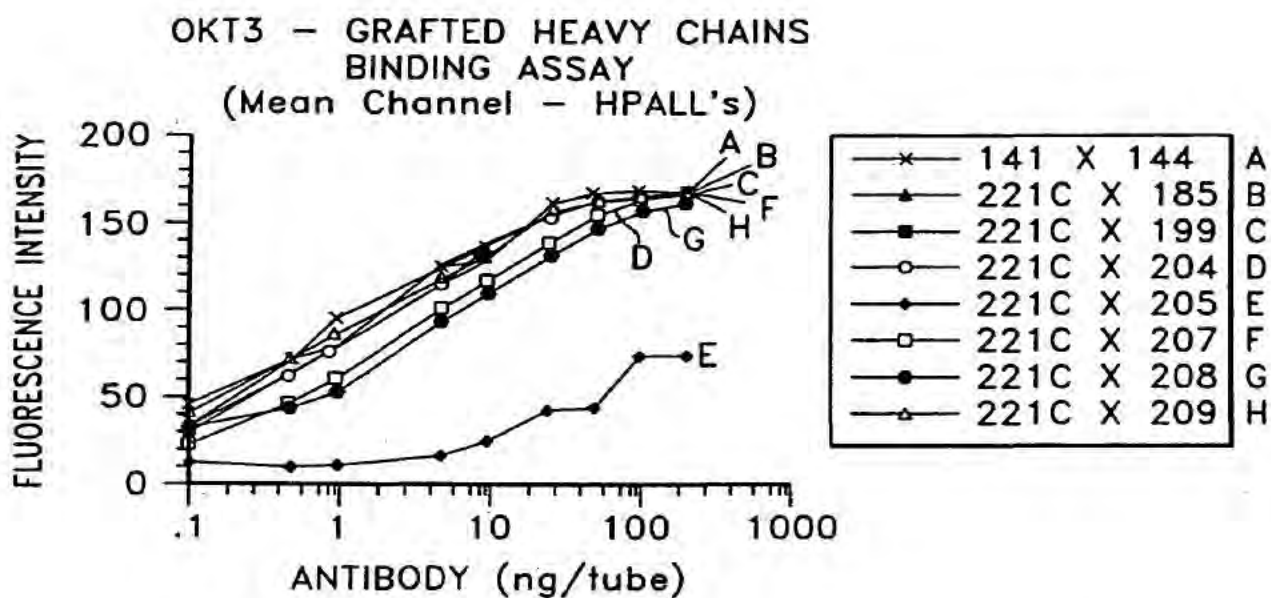


FIG. 9

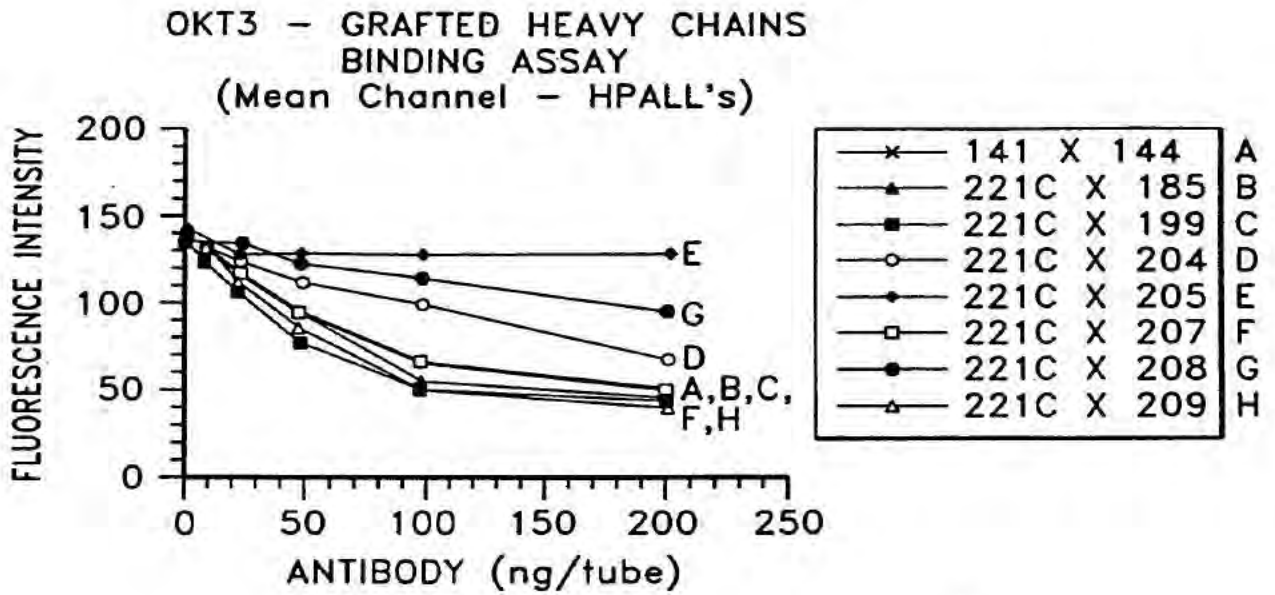
13/18



—●—	(205)	—, —, —, 24, 48, 49, 71, 73, 76, 78, 88, 91,
—●—	(208)	6, —, —, 24, 48, 49, 71, 73, —, 78, —, —,
—○—	(204)	6, —, —, 24, 48, 49, 71, 73, 76, 78, —, —,
—■—	(199)	6, 23, 24, 48, 49, —, —, —, —, —, —,
—□—	(207)	6, 23, 24, 48, 49, 71, 73, —, 78, —, —,
—▲—	(185)	6, 23, 24, 48, 49, 71, 73, 76, 78, 88, 91,
—△—	(209)	6, 23, 24, 48, 49, —, —, —, —, 78, —, —,
—x—	141 X 144	

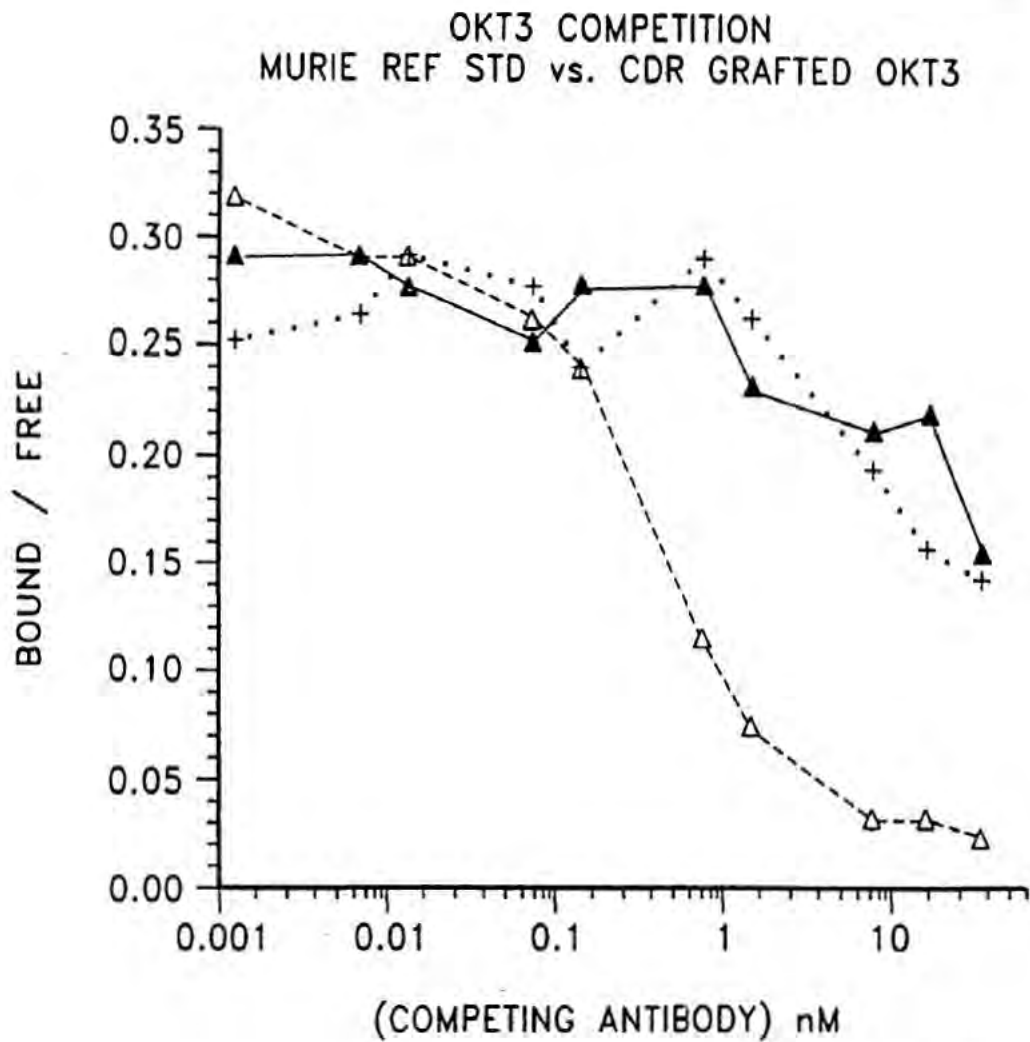
FIG. 10a

14/18



—●—	(205)	—, —, —, 24, 48, 49, 71, 73, 76, 78, 88, 91,
—●—	(208)	6, —, —, 24, 48, 49, 71, 73, —, 78, —, —,
—○—	(204)	6, —, —, 24, 48, 49, 71, 73, 76, 78, —, —,
—■—	(199)	6, 23, 24, 48, 49, —, —, —, —, —, —,
—□—	(207)	6, 23, 24, 48, 49, 71, 73, —, 78, —, —,
—▲—	(185)	6, 23, 24, 48, 49, 71, 73, 76, 78, 88, 91,
—▲—	(209)	6, 23, 24, 48, 49, —, —, —, —, 78, —, —,
—x—	141 X 144	—, —, —, —, —, —, —, —, —, —, —,

FIG. 10b



17/18

- △--- MEDIA CNTRL
REF IN MEDIA
-+..... CDR 221 x 178 *
#1
- ▲— CDR 221 x 178 *
#2

* PROTEIN CONCENTRATIONS
APPROXIMATE [ELISA]

FIG. 12

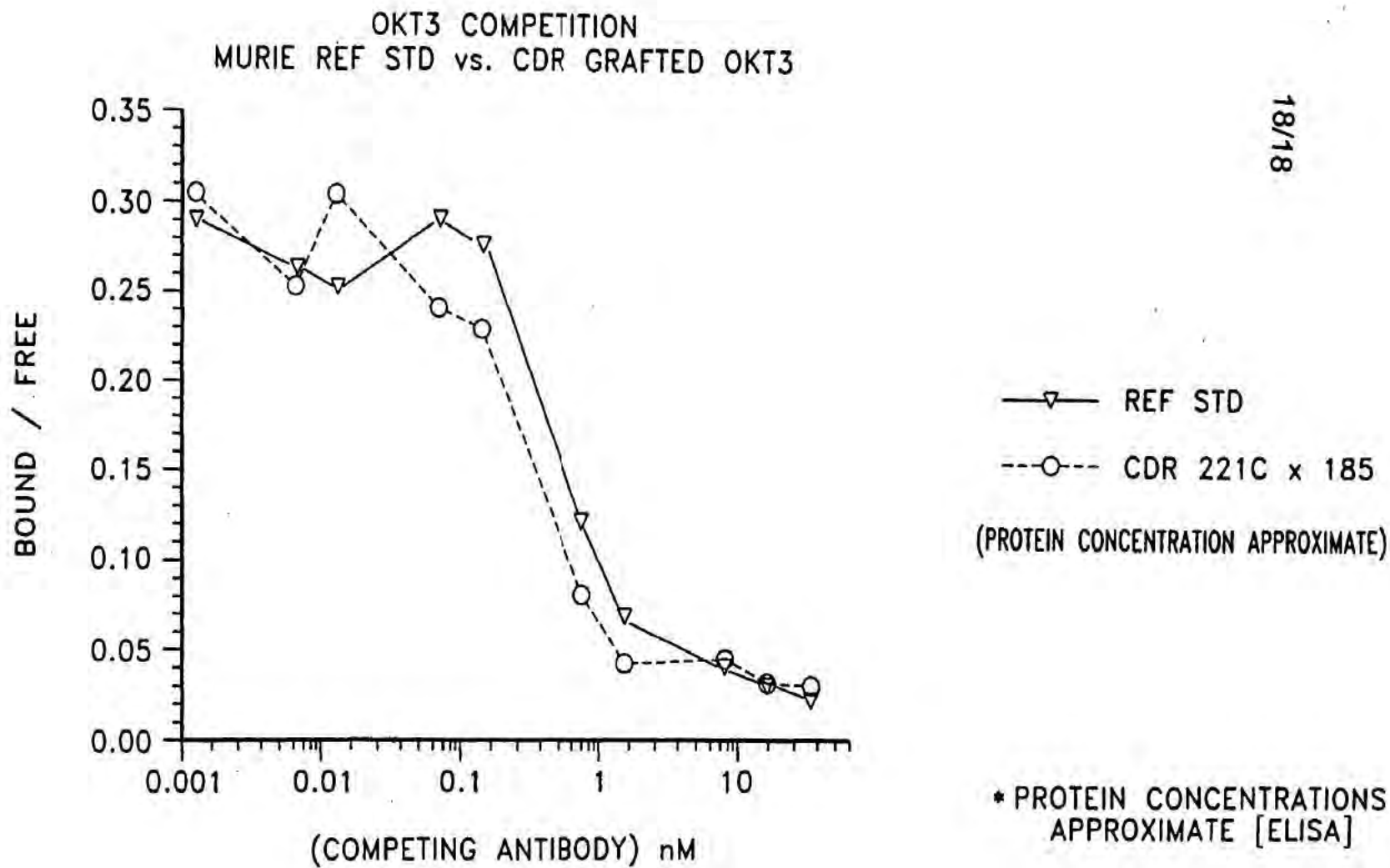


FIG. 13

COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name; and

I verily believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: HUMANISED ANTIBODIES the specification of which:

is attached hereto.

was filed on 21 December 1990 as International Application Serial No. PCT/GB90/02017 and was amended on _____ (if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to the examination of this application in accordance with 37 CFR § 1.56(a).

I hereby claim foreign priority benefits under 35 U.S.C. § 119 of any foreign application(s) for patent or inventor's certificate listed below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of any application on which priority is claimed:

Country	Number	Date Filed	Priority Claimed
<u>U.K.</u>	<u>8928874.0</u>	<u>21.12.89</u>	<u>yes</u>
_____	_____	_____	_____
_____	_____	_____	_____

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I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose material information as defined in 37 CFR § 1.56(a) which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

Application Serial No.	Filing Date	Status (patented, pending)
_____	_____	_____
_____	_____	_____
_____	_____	_____

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:
Francis A. Paintin

Registration Nos. 19,386
of the firm of **WOODCOCK WASHBURN KURTZ MACKIEWICZ & NORRIS**, One Liberty Place - 46th Floor, Philadelphia, Pennsylvania 19103, and

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the

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United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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	Post Office Address		

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DATE FILED: 05/28/2010
DOCUMENT NO: 28

DOCKET NO.: CARP0001-112 PATENT
PRELIMINARY AMENDMENT AND REQUEST FOR INTERFERENCE UNDER 37
C.F.R. § 42.202 DATED NOVEMBER 21, 2005

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application of: John R. Adair, Diljeet S. Athwal and John S. Emtage

Serial No.: Not Yet Assigned

Art Unit: Not Yet Assigned

Filing Date: November 21, 2005

Examiner: Not Yet Assigned

For: HUMANISED ANTIBODIES

Customer No.: 34132

EXPRESS MAIL LABEL NO.: EV146 601 565US
DATE OF DEPOSIT: November 21, 2005

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

PRELIMINARY AMENDMENT
AND
REQUEST FOR INTERFERENCE UNDER 37 CFR § 42.202

Applicant respectfully requests entry of the following amendments prior to the calculation of filing fees:

Amendments To The Specification begin on page 2 of this paper.

Listing of the Claims, reflecting current amendments, begins on page 3 of this paper.

Remarks begin on page 4 of this paper.

The **Conclusion** is found on page 12.

Appendix A is found on page 14.

Appendix B is found on page 17.

Appendix C is found on page 19.

Appendix D is found on page 20.

Appendix E is found on page 21.

Carter Exhibit 2003
Carter v. Adair
Interference No. 105,744

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph containing the cross-reference to related applications on page 1 of the specification with the following:

This application is a Continuation of U.S. Application Serial No. 08/846,658, Filed May 1, 1997, which is a Continuation of U.S. Application Serial No. 08/303,569, Filed September 7, 1994, now U.S. Patent No. 5,859,205, Issued January 12, 1999, which is a File Wrapper Continuation of U.S. Application Serial No. 07/743,329, Filed September 17, 1991, Abandoned, which is a 35 U.S.C. 371 National Stage Application of International Application No. PCT/GB90/02017, International Filing Date of December 21, 1990, which claims priority to Great Britain Application No. 8928874.0, Filed December 21, 1989, all applications are incorporated by reference herein in their entireties.

LISTING OF CLAIMS

This listing of claims represents the current status of the claims.

Claims 1-23 (**cancelled**)

Claim 24 (new) A humanised antibody heavy chain variable domain comprising non-human complementarity determining region amino acid residues which bind an antigen and a human framework region wherein said framework region comprises an amino acid substitution at a residue selected from the group consisting of 23, 24, 49, 71, 73, and 78, and combinations thereof, as numbered according to Kabat.

Claim 25 (new) A humanised antibody comprising the variable domain of claim 24.

REMARKS

Claims 24 to 25 are pending. Applicants hereby request an interference in accordance with 37 CFR § 42.202. It is noted that U.S. Patent No. 6,407,213, whose claims present the basis for an interference, is classified in Class 530, and was examined by Examiners Minh-Tam Davis and Anthony C. Caputa.

Compliance with 37 CFR § 42.202

Applicants respectfully submit that all requirements of 37 CFR § 42.202 have been met and respectfully request examination of the present application and declaration of an interference.

(a) Identifying The Patent

Applicants request that an interference be declared between Applicants' above-identified application and U.S. Patent No. 6,407,213 B1 (hereinafter the 213 patent), issued to Carter et al. on June 18, 2002, a copy of which is enclosed herewith.

(b) Compliance with 35 USC § 135(b)

Although the present rules do not require a showing of compliance under 35 USC § 135(b), Applicants submit the following to advance the examination of the present application to allowability. The present application is a Continuation of U.S. Application Serial No. 08/846,658, Filed May 1, 1997, which is a Continuation of U.S. Application Serial No. 08/303,569, Filed September 7, 1994, now U.S. Patent No. 5,859,205, Issued January 12, 1999, which is a File Wrapper Continuation of U.S. Application Serial No. 07/743,329, Filed September 17, 1991, Abandoned, which is a 35 U.S.C. 371 National Stage Application of International Application No. PCT/GB90/02017, International Filing Date of December 21, 1990 (hereinafter "the PCT application," a copy of which is enclosed herewith), which claims priority to Great Britain Application No. 8928874.0, Filed December 21, 1989. Claims 1-23 as filed in the PCT application are attached as Appendix A.

Under 35 USC § 135(b)(1), Applicants must show that they had a claim to the same, or substantially the same, subject matter as a claim of the 213 patent within one year of the issuance of the 213 patent, or June 18, 2003. The 213 patent issued on June 18, 2002. The PCT application was filed on December 21, 1990, over 10 years earlier than the 213 patent issued. The time limit of Section 135(b)(1) has been complied with fully. See *Corbett v. Chisholm*, 196 USPQ 337 (CCPA 1977).

To meet the "same or substantially the same invention" requirement of Section 135(b)(1), Applicants must show that their claim contained all material limitations, i.e. limitations necessary to patentability, of the claim of the 213 patent alleged to be to the same, or substantially the same, invention. *Corbett v. Chisholm*, 196 USPQ 337 (C.C.P.A. 1977), citing *Wetmore v. Miller*, 477 F.2d 960, 177 USPQ 699 (C.C.P.A. 1973).

As is evident from Appendix A, Applicants made a claim for the same, or substantially the same, subject matter as a claim of the 213 patent well before the issuance of the 213 patent. Claim 16 of the PCT application, as depending from claim 8, is to substantially the same subject matter as at least claim 1 of the 213 patent. For the Office's convenience, all three claims are duplicated below.

Claim 8 of the PCT application: A CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 46, 48, 58 and 71.

Claim 16 of the PCT application: A CDR-grafted antibody heavy or light chain or molecule according to any one of the preceding claims comprising human acceptor residues and non-human donor residues.

Claim 1 of the 213 patent: A humanized antibody variable domain comprising non-human Complementarity Determining Region (CDR) amino acid residues

DOCKET NO.: CARP0001-112 **PATENT**
PRELIMINARY AMENDMENT AND REQUEST FOR INTERFERENCE UNDER 37
C.F.R. § 42.202 DATED NOVEMBER 21, 2005

which bind an antigen incorporated into a human antibody variable domain, and further comprising a Framework Region (FR) amino acid substitution at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 36H, 39H, 43H, 45H, 69H, 70H, 74H, and 92H, utilizing the numbering system set forth in Kabat.

Both claim 16 of the PCT application, as it depends from claim 8, and claim 1 of the 213 patent are directed to variable domains comprising non-human Complementarity Determining Regions (“CDRs”) that bind antigen, i.e., antigen binding regions, human framework regions, and a non-human framework amino acid at residue 58 of the light chain, using Kabat numbering. Both claims also comprise a human framework region; claim 1 of the 213 patent simply recites it differently -- if one incorporates non-human CDR amino acid residues into a human antibody variable domain, one ends up with a human framework region. Further, the 213 patent defines “humanized antibody” as an antibody having a framework region “having substantially the amino acid sequence of a human immunoglobulin,” i.e., a human framework region (see column 8, lines 11-17, of the 213 patent). “Antigen binding regions,” as recited in claim 8 of the PCT application, refers to CDRs (see page 8, lines 10-13, of the PCT application). As indicated on page 8, lines 22-24 of the PCT application, all numbering is according to Kabat. Claim 16 implicitly contains the recitation that the amino acid be substituted. As indicated on page 17, lines 1-19 of the PCT application, substitution of the non-human framework residues for the human framework residues is required when the donor and framework residue at any of the recited positions differ. While Applicants’ claim recites a “light chain” and claim 1 of the 213 patent recites a “variable domain,” Applicants submit that this is merely a difference in scope, and not a material difference. *See Corbett.*

(c) Presentation Of A Proposed Count

Applicants present in Appendix B, attached hereto, a proposed count that is presented in the “alternative” format as claim 30 or claim 80 of the 213 patent or Applicants’ claim 24. All alternatives are to the same patentable invention.

All alternatives recite that the variable domain comprises non-human complementarity determining region amino acid residues which bind an antigen. All alternatives also comprise a human framework region. As discussed above for compliance with Section 135(b), the 213 patent defines “humanized antibody” as an antibody having a framework region “having substantially the amino acid sequence of a human immunoglobulin,” i.e., a human framework region (see column 8, lines 11-17, of the 213 patent). And, if one incorporates non-human CDR amino acid residues into a human antibody variable domain, as recited in claims 30 and 80, one ends up with a human framework region. Further, all alternatives require only that one of the listed framework residues be substituted. Claims 30 and 80 of the 213 patent and Applicants’ claim 24 recite substituting, *inter alia*, residue 78 of the heavy chain.

Although claim 30 of the 213 patent and Applicants’ claim 24 do not recite the alternative recitations (a) through (c) of claim 80 of the 213 patent, e.g., “noncovalently binds antigen directly,” such limitations are clearly implicit for all the framework residue substitutions recited in claim 80.

Although claims 30 and 80 of the 213 patent do not recite that the variable domain is from the light chain, it clearly must be the case when a light chain framework residue, i.e., one designated with an “L,” is to be substituted.

Claim 30 of the 213 patent recites an “antibody” while the remaining alternatives recite a “variable domain.” The antibody recitation is anticipated by and/or obvious over the recitation of variable domain and *vice versa*. “Humanized antibody” is defined in the 213 patent to comprise, *inter alia*, at least one variable domain (see column 8, lines 26-28, of the 213 patent).

Claim 30 of the 213 patent further recites a specific antibody target. The alternatives of the count that do not recite a particular target are clearly anticipated thereby. Considering the target, i.e., the tyrosine kinase receptor for HER2, p185^{HER2}, Applicants submit that claim 30 is clearly obvious over the other alternatives of the count for the reasons that follow.

The import of p185^{HER2} to cancer, particularly breast cancer, had been well documented well before the priority date of the 213 patent. See, for example, Slamon, D.J. et al., *Science*, 235:177-182, 1987. The development of antibodies against p185^{HER2} for use in therapy had also

been well documented, as was the use of antibodies other than hybridoma-produced monoclonal antibodies. Applicants respectfully submit that, in view of the knowledge of the art at the time, a humanized antibody against p185^{HER2} would have been obvious over the remaining alternatives of the count.

(d) Identification of claims corresponding to the count

Applicants identify all of the 213 patent claims, claims 1-82, and all of Applicants' pending claims, claims 24-25, as corresponding to the proposed count. All of said claims are either anticipated by, or obvious over, the proposed count as required by 37 CFR § 41.207(b)(2).

More specifically, the alternatives of the proposed count recite framework residue substitutions recited in claims 1, 5-28, 34-63, 66, 70-77, and 79 of the 213 patent.

Claims 2, 31, 67, and 81 of the 213 patent recite that the substituted residue is the residue found at the corresponding location of the non-human antibody from which the non-human CDR amino acids are obtained. Such a claim is anticipated by the proposed count – the goal of substituting framework residues is to improve affinity to approach that of the antibody from which the CDRs are obtained. See, for example, Riechmann, et al., *Nature*, 332:323-327, 1988.

Claims 3, 32, 68, and 82 of the 213 patent recite that no human framework residue other than those set forth in the claim from which they depend has been substituted. Such claims are anticipated by, or clearly obvious over, the proposed count in view of the use of the Markush language “selected from the group consisting of.” The transitional phrase “consisting of” is closed, meaning that it excludes any element not listed. See MPEP 2111.03.

Claims 29 and 78 recite an antibody comprising the humanized variable domains of the claims from which they depend. Such claims are clearly anticipated by claim 30 of the proposed count.

While claims 4, 33, 62 and 69 of the 213 patent further recite that the variable domain is a “consensus” human variable domain, use of such framework regions in making humanized antibodies was known by the priority date of the 213 patent. See, for example, column 13, lines

6-9, of U.S. Patent No. 5,530,101, issued to Queen et al., filed on December 19, 1990. Claims 62 and 69 are, thus, obvious in view of the proposed count and the art.

The recitation in claim 63 that the humanized antibody lacks immunogenicity when compared to the non-human parent upon repeated administration is the very goal of humanization and is, thus, implicit. The motivation for preparing humanized antibodies was to reduce immunogenicity. See column 1, lines 51-58, of the 213 patent, discussing the "Background of the Invention." References from the early 1980's are cited therein disclosing the anti-globulin response to rodent monoclonal antibodies. Claim 63 is, at a minimum, obvious over the proposed count and the art.

The alternatives recited in claim 64 include the alternatives recited in claim 80 of the count. Claim 64 is, thus, anticipated by the proposed count.

The recitation in claim 65 that the variant of claim 63 binds the antigen "up to 3-fold more in the binding affinity than the parent antibody binds antigen" broadly includes variants that have binding affinities equal to and less than the parent. As recognized in the "Background of the Invention" section of the 213 patent, at column 3, lines 50-55, humanizing antibody while retaining high affinity for antigen was difficult to achieve; achieving lower affinity was not. This recitation, thus, is also either anticipated by, or obvious over, the proposed count in view of the art.

All of Applicants claims, claims 24-25, are anticipated by or obvious over the proposed count. Claim 25 is anticipated by claim 30 of the count.

(e) Interference-In-Fact

"An interference-in-fact exists if the subject matter of a claim of one party would, if prior art, have anticipated or rendered obvious the subject matter of a claim of the opposing party and vice versa." 37 CFR § 41.203(a) (2004). Applicants set forth in attached Appendix C a comparison of claim 66 of the 213 patent with Applicants' claim 24, both of which correspond to the present count.

As is clear from Appendix C, each claim anticipates and/or renders obvious the other. Both claims recite a humanized variable domain. Both claims are directed to a heavy chain

variable domain. Both claims also recite that the variable domain comprises non-human complementarity determining region amino acid residues which bind an antigen. Both claims also comprise a human framework region; claim 66 of the 213 patent simply recites it differently -- if one incorporates non-human CDR amino acid residues into a human antibody variable domain, one ends up with a human framework region. Indeed, as discussed above, the 213 patent defines "humanized antibody" as an antibody having a framework region "having substantially the amino acid sequence of a human immunoglobulin," i.e., a human framework region (see column 8, lines 11-17, of the 213 patent). Both claims recite a single amino acid substitution in the framework region to be selected from a Markush group listed thereafter; both recite that residue 24 of the heavy chain is to be substituted. Finally, both claims recite that numbering is according to Kabat.

(f) Support for Applicants Claims

In attached Appendix D, Applicants illustrate the representative support in their disclosure for the limitations of their claims 24 to 25. There is, of course, additional support in Applicants' application omitted herein for the sake of brevity. In Appendix E, Applicants show support for their claim 24, filed December 21, 1989. Methods for preparing exemplary antibodies having framework substitutions are described, *inter alia*, on pages 18-23, Sections 13.1.1 through 15.3, of the GB priority application.

(g) Applicants Will Prevail on Priority

US Serial No. 08/146,206, which issued as the 213 patent, was filed on June 15, 1992 as a PCT continuation-in-part of U.S. Serial No. 07/715,272, filed June 14, 1991.

The present application is a continuation of Application Serial No. 08/846,658, filed May 1, 1997, which is a continuation of Application Serial No. 08/303,569, filed September 7, 1994, now U.S. Patent No. 5,859,205, which is a continuation of Application Serial No. 07/743,329, filed as PCT/GB90/02017, filed December 21, 1990 and which claims priority benefit of GB 8928874.0, filed December 21, 1989. Applicants' earliest constructive reduction to practice date to which they are entitled is at least as early as December 21, 1989, but not later than December

DOCKET NO.: CARP0001-112

PATENT

**PRELIMINARY AMENDMENT AND REQUEST FOR INTERFERENCE UNDER 37
C.F.R. § 42.202 DATED NOVEMBER 21, 2005**

21, 1990. Regardless, both dates are earlier than the earliest filing date of the 213 patent , or
June 14, 1991.

CONCLUSION

The Requested Interference Should Be Declared

Early consideration and indication of allowability of all pending claims is respectfully requested. For an interference to be declared, however, only one claim needs to be allowable. MPEP § 2307.02. Should the present examination involve rejections of applicant's claims that would have been equally applicable against the 213 patent claims, applicants respectfully note MPEP § 2307.02, which requires the approval of the Group Director for such a rejection. Applicants are presumptively the prior inventors of the claimed subject matter and only desire an interference to prove that they are the actual prior inventors. Their opportunity to do so should not be unduly delayed. In view of the foregoing, Applicants respectfully request that an interference be declared between the present application and the 213 patent.

To assist the Examiner, Applicants note the following.

- (1) the proposed count for the interference should be the Proposed Count set forth in Appendix B.
- (2) the claims of the 213 patent which should be designated as corresponding to the count are claims 1-82, all of the issued claims of the patent.
- (3) the claims of Applicants that should be designated as corresponding to the count are claims 24-25, all pending claims of the Applicants' above-identified application.
- (4) no claims of either party should be designated as not corresponding to the count since none are directed to a separate patentable invention when considering the proposed count.

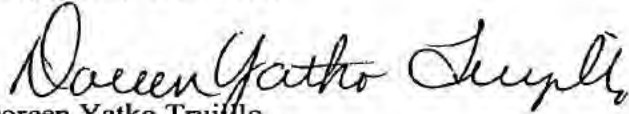
DOCKET NO.: CARP0001-112

PATENT

**PRELIMINARY AMENDMENT AND REQUEST FOR INTERFERENCE UNDER 37
C.F.R. § 42.202 DATED NOVEMBER 21, 2005**

The examiner is requested to contact the undersigned attorney if an interview, telephonic or personal, would facilitate allowance of the claims or declaration of an interference.

Respectfully submitted,



Doreen Yatko Trujillo
Registration No. 35,719

Date: *November 21, 2005*

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(215) 665-5593 - Telephone
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Attachments: **Appendices A-E**
Copy of U.S. Patent No. 6,407,213 B1
Copy of PCT Publication WO 91/09967

APPENDIX A

1. A CDR-grafted antibody heavy chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 6, 23 and/or 24, 48 and/or 49, 71 and/or 73, 75 and/or 76 and/or 78 and 88 and/or 91.
2. A CDR-grafted heavy chain according to claim 1 comprising donor residues at positions 23, 24, 49, 71, 73 and 78, or at positions 23, 24 and 49.
3. A CDR-grafted heavy chain according to claim 2 comprising donor residues at positions 2, 4, 6, 25, 36, 37, 39, 47, 48, 93, 94, 103, 104, 106 and 107.
4. A CDR-grafted heavy chain according to claim 2 or 3, comprising donor residues at one, some or all of positions: 1 and 3, 69 (if 48 is different between donor and acceptor), 38 and 46 (if 48 is the donor residue), 67, 82 and IS (if 67 is the donor residue), 91, and any one or more of 9, 11, 41, 87, 108, 110 and 112.
5. A CDR-grafted heavy chain according to any of the preceding comprising donor CDRs at positions 26-35, 50-65 and 95-100.
6. A CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor residues at at least one of positions 1 and/or 3 and 46 and/or 47.
7. A CDR-grafted light chain according to claim 6 comprising donor residues at positions 46 and 47.
8. A CDR-grafted antibody light chain having a variable region domain comprising acceptor framework and donor antigen binding regions wherein the framework comprises donor

residues at at least one of positions 46, 48, 58 and 71.

9. A CDR-grafted light chain according to claim 8 comprising donor residues at positions 46, 48, 58 and 71.

10. A CDR-grafted light chain according to claim 8 or 9, comprising donor residues at positions 2, 4, 6, 35, 36, 38, 44, 47, 49, 62, 64-69, 85, 87, 98, 99, 101 and 102.

11. A CDR-grafted light chain according to claim 9 or 10, comprising donor residues at one, some or all of positions: 1 and 3, 63, 60 (if 60 and 54 are able to form a potential saltbridge), 70 (if 70 and 24 are able to form a potential saltbridge), 73 and 21 (if 47 is different between donor and acceptor), 37 and 45 (if 47 is different between donor and acceptor), and any one or more of 10, 12, 40, 83, 103 and 105.

12. A CDR-grafted light chain according to any one of claims 6-11, comprising donor CDRs at positions 24-34, 50-56 and 89-97.

13. A CDR-grafted antibody molecule comprising at least one CDR-grafted heavy chain according to any one of claims 1-5 and at least one CDR-grafted light chain according to any one of claims 6-12.

14. A CDR-grafted antibody molecule according to claim 13, which is a site-specific antibody molecule.

15. A CDR-grafted antibody molecule according to claim 13 which has specificity for an interleukin, hormone or other biologically active compound or a receptor therefor.

16. A CDR-grafted antibody heavy or light chain or molecule according to any one of the preceding claims comprising human acceptor residues and non-human donor residues.

17. A DNA sequence which codes for a CDR-grafted heavy chain according to claim 1 or a

CDR-grafted light chain according to claim 6 or claim 8.

18. A cloning or expression vector containing a DNA sequence according to claim 17.

19. A host cell transformed with a DNA sequence according to claim 17.

20. A process for the production of a CDR-grafted antibody sequence according to claim 17 in a transformed host cell.

21. A process for producing a CDR-grafted antibody product comprising: (a) producing in an expression vector an operon having a DNA sequence which encodes an antibody heavy chain according to claim 1; and/or (b) producing in an expression vector an operon having a DNA sequence which encodes a complementary antibody light chain according to claim 6 or claim 8; (c) transfecting a host cell with the or each vector; and (d) culturing the transfected cell line to produce the CDR-grafted antibody product.

22. A therapeutic or diagnostic composition comprising a CDR-grafted antibody heavy chain according to claim 1, or a CDR-grafted light chain according to claim 6 or claim 8, or a CDR-grafted antibody molecule according to claim 13 in combination with a pharmaceutically acceptable carrier, diluent or excipient.

23. A method of therapy or diagnosis comprising administering an effective amount of a CDR-grafted heavy chain according to claim 1, or a CDR-grafted light chain according to claim 6 or claim 8, or a CDR-grafted antibody molecule according to claim 13 to a human or animal subject.

APPENDIX B**Proposed Count for interference****Claim 30 of the 213 patent**

An antibody which binds p185^{HER2} and comprises a humanized antibody variable domain, wherein the humanized antibody variable domain comprises non-human Complementarity Determining Region (CDR) amino acid residues which bind p185^{HER2} incorporated into a human antibody variable domain, and further comprises a Framework Region (FR) amino acid substitution at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 46L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 36H, 39H, 43H, 45H, 69H, 70H, 74H, 75H, 76H, **78H** and 92H, utilizing the numbering system set forth in Kabat.

OR**Claim 80 of the 213 patent**

A humanized antibody variable domain comprising non-human Complementarity Determining Region (CDR) amino acid residues which bind an antigen incorporated into a human antibody variable domain, and further comprising a Framework Region (FR) amino acid substitution where the substituted FR residue:

(a) noncovalently binds antigen directly;

(b) interacts with a CDR; or

(c) participates in the $V_L - V_H$ interface by affecting the proximity or orientation of the V_L and V_H regions with respect to one another, and wherein the substituted FR residue is at a site selected from the group consisting of: 4L, 38L, 43L, 44L, 58L, 62L, 65L, 66L, 67L, 68L, 69L, 73L, 85L, 98L, 2H, 4H, 24H, 36H, 39H, 43H, 45H, 69H, 70H, 73H, 74H, 76H, **78H**, 92H and 93H, utilizing the numbering system set forth in Kabat.

DOCKET NO.: CARP0001-112 **PATENT**
PRELIMINARY AMENDMENT AND REQUEST FOR INTERFERENCE UNDER 37
C.F.R. § 42.202 DATED NOVEMBER 21, 2005

OR

Applicants' claim 24

A humanised antibody **heavy chain** variable domain comprising non-human complementarity determining region amino acid residues which bind an antigen and a human framework region wherein said framework region comprises an amino acid substitution at a residue selected from the group consisting of 23, 24, 49, 71, 73, and 78, and combinations thereof, as numbered according to Kabat.

APPENDIX C

Comparison of Applicants' claim 24 and claim 66 of the 213 patent

Applicants' Claim 24	213 patent Claim 66
Claim 24 – A humanised antibody heavy chain variable domain comprising	A humanized antibody heavy chain variable domain comprising
non-human complementarity determining region amino acid residues which bind an antigen and	non-human Complementarity Determining Region (CDR) amino acid residues which bind an antigen
a human framework region wherein said framework region comprises an amino acid substitution at a residue selected from the group consisting of	incorporated into a human antibody variable domain, and further comprising a Framework Region (FR) amino acid substitution at a site selected from the group consisting of:
23, 24, 49, 71, 73, and 78, and combinations thereof,	24H, 73H, 76H, 78H, and 93H
as numbered according to Kabat.	utilizing the numbering system as set forth in Kabat.

APPENDIX D**Support for Applicants' claims in Applicants' Present Specification**

Claim	Present Specification
Claim 24 -- A humanised antibody heavy chain variable domain comprising	page 6, lines 29-31
non-human complementarity determining region amino acid residues which bind an antigen and	page 7, line 29, through page 8, line 7 and page 17, lines 6-7
a human framework region wherein said framework region comprises an amino acid substitution at a residue selected from the group consisting of	page 7, line 29, through page 8, line 7 and page 17, lines 1-19
23, 24, 49, 71, 73, and 78, and combinations thereof,	page 7, lines 1-3
as numbered according to Kabat.	page 8, lines 22-24
Claim 25 -- A humanised antibody comprising the variable domain of claim 24.	see above support for claim 24

APPENDIX E

Support For Applicants' Claims in the GB Application, filed December 21, 1989

Claim	1989 GB Application
Claim 24 – A humanised antibody heavy chain variable domain comprising	page 5, lines 8-10
non-human complementarity determining region amino acid residues which bind an antigen and	page 5, lines 8-21
a human framework region wherein said framework region comprises an amino acid substitution at a residue selected from the group consisting of	page 5, line 10 and page 26, lines 31-33
23, 24, 49, 71, 73, and 78, and combinations thereof,	page 6, lines 8-10 and Table 1
as numbered according to Kabat.	page 6, lines 5-7

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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re application of: **John R. Adair et al.**

Confirmation No. **5305**

Serial No.: **11/284,261**

Art Unit: **1643**

Filed: **November 21, 2005**

Examiner: **Anne Gussow**

Title: **HUMANISED ANTIBODIES**

Customer No.: **34132**

Via EFS Web:
DATE FILED: September 9, 2009

MAIL STOP AMENDMENT

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

REQUEST FOR RECONSIDERATION

Dear Sir:

This paper is being filed in response to the Non-Final Office Action dated as mailed March 9, 2009. Applicants hereby petition for a three-month extension of time to respond to the Non-Final Office Action and request the Commissioner to charge Deposit Account 50-3111 the appropriate extension of time fee.

Listing of the Claims, begin on page 2.

Remarks begin on page 3.

The **Conclusion** is found on page 5.

Carter Exhibit 2004
Carter v. Adair
Interference No. 105,744

LISTING OF THE CLAIMS

Claims 1-23 (**cancelled**)

Claim 24 (**currently amended**): A humanised antibody comprising a heavy chain variable domain comprising non-human complementarity determining region amino acid residues which bind an antigen and a human framework region wherein said framework region comprises a non-human amino acid substitution at a residue selected from the group consisting of 23, 24, 49, 71, 73, and 78, and combinations thereof, as numbered according to Kabat.

Claim 25 (**cancelled**)