(12) STANDARD PATENT (11) Application No. **AU 2015327819 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Antibodies that bind ebola glycoprotein and uses thereof

(51) International Patent Classification(s)
C07K 16/10 (2006.01)

(21) Application No: **2015327819** (22) Date of Filing: **2015.10.02**

(87) WIPO No: **WO16/054598**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/059,746	**2014.10.03**	**US**

(43) Publication Date: **2016.04.07**
(44) Accepted Journal Date: **2021.07.01**

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(56) Related Art
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WO 2004018649 A2
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(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 April 2016 (07.04.2016)

WIPO | PCT

(10) International Publication Number
WO 2016/054598 A3

(51) International Patent Classification:
C07K 16/10 (2006.01)

(21) International Application Number:
PCT/US2015/053871

(22) International Filing Date:
2 October 2015 (02.10.2015)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/059,746 3 October 2014 (03.10.2014) US

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(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
- *with international search report (Art. 21(3))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

(88) **Date of publication of the international search report**:
19 May 2016

WO 2016/054598 A3

(54) **Title**: ANTIBODIES THAT BIND EBOLA GLYCOPROTEIN AND USES THEREOF

(57) **Abstract**: Isolated monoclonal antibodies which bind to Ebola virus glycoprotein and related antibody-based compositions and molecules are disclosed. Also disclosed are therapeutic and diagnostic methods for using the antibodies.

08 Jun 2021
2015327819

ANTIBODIES THAT BIND EBOLA GLYCOPROTEIN AND USES THEREOF

RELATED APPLICATIONS

This application claims the benefit of the priority date of U.S. Provisional Application No. 62/059,746, which was filed on October 3, 2014. The content of this provisional application is hereby incorporated by reference in its entirety.

GOVERNMENT FUNDING

This invention was made with Government support under Grant No. 6922267 awarded by the National Institute of General Medical Sciences, and under Grant No. 6930370 awarded by the National Institute of Allergy and Infectious Diseases. The Government has certain rights in the invention.

BACKGROUND

Ebola virus (EBOV) is a virulent pathogen which causes severe hemorrhagic fever in humans with a fatality rate of 50-90%. The acute form of the i llness (approximately 3-5 weeks from contraction to death) means that there is little opportunity to develop an adaptive immunity. There is an urgent need for effective counter measures as there are no approved vaccines or therapies against EBOV.

The EBOV glycoprotein (GP) is the predominant surface protein expressed by the virus. The GP protein is responsible for two main functions: (1) viral entry into host cells and (2) catalysis of membrane fusion. Mice experiments have demonstrated that EBOV GP is the main target of neutralizing anti bodies. Additionally, animal studies have shown that such antibodies have prophylactic and therapeutic potential in non-human primates, which mimic important aspects of EBOV infection in humans. However, mutations in the Ebola virus glycoprotein may affect the efficacy of current vaccines or antibody treatments. Therefore, new antibody-based agents and vaccines against EBOV GP provide a promising option for combating EBOV outbreaks in humans.

SUMMARY

According to a first aspect, the present invention provides an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, wherein the monoclonal antibody is selected from the group consisting of:

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(a) a monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14;

(b) a monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37; and

(c) a monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17.

According to a second aspect, the present invention provides a pharmaceutical composition comprising a monoclonal antibody or antigen binding portion thereof of the first aspect and a pharmaceutically acceptable carrier.

According to a third aspect, the present invention provides a pharmaceutical composition comprising two or more of the monoclonal antibodies or antigen binding portions thereof of the first aspect and a pharmaceutically acceptable carrier.

According to a fourth aspect, the present invention provides a method for treating Ebola virus infection comprising administering to a subject in need thereof an effective amount of the pharmaceutical composition of the second or third aspects.

According to a fifth aspect, the present invention provides use of a pharmaceutical composition of the second or third aspects in the manufacture of a medicament for treating Ebola virus infection.

According to a sixth aspect, the present invention provides a nucleic acid molecule comprising a nucleotide sequence encoding the light chain, heavy chain, or both the light and heavy chains of the monoclonal antibody or antigen binding portion thereof of the first aspect.

According to a seventh aspect, the present invention provides an expression vector comprising the nucleic acid molecule of the sixth aspect.

According to an eighth aspect, the present invention provides a host cell comprising an expression vector of the seventh aspect.

According to a ninth aspect, the present invention provides a method for producing a monoclonal antibody, or antigen binding portion thereof, comprising culturing a host cell transformed to express the monoclonal antibody, or antigen binding portion thereof, of the first aspect.

The invention described herein pertains to monoclonal antibodies and antigen binding portions thereof directed towards Ebola virus glycoprotein (GP), which have desirable functional properties. These properties include high affinity binding to Ebola virus GP and neutralizing activity against the Zaire Ebola Virus, including the Makona 2014 strain. As described herein, the present invention identifies regions within Ebola virus GP that serve as specific neutralization epitopes for the monoclonal antibodies of the invention. These epitopes also serve to provide fragments of Ebola virus GP that are useful for eliciting an active and specific immune response against Ebola virus GP, both *in vitro*, e.g., for detection of GP, and *in vivo*, for inducing a protective immune response in subjects in need thereof. The epitopes are useful in vaccine compositions as immunogens for eliciting an anti-Ebola virus GP immune response in subjects. Also provided herein are methods for treating Ebola virus infection in patients in need thereof as well as methods of detecting Ebola virus in a sample.

In one aspect, provided herein are isolated monoclonal antibodies, or antigen binding portions thereof, which binds to Ebola virus glycoprotein, wherein the monoclonal antibody is selected from the group consisting of:

(a) a monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14;

(b) a monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37; and

(c) a monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17.

In some aspects, the invention relates to a monoclonal antibody 4G7.9, or antigen binding portion thereof. In other aspects, the invention relates to a monoclonal antibody 2G4.6, or antigen binding portion thereof. Yet other aspects of the invention relate to a monoclonal antibody 13C6.1, or antigen binding portion thereof.

In one aspect, provided herein are pharmaceutical compositions comprising a combination of monoclonal antibodies or antigen binding portions thereof, which bind to Ebola virus glycoprotein, and a pharmaceutically acceptable carrier, wherein the combination of monoclonal antibodies is selected from the group consisting of:

(a) monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14 and monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37, and optionally, monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17;

(b) monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14 and monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17, and optionally monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37; and

(c) monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17, and optionally monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37, and optionally, monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14.

In some aspects, the invention relates to a pharmaceutical composition comprising monoclonal antibodies 4G7.9, 2G4.6 and 13C6.1, and a pharmaceutically acceptable carrier.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, wherein the remainder of the light chain is from a human immunoglobulin.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 75, and 76, respectively, and variable region framework residues selected from the group consisting of 49H, 50H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 94, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 45, 46, and 47, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 48, 50, and 51, respectively, wherein the remainder of the light chain is from a human immunoglobulin.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, and comprises a heavy chain variable region and light chain variable region comprising an amino acid sequence at least 90% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 15 and 17, respectively;

(b) SEQ ID NOs: 32 and 37, respectively; and

(c) SEQ IS NOs: 39 and 14, respectively;

wherein the monoclonal antibody is a neutralizing antibody and specifically binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, wherein the remainder of the light chain is from a human immunoglobulin.

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89, respectively, and variable region framework residues selected from the group consisting of 43L, 87L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 75, and 76, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

Yet another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, and variable region framework residues selected from the group consisting of 43L, 87L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

Another aspect of the inventions relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising:

a) a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and

b) a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 90, and 89 respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 52L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which specifically binds to Ebola virus glycoprotein and competes for binding to Ebola virus glycoprotein with a monoclonal antibody selected from the group consisting of 13C6.1, 2G4.6, and 4G7.9, wherein the monoclonal antibody exhibits at least one (or more) of the following properties:

(a) binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA;

(b) binds to a conformational epitope on Ebola virus glycoprotein (SEQ ID NO: 91);

(c) binds within the region V505-C511 of Ebola virus glycoprotein (SEQ ID NO: 91);

(d) binds within the region N550-E564 of Ebola virus glycoprotein (SEQ ID NO: 91);

(e) binds within the region T270-P279 of Ebola virus glycoprotein (SEQ ID NO: 91);

(f) binds within the region Y394-R404 of Ebola virus glycoprotein (SEQ ID NO: 91); and

(g) engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, which specifically bind to a conformational epitope on Ebola virus glycoprotein (SEQ ID NO: 91) that spans V505-C511 and N550-E564.

Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, which specifically binds to a conformational epitope on Ebola virus glycoprotein (SEQ ID NO: 91) that spans T270-P279 and Y394-R409.

In other aspects, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which specifically binds to Ebola virus glycoprotein, comprises a variable heavy chain and a variable light chain selected from the group consisting of:

(a) SEQ ID NOs: 15 and 17;

(b) SEQ ID NOs: 32 and 37;

(c) SEQ IS NOs: 39 and 14;

(d) SEQ ID NOs: 11 and 37;

(e) SEQ ID NOs: 13 and 14;

(f) SEQ ID NOs: 13 and 42;

(g) SEQ ID NOs: 13 and 43;

(h) SEQ ID NOs: 39 and 42;

(i) SEQ ID NOs: 39 and 43; and

(j) SEQ ID NOs: 39 and 44.

Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, having neutralizing activity against the Zaire Ebola Virus.

Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, which specifically bind to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, 150 pM or less, or 100 pM or less, as measured by ELISA. Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, which specifically bind to Ebola virus glycoprotein with an EC_{50} of 150 pM or less, as measured by ELISA. Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, which specifically bind to Ebola virus glycoprotein with an EC_{50} of 100 pM or less, as measured by ELISA.

One aspect of the invention relates to a monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14, which binds to V505-C511 and N550-E564 of Ebola virus glycoprotein (SEQ ID NO: 91). Other aspects of the invention relate to monoclonal antibodies 4G7.1, 4G7.2, 4G7.3, 4G7.10, 4G7.11, and 4G7.12, which bind within the region V505-C511 or within the region N550-E564, or both.

Yet other aspects of the invention relate to a monoclonal antibody 4G7.9 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Another aspect of the invention relates to a monoclonal antibody 4G7.9 which binds to Ebola virus glycoprotein with an EC_{50} of 100 pM or less, as measured by ELISA. Other aspects of the invention relate to monoclonal antibody 4G7.9 which binds to Ebola virus glycoprotein with an EC_{50} of 99.7 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.1 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.1 which binds to Ebola virus glycoprotein with an EC_{50} of 182 pM or less, as measured by ELISA. In other aspects, the invention relates to a monoclonal antibody 4G7.2 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.2 which binds to Ebola virus glycoprotein with an EC_{50} of 95.2 pM or less, as measured by ELISA. In other aspects, the invention relates to a monoclonal antibody 4G7.3 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.3 which binds to Ebola virus glycoprotein with an EC_{50} of 176 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.10 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Another aspect of the invention relates to monoclonal antibody 4G7.10 which binds to Ebola virus glycoprotein with an EC_{50} of 120 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.11 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Another aspect of the invention relates to monoclonal antibody 4G7.11 which binds to Ebola virus glycoprotein with an EC_{50} of 145 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 4G7.12 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Another aspect of the invention relates to monoclonal antibody 4G7.12 which binds to Ebola virus glycoprotein with an EC_{50} of 88.8 pM or less, as measured by ELISA.

Yet other aspects of the invention relate to a monoclonal antibody 4G7.9 which has neutralizing activity against Zaire Ebola Virus. In one aspect, the invention relates to a monoclonal antibody 4G7.9 which neutralizes Ebola virus Mayinga 1976 strain at 1 μg/mL, as measured by a plaque reduction neutralization assay. In another aspect, the invention relates to a monoclonal antibody 4G7.9 which neutralizes Ebola virus Kikwit 1995 strain at 1 μg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody 4G7.9 neutralizes Ebola virus Makon 2014 strain at 1 μg/mL, as measured by a plaque reduction neutralization assay.

Other aspects of the invention relate to a monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14, which engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC). Yet other aspects of the invention relate to monoclonal antibodies 4G7.1, 4G7.2, 4G7.3, 4G7.10, 4G7.11, and 4G7.12, which engage immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which specifically binds to Ebola virus glycoprotein and competes for binding to Ebola virus glycoprotein with a monoclonal antibody 4G7.9, wherein the monoclonal antibody exhibits at least one, two, three, four, five or all of the following properties:

(a) binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA;

(b) binds to a conformational epitope on Ebola virus glycoprotein (SEQ ID NO: 91);

(c) binds within the region V505-C511 of Ebola virus glycoprotein (SEQ ID NO: 91);

(d) binds within the region N550-E564 of Ebola virus glycoprotein (SEQ ID NO: 91); and

(e) engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

One aspect of the invention relates to a monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17, which binds to T270-P279 and Y394-R409 of Ebola virus glycoprotein (SEQ ID NO: 91).

Yet other aspects of the invention relate to a monoclonal antibody 13C6.1 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA.

Other aspects of the invention relate to monoclonal antibody 13C6.1 which binds to Ebola virus glycoprotein with an EC_{50} of 136 pM or less, as measured by ELISA.

Yet other aspects of the invention relate to a monoclonal antibody 13C6.1 which has neutralizing activity against Zaire Ebola Virus. In one aspect, the invention relates to a monoclonal antibody 13C6.1 which neutralizes Ebola virus Mayinga 1976 strain at >50 μg/mL, as measured by a plaque reduction neutralization assay. In another aspect, the invention relates to a monoclonal antibody 13C6.1 which neutralizes Ebola virus Kikwit 1995 strain at >50 μg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody 13C6.1 neutralizes Ebola virus Makon 2014 strain at >50 μg/mL, as measured by a plaque reduction neutralization assay.

Other aspects of the invention relate to a monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17, which engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which specifically binds to Ebola virus glycoprotein and competes for binding to Ebola virus glycoprotein with a monoclonal antibody 13C6.1, wherein the monoclonal antibody exhibits at least one, two, three, four, five or all of the following properties:

(a) binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA;

(b) binds to a conformational epitope on Ebola virus glycoprotein (SEQ ID NO: 91);

(c) binds within the region T270-P279 of Ebola virus glycoprotein (SEQ ID NO: 91);

(d) binds within the region Y394-R409 of Ebola virus glycoprotein (SEQ ID NO: 91); and

(e) engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

One aspect of the invention relates to a monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37, which binds to V505-C511 and N550-E564 of Ebola virus glycoprotein (SEQ ID NO: 91). Other aspects of the invention relate to monoclonal antibody 2G4.3, which binds within the region V505-C511 or within the region N550-E562, or both.

Yet other aspects of the invention relate to a monoclonal antibody 2G4.6 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Another aspect of the invention relates to a monoclonal antibody 2G4.6 which binds to Ebola virus glycoprotein with an EC_{50} of 109 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 2G4.3 which binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. Other aspects of the invention relate to a monoclonal antibody 2G4.3 which binds to Ebola virus glycoprotein with an EC_{50} of 129 pM or less, as measured by ELISA.

Yet other aspects of the invention relate to a monoclonal antibody 2G4.6 which has neutralizing activity against Zaire Ebola Virus. In one aspect, the invention relates to a monoclonal antibody 2G4.6 which neutralizes Ebola virus Mayinga 1976 strain at 2 µg/mL, as measured by a plaque reduction neutralization assay. In another aspect, the invention relates to a monoclonal antibody 2G4.6 which neutralizes Ebola virus Kikwit 1995 strain at 4 µg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody 2G4.6 neutralizes Ebola virus Makon 2014 strain at 2 µg/mL, as measured by a plaque reduction neutralization assay.

Other aspects of the invention relate to a monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37, which engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC). Yet other aspects of the invention relate to monoclonal antibodies 2G4.3, which engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which specifically binds to Ebola virus glycoprotein and competes for binding to Ebola virus glycoprotein with a monoclonal antibody 2G4.6, wherein the monoclonal antibody exhibits at least one, two, three, four, five or all of the following properties:

(a) binds to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA;

(b) binds to a conformational epitope on Ebola virus glycoprotein (SEQ ID NO: 91);

(c) binds within the region V505-C511 of Ebola virus glycoprotein (SEQ ID NO: 91);

(d) binds within the region N550-E564 of Ebola virus glycoprotein (SEQ ID NO: 91); and

(e) engages immune components such as antibody-dependent cellular cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC).

Yet other aspects of the invention relate to a pharmaceutical composition comprising a combination of monoclonal antibodies or antigen binding portions thereof, which bind to Ebola virus glycoprotein, and a pharmaceutically acceptable carrier, wherein the combination of monoclonal antibodies is selected from the foregoing monoclonal antibodies.

Some aspects of the invention relate to any of the preceding antibodies, or antigen binding portions thereof, in which the monoclonal antibody is an IgG1, an IgG2, an IgG3, an IgG4, an IgM, an IgA1, an IgA2, an IgD, or an IgE antibody. In some aspects of the invention, any of the preceding antibodies, or antigen binding portions thereof, is a monoclonal IgG1 antibody.

Other aspects of the invention relate to pharmaceutical compositions comprising any of the preceding monoclonal antibodies or antigen binding portions thereof, and a pharmaceutically acceptable carrier.

Other aspects of the invention relate to pharmaceutical compositions comprising one or more (e.g., two or three different monoclonal antibodies) of the preceding monoclonal antibodies or antigen binding portions thereof, and a pharmaceutically acceptable carrier.

Another aspect of the invention relates to methods for treating Ebola virus infection in a subject in need thereof, comprising administering a pharmaceutical composition comprising an effective amount of any of the preceding monoclonal antibodies or antigen binding portions thereof, or a combination of monoclonal antibodies (e.g., two or three different monoclonal antibodies) or antigen binding portions thereof; and a pharmaceutically acceptable carrier.

Other aspects of the invention relate to methods for treating Ebola virus infection in a subject in need thereof, comprising administering a first pharmaceutical composition comprising an effective amount of a first monoclonal antibody of any of the preceding monoclonal antibodies or antigen binding portions thereof, and a pharmaceutically acceptable carrier; and a second pharmaceutical composition comprising an effective amount of a second monoclonal antibody (different from the first) from any of the preceding monoclonal antibodies or antigen binding portions thereof, and a pharmaceutically acceptable carrier. In other aspects, a third pharmaceutical composition comprising an effective amount of a third monoclonal antibody (different from the first and second) from any of the preceding monoclonal antibodies or antigen binding portions thereof, and a pharmaceutically acceptable carrier is administered to the subject in need thereof.

In another aspect, the methods of the invention further comprise administering a therapeutic agent to a subject in need thereof. In one aspect, the therapeutic agent is interferon alpha.

Other aspects of the invention relate to a monoclonal antibody or antigen binding portion thereof of the preceding antibody, or one or more monoclonal antibodies or antigen binding portions thereof of the preceding antibodies, for use in treating Ebola virus infection. In some aspects, the use further comprises administering a therapeutic agent. In some embodiments, the therapeutic agent is interferon alpha.

Yet other aspects of the invention relate to methods for detecting Ebola virus infection in a subject, comprising obtaining a sample from the subject and contacting the sample with any of the preceding monoclonal antibodies or antigen binding portions thereof, or a combination of monoclonal antibodies (e.g., two or three different monoclonal antibodies) or antigen binding portions thereof; and detecting the presence of Ebola virus glycoprotein in the subject.

Some aspects of the invention relate to peptide or peptide mimetics based on one or more epitopes within Ebola virus glycoprotein region V505-C511, region N550-E564, region T270-P279, or region Y394-R404 of Ebola virus glycoprotein (SEQ ID NO: 91). Some aspects of the invention relate to peptide or peptide mimetics based on one or more epitopes within Ebola virus glycoprotein (SEQ ID NO: 91) that spans V505-C511 and N550-E564. Some aspects of the invention relate to peptide or peptide mimetics based on one or more conformational epitopes on Ebola virus glycoprotein (SEQ ID NO: 91) that spans T270-P279 and Y394-R409.

Some aspects of the invention relate to peptide or peptide mimetics based on one or more epitopes Ebola virus glycoprotein TGKLIWKVNP (SEQ ID NO: 98), YKLDISEATQVGQHHR (SEQ ID NO: 99), VNAQPKC (SEQ ID NO: 100), and NQDGLICGLRQLANE (SEQ ID NO: 101).

Other aspects of the invention relate to vaccine compositions that comprise the foregoing peptides, peptide mimetics (or fusion protein thereof). Such vaccine compositions may include one or more adjuvants. Methods of eliciting an anti-Ebola virus GP immune response in a subject, comprising administering to the animal an effective amount of the vaccine composition, are also provided.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a heat map showing the effects of various point mutations in the Ebola virus glycoprotein on the binding of antibodies 4G7, 13C6, KZ52, and 2G4. Mutations that result in higher binding affinity are shown as a light color and mutations that that result in lower binding affinity are shown in a darker color. WT=wild-type Ebola virus glycoprotein.

Figure 2 is the sequence of the Ebola virus glycoprotein with amino acids marked as black or black with an underline if they had an effect on binding as determined in Figure 1. GP=glycoprotein.

Figures 3A-3C are graphs showing the binding affinities of antibodies 2G4 (**Figure 3A**), 4G7 (**Figure 3B**), and 13C6 (**Figure 3C**) for Ebola virus glycoprotein, as determined by ELISA. Both wild-type antibodies and related constructs are shown.

Figure 4 is a phylogram of the variable region heavy chains (VH) and variable region light chains (VL) for antibodies 2G4, 4G7, and 13C6. The lead candidates are circled by dotted ovals.

Figure 5 is a table showing the neutralization titers of antibodies 13C6.1, 2G4.6, and 4G7.9 on three different Ebola virus strains.

DETAILED DESCRIPTION

The invention described herein pertains to monoclonal antibodies and antigen binding portions thereof directed towards Ebola virus glycoprotein (GP), which have desirable functional properties. These properties include high affinity binding to Ebola virus GP and neutralizing activity against the Zaire Ebola Virus, including the Makona 2014 strain. As described herein, the present invention identifies regions within Ebola virus GP that serve as specific neutralization epitopes for the monoclonal antibodies of the invention. These epitopes also serve to provide fragments of Ebola virus GP that are useful for eliciting an active and specific immune response against Ebola virus GP, both *in vitro*, e.g., for detection of GP, and *in vivo*, for inducing a protective immune response in subjects in need thereof.

Definitions

Terms used in the claims and specification are defined as set forth below unless otherwise specified.

The term "Ebola virus", refers to members of the family Filoviridae, which are associated with outbreaks of highly lethal hemorrhagic fever in humans and nonhuman primates. Human pathogens include Ebola Zaire, Ebola Sudan, and Ebola Ivory Coast. Ebola

Reston is a monkey pathogen and is not considered a human pathogen. The natural reservoir of the virus is unknown and there are currently no available vaccines or effective therapeutic treatments for filovirus infections. The genome of Ebola virus consists of a single strand of negative sense RNA that is approximately 19 kb in length. This RNA contains seven sequentially arranged genes that produce 8 mRNAs upon infection. Ebola virions, like virions of other filoviruses, contain seven proteins: a surface glycoprotein (GP), a nucleoprotein (NP), four virion structural proteins (VP40, VP35, VP30, and VP24), and an RNA-dependent RNA polymerase (L) (Feldmann et al.(1992) Virus Res. 24, 1-19; Sanchez et al.,(1993) Virus Res. 29, 215-240; reviewed in Peters et al. (1996) In *Fields Virolooy,* Third ed. pp. 1161-1176. Fields, B. N., Knipe, D. M., Howley, P. M., et al. eds. Lippincott-Raven Publishers, Philadelphia).

The term "Ebola virus glycoprotein (GP)" refers to the predominant surface protein expressed by the virus. The sequence of the Ebola virus GP (Zaire Ebola virus glycoprotein precursor, Genebank Accession: AIG96634.1) is set forth as SEQ ID NO: 91.

The glycoprotein of Ebola virus is the main surface antigen and responsible for viral entry and fusion, expressed as a trimer on the viral surface. It is unusual in that it is encoded in two open reading frames. Transcriptional editing is needed to express the transmembrane form that is incorporated into the virion (Sanchez et al. (1996) *Proc. Natl. Acad. Sci. USA* 93, 3602-3607; Volchkov et al, (1995) *Virology* 214, 421-430). The unedited form produces a nonstructural secreted glycoprotein (sGP) that is synthesized in large amounts early during the course of infection. During assembly of the virus, the glycoprotein undergoes enzymatic cleavage by furin and generates GP1 and GP2 domains. Little is known about the biological functions of these proteins and it is not known which antigens significantly contribute to protection and should therefore be used to induce an immune response.

The term “antibody” as referred to herein includes whole antibodies and any antigen binding fragment (*i.e.*, “antigen-binding portion”) or single chain thereof. An “antibody” refers, in certain embodiments, to a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen binding portion thereof. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as V_H) and a heavy chain constant region. The heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. Each light chain is comprised of a light chain variable region (abbreviated herein as V_L) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (*e.g.*, effector cells) and the first component (Clq) of the classical complement system.

The term “antigen-binding portion” of an antibody (or simply “antibody portion”), as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen (*e.g.*, Ebola virus GP). Such "fragments" are, for example between about 8 and about 1500 amino acids in length, suitably between about 8 and about 745 amino acids in length, suitably about 8 to about 300, for example about 8 to about 200 amino acids, or about 10 to about 50 or 100 amino acids in length. It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term “antigen-binding portion” of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the V_L, V_H, CL and CH1 domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and CH1 domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al.*, (1989) *Nature* 341:544-546), which consists of a V_H domain; and (vi) an isolated complementarity determining region (CDR) or (vii) a combination of two or more isolated CDRs which may optionally be joined by a synthetic linker. Furthermore, although the two domains of the Fv fragment, V_L and V_H, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain Fv (scFv); see *e.g.*, Bird *et al.* (1988) *Science* 242:423-426; and Huston *et al.* (1988) *Proc. Natl. Acad. Sci. USA* 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term “antigen-binding portion” of an antibody. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies. Antigen-binding portions can be produced by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact immunoglobulins.

The term "monoclonal antibody," as used herein, refers to an antibody which displays a single binding specificity and affinity for a particular epitope. Accordingly, the term "human monoclonal antibody" refers to an antibody which displays a single binding specificity and which has variable and optional constant regions derived from human germline immunoglobulin sequences. In one embodiment, human monoclonal antibodies are produced by a hybridoma which includes a B cell obtained from a transgenic non-human animal, *e.g.*, a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell.

The term "recombinant human antibody," as used herein, includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as (a) antibodies isolated from an animal (*e.g.*, a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom, (b) antibodies isolated from a host cell transformed to express the antibody, *e.g.*, from a transfectoma, (c) antibodies isolated from a recombinant, combinatorial human antibody library, and (d) antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies comprise variable and constant regions that utilize particular human germline immunoglobulin sequences are encoded by the germline genes, but include subsequent rearrangements and mutations which occur, for example, during antibody maturation. As known in the art (see, *e.g.*, Lonberg (2005) Nature Biotech. 23(9):1117-1125), the variable region contains the antigen binding domain, which is encoded by various genes that rearrange to form an antibody specific for a foreign antigen. In addition to rearrangement, the variable region can be further modified by multiple single amino acid changes (referred to as somatic mutation or hypermutation) to increase the affinity of the antibody to the foreign antigen. The constant region will change in further response to an antigen (*i.e.*, isotype switch). Therefore, the rearranged and somatically mutated nucleic acid molecules that encode the light chain and heavy chain immunoglobulin polypeptides in response to an antigen may not have sequence identity with the original nucleic acid molecules, but instead will be substantially identical or similar (*i.e.*, have at least 80% identity).

The term "human antibody" includes antibodies having variable and constant regions (if present) of human germline immunoglobulin sequences. Human antibodies of the invention can include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*) (*see*, Lonberg, N. *et al.* (1994) *Nature* 368(6474): 856-859);

Lonberg, N. (1994) *Handbook of Experimental Pharmacology* 113:49-101; Lonberg, N. and Huszar, D. (1995) *Intern. Rev. Immunol.* Vol. 13: 65-93, and Harding, F. and Lonberg, N. (1995) *Ann. N.Y. Acad. Sci* 764:536-546). However, the term "human antibody" does not include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences (*i.e.*, humanized antibodies).

As used herein, a "heterologous antibody" is defined in relation to the transgenic non-human organism producing such an antibody. This term refers to an antibody having an amino acid sequence or an encoding nucleic acid sequence corresponding to that found in an organism not consisting of the transgenic non-human animal, and generally from a species other than that of the transgenic non-human animal.

As used herein, "neutralizing antibody" refers to an antibody, for example, a monoclonal antibody, capable of disrupting a formed viral particle or inhibiting formatting of a viral particle or prevention of binding to or infection of mammalian cells by a viral particle.

As used herein, "diagnostic antibody" or "detection antibody" or "detecting antibody" refers to an antibody, for example, a monoclonal antibody, capable of detecting the presence of an antigenic target within a sample. As will be appreciated by one of skill in the art, such diagnostic antibodies preferably have high specificity for their antigenic target.

The term "humanized immunoglobulin" or "humanized antibody" refers to an immunoglobulin or antibody that includes at least one humanized immunoglobulin or antibody chain (i.e., at least one humanized light or heavy chain). The term "humanized immunoglobulin chain" or "humanized antibody chain" (i.e., a "humanized immunoglobulin light chain" or "humanized immunoglobulin heavy chain") refers to an immunoglobulin or antibody chain (i.e., a light or heavy chain, respectively) having a variable region that includes a variable framework region substantially from a human immunoglobulin or antibody and complementarity determining regions (CDRs) (e.g., at least one CDR, preferably two CDRs, more preferably three CDRs) substantially from a non-human immunoglobulin or antibody, and further includes constant regions (e.g., at least one constant region or portion thereof, in the case of a light chain, and preferably three constant regions in the case of a heavy chain). The term "humanized variable region" (e.g., "humanized light chain variable region" or "humanized heavy chain variable region") refers to a variable region that includes a variable framework region substantially from a human immunoglobulin or antibody and complementarity determining regions (CDRs) substantially from a non-human immunoglobulin or antibody.

The phrase "substantially from a human immunoglobulin or antibody" or "substantially human" means that, when aligned to a human immunoglobulin or antibody amino acid sequence for comparison purposes, the region shares at least 80-90%, preferably at least 90-95%, more preferably at least 95-99% identity (i.e., local sequence identity) with the human framework or constant region sequence, allowing, for example, for conservative substitutions, consensus sequence substitutions, germline substitutions, backmutations, and the like. The introduction of conservative substitutions, consensus sequence substitutions, germline substitutions, backmutations, and the like, is often referred to as "optimization" of a humanized antibody or chain. The phrase "substantially from a non-human immunoglobulin or antibody" or "substantially non-human" means having an immunoglobulin or antibody sequence at least 80-95%, preferably at least 90-95%, more preferably, 96%, 97%, 98%, or 99% identical to that of a non-human organism, e.g., a non-human mammal.

Preferably, residue positions which are not identical differ by conservative amino acid substitutions. For purposes of classifying amino acids substitutions as conservative or nonconservative, amino acids are grouped as follows: Group I (hydrophobic sidechains): leu, met, ala, val, leu, ile; Group II (neutral hydrophilic side chains): cys, ser, thr; Group III (acidic side chains): asp, glu; Group IV (basic side chains): asn, gln, his, lys, arg; Group V (residues influencing chain orientation): gly, pro; and Group VI (aromatic side chains): trp, tyr, phe. Conservative substitutions involve substitutions between amino acids in the same class. Non-conservative substitutions constitute exchanging a member of one of these classes for a member of another.

A mutation (e.g., a backmutation) is said to substantially affect the ability of a heavy or light chain to direct antigen binding if it affects (e.g., decreases) the binding affinity of an intact immunoglobulin or antibody (or antigen binding fragment thereof) comprising said chain by at least an order of magnitude compared to that of the antibody (or antigen binding fragment thereof) comprising an equivalent chain lacking said mutation. A mutation "does not substantially affect (e.g., decrease) the ability of a chain to direct antigen binding" if it affects (e.g., decreases) the binding affinity of an intact immunoglobulin or antibody (or antigen binding fragment thereof) comprising said chain by only a factor of two, three, or four of that of the antibody (or antigen binding fragment thereof) comprising an equivalent chain lacking said mutation.

Preferably, humanized immunoglobulins or antibodies bind antigen with an affinity that is within a factor of three, four, or five of that of the corresponding non-humanized antibody. For example, if the nonhumanized antibody has a binding affinity of 10^9 M^{-1}, humanized antibodies will have a binding affinity of at least 3 times 10^9 M^{-1}, 4 times 10^9 M^{-1} or 10^9 M^{-1}. When describing the binding properties of an immunoglobulin or antibody chain, the chain can be described based on its ability to "direct antigen (e.g., Ebola GP) binding". A chain is said to "direct antigen binding" when it confers upon an intact immunoglobulin or antibody (or antigen binding fragment thereof) a specific binding property or binding affinity. A mutation (e.g., a backmutation) is said to substantially affect the ability of a heavy or light chain to direct antigen binding if it affects (e.g., decreases) the binding affinity of an intact immunoglobulin or antibody (or antigen binding fragment thereof) comprising said chain by at least an order of magnitude compared to that of the antibody (or antigen binding fragment thereof) comprising an equivalent chain lacking said mutation. A mutation "does not substantially affect (e.g., decrease) the ability of a chain to direct antigen binding" if it affects (e.g., decreases) the binding affinity of an intact immunoglobulin or antibody (or antigen binding fragment thereof) comprising said chain by only a factor of two, three, or four of that of the antibody (or antigen binding fragment thereof) comprising an equivalent chain lacking said mutation.

The term "chimeric immunoglobulin" or antibody refers to an immunoglobulin or antibody whose variable regions derive from a first species and whose constant regions derive from a second species. Chimeric immunoglobulins or antibodies can be constructed, for example by genetic engineering, from immunoglobulin gene segments belonging to different species. The terms "humanized immunoglobulin" or "humanized antibody" are not intended to encompass chimeric immunoglobulins or antibodies, as defined infra. Although humanized immunoglobulins or antibodies are chimeric in their construction (i.e., comprise regions from more than one species of protein), they include additional features (i.e., variable regions comprising donor CDR residues and acceptor framework residues) not found in chimeric immunoglobulins or antibodies, as defined herein.

An “isolated antibody,” as used herein, is intended to refer to an antibody which is substantially free of other antibodies having different antigenic specificities (*e.g.*, an isolated antibody that specifically binds to Ebola virus GP is substantially free of antibodies that specifically bind antigens other than Ebola virus GP). An isolated antibody is typically substantially free of other cellular material and/or chemicals. In certain embodiments of the invention, a combination of “isolated” antibodies having different Ebola virus GP specificities is combined in a well defined composition.

The term “epitope” or “antigenic determinant” refers to a site on an antigen to which an immunoglobulin or antibody specifically binds. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from contiguous amino acids are typically retained on exposure to denaturing solvents, whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids in a unique spatial conformation. Methods for determining what epitopes are bound by a given antibody (*i.e.*, epitope mapping) are well known in the art and include, for example, immunoblotting and immunoprecipitation assays, wherein overlapping or contiguous peptides from Ebola virus GP are tested for reactivity with the given anti-GP antibody. Methods of determining spatial conformation of epitopes include techniques in the art and those described herein, for example, x-ray crystallography and 2-dimensional nuclear magnetic resonance (see, *e.g.*, *Epitope Mapping Protocols in Methods in Molecular Biology,* Vol. 66, G. E. Morris, Ed. (1996)).

Antibodies that recognize the same epitope can be identified in a simple immunoassay showing the ability of one antibody to block the binding of another antibody to a target antigen, i.e., a competitive binding assay. Competitive binding is determined in an assay in which the immunoglobulin under test inhibits specific binding of a reference antibody to a common antigen. Numerous types of competitive binding assays are known, for example: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see Stahli et al., Methods in Enzymology 9:242 (1983)); solid phase direct biotin-avidin EIA (see Kirkland et al., J. Immunol. 137:3614 (1986)); solid phase direct labeled assay, solid phase direct labeled sandwich assay (see Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Press (1988)); solid phase direct label RIA using 1-125 label (see Morel et al., Mol. Immunol. 25(1):7 (1988)); solid phase direct biotin-avidin EIA (Cheung et al., Virology 176:546 (1990)); and direct labeled RIA. (Moldenhauer et al., Scand. J. Immunol. 32:77 (1990)). Typically, such an assay involves the use of purified antigen bound to a solid surface or cells bearing either of these, an unlabeled test immunoglobulin and a labeled reference immunoglobulin. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test immunoglobulin. Usually the test immunoglobulin is present in excess. Usually, when a competing antibody is present in excess, it will inhibit specific binding of a reference antibody to a common antigen by at least 50-55%, 55-60%, 60-65%, 65-70% 70-75% or more.

The term "epitope mapping" refers to the process of identification of the molecular determinants for antibody-antigen recognition. Numerous methods for epitope mapping are known in the art, such as x-ray analysis, protease mapping, hydrogen/deuterium exchange mass spectrometry (HDX-MS), 2D nuclear magnetic resonance, alanine scanning, and deep mutational scanning.

To facilitate the engineering of antibodies that target the Ebola virus glycoprotein (GP), epitope hotspots were determined using alanine scanning, as described herein. Based on the binding analysis, antibodies 4G7, K252, and 2G4 were found to bind to a conformational epitope that included regions V505-C511 and N550-E564 of SEQ ID NO: 91, whereas antibody 13C6 was found to bind within the regions T270-P279 and Y394-R409 of SEQ ID NO: 91 (Figure 1). Figure 2 summarizes the hotspots in the Ebola virus glycoprotein identified through this mutational analysis. Some aspects of the invention relate to peptide or peptide mimetics based on one or more epitopes within Ebola virus glycoprotein region V505-C511, region N550-E564, region T270-P279, or region Y394-R404 of Ebola virus glycoprotein (SEQ ID NO: 91). Some aspects of the invention relate to peptide or peptide mimetics based on one or more epitopes within Ebola virus glycoprotein (SEQ ID NO: 91) that spans V505-C511 and N550-E564. Some aspects of the invention relate to peptide or peptide mimetics based on one or more conformational epitopes on Ebola virus glycoprotein (SEQ ID NO: 91) that spans T270-P279 and Y394-R409. Some aspects of the invention relate to peptide or peptide mimetics based on one or more epitopes Ebola virus glycoprotein TGKLIWKVNP (SEQ ID NO: 98), YKLDISEATQVGQHHR (SEQ ID NO: 99), VNAQPKC (SEQ ID NO: 100), and NQDGLICGLRQLANE (SEQ ID NO: 101).

As used herein, the terms “specific binding,” “selective binding,” “selectively binds,” and “specifically binds,” refer to antibody binding to an epitope on a predetermined antigen. Typically, the antibody binds with an equilibrium dissociation constant (K_D) of approximately less than 10^{-7} M, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower when determined by surface plasmon resonance (SPR) technology in a BIACORE 2000 instrument using recombinant Ebola virus GP as the analyte and the antibody as the ligand and binds to the predetermined antigen with an affinity that is at least two-fold greater than its affinity for binding to a non-specific antigen (*e.g.*, BSA, casein) other than the predetermined antigen or a closely-related antigen. The phrases “an antibody recognizing an antigen” and “an antibody specific for an antigen” are used interchangeably herein with the term “an antibody which binds specifically to an antigen.”

The term “K_D,” as used herein, is intended to refer to the dissociation equilibrium constant of a particular antibody-antigen interaction.

The term “kd” as used herein, is intended to refer to the off rate constant for the dissociation of an antibody from the antibody/antigen complex.

The term “ka” as used herein, is intended to refer to the on rate constant for the association of an antibody with the antigen.

The term “EC50,” as used herein, refers to the concentration of an antibody or an antigen-binding portion thereof, which induces a response, either in an *in vitro* or an *in vivo* assay, which is 50% of the maximal response, *i.e.*, halfway between the maximal response and the baseline. In some aspects of the invention, monoclonal antibodies or antigen binding portions thereof, bind to Ebola virus glycoprotein with an EC_{50} of 300 pM or less, as measured by ELISA. In some aspects of the invention, monoclonal antibodies or antigen binding portions thereof, bind to Ebola virus glycoprotein with an EC_{50} of 200 pM or less, as measured by ELISA. In some aspects of the invention, monoclonal antibodies or antigen binding portions thereof, bind to Ebola virus glycoprotein with an EC_{50} of 150 pM or less, as measured by ELISA. In some aspects of the invention, monoclonal antibodies or antigen binding portions thereof, bind to Ebola virus glycoprotein with an EC_{50} of 100 pM or less, as measured by ELISA.

As used herein, “isotype” refers to the antibody class (*e.g.*, IgM or IgGl) that is encoded by heavy chain constant region genes. In one embodiment, a human monoclonal antibody of the invention is of the IgG1 isotype. In certain embodiments, the human IgG1 has a heavy chain constant domain sequence as set forth in SEQ ID NO: 1 and a light chain constant domain sequence as set forth in SEQ ID NO: 2.

The term “binds to Ebola virus glycoprotein (GP),” refers to the ability of a monoclonal antibody of the invention to specifically bind to Ebola virus GP, for example, expressed on the surface of a cell or which is attached to a solid support.

As used herein, the term "having neutralizing activity" refers to the reduction in viral infectivity by the binding of a monoclonal antibody of the invention, or antigen binding portion thereof, to Ebola Virus GP. Neutralization is measured in the presence or absence of complement.

As used herein, a plaque reduction neutralization assay is used to quantify the titre of neutralizing antibody for a virus. A serum sample or solution of antibody to be tested is diluted and mixed with a viral suspension. This is incubated to allow the antibody to react with the virus and poured over a confluent monolayer of host cells. The concentration of plaque forming units can be estimated by the number of plaques (regions of infected cells) formed after a few days. The concentration of serum to reduce the number of plaques by

50% compared to the serum free virus gives the measure of how much antibody is present or how effective it is. This measurement is denoted as the plaque reduction neutralization $(PRNT)_{50}$ value.

The term “nucleic acid molecule,” as used herein, is intended to include DNA molecules and RNA molecules. A nucleic acid molecule may be single-stranded or double-stranded, but preferably is double-stranded DNA.

The present invention also encompasses “conservative sequence modifications” of the sequences set forth in the Sequence Table *i.e*., nucleotide and amino acid sequence modifications which do not abrogate the binding of the antibody encoded by the nucleotide sequence or containing the amino acid sequence, to the antigen. Such conservative sequence modifications include conservative nucleotide and amino acid substitutions, as well as, nucleotide and amino acid additions and deletions. For example, modifications can be introduced into sequences set forth in the Sequence Table by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative amino acid substitutions include ones in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a human anti-GP antibody is preferably replaced with another amino acid residue from the same side chain family. Methods of identifying nucleotide and amino acid conservative substitutions which do not eliminate antigen binding are well-known in the art (see, *e.g*., Brummell *et al*., *Biochem.* 32:1180-1187 (1993); Kobayashi *et al. Protein Eng.* 12(10):879-884 (1999); and Burks *et al. Proc. Natl. Acad. Sci. USA* 94:412-417 (1997))

Alternatively, in certain embodiments, mutations can be introduced randomly along all or part of an anti-Ebola Virus GP antibody coding sequence, such as by saturation mutagenesis, and the resulting modified anti-Ebola Virus GP antibodies can be screened for binding activity.

For nucleic acids, the term “substantial homology” indicates that two nucleic acids, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least about 80% of the nucleotides, usually at least about 90% to 95%, and more preferably at least about 98% to 99.5% of the nucleotides. Alternatively, substantial homology exists when the segments will hybridize under selective hybridization conditions, to the complement of the strand.

The percent identity between two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100), taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm, as described in the non-limiting examples below.

The percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. The percent identity between two nucleotide or amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

The nucleic acid and protein sequences of the present invention can further be used as a “query sequence” to perform a search against public databases to, for example, identify related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

The nucleic acids may be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form. A nucleic acid is "isolated" or "rendered substantially pure" when purified away from other cellular components or other contaminants, *e.g.*, other cellular nucleic acids or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, agarose gel electrophoresis and others well known in the art. *See*, F. Ausubel, *et al.*, ed. Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York (1987).

When given an amino acid sequence, one versed in the art can make conservative substitutions to the nucleotide sequence encoding it without altering the amino acid sequence, given the redundancy in the genetic code. The nucleic acid compositions, while often in a native sequence (except for modified restriction sites and the like), from either cDNA, genomic or mixtures thereof may be mutated, in accordance with standard techniques to provide gene sequences. For coding sequences, these mutations, may affect amino acid sequence as desired. In particular, DNA sequences substantially homologous to or derived from native V, D, J, constant, switches and other such sequences described herein are contemplated (where "derived" indicates that a sequence is identical or modified from another sequence).

The term "peptide" as used herein is defined as a chain of amino acid residues, usually having a defined sequence. As used herein the term peptide is interchangeable with the terms "polypeptide" and "protein". In the context of the present invention, the term "peptide" is defined as being any peptide or protein comprising at least two amino acids linked by a modified or unmodified peptide bond. The term "peptide" refers to short-chain molecules such as oligopeptides or oligomers or to long-chain molecules such as proteins. A peptide according to the present invention can comprise modified amino acids. Thus, the peptide of the present invention can also be modified by natural processes such as post-transcriptional modifications or by a chemical process. Some examples of these modifications are: acetylation, acylation, ADP-ribosylation, amidation, covalent bonding with flavine, covalent bonding with a heme, covalent bonding with a nucleotide or a nucleotide derivative, covalent bonding to a modified or unmodified carbohydrate moiety, bonding with a lipid or a lipid derivative, covalent bonding with a phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, cysteine molecule formation, pyroglutamate formation, formylation, gamma-carboxylation, hydroxylation, iodination, methylation, oxidation, phosphorylation, racemization, hydroxylation, etc. Thus, any modification of the peptide which does not have the effect of eliminating the immunogenicity of the peptide, is covered within the scope of the present invention.

The individual residues of the peptides of the invention protein can be incorporated in the peptide by a peptide bond or peptide bond mimetic. A peptide bond mimetic of the invention includes peptide backbone modifications well known to those skilled in the art. Such modifications include modifications of the amide nitrogen, the a-carbon, amide carbonyl, complete replacement of the amide bond, extensions, deletions or backbone cross-links. See, generally, Spatola, Chemistry and Biochemistry of Amino Acids, Peptides and Proteins, Vol. VII (Weinstein ed., 1983). Several peptide backbone modifications are known, these include, ψ [CH_2S], ψ [CH_2NH], ψ [$CSNH_2$], ψ [NHCO], ψ [$COCH_2$] and ψ [(E) or (Z) CH=CH]. The nomenclature used above, follows that suggested by Spatola, above. In this context, ψ indicates the absence of an amide bond. The structure that replaces the amide group is specified within the brackets.

Amino acid mimetics may also be incorporated in the peptides. An "amino acid mimetic" as used here is a moiety other than a naturally occurring amino acid that conformationally and functionally serves as a substitute for an amino acid in a peptide of the present invention. Such a moiety serves as a substitute for an amino acid residue if it does not interfere with the ability of the peptide to bind to Ebola virus antibodies. Amino acid mimetics may include non-protein amino acids, such as β-, γ-, δ-amino acids, β-, γ-, δ----imino acids (such as piperidine-4- carboxylic acid) as well as many derivatives of L-a-amino acids. A number of suitable amino acid mimetics are known to the skilled artisan, they include cyclohexylalanine, 3-cyclohexylpropionic acid, L-adamantyl alanine, adamantylacetic acid and the like. In addition, D-amino acids can be regarded as mimetics. Peptide mimetics suitable for peptides of the present invention are discussed by Morgan and Gainor, (1989) Ann. Repts. Med. Chem. 24:243-252.

The term “vector,” as used herein, is intended to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a “plasmid,” which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome.

Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors"). In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The term "recombinant host cell" (or simply "host cell"), as used herein, is intended to refer to a cell into which a recombinant expression vector has been introduced. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein.

The terms "treat," "treating," and "treatment," as used herein, refer to therapeutic or preventative measures described herein. The methods of "treatment" employ administration to a subject, in need of such treatment, a human antibody of the present invention, for example, a subject in need of an enhanced immune response against a particular antigen or a subject who ultimately may acquire such a disorder, in order to prevent, cure, delay, reduce the severity of, or ameliorate one or more symptoms of the disorder or recurring disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts effective for this use will depend upon the severity of the disorder being treated and the general state of the patient's own immune system.

The term "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

As used herein, the term "subject" includes any human or non-human animal. For example, the methods and compositions of the present invention can be used to treat a subject with an immune disorder. The term "non-human animal" includes all vertebrates, *e.g.*, mammals and non-mammals, such as non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, *etc.*

Various aspects of the invention are described in further detail in the following subsections.

Production of Antibodies to Ebola Virus Glycoprotein

The present invention encompasses antibodies, e.g., monoclonal antibodies that bind Ebola virus GP. Exemplary monoclonal antibodies that bind Ebola virus GP are optimized monoclonal antibodies which include CDRs or optimized CDRs based on the mouse monoclonal antibodies 13C6, 6D8, and 13F6 (as disclosed in US 6,630,144 and US 7,335,356), and mouse monoclonal antibodies 1H3, 2G4, and 4G7 (as disclosed in US 8,513,391). Provided herein are isolated monoclonal antibodies or antigen binding portions thereof, comprising heavy and light chain variable sequences comprising (further described in Tables 1 and 2):

(a) SEQ ID NOs: 15 and 17, respectively;
(b) SEQ ID NOs: 15 and 18, respectively;
(c) SEQ ID NOs: 16 and 17, respectively;
(d) SEQ ID NOs: 16 and 18, respectively;
(e) SEQ ID NOs: 19 and 20, respectively;
(f) SEQ ID NOs:19 and 21, respectively;
(g) SEQ ID NOs: 22 and 23, respectively;
(h) SEQ ID NOs: 22 and 24, respectively;
(i) SEQ ID NOs: 9 and 10, respectively;
(j) SEQ ID NOs: 9 and 27, respectively;
(k) SEQ ID NOs: 9 and 28, respectively;
(l) SEQ ID NOs: 9 and 29, respectively;
(m) SEQ ID NOs: 9 and 30, respectively;
(n) SEQ ID NOs: 9 and 31, respectively;
(o) SEQ ID NOs: 25 and 10, respectively;
(p) SEQ ID NOs: 25 and 27, respectively;
(q) SEQ ID NOs: 25 and 28, respectively;
(r) SEQ ID NOs: 25 and 29, respectively;
(s) SEQ ID NOs: 25 and 30, respectively;
(t) SEQ ID NOs: 25 and 31, respectively;

(u) SEQ ID NOs: 26 and 10, respectively;

(v) SEQ ID NOs: 26 and 27, respectively;

(w) SEQ ID NOs: 26 and 28, respectively;

(x) SEQ ID NOs: 26 and 29, respectively;

(y) SEQ ID NOs: 26 and 30, respectively;

(z) SEQ ID NOs: 26 and 31, respectively;

(aa) SEQ ID NOs: 11 and 12, respectively;

(bb) SEQ ID NOs: 11 and 36, respectively;

(cc) SEQ ID NOs: 11 and 37, respectively;

(dd) SEQ ID NOs: 32 and 12, respectively;

(ee) SEQ ID NOs: 32 and 36, respectively;

(ff) SEQ ID NOs: 32 and 37, respectively;

(gg) SEQ ID NOs: 33 and 12, respectively;

(hh) SEQ ID NOs: 33 and 36, respectively;

(ii) SEQ ID NOs: 33 and 37, respectively;

(jj) SEQ ID NOs: 34 and 12, respectively;

(kk) SEQ ID NOs: 34 and 36, respectively;

(ll) SEQ ID NOs: 34 and 37, respectively;

(mm) SEQ ID NOs: 35 and 12, respectively;

(nn) SEQ ID NOs: 35 and 36, respectively;

(oo) SEQ ID NOs: 35 and 37, respectively;

(pp) SEQ ID NOs: 13 and 14, respectively;

(qq) SEQ ID NOs: 13 and 42, respectively;

(rr) SEQ ID NOs: 13 and 43, respectively;

(ss) SEQ ID NOs: 13 and 44, respectively;

(tt) SEQ ID NOs: 38 and 14, respectively;

(uu) SEQ ID NOs: 38 and 42, respectively;

(vv) SEQ ID NOs: 38 and 43, respectively;

(ww) SEQ ID NOs: 38 and 44, respectively;

(xx) SEQ ID NOs: 39 and 14, respectively;

(yy) SEQ ID NOs: 39 and 42, respectively;

(zz) SEQ ID NOs: 39 and 43, respectively;

(aaa) SEQ ID NOs: 39 and 44, respectively;

(bbb) SEQ ID NOs: 40 and 14, respectively;

(ccc) SEQ ID NOs: 40 and 42, respectively;
(ddd) SEQ ID NOs: 40 and 43, respectively;
(eee) SEQ ID NOs: 40 and 44, respectively;
(fff) SEQ ID NOs: 41 and 14, respectively;
(ggg) SEQ ID NOs: 41 and 42, respectively;
(hhh) SEQ ID NOs: 41 and 43, respectively; and
(iii) SEQ ID NOs: 41 and 44, respectively.

Monoclonal antibodies of the invention can be produced using a variety of known techniques, such as the standard somatic cell hybridization technique described by Kohler and Milstein, Nature 256: 495 (1975). Although somatic cell hybridization procedures are preferred, in principle, other techniques for producing monoclonal antibodies also can be employed, *e.g.*, viral or oncogenic transformation of B lymphocytes, phage display technique using libraries of human antibody genes.

Accordingly, in certain embodiments, a hybridoma method is used for producing an antibody that binds Ebola virus GP. In this method, a mouse or other appropriate host animal can be immunized with a suitable antigen in order to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the antigen used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes can then be fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, Monoclonal Antibodies: Principles and Practice, pp.59-103 (Academic Press, 1986)). Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, Monoclonal Antibodies:Principles and Practice, pp. 59-103 (Academic Press, 1986)). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as ascites tumors in an animal. The monoclonal antibodies secreted by the subclones can be separated from the culture medium, ascites fluid, or serum by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

In certain embodiments, antibodies and antibody portions that bind Ebola virus GP can be isolated from antibody phage libraries generated using the techniques described in, for example, McCafferty *et al.*, *Nature*, 348:552-554 (1990). Clackson *et al.*, Nature, 352:624-628 (1991), Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991) and Hoet *et al* (2005) *Nature Biotechnology* 23, 344-348 ; U.S. Patent Nos. 5,223,409; 5,403,484; and 5,571,698 to Ladner *et al.*; U.S. Patent Nos. 5,427,908 and 5,580,717 to Dower *et al.*; U.S. Patent Nos. 5,969,108 and 6,172,197 to McCafferty *et al.*; and U.S. Patent Nos. 5,885,793; 6,521,404; 6,544,731; 6,555,313; 6,582,915 and 6,593,081 to Griffiths *et al.*. Additionally, production of high affinity (nM range) human antibodies by chain shuffling (Marks *et al.*, *Bio/Technology*, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries (Waterhouse *et al.*, *Nuc. Acids. Res.*, 21:2265-2266 (1993)) may also be used.

In certain embodiments, the antibody that binds Ebola virus GP is produced using the phage display technique described by Hoet *et al.*, *supra*. This technique involves the generation of a human Fab library having a unique combination of immunoglobulin sequences isolated from human donors and having synthetic diversity in the heavy-chain CDRs is generated. The library is then screened for Fabs that bind to Ebola virus GP.

The preferred animal system for generating hybridomas which produce antibodies of the invention is the murine system. Hybridoma production in the mouse is well known in the art, including immunization protocols and techniques for isolating and fusing immunized splenocytes.

In certain embodiments, antibodies directed against Ebola virus GP are generated using transgenic or transchromosomal mice carrying parts of the human immune system rather than the mouse system. In one embodiment, the invention employs transgenic mice, referred to herein as "HuMAb mice" which contain a human immunoglobulin gene miniloci that encodes unrearranged human heavy (μ and γ) and κ light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous μ and κ chain loci (Lonberg, N. *et al.* (1994) *Nature* 368(6474): 856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or κ, and in response to immunization, the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgGκ monoclonal antibodies (Lonberg, N. *et al.* (1994), *supra*; reviewed in Lonberg, N. (1994) *Handbook of Experimental Pharmacology* 113:49-101; Lonberg, N. and Huszar, D. (1995) *Intern. Rev. Immunol.* Vol. 13: 65-93, and Harding, F. and Lonberg, N. (1995) *Ann. N.Y. Acad. Sci* 764:536-546). The preparation of HuMAb mice is described in detail below and in Taylor, L. *et al.* (1992) *Nucleic Acids Research* 20:6287-

6295; Chen, J. *et al.* (1993) *International Immunology* 5: 647-656; Tuaillon *et al.* (1993) *Proc. Natl. Acad. Sci USA* 90:3720-3724; Choi *et al.* (1993) *Nature Genetics* 4:117-123; Chen, J. *et al.* (1993) *EMBO J.* 12: 821-830; Tuaillon *et al.* (1994) *J. Immunol.* 152:2912-2920; Lonberg *et al.*, (1994) *Nature* 368(6474): 856-859; Lonberg, N. (1994) *Handbook of Experimental Pharmacology* 113:49-101; Taylor, L. *et al.* (1994) *International Immunology* 6: 579-591; Lonberg, N. and Huszar, D. (1995) *Intern. Rev. Immunol.* Vol. 13: 65-93; Harding, F. and Lonberg, N. (1995) *Ann. N.Y. Acad. Sci* 764:536-546; Fishwild, D. *et al.* (1996) *Nature Biotechnology* 14: 845-851. See further, U.S. Patent Nos. 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,789,650; 5,877,397; 5,661,016; 5,814,318; 5,874,299; and 5,770,429; all to Lonberg and Kay, and GenPharm International; U.S. Patent No. 5,545,807 to Surani *et al.*; International Publication Nos. WO 98/24884, published on June 11, 1998; WO 94/25585, published November 10, 1994; WO 93/1227, published June 24, 1993; WO 92/22645, published December 23, 1992; WO 92/03918, published March 19, 1992.

In certain embodiments, human antibodies of the invention can be raised using a mouse that carries human immunoglobulin sequences on transgenes and transchomosomes, such as a mouse that carries a human heavy chain transgene and a human light chain transchromosome. Such mice, referred to in the art as "KM mice", are described in detail in PCT Publication WO 02/43478 to Ishida et al.

Still further, alternative transgenic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise anti-Ebola virus GP antibodies of the invention. For example, an alternative transgenic system referred to as the Xenomouse (Abgenix, Inc.) can be used; such mice are described in, for example, U.S. Pat. Nos. 5,939,598; 6,075,181; 6,114,598; 6,150,584 and 6,162,963 to Kucherlapati et al.

Moreover, alternative transchromosomic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise anti-Ebola virus GP antibodies of the invention. For example, mice carrying both a human heavy chain transchromosome and a human light chain tranchromosome, referred to in the art as "TC mice" can be used; such mice are described in Tomizuka et al. (2000) Proc. Natl. Acad. Sci. USA 97:722-727. Furthermore, cows carrying human heavy and light chain transchromosomes have been described in the art (Kuroiwa et al. (2002) Nature Biotechnology 20:889-894) and can be used to raise anti-Ebola virus GP antibodies of the invention.

Additional mouse systems described in the art for raising human antibodies also can be applied to raising anti-Ebola virus GP antibodies of the invention, including but not limited to (i) the VelocImmune® mouse (Regeneron Pharmaceuticals, Inc.), in which the endogenous mouse heavey and light chain variable regions have been replaced, via homologous recombination, with human heavy and light chain variable regions, operatively linked to the endogenous mouse constant regions, such that chimeric antibodies (human V/mouse C) are raised in the mice, and then subsequently converted to fully human antibodies using standard recombinant DNA techniques; and (ii) the MeMo® mouse (Merus Biopharmaceuticals, Inc.), in which the mouse contains unrearranged human heavy chain variable regions but a single rearranged human common light chain variable region. Such mice, and use thereof to raise antibodies, are described in, for example, WO 2009/15777, US 2010/0069614, WO 2011/072204, WO 2011/097603, WO 2011/163311, WO 2011/163314, WO 2012/148873, US 2012/0070861 and US 2012/0073004.

Human monoclonal antibodies of the invention can also be prepared using SCID mice into which human immune cells have been reconstituted such that a human antibody response can be generated upon immunization. Such mice are described in, for example, U.S. Pat. Nos. 5,476,996 and 5,698,767 to Wilson et al.

In certain embodiments, the mAbs described herein can be produced in plants using deconstructed viral vectors, as described in Olinger et al., *PNAS* 2012; 109, 18030-18035, herein incorporated by reference. In certain embodiments, the mAbs are produced in tobacco plants.

In certain embodiments, chimeric antibodies can be prepared based on the sequence of a murine monoclonal antibodies described herein. A chimeric antibody refers to an antibody whose light and heavy chain genes have been constructed, typically by genetic engineering, from immunoglobulin gene segments belonging to different species. For example, the variable (V) segments of the genes from a mouse monoclonal antibody may be joined to human constant (C) segments, such as IgG1 and IgG4. Human isotype IgG1 is preferred. A typical chimeric antibody is thus a hybrid protein consisting of the V or antigen-binding domain from a mouse antibody and the C or effector domain from a human antibody.

Production of Humanized Antibodies

The term "humanized antibody" refers to an antibody comprising at least one chain comprising variable region framework residues substantially from a human antibody chain (referred to as the acceptor immunoglobulin or antibody) and at least one complementarity determining region substantially from a mouse antibody, (referred to as the donor immunoglobulin or antibody). See, Queen et al., Proc. Natl. Acad. Sci. USA 86:10029-10033 (1989), U.S. Pat. No. 5,530,101, U.S. Pat. No. 5,585,089, U.S. Pat. No. 5,693,761, U.S. Pat. No. 5,693,762, Selick et al., WO 90/07861, and Winter, U.S. Pat. No. 5,225,539 (incorporated by reference in their entirety for all purposes). The constant region(s), if present, are also substantially or entirely from a human immunoglobulin.

The substitution of mouse CDRs into a human variable domain framework is most likely to result in retention of their correct spatial orientation if the human variable domain framework adopts the same or similar conformation to the mouse variable framework from which the CDRs originated. This is achieved by obtaining the human variable domains from human antibodies whose framework sequences exhibit a high degree of sequence identity with the murine variable framework domains from which the CDRs were derived. The heavy and light chain variable framework regions can be derived from the same or different human antibody sequences. The human antibody sequences can be the sequences of naturally occurring human antibodies or can be consensus sequences of several human antibodies. See Kettleborough et al., Protein Engineering 4:773 (1991); Kolbinger et al., Protein Engineering 6:971 (1993) and Carter et al., WO 92/22653.

Having identified the complementarity determining regions of the murine donor immunoglobulin and appropriate human acceptor immunoglobulins, the next step is to determine which, if any, residues from these components should be substituted to optimize the properties of the resulting humanized antibody. In general, substitution of human amino acid residues with murine should be minimized, because introduction of murine residues increases the risk of the antibody eliciting a human-anti-mouse-antibody (HAMA) response in humans. Art-recognized methods of determining immune response can be performed to monitor a HAMA response in a particular patient or during clinical trials. Patients administered humanized antibodies can be given an immunogenicity assessment at the beginning and throughout the administration of said therapy. The HAMA response is measured, for example, by detecting antibodies to the humanized therapeutic reagent, in serum samples from the patient using a method known to one in the art, including surface plasmon resonance technology (BIACORE) and/or solid-phase ELISA analysis.

Certain amino acids from the human variable region framework residues are selected for substitution based on their possible influence on CDR conformation and/or binding to antigen. The unnatural juxtaposition of murine CDR regions with human variable framework region can result in unnatural conformational restraints, which, unless corrected by substitution of certain amino acid residues, lead to loss of binding affinity.

The selection of amino acid residues for substitution is determined, in part, by computer modeling. Computer hardware and software are described herein for producing three-dimensional images of immunoglobulin molecules. In general, molecular models are produced starting from solved structures for immunoglobulin chains or domains thereof. The chains to be modeled are compared for amino acid sequence similarity with chains or domains of solved three-dimensional structures, and the chains or domains showing the greatest sequence similarity is/are selected as starting points for construction of the molecular model. Chains or domains sharing at least 50% sequence identity are selected for modeling, and preferably those sharing at least 60%, 70%, 80%, 90% sequence identity or more are selected for modeling. The solved starting structures are modified to allow for differences between the actual amino acids in the immunoglobulin chains or domains being modeled, and those in the starting structure. The modified structures are then assembled into a composite immunoglobulin. Finally, the model is refined by energy minimization and by verifying that all atoms are within appropriate distances from one another and that bond lengths and angles are within chemically acceptable limits.

The selection of amino acid residues for substitution can also be determined, in part, by examination of the characteristics of the amino acids at particular locations, or empirical observation of the effects of substitution or mutagenesis of particular amino acids. For example, when an amino acid differs between a murine variable region framework residue and a selected human variable region framework residue, the human framework amino acid should usually be substituted by the equivalent framework amino acid from the mouse antibody when it is reasonably expected that the amino acid:

(1) noncovalently binds antigen directly,

(2) is adjacent to a CDR region,

(3) otherwise interacts with a CDR region (e.g., is within about 3-6 angstroms of a CDR region as determined by computer modeling), or

(4) participates in the VL-VH interface.

Residues which "noncovalently bind antigen directly" include amino acids in positions in framework regions which have a good probability of directly interacting with amino acids on the antigen according to established chemical forces, for example, by hydrogen bonding, Van der Waals forces, hydrophobic interactions, and the like.

CDR and framework regions are as defined by Kabat et al. or Chothia et al., supra. When framework residues, as defined by Kabat et al., supra, constitute structural loop residues as defined by Chothia et al., supra, the amino acids present in the mouse antibody may be selected for substitution into the humanized antibody. Residues which are "adjacent to a CDR region" include amino acid residues in positions immediately adjacent to one or more of the CDRs in the primary sequence of the humanized immunoglobulin chain, for example, in positions immediately adjacent to a CDR as defined by Kabat, or a CDR as defined by Chothia (See e.g., Chothia and Lesk J M B 196:901 (1987)). These amino acids are particularly likely to interact with the amino acids in the CDRs and, if chosen from the acceptor, to distort the donor CDRs and reduce affinity. Moreover, the adjacent amino acids may interact directly with the antigen (Amit et al., Science, 233:747 (1986), which is incorporated herein by reference) and selecting these amino acids from the donor may be desirable to keep all the antigen contacts that provide affinity in the original antibody.

Residues that "otherwise interact with a CDR region" include those that are determined by secondary structural analysis to be in a spatial orientation sufficient to affect a CDR region. In certain embodiments, residues that "otherwise interact with a CDR region" are identified by analyzing a three-dimensional model of the donor immunoglobulin (e.g., a computer-generated model). A three-dimensional model, typically of the original donor antibody, shows that certain amino acids outside of the CDRs are close to the CDRs and have a good probability of interacting with amino acids in the CDRs by hydrogen bonding, Van der Waals forces, hydrophobic interactions, etc. At those amino acid positions, the donor immunoglobulin amino acid rather than the acceptor immunoglobulin amino acid may be selected. Amino acids according to this criterion will generally have a side chain atom within about 3 angstrom units (A) of some atom in the CDRs and must contain an atom that could interact with the CDR atoms according to established chemical forces, such as those listed above.

In the case of atoms that may form a hydrogen bond, the 3 Angstroms is measured between their nuclei, but for atoms that do not form a bond, the 3 Angstroms is measured between their Van der Waals surfaces. Hence, in the latter case, the nuclei must be within about 6 Angstroms (3 Angstroms plus the sum of the Van der Waals radii) for the atoms to be considered capable of interacting. In many cases the nuclei will be from 4 or 5 to 6 Angstroms apart. In determining whether an amino acid can interact with the CDRs, it is preferred not to consider the last 8 amino acids of heavy chain CDR 2 as part of the CDRs, because from the viewpoint of structure, these 8 amino acids behave more as part of the framework.

Amino acids that are capable of interacting with amino acids in the CDRs, may be identified in yet another way. The solvent accessible surface area of each framework amino acid is calculated in two ways: (1) in the intact antibody, and (2) in a hypothetical molecule consisting of the antibody with its CDRs removed. A significant difference between these numbers of about 10 square angstroms or more shows that access of the framework amino acid to solvent is at least partly blocked by the CDRs, and therefore that the amino acid is making contact with the CDRs. Solvent accessible surface area of an amino acid may be calculated based on a three-dimensional model of an antibody, using algorithms known in the art (e.g., Connolly, J. Appl. Cryst. 16:548 (1983) and Lee and Richards, J. Mol. Biol. 55:379 (1971), both of which are incorporated herein by reference). Framework amino acids may also occasionally interact with the CDRs indirectly, by affecting the conformation of another framework amino acid that in turn contacts the CDRs.

The amino acids at several positions in the framework are known to be capable of interacting with the CDRs in many antibodies (Chothia and Lesk, supra, Chothia et al., supra and Tramontano et al., J. Mol. Biol. 215:175 (1990), all of which are incorporated herein by reference). Notably, the amino acids at positions 2, 48, 64 and 71 of the light chain and 26-30, 71 and 94 of the heavy chain (numbering according to Kabat) are known to be capable of interacting with the CDRs in many antibodies. The amino acids at positions 35 in the light chain and 93 and 103 in the heavy chain are also likely to interact with the CDRs. At all these numbered positions, choice of the donor amino acid rather than the acceptor amino acid (when they differ) to be in the humanized immunoglobulin is preferred. On the other hand, certain residues capable of interacting with the CDR region, such as the first 5 amino acids of the light chain, may sometimes be chosen from the acceptor immunoglobulin without loss of affinity in the humanized immunoglobulin.

Residues which "participate in the VL-VH interface" or "packing residues" include those residues at the interface between VL and VH as defined, for example, by Novotny and Haber, Proc. Natl. Acad. Sci. USA, 82:4592-66 (1985) or Chothia et al, supra. Generally, unusual packing residues should be retained in the humanized antibody if they differ from those in the human frameworks.

In general, one or more of the amino acids fulfilling the above criteria is substituted. In some embodiments, all or most of the amino acids fulfilling the above criteria are substituted. Occasionally, there is some ambiguity about whether a particular amino acid meets the above criteria, and alternative variant immunoglobulins are produced, one of which has that particular substitution, the other of which does not. Alternative variant immunoglobulins so produced can be tested in any of the assays described herein for the desired activity, and the preferred immunoglobulin selected.

Usually the CDR regions in humanized antibodies are substantially identical, and more usually, identical to the corresponding CDR regions of the donor antibody. Although not usually desirable, it is sometimes possible to make one or more conservative amino acid substitutions of CDR residues without appreciably affecting the binding affinity of the resulting humanized immunoglobulin. By conservative substitutions is intended combinations such as gly, ala; val, ile, leu; asp, glu; asn, gln; ser, thr; lys, arg; and phe, tyr.

Additional candidates for substitution are acceptor human framework amino acids that are unusual or "rare" for a human immunoglobulin at that position. These amino acids can be substituted with amino acids from the equivalent position of the mouse donor antibody or from the equivalent positions of more typical human immunoglobulins. For example, substitution may be desirable when the amino acid in a human framework region of the acceptor immunoglobulin is rare for that position and the corresponding amino acid in the donor immunoglobulin is common for that position in human immunoglobulin sequences; or when the amino acid in the acceptor immunoglobulin is rare for that position and the corresponding amino acid in the donor immunoglobulin is also rare, relative to other human sequences. These criteria help ensure that an atypical amino acid in the human framework does not disrupt the antibody structure. Moreover, by replacing an unusual human acceptor amino acid with an amino acid from the donor antibody that happens to be typical for human antibodies, the humanized antibody may be made less immunogenic.

The term "rare", as used herein, indicates an amino acid occurring at that position in less than about 20% but usually less than about 10% of sequences in a representative sample of sequences, and the term "common", as used herein, indicates an amino acid occurring in more than about 25% but usually more than about 50% of sequences in a representative sample. For example, all human light and heavy chain variable region sequences are respectively grouped into "subgroups" of sequences that are especially homologous to each other and have the same amino acids at certain critical positions (Kabat et al., supra). When deciding whether an amino acid in a human acceptor sequence is "rare" or "common" among human sequences, it will often be preferable to consider only those human sequences in the same subgroup as the acceptor sequence.

Additional candidates for substitution are acceptor human framework amino acids that would be identified as part of a CDR region under the alternative definition proposed by Chothia et al., supra. Additional candidates for substitution are acceptor human framework amino acids that would be identified as part of a CDR region under the AbM and/or contact definitions.

Additional candidates for substitution are acceptor framework residues that correspond to a rare or unusual donor framework residue. Rare or unusual donor framework residues are those that are rare or unusual (as defined herein) for murine antibodies at that position. For murine antibodies, the subgroup can be determined according to Kabat and residue positions identified which differ from the consensus. These donor specific differences may point to somatic mutations in the murine sequence which enhance activity. Unusual residues that are predicted to affect binding are retained, whereas residues predicted to be unimportant for binding can be substituted.

Additional candidates for substitution are non-germline residues occurring in an acceptor framework region. For example, when an acceptor antibody chain (i.e., a human antibody chain sharing significant sequence identity with the donor antibody chain) is aligned to a germline antibody chain (likewise sharing significant sequence identity with the donor chain), residues not matching between acceptor chain framework and the germline chain framework can be substituted with corresponding residues from the germline sequence.

Other than the specific amino acid substitutions discussed above, the framework regions of humanized immunoglobulins are usually substantially identical, and more usually, identical to the framework regions of the human antibodies from which they were derived. Of course, many of the amino acids in the framework region make little or no direct contribution to the specificity or affinity of an antibody. Thus, many individual conservative substitutions of framework residues can be tolerated without appreciable change of the specificity or affinity of the resulting humanized immunoglobulin. Thus, in one embodiment the variable framework region of the humanized immunoglobulin shares at least 85% sequence identity to a human variable framework region sequence or consensus of such sequences. In another embodiment, the variable framework region of the humanized immunoglobulin shares at least 90%, preferably 95%, more preferably 96%, 97%, 98% or 99% sequence identity to a human variable framework region sequence or consensus of such sequences. In general, however, such substitutions are undesirable.

The humanized antibodies preferably exhibit a specific binding affinity for antigen of at least 10^7, 10^8, 10^9 or 10^{10} M^{-1}. Usually the upper limit of binding affinity of the humanized antibodies for antigen is within a factor of three, four or five of that of the donor immunoglobulin. Often the lower limit of binding affinity is also within a factor of three, four or five of that of donor immunoglobulin. Alternatively, the binding affinity can be compared to that of a humanized antibody having no substitutions (e.g., an antibody having donor CDRs and acceptor FRs, but no FR substitutions). In such instances, the binding of the optimized antibody (with substitutions) is preferably at least two- to three-fold greater, or three- to four-fold greater, than that of the unsubstituted antibody. For making comparisons, activity of the various antibodies can be determined, for example, by BIACORE (i.e., surface plasmon resonance using unlabelled reagents) or competitive binding assays.

Immunizations

To generate fully human antibodies to Ebola virus GP, transgenic or transchromosomal mice containing human immunoglobulin genes (*e.g.*, HCo12, HCo7 or KM mice) can be immunized with a purified or enriched preparation of the Ebola virus GP antigen and/or cells expressing Ebola virus GP, as described, for example, by Lonberg *et al.* (1994) *Nature* 368(6474): 856-859; Fishwild *et al.* (1996) *Nature Biotechnology* 14: 845-851 and WO 98/24884. As described herein, HuMAb mice are immunized either with recombinant Ebola virus GP proteins or cell lines expressing Ebola virus GP as immunogens. Alternatively, mice can be immunized with DNA encoding Ebola virus GP. Preferably, the mice will be 6-16 weeks of age upon the first infusion. For example, a purified or enriched preparation (5-50 μg) of the recombinant Ebola virus GP antigen can be used to immunize the HuMAb mice intraperitoneally.

Cumulative experience with various antigens has shown that the transgenic mice respond best when initially immunized intraperitoneally (IP) or subcutaneously (SC) with antigen in complete Freund's adjuvant, followed by every other week IP/SC immunizations (up to a total of 10) with antigen in incomplete Freund's adjuvant. The immune response can be monitored over the course of the immunization protocol with plasma samples being obtained by retroorbital bleeds. The plasma can be screened by ELISA (as described below), and mice with sufficient titers of anti-Ebola virus GP human immunoglobulin can be used for fusions. Mice can be boosted intravenously with antigen 3 days before sacrifice and removal of the spleen.

Generation of Hybridomas Producing Monoclonal Antibodies to Ebola virus GP

To generate hybridomas producing monoclonal antibodies to Ebola virus GP, splenocytes and lymph node cells from immunized mice can be isolated and fused to an appropriate immortalized cell line, such as a mouse myeloma cell line. The resulting hybridomas can then be screened for the production of antigen-specific antibodies. For example, single cell suspensions of splenic lymphocytes from immunized mice can be fused to SP2/0-Ag8.653 nonsecreting mouse myeloma cells (ATCC, CRL 1580) with 50% PEG (w/v). Cells can be plated at approximately 1 x 10^5 in flat bottom microtiter plate, followed by a two week incubation in selective medium containing besides usual reagents 10% fetal Clone Serum, 5-10% origen hybridoma cloning factor (IGEN) and 1X HAT (Sigma). After approximately two weeks, cells can be cultured in medium in which the HAT is replaced with HT. Individual wells can then be screened by ELISA for human anti-Ebola virus GP monoclonal IgM and IgG antibodies. Once extensive hybridoma growth occurs, medium can be observed usually after 10-14 days. The antibody secreting hybridomas can be replated, screened again, and if still positive for IgG, anti-Ebola virus GP monoclonal antibodies can be subcloned at least twice by limiting dilution. The stable subclones can then be cultured *in vitro* to generate antibody in tissue culture medium for characterization.

Generation of Transfectomas Producing Monoclonal Antibodies to Ebola virus GP

Antibodies of the invention also can be produced in a host cell transfectoma using, for example, a combination of recombinant DNA techniques and gene transfection methods as is well known in the art (Morrison, S. (1985) Science 229:1202).

For example, in certain embodiments, the gene(s) of interest, *e.g.*, human antibody genes, can be ligated into an expression vector such as a eukaryotic expression plasmid such as used by GS gene expression system disclosed in WO 87/04462, WO 89/01036 and EP 338 841 or other expression systems well known in the art. The purified plasmid with the cloned antibody genes can be introduced in eukaryotic host cells such as CHO-cells or NSO-cells or alternatively other eukaryotic cells like a plant derived cells, fungi or yeast cells. The method used to introduce these genes could be methods described in the art such as electroporation, lipofectine, lipofectamine or other. After introducing these antibody genes in the host cells, cells expressing the antibody can be identified and selected. These cells represent the transfectomas which can then be amplified for their expression level and upscaled to produce antibodies. Recombinant antibodies can be isolated and purified from these culture supernatants and/or cells.

Alternatively these cloned antibody genes can be expressed in other expression systems such as *E. coli* or in complete organisms or can be synthetically expressed.

Use of Partial Antibody Sequences to Express Intact Antibodies

Antibodies interact with target antigens predominantly through amino acid residues that are located in the six heavy and light chain complementarity determining regions (CDRs). For this reason, the amino acid sequences within CDRs are more diverse between individual antibodies than sequences outside of CDRs. Because CDR sequences are responsible for most antibody-antigen interactions, it is possible to express recombinant antibodies that mimic the properties of specific naturally occurring antibodies by constructing expression vectors that include CDR sequences from the specific naturally occurring antibody grafted onto framework sequences from a different antibody with different properties (see, *e.g.*, Riechmann, L. *et al.,* 1998, *Nature* 332:323-327; Jones, P. *et al.,* 1986, *Nature* 321:522-525; and Queen, C. *et al.,* 1989, *Proc. Natl. Acad. See.* U.S.A. 86:10029-10033). Such framework sequences can be obtained from public DNA databases that include germline antibody gene sequences. These germline sequences will differ from mature antibody gene sequences because they will not include completely assembled variable genes, which are formed by V(D)J joining during B cell maturation. Germline gene sequences will also differ from the sequences of a high affinity secondary repertoire antibody at individual evenly across the variable region. For example, somatic mutations are relatively infrequent in the amino-terminal portion of framework region. For example, somatic mutations are relatively infrequent in the amino terminal portion of framework region 1 and in the carboxy-terminal portion of framework region 4. Furthermore, many somatic mutations do not significantly alter the binding properties of the antibody. For this reason, it is not necessary to obtain the entire DNA sequence of a particular antibody in order to recreate an intact recombinant antibody having binding properties similar to those of the original antibody (see PCT/US99/05535 filed on March 12, 1999). Partial heavy and light chain sequence spanning the CDR regions is typically sufficient for this purpose. The partial sequence is used to determine which germline variable and joining gene segments contributed to the recombined antibody variable genes. The germline sequence is then used to fill in missing portions of the variable regions. Heavy and light chain leader sequences are cleaved during protein maturation and do not contribute to the properties of the final antibody. To add missing sequences, cloned cDNA sequences can be combined with synthetic oligonucleotides by ligation or PCR amplification. Alternatively, the entire variable region can be synthesized as a set of short, overlapping, oligonucleotides and combined by PCR amplification to create an entirely synthetic variable region clone. This process has certain advantages such as elimination or inclusion or particular restriction sites, or optimization of particular codons.

The nucleotide sequences of heavy and light chain transcripts from a hybridoma are used to design an overlapping set of synthetic oligonucleotides to create synthetic V sequences with identical amino acid coding capacities as the natural sequences. The synthetic heavy and kappa chain sequences can differ from the natural sequences in three ways: strings of repeated nucleotide bases are interrupted to facilitate oligonucleotide synthesis and PCR amplification; optimal translation initiation sites are incorporated according to Kozak's rules (Kozak, 1991, J. Biol. Chem. 266:19867-19870); and, HindIII sites are engineered upstream of the translation initiation sites.

For both the heavy and light chain variable regions, the optimized coding, and corresponding non-coding, strand sequences are broken down into 30 – 50 nucleotide approximately the midpoint of the corresponding non-coding oligonucleotide. Thus, for each chain, the oligonucleotides can be assembled into overlapping double stranded sets that span segments of 150 – 400 nucleotides. The pools are then used as templates to produce PCR amplification products of 150 – 400 nucleotides. Typically, a single variable region oligonucleotide set will be broken down into two pools which are separately amplified to generate two overlapping PCR products. These overlapping products are then combined by PCR amplification to form the complete variable region. It may also be desirable to include an overlapping fragment of the heavy or light chain constant region (including the BbsI site of the kappa light chain, or the AgeI site if the gamma heavy chain) in the PCR amplification to generate fragments that can easily be cloned into the expression vector constructs.

The reconstructed heavy and light chain variable regions are then combined with cloned promoter, leader sequence, translation initiation, leader sequence, constant region, 3' untranslated, polyadenylation, and transcription termination, sequences to form expression vector constructs. The heavy and light chain expression constructs can be combined into a single vector, co-transfected, serially transfected, or separately transfected into host cells which are then fused to form a host cell expressing both chains.

Plasmids for use in construction of expression vectors were constructed so that PCR amplified V heavy and V kappa light chain cDNA sequences could be used to reconstruct complete heavy and light chain minigenes. These plasmids can be used to express completely human $IgG_1\kappa$ or $IgG_4\kappa$ antibodies.

Fully human, humanized, and chimeric antibodies of the present invention also include IgG2, IgG3, IgE, IgA, IgM, and IgD antibodies. Similar plasmids can be constructed for expression of other heavy chain isotypes, or for expression of antibodies comprising lambda light chains.

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 45-47; and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 48, 50, and 51; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 52-54; and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 55, 56, and 58; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 52-54 and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 55, 56, and 59; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 60, 61, and 63; and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 64, 65, and 67; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 74, 77, and 78; and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 80-82; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 74, 77, and 79 and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 80-82 where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 83-85 and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 87, 90, and 89; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 86, 84, and 85; and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs:87-89 where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

In certain embodiments, the invention provides a method for preparing an anti-Ebola virus GP antibody including: preparing an antibody including (1) heavy chain framework regions and heavy chain CDRs, where at least one of the heavy chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 86, 84, and 85; and (2) light chain framework regions and light chain CDRs, where at least one of the light chain CDRs includes an amino acid sequence selected from the amino acid sequences of CDRs shown in SEQ ID NOs: 87, 90, and 89; where the antibody retains the ability to bind to Ebola virus GP. The ability of the antibody to bind Ebola virus GP can be determined using standard binding assays (*e.g.*, an ELISA or a FLISA).

Accordingly, in certain embodiments, the invention further provides anti-Ebola virus GP antibodies comprising: (1) heavy chain framework regions, a heavy chain CDR1 region, a heavy chain CDR2 region, and a heavy chain CDR3 region, wherein the heavy chain CDR3 region is selected from the CDR3s of the antibodies disclosed herein and (2) light chain framework regions, a light chain CDR1 region, a light chain CDR2 region, and a light chain CDR3 region, wherein the light chain CDR3 region is selected from the CDR3s of the antibodies disclosed herein, wherein the antibody binds Ebola virus GP. The antibody may further include the heavy chain CDR2 and/or the light chain CDR2 of the antibodies disclosed herein. The antibody may further comprise the heavy chain CDR1 and/or the light chain CDR1 of the antibodies disclosed herein.

Generation of Antibodies Having Modified Sequences

In another embodiment, the variable region sequences, or portions thereof, of the anti-Ebola virus GP antibodies of the invention are modified to create structurally related anti-Ebola virus GP antibodies that retain binding (*i.e.*, to the same epitope as the unmodified antibody).

Accordingly, in one aspect of the invention, the CDR1, 2, and/or 3 regions of the engineered antibodies described above can comprise the exact amino acid sequence(s) as those of antibodies disclosed herein. However, in other aspects of the invention, the antibodies comprise derivatives from the exact CDR sequences of the antibodies disclosed herein, still retain the ability of to bind Ebola virus GP effectively. Such sequence modifications may include one or more amino acid additions, deletions, or substitutions, *e.g.*, conservative sequence modifications as described above. Sequence modifications may also be based on the consensus sequences described above for the particular CDR1, CDR2, and CDR3 sequences of antibodies disclosed herein.

Accordingly, in another embodiment, the engineered antibody may be composed of one or more CDRs that are, for example, 90%, 95%, 98% or 99.5% identical to one or more CDRs of antibodies disclosed herein. Ranges intermediate to the above-recited values, *e.g.*, CDRs that are 90-95%, 95-98%, or 98-100% identical identity to one or more of the above sequences are also intended to be encompassed by the present invention.

In another embodiment, one or more residues of a CDR may be altered to modify binding to achieve a more favored on-rate of binding, a more favored off-rate of binding, or both, such that an idealized binding constant is achieved. Using this strategy, an antibody having ultra high binding affinity of, for example, 10^{10} M^{-1} or more, can be achieved. Affinity maturation techniques, well known in the art and those described herein, can be used to alter the CDR region(s) followed by screening of the resultant binding molecules for the desired change in binding. Accordingly, as CDR(s) are altered, changes in binding affinity as well as immunogenicity can be monitored and scored such that an antibody optimized for the best combined binding and low immunogenicity are achieved.

Thus, for variable region modification within the VH and/or VL CDR1, CDR2 and/or CDR3 regions, site-directed mutagenesis or PCR-mediated mutagenesis can be performed to introduce the mutation(s) and the effect on antibody binding, or other functional property of interest, can be evaluated in in vitro or in vivo assays. Preferably conservative modifications (as discussed herein) are introduced. The mutations can be amino acid substitutions, additions or deletions, but are preferably substitutions. Moreover, typically no more than one, two, three, four or five residues within a CDR region are altered.

Accordingly, in another embodiment, the instant invention provides isolated anti-Ebola virus GP monoclonal antibodies, or antigen binding portions thereof, comprising: (a) a VH CDR1 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 45, 52, 60, 68, 74, and 83, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 45, 52, 60, 68, 74, and 83; (b) a VH CDR2 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 46, 53, 61, 69, 75, and 84, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 46, 53, 61, 69, 75, and 84; (c) a VH CDR3 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 47, 54, 62, 70, 76, and 85, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 47, 54, 62, 70, 76, and 85; (d) a VL CDR1 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 48, 55, 64, 71, 80, and 87, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 48, 55, 64, 71, 80, and 87; (e) a VL CDR2 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 49, 56, 65, 72, 81, and 88, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 49, 56, 65, 72, 81, and 88; and (f) a VL CDR3 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 51, 57, 66, 73, 82, and 89, or an amino acid sequence having one, two, three, four or five amino acid substitutions, deletions or additions as compared to SEQ ID NOs: 51, 57, 66, 73, 82, and 89.

In addition to or instead of modifications within the CDRs, modifications can also be made within one or more of the framework regions, FR1, FR2, FR3 and FR4, of the heavy and/or the light chain variable regions of an antibody, so long as these modifications do not eliminate the binding affinity of the antibody. In certain embodiments, the isolated monoclonal antibody comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 68, 69, and 70, respectively, and any one of variable region framework residue mutations 49H, 71H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 92, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 71, 72, and 73, respectively, and any one of variable region framework residue mutations 42L, 59L, 70L, 99L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 93, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 75, and 76, respectively, and any one of variable region framework residue mutations 49H, 50H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 94, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and variable region framework residue mutations 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 77, and 78, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and any one of variable region framework residue mutations 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 77, and 79, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and any one of variable region framework residue mutations 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and any one of variable region framework residue mutations 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs : 87, 88, and 89, respectively, and any one of variable region framework residue mutations of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 86, 84, and 85, respectively, and any one of variable region framework residue mutations 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89, respectively, and any one of variable region framework residue mutations 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and any one of variable region framework residue mutations 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 90, and 89, respectively, and any one of variable region framework residue mutations 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the monoclonal antibody used herein comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 86, 84, and 85, respectively, and any one of variable region framework residue mutations 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 90, and 89, respectively, and any one of variable region framework residue mutations 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In general, the framework regions of antibodies are usually substantially identical, and more usually, identical to the framework regions of the human germline sequences from which they were derived. Of course, many of the amino acids in the framework region make little or no direct contribution to the specificity or affinity of an antibody. Thus, many individual conservative substitutions of framework residues can be tolerated without appreciable change of the specificity or affinity of the resulting immunoglobulin. Thus, in one embodiment the variable framework region of the antibody shares at least 85% sequence identity to a human germline variable framework region sequence or consensus of such sequences. In another embodiment, the variable framework region of the antibody shares at least 90%, 95%, 96%, 97%, 98% or 99% sequence identity to a human germline variable framework region sequence or consensus of such sequences.

In certain embodiments, framework regions are mutated. In certain embodiments, alanine is substituted for a glycine at residue 49 in the heavy chain variable region of SEQ ID NO: 9. In certain embodiments, serine is substituted for a threonine at residue 71 in the heavy chain variable region of SEQ ID NO: 9. In certain embodiments, alanine is substituted for a serine at residue 42 in the light chain variable region of SEQ ID NO: 10. In certain embodiments alanine is substituted for a valine at residue 59, phenylalanine is substituted for tyrosine at residue 70, and glutamine is substituted for glycine at residue 99 in the light chain variable region of SEQ ID NO: 10.

In certain embodiments, glycine is substituted for an alanine at residue 49 and phenylalanine is substituted for glutamic acid at residue 50 in the heavy chain variable region of SEQ ID NO: 11. In certain embodiments, alanine is substituted for a valine at residue 102 in the heavy chain variable region of SEQ ID NO: 11. In certain embodiments, alanine is substituted for a serine at residue 43, lysine is substituted for a glutamine at residue 45, and glutamine is substituted for a glycine at residue 100 in the light chain variable region of SEQ ID NO: 12. In certain embodiments, glutamine is substituted for valine at residue 3, aspartic acid is substituted for glutamine at residue 70, and phenylalanine is substituted for tyrosine at reside 71, in the light chain variable region of SEQ ID NO: 12.

In certain embodiments, glycine is substituted for serine at residue 44 in the heavy chain variable region of SEQ ID NO: 13. In certain embodiments, methionine is substituted for isoleucine at residue 48, isoleucine is substituted for leucine at residue 70, and alanine is substituted for valine at reside 72, in the heavy chain variable region of SEQ ID NO: 13. In certain embodiments, asparagine is substituted for valine at residue 50 in the heavy chain variable region of SEQ ID NO: 13. In certain embodiments, phenylalanine is substituted for valine at residue 32 in the heavy chain variable region of SEQ ID NO: 13. In certain embodiments, alanine is substituted for serine at residue 43 and tyrosine is substituted for phenylalanine at residue 87, in the light chain variable region of SEQ ID NO: 14. In certain embodiments, glutamine is substituted for valine at residue 3, aspartic acid is substituted for glutamine at residue 70, threonine is substituted for serine at residue 72, phenylalanine is substituted for leucine at residue 73, and glutamine is substituted for serine at residue 100, in the light chain variable region of SEQ ID NO: 14. In certain embodiments, lysine is substituted for valine at residue 52 in the light chain variable region of SEQ ID NO: 14.

Framework modifications can also be made to reduce immunogenicity of the antibody or to reduce or remove T cell epitopes that reside therein, as described for instance by Carr et al in US2003/0153043.

Engineered antibodies of the invention include those in which modifications have been made to framework residues within V_H and/or V_L, e.g. to improve the properties of the antibody. Typically such framework modifications are made to decrease the immunogenicity of the antibody. For example, one approach is to "backmutate" one or more framework residues to the corresponding germline sequence. More specifically, an antibody that has undergone somatic mutation can contain framework residues that differ from the germline sequence from which the antibody is derived. Such residues can be identified by comparing the antibody framework sequences to the germline sequences from which the antibody is derived.

Another type of framework modification involves mutating one or more residues within the framework region, or even within one or more CDR regions, to remove T cell epitopes to thereby reduce the potential immunogenicity of the antibody. This approach is also referred to as "deimmunization" and is described in further detail in U.S. Patent Publication No. 20030153043.

Additional Antibody Modifications

Antibodies of the present disclosure can contain one or more glycosylation sites in either the light or heavy chain variable region. Such glycosylation sites may result in increased immunogenicity of the antibody or an alteration of the pK of the antibody due to altered antigen binding (Marshall et al (1972) Annu Rev Biochem 41:673-702; Gala and Morrison (2004) J Immunol 172:5489-94; Wallick et al (1988) J Exp Med 168:1099-109; Spiro (2002) Glycobiology 12:43R-56R; Parekh et al (1985) Nature 316:452-7; Mimura et al. (2000) Mol Immunol 37:697-706). Glycosylation has been known to occur at motifs containing an N-X-S/T sequence. In some instances, it is preferred to have an anti-Ebola virus antibody that does not contain variable region glycosylation. This can be achieved either by selecting antibodies that do not contain the glycosylation motif in the variable region or by mutating residues within the glycosylation region.

For example, in certain embodiments, the glycosylation of an antibody is modified, e.g., the variable region is altered to eliminate one or more glycosylation sites resident in the variable region. More particularly, it is desirable in the sequence of the present antibodies to eliminate sites prone to glycosylation. This is achieved by altering the occurrence of one or more N-X-(S/T) sequences that occur in the parent variable region (where X is any amino acid residue), particularly by substituting the N residue and/or the S or T residue. In one embodiment, T95 is mutated to K95. In another embodiment, N47 is mutated to R47.

For example, aglycoslated antibodies can be made (i.e., which lack glycosylation). Glycosylation can be altered to, for example, increase the affinity of the antibody for antigen. Such carbohydrate modifications can be accomplished by, for example, altering one or more sites of glycosylation within the antibody sequence. For example, one or more amino acid substitutions can be made that result in elimination of one or more variable region framework glycosylation sites to thereby eliminate glycosylation at that site. Such aglycosylation may increase the affinity of the antibody for antigen. See, e.g., U.S. Patent Nos. 5,714,350 and 6,350,861.

Additionally or alternatively, the antibody can have an altered type of glycosylation, such as a hypofucosylated antibody having reduced amounts of fucosyl residues or an antibody having increased bisecting GlcNac structures. Such altered glycosylation patterns have been demonstrated to increase the ADCC ability of antibodies. Such carbohydrate modifications can be accomplished by, for example, expressing the antibody in a host cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies of the invention to thereby produce an antibody with altered glycosylation. For example, the cell lines Ms704, Ms705, and Ms709 lack the fucosyltransferase gene, FUT8 (α (1,6)-fucosyltransferase), such that antibodies expressed in the Ms704, Ms705, and Ms709 cell lines lack fucose on their carbohydrates. The Ms704, Ms705, and Ms709 FUT8$^{-/-}$ cell lines were created by the targeted disruption of the FUT8 gene in CHO/DG44 cells using two replacement vectors (see U.S. Patent Publication No. 20040110704 and Yamane-Ohnuki et al. (2004) Biotechnol Bioeng 87:614-22). As another example, EP 1,176,195 describes a cell line with a functionally disrupted FUT8 gene, which encodes a fucosyl transferase, such that antibodies expressed in such a cell line exhibit hypofucosylation by reducing or eliminating the α-1,6 bond-related enzyme. EP 1,176,195 also describes cell lines which have a low enzyme activity for adding fucose to the N-acetylglucosamine that binds to the Fc region of the antibody or does not have the enzyme activity, for example the rat myeloma cell line YB2/0 (ATCC CRL 1662). PCT Publication WO 03/035835 describes a variant CHO cell line, Lec13 cells, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell (see also Shields et al. (2002) J. Biol. Chem. 277:26733-26740). Antibodies with a modified glycosylation profile can also be produced in chicken eggs, as described in PCT Publication WO 06/089231. Alternatively, antibodies with a modified glycosylation profile can be produced in plant cells, such as Lemna. Methods for production of antibodies in a plant system are disclosed in the U.S. Patent application corresponding to Alston & Bird LLP attorney docket No. 040989/314911, filed on August 11, 2006. PCT Publication WO 99/54342 describes cell lines engineered to express glycoprotein-modifying glycosyl transferases (e.g., β(1,4)-N-acetylglucosaminyltransferase III (GnTIII)) such that antibodies expressed in the engineered cell lines exhibit increased bisecting GlcNac structures which results in increased ADCC activity of the antibodies (see also Umana et al. (1999) Nat. Biotech. 17:176-180). Alternatively, the fucose residues of the antibody can be cleaved off using a fucosidase enzyme; e.g., the fucosidase α-L-fucosidase removes fucosyl residues from antibodies (Tarentino et al. (1975) Biochem. 14:5516-23).

The variable segments of antibodies produced as described supra (e.g., the heavy and light chain variable regions of chimeric or humanized antibodies) are typically linked to at least a portion of an immunoglobulin constant region (Fc region), typically that of a human immunoglobulin. Human constant region DNA sequences can be isolated in accordance with well known procedures from a variety of human cells, but preferably immortalized B cells (see Kabat et al., supra, and Liu et al., WO87/02671) (each of which is incorporated by reference in its entirety for all purposes). Ordinarily, the antibody will contain both light chain and heavy chain constant regions. The heavy chain constant region usually includes CH1, hinge, CH2, CH3, and CH4 regions. The antibodies described herein include antibodies having all types of constant regions, including IgM, IgG, IgD, IgA and IgE, and any isotype, including IgG1, IgG2, IgG3 and IgG4. When it is desired that the antibody (e.g., humanized antibody) exhibit cytotoxic activity, the constant domain is usually a complement fixing constant domain and the class is typically IgG1. Human isotype IgG1 is preferred. Light chain constant regions can be lambda or kappa. The humanized antibody may comprise sequences from more than one class or isotype. Antibodies can be expressed as tetramers containing two light and two heavy chains, as separate heavy chains, light chains, as Fab, Fab' F(ab')2, and Fv, or as single chain antibodies in which heavy and light chain variable domains are linked through a spacer.

In certain embodiments, the antibody comprises a variable region that is mutated to improve the physical stability of the antibody. In one embodiment, the antibody is an IgG4 isotype antibody comprising a serine to proline mutation at a position corresponding to position 228 (S228P; EU index) in the hinge region of the heavy chain constant region. This mutation has been reported to abolish the heterogeneity of inter-heavy chain disulfide bridges in the hinge region (Angal et al. supra; position 241 is based on the Kabat numbering system). For example, in certain embodiments, an anti-Ebola virus GP antibody of the invention can comprise the heavy chain variable region of any of the antibodies described herein linked to a human IgG4 constant region in which the Serine at a position corresponding to position 241 as described in Angal et al., supra, has been mutated to Proline. Thus, for the heavy chain variable regions linked to a human IgG4 constant region, this mutation corresponds to an S228P mutation by the EU index.

In certain embodiments, the hinge region of CH1 is modified such that the number of cysteine residues in the hinge region is altered, e.g., increased or decreased. This approach is described further in U.S. Patent No. 5,677,425. The number of cysteine residues in the hinge region of CH1 is altered to, for example, facilitate assembly of the light and heavy chains or to increase or decrease the stability of the antibody.

In addition, the antibody can be pegylated, for example, to increase the biological (e.g., serum) half life of the antibody. To pegylate an antibody, the antibody, or fragment thereof, typically is reacted with polyethylene glycol (PEG), such as a reactive ester or aldehyde derivative of PEG, under conditions in which one or more PEG groups become attached to the antibody or antibody fragment. Preferably, the pegylation is carried out via an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" is intended to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (C1-C10) alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide. In certain embodiments, the antibody to be pegylated is an aglycosylated antibody. Methods for pegylating proteins are known in the art and can be applied to the antibodies of the invention. See, e.g., EP 0 154 316 and EP 0 401 384.

Expression of Recombinant Antibodies

Chimeric and humanized antibodies are typically produced by recombinant expression. Nucleic acids encoding light and heavy chain variable regions, optionally linked to constant regions, are inserted into expression vectors. The light and heavy chains can be cloned in the same or different expression vectors. The DNA segments encoding immunoglobulin chains are operably linked to control sequences in the expression vector(s) that ensure the expression of immunoglobulin polypeptides. Expression control sequences include, but are not limited to, promoters (e.g., naturally-associated or heterologous promoters), signal sequences, enhancer elements, and transcription termination sequences. Preferably, the expression control sequences are eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells. Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences, and the collection and purification of the crossreacting antibodies.

These expression vectors are typically replicable in the host organisms either as episomes or as an integral part of the host chromosomal DNA. Commonly, expression vectors contain selection markers (e.g., ampicillin-resistance, hygromycin-resistance, tetracycline resistance, kanamycin resistance or neomycin resistance) to permit detection of those cells transformed with the desired DNA sequences (see, e.g., Itakura et al., U.S. Pat. No. 4,704,362).

E. coli is one prokaryotic host particularly useful for cloning the polynucleotides (e.g., DNA sequences) of the present invention. Other microbial hosts suitable for use include bacilli, such as Bacillus subtilis, and other enterobacteriaceae, such as Salmonella, Serratia, and various Pseudomonas species. In these prokaryotic hosts, one can also make expression vectors, which will typically contain expression control sequences compatible with the host cell (e.g., an origin of replication). In addition, any number of a variety of well-known promoters will be present, such as the lactose promoter system, a tryptophan (trp) promoter system, a beta-lactamase promoter system, or a promoter system from phage lambda. The promoters will typically control expression, optionally with an operator sequence, and have ribosome binding site sequences and the like, for initiating and completing transcription and translation. Other microbes, such as yeast, are also useful for expression.

Saccharomyces is a preferred yeast host, with suitable vectors having expression control sequences (e.g., promoters), an origin of replication, termination sequences and the like as desired. Typical promoters include 3-phosphoglycerate kinase and other glycolytic enzymes. Inducible yeast promoters include, among others, promoters from alcohol dehydrogenase, isocytochrome C, and enzymes responsible for maltose and galactose utilization.

In addition to microorganisms, mammalian tissue cell culture may also be used to express and produce the polypeptides of the present invention (e.g., polynucleotides encoding immunoglobulins or fragments thereof). See Winnacker, From Genes to Clones, VCH Publishers, N.Y., N.Y. (1987). Eukaryotic cells are actually preferred, because a number of suitable host cell lines capable of secreting heterologous proteins (e.g., intact immunoglobulins) have been developed in the art, and include CHO cell lines, various Cos cell lines, HeLa cells, preferably, myeloma cell lines, or transformed B-cells or hybridomas. Preferably, the cells are nonhuman. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter, and an enhancer (Queen et al., Immunol. Rev. 89:49 (1986)), and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites, and transcriptional terminator sequences. Preferred expression control sequences are promoters derived from immunoglobulin genes, SV40, adenovirus, bovine papilloma virus, cytomegalovirus and the like. See Co et al., J. Immunol. 148:1149 (1992).

Alternatively, antibody-coding sequences can be incorporated in transgenes for introduction into the genome of a transgenic animal and subsequent expression in the milk of the transgenic animal (see, e.g., Deboer et al., U.S. Pat. No. 5,741,957, Rosen, U.S. Pat. No. 5,304,489, and Meade et al., U.S. Pat. No. 5,849,992). Suitable transgenes include coding sequences for light and/or heavy chains in operable linkage with a promoter and enhancer from a mammary gland specific gene, such as casein or beta lactoglobulin.

The vectors containing the polynucleotide sequences of interest (e.g., the heavy and light chain encoding sequences and expression control sequences) can be transferred into the host cell by well-known methods, which vary depending on the type of cellular host. For example, calcium chloride transfection is commonly utilized for prokaryotic cells, whereas calcium phosphate treatment, electroporation, lipofection, biolistics or viral-based transfection may be used for other cellular hosts. (See generally Sambrook et al., Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Press, 2nd ed., 1989) (incorporated by reference in its entirety for all purposes). Other methods used to transform mammalian cells include the use of polybrene, protoplast fusion, liposomes, electroporation, and microinjection (see generally, Sambrook et al., supra). For production of transgenic animals, transgenes can be microinjected into fertilized oocytes, or can be incorporated into the genome of embryonic stem cells, and the nuclei of such cells transferred into enucleated oocytes.

When heavy and light chains are cloned on separate expression vectors, the vectors are co-transfected to obtain expression and assembly of intact immunoglobulins. Once expressed, the whole antibodies, their dimers, individual light and heavy chains, or other immunoglobulin forms of the present invention can be purified according to standard procedures of the art, including ammonium sulfate precipitation, affinity columns, column chromatography, HPLC purification, gel electrophoresis and the like (see generally Scopes, Protein Purification (Springer-Verlag, N.Y., (1982)). Substantially pure immunoglobulins of at least about 90 to 95% homogeneity are preferred, and 98 to 99% or more homogeneity most preferred, for pharmaceutical uses.

Antibody Fragments

Also contemplated within the scope of the instant invention are antibody fragments. In one embodiment, fragments of non-human, and/or chimeric antibodies are provided. In another embodiment, fragments of humanized antibodies are provided. Typically, these fragments exhibit specific binding to antigen with an affinity of at least 10^7, and more typically 10^8 or 10^9 M^{-1}. Humanized antibody fragments include separate heavy chains, light chains, Fab, Fab', F(ab')2, Fabc, and Fv. Fragments are produced by recombinant DNA techniques, or by enzymatic or chemical separation of intact immunoglobulins.

Assays for Characterization of Antibodies

Antibodies described herein can be tested for binding to Ebola virus glycoprotein (GP) by, for example, standard ELISA. Briefly, microtiter plates are coated with purified Ebola virus (i.e., Ebola Zaire 1995 virions) at 10-20 µg/ml in PBS, and then blocked with 5% nonfat dry milk in PBS. After washing, 0.05 mL of purified mAbs were added to wells containing antigen and incubated for 2 hours at room temperature. Bound mAbs were detected using horseradish peroxidase conjugated goat anti-mouse IgA+IgG+IgM secondary antibodies and ABTS substrate (Kirkegaard and Perry Laboratories).

An ELISA assay as described above can be used to screen for antibodies and, thus, hybridomas that produce antibodies that show positive reactivity with the Ebola virus GP. Hybridomas that produce antibodies that bind, preferably with high affinity, to Ebola virus GP can then be subcloned and further characterized. One clone from each hybridoma, which retains the reactivity of the parent cells (by ELISA), can then be chosen for making a cell bank, and for antibody purification.

The ELISA assay described above can also be used to confirm that framework mutation(s) do not affect the ability of the anti-GP antibodies disclosed herein to bind to GP.

To purify anti-Ebola virus GP antibodies, selected hybridomas can be grown in two-liter spinner-flasks for monoclonal antibody purification. Supernatants can be filtered and concentrated before affinity chromatography with protein A-sepharose (Pharmacia, Piscataway, NJ). Eluted IgG can be checked by gel electrophoresis and high performance liquid chromatography to ensure purity. The buffer solution can be exchanged into PBS, and the concentration can be determined by OD_{280} using 1.43 extinction coefficient. The monoclonal antibodies can be aliquoted and stored at -80 °C.

To determine if the selected anti-Ebola virus GP monoclonal antibodies bind to unique epitopes, each antibody can be biotinylated using commercially available reagents (Pierce, Rockford, IL). Biotinylated MAb binding can be detected with a streptavidin labeled probe. Competition studies using unlabeled monoclonal antibodies and biotinylated monoclonal antibodies can be performed using Ebola virus GP coated-ELISA plates as described above.

To determine the isotype of purified antibodies, isotype ELISAs can be performed using reagents specific for antibodies of a particular isotype. For example, plates are coated with anti-IgG, IgA, or IgM heavy-chain specific antibodies (100 ng/well) and incubated with hybridoma culture supernatants. The subtype of the mAb is detected by using anti-IgG1, IgG2a, IgG2b, IgG3, IgM, or IgA heavy-chain specific antibodies conjugated to alkaline phosphatase.

Anti-Ebola virus GP antibodies can be further tested for reactivity with the Ebola virus GP antigen by Western blotting. Briefly, unlabeled Ebola Zaire 1995 virion proteins are resolved on a 10% SDS-polyacrylaminde gel and transferred to PVDF membranes. After nonspecific bindings sites are blocked using nonfat dry milk in PBS containing 0.02% Tween-20, purified mAb (10 ug/ml) are added to the membranes for 1 hour at room temperature. Membranes are then incubated with horseradish peroxidase-conjugated goat anti-mouse IgA+IgG+IgM secondary antibodies for 1 hour and develobed using ECL chemiluminescence kit (Amersham).

Methods for analyzing binding affinity, cross-reactivity, and binding kinetics of various anti-Ebola virus GP antibodies include standard assays known in the art, for example, Biacore™ surface plasmon resonance (SPR) analysis using a Biacore™ 2000 SPR instrument (Biacore AB, Uppsala, Sweden).

To determine the neutralization of mAbs described herein, i*n vitro* plaque reduction neutralization assays can be performed. Briefly, plaque assays are done using confluent Vero-E6 cells. Four-fold serial dilutions of mAbs are mixed with 100 pfu of mouse-adapted Ebola virus at 37^0C for 1 hour. In certain embodiments, the Ebloa virus is the Mayinga 1976 strain. In certain embodiments, the Ebola virus is the Kikwit 1995 strain. In certain embodiments, the Ebola virus is the Makona 2014 strain. Cells are covered with an agarose overlay and a second overlay containing 5% neutral red solution in PBS or agarose is added 6 days later. Plaques are counted the following day and endpoint titers are determined to be the last dilution of mAb that reduced the number of plaques by 80% of cells not incubated with mAbs.

Some aspects of the invention relate to a monoclonal antibody or antigen binding portion thereof which has neutralizing activity against Zaire Ebola Virus. In one aspect, the invention relates to a monoclonal antibody which neutralizes Ebola virus at 50 ug/mL, as measured by a plaque reduction neutralization assay. In another aspect, the invention relates to a monoclonal antibody which neutralizes Ebola virus at less than 50 µg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody which neutralizes Ebola virus at less than 20 µg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody which neutralizes Ebola virus at less than 10 µg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody which neutralizes Ebola virus at less than 5 µg/mL, as measured by a plaque reduction neutralization assay. Another aspect of the invention relates to a monoclonal antibody which neutralizes Ebola virus at 1-5 or 2-4 µg/mL, as measured by a plaque reduction neutralization assay.

To determine the *in vivo* capability of the mAbs described herein, BALB/c or C57BL/6 mice are used. Mice are challenged with mouse-adapted Ebola Zaire virus 24 hours after injection of purified mAbs or combinations of mAbs to determine the prophylactic benefits. To determine the therapeutic benefit of the mAbs described herein, mAbs are injected 1, 2 or 3 days after Ebola Zaire virus challenge. Animals are monitored for morbidity and mortality for 28 days post infection.

Competitive Binding Antibodies

In certain embodiments, antibodies of the invention compete (e.g., cross-compete) for binding to Ebola virus GP with the particular anti-GP antibodies described herein. Such competing antibodies can be identified based on their ability to competitively inhibit binding to Ebola virus GP of one or more of mAbs described herein in standard Ebola virus GP binding assays. For example, standard ELISA assays can be used in which a recombinant Ebola virus GP is immobilized on the plate, one of the antibodies is fluorescently labeled and the ability of non-labeled antibodies to compete off the binding of the labeled antibody is evaluated. Additionally or alternatively, BIAcore analysis can be used to assess the ability of the antibodies to cross-compete. The ability of a test antibody to inhibit the binding of an anti-GP antibody of the invention to Ebola virus GP demonstrates that the test antibody can compete with the antibody for binding to Ebola virus GP

In certain embodiments, the competing antibody is an antibody that binds to the same epitope on Ebola virus GP as the particular anti-GP monoclonal antibodies described herein. Standard epitope mapping techniques, such as x-ray crystallography and 2-dimensional nuclear magnetic resonance, can be used to determine whether an antibody binds to the same epitope as a reference antibody (see, e.g., Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, G. E. Morris, Ed. (1996)).

In certain embodiments, the antibody that competes for binding to Ebola virus GP and/or binds to the same epitope on Ebola virus GP is a humanized antibody.

Once a single, archtypal anti-GP mAb has been isolated that has the desired properties described herein, it is straightforward to generate other mAbs with similar properties, e.g., having the same epitope, by using art-known methods. For example, mice may be immunized with Ebola virus as described herein, hybridomas produced, and the resulting mAbs screened for the ability to compete with the archtypal mAb for binding to Ebola virus GP. Mice can also be immunized with a smaller fragment of Ebola virus GP containing the epitope to which the archtypal mAb binds. The epitope can be localized by, e.g., screening for binding to a series of overlapping peptides spanning Ebola virus GP. Alternatively, the method of Jespers et al., Biotechnology 12:899, 1994 ma be used to guide the selection of mAbs having the same epitope and therefore similar properties to the archtypal mAb. Using phage display, first the heavy chain of the archtypal antibody is paired with a repertoire of (preferably human) light chains to select an Ebola virus GP-binding mAb, and then the new light chain is paired with a repertoire of (preferably human) heavy chains to select an (preferably human) Ebola virus GP-binding mAb having the same epitope as the archtypal mAb. Alternatively variants of the archetypal mAb can be obtained by mutagenesis of cDNA encoding the heavy and light chains of the antibody.

Epitope mapping, e.g., as described in Champe et al. (1995) J. Biol. Chem. 270:1388-1394, can be performed to determine whether the antibody binds an epitope of interest. "Alanine scanning mutagenesis," as described by Cunningham and Wells (1989) Science 244: 1081-1085, or some other form of point mutagenesis of amino acid residues in human Ebola virus GP may also be used to determine the functional epitope for an anti-GP antibody of the present invention. Mutagenesis studies, however, may also reveal amino acid residues that are crucial to the overall three-dimensional structure of Eboal virus GP but that are not directly involved in antibody-antigen contacts, and thus other methods may be necessary to confirm a functional epitope determined using this method.

The epitope bound by a specific antibody may also be determined by assessing binding of the antibody to peptides comprising fragments of Ebola virus GP. A series of overlapping peptides encompassing the sequence of Ebola virus GP may be synthesized and screened for binding, e.g. in a direct ELISA, a competitive ELISA (where the peptide is assessed for its ability to prevent binding of an antibody to Ebola virus GP bound to a well of a microtiter plate), or on a chip. Such peptide screening methods may not be capable of detecting some discontinuous functional epitopes, i.e. functional epitopes that involve amino acid residues that are not contiguous along the primary sequence of the Ebola virus GP polypeptide chain.

The epitope bound by antibodies of the present invention may also be determined by structural methods, such as X-ray crystal structure determination (e.g., WO2005/044853), molecular modeling and nuclear magnetic resonance (NMR) spectroscopy, including NMR determination of the H-D exchange rates of labile amide hydrogens in Ebola virus GP when free and when bound in a complex with an antibody of interest (Zinn-Justin et al. (1992) Biochemistry 31, 11335-11347; Zinn-Justin et al. (1993) Biochemistry 32, 6884-6891).

With regard to X-ray crystallography, crystallization may be accomplished using any of the known methods in the art (e.g. Giege et al. (1994) Acta Crystallogr. D50:339-350; McPherson (1990) Eur. J. Biochem. 189:1-23), including microbatch (e.g. Chayen (1997) Structure 5:1269-1274), hanging-drop vapor diffusion (e.g. McPherson (1976) J. Biol. Chem. 251:6300-6303), seeding and dialysis. It is desirable to use a protein preparation having a concentration of at least about 1 mg/mL and preferably about 10 mg/mL to about 20 mg/mL. Crystallization may be best achieved in a precipitant solution containing polyethylene glycol 1000-20,000 (PEG; average molecular weight ranging from about 1000 to about 20,000 Da), preferably about 5000 to about 7000 Da, more preferably about 6000 Da, with concentrations ranging from about 10% to about 30% (w/v). It may also be desirable to include a protein stabilizing agent, e.g. glycerol at a concentration ranging from about 0.5% to about 20%. A suitable salt, such as sodium chloride, lithium chloride or sodium citrate may also be desirable in the precipitant solution, preferably in a concentration ranging from about 1 mM to about 1000 mM. The precipitant is preferably buffered to a pH of from about 3.0 to about 5.0, preferably about 4.0. Specific buffers useful in the precipitant solution may vary and are well-known in the art (Scopes, Protein Purification: Principles and Practice, Third ed., (1994) Springer-Verlag, New York). Examples of useful buffers include, but are not limited to, HEPES, Tris, MES and acetate. Crystals may be grow at a wide range of temperatures, including 2° C, 4° C, 8° C and 26° C.

Antibody:antigen crystals may be studied using well-known X-ray diffraction techniques and may be refined using computer software such as X-PLOR (Yale University, 1992, distributed by Molecular Simulations, Inc.; see e.g. Blundell & Johnson (1985) Meth. Enzymol. 114 & 115, H. W. Wyckoff et al., eds., Academic Press; U.S. Patent Application Publication No. 2004/0014194), and BUSTER (Bricogne (1993) Acta Cryst. D49:37-60; Bricogne (1997) Meth. Enzymol. 276A:361-423, Carter & Sweet, eds.; Roversi et al. (2000) Acta Cryst. D56:1313-1323), the disclosures of which are hereby incorporated by reference in their entireties.

Antibody competition assays, as described herein, can be used to determine whether an antibody "binds to the same epitope" as another antibody. Typically, competition of 50% or more, 60% or more, 70% or more, such as 70%, 71%, 72%, 73%, 74%, 75%, 80%, 85%, 90%, 95% or more, of an antibody known to interact with the epitope by a second antibody under conditions in which the second antibody is in excess and the first saturates all sites, is indicative that the antibodies "bind to the same epitope." To assess the level of competition between two antibodies, for example, radioimmunoassays or assays using other labels for the antibodies, can be used. For example, an Ebola virus GP antigen can be incubated with a saturating amount of a first anti-GP antibody or antigen-binding fragment thereof conjugated to a labeled compound (e.g., ^{3}H, ^{125}I, biotin, or rubidium) in the presence the same amount of a second unlabeled anti-GP antibody. The amount of labeled antibody that is bound to the antigen in the presence of the unlabeled blocking antibody is then assessed and compared to binding in the absence of the unlabeled blocking antibody. Competition is determined by the percentage change in binding signals in the presence of the unlabeled blocking antibody compared to the absence of the blocking antibody. Thus, if there is a 50% inhibition of binding of the labeled antibody in the presence of the blocking antibody compared to binding in the absence of the blocking antibody, then there is competition between the two antibodies of 50%. Thus, reference to competition between a first and second antibody of 50% or more, 60% or more, 70% or more, such as 70%, 71%, 72%, 73%, 74%, 75%, 80%, 85%, 90%, 95% or more, means that the first antibody inhibits binding of the second antibody (or vice versa) to the antigen by 50%, 60%, 70%, 71%, 72%, 73%, 74%, 75%, 80%, 85%, 90%, 95% or more (compared to binding of the antigen by the second antibody in the absence of the first antibody). Thus, inhibition of binding of a first antibody to an antigen by a second antibody of 50%, 60%, 70%, 71%, 72%, 73%, 74%, 75%, 80%, 85%, 90%, 95% or more indicates that the two antibodies bind to the same epitope.

Testing Antibodies for Therapeutic Efficacy in Animal Models

Animal models are effective for testing the therapeutic efficacy of antibodies against Ebola virus GP. In certain embodiments, rodents (i.e., mice) can be used for Ebola infection. Briefly, mice are challenged with a strain of mouse adapted Ebola virus (e.g., Ebola Zaire 1976) by intraperitoneal inoculation, approximately 300 times the dose lethal for 50% of adult mice. In certain embodiments, guinea pigs can be used for Ebola infection. Guinea pigs are challenged with guinea pig-adapted virus. Additionally, in certain embodiments, non-human primates are used as an animal model of infection, as described in the Example below. In all animal models, antibodies can be administered 24 or 48 hours after infection to test for therapeutic efficacy.

Immunotoxins, Immunoconjugates and Antibody Derivatives

In another embodiment, the antibodies of the present invention are linked to a therapeutic moiety, such as a cytotoxin, a drug or a radioisotope. When conjugated to a cytotoxin, these antibody conjugates are referred to as "immunotoxins." A cytotoxin or cytotoxic agent includes any agent that is detrimental to (*e.g.*, kills) cells.

Techniques for conjugating such therapeutic moiety to antibodies are well known in the art.

The toxin component of the immunotoxin can be, for example, a chemotherapeutic agent, a toxin such as an enzymatically active toxin of bacterial, fungal, plant or animal origin, or fragments thereof, or a small molecule toxin.

Additional toxins and fragments thereof which can be used include diphtheria A chain, nonbonding active fragments of diphtheria toxin, cholera toxin, botulinus toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, phytolaca Americana proteins (PAPI, PAPII, and PAP-S), Momordica charantia inhibitor, curcin, crotin, sapaonaria, officinalis inhibitor, gelonin, saporin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothcenes. Small molecule toxins include, for example, calicheamicins, maytansinoids, palytoxin and CC1065.

Antibodies of the invention also can be used for diagnostic purposes, including sample testing and in vivo imaging, and for this purpose the antibody (or binding fragment thereof) can be conjugated to an appropriate detectable agent, to form an immunoconjugate. For diagnostic purposes, appropriate agents are detectable labels that include radioisotopes, for whole body imaging, and radioisotopes, enzymes, fluorescent labels and other suitable antibody tags for sample testing.

For Ebola virus GP detection, the detectable labels can be any of the various types used currently in the field of in vitro diagnostics, including particulate labels including metal sols such as colloidal gold, isotopes such as I^{125} or Tc^{99} presented for instance with a peptidic chelating agent of the N_2S_2, N_3S or N_4 type, chromophores including fluorescent markers, luminescent markers, phosphorescent markers and the like, as well as enzyme labels that convert a given substrate to a detectable marker, and polynucleotide tags that are revealed following amplification such as by polymerase chain reaction. Suitable enzyme labels include horseradish peroxidase, alkaline phosphatase and the like. For instance, the label can be the enzyme alkaline phosphatase, detected by measuring the presence or formation of chemiluminescence following conversion of 1,2 dioxetane substrates such as adamantyl methoxy phosphoryloxy phenyl dioxetane (AMPPD), disodium 3-(4-(methoxyspiro{1,2-dioxetane-3,2'-(5'-chloro)tricyclo{3.3.1.1 3,7}decan}-4-yl) phenyl phosphate (CSPD), as well as CDP and CDP-star® or other luminescent substrates well-known to those in the art, for example the chelates of suitable lanthanides such as Terbium(III) and Europium(III). The detection means is determined by the chosen label. Appearance of the label or its reaction products can be achieved using the naked eye, in the case where the label is particulate and accumulates at appropriate levels, or using instruments such as a spectrophotometer, a luminometer, a fluorimeter, and the like, all in accordance with standard practice.

In certain embodiments, an antibody provided herein may be further modified to contain additional non-proteinaceous moieties that are known in the art and readily available. The moieties suitable for derivatization of the antibody include but are not limited to water soluble polymers. Non-limiting examples of water soluble polymers include, but are not limited to, polyethylene glycol (PEG), copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1,3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, propropylene glycol homopolymers, prolypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (e.g., glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. The polymer may be of any molecular weight, and may be branched or unbranched. The number of polymers attached to the antibody may vary, and if more than one polymer is attached, they can be the same or different molecules. In general, the number and/or type of polymers used for derivatization can be determined based on considerations including, but not limited to, the particular properties or functions of the antibody to be improved, whether the antibody derivative will be used in a therapy under defined conditions, etc.

Compositions

In certain embodiments, the present invention provides a composition, *e.g.*, a composition, containing one or more monoclonal antibodies described herein, formulated together with a carrier (*e.g.*, a pharmaceutically acceptable carrier). In one embodiment, the compositions include a combination of multiple (*e.g.*, two or more) isolated antibodies of the invention. Preferably, each of the antibodies of the composition binds to a distinct, pre-selected epitope of Ebola virus GP.

Pharmaceutical compositions of the invention also can be administered in combination therapy, *i.e.*, combined with other agents. For example, the combination therapy can include a composition of the present invention with at least one or more additional therapeutic agents. Co-administration with other antibodies is also encompassed by the invention.

As used herein, the terms “carrier” and “pharmaceutically acceptable carrier” includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (*e.g.*, by injection or infusion). Depending on the route of administration, the active compound, *e.g.*, antibody, may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

A "pharmaceutically acceptable salt" refers to a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see *e.g.*, Berge, S.M., *et al.* (1977) J. Pharm. Sci. 66:1-19). Examples of such salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted alkanoic acids, hydroxy alkanoic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chloroprocaine, choline, diethanolamine, ethylenediamine, procaine and the like.

A composition of the present invention can be administered by a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. The active compounds can be prepared with carriers that will protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are patented or generally known to those skilled in the art. *See, e.g., Sustained and Controlled Release Drug Delivery Systems*, J.R. Robinson, ed., Marcel Dekker, Inc., New York, 1978.

To administer a compound of the invention by certain routes of administration, it may be necessary to coat the compound with, or co-administer the compound with, a material to prevent its inactivation. For example, the compound may be administered to a subject in an appropriate carrier, for example, liposomes, or a diluent. Acceptable diluents include saline and aqueous buffer solutions. Liposomes include water-in-oil-in-water CGF emulsions as well as conventional liposomes (Strejan *et al.* (1984) *J. Neuroimmunol.* 7:27).

Carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions of the invention is contemplated. Supplementary active compounds can also be incorporated into the compositions.

Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Dosage regimens are adjusted to provide the optimum desired response (*e.g.*, a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. For example, the antibodies of the invention may be administered once or twice weekly by subcutaneous or intramuscular injection or once or twice monthly by subcutaneous or intramuscular injection.

It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

Examples of pharmaceutically-acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

For the therapeutic compositions, formulations of the present invention include those suitable for oral, nasal, topical (including buccal and sublingual), rectal, vaginal and/or parenteral administration. The formulations may conveniently be presented in unit dosage form and may be prepared by any methods known in the art of pharmacy. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will vary depending upon the subject being treated, and the particular mode of administration. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will generally be that amount of the composition which produces a therapeutic effect. Generally, out of one hundred per cent, this amount will range from about 0.001 percent to about ninety percent of active ingredient, preferably from about 0.005 percent to about 70 percent, most preferably from about 0.01 percent to about 30 percent.

Formulations of the present invention which are suitable for vaginal administration also include pessaries, tampons, creams, gels, pastes, foams or spray formulations containing such carriers as are known in the art to be appropriate. Dosage forms for the topical or transdermal administration of compositions of this invention include powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and inhalants. The active compound may be mixed under sterile conditions with a pharmaceutically acceptable carrier, and with any preservatives, buffers, or propellants which may be required.

The phrases "parenteral administration" and "administered parenterally" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion.

Examples of suitable aqueous and nonaqueous carriers which may be employed in the pharmaceutical compositions of the invention include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms may be ensured both by sterilization procedures, supra, and by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

When the compounds of the present invention are administered as pharmaceuticals, to humans and animals, they can be given alone or as a pharmaceutical composition containing, for example, 0.001 to 90% (more preferably, 0.005 to 70%, such as 0.01 to 30%) of active ingredient in combination with a pharmaceutically acceptable carrier.

Regardless of the route of administration selected, the compounds of the present invention, which may be used in a suitable hydrated form, and/or the pharmaceutical compositions of the present invention, are formulated into pharmaceutically acceptable dosage forms by conventional methods known to those of skill in the art.

Actual dosage levels of the active ingredients in the pharmaceutical compositions of the present invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions of the present invention employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts. A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the effective amount of the pharmaceutical composition required. For example, the physician or veterinarian could start doses of the compounds of the invention employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved. In general, a suitable daily dose of a composition of the invention will be that amount of the compound which is the lowest dose effective to produce a therapeutic effect. Such an effective dose will generally depend upon the factors described above. It is preferred that administration be intravenous, intramuscular, intraperitoneal, or subcutaneous, preferably administered proximal to the site of the target. If desired, the effective daily dose of a therapeutic composition may be administered as two, three, four, five, six or more sub-doses administered separately at appropriate intervals throughout the day, optionally, in unit dosage forms. While it is possible for a compound of the present invention to be administered alone, it is preferable to administer the compound as a pharmaceutical formulation (composition).

Therapeutic compositions can be administered with medical devices known in the art. For example, in certain embodiments, a therapeutic composition of the invention can be administered with a needleless hypodermic injection device, such as the devices disclosed in U.S. Patent Nos. 5,399,163, 5,383,851, 5,312,335, 5,064,413, 4,941,880, 4,790,824, or 4,596,556. Examples of well-known implants and modules useful in the present invention include: U.S. Patent No. 4,487,603, which discloses an implantable micro-infusion pump for dispensing medication at a controlled rate; U.S. Patent No. 4.,486,194, which discloses a therapeutic device for administering medicants through the skin; U.S. Patent No. 4,447,233, which discloses a medication infusion pump for delivering medication at a precise infusion rate; U.S. Patent No. 4,447,224, which discloses a variable flow implantable infusion apparatus for continuous drug delivery; U.S. Patent No. 4,439,196, which discloses an osmotic drug delivery system having multi-chamber compartments; and U.S. Patent No. 4,475,196, which discloses an osmotic drug delivery system. Many other such implants, delivery systems, and modules are known to those skilled in the art.

In certain embodiments, the antibodies of the invention can be formulated to ensure proper distribution *in vivo*. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. To ensure that the therapeutic compounds of the invention cross the BBB (if desired), they can be formulated, for example, in liposomes. For methods of manufacturing liposomes, see, *e.g.*, U.S. Patents 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties which are selectively transported into specific cells or organs, thus enhance targeted drug delivery (*see, e.g.*, V.V. Ranade (1989) *J. Clin. Pharmacol.* 29:685). Exemplary targeting moieties include folate or biotin (see, *e.g.*, U.S. Patent 5,416,016 to Low *et al.*); mannosides (Umezawa *et al.*, (1988) *Biochem. Biophys. Res. Commun.* 153:1038); antibodies (P.G. Bloeman *et al.* (1995) *FEBS Lett.* 357:140; M. Owais *et al.* (1995) *Antimicrob. Agents Chemother.* 39:180); surfactant protein A receptor (Briscoe *et al.* (1995) *Am. J. Physiol.* 1233:134), different species of which may comprise the formulations of the inventions, as well as components of the invented molecules; p120 (Schreier *et al.* (1994) *J. Biol. Chem.* 269:9090); see also K. Keinanen; M.L. Laukkanen (1994) *FEBS Lett.* 346:123; J.J. Killion; I.J. Fidler (1994) *Immunomethods* 4:273. In one embodiment of the invention, the therapeutic compounds of the invention are formulated in liposomes; in certain embodiments, the liposomes include a targeting moiety. In certain embodiments, the therapeutic compounds in the liposomes are delivered by bolus injection to a site proximal to the tumor or infection. The composition must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi.

The composition must be sterile and fluid to the extent that the composition is deliverable by syringe. In addition to water, the carrier can be an isotonic buffered saline solution, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. Proper fluidity can be maintained, for example, by use of coating such as lecithin, by maintenance of required particle size in the case of dispersion and by use of surfactants. In many cases, it is preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol or sorbitol, and sodium chloride in the composition. Long-term absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate or gelatin.

When the active compound is suitably protected, as described above, the compound may be orally administered, for example, with an inert diluent or an assimilable edible carrier.

Uses and Methods of the Invention

In certain embodiments, the antibodies, bispecific molecules, and compositions of the present invention can be used to treat and/or prevent (*e.g.*, immunize against) Ebola virus infection in a subject. In other aspects, the antibodies, and compositions of the present invention can be used to detect Ebola virus infection in a sample.

For use in therapy, the antibodies of the invention can be administered to a subject directly (*i.e.*, *in vivo*), either alone or with other therapies such as an immunostimulatory agent. In all cases, the antibodies, compositions, and immunostimulatory agents and other therapies are administered in an effective amount to exert their desired therapeutic effect. The term "effective amount" refers to that amount necessary or sufficient to realize a desired biologic effect. One of ordinary skill in the art can empirically determine the effective amount of a particular molecule without necessitating undue experimentation.

Additionally, in certain embodiments, these optimized antibodies can be combined with monoclonal antibodies against Ebola virus glycoprotein characterized in US 6, 630, 144, Olinger et al., *PNAS* 2012; 109, 18030-18035, and Pettitt et al., *Sci Transl Med* 2013; 5, 199ra113.

Preferred routes of administration for vaccines include, for example, injection (*e.g.*, subcutaneous, intravenous, parenteral, intraperitoneal, intrathecal). The injection can be in a bolus or a continuous infusion. Other routes of administration include oral administration.

Antibodies of the invention also can be coadministered with adjuvants and other therapeutic agents. It will be appreciated that the term “coadministered” as used herein includes any or all of simultaneous, separate, or sequential administration of the antibodies and conjugates of the present invention with adjuvants and other agents, including administration as part of a dosing regimen. The antibodies are typically formulated in a carrier alone or in combination with such agents. Examples of such carriers include solutions, solvents, dispersion media, delay agents, emulsions and the like. The use of such media for pharmaceutically active substances is well known in the art. Any other conventional carrier suitable for use with the molecules falls within the scope of the instant invention.

The present invention is further illustrated by the following examples which should not be construed as further limiting. The contents of Sequence Listing, figures and all references, patents and published patent applications cited throughout this application are expressly incorporated herein by reference.

Antibody Combinations

In certain embodiments, a subject is administered a pharmaceutical composition comprising one or more antibodies or antigen binding fragments of the invention with a pharmaceutically acceptable carrier. In some embodiments, a combination of antibodies is formulated with a pharmaceutically acceptable carrier in a single pharmaceutical composition. In other embodiments, each antibody is formulated with a pharmaceutically acceptable carrier and a combination or two or more pharmaceutical compositions is administered to a subject.

In certain embodiments of the invention, a combination of two, three, or more antibodies is selected from the group consisting of the antibodies set forth in Table 1 and Table 2. In certain embodiments, three antibodies from Table 1 or Table 2 are formulated with a pharmaceutically acceptable carrier in a single pharmaceutical composition. In certain embodiments, the combination is administered to a subject for treatment of an Ebola virus infection. In other embodiments, each antibody from Table 1 or Table 2 is formulated with a pharmaceutically acceptable carrier and a combination or two or more pharmaceutical compositions is administered to a subject. The subject can be administered a composition comprising the antibodies disclosed herein alone or in combination, along with a therapeutic agent. In certain embodiments, the therapeutic agent is interferon-alpha. The combinations described herein may be more effective at neutralizing Ebola virus.

Peptides and Compositions Based on Ebola virus glycoprotein (GP) Epitopes

To facilitate the engineering of antibodies that target the Ebola virus glycoprotein (GP), epitope hotspots were determined using alanine scanning, as described herein. Based on the binding analysis, antibodies 4G7, K252, and 2G4 were found to bind to a conformational epitope that included regions V505-C511 and N550-E564 of SEQ ID NO: 91, whereas antibody 13C6 was found to bind within the regions T270-P279 and Y394-R409 of SEQ ID NO: 91 (Figure 1). Figure 2 summarizes the hotspots in the Ebola virus glycoprotein identified through this mutational analysis.

Peptides or peptide mimetics based on one or more epitopes within Ebola virus glycoprotein include region V505-C511, region N550-E564, region T270-P279, or region Y394-R404 of Ebola virus glycoprotein (SEQ ID NO: 91). Other peptide or peptide mimetics based on one or more epitopes Ebola virus glycoprotein include TGKLIWKVNP (SEQ ID NO: 98), YKLDISEATQVGQHHR (SEQ ID NO: 99), VNAQPKC (SEQ ID NO: 100), and NQDGLICGLRQLANE (SEQ ID NO: 101).

Generally, peptides for use as immunogens range in size from about 10 to about 50 amino acid residues in length, more preferably from about 15 to about 30 amino acid residues, and in particular, is about 20 amino acid residues in length.

A peptide of the invention can be readily modified to include at least one conservative amino acid substitution, and at any position. Preferably, that peptide specifically binds to an anti-Ebola monoclonal antibody as described herein. Peptides of the invention are chemically synthesized *in vitro* using known techniques.

The peptides described above are formulated into vaccine compositions. These vaccine compositions may be employed to immunize an animal in order to elicit a highly anti-Ebola antibody immune response. Vaccine compositions are also useful to administer to subjects in need thereof to induce a protective immune response. Such vaccine compositions are well known to the art and include, for example, physiologically compatible buffers, preservatives, and saline and the like, as well as adjuvants.

"Adjuvants" are agents that nonspecifically increase an immune response to a particular antigen, thus reducing the quantity of antigen necessary in any given vaccine, and/or the frequency of injection necessary in order to generate an adequate immune response to the antigen of interest. Suitable adjuvants for the vaccination of animals include, but are not limited to, Adjuvant 65 (containing peanut oil, mannide monooleate and aluminum monostearate); Freund's complete or incomplete adjuvant; mineral gels, such as aluminum hydroxide, aluminum phosphate and alum; surfactants, such as hexadecylamine, octadecylamine, lysolecithin, dimethyldioctadecylammonium bromide, N,N-dioctadecyl-N',N'-bis(2-hydroxymethyl) propanediamine, methoxyhexadecylglycerol and pluronic polyols; polyanions, such as pyran, dextran sulfate, poly IC, polyacrylic acid and carbopol; peptides, such as muramyl dipeptide, dimethylglycine and tuftsin; and oil emulsions. The protein or peptides could also be administered following incorporation into liposomes or other microcarriers. Information concerning adjuvants and various aspects of immunoassays are disclosed, e.g., in the series by P. Tijssen, Practice and Theory of Enzyme Immunoassays, 3rd Edition, 1987, Elsevier, N.Y., incorporated by reference herein.

The vaccine composition includes a sufficient amount of the desired immunogen, such as the peptides of the invention, to elicit an immune response. The amount administered can range from about 0.0001 g/kg to about 1.0 g/kg, relative to the mass of the animal. Any suitable vertebrate animal is readily employed to obtain polyclonal antiserum. Preferably, the animal is a mammal, and includes, but is not limited to, rodents, such as a mice, rats, rabbits, horses, canines, felines, bovines, ovines, e.g., goats and sheep, primates, e.g., monkeys, great apes and humans, and the like.

The vaccine composition is readily administered by any standard route, including intravenously, intramuscularly, subcutaneously, intraperitoneally, and/or orally. The artisan will appreciate that the vaccine composition is preferably formulated appropriately for each type of recipient animal and route of administration.

Other aspects of the invention relate to methods of treating or preventing of Ebola virus infection by administering to a subject in need thereof an effective amount of a vaccine according to the invention.

Other Embodiments

The invention described herein pertains to antibodies directed towards Ebola virus glycoprotein (GP). In one aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which specifically binds to Ebola virus glycoprotein, comprises a variable heavy chain and a variable light chain selected from the group consisting of:

(a) SEQ ID NOs: 15 and 17;
(b) SEQ ID NOs: 15 and 18;
(c) SEQ ID NOs: 16 and 17;
(d) SEQ ID NOs: 16 and 18;
(e) SEQ ID NOs: 19 and 20;
(f) SEQ ID NOs:19 and 21;
(g) SEQ ID NOs: 22 and 23;
(h) SEQ ID NOs: 22 and 24;
(i) SEQ ID NOs: 9 and 10;
(j) SEQ ID NOs: 9 and 27;
(k) SEQ ID NOs: 9 and 28;
(l) SEQ ID NOs: 9 and 29;
(m) SEQ ID NOs: 9 and 30;
(n) SEQ ID NOs: 9 and 31;
(o) SEQ ID NOs: 25 and 10;
(p) SEQ ID NOs: 25 and 27;
(q) SEQ ID NOs: 25 and 28;

(r) SEQ ID NOs: 25 and 29;

(s) SEQ ID NOs: 25 and 30;

(t) SEQ ID NOs: 25 and 31;

(u) SEQ ID NOs: 26 and 10;

(v) SEQ ID NOs: 26 and 27;

(w) SEQ ID NOs: 26 and 28;

(x) SEQ ID NOs: 26 and 29;

(y) SEQ ID NOs: 26 and 30;

(z) SEQ ID NOs: 26 and 31;

(aa) SEQ ID NOs: 11 and 12;

(bb) SEQ ID NOs: 11 and 36;

(cc) SEQ ID NOs: 11 and 37;

(dd) SEQ ID NOs: 32 and 12;

(ee) SEQ ID NOs: 32 and 36;

(ff) SEQ ID NOs: 32 and 37;

(gg) SEQ ID NOs: 33 and 12;

(hh) SEQ ID NOs: 33 and 36;

(ii) SEQ ID NOs: 33 and 37;

(jj) SEQ ID NOs: 34 and 12;

(kk) SEQ ID NOs: 34 and 36;

(ll) SEQ ID NOs: 34 and 37;

(mm) SEQ ID NOs: 35 and 12;

(nn) SEQ ID NOs: 35 and 36;

(oo) SEQ ID NOs: 35 and 37;

(pp) SEQ ID NOs: 13 and 14;

(qq) SEQ ID NOs: 13 and 42;

(rr) SEQ ID NOs: 13 and 43;

(ss) SEQ ID NOs: 13 and 44;

(tt) SEQ ID NOs: 38 and 14;

(uu) SEQ ID NOs: 38 and 42;

(vv) SEQ ID NOs: 38 and 43;

(ww) SEQ ID NOs: 38 and 44;

(xx) SEQ ID NOs: 39 and 14;

(yy) SEQ ID NOs: 39 and 42;

(zz) SEQ ID NOs: 39 and 43;

(aaa) SEQ ID NOs: 39 and 44;

(bbb) SEQ ID NOs: 40 and 14;

(ccc) SEQ ID NOs: 40 and 42;

(ddd) SEQ ID NOs: 40 and 43;

(eee) SEQ ID NOs: 40 and 44;

(fff) SEQ ID NOs: 41 and 14;

(ggg) SEQ ID NOs: 41 and 42;

(hhh) SEQ ID NOs: 41 and 43; and

(iii) SEQ ID NOs: 41 and 44.

Certain aspects of the invention relate to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein and comprises heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence is selected from the group consisting of SEQ ID NOs: 9, 11, 13, 15, 16, 19, 22, 25, 26, 32, 33, 34, 35, 38, 39, 40, and 41.

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein and comprises heavy and light chain variable regions, wherein the light chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence is selected from the group consisting of SEQ ID NOs: 10, 12, 14, 17, 18, 20, 21, 23, 24, 27, 28, 29, 30, 31, 36, 37, 42, 43, and 44.

In a further aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein and comprises heavy chain and light chain sequences is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 15 and 17, respectively;

(b) SEQ ID NOs: 15 and 18, respectively;

(c) SEQ ID NOs: 16 and 17, respectively;

(d) SEQ ID NOs: 16 and 18, respectively;

(e) SEQ ID NOs: 19 and 20, respectively;

(f) SEQ ID NOs:19 and 21, respectively;

(g) SEQ ID NOs: 22 and 23, respectively;

(h) SEQ ID NOs: 22 and 24, respectively;

(i) SEQ ID NOs: 9 and 10, respectively;

(j) SEQ ID NOs: 9 and 27, respectively;

(k) SEQ ID NOs: 9 and 28, respectively;

(l) SEQ ID NOs: 9 and 29, respectively;

(m) SEQ ID NOs: 9 and 30, respectively;

(n) SEQ ID NOs: 9 and 31, respectively;

(o) SEQ ID NOs: 25 and 10, respectively;

(p) SEQ ID NOs: 25 and 27, respectively;

(q) SEQ ID NOs: 25 and 28, respectively;

(r) SEQ ID NOs: 25 and 29, respectively;

(s) SEQ ID NOs: 25 and 30, respectively;

(t) SEQ ID NOs: 25 and 31, respectively;

(u) SEQ ID NOs: 26 and 10, respectively;

(v) SEQ ID NOs: 26 and 27, respectively;

(w) SEQ ID NOs: 26 and 28, respectively;

(x) SEQ ID NOs: 26 and 29, respectively;

(y) SEQ ID NOs: 26 and 30, respectively;

(z) SEQ ID NOs: 26 and 31, respectively;

(aa) SEQ ID NOs: 11 and 12, respectively;

(bb) SEQ ID NOs: 11 and 36, respectively;

(cc) SEQ ID NOs: 11 and 37, respectively;

(dd) SEQ ID NOs: 32 and 12, respectively;

(ee) SEQ ID NOs: 32 and 36, respectively;

(ff) SEQ ID NOs: 32 and 37, respectively;

(gg) SEQ ID NOs: 33 and 12, respectively;

(hh) SEQ ID NOs: 33 and 36, respectively;

(ii) SEQ ID NOs: 33 and 37, respectively;

(jj) SEQ ID NOs: 34 and 12, respectively;

(kk) SEQ ID NOs: 34 and 36, respectively;

(ll) SEQ ID NOs: 34 and 37, respectively;

(mm) SEQ ID NOs: 35 and 12, respectively;

(nn) SEQ ID NOs: 35 and 36, respectively;

(oo) SEQ ID NOs: 35 and 37, respectively;

(pp) SEQ ID NOs: 13 and 14, respectively;

(qq) SEQ ID NOs: 13 and 42, respectively;

(rr) SEQ ID NOs: 13 and 43, respectively;

(ss) SEQ ID NOs: 13 and 44, respectively;

(tt) SEQ ID NOs: 38 and 14, respectively;

(uu) SEQ ID NOs: 38 and 42, respectively;

(vv) SEQ ID NOs: 38 and 43, respectively;

(ww) SEQ ID NOs: 38 and 44, respectively;

(xx) SEQ ID NOs: 39 and 14, respectively;

(yy) SEQ ID NOs: 39 and 42, respectively;

(zz) SEQ ID NOs: 39 and 43, respectively;

(aaa) SEQ ID NOs: 39 and 44, respectively;

(bbb) SEQ ID NOs: 40 and 14, respectively;

(ccc) SEQ ID NOs: 40 and 42, respectively;

(ddd) SEQ ID NOs: 40 and 43, respectively;

(eee) SEQ ID NOs: 40 and 44, respectively;

(fff) SEQ ID NOs: 41 and 14, respectively;

(ggg) SEQ ID NOs: 41 and 42, respectively;

(hhh) SEQ ID NOs: 41 and 43, respectively; and

(iii) SEQ ID NOs: 41 and 44, respectively.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises heavy and light chain variable regions comprising an amino acid sequence at least 90% identical to the heavy and light chain variable regions selected from the group consisting of (a)-(iii). In certain embodiments, antibody, or antigen binding portion thereof comprises an amino acid sequence at least 95% identical to the heavy and light chain variable regions selected from the group consisting of (a)-(iii). In another embodiment, the antibody, or antigen binding portion thereof comprises a heavy and light chain variable region comprising an amino acid sequence at least 90% identical to the heavy and light chain variable regions selected from the group consisting of (a)-(iii).

In a further embodiment, the antibody is selected from the group consisting of an IgG1,an IgG2, an IgG3, an IgG4,an IgM, an IgA1, an IgA2,an IgD, and an IgE antibody. In an even further embodiment, the antibody, or antigen binding portion thereof is an IgG1 antibody.

Another aspect of the invention relates to an isolated monoclonal antibody that competes for binding to Ebola virus GP with an antibody described herein.

In a further aspect, the invention relates to a pharmaceutical composition comprising a monoclonal antibody or antigen binding potion thereof of and a pharmaceutically acceptable carrier. In certain embodiments the pharmaceutical composition comprises one or more of the monoclonal antibodies (a combination of monoclonal antibodies) or antigen binding portions thereof of and a pharmaceutically acceptable carrier. In one embodiment, a combination of antibodies is formulated with a pharmaceutically acceptable carrier in a single pharmaceutical composition. In another embodiment, each antibody is formulated with a pharmaceutically acceptable carrier and two or more pharmaceutical compositions with one or more antibodies is administered to a subject.

One aspect of the invention relates to a method for treating Ebola virus infection comprising administering an effective amount of the pharmaceutical compositions described above. In a further embodiment, the method further comprises administering a therapeutic agent. In certain embodiments the therapeutic agent is interferon alpha.

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises a heavy chain comprising CDR1, CDR2, and CDR3, sequences set forth in SEQ ID NOs: 68, 69, and 70, respectively, and variable region framework residues selected from the group consisting of 49H, 71H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 92, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 71, 72, and 73, respectively, and variable region framework residues selected from the group consisting of 42L, 59L, 70L, 99L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 93, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 49G (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 71T (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 42S (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 59V, 70Y, and 99G (Kabat numbering convention).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 75, and 76, respectively, and variable region framework residues selected from the group consisting of 49H, 50H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 94, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 49A and 50E (Kabat numbering convention). In certain embodiments the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S, 45Q, and 100G (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, and 71Y (Kabat numbering convention).

Another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprising a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 77, and 78, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S, 45Q, and 100G (Kabat numbering convention). In certain embodiments the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, and 71Y (Kabat numbering convention).

In another aspect of the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprise a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 74, 77, and 79, respectively, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 80, 81, and 82, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 45L, 70L, 71L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 95, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S, 45Q, and 100G (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, and 71Y (Kabat numbering convention).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 44S (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 48I, 70L, and 72V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 50V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S and 87F (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, 72S, 73L, and 100S (Kabat numbering convention).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 86, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 88, and 89 respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 44S (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 48I, 70L, and 72V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 50V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S and 87F (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, 72S, 73L, and 100S (Kabat numbering convention).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 83, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96 wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 90, and 89, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 44S (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 48I, 70L, and 72V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 50V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S and 87F (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, 72S, 73L, and 100S (Kabat numbering convention).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises a heavy chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 86, 84, and 85, respectively, and variable region framework residues selected from the group consisting of 44H, 48H, 70H, 72H, or a combination thereof (Kabat numbering convention) from the heavy chain variable region set forth in SEQ ID NO: 96, wherein the remainder of the heavy chain is from a human immunoglobulin; and a light chain comprising CDR1, CDR2, and CDR3 sequences set forth in SEQ ID NOs: 87, 90, and 89, respectively, and variable region framework residues selected from the group consisting of 3L, 43L, 70L, 72L, 73L, 87L, 100L, or a combination thereof (Kabat numbering convention) from the light chain variable region set forth in SEQ ID NO: 97, wherein the remainder of the light chain is from a human immunoglobulin.

In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 44S (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 48I, 70L, and 72V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residue 50V (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 43S and 87F (Kabat numbering convention). In certain embodiments, the preceding antibody, or antigen binding portion thereof comprises variable region framework residues 3V, 70Q, 72S, 73L, and 100S (Kabat numbering convention).

In another aspect, the invention relates to an isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, comprises:

a) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 45, 46, and 47, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 48, 50, and 51 respectively;
b) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 52, 53, and 54, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 55, 56, and 58 respectively;
c) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 52, 53, and 54, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 55, 56, and 59, respectively;
d) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 60, 61, and 63, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 64, 65, and 67, respectively;
e) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 74, 77, and 78, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 80, 81, and 82, respectively;
f) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 74, 77, and 79, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 80, 81, and 82, respectively;
g) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 83, 84 and 85, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 87, 90 and 89, respectively;
h) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 86, 84, and 85, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 87, 88, and 89, respectively; or
i) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 86, 84, and 85, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 87, 90, and 89, respectively.

One aspect of the invention is a pharmaceutical composition comprising the preceding antibody or antigen binding potion thereof and a pharmaceutically acceptable carrier.

A further aspect of the invention is a pharmaceutical composition comprising one or more of the preceding antibodies or antigen binding positions thereof and a pharmaceutically acceptable carrier.

One aspect of the invention is a method for treating Ebola virus infection comprising administering an effective amount of the pharmaceutical compositions described herein. In certain embodiments the method includes administering a therapeutic agent. In certain embodiments, the therapeutic agent is interferon alpha.

Examples

The examples below utilize monoclonal antibodies of the invention which have been optimized based on previously characterized mouse monoclonal antibodies 1H3, 2G4, and 4G7 (US 8, 513, 391, Qiu et al., *Sci Transl Med* 2012; 4, 138ra81, and Qiu et al., *Clin Immunol* 2011; 141, 218-227, herein incorporated by reference)), and mouse monoclonal antibodies 13C6, 6D8, and 13F6 (US 6,630,144 and 7,335,356, herein incorporated by reference).

Example 1

Epitope Mapping of the Ebola virus glycoprotein

To facilitate the engineering of antibodies that target the Ebola virus glycoprotein (GP), epitope hotspots were determined using alanine scanning, as described below.

GP Expression Platform

A GP expression platform that allows for alanine mutations to be made and for their binding properties to be assayed was first established. A pcDNA 3.3 expression vector containing a sequence encoding GPΔTMΔmuc (missing transmembrane and mucin domains) was transiently transfected into HEK 293F cells. After 6 days, supernatant was harvested and purified using a 1 mL HisTrap HP column on an AKTA FPLC (GE Healthcare). Fractions were collected and analyzed using Native PAGE (Invitrogen). Fractions containing trimeric GP species were combined and buffer exchanged into PBS using Amicon Ultra Centrifugation Filters (Millipore). Protein concentration was determined using a BCA assay (Pierce) and GP was assessed again using Native PAGE to confirm purity.

Site-directed mutagenesis for alanine-scanning studies

GPΔTMΔmuc point mutants were created using site-directed mutagenesis. Mutagenesis primers were designed corresponding to the mutant sequence, and a PCR amplification reaction was carried out using a QuikChange Mutagenesis Kit (Agilent). PCR reactions were then digested using Dpn1 for 3 hours, transformed into One Shot TOP10 Chemically Competent cells (Thermo) and then plated onto LB agar plates containing ampicillin. Plasmid DNA was generated by growing colonies in LB broth containing ampicillin overnight and then by purifying using Plasmid DNA preparation kits (Invitrogen). Positive colonies were confirmed using Sanger sequencing (Genewiz). The functional consequences of the alanine mutations were assessed by assaying the binding of various mAbs (e.g. 13C6, 2G4, 4G7) to the mutants. An ELISA was used wherein either the mutant or WT GP was coated on the plate and antibodies were added. Change in binding between the specific mutant and WT was analyzed to determine the effect of the mutation on binding.

Based on the binding analysis, antibodies 4G7, K252, and 2G4 were found to bind to a conformational epitope that included regions V505-C511 and N550-E564 of SEQ ID NO: 91, whereas antibody 13C6 was found to bind within the regions T270-P279 and Y394-R409 of SEQ ID NO: 91 (**Figure 1**). **Figure 2** summarizes the hotspots in the glycoprotein identified through this mutational analysis.

<u>Example 2</u>

Binding Affinity of Ebola Glycoprotein-Specific Antibodies

Based on the epitope hostspot data from Example 1, antibodies from Table 1 were further selected based on their binding affinity to the Ebola virus glycoprotein using ELISA.

For the ELISA, 100 µL of Ebola GPdTM (IBT Bioservices) was plated onto a Maxisorp 96 well plate (Nunc) at a concentration of 1 µg/mL and left at 4°C overnight. The following day, the plate was washed 3x with PBST (PBS + 0.05% TWEEN) and 100 µL of 1% BSA in PBST was incubated for 1 hour at room temperature. The plate was then washed 3x and 100 µL of an antibody dilution series was added. For each antibody dilution series, the first well contained antibody at a concentration of 9 µg/mL, and then each well was a 3-fold dilution across an 11-point series (12th well was PBST). After antibody addition, plates were incubated for 2 hours at room temperature. Plates were then washed 3x and 100 µL secondary antibody (Rabbit anti-human IgG Fc with HRP, Jackson Immunoresearch) was added to each well at a dilution of 1:5000 (from 0.8 mg/mL stock) for 1 hour. Plates were then washed 3x, and 100 µL TMB microwell peroxidase (KPL) was added for 5 minutes before neutralization with 100 µL 1N H_2SO_4. Plates were then read using a SpectraMax M5e plate reader at 450 nm.

Figures 3A-3C show the data generated from the ELISA. The data is a representation of different antibodies (13C6.X, 2G4.X, 4G7.X) from the screening process. The 2G4 antibodies tested were wild type (WT), 2G4.3, and 2G4.6, with EC50 values of 154 pM, 129 pM, and 109 pM, respectively (**Figure 3A**). The 4G7 antibodies tested were Wt, 4G7.2, 4G7.3, 4G7.1, 4G7.10, 4G7.9, 4G7.11, and 4G7.12, with EC50 values of 72.5 pM, 95.2 pM, 176 pM, 182 pM, 120 pM, 99.7 pM, 145 pM, and 88.8 pM, respectively (**Figure 3B**). The 13C6 antibodies tested were WT and 13C6.1, having EC50 values of 74.7 pM and 136 pM, respectively (**Figure 3C**). These data show that the antibodies bound to Ebola glycoprotein with an EC50 of 200 pM or less, as measured by ELISA

The candidates were generated using in silico antibody design, and the lead candidates were selected on the basis of binding affinity values. The phylogram shown in **Figure 4** illustrates the sequence similarity between the different antibodies. In each case, the lead candidate is circled in a dotted oval. For each candidate there is a large distance from the parent monoclonal antibody (WT). In addition, the in silico generated candidates cluster closely, illustrating the similarity between these candidates. Phylogeny trees were constructed for the representative antibody amino acid sequences by Neighbor-Joining method using Geneious (http://www.geneious.com/).

Example 3

Neutralization of Ebola virus glycoprotein by optimized monoclonal antibodies

In order to determine if the anti-Ebola glycoprotein antibodies neutralize Ebola virus *in vitro*, purified mAbs were evaluated for their ability to inhibit plaque formation by various strains of Ebola virus as compared to plaques formation in the absence of the antibodies (i.e., control). Known amounts of antibody were mixed with 200 pfu of Ebola virus and incubated at 37^0C for 30 minutes. The virus/antibody mix was then added to a monolayer of vero E6 cells and allowed to adsorb for 30 minutes at 37^0C. After this, the cells were washed twice with PBS and then overlayed with media containing 1% methyl cellulose. Cells were incubated for 4 days at 37^0C and then fixed with formalin for removal from BSL4 lab. Ebola virus infected plaques were visualized by IFA staining and the number of plaques in each well counted. Percent reduction in plaque number was calculated from wells with no serum. Titre is expressed as either 50 or 80% plaque reduction.

Figure 5 shows the results of the neutralization assay. Antibody 13C6.1 neutralized each of the three Ebola strains at a concentration of greater than 50 μg/mL. Antibody 2G4.6 neutralized the three Ebola strains at concentrations of 2 to 4 μg/mL. Antibody 4G7.9 neutralized the three strains at a concentration of 1 μg/mL.

Example 4

In vivo non-human primate study

Cynomolgus macaques are used to test whether and how effectively an anti-GP mAb can improve survival when administered after high-dose EBOV infection.

Ebola virus (EBOV) strain Kikwit 95 is produced on Vero E6 cells in complete minimal essential medium (cMEM), 2% FBS, and 1% penicillin/stretopmycin.

Macaques are randomized into groups on the basis of treatment regimens, plus one receiving only PBS as a positive control for infection. Each subject is infected with 1000 PFU (1 mL each into two sites intramuscularly) of EBOV in Dulbecco's modified Eagle's medium (DMEM). Half of the groups begin treatment 24 hours post infection and the other half of the groups begin treatment 48 hours post infection. The subjects are treated intravenously with one of the EBOV-GP-specific neutralizing antibodies disclosed herein at 25 mg/kg, or a mixture of antibodies disclosed herein, as a 5 mL slow bolus in the saphenous vein. The subjects are monitored daily and scored for disease progression with an internal filovirus scoring protocol. Changes in the subject's posture/activity, attitude, activity level, feces/urine output, food/water intake, weight, temperature, respiration, and scored disease manifestations such as a visible rash, hemorrhage, cyanosis, or flushed skin are scored. Tests for weight, temperature, blood, and oropharyngeal, nasal, and rectal swabs are taken at days 1, 4, 7, 14, 21, and 28 post infection for the 24-hour group or at 2, 5, 8, 14, 21, and 28 days post infection for the 48-hour group, before the animals receive the mAb or mAb mixture.

Example 5

Human Study

Humans infected with Ebola virus are administered a single anti-GP antibody disclosed herein, or a combination thereof. Ideally, the antibodies will be given 24 or 48 hours post infection. Subjects are monitored for disease manifestations such as visible rash, hemorrhage, cyanosis, or flushed skin. Viral titers are also be monitored.

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

Table 1: Antibody Pairs by SEQ ID Number

			VH CDR			VL CDR		
Antibody	**VH**	**VL**	**CDR1**	**CDR2**	**CDR3**	**CDR1**	**CDR2**	**CDR3**
13C6.1	15	17	45	46	47	48	50	51
13C6.2	15	18	45	46	47	48	50	51
13C6.3	16	17	45	46	47	48	50	51
13C6.4	16	18	45	46	47	48	50	51
6D8.1	19	20	52	53	54	55	56	58
6D8.2	19	21	52	53	54	55	56	59
13F6.1	22	23	60	61	63	64	65	67
13F6.2	22	24	60	61	63	64	65	67
1H3.1	9	10	68	69	70	71	72	73
1H3.2	9	27	68	69	70	71	72	73
1H3.3	9	28	68	69	70	71	72	73
1H3.4	9	29	68	69	70	71	72	73
1H3.5	9	30	68	69	70	71	72	73
1H3.6	9	31	68	69	70	71	72	73
1H3.7	25	10	68	69	70	71	72	73
1H3.8	25	27	68	69	70	71	72	73
1H3.9	25	28	68	69	70	71	72	73
1H3.10	25	29	68	69	70	71	72	73
1H3.11	25	30	68	69	70	71	72	73
1H3.12	25	31	68	69	70	71	72	73
1H3.13	26	10	68	69	70	71	72	73
1H3.14	26	27	68	69	70	71	72	73
1H3.15	26	28	68	69	70	71	72	73
1H3.16	26	29	68	69	70	71	72	73
1H3.17	26	30	68	69	70	71	72	73
1H3.16	26	31	68	69	70	71	72	73
2G4.1	11	12	74	75	76	80	81	82
2G4.2	11	36	74	75	76	80	81	82
2G4.3	11	37	74	75	76	80	81	82
2G4.4	32	12	74	75	76	80	81	82
2G4.5	32	36	74	75	76	80	81	82
2G4.6	32	37	74	75	76	80	81	82
2G4.7	33	12	74	75	76	80	81	82
2G4.8	33	36	74	75	76	80	81	82
2G4.9	33	37	74	75	76	80	81	82
2G4.10	34	12	74	77	78	80	81	82
2G4.11	34	36	74	77	78	80	81	82
2G4.12	34	37	74	77	78	80	81	82
2G4.13	35	12	74	77	79	80	81	82
2G4.14	35	36	74	77	79	80	81	82
2G4.15	35	37	74	77	79	80	81	82
4G7.1	13	14	83	84	85	87	88	89
4G7.2	13	42	83	84	85	87	88	89
4G7.3	13	43	83	84	85	87	88	89

4G7.4	13	44	83	84	85	87	90	89
4G7.5	38	14	83	84	85	87	88	89
4G7.6	38	42	83	84	85	87	88	89
4G7.7	38	43	83	84	85	87	88	89
4G7.8	38	44	83	84	85	87	90	89
4G7.9	39	14	83	84	85	87	88	89
4G7.10	39	42	83	84	85	87	88	89
4G7.11	39	43	83	84	85	87	88	89
4G7.12	39	44	83	84	85	87	90	89
4G7.13	40	14	83	84	85	87	88	89
4G7.14	40	42	83	84	85	87	88	89
4G7.15	40	43	83	84	85	87	88	89
4G7.16	40	44	83	84	85	87	90	89
4G7.17	41	14	86	84	85	87	88	89
4G7.18	41	42	86	84	85	87	88	89
4G7.19	41	43	86	84	85	87	88	89
4G7.20	41	44	86	84	85	87	90	89

Table 2: Summary Sequence Table

SEQ ID Number	Description	Sequence
1	Human IgG1 Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
2	Human IgG1 Light chain (kappa)	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWK VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC
3	13C6 V_H Wild Type	QLTLKESGPGILKPSQTLSLTCSLSGFSLSTSGVGVGWFRQPSG KGLEWLALIWWDDDKYYNPSLKSQLSISKDFSRNQVFLKISN VDIADTATYYCARRDPFGYDNAMGYWGQGTSVTVSS
4	13C6 V_L Wild Type	DIVMTQSQKFMSTSVGDRVSLTCKASQNVGTAVAWYQQKPG QSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQSEDLA DYFCQQYSSYPLTFGAGTKLELR
5	6D8 V_H Wild Type	DVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAP GKGLEWIGEINPDSSTINYTPSLKDKFIISRDNAKNTLYLQMSK VRSEDTALYYCTRQGYGYNYWGQGTTLIVSS
6	6D8 V_L Wild Type	DVLLTQIPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQK PGQSPKLLIYKASNRFSGVPDRFSGSGSGTDFTLKINRVEAEDL GVYYCLQGSHVPSTFGGGTKLEIK
7	13F6 V_H Wild Type	EVQVVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTPE KRLEWVAYISRGGGYTYYPDTVKGRFTISRDNAKNTLYLQMS SLKSEDTAMYYCSRHIYYGSSHYYAMDYWGQGTSVTVSS
8	13F6 V_L Wild Type	QLVLTQSSSASFSLGASAKLTCTLSRQHSTYTIEWYQQQPLKP PRYVMELKKDGSHSTGDGIPDRFSGSSSGADRYLSISNIQPEDE AIYICGVGDTIKEQFVYVFGGGTKVTVLG
9	1H3V_H.1	EVQLVESGGGLVQPGGSLRLSCTASGFNIKDTYIHWVRQAPG KGLEWVARIDPANGNTKYADSVKGRFTISADTSKNTAYLQM NSLRAEDTAVYYCARESRISTMLTTGYFDYWGQGTLVTVSS
10	1H3V_L.1	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKA PKLLIYDTSNLASGVPARFSGSGSGTEFTLTISSLQPDDFATYY CQQWSSYPYTFGQGTKVEVK
11	2G4V_H.1	EVQLLESGGGLVQPGGSLRLSCVASGFTFSNYWMNWVRQAP GKGLEWLGFIRLKSNNYATHYSASVKGRFTISRDKSKSTLYLQ MNTLQAEDSAIYYCTRGNGNYRAMDYWGQGTLVTVSS
12	2G4V_L.1	DIQMTQSPSSLSASVGDRVTITCRASENIYSSLAWYQQKPGKA PKLLVYSATILADGVPSRFSGSGSGTDFTLTISSLQPEDFATYY CQHFWGTPYTFGQGTKVEIK
13	4G7V_H.1	QVQLVQSGAEVKKPGSSVKVSCKASGSSFTGFSMNWVRQAP GQGLEWMGNIDTYYGGTTYNGKFKGRVTITADKSTSTAYME LSSLRSEDTAVYYCARSAYYGSTFAYWGQGTLVTVSS

14	4G7V_L.1	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKAPKLLVYNAKTLIEGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQHHFGTPFTFGQGTKVEIK
15	13C6 V_H.1 (T56S)	QLTLKESGPTLVKPTQTLSLTCTFSGFSLSTSGVGVGWFRQPPGKALEWLALIWWDDDKYYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARRDPFGYDNAMGYWGQGTTVTVSS
16	13C6 V_H.2 (T56S)	QLTLKESGPTLVKPTQTLSLTCTFSGFSLSTSGVGVGWFRQPPGKALEWLALIWWDDDKYYGPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCARRDPFGYDNAMGYWGQGTTVTVSS
17	13C6 V_L.1	DIVMTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQYSSYPLTFGGGTKLEIK
18	13C6 V_L.2	DIVMTQSPSFLSASVGDRVTITCKASQNVGTAVAWYQQKPGKAPKLLIYSASNRYSGVPSRFSGSGSGTDFTLTISSLQPEDFATYFCQQYSSYPLTFGQGTKLEIK
19	6D8 V_H.3	EVKLVESGGGLVQPGGSLRLSCAASGFDFSRYWMSWVRQAPGKGLVWVSEINPDSSTINYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCTRQGYGYNYWGQGTTVTVSS
20	6D8 V_L.3	DVLLTQSPLSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPRLLIYKASNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLNGSHVPSTFGGGTKVEIK
21	6D8 V_L.4	DVLLTQTPLSLPVTLGQPASISCRSSQSIVHSNGNTYLEWYLQKPGQSPQLLIYKASNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCLQGSHVPSSFGGGTKVEIK
22	13F6 V_H.4	EVQVVESGGGLVQPGGSLRLSCAASGFAFSSYDMSWVRQAPGKGLEWVSYISRGGGYTYYADSVKGRFTISRDNAKNTLYLQMNSLKAEDTAVYYCSRHIYYGSSHYYAMDVWGQGTTVTVSS
23	13F6 V_L.5	QLVLTQSPSASASLGASIKLTCTLSRQHSTYTIEWYQQQPGKSPRYVMELKKDGSHSTGDGIPDRFSGSSSGADRYLTISNLQSEDEAEYICGEGDTIKEQFVYVFGGGTKVTVLG
24	13F6 V_L.6	QLVLTQSPSASASLGASIKLTCTLSRQHSTYTIEWYQQQPEKGPRYVMELKKDGSHSTGDGIPDRFSGSSSGADRYLTISNLQSEDEADYICGEGDTIKEQFVYVFGGGTKVTVLG
25	1H3V_H.2 (A49G)	EVQLVESGGGLVQPGGSLRLSCTASGFNIKDTYIHWVRQAPGKGLEWVGRIDPANGNTKYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARESRISTMLTTGYFDYWGQGTLVTVSS
26	1H3V_H.3 (A49G, S71T)	EVQLVESGGGLVQPGGSLRLSCTASGFNIKDTYIHWVRQAPGKGLEWVGRIDPANGNTKYADSVKGRFTITADTSKNTAYLQMNSLRAEDTAVYYCARESRISTMLTTGYFDYWGQGTLVTVSS
27	1H3V_L.2 (A42S)	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKSPKLLIYDTSNLASGVPARFSGSGSGTEFTLTISSLQPDDFATYYCQQWSSYPYTFGQGTKVEVK
28	1H3V_L.3 (A42S, A59V, F70Y, Q99G)	DIQMTQSPSTLSASVGDRVTITCSASSSVSYMYWYQQKPGKSPKLLIYDTSNLASGVPVRFSGSGSGTEYTLTISSLQPDDFATYYCQQWSSYPYTFGGGTKVEVK
29	1H3V_L.4	DIQMTQSPASVGDRVTITCSASSSVSYMYWYQQKPGKSPKLLIYDTSNLASGVPARFSGSGSGTEFTLTISSLQPDDFATYYCQQWSSYPYTFGQGTKVEVK

30	1H3V$_L$.5 (A59V, F70Y, Q99G)	DIQMTQSPASVGDRVTITCSASSSVSYMYWYQQKPGKSPKLLIYDTSNLASGVPVRFSGSGSGTEYTLTISSLQPDDFATYYCQQWSSYPYTFGGGTKVEVK
31	1H3V$_L$.6	MTQTPAIMSASPGEKVTMTCSASSSVSYMYWYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPYTFGGGTKLEIK
32	2G4V$_H$.2 (G49A, F50E)	EVQLLESGGGLVQPGGSLRLSCVASGFTFSNYWMNWVRQAPGKGLEWLAEIRLKSNNYATHYSASVKGRFTISRDKSKSTLYLQMNTLQAEDSAIYYCTRGNGNYRAMDYWGQGTLVTVSS
33	2G4V$_H$.3	EVQLLESGGGLVQPGGSLRLSCVASGFTFSNYWMNWVRQAPGKGLEWLAEIRLKSNNYATHYSASVKGRFTISRDDSKRSVYLQMNTLQAEDSAIYYCTRGNGNYRAMDYWGQGTLVTVSS
34	2G4V$_H$.4	EVQLLESGGGLVQPGGSLRLSCVASGFTFSNYWMNWVRQAPGKGLEWLAEIRLKSVNYATHYSASVKGRFTISRDDSKRSVYLQMNTLQAEDSAIYYCTRGAGVFRAMFYWGQGTLVTVSS
35	2G4V$_H$.5 (A102V)	EVQLLESGGGLVQPGGSLRLSCVASGFTFSNYWMNWVRQAPGKGLEWLAEIRLKSVNYATHYSASVKGRFTISRDDSKRSVYLQMNTLQAEDSAIYYCTRGVGVFRAMFYWGQGTLVTVSS
36	2G4V$_L$.2 (A43S, K45Q, Q100G)	DIQMTQSPSSLSASVGDRVTITCRASENIYSSLAWYQQKPGKSPQLLVYSATILADGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQHFWGTPYTFGGGTKVEIK
37	2G4V$_L$.3 (Q3V, A43S, K45Q, D70Q, F71Y, Q100G)	DIVMTQSPSSLSASVGDRVTITCRASENIYSSLAWYQQKPGKSPQLLVYSATILADGVPSRFSGSGSGTQYTLTISSLQPEDFATYYCQHFWGTPYTFGGGTKVEIK
38	4G7V$_H$.2 (G44S)	QVQLVQSGAEVKKPGSSVKVSCKASGSSFTGFSMNWVRQAPGQSLEWMGNIDTYYGGTTYNGKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARSAYYGSTFAYWGQGTLVTVSS
39	4G7V$_H$.3 (G44S, M48I, I70L, A72V)	QVQLVQSGAEVKKPGSSVKVSCKASGSSFTGFSMNWVRQAPGQSLEWIGNIDTYYGGTTYNGKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCARSAYYGSTFAYWGQGTLVTVSS
40	4G7V$_H$.3.1 (G44S, M48I, N50V, I70L, A72V)	QVQLVQSGAEVKKPGSSVKVSCKASGSSFTGFSMNWVRQAPGQSLEWIGVIDTYYGGTTYNGKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCARSAYYGSTFAYWGQGTLV
41	4G7V$_H$.3.2 (F32V, G44S, M48I, I70L, A72V)	QVQLVQSGAEVKKPGSSVKVSCKASGSSFTGVSMNWVRQAPGQSLEWIGNIDTYYGGTTYNGKFKGRVTLTVDKSTSTAYMELSSLRSEDTAVYYCARSAYYGSTFAYWGQGTLVTVSS
42	4G7V$_L$.2 (A43S, Y87F)	DIQMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKSPKLLVYNAKTLIEGVPSRFSGSGSGTDFTFTISSLQPEDIATYFCQHHFGTPFTFGQGTKVEIK
43	4G7V$_L$.3 (Q3V, A48S, D70Q, T72S, F73L, Y87F,	DIVMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKSPKLLVYNAKTLIEGVPSRFSGSGSGTQFSLTISSLQPEDIATYFCQHHFGTPFTFGSGTKVEIK

	Q100S)	
44	4G7V$_L$.4 (Q3V, A48S, K52V, D70Q, T72S, F73L, Y87F, Q100S)	DIVMTQSPSSLSASVGDRVTITCRASENIYSYLAWYQQKPGKSPKLLVYNAVTLIEGVPSRFSGSGSGTQFSLTISSLQPEDIATYFCQHHFGTPFTFGSGTKVEIK
45	13C6 V$_H$ CDR1	GFSLSTSGV
46	13C6 V$_H$ CDR2	WWDDD
47	13C6 V$_H$ CDR3	RDPFGYDNAMGY
48	13C6 V$_L$ CDR1	KASQNVGTAVA
49	13C6 V$_L$ WT CDR2	SASNRYT
50	13C6 VL.1 and V$_L$.2 CDR2	SASNRYS
51	13C6 V$_L$ CDR3	QQYSSYPLT
52	6D8 V$_H$ CDR1	GFDFSRY
53	6D8 V$_H$ CDR2	NPDSST
54	6D8 V$_H$ CDR3	QGYGYNY
55	6D8 V$_L$ CDR1	RSSQSIVHSNGNTYLE
56	6D8 V$_L$ CDR2	KASNRFS
57	6D8 V$_L$ WT CDR3	LQGSHVPST
58	6D8 V$_L$.3 CDR3	LNGSHVPST
59	6D8 V$_L$.4 CDR3	LQGSHVPSS
60	13F6 V$_H$ CDR1	GFAFSSY
61	13F6 V$_H$ CDR2	SRGGGY
62	13F6 V$_H$ WT CDR3	HIYYGSSHYYAMDY
63	13F6 V$_H$.4 CDR3	HIYYGSSHYYAMDV
64	13F6 V$_L$ CDR1	TLSRQHSTYTIE

65	13F6 V_L CDR2	LKKDGSHSTGD
66	13F6 V_L WT CDR3	GVGDTIKEQFVYV
67	13F6 V_L.5 and V_L.6 CDR3	GEGDTIKEQFVYV
68	1H3 V_H CDR1	GFNIKDT
69	1H3 V_H CDR2	DPANGN
70	1H3 V_H CDR3	ESRISTMLTTGYFDY
71	1H3 V_L CDR1	SASSSVSYMY
72	1H3 V_L CDR2	DTSNLAS
73	1H3 V_L CDR3	QQWSSYPYT
74	2G4 V_H CDR1	GFTFSNY
75	2G4 V_H CDR2	RLKSNNYA
76	2G4 V_H CDR3	GNGNYRAMDY
77	2G4V_H.4 and 2G4V_H.5 CDR2	RLKSVNYA
78	2G4V_H.4 CDR3	GAGVFRAMFY
79	2G4V_H.5 CDR3	GVGVFRAMFY
80	2G4 V_L CDR1	RASENIYSSLA
81	2G4 V_L CDR2	SATILAD
82	2G4 V_L CDR3	QHFWGTPYT
83	4G7 V_H CDR1	GSSFTGF
84	4G7 V_H CDR2	DTYYGG
85	4G7 V_H CDR3	SAYYGSTFAY
86	4G7V_H.3.2 CDR1	GSSFTGV
87	4G7 V_L CDR1	RASENIYSYLA

88	4G7 V_L CDR2	NAKTLIE
89	4G7 V_L CDR3	QHHFGTPFT
90	4G7V_L.4 CDR2	NAVTLIEG
91	Ebola virus glycoprotein precursor, Genebank Accession: AIG96634.1	MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQV SDVDKLVCRDKLSSTNQLRSVGLNLEGNGVATDVPSVTKRW GFRSGVPPKVVNYEAGEWAENCYNLEIKKPDGSECLPAAPDG IRGFPRCRYVHKVSGTGPCAGDFAFHKEGAFFLYDRLASTVIY RGTTFAEGVVAFLILPQAKKDFFSSHPLREPVNATEDPSSGYY STTIRYQATGFGTNETEYLFEVDNLTYVQLESRFTPQFLLQLN ETIYASGKRSNTTGKLIWKVNPEIDTTIGEWAFWETKKNLTRK IRSEELSFTAVSNGPKNISGQSPARTSSDPETNTTNEDHKIMAS ENSSAMVQVHSQGRKAAVSHLTTLATISTSPQPPTTKTGPDNS THNTPVYKLDISEATQVGQHHRRADNDSTASDTPPATTAAGP LKAENTNTSKSADSLDLATTTSPQNYSETAGNNNTHHQDTGE ESASSGKLGLITNTIAGVAGLITGGRRTRREVIVNAQPKCNPNL HYWTTQDEGAAIGLAWIPYFGPAAEGIYTEGLMHNQDGLICG LRQLANETTQALQLFLRATTELRTFSILNRKAIDFLLQRWGGT CHILGPDCCIEPHDWTKNITDKIDQIIHDFVDKTLPDQGDNDN WWTGWRQWIPAGIGVTGVIIAVIALFCICKFVF
92	1H3-V_H (mouse)	EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWVKQGPE QGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLS GLTSEDTAVYYCARESRISTMLTTGYFDYWGQGTTLTVSS
93	1H3-V_L (mouse)	DIVMTQSPASPGEKVTMTCSASSSVSYMYWYQQKPGSSPRLL IYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQ WSSYPYTFGGGTKLEIK
94	2G4-V_H (mouse)	EVQLQQSGGGLMQPGGSMKLSCVASGFTFSNYWMNWVRQS PEKGLEWVAEIRLKSNNYATHYAESVKGRFTISRDDSKRSVY LQMNTLRAEDTGIYYCTRGNGNYRAMDYWGQGTSVTVSS
95	2G4-V_L (mouse)	DIVMTQSPASLSVSVGETVSITCRASENIYSSLAWYQQKQGKS PQLLVYSATILADGVPSRFSGSGSGTQYSLKINSLQSEDFGTYY CQHFWGTPYTFGGGTKLEIK
96	4G7-V_H (mouse)	EVQLQQSGPELEMPGASVKISCKASGSSFTGFSMNWVKQSNG KSLEWIGNIDTYYGGTTYNQKFKGKATLTVDKSSSTAYMQLK SLTSEDSAVYYCARSAYYGSTFAYWGQGTLVTVSS
97	4G7-V_L (mouse)	DIVMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKS PQLLVYNAKTLIEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYF CQHHFGTPFTFGSGTELEIK
98	Ebola virus GP T270-P279	TGKLIWKVNP
99	Ebola virus GP Y394-R409	YKLDISEATQVGQHHR
100	Ebola virus GPV505-C511	VNAQPKC

101	Ebola virus GP N550-E564	NQDGLICGLRQLANE

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CLAIMS:

1. An isolated monoclonal antibody, or antigen binding portion thereof, which binds to Ebola virus glycoprotein, wherein the monoclonal antibody is selected from the group consisting of:

(a) a monoclonal antibody 4G7.9 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14;

(b) a monoclonal antibody 2G4.6 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37; and

(c) a monoclonal antibody 13C6.1 comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17.

2. The monoclonal antibody of claim 1, comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 39 and 14.

3. The monoclonal antibody of claim 1, comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 32 and 37.

4. The monoclonal antibody of claim 1, comprising a variable heavy chain and a variable light chain set forth in SEQ ID NOs: 15 and 17.

5. A pharmaceutical composition comprising a monoclonal antibody or antigen binding portion thereof of any one of claims 1-4 and a pharmaceutically acceptable carrier.

6. A pharmaceutical composition comprising two or more of the monoclonal antibodies or antigen binding portions thereof of any one of claims 1-4 and a pharmaceutically acceptable carrier.

7. A method for treating Ebola virus infection comprising administering to a subject in need thereof an effective amount of the pharmaceutical composition of claim 5 or 6.

8. The method of claim 7, further comprising administering a therapeutic agent.

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9. The method of claim 7, wherein the therapeutic agent is interferon alpha.

10. Use of a pharmaceutical composition of claim 5 or 6 in the manufacture of a medicament for treating Ebola virus infection.

11. The use of claim 10, wherein the pharmaceutical composition is further in combination with an additional therapeutic agent.

12. The use of claim 11, wherein the therapeutic agent is interferon alpha.

13. A nucleic acid molecule comprising a nucleotide sequence encoding the light chain, heavy chain, or both the light and heavy chains of the monoclonal antibody or antigen binding portion thereof of any one of claims 1-4.

14. An expression vector comprising the nucleic acid molecule of claim 13.

15. A host cell comprising an expression vector of claim 14.

16. A method for producing a monoclonal antibody, or antigen binding portion thereof, comprising culturing a host cell transformed to express the monoclonal antibody, or antigen binding portion thereof, of any one of claims 1-4.

17. The method of claim 16, further comprising obtaining the monoclonal antibody, or antigen binding portion thereof.

Massachusetts Institute of Technology

Patent Attorneys for the Applicant/Nominated Person

SPRUSON & FERGUSON

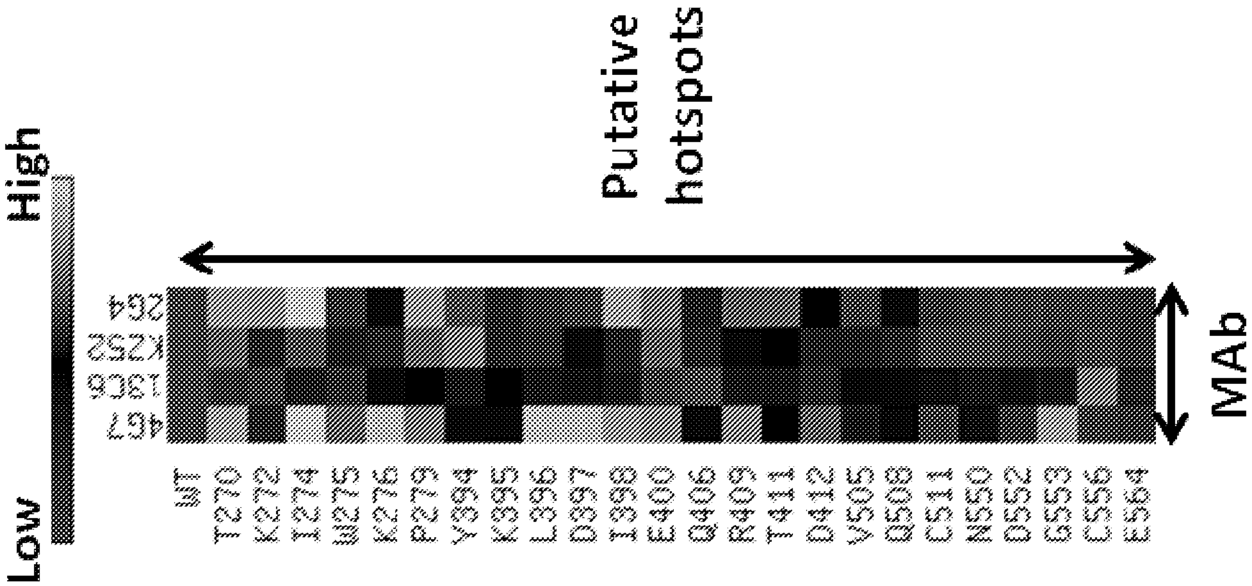
High
Low
Putative hotspots
MAb
2G4
K252
13C6
4G7
WT
T270
K272
I274
W275
K276
P279
Y394
K395
L396
D397
I398
E400
Q406
R409
T411
D412
V505
Q508
C511
N550
D552
G553
C556
E564

Figure 1

Figure 2

> ZEBOV 2014 GP

MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQVSDVDKLVCR
DKLSSTNQLRSVGLNLEGNGVATDVPSVTKRWGFRSGVPPKVVNYEAGEWAENC
YNLEIKKPDGSECLPAAPDGIRGFPRCRYVHKVSGTGPCAGDFAFHKEGAFFLY
DRLASTVIYRGTTFAEGVVAFLILPQAKKDFFSSHPLREPVNATEDPSSGYYST
TIRYQATGFGTNETEYLFEVDNLTYVQLESRFTPQFLLQLNETIYASGKRSNT**T**
G**K**L**IWK**VN**P**EIDTTIGEWAFWETKKNLTRKIRSEELSFTAVSNGPKNISGQSPA
RTSSDPETNTTNEDHKIMASENSSAMVQVHSQGRKAAVSHLTTLATISTSPQPP
TTKTGPDNSTHNTPV**YKLDI**S**E**ATQVG**Q**HH**R**R**AD**NDSTASDTPPATTAAGPLKA
ENTNTSKSADSLDLATTTSPQNYSETAGNNNTHHQDTGEESASSGKLGLITNTI
AGVAGLITGGRRTRREVI**V**NA**Q**PK**C**NPNLHYWTTQDEGAAIGLAWIPYFGPAAE
GIYTEGLMH**N**Q**DG**LI**C**GLRQLAN**E**TTQALQLFLRATTELRTFSILNRKAIDFLL
QRWGGTCHILGPDCCIEPHDWTKNITDKIDQIIHDFVDKTLPDQGDNDNWWTGW
RQWIPAGIGVTGVIIAVIALFCICKFVF (SEQ ID NO: 91)

GP1 AMINO ACIDS **GP2 AMINO ACIDS**

Figure 3A

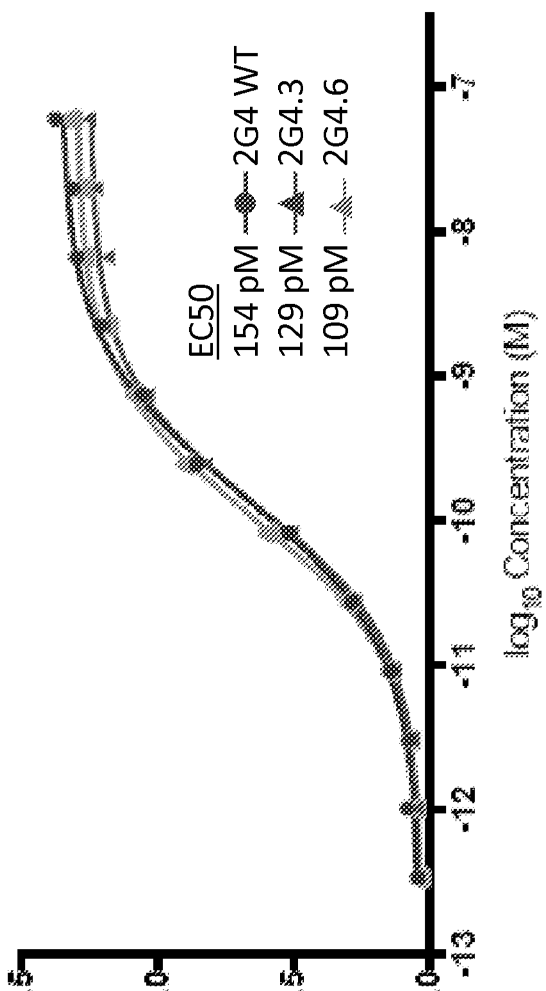

Figure 3B

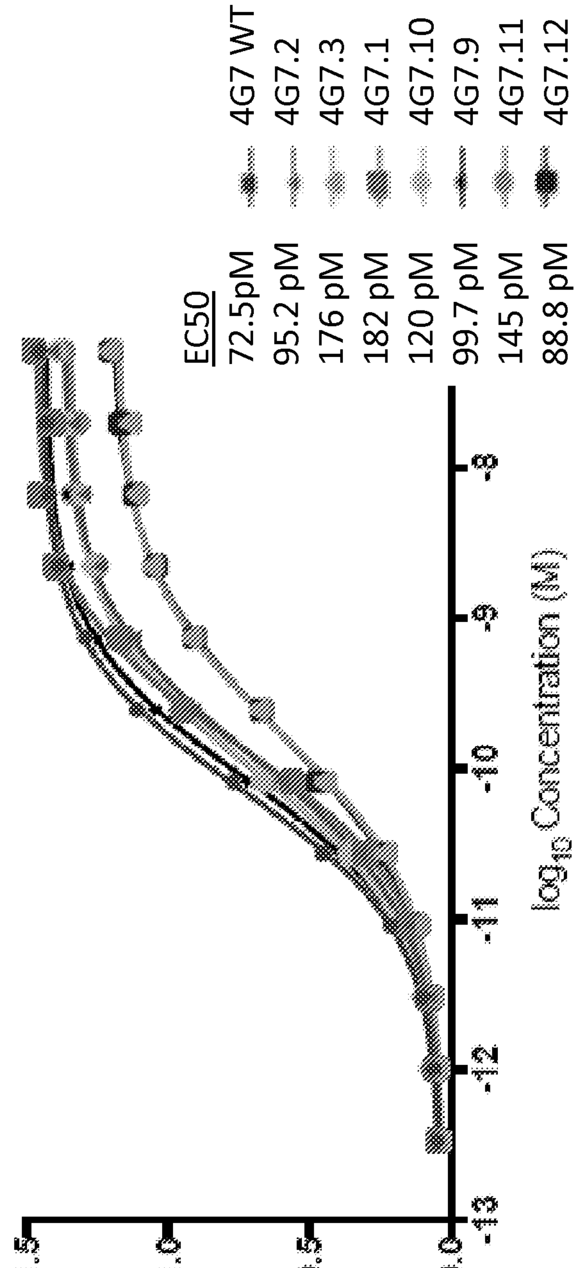

Figure 3C

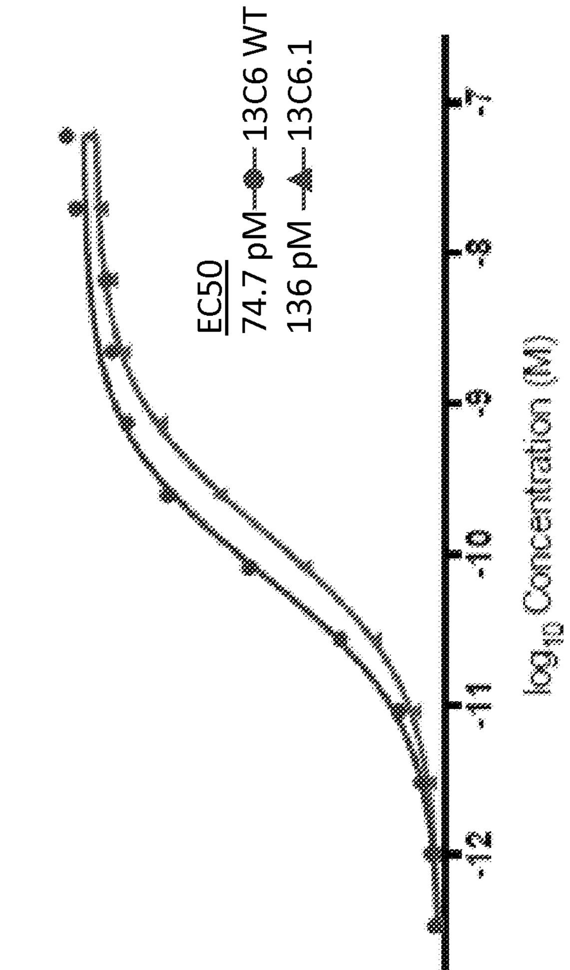
EC50
74.7 pM 13C6 WT
136 pM 13C6.1
Absorbance
2.0
1.5
1.0
0.5
0.0
-13
-12
-11
-10
-9
-8
-7
log10 Concentration (M)

Figure 4

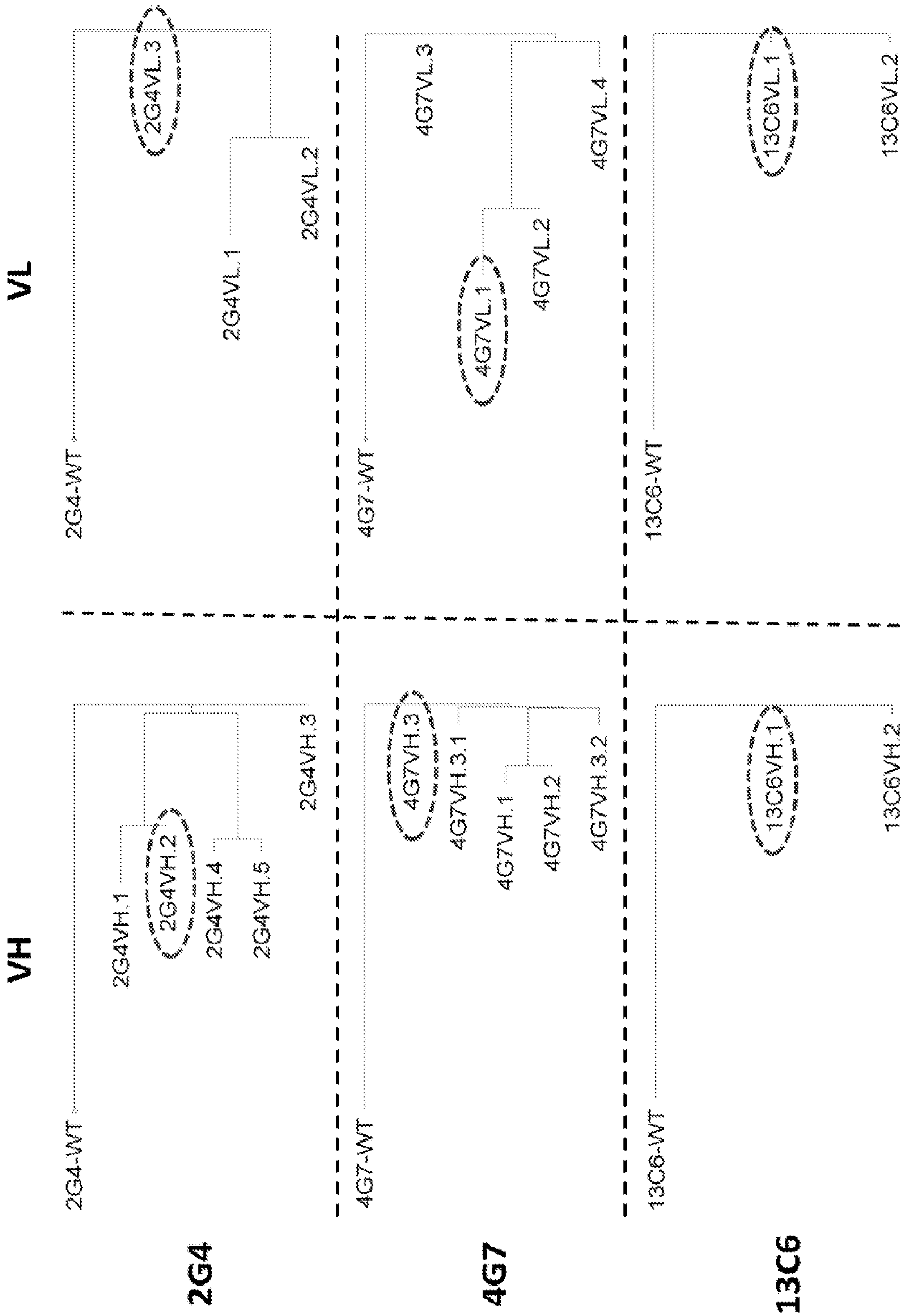
VL
VH
2G4
4G7
13C6
2G4-WT
2G4VL.1
2G4VL.2
2G4VL.3
4G7-WT
4G7VL.1
4G7VL.2
4G7VL.3
4G7VL.4
13C6-WT
13C6VL.1
13C6VL.2
2G4VH.1
2G4VH.2
2G4VH.3
2G4VH.4
2G4VH.5
4G7VH.1
4G7VH.2
4G7VH.3
4G7VH.3.1
4G7VH.3.2
13C6VH.1
13C6VH.2

Figure 5

Antibody	Neutralising titre (PRNT80)		
	Mayinga 1976 strain	Kikwit 1995 strain	Makona 2014 strain
13C6.1	>50 µg/mL	>50 µg/mL	>50 µg/mL
2G4.6	2 µg/mL	4 µg/mL	2 µg/mL
4G7.9	1 µg/mL	1 µg/mL	1 µg/mL