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(54) Titre : ANTICORPS THERAPEUTIQUES QUI SE LIENT A OPRF ET OPRL

(54) Title: ANTIBODY THERAPEUTICS THAT BIND OPRF AND OPRL

(57) **Abrégé/Abstract:**

There is disclosed compositions and methods relating to or derived from anti-OprF and anti-OprI antibodies. More specifically, there is disclosed fully human antibodies that bind OprF and OprI, OprF and OprI-antibody binding fragments and derivatives of such antibodies, and OprF and OprI-binding polypeptides comprising such fragments. Further still, there is disclosed nucleic acids encoding such antibodies, antibody fragments and derivatives and polypeptides, cells comprising such polynucleotides, methods of making such antibodies, antibody fragments and derivatives and polypeptides, and methods of using such antibodies, antibody fragments and derivatives and polypeptides, including methods of treating or diagnosing subjects having *Pseudomonas aeruginosa* infections. There is disclosed a method for treating or preventing *Pseudomonas aeruginosa* infections, wherein the disease is selected from the group consisting of burns, surgical site infections, diabetic foot ulcers, infected wounds, and cystic fibrosis.



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(54) Title: ANTIBODY THERAPEUTICS THAT BIND OPRF AND OPR1

(57) Abstract: There is disclosed compositions and methods relating to or derived from anti-OprF and anti-Opr1 antibodies. More specifically, there is disclosed fully human antibodies that bind OprF and Opr1, OprF and Opr1-antibody binding fragments and derivatives of such antibodies, and OprF and Opr1-binding polypeptides comprising such fragments. Further still, there is disclosed nucleic acids encoding such antibodies, antibody fragments and derivatives and polypeptides, cells comprising such polynucleotides, methods of making such antibodies, antibody fragments and derivatives and polypeptides, and methods of using such antibodies, antibody fragments and derivatives and polypeptides, including methods of treating or diagnosing subjects having *Pseudomonas aeruginosa* infections. There is disclosed a method for treating or preventing *Pseudomonas aeruginosa* infections, wherein the disease is selected from the group consisting of burns, surgical site infections, diabetic foot ulcers, infected wounds, and cystic fibrosis.



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Antibody Therapeutics That Bind OprF and OprI

Technical Field

The present disclosure provides compositions and methods relating to or derived from anti-OprF and anti-OprI antibodies. More specifically, the present disclosure provides fully human antibodies that bind OprF and OprI, OprF and OprI-antibody binding fragments and derivatives of such antibodies, and OprF and OprI-binding polypeptides comprising such fragments. Further still, the present disclosure provides nucleic acids encoding such antibodies, antibody fragments and derivatives and polypeptides, cells comprising such polynucleotides, methods of making such antibodies, antibody fragments and derivatives and polypeptides, and methods of using such antibodies, antibody fragments and derivatives and polypeptides, including methods of treating or preventing spread of subjects having *Pseudomonas aeruginosa* infections. The present disclosure further provides a method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections, wherein the disease is selected from the group consisting of burns, surgical site infections, diabetic foot ulcers, infected wounds, and cystic fibrosis.

Background

Pseudomonas aeruginosa is a common environmental microorganism that has acquired the ability to take advantage of weaknesses in the host defenses to become an opportunistic pathogen in humans. It is the most common Gram-negative cause of hospital-acquired infections. In general, *P. aeruginosa* infections are especially troublesome due to the fact that this bacterium continues to acquire resistance to commonly-used antibiotics. *P. aeruginosa* is a part of the drug-resistant ESKAPE microbe group, which considered one of the biggest threats infectious diseases today. Notably, it is intrinsically resistant to a number of antibiotics due to its multidrug efflux pump systems, and a bacterial envelop that has low permeability. These attributes, plus a predilection towards hypermutation and efficient horizontal gene transfers of antibiotic resistance genes give rise to infections that become refractory to antibiotic therapy.

***Pseudomonas aeruginosa* infections.** *P. aeruginosa* is the most common Gram-negative pathogen isolated from chronic wound infections. Infections of the dermis, including burns, surgical-site infections and non-healing diabetic foot ulcers affect over a million people, cause thousands of amputations and deaths and cost billions of dollars in direct medical costs in the United States annually. The microbial populations of these infections are biofilm-associated and display increased tolerance to antimicrobials.

In burn wound infections, *P. aeruginosa* is the most common Gram-negative isolated and is associated with very high mortality. The American Burn Association estimates that approximately 500,000 individuals in the United States are treated for thermal injury each year, resulting in over 4,000 deaths. Worldwide, the numbers are significantly larger, especially in areas of conflict. As thermal injury removes or impairs the body's natural barrier to microbes, the cause of death in over 75% of these burned individuals is infection. While not as dramatic, secondary sepsis, originating from infected wounds, affects trauma patients and those with surgical-site infections. Approximately 10% of burn patients become infected with *P. aeruginosa* and of those, up to 75% die of septicemia. Sepsis is the most common cause of death among ICU patients, and ranks 10th among all patients.

Most prominent is the role of *P. aeruginosa* in patients suffering from cystic fibrosis (CF). CF is the most common lethal inherited genetic disorder that follows an autosomal recessive inheritance pattern in Caucasian people. Approximately 30,000 people in the United States suffer from CF. Due to impaired lung defense functions, CF patients are vulnerable targets for *P. aeruginosa*. As a result, infections with *P. aeruginosa*, and the damage caused by the inflammatory infection process leads to death in more than 90% of CF patients.

OprF and OprI. Both proteins are *P. aeruginosa* outer membrane proteins that are surface exposed and antigenically conserved in various strains of *P. aeruginosa*. Antibodies against OprF are associated with protection in animal models and are present following immunization in humans. It has also been reported that OprF function is required for full *P. aeruginosa* virulence as it is a modulator of quorum sensing. The binding of OprF to interferon- γ (IFN- γ) has been shown to up-regulate another adhesin, LecA, through quorum sensing. Activation of IFN- γ also increased expression of pyocyanin, which is another quorum-sensing-related virulence product. Activation of LecA and pyocyanin leads to the disruption of epithelial cell function. OprF is essential for microaerobic growth of *P. aeruginosa*, and expression is also imperative for the formation of anaerobic biofilms. OprF mutants are unable to adhere to animal cells and lack the ability to secrete ExoT and ExoS toxins via the type III secretion system. An OprF mutant was deficient in the production of signal molecules *N*-(3-oxododecanoyl)-L-homoserine lactone and *N*-butanoyl-L-homoserine lactone, both of which regulate the timing and production of pyocyanin, elastase, lectin PA-1L and exotoxin A. There, there is a need in the art for effective anti-infective agents.

Summary

The present disclosure provides a fully human antibody of an IgG class that binds to a OprF and OprI epitope with a binding affinity of at least 10^{-6} M, which has a heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof. Preferably, the fully human antibody has both a heavy chain and a light chain wherein the antibody has a heavy chain/light chain variable domain

sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2 (called OFA1 herein), SEQ ID NO. 3/SEQ ID NO. 4 (called OFC7 herein), SEQ ID NO. 5/SEQ ID NO. 6 (called OFC10 herein), SEQ ID NO. 7/SEQ ID NO. 8 (called OFF7 herein), SEQ ID NO. 9/SEQ ID NO. 10 (called OFF8 herein), SEQ ID NO. 11/SEQ ID NO. 12 (called OFG5 herein), SEQ ID NO. 13/SEQ ID NO. 14 (called OFH10 herein), SEQ ID NO. 15/SEQ ID NO. 16 (called OIA1 herein), SEQ ID NO. 17/SEQ ID NO. 18 (called OIA10 herein), SEQ ID NO. 19/SEQ ID NO. 20 (called OIA2 herein), SEQ ID NO. 21/SEQ ID NO. 22 (called OIA4 herein), SEQ ID NO. 23/SEQ ID NO. 24 (called OIA5 herein), SEQ ID NO. 25/SEQ ID NO. 26 (called OIA6 herein), SEQ ID NO. 27/SEQ ID NO. 28 (called OIA7 herein), SEQ ID NO. 29/SEQ ID NO. 30 (called OIA8 herein), SEQ ID NO. 31/SEQ ID NO. 32 (called OIA9 herein), SEQ ID NO. 33/SEQ ID NO. 34 (called OIB1 herein), SEQ ID NO. 35/SEQ ID NO. 36 (called OIB11 herein), SEQ ID NO. 37/SEQ ID NO. 38 (called OIB12 herein), SEQ ID NO. 39/SEQ ID NO. 40 (called OIB2 herein), SEQ ID NO. 41/SEQ ID NO. 42 (called OIB3 herein), SEQ ID NO. 43/SEQ ID NO. 44 (called OIB8 herein), SEQ ID NO. 45/SEQ ID NO. 46 (called OIB9 herein), SEQ ID NO. 47/SEQ ID NO. 48 (called OIC1 herein), SEQ ID NO. 49/SEQ ID NO. 50 (called OIC3 herein), SEQ ID NO. 51/SEQ ID NO. 52 (called OIC6 herein), SEQ ID NO. 53/SEQ ID NO. 54 (called OIC9 herein), SEQ ID NO. 55/SEQ ID NO. 56 (called OID1 herein), SEQ ID NO. 57/SEQ ID NO. 58 (called OID10 herein), SEQ ID NO. 59/SEQ ID NO. 60 (called OID12 herein), SEQ ID NO. 61/SEQ ID NO. 62 (called OID3 herein), SEQ ID NO. 63/SEQ ID NO. 64 (called OID3 herein), SEQ ID NO. 65/SEQ ID NO. 66 (called OID5 herein), SEQ ID NO. 67/SEQ ID NO. 68 (called OID6 herein), SEQ ID NO. 69/SEQ ID NO. 70 (called OID8 herein), SEQ ID NO. 71/SEQ ID NO. 72 (called OIE12 herein), SEQ ID NO. 73/SEQ ID NO. 74 (called OIE3 herein), SEQ ID NO. 75/SEQ ID NO. 76 (called OIE9 herein), SEQ ID NO. 77/SEQ ID NO. 78 (called OIF10 herein), SEQ ID NO. 79/SEQ ID NO. 80 (called OIF4 herein), SEQ ID NO. 81/SEQ ID NO. 82 (called OIF6 herein), SEQ ID NO. 83/SEQ ID NO. 84 (called OIF9 herein), SEQ ID NO. 85/SEQ ID NO. 86 (called OIG1 herein), SEQ ID NO. 87/SEQ ID NO. 88 (called OIG11 herein), SEQ ID NO. 89/SEQ ID NO. 90 (called OIG12 herein), SEQ ID NO. 91/SEQ ID NO. 92 (called OIG2 herein), SEQ ID NO. 93/SEQ ID NO. 94 (called OIG5 herein), SEQ ID NO. 95/SEQ ID NO. 96 (called OIG7 herein), SEQ ID NO. 97/SEQ ID NO. 98 (called OIG8 herein), SEQ ID NO. 99/SEQ ID NO. 100 (called OIG9 herein), SEQ ID NO. 101/SEQ ID NO. 102 (called OIH10 herein), SEQ ID NO. 103/SEQ ID NO. 104 (called OIH11 herein), SEQ ID NO. 105/SEQ ID NO. 106 (called OIH12 herein), SEQ ID NO. 107/SEQ ID NO. 108 (called OIH3 herein), SEQ ID NO. 109/SEQ ID NO. 110 (called OIH5 herein), SEQ ID

NO. 111/SEQ ID NO. 112 (called OIH6 herein), SEQ ID NO. 113/SEQ ID NO. 114 (called FEA2 herein), SEQ ID NO. 115/SEQ ID NO. 116 (called FEA3 herein), SEQ ID NO. 117/SEQ ID NO. 118 (called FEA4 herein), SEQ ID NO. 119/SEQ ID NO. 120 (called FEA7 herein), SEQ ID NO. 121/SEQ ID NO. 122 (called FEA12 herein), SEQ ID NO. 123/SEQ ID NO. 124 (called FEC2 herein), SEQ ID NO. 125/SEQ ID NO. 126 (called FEC4 herein), SEQ ID NO. 127/SEQ ID NO. 128 (called FEC10 herein), SEQ ID NO. 129/SEQ ID NO. 130 (called FED2 herein), SEQ ID NO. 131/SEQ ID NO. 132 (called FED5 herein), SEQ ID NO. 133/SEQ ID NO. 134 (called FED8 herein), SEQ ID NO. 135/SEQ ID NO. 136 (called FEE10 herein), SEQ ID NO. 137/SEQ ID NO. 138 (called FEF8 herein), SEQ ID NO. 139/SEQ ID NO. 140 (called FEH2 herein), SEQ ID NO. 141/SEQ ID NO. 142 (called FEH7 herein), and combinations thereof.

The present disclosure provides a Fab fully human antibody fragment, having a variable domain region from a heavy chain and a variable domain region from a light chain, wherein the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ

ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof. Preferably, the fully human antibody Fab fragment has both a heavy chain variable domain region and a light chain variable domain region wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO.

117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

The present disclosure provides a single chain human antibody, having a variable domain region from a heavy chain and a variable domain region from a light chain and a peptide linker connection the heavy chain and light chain variable domain regions, wherein the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ

ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof. Preferably, the fully human single chain antibody has both a heavy chain variable domain region and a light chain variable domain region, wherein the single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO.

137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

The present disclosure further provides a method for treating or preventing spread of infection for subjects having *Pseudomonas aeruginosa* infections. comprising administering

5 an anti-OprF and anti-OprI polypeptide, wherein the fully human antibody has a heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO.

10 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ

15 ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131,

20 SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO.

25 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ

30 ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132,

SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof;

wherein the Fab fully human antibody fragment has the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has the light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof; and

wherein the single chain human antibody has the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has the light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof.

Preferably, the fully human antibody has both a heavy chain and a light chain wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group

consisting of SEQ ID NO. 1/SEQ ID NO. 2 (called OFA1 herein), SEQ ID NO. 3/SEQ ID NO. 4 (called OFC7 herein), SEQ ID NO. 5/SEQ ID NO. 6 (called OFC10 herein), SEQ ID NO. 7/SEQ ID NO. 8 (called OFF7 herein), SEQ ID NO. 9/SEQ ID NO. 10 (called OFF8 herein), SEQ ID NO. 11/SEQ ID NO. 12 (called OFG5 herein), SEQ ID NO. 13/SEQ ID NO. 14 (called OFH10 herein), SEQ ID NO. 15/SEQ ID NO. 16 (called OIA1 herein), SEQ ID NO. 17/SEQ ID NO. 18 (called OIA10 herein), SEQ ID NO. 19/SEQ ID NO. 20 (called OIA2 herein), SEQ ID NO. 21/SEQ ID NO. 22 (called OIA4 herein), SEQ ID NO. 23/SEQ ID NO. 24 (called OIA5 herein), SEQ ID NO. 25/SEQ ID NO. 26 (called OIA6 herein), SEQ ID NO. 27/SEQ ID NO. 28 (called OIA7 herein), SEQ ID NO. 29/SEQ ID NO. 30 (called OIA8 herein), SEQ ID NO. 31/SEQ ID NO. 32 (called OIA9 herein), SEQ ID NO. 33/SEQ ID NO. 34 (called OIB1 herein), SEQ ID NO. 35/SEQ ID NO. 36 (called OIB11 herein), SEQ ID NO. 37/SEQ ID NO. 38 (called OIB12 herein), SEQ ID NO. 39/SEQ ID NO. 40 (called OIB2 herein), SEQ ID NO. 41/SEQ ID NO. 42 (called OIB3 herein), SEQ ID NO. 43/SEQ ID NO. 44 (called OIB8 herein), SEQ ID NO. 45/SEQ ID NO. 46 (called OIB9 herein), SEQ ID NO. 47/SEQ ID NO. 48 (called OIC1 herein), SEQ ID NO. 49/SEQ ID NO. 50 (called OIC3 herein), SEQ ID NO. 51/SEQ ID NO. 52 (called OIC6 herein), SEQ ID NO. 53/SEQ ID NO. 54 (called OIC9 herein), SEQ ID NO. 55/SEQ ID NO. 56 (called OID1 herein), SEQ ID NO. 57/SEQ ID NO. 58 (called OID10 herein), SEQ ID NO. 59/SEQ ID NO. 60 (called OID12 herein), SEQ ID NO. 61/SEQ ID NO. 62 (called OID3 herein), SEQ ID NO. 63/SEQ ID NO. 64 (called OID3 herein), SEQ ID NO. 65/SEQ ID NO. 66 (called OID5 herein), SEQ ID NO. 67/SEQ ID NO. 68 (called OID6 herein), SEQ ID NO. 69/SEQ ID NO. 70 (called OID8 herein), SEQ ID NO. 71/SEQ ID NO. 72 (called OIE12 herein), SEQ ID NO. 73/SEQ ID NO. 74 (called OIE3 herein), SEQ ID NO. 75/SEQ ID NO. 76 (called OIE9 herein), SEQ ID NO. 77/SEQ ID NO. 78 (called OIF10 herein), SEQ ID NO. 79/SEQ ID NO. 80 (called OIF4 herein), SEQ ID NO. 81/SEQ ID NO. 82 (called OIF6 herein), SEQ ID NO. 83/SEQ ID NO. 84 (called OIF9 herein), SEQ ID NO. 85/SEQ ID NO. 86 (called OIG1 herein), SEQ ID NO. 87/SEQ ID NO. 88 (called OIG11 herein), SEQ ID NO. 89/SEQ ID NO. 90 (called OIG12 herein), SEQ ID NO. 91/SEQ ID NO. 92 (called OIG2 herein), SEQ ID NO. 93/SEQ ID NO. 94 (called OIG5 herein), SEQ ID NO. 95/SEQ ID NO. 96 (called OIG7 herein), SEQ ID NO. 97/SEQ ID NO. 98 (called OIG8 herein), SEQ ID NO. 99/SEQ ID NO. 100 (called OIG9 herein), SEQ ID NO. 101/SEQ ID NO. 102 (called OIH10 herein), SEQ ID NO. 103/SEQ ID NO. 104 (called OIH11 herein), SEQ ID NO. 105/SEQ ID NO. 106 (called OIH12 herein), SEQ ID NO. 107/SEQ ID NO. 108 (called OIH3 herein), SEQ ID NO. 109/SEQ ID NO. 110 (called OIH5 herein), SEQ ID NO.

111/SEQ ID NO. 112 (called OIH6 herein), SEQ ID NO. 113/SEQ ID NO. 114 (called FEA2 herein), SEQ ID NO. 115/SEQ ID NO. 116 (called FEA3 herein), SEQ ID NO. 117/SEQ ID NO. 118 (called FEA4 herein), SEQ ID NO. 119/SEQ ID NO. 120 (called FEA7 herein), SEQ ID NO. 121/SEQ ID NO. 122 (called FEA12 herein), SEQ ID NO. 123/SEQ ID NO. 124 (called FEC2 herein), SEQ ID NO. 125/SEQ ID NO. 126 (called FEC4 herein), SEQ ID NO. 127/SEQ ID NO. 128 (called FEC10 herein), SEQ ID NO. 129/SEQ ID NO. 130 (called FED2 herein), SEQ ID NO. 131/SEQ ID NO. 132 (called FED5 herein), SEQ ID NO. 133/SEQ ID NO. 134 (called FED8 herein), SEQ ID NO. 135/SEQ ID NO. 136 (called FEE10 herein), SEQ ID NO. 137/SEQ ID NO. 138 (called FEF8 herein), SEQ ID NO. 139/SEQ ID NO. 140 (called FEH2 herein), SEQ ID NO. 141/SEQ ID NO. 142 (called FEH7 herein), and combinations thereof. Preferably, the fully human single chain antibody has both a heavy chain variable domain region and a light chain variable domain region, wherein the single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID

NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

Preferably, the method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections, wherein the disease is selected from the group consisting of burns, surgical site infections, diabetic foot ulcers, infected wounds, and cystic fibrosis.

Description of the Drawings

Figures 1-4 show a bar graph of various listed antibodies binding to their respective antigen Oprf or OprI based on a standard ELISA assay to measure antibody-target binding. Figure 1 shows OprI antibodies. Figure 2 shows OprF single chain antibodies. Figure 3 shows OprF fully human IgG antibodies and Figure 4 shows OprF epitope 8 single chain antibodies.

Figure 5 shows a whole cell *Pseudomonas* ELISA to characterize binding specificity of anti-OprF antibodies. The blue bar should be larger than the green signal to indicate preferential binding to wild type *Pseudomonas* (OprF-positive cells).

Figure 6 shows a Western blot analysis of anti-OprI antibody oprIA5. This blot shows that the mAb reacts with cell lysates from wildtype *P. aeruginosa* as well as OprF mutant cells but not with OprI-deficient cell lysate.

Figure 7 shows a western blot analysis of anti-OprI antibody STI-oprFF7. This blot shows that the mAb reacts with cell lysates from wild type *P. aeruginosa* as well as OprI mutant cells but not with OprF-deficient cell lysate.

Figure 8A shows attachment prevention assay's normalized to IgG1 treatment.

Figure 8B shows biofilm disruption assays, normalized to IgG1 treatment.

Detailed Description

The present disclosure provides a fully human antibody of an IgG class that binds to a OprF and OprI epitope with a binding affinity of 10^{-6} M or less, that has a heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO.

27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof. Preferably, the fully human antibody has both a heavy chain and a light chain wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2 (called OFA1 herein), SEQ ID NO. 3/SEQ ID NO. 4 (called OFC7 herein), SEQ ID NO. 5/SEQ ID NO. 6 (called OFC10 herein), SEQ ID NO. 7/SEQ ID NO. 8 (called OFF7 herein), SEQ ID NO. 9/SEQ ID NO. 10 (called OFF8 herein), SEQ ID NO. 11/SEQ ID NO. 12 (called OFG5 herein), SEQ ID NO. 13/SEQ ID NO. 14 (called OFH10 herein), SEQ ID NO. 15/SEQ ID NO. 16 (called OIA1 herein), SEQ ID NO. 17/SEQ ID NO. 18 (called OIA10 herein), SEQ

ID NO. 19/SEQ ID NO. 20 (called OIA2 herein), SEQ ID NO. 21/SEQ ID NO. 22 (called
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 ID NO. 29/SEQ ID NO. 30 (called OIA8 herein), SEQ ID NO. 31/SEQ ID NO. 32 (called
 5 OIA9 herein), SEQ ID NO. 33/SEQ ID NO. 34 (called OIB1 herein), SEQ ID NO. 35/SEQ
 ID NO. 36 (called OIB11 herein), SEQ ID NO. 37/SEQ ID NO. 38 (called OIB12 herein),
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 (called OIB3 herein), SEQ ID NO. 43/SEQ ID NO. 44 (called OIB8 herein), SEQ ID NO.
 45/SEQ ID NO. 46 (called OIB9 herein), SEQ ID NO. 47/SEQ ID NO. 48 (called OIC1
 10 herein), SEQ ID NO. 49/SEQ ID NO. 50 (called OIC3 herein), SEQ ID NO. 51/SEQ ID NO.
 52 (called OIC6 herein), SEQ ID NO. 53/SEQ ID NO. 54 (called OIC9 herein), SEQ ID NO.
 55/SEQ ID NO. 56 (called OID1 herein), SEQ ID NO. 57/SEQ ID NO. 58 (called OID10
 herein), SEQ ID NO. 59/SEQ ID NO. 60 (called OID12 herein), SEQ ID NO. 61/SEQ ID
 NO. 62 (called OID3 herein), SEQ ID NO. 63/SEQ ID NO. 64 (called OID3 herein), SEQ ID
 15 NO. 65/SEQ ID NO. 66 (called OID5 herein), SEQ ID NO. 67/SEQ ID NO. 68 (called OID6
 herein), SEQ ID NO. 69/SEQ ID NO. 70 (called OID8 herein), SEQ ID NO. 71/SEQ ID NO.
 72 (called OIE12 herein), SEQ ID NO. 73/SEQ ID NO. 74 (called OIE3 herein), SEQ ID
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 20 82 (called OIF6 herein), SEQ ID NO. 83/SEQ ID NO. 84 (called OIF9 herein), SEQ ID NO.
 85/SEQ ID NO. 86 (called OIG1 herein), SEQ ID NO. 87/SEQ ID NO. 88 (called OIG11
 herein), SEQ ID NO. 89/SEQ ID NO. 90 (called OIG12 herein), SEQ ID NO. 91/SEQ ID
 NO. 92 (called OIG2 herein), SEQ ID NO. 93/SEQ ID NO. 94 (called OIG5 herein), SEQ ID
 NO. 95/SEQ ID NO. 96 (called OIG7 herein), SEQ ID NO. 97/SEQ ID NO. 98 (called OIG8
 25 herein), SEQ ID NO. 99/SEQ ID NO. 100 (called OIG9 herein), SEQ ID NO. 101/SEQ ID
 NO. 102 (called OIH10 herein), SEQ ID NO. 103/SEQ ID NO. 104 (called OIH11 herein),
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 108 (called OIH3 herein), SEQ ID NO. 109/SEQ ID NO. 110 (called OIH5 herein), SEQ ID
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 30 FEA2 herein), SEQ ID NO. 115/SEQ ID NO. 116 (called FEA3 herein), SEQ ID NO.
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130 (called FED2 herein), SEQ ID NO. 131/SEQ ID NO. 132 (called FED5 herein), SEQ ID NO. 133/SEQ ID NO. 134 (called FED8 herein), SEQ ID NO. 135/SEQ ID NO. 136 (called FEE10 herein), SEQ ID NO. 137/SEQ ID NO. 138 (called FEF8 herein), SEQ ID NO.

139/SEQ ID NO. 140 (called FEH2 herein), SEQ ID NO. 141/SEQ ID NO. 142 (called FEH7 herein), and combinations thereof.

The present disclosure provides a Fab fully human antibody fragment, having a variable domain region from a heavy chain and a variable domain region from a light chain, wherein the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108,

SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof. Preferably, the fully human

5 antibody Fab fragment has both a heavy chain variable domain region and a light chain variable domain region wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ

10 ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO.

15 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ

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25 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO.

30 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

The present disclosure provides a single chain human antibody, having a variable domain region from a heavy chain and a variable domain region from a light chain and a peptide linker connection the heavy chain and light chain variable domain regions, wherein the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof. Preferably, the fully human

single chain antibody has both a heavy chain variable domain region and a light chain variable domain region, wherein the single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

The present disclosure further provides a method for treating or preventing various cancers or diseases of the heart, bone/joints or lung, wherein such diseases are selected from the group consisting of hepatocellular carcinoma, colon adenocarcinoma, lung carcinoma, breast cancer, myocardial infarction, angina, osteoarthritis, pulmonary fibrosis, asthma, cystic

fibrosis, bronchitis, and asthma, comprising administering an anti-OprF and anti-OprI polypeptide, wherein the anti-OprF and anti-OprI polypeptide is selected from the group consisting of a fully human antibody of an IgG class that binds to a OprF and OprI epitope with a binding affinity of at least 10^{-6} M, a Fab fully human antibody fragment, having a
 5 variable domain region from a heavy chain and a variable domain region from a light chain, a single chain human antibody, having a variable domain region from a heavy chain and a variable domain region from a light chain and a peptide linker connection the heavy chain and light chain variable domain regions, and combinations thereof;

wherein the fully human antibody has a heavy chain variable domain sequence that is
 10 at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41,
 15 SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO.
 20 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has
 25 a light chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38,
 30 SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO.

92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof;

wherein the Fab fully human antibody fragment has the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has the light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID

NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof; and

5 wherein the single chain human antibody has the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has the light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ

ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof.

Preferably, the fully human antibody has both a heavy chain and a light chain wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group

5 consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO.

10 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ

15 ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO.

20 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID

25 NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID

30 NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

Preferably, the fully human antibody Fab fragment has both a heavy chain variable domain region and a light chain variable domain region wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID

NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof. Preferably, the fully human single chain antibody has both a heavy chain variable domain region and a light chain variable domain region, wherein the single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO.

25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

Preferably, the method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections, wherein the disease is selected from the group consisting of burns, surgical site infections, diabetic foot ulcers, infected wounds, and cystic fibrosis.

An "antigen binding protein" is a protein comprising a portion that binds to an antigen and, optionally, a scaffold or framework portion that allows the antigen binding portion to adopt a conformation that promotes binding of the antigen binding protein to the antigen.

Examples of antigen binding proteins include antibodies, antibody fragments (*e.g.*, an antigen binding portion of an antibody), antibody derivatives, and antibody analogs. The antigen binding protein can comprise, for example, an alternative protein scaffold or artificial scaffold with grafted CDRs or CDR derivatives. Such scaffolds include, but are not limited to, antibody-derived scaffolds comprising mutations introduced to, for example, stabilize the

three-dimensional structure of the antigen binding protein as well as wholly synthetic scaffolds comprising, for example, a biocompatible polymer. See, for example, Korndorfer et al., 2003, *Proteins: Structure, Function, and Bioinformatics*, Volume 53, Issue 1:121-129; Roque et al., 2004, *Biotechnol. Prog.* 20:639-654. In addition, peptide antibody mimetics ("PAMs") can be used, as well as scaffolds based on antibody mimetics utilizing fibronectin components as a scaffold.

An antigen binding protein can have, for example, the structure of a naturally occurring immunoglobulin. An "immunoglobulin" is a tetrameric molecule. In a naturally occurring immunoglobulin, each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Human light chains are classified as kappa or lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. See generally, *Fundamental Immunology* Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)) (incorporated by reference in its entirety for all purposes). The variable regions of each light/heavy chain pair form the antibody binding site such that an intact immunoglobulin has two binding sites.

The variable regions of naturally occurring immunoglobulin chains exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, also called complementarity determining regions or CDRs. From N-terminus to C-terminus, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain is in accordance with the definitions of Kabat et al. in *Sequences of Proteins of Immunological Interest*, 5th Ed., US Dept. of Health and Human Services, PHS, NIH, NIH Publication no. 91-3242, 1991. Other numbering systems for the amino acids in immunoglobulin chains include IMGT.RTM. (international ImMunoGeneTics information system; Lefranc et al, *Dev. Comp. Immunol.* 29:185-203; 2005) and AHo (Honegger and Pluckthun, *J. Mol. Biol.* 309(3):657-670; 2001).

Antibodies can be obtained from sources such as serum or plasma that contain immunoglobulins having varied antigenic specificity. If such antibodies are subjected to

affinity purification, they can be enriched for a particular antigenic specificity. Such enriched preparations of antibodies usually are made of less than about 10% antibody having specific binding activity for the particular antigen. Subjecting these preparations to several rounds of affinity purification can increase the proportion of antibody having specific binding activity for the antigen. Antibodies prepared in this manner are often referred to as "monospecific." Monospecific antibody preparations can be made up of about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99%, or 99.9% antibody having specific binding activity for the particular antigen.

An "antibody" refers to an intact immunoglobulin or to an antigen binding portion thereof that competes with the intact antibody for specific binding, unless otherwise specified. Antigen binding portions may be produced by recombinant DNA techniques or by enzymatic or chemical cleavage of intact antibodies. Antigen binding portions include, *inter alia*, Fab, Fab', F(ab')₂, Fv, domain antibodies (dAbs), and complementarity determining region (CDR) fragments, single-chain antibodies (scFv), chimeric antibodies, diabodies, triabodies, tetrabodies, and polypeptides that contain at least a portion of an immunoglobulin that is sufficient to confer specific antigen binding to the polypeptide.

A Fab fragment is a monovalent fragment having the V_L, V_H, C_L and C_{H1} domains; a F(ab')₂ fragment is a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; a Fd fragment has the V_H and C_{H1} domains; an Fv fragment has the V_L and V_H domains of a single arm of an antibody; and a dAb fragment has a V_H domain, a V_L domain, or an antigen-binding fragment of a V_H or V_L domain (U.S. Patents 6,846,634; 6,696,245, US App. Pub.20/0202512; 2004/0202995; 2004/0038291; 2004/0009507; 2003/0039958, and Ward et al., *Nature* 341:544-546, 1989).

A single-chain antibody (scFv) is an antibody in which a V_L and a V_H region are joined via a linker (*e.g.*, a synthetic sequence of amino acid residues) to form a continuous protein chain wherein the linker is long enough to allow the protein chain to fold back on itself and form a monovalent antigen binding site (see, *e.g.*, Bird et al., 1988, *Science* 242:423-26 and Huston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879-83). Diabodies are bivalent antibodies comprising two polypeptide chains, wherein each polypeptide chain comprises V_H and V_L domains joined by a linker that is too short to allow for pairing between two domains on the same chain, thus allowing each domain to pair with a complementary domain on another polypeptide chain (see, *e.g.*, Holliger et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:6444-48, and Poljak et al., 1994, *Structure* 2:1121-23). If the two polypeptide chains of a diabody are identical, then a diabody resulting from their pairing will have two identical

antigen binding sites. Polypeptide chains having different sequences can be used to make a diabody with two different antigen binding sites. Similarly, tribodies and tetrabodies are antibodies comprising three and four polypeptide chains, respectively, and forming three and four antigen binding sites, respectively, which can be the same or different.

5 Complementarity determining regions (CDRs) and framework regions (FR) of a given antibody may be identified using the system described by Kabat et al. *supra*; Lefranc et al., *supra* and/or Honegger and Pluckthun, *supra*. One or more CDRs may be incorporated into a molecule either covalently or noncovalently to make it an antigen binding protein. An antigen binding protein may incorporate the CDR(s) as part of a larger polypeptide chain, may
10 covalently link the CDR(s) to another polypeptide chain, or may incorporate the CDR(s) noncovalently. The CDRs permit the antigen binding protein to specifically bind to a particular antigen of interest.

 An antigen binding protein may have one or more binding sites. If there is more than one binding site, the binding sites may be identical to one another or may be different. For
15 example, a naturally occurring human immunoglobulin typically has two identical binding sites, while a "bispecific" or "bifunctional" antibody has two different binding sites.

 The term "human antibody" includes all antibodies that have one or more variable and constant regions derived from human immunoglobulin sequences. In one embodiment, all of the variable and constant domains are derived from human immunoglobulin sequences (a
20 fully human antibody). These antibodies may be prepared in a variety of ways, examples of which are described below, including through the immunization with an antigen of interest of a mouse that is genetically modified to express antibodies derived from human heavy and/or light chain-encoding genes.

 A humanized antibody has a sequence that differs from the sequence of an antibody
25 derived from a non-human species by one or more amino acid substitutions, deletions, and/or additions, such that the humanized antibody is less likely to induce an immune response, and/or induces a less severe immune response, as compared to the non-human species antibody, when it is administered to a human subject. In one embodiment, certain amino acids in the framework and constant domains of the heavy and/or light chains of the non-
30 human species antibody are mutated to produce the humanized antibody. In another embodiment, the constant domain(s) from a human antibody are fused to the variable domain(s) of a non-human species. In another embodiment, one or more amino acid residues in one or more CDR sequences of a non-human antibody are changed to reduce the likely immunogenicity of the non-human antibody when it is administered to a human subject,

wherein the changed amino acid residues either are not critical for immunospecific binding of the antibody to its antigen, or the changes to the amino acid sequence that are made are conservative changes, such that the binding of the humanized antibody to the antigen is not significantly worse than the binding of the non-human antibody to the antigen. Examples of
5 how to make humanized antibodies may be found in U.S. Patents 6,054,297, 5,886,152 and 5,877,293.

The term "chimeric antibody" refers to an antibody that contains one or more regions from one antibody and one or more regions from one or more other antibodies. In one embodiment, one or more of the CDRs are derived from a human anti-OprF and anti-OprI
10 antibody. In another embodiment, all of the CDRs are derived from a human anti-OprF and anti-OprI antibody. In another embodiment, the CDRs from more than one human anti-OprF and anti-OprI antibodies are mixed and matched in a chimeric antibody. For instance, a chimeric antibody may comprise a CDR1 from the light chain of a first human anti-PAR-2 antibody, a CDR2 and a CDR3 from the light chain of a second human anti-OprF and anti-
15 OprI antibody, and the CDRs from the heavy chain from a third anti-OprF and anti-OprI antibody. Other combinations are possible.

Further, the framework regions may be derived from one of the same anti-OprF and anti-OprI antibodies, from one or more different antibodies, such as a human antibody, or from a humanized antibody. In one example of a chimeric antibody, a portion of the heavy
20 and/or light chain is identical with, homologous to, or derived from an antibody from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with, homologous to, or derived from an antibody (-ies) from another species or belonging to another antibody class or subclass. Also included are fragments of such antibodies that exhibit the desired biological activity (*i.e.*, the ability to
25 specifically bind OprF and OprI).

A "neutralizing antibody" or an "inhibitory antibody" is an antibody that inhibits the proteolytic activation of OprF and OprI when an excess of the anti-OprF and anti-OprI antibody reduces the amount of activation by at least about 20% using an assay such as those described herein in the Examples. In various embodiments, the antigen binding protein
30 reduces the amount of amount of proteolytic activation of OprF and OprI by at least 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 99%, and 99.9%.

Fragments or analogs of antibodies can be readily prepared by those of ordinary skill in the art following the teachings of this specification and using techniques known in the art. Preferred amino- and carboxy-termini of fragments or analogs occur near boundaries of

functional domains. Structural and functional domains can be identified by comparison of the nucleotide and/or amino acid sequence data to public or proprietary sequence databases.

Computerized comparison methods can be used to identify sequence motifs or predicted protein conformation domains that occur in other proteins of known structure and/or function.

5 Methods to identify protein sequences that fold into a known three-dimensional structure are known. See, Bowie et al., 1991, *Science* 253:164.

A "CDR grafted antibody" is an antibody comprising one or more CDRs derived from an antibody of a particular species or isotype and the framework of another antibody of the same or different species or isotype.

10 A "multi-specific antibody" is an antibody that recognizes more than one epitope on one or more antigens. A subclass of this type of antibody is a "bi-specific antibody" which recognizes two distinct epitopes on the same or different antigens.

An antigen binding protein "specifically binds" to an antigen (*e.g.*, human OprF and OprI) if it binds to the antigen with a dissociation constant of 1 nanomolar or less.

15 An "antigen binding domain," "antigen binding region," or "antigen binding site" is a portion of an antigen binding protein that contains amino acid residues (or other moieties) that interact with an antigen and contribute to the antigen binding protein's specificity and affinity for the antigen. For an antibody that specifically binds to its antigen, this will include at least part of at least one of its CDR domains.

20 An "epitope" is the portion of a molecule that is bound by an antigen binding protein (*e.g.*, by an antibody). An epitope can comprise non-contiguous portions of the molecule (*e.g.*, in a polypeptide, amino acid residues that are not contiguous in the polypeptide's primary sequence but that, in the context of the polypeptide's tertiary and quaternary structure, are near enough to each other to be bound by an antigen binding protein).

25 The "percent identity" of two polynucleotide or two polypeptide sequences is determined by comparing the sequences using the GAP computer program (a part of the GCG Wisconsin Package, version 10.3 (Accelrys, San Diego, Calif.)) using its default parameters.

The terms "polynucleotide," "oligonucleotide" and "nucleic acid" are used interchangeably throughout and include DNA molecules (*e.g.*, cDNA or genomic DNA),
30 RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs (*e.g.*, peptide nucleic acids and non-naturally occurring nucleotide analogs), and hybrids thereof. The nucleic acid molecule can be single-stranded or double-stranded. In one embodiment, the nucleic acid molecules of the invention comprise a contiguous open reading frame encoding an antibody, or a fragment, derivative, mutein, or variant thereof.

Two single-stranded polynucleotides are "the complement" of each other if their sequences can be aligned in an anti-parallel orientation such that every nucleotide in one polynucleotide is opposite its complementary nucleotide in the other polynucleotide, without the introduction of gaps, and without unpaired nucleotides at the 5' or the 3' end of either
5 sequence. A polynucleotide is "complementary" to another polynucleotide if the two polynucleotides can hybridize to one another under moderately stringent conditions. Thus, a polynucleotide can be complementary to another polynucleotide without being its complement.

A "vector" is a nucleic acid that can be used to introduce another nucleic acid linked
10 to it into a cell. One type of vector is a "plasmid," which refers to a linear or circular double stranded DNA molecule into which additional nucleic acid segments can be ligated. Another type of vector is a viral vector (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), wherein additional DNA segments can be introduced into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they
15 are introduced (*e.g.*, bacterial vectors comprising a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. An "expression vector" is a type of vector that can direct the expression of a chosen polynucleotide.

A nucleotide sequence is "operably linked" to a regulatory sequence if the regulatory
20 sequence affects the expression (*e.g.*, the level, timing, or location of expression) of the nucleotide sequence. A "regulatory sequence" is a nucleic acid that affects the expression (*e.g.*, the level, timing, or location of expression) of a nucleic acid to which it is operably linked. The regulatory sequence can, for example, exert its effects directly on the regulated
25 nucleic acid, or through the action of one or more other molecules (*e.g.*, polypeptides that bind to the regulatory sequence and/or the nucleic acid). Examples of regulatory sequences include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Further examples of regulatory sequences are described in, for example, Goeddel, 1990, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San
30 Diego, Calif. and Baron et al., 1995, *Nucleic Acids Res.* 23:3605-06.

A "host cell" is a cell that can be used to express a nucleic acid, *e.g.*, a nucleic acid of the invention. A host cell can be a prokaryote, for example, *E. coli*, or it can be a eukaryote, for example, a single-celled eukaryote (*e.g.*, a yeast or other fungus), a plant cell (*e.g.*, a tobacco or tomato plant cell), an animal cell (*e.g.*, a human cell, a monkey cell, a hamster

cell, a rat cell, a mouse cell, or an insect cell) or a hybridoma. Examples of host cells include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (see Gluzman et al., 1981, *Cell* 23:175), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media (see Rasmussen et al., 1998, *Cytotechnology* 28:31) or CHO strain DX-B11, which is deficient in DHFR (see Urlaub et al., 1980, *Proc. Natl. Acad. Sci. USA* 77:4216-20), HeLa cells, BHK (ATCC CRL 10) cell lines, the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) (see McMahan et al., 1991, *EMBO J.* 10:2821), human embryonic kidney cells such as 293,293 EBNA or MSR 293, human epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Typically, a host cell is a cultured cell that can be transformed or transfected with a polypeptide-encoding nucleic acid, which can then be expressed in the host cell. The phrase "recombinant host cell" can be used to denote a host cell that has been transformed or transfected with a nucleic acid to be expressed. A host cell also can be a cell that comprises the nucleic acid but does not express it at a desired level unless a regulatory sequence is introduced into the host cell such that it becomes operably linked with the nucleic acid. It is understood that the term host cell refers not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to, *e.g.*, mutation or environmental influence, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

Polypeptides of the present disclosure can be produced using any standard methods known in the art. In one example, the polypeptides are produced by recombinant DNA methods by inserting a nucleic acid sequence (*e.g.*, a cDNA) encoding the polypeptide into a recombinant expression vector and expressing the DNA sequence under conditions promoting expression.

Nucleic acids encoding any of the various polypeptides disclosed herein may be synthesized chemically. Codon usage may be selected so as to improve expression in a cell. Such codon usage will depend on the cell type selected. Specialized codon usage patterns have been developed for *E. coli* and other bacteria, as well as mammalian cells, plant cells, yeast cells and insect cells. See for example: Mayfield et al., *Proc. Natl. Acad. Sci. USA*. 2003 100(2):438-42; Sinclair et al. *Protein Expr. Purif.* 2002 (1):96-105; Connell N D. *Curr.*

Opin. Biotechnol. 2001 12(5):446-9; Makrides et al. *Microbiol. Rev.* 1996 60(3):512-38; and Sharp et al. *Yeast.* 1991 7(7):657-78.

General techniques for nucleic acid manipulation are described for example in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Vols. 1-3, Cold Spring Harbor Laboratory Press, 2 ed., 1989, or F. Ausubel et al., *Current Protocols in Molecular Biology* (Green Publishing and Wiley-Interscience: New York, 1987) and periodic updates, herein incorporated by reference. The DNA encoding the polypeptide is operably linked to suitable transcriptional or translational regulatory elements derived from mammalian, viral, or insect genes. Such regulatory elements include a transcriptional promoter, an optional operator sequence to control transcription, a sequence encoding suitable mRNA ribosomal binding sites, and sequences that control the termination of transcription and translation. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants is additionally incorporated.

The recombinant DNA can also include any type of protein tag sequence that may be useful for purifying the protein. Examples of protein tags include but are not limited to a histidine tag, a FLAG tag, a myc tag, an HA tag, or a GST tag. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts can be found in *Cloning Vectors: A Laboratory Manual*, (Elsevier, N.Y., 1985).

The expression construct is introduced into the host cell using a method appropriate to the host cell. A variety of methods for introducing nucleic acids into host cells are known in the art, including, but not limited to, electroporation; transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is an infectious agent). Suitable host cells include prokaryotes, yeast, mammalian cells, or bacterial cells.

Suitable bacteria include gram negative or gram positive organisms, for example, *E. coli* or *Bacillus spp.* Yeast, preferably from the *Saccharomyces* species, such as *S. cerevisiae*, may also be used for production of polypeptides. Various mammalian or insect cell culture systems can also be employed to express recombinant proteins. *Baculovirus* systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, (Bio/Technology, 6:47, 1988). Examples of suitable mammalian host cell lines include endothelial cells, COS-7 monkey kidney cells, CV-1, L cells, C127, 3T3, Chinese hamster ovary (CHO), human embryonic kidney cells, HeLa, 293, 293T, and BHK cell lines. Purified polypeptides are prepared by culturing suitable host/vector systems to express the recombinant proteins. For many applications, the small size of many of the polypeptides

disclosed herein would make expression in *E. coli* as the preferred method for expression.

The protein is then purified from culture media or cell extracts.

Proteins disclosed herein can also be produced using cell-translation systems. For such purposes the nucleic acids encoding the polypeptide must be modified to allow in vitro

5 transcription to produce mRNA and to allow cell-free translation of the mRNA in the particular cell-free system being utilized (eukaryotic such as a mammalian or yeast cell-free translation system or prokaryotic such as a bacterial cell-free translation system).

OprF and OprI-binding polypeptides can also be produced by chemical synthesis (*e.g.*, by the methods described in Solid Phase Peptide Synthesis, 2nd ed., 1984, The Pierce Chemical Co.,
10 Rockford, Ill.). Modifications to the protein can also be produced by chemical synthesis.

The polypeptides of the present disclosure can be purified by isolation/purification methods for proteins generally known in the field of protein chemistry. Non-limiting examples include extraction, recrystallization, salting out (*e.g.*, with ammonium sulfate or sodium sulfate), centrifugation, dialysis, ultrafiltration, adsorption chromatography, ion exchange

15 chromatography, hydrophobic chromatography, normal phase chromatography, reversed-phase chromatography, gel filtration, gel permeation chromatography, affinity chromatography, electrophoresis, countercurrent distribution or any combinations of these. After purification, polypeptides may be exchanged into different buffers and/or concentrated by any of a variety of methods known to the art, including, but not limited to, filtration and
20 dialysis.

The purified polypeptide is preferably at least 85% pure, more preferably at least 95% pure, and most preferably at least 98% pure. Regardless of the exact numerical value of the purity, the polypeptide is sufficiently pure for use as a pharmaceutical product.

Post-Translational Modifications of Polypeptides

25 In certain embodiments, the binding polypeptides of the invention may further comprise post-translational modifications. Exemplary post-translational protein modifications include phosphorylation, acetylation, methylation, ADP-ribosylation, ubiquitination, glycosylation, carbonylation, sumoylation, biotinylation or addition of a polypeptide side chain or of a hydrophobic group. As a result, the modified soluble polypeptides may contain
30 non-amino acid elements, such as lipids, poly- or mono-saccharide, and phosphates. A preferred form of glycosylation is sialylation, which conjugates one or more sialic acid moieties to the polypeptide. Sialic acid moieties improve solubility and serum half-life while also reducing the possible immunogenicity of the protein. See Raju et al. *Biochemistry*. 2001 31; 40(30):8868-76.

In one embodiment, modified forms of the subject soluble polypeptides comprise linking the subject soluble polypeptides to nonproteinaceous polymers. In one embodiment, the polymer is polyethylene glycol ("PEG"), polypropylene glycol, or polyoxyalkylenes, in the manner as set forth in U.S. Patents 4,640,835; 4,496,689; 4,301,144; 4,670,417;

5 4,791,192 or 4,179,337.

PEG is a water soluble polymer that is commercially available or can be prepared by ring-opening polymerization of ethylene glycol according to methods well known in the art (Sandler and Karo, Polymer Synthesis, Academic Press, New York, Vol. 3, pages 138-161). The term "PEG" is used broadly to encompass any polyethylene glycol molecule, without
 10 regard to size or to modification at an end of the PEG, and can be represented by the formula: $X-O(CH_2CH_2O)_n-CH_2CH_2OH$ (1), where n is 20 to 2300 and X is H or a terminal modification, *e.g.*, a C_{1-4} alkyl. In one embodiment, the PEG of the invention terminates on one end with hydroxy or methoxy, *i.e.*, X is H or CH_3 ("methoxy PEG"). A PEG can contain further chemical groups which are necessary for binding reactions; which results from the
 15 chemical synthesis of the molecule; or which is a spacer for optimal distance of parts of the molecule. In addition, such a PEG can consist of one or more PEG side-chains which are linked together. PEGs with more than one PEG chain are called multiarmed or branched PEGs. Branched PEGs can be prepared, for example, by the addition of polyethylene oxide to various polyols, including glycerol, pentaerythriol, and sorbitol. For example, a four-armed
 20 branched PEG can be prepared from pentaerythriol and ethylene oxide. Branched PEG are described in, for example, EP-A 0 473 084 and U.S. Patent. 5,932,462. One form of PEGs includes two PEG side-chains (PEG2) linked via the primary amino groups of a lysine (Monfardini et al., *Bioconjugate Chem.* 6 (1995) 62-69).

The serum clearance rate of PEG-modified polypeptide may be decreased by about
 25 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or even 90%, relative to the clearance rate of the unmodified binding polypeptide. The PEG-modified polypeptide may have a half-life ($t_{1/2}$) which is enhanced relative to the half-life of the unmodified protein. The half-life of PEG-binding polypeptide may be enhanced by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 100%, 125%, 150%, 175%, 200%, 250%, 300%, 400% or 500%, or even by
 30 1000% relative to the half-life of the unmodified binding polypeptide. In some embodiments, the protein half-life is determined *in vitro*, such as in a buffered saline solution or in serum. In other embodiments, the protein half-life is an *in vivo* half life, such as the half-life of the protein in the serum or other bodily fluid of an animal.

Therapeutic Formulations and Modes of Administration

The present disclosure features method for treating or preventing the *S. aureus* infection comprising administering an anti-OprF and anti-OprI polypeptide. Techniques and dosages for administration vary depending on the type of specific polypeptide and the specific condition being treated but can be readily determined by the skilled artisan. In general, regulatory agencies require that a protein reagent to be used as a therapeutic is formulated so as to have acceptably low levels of pyrogens. Accordingly, therapeutic formulations will generally be distinguished from other formulations in that they are substantially pyrogen free, or at least contain no more than acceptable levels of pyrogen as determined by the appropriate regulatory agency (*e.g.*, FDA).

Therapeutic compositions of the present disclosure may be administered with a pharmaceutically acceptable diluent, carrier, or excipient, in unit dosage form. Administration may be parenteral (*e.g.*, intravenous, subcutaneous), oral, or topical, as non-limiting examples. In addition, any gene therapy technique, using nucleic acids encoding the polypeptides of the invention, may be employed, such as naked DNA delivery, recombinant genes and vectors, cell-based delivery, including *ex vivo* manipulation of patients' cells, and the like.

The composition can be in the form of a pill, tablet, capsule, liquid, or sustained release tablet for oral administration; or a liquid for intravenous, subcutaneous or parenteral administration; gel, lotion, ointment, cream, or a polymer or other sustained release vehicle for local administration.

Methods well known in the art for making formulations are found, for example, in "Remington: The Science and Practice of Pharmacy" (20th ed., ed. A. R. Gennaro A R., 2000, Lippincott Williams & Wilkins, Philadelphia, Pa.). Formulations for parenteral administration may, for example, contain excipients, sterile water, saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, or hydrogenated naphthalenes. Biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be used to control the release of the compounds. Nanoparticulate formulations (*e.g.*, biodegradable nanoparticles, solid lipid nanoparticles, liposomes) may be used to control the biodistribution of the compounds. Other potentially useful parenteral delivery systems include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. The concentration of the compound in the formulation varies depending upon a number of factors, including the dosage of the drug to be administered, and the route of administration.

The polypeptide may be optionally administered as a pharmaceutically acceptable salt, such as non-toxic acid addition salts or metal complexes that are commonly used in the pharmaceutical industry. Examples of acid addition salts include organic acids such as acetic, lactic, pantoic, maleic, citric, malic, ascorbic, succinic, benzoic, palmitic, suberic, salicylic, tartaric, methanesulfonic, toluenesulfonic, or trifluoroacetic acids or the like; polymeric acids such as tannic acid, carboxymethyl cellulose, or the like; and inorganic acid such as hydrochloric acid, hydrobromic acid, sulfuric acid phosphoric acid, or the like. Metal complexes include zinc, iron, and the like. In one example, the polypeptide is formulated in the presence of sodium acetate to increase thermal stability.

Formulations for oral use include tablets containing the active ingredient(s) in a mixture with non-toxic pharmaceutically acceptable excipients. These excipients may be, for example, inert diluents or fillers (*e.g.*, sucrose and sorbitol), lubricating agents, glidants, and anti-adhesives (*e.g.*, magnesium stearate, zinc stearate, stearic acid, silicas, hydrogenated vegetable oils, or talc).

Formulations for oral use may also be provided as chewable tablets, or as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium.

A therapeutically effective dose refers to a dose that produces the therapeutic effects for which it is administered. The exact dose will depend on the disorder to be treated, and may be ascertained by one skilled in the art using known techniques. In general, the polypeptide is administered at about 0.01 $\mu\text{g/kg}$ to about 50 mg/kg per day, preferably 0.01 mg/kg to about 30 mg/kg per day, most preferably 0.1 mg/kg to about 20 mg/kg per day. The polypeptide may be given daily (*e.g.*, once, twice, three times, or four times daily) or preferably less frequently (*e.g.*, weekly, every two weeks, every three weeks, monthly, or quarterly). In addition, as is known in the art, adjustments for age as well as the body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the disease may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

95% Homology

The present disclosure provides a number of antibodies structurally characterized by the amino acid sequences of their variable domain regions. However, the amino acid sequences can undergo some changes while retaining their high degree of binding to their specific targets. More specifically, many amino acids in the variable domain region can be

changed with conservative substitutions and it is predictable that the binding characteristics of the resulting antibody will not differ from the binding characteristics of the wild type antibody sequence. There are many amino acids in an antibody variable domain that do not directly interact with the antigen or impact antigen binding and are not critical for determining antibody structure. For example, a predicted nonessential amino acid residue in any of the disclosed antibodies is preferably replaced with another amino acid residue from the same class. Methods of identifying 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)). Near et al. *Mol. Immunol.* 30:369-377, 1993 explains how to impact or not impact binding through site-directed mutagenesis. Near et al. only mutated residues that they thought had a high probability of changing antigen binding. Most had a modest or negative effect on binding affinity (Near et al. Table 3) and binding to different forms of digoxin (Near et al. Table 2).

Exemplary Uses

An OprF and OprI binding polypeptide can be administered alone or in combination with one or more additional therapies such as chemotherapy radiotherapy, immunotherapy, surgical intervention, or any combination of these. Long-term therapy is equally possible as is adjuvant therapy in the context of other treatment strategies, as described above.

In certain embodiments of such methods, one or more polypeptide therapeutic agents can be administered, together (simultaneously) or at different times (sequentially). In addition, polypeptide therapeutic agents can be administered with another type of compounds for treating cancer or for inhibiting angiogenesis.

In certain embodiments, the subject anti-OprF and anti-OprI antibodies agents of the invention can be used alone.

In certain embodiments, the binding polypeptides or fragments thereof can be labeled or unlabeled for diagnostic purposes. Typically, diagnostic assays entail detecting the formation of a complex resulting from the binding of a binding polypeptide to OprF and OprI. The binding polypeptides or fragments can be directly labeled, similar to antibodies. A variety of labels can be employed, including, but not limited to, radionuclides, fluorescers, enzymes, enzyme substrates, enzyme cofactors, enzyme inhibitors and ligands (e.g., biotin, haptens). Numerous appropriate immunoassays are known to the skilled artisan (see, for example, U.S. Patents. 3,817,827; 3,850,752; 3,901,654; and 4,098,876). When unlabeled, the binding polypeptides can be used in assays, such as agglutination assays. Unlabeled

binding polypeptides can also be used in combination with another (one or more) suitable reagent which can be used to detect the binding polypeptide, such as a labeled antibody reactive with the binding polypeptide or other suitable reagent (*e.g.*, labeled protein A).

In one embodiment, the binding polypeptides of the present invention can be utilized
5 in enzyme immunoassays, wherein the subject polypeptides are conjugated to an enzyme. When a biological sample comprising an OprF and OprI protein is combined with the subject binding polypeptides, binding occurs between the binding polypeptides and the OprF and OprI protein. In one embodiment, a sample containing cells expressing an OprF and OprI protein (*e.g.*, endothelial cells) is combined with the subject antibodies, and binding occurs
10 between the binding polypeptides and cells bearing an OprF and OprI protein recognized by the binding polypeptide. These bound cells can be separated from unbound reagents and the presence of the binding polypeptide-enzyme conjugate specifically bound to the cells can be determined, for example, by contacting the sample with a substrate of the enzyme which produces a color or other detectable change when acted on by the enzyme. In another
15 embodiment, the subject binding polypeptides can be unlabeled, and a second, labeled polypeptide (*e.g.*, an antibody) can be added which recognizes the subject binding polypeptide.

In certain aspects, kits for use in detecting the presence of an OprF and OprI protein in a biological sample can also be prepared. Such kits will include an OprF and OprI binding
20 polypeptide which binds to an OprF and OprI protein or portion of said receptor, as well as one or more ancillary reagents suitable for detecting the presence of a complex between the binding polypeptide and the receptor protein or portions thereof. The polypeptide compositions of the present invention can be provided in lyophilized form, either alone or in combination with additional antibodies specific for other epitopes. The binding polypeptides
25 and/or antibodies, which can be labeled or unlabeled, can be included in the kits with adjunct ingredients (*e.g.*, buffers, such as Tris, phosphate and carbonate, stabilizers, excipients, biocides and/or inert proteins, *e.g.*, bovine serum albumin). For example, the binding polypeptides and/or antibodies can be provided as a lyophilized mixture with the adjunct ingredients, or the adjunct ingredients can be separately provided for combination by the
30 user. Generally these adjunct materials will be present in less than about 5% weight based on the amount of active binding polypeptide or antibody, and usually will be present in a total amount of at least about 0.001% weight based on polypeptide or antibody concentration. Where a second antibody capable of binding to the binding polypeptide is employed, such antibody can be provided in the kit, for instance in a separate vial or container. The second

antibody, if present, is typically labeled, and can be formulated in an analogous manner with the antibody formulations described above.

Polypeptide sequences are indicated using standard one- or three-letter abbreviations. Unless otherwise indicated, each polypeptide sequence has amino termini at the left and a
5 carboxy termini at the right; each single-stranded nucleic acid sequence, and the top strand of each double-stranded nucleic acid sequence, has a 5' termini at the left and a 3' termini at the right. A particular polypeptide sequence also can be described by explaining how it differs from a reference sequence.

10 The following terms, unless otherwise indicated, shall be understood to have the following meanings:

The terms "peptide," "polypeptide" and "protein" each refers to a molecule comprising two or more amino acid residues joined to each other by peptide bonds. These terms encompass, *e.g.*, native and artificial proteins, protein fragments and polypeptide analogs (such as muteins, variants, and fusion proteins) of a protein sequence as well as post-
15 translationally, or otherwise covalently or non-covalently, modified proteins. A peptide, polypeptide, or protein may be monomeric or polymeric.

A "variant" of a polypeptide (for example, an antibody) comprises an amino acid sequence wherein one or more amino acid residues are inserted into, deleted from and/or substituted into the amino acid sequence relative to another polypeptide sequence. Disclosed
20 variants include, for example, fusion proteins.

A "derivative" of a polypeptide is a polypeptide (*e.g.*, an antibody) that has been chemically modified, *e.g.*, via conjugation to another chemical moiety (such as, for example, polyethylene glycol or albumin, *e.g.*, human serum albumin), phosphorylation, and glycosylation. Unless otherwise indicated, the term "antibody" includes, in addition to
25 antibodies comprising two full-length heavy chains and two full-length light chains, derivatives, variants, fragments, and muteins thereof, examples of which are described below.

An "antigen binding protein" is a protein comprising a portion that binds to an antigen and, optionally, a scaffold or framework portion that allows the antigen binding portion to adopt a conformation that promotes binding of the antigen binding protein to the antigen.
30 Examples of antigen binding proteins include antibodies, antibody fragments (*e.g.*, an antigen binding portion of an antibody), antibody derivatives, and antibody analogs. The antigen binding protein can comprise, for example, an alternative protein scaffold or artificial scaffold with grafted CDRs or CDR derivatives. Such scaffolds include, but are not limited to, antibody-derived scaffolds comprising mutations introduced to, for example, stabilize the

three-dimensional structure of the antigen binding protein as well as wholly synthetic scaffolds comprising, for example, a biocompatible polymer. See, for example, Korndorfer et al., 2003, *Proteins: Structure, Function, and Bioinformatics*, Volume 53, Issue 1:121-129; Roque et al., 2004, *Biotechnol. Prog.* 20:639-654. In addition, peptide antibody mimetics ("PAMs") can be used, as well as scaffolds based on antibody mimetics utilizing fibronectin components as a scaffold.

An antigen binding protein can have, for example, the structure of a naturally occurring immunoglobulin. An "immunoglobulin" is a tetrameric molecule. In a naturally occurring immunoglobulin, each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Human light chains are classified as kappa or lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. Preferably, the anti-EGFR antibodies disclosed herein are characterized by their variable domain region sequences in the heavy V_H and light V_L amino acid sequences. The preferred antibody is A6 which is a kappa IgG antibody. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. See generally, *Fundamental Immunology* Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)). The variable regions of each light/heavy chain pair form the antibody binding site such that an intact immunoglobulin has two binding sites.

A "multi-specific antibody" is an antibody that recognizes more than one epitope on one or more antigens. A subclass of this type of antibody is a "bi-specific antibody" which recognizes two distinct epitopes on the same or different antigens.

An antigen binding protein "specifically binds" to an antigen (*e.g.*, OprF and OprI) if it binds to the antigen with a dissociation constant of 1 nanomolar or less.

An "antigen binding domain," "antigen binding region," or "antigen binding site" is a portion of an antigen binding protein that contains amino acid residues (or other moieties) that interact with an antigen and contribute to the antigen binding protein's specificity and affinity for the antigen. For an antibody that specifically binds to its antigen, this will include at least part of at least one of its CDR domains.

An "epitope" is the portion of a molecule that is bound by an antigen binding protein (e.g., by an antibody). An epitope can comprise non-contiguous portions of the molecule (e.g., in a polypeptide, amino acid residues that are not contiguous in the polypeptide's primary sequence but that, in the context of the polypeptide's tertiary and quaternary structure, are near enough to each other to be bound by an antigen binding protein).

The "percent homology" of two polynucleotide or two polypeptide sequences is determined by comparing the sequences using the GAP computer program (a part of the GCG Wisconsin Package, version 10.3 (Accelrys, San Diego, Calif.)) using its default parameters.

A "host cell" is a cell that can be used to express a nucleic acid. A host cell can be a prokaryote, for example, *E. coli*, or it can be a eukaryote, for example, a single-celled eukaryote (e.g., a yeast or other fungus), a plant cell (e.g., a tobacco or tomato plant cell), an animal cell (e.g., a human cell, a monkey cell, a hamster cell, a rat cell, a mouse cell, or an insect cell) or a hybridoma. Examples of host cells include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., 1981, *Cell* 23:175), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media (Rasmussen et al., 1998, *Cytotechnology* 28:31) or CHO strain DX-B11, which is deficient in DHFR (Urlaub et al., 1980, *Proc. Natl. Acad. Sci. USA* 77:4216-20), HeLa cells, BHK (ATCC CRL 10) cell lines, the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) (McMahan et al., 1991, *EMBO J.* 10:2821), human embryonic kidney cells such as 293,293 EBNA or MSR 293, human epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Typically, a host cell is a cultured cell that can be transformed or transfected with a polypeptide-encoding nucleic acid, which can then be expressed in the host cell. The phrase "recombinant host cell" can be used to denote a host cell that has been transformed or transfected with a nucleic acid to be expressed. A host cell also can be a cell that comprises the nucleic acid but does not express it at a desired level unless a regulatory sequence is introduced into the host cell such that it becomes operably linked with the nucleic acid. It is understood that the term host cell refers not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to, e.g., mutation or environmental influence, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

Antigen Binding Proteins

Antigen binding proteins (*e.g.*, antibodies, antibody fragments, antibody derivatives, antibody muteins, and antibody variants) are polypeptides that bind to OprF and OprI.

Oligomers that contain one or more antigen binding proteins may be employed as OprF and OprI antagonists. Oligomers may be in the form of covalently-linked or non-covalently-linked dimers, trimers, or higher oligomers. Oligomers comprising two or more
5 covalently-linked dimers, trimers, or higher oligomers. Oligomers comprising two or more antigen binding protein are contemplated for use, with one example being a homodimer. Other oligomers include heterodimers, homotrimers, heterotrimers, homotetramers, heterotetramers, etc.

One embodiment is directed to oligomers comprising multiple antigen binding
10 proteins joined via covalent or non-covalent interactions between peptide moieties fused to the antigen binding proteins. Such peptides may be peptide linkers (spacers), or peptides that have the property of promoting oligomerization. Leucine zippers and certain polypeptides derived from antibodies are among the peptides that can promote oligomerization of antigen binding proteins attached thereto, as described in more detail below.

15 In particular embodiments, the oligomers comprise from two to four antigen binding proteins. The antigen binding proteins of the oligomer may be in any form, such as any of the forms described above, *e.g.*, variants or fragments. Preferably, the oligomers comprise antigen binding proteins that have OprF and OprI binding activity.

In one embodiment, an oligomer is prepared using polypeptides derived from
20 immunoglobulins. Preparation of Fusion Proteins Comprising Certain Heterologous Polypeptides Fused to Various Portions of antibody-derived polypeptides (including the Fc domain) has been described, *e.g.*, by Ashkenazi et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:10535; Byrn et al., 1990, *Nature* 344:677; and Hollenbaugh et al., 1992 "Construction of Immunoglobulin Fusion Proteins", in *Current Protocols in Immunology*, Suppl. 4, pages
25 10.19.1-10.19.11.

One embodiment is directed to a dimer comprising two fusion proteins created by fusing an OprF and OprI binding fragment of an anti-OprF and anti-OprI antibody to the Fc region of an antibody. The dimer can be made by, for example, inserting a gene fusion encoding the fusion protein into an appropriate expression vector, expressing the gene fusion
30 in host cells transformed with the recombinant expression vector, and allowing the expressed fusion protein to assemble much like antibody molecules, whereupon interchain disulfide bonds form between the Fc moieties to yield the dimer.

The term "Fc polypeptide" includes native and mutein forms of polypeptides derived from the Fc region of an antibody. Truncated forms of such polypeptides containing the hinge

region that promotes dimerization also are included. Fusion proteins comprising Fc moieties (and oligomers formed therefrom) offer the advantage of facile purification by affinity chromatography over Protein A or Protein G columns.

Another method for preparing oligomeric antigen binding proteins involves use of a leucine zipper. Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., 1988, *Science* 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe et al., 1994, *FEBS Letters* 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow et al., 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising an anti-OprF and OprI antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric anti-OprF and OprI antibody fragments or derivatives that form are recovered from the culture supernatant.

Antigen-binding fragments of antigen binding proteins of the invention may be produced by conventional techniques. Examples of such fragments include, but are not limited to, Fab and F(ab')₂ fragments.

The present disclosure provides monoclonal antibodies that bind to OprF and OprI. Monoclonal antibodies may be produced using any technique known in the art, *e.g.*, by immortalizing spleen cells harvested from the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, *e.g.*, by fusing them with myeloma cells to produce hybridomas. Myeloma cells for use in hybridoma-producing fusion procedures preferably are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain selective media which support the growth of only the desired fused cells (hybridomas). Examples of suitable cell lines for use in mouse fusions include Sp-20, P3-X63/Ag8, P3-X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XX0 Bul; examples of cell lines used in rat fusions include R210.RCY3, Y3-Ag 1.2.3, IR983F and 48210. Other cell lines useful for cell fusions are U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6.

Antigen binding proteins directed against OprF and OprI can be used, for example, in assays to detect the presence of OprF and OprI polypeptides, either *in vitro* or *in vivo*. The antigen binding proteins also may be employed in purifying OprF and OprI proteins by immunoaffinity chromatography. Blocking antigen binding proteins can be used in the methods disclosed herein. Such antigen binding proteins that function as OprF and OprI antagonists may be employed in treating any OprF and OprI-induced condition, including but not limited to various cancers.

Antigen binding proteins may be employed in an *in vitro* procedure, or administered *in vivo* to inhibit OprF and OprI-induced biological activity. Disorders caused or exacerbated (directly or indirectly) by the proteolytic activation of OprF and OprI, examples of which are provided herein, thus may be treated. In one embodiment, the present invention provides a therapeutic method comprising *in vivo* administration of an OprF and OprI blocking antigen binding protein to a mammal in need thereof in an amount effective for reducing an OprF and OprI-induced biological activity.

Antigen binding proteins include fully human monoclonal antibodies that inhibit a biological activity of OprF and OprI.

Antigen binding proteins may be prepared by any of a number of conventional techniques. For example, they may be purified from cells that naturally express them (*e.g.*, an antibody can be purified from a hybridoma that produces it), or produced in recombinant expression systems, using any technique known in the art. See, for example, Monoclonal Antibodies, Hybridomas: A New Dimension in Biological Analyses, Kennet et al. (eds.), Plenum Press, New York (1980); and Antibodies: A Laboratory Manual, Harlow and Land (eds.), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1988).

Any expression system known in the art can be used to make the recombinant polypeptides of the invention. In general, host cells are transformed with a recombinant expression vector that comprises DNA encoding a desired polypeptide. Among the host cells that may be employed are prokaryotes, yeast or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or *bacilli*. Higher eukaryotic cells include insect cells and established cell lines of mammalian origin. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., 1981, *Cell* 23:175), L cells, 293 cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, BHK (ATCC CRL 10) cell lines, and the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) as described by McMahan et al., 1991, *EMBO J.* 10: 2821. Appropriate

cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels et al. (Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., 1985).

The transformed cells can be cultured under conditions that promote expression of the polypeptide, and the polypeptide recovered by conventional protein purification procedures. One such purification procedure includes the use of affinity chromatography, *e.g.*, over a matrix having all or a portion (*e.g.*, the extracellular domain) of OprF and OprI bound thereto. Polypeptides contemplated for use herein include substantially homogeneous recombinant mammalian anti-OprF and anti-OprI antibody polypeptides substantially free of contaminating endogenous materials.

Antigen binding proteins may be prepared, and screened for desired properties, by any of a number of known techniques. Certain of the techniques involve isolating a nucleic acid encoding a polypeptide chain (or portion thereof) of an antigen binding protein of interest (*e.g.*, an anti-OprF and anti-OprI antibody), and manipulating the nucleic acid through recombinant DNA technology. The nucleic acid may be fused to another nucleic acid of interest, or altered (*e.g.*, by mutagenesis or other conventional techniques) to add, delete, or substitute one or more amino acid residues, for example.

Single chain antibodies may be formed by linking heavy and light chain variable domain (Fv region) fragments via an amino acid bridge (short peptide linker), resulting in a single polypeptide chain. Such single-chain Fvs (scFvs) have been prepared by fusing DNA encoding a peptide linker between DNAs encoding the two variable domain polypeptides (V_L and V_H). The resulting polypeptides can fold back on themselves to form antigen-binding monomers, or they can form multimers (*e.g.*, dimers, trimers, or tetramers), depending on the length of a flexible linker between the two variable domains (Kortt et al., 1997, *Prot. Eng.* 10:423; Kortt et al., 2001, *Biomol. Eng.* 18:95-108). By combining different V_L and V_H -comprising polypeptides, one can form multimeric scFvs that bind to different epitopes (Kriangkum et al., 2001, *Biomol. Eng.* 18:31-40). Techniques developed for the production of single chain antibodies include those described in U.S. Patent 4,946,778; Bird, 1988, *Science* 242:423; Huston et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:5879; Ward et al., 1989, *Nature* 334:544; de Graaf et al., 2002, *Methods Mol. Biol.* 178:379-87.

Techniques are known for deriving an antibody of a different subclass or isotype from an antibody of interest, *i.e.*, subclass switching. Thus, IgG antibodies may be derived from an IgM antibody, for example, and vice versa. Such techniques allow the preparation of new antibodies that possess the antigen-binding properties of a given antibody (the parent

antibody), but also exhibit biological properties associated with an antibody isotype or subclass different from that of the parent antibody. Recombinant DNA techniques may be employed. Cloned DNA encoding particular antibody polypeptides may be employed in such procedures, *e.g.*, DNA encoding the constant domain of an antibody of the desired isotype (Lantto et al., 2002, *Methods Mol. Biol.* 178:303-16). Moreover, if an IgG4 is desired, it may also be desired to introduce a point mutation (CPSC->CPPC) in the hinge region (Bloom et al., 1997, *Protein Science* 6:407) to alleviate a tendency to form intra-H chain disulfide bonds that can lead to heterogeneity in the IgG4 antibodies.

In particular embodiments, antigen binding proteins of the present invention have a binding affinity (K_a) for OprF and OprI of at least 10^6 . In other embodiments, the antigen binding proteins exhibit a K_a of at least 10^7 , at least 10^8 , at least 10^9 , or at least 10^{10} . In another embodiment, the antigen binding protein exhibits a K_a substantially the same as that of an antibody described herein in the Examples.

In another embodiment, the present disclosure provides an antigen binding protein that has a low dissociation rate from OprF and OprI. In one embodiment, the antigen binding protein has a K_{off} of 1×10^{-4} to $^{-1}$ or lower. In another embodiment, the K_{off} is 5×10^{-5} to $^{-1}$ or lower. In another embodiment, the K_{off} is substantially the same as an antibody described herein. In another embodiment, the antigen binding protein binds to OprF and OprI with substantially the same K_{off} as an antibody described herein.

In another aspect, the present disclosure provides an antigen binding protein that inhibits an activity of OprF and OprI. In one embodiment, the antigen binding protein has an IC_{50} of 1000 nM or lower. In another embodiment, the IC_{50} is 100 nM or lower; in another embodiment, the IC_{50} is 10 nM or lower. In another embodiment, the IC_{50} is substantially the same as that of an antibody described herein in the Examples. In another embodiment, the antigen binding protein inhibits an activity of OprF and OprI with substantially the same IC_{50} as an antibody described herein.

In another aspect, the present disclosure provides an antigen binding protein that binds to OprF and OprI expressed on the surface of a cell and, when so bound, inhibits OprF and OprI signaling activity in the cell without causing a significant reduction in the amount of OprF and OprI on the surface of the cell. Any method for determining or estimating the amount of OprF and OprI on the surface and/or in the interior of the cell can be used. In other embodiments, binding of the antigen binding protein to the OprF and OprI-expressing cell causes less than about 75%, 50%, 40%, 30%, 20%, 15%, 10%, 5%, 1%, or 0.1% of the cell-surface OprF and OprI to be internalized.

In another aspect, the present disclosure provides an antigen binding protein having a half-life of at least one day *in vitro* or *in vivo* (e.g., when administered to a human subject). In one embodiment, the antigen binding protein has a half-life of at least three days. In another embodiment, the antigen binding protein has a half-life of four days or longer. In another
5 embodiment, the antigen binding protein has a half-life of eight days or longer. In another embodiment, the antigen binding protein is derivatized or modified such that it has a longer half-life as compared to the underivatized or unmodified antigen binding protein. In another embodiment, the antigen binding protein contains one or more point mutations to increase serum half life, such as described in WO00/09560, incorporated by reference herein.

10 The present disclosure further provides multi-specific antigen binding proteins, for example, bispecific antigen binding protein, e.g., antigen binding protein that bind to two different epitopes of OprF and OprI, or to an epitope of OprF and OprI and an epitope of another molecule, via two different antigen binding sites or regions. Moreover, bispecific antigen binding protein as disclosed herein can comprise an OprF and OprI binding site from
15 one of the herein-described antibodies and a second OprF and OprI binding region from another of the herein-described antibodies, including those described herein by reference to other publications. Alternatively, a bispecific antigen binding protein may comprise an antigen binding site from one of the herein described antibodies and a second antigen binding site from another OprF and OprI antibody that is known in the art, or from an antibody that is
20 prepared by known methods or the methods described herein.

Numerous methods of preparing bispecific antibodies are known in the art. Such methods include the use of hybrid-hybridomas as described by Milstein et al., 1983, *Nature* 305:537, and chemical coupling of antibody fragments (Brennan et al., 1985, *Science* 229:81; Glennie et al., 1987, *J. Immunol.* 139:2367; U.S. Patent 6,010,902). Moreover, bispecific
25 antibodies can be produced via recombinant means, for example by using leucine zipper moieties (i.e., from the *Fos* and *Jun* proteins, which preferentially form heterodimers; Kostelny et al., 1992, *J. Immunol.* 148:1547) or other lock and key interactive domain structures as described in U.S. Patent 5,582,996. Additional useful techniques include those described in U.S. Patents 5,959,083; and 5,807,706.

30 In another aspect, the antigen binding protein comprises a derivative of an antibody. The derivatized antibody can comprise any molecule or substance that imparts a desired property to the antibody, such as increased half-life in a particular use. The derivatized antibody can comprise, for example, a detectable (or labeling) moiety (e.g., a radioactive, colorimetric, antigenic or enzymatic molecule, a detectable bead (such as a magnetic or

electrodense (*e.g.*, gold) bead), or a molecule that binds to another molecule (*e.g.*, biotin or streptavidin), a therapeutic or diagnostic moiety (*e.g.*, a radioactive, cytotoxic, or pharmaceutically active moiety), or a molecule that increases the suitability of the antibody for a particular use (*e.g.*, administration to a subject, such as a human subject, or other *in vivo* or *in vitro* uses). Examples of molecules that can be used to derivatize an antibody include albumin (*e.g.*, human serum albumin) and polyethylene glycol (PEG). Albumin-linked and PEGylated derivatives of antibodies can be prepared using techniques well known in the art. In one embodiment, the antibody is conjugated or otherwise linked to transthyretin (TTR) or a TTR variant. The TTR or TTR variant can be chemically modified with, for example, a chemical selected from the group consisting of dextran, poly(*n*-vinyl pyrrolidone), polyethylene glycols, propylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols and polyvinyl alcohols.

Preferably, the disclosed antibodies are administered by inhalation, but aerosolization of full IgG antibodies may prove limiting due to their molecular size (~150kDa). To maximize available commercial aerosolization devices, smaller Fab fragments may be required. In this case, we may also need to generate Fab fragments from the parental IgG molecules. Therefore, we will perform initial studies using standard enzyme-based digestion methodologies for the generation of Fab fragments, which will then be characterized in parallel with full IgG molecules.

Example 1

This example illustrates an ELISA assay that was conducted to check binding of various candidate antibodies. Figures 1-4 show the results of the ELISA studies showing the disclosed antibodies that bind to their respective targets.

Example 2

This example illustrates that ELISA plates were coated with 100 μ L of wild type *P. aeruginosa* PAO1, Δ *oprF*, and Δ *oprI* strains and incubated at 37°C for two hours. The plates were blocked with PBS plus 10% fetal calf serum and then washed in PBST (PBS + 0.05% Tween) for 2 h. The plates were then incubated with specific mAbs to *oprF*, *oprI*, *P. aeruginosa* and a non-specific human IgG control antibody at 0.5 μ g/ml, 2.5 μ g/mL and 5 μ g/mL for 1hr at 37 °C. After washing, anti-human secondary antibody (1:10,000 in PBS) was added, followed by further washing. 3,3',5,5'-Tetramethylbenzidine (TMB) was added to each well at RT for 30 minutes, followed by 50 μ L of 2N H₂SO₄. The plates were then read at 450nm with a Molecular Devices SpectraMax plate reader.

As in many cell-based ELISAs, the data here (Figure 5) show significant background signal but nonetheless, there were a few clones that demonstrated specificity for the OprF- or OprI-expressing strain over the knockout bacteria. To further investigate these potential binders, Western blots were performed using bacterial cell lysates.

Example 3

This example illustrates Western blots using bacterial cell lysates. Strains were grown as described to an OD600 of ~1.0. Cells were pelleted, suspended in 5X SDS loading buffer and boiled for 5 minutes. Suspensions were then run through a 26-gauge needle to disperse the viscous cell components. Samples were resolved on a 12% SDS-PAGE gel, followed by semi-dry transfer to a nitrocellulose membrane. Blots were probed with primary anti-OprF, anti-OprI, and anti-*P.aeruginosa* antibodies followed by anti-human HRP-conjugated secondary antibody. Blots were visualized using chemiluminescent detection via a BioRad GelDoc XR+ system (Figures 6 and 7). The Western blot data confirm that the mAbs oprIA5 and oprFF7 specifically recognize OprI and OprF, respectively. Importantly, both mAbs recognize wild type *P. aeruginosa*.

Example 4

This example illustrates the effects of our antibody on the ability of *P. aeruginosa* to form biofilm or to disperse already formed biofilm. Attachment assays were performed as follows: 5 ml of LBNS was inoculated with a single colony of *P. aeruginosa* PAO1, $\Delta oprF$, and $\Delta oprI$ into a culture tube and grown overnight at 37 °C. The following morning, 50 μ L of the overnight culture was seeded into a new test tube with 5 mls fresh media and grown to OD600 0.5-0.7 at 37 °C. 50 μ L of the bacterial culture was added to 50 μ L of the appropriate concentration of mAb to get a final concentration of either 2.5 μ g/mL, 5 μ g/mL, or 10 μ g/mL, mixed and plated into 96-well PVC microtiter dishes and incubated statically at 37 °C for 2 h. The plates were then washed vigorously by immersion in water. Biomass was stained with 0.1% crystal violet for 30 minutes, followed by vigorous washing. Remaining crystal violet was solubilized in 100 μ L of 95% ethanol for 30 minutes and transferred to a fresh 96-well plate. Absorbance was determined at OD540. The data are shown in Figure 8A.

Example 5

This example illustrates a biofilm disruption assay. Disruption assays were performed as follows: 5 ml of LBNS was inoculated with a single colony of *P. aeruginosa* PAO1, $\Delta oprF$, and $\Delta oprI$ into an overnight culture tube and grown at 37 °C. The following morning, 50 μ L of the overnight culture was seeded into a new test tube with 5 mls fresh media and grown to OD600 0.5-0.7 at 37 °C. 100 μ L of the bacterial culture was added to a 96-well

MBEC peg plate and incubated at 37 °C overnight. The next morning the pegs were washed using another flat bottom 96 well plate with sterile ddH₂O. 100 µl of mAbs were then added to a new 96 well flat bottom plate and the peg lid (containing the overnight biofilm) was incubated with the mAbs at the above concentrations for two hours at room temperature.

- 5 Plates were then washed vigorously using another flat bottom 96 well plate with sterile ddH₂O. Biomass was stained with 0.1% crystal violet for 30 minutes, followed by vigorous washing. Remaining crystal violet was solubilized in 100 µl of 95% ethanol for 30 minutes and transferred to a fresh 96-well plate and absorbance was measured at OD540.

The biofilm assays suggest that neither mAb has a profound effect on biofilm

- 10 formation nor established biofilm. However, it appears that higher concentration of oprFF7 might disrupt existing biofilm to a moderate extent.

Sequence Listing OprF-binding Antibodies

	Heavy chain variable domain region	Light chain variable domain region
OFA1	EVQLVQSGAEMKKPGSSVKVSCAS GDTFSNYNFWVRQAPGQGLEWMG GITPIFGAAQYAQKFQDRVTIIADESTS TAYMELRSLRSDDTAVYYCAGGWAG FCSSASCYRFDYWGGGTTVTVSS SEQ ID NO. 1	SYELTQPPSVSAAPGQKVTISCS GSSSNIGNYYVSWYQQLPGTAP KLLIYDNDKRPSGIPDRFSASKS GTSASLAITGLQAEDEADYYCQ SYDRTLSGGILGTGKLTVL SEQ ID NO. 2
OFC7	QVQLVVGSGDEVKKPGASVKVSCAS GYTFTSYDINWVRQAPGQGLEWLWV MSPNSGNTDYAEKFQGRVTMTSDTSI TTAYMELSSLASEDTAVYYCARGVAA GLDYWGQGTLVTVSS SEQ ID NO. 3	LPVLTQSASVSGSPGQSITISCT GTSTDVDYSNYVSWYQHHPGK APKLMYDVSRRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTS GTTLVFGGGTKVTVL SEQ ID NO. 4
OFC10	EVQLVESGPGGLAKPSETLSLTCSVFG GSIRRYYSWIRQSPGKGLEWIGFFY HSGSADYNPSPNYNPSFKSRVTISVD TSKTQFSLKMTSVTAADTAVYYCAKG DGSWYLD SWGGTTLVTVSS SEQ ID NO. 5	DIVMTQSPSSLSASVGDRVTITC RASHSISRSLNWFYQQKPGKAPK LLIYAASILQSGVSSRFSGSGSG TDFTLTISRLQPEDFATYYCQES DSPPPFTFGPGTKVEIK SEQ ID NO. 6
OFF7	EVQLVQSGAEMKKPGSSVKVSCAS GDTFSNYNFWVRQAPGQGLEWMG GITPIFGAAQYAQKFQDRVTIIADESTS TAYMELRSLRSDDTAVYYCAGGWAG FCSSASCYRFDYWGGGTTVTVSS SEQ ID NO. 7	SYELTQPPSVSAAPGQKVTISCS GSSSNIGNYYVSWYQQLPGTAP KLLIYDNDKRPSGIPDRFSASKS GTSASLAITGLQAEDEADYYCQ SYDRTLSGGILGTGKLTVL SEQ ID NO. 8

OFF8	QVQLVQSGAEVKKPGASVRVSCAS EYFTTAYYLHWVRQAPGQGLEWMGR IDPNSGGTNFAQKFQGRVTMTSDTSV STAYMELRGLRSDDTAVYYCARAQYA AKDYWGQGTLLTVSS SEQ ID NO. 9	SYELMQPPSVSVAPGKTARITC GGNNIGSKSVHWYQQKPGQAP VLVYDDSDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYC QVWDSSSAHVVFGGGTCLTVL SEQ ID NO. 10
OFG5	QVQLVQSGAEVKKPGASVKVSCAS GYFTTGYYMHWVRQAPGQGLEWMG WINPNSGGTNFAQKFQGRVTITRDT ASTAYMELSSLRSEDVAVYYCATLGG AAAGLNTDYWGQGTLLTVSS SEQ ID NO. 11	SYELMQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSNRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSSSTRVFGTGKTVL SEQ ID NO. 12
OFH10	QVQLVESGGGLIQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVI YSGGTYKYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYFCARGDDAFD IWGQGTMTVTVSS SEQ ID NO. 13	QSVLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSNRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSSNTIVFGSGTKTVL SEQ ID NO. 14

Sequence Listing
OprI-binding Antibodies

	Heavy chain variable domain region	Light chain variable domain region
OIA1	EVQLVESGGGLVQPGGSLRLSCAAS GFTGSNNYMSWVRQAPGKGLEWVSII YSGGNAYYADSVKGRFTISRDNKNT YFQMNSLRVEDTAVYYCAEGYGGVD YWGQGTLLTVSS SEQ ID NO. 15	DVVMQTQSPDSLAVSLGERATIN CKSSQSVLYSSNNKNYLAWYQ QKPGQPPKLLIYWASTRESGVP DRFSGSGSGTDFTLTISLQAE VAVYYCQQYYSSPFSFGPGTKV DIK SEQ ID NO. 16
OIA10	QVQLVQSGAEVKKPGASVKVSCAS GYFTTSYYMHWVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTTRDTST STVYMELSSLRAEDMAVYYCAREGLP DAFDIWGQGTMTVTVSS SEQ ID NO. 17	QAGLTQPASVSGSPGQSITLSC TGTSSDVGGYNYVTWFQQHPG KAPKLMYDVSKRPSGASNRFS GSKSGNTASLTISGLQAEDEAD YYCSSYTSSGTYVFGTGKCLTVL SEQ ID NO. 18
OIA2	QVQLVQSGAEVKKPGASVKVSCAS GYFTTGYYMHWVRQAPGQGLEWMG WINPNSGGTNFAQKFQGRVTMTTRNT SISTAYMELSSLRSEDVAVYYCAREIY DFDAFDIWGQGTMTVTVSS SEQ ID NO. 19	SYELMQPPSVSVAPGKTARITC GGNNIGSKSVHWYQQKPGQAP VLVIYYDSDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQ VWDSRSDQVIFGGGTQLTVL SEQ ID NO. 20
OIA4	QVQLVESGGGLVQPGGSLRLSCAAS GFTVSSNYMSWVRQAPGKGLEWVSV IYSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYYCAREDSSSW YWNADFIDWGQGTMTVTVSS SEQ ID	YELMQPPSVSVAPGKTARITCG GNNIGSKSVHWYQQKPGQAPV LVIYYDSDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQV WDSSSDHPVFGGGTKCLTVL

	NO. 21	SEQ ID NO. 22
OIA5	QVQLVQSGSELKKPGASVKVSCKASG YTFTSYAMNWVRQAPGQGLEWMGII NPSGGSTSYAQKFQGRVTMTRDTST STVYMELSSLRSEDVAVYYCARSTLW FSEFDYWGGGTLVTVSS SEQ ID NO. 23	EIVLTQSPGTLSSLSPGERATLSC RASQSVTIYLAWYQQKPGQAPR LLIYDASNRAAGIPARFSGSGSG TDFTLTISSELEPEDFATYYCQQY DTSSTFGGQGTKVDIK SEQ ID NO. 24
OIA6	EVQLLESQGGGLVQPGGSLRLSCAASG FTFSSYEMNWVRQAPGKGLEWVSYIS SSGSTIYYADSVKGRFTISRDNKNSL YLQMNSLRAEDTAVYYCARLIYDSSG YYFDYWGGGTLVTVSS SEQ ID NO. 25	DIQLTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLKISRVEAEDV GVYYCMQGSHPHTFGGQGTKL EIK SEQ ID NO. 26
OIA7	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYMHVVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTMDTSA NTVYMELSLRSDDTAVYYCARDWFS EDYFDYWGGGTLVTVSS SEQ ID NO. 27	QSVVTQPPSVSAAPGQKVTISC SGSNSNIGNNNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSGSK SGTSATLAITGLQTGDEADYYC GTWDSSLSGGVFGGGTKLTVL SEQ ID NO. 28
OIA8	EVQLVQSGGGVVPGRSLRLSCAAS GFTFSIYGMHWVRQAPGKGLEWVAVI WDDGSKKYYADSVKGRFTISRDNKNSL TLYLQMNTLRADDTAVYYCAGELWKY YDSSGFYSINPEYFQHWGGGTLVTVS S SEQ ID NO. 29	QAGLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLIYDVSRPSGVSNRFSGS KSGNTASLTISGLQAEDEADYYC SSYTTSTLLFGGGTKLTVL SEQ ID NO. 30
OIA9	EVQLVQSGGGGLIQPGGSLRLSCAASG FSVSSDYMSWVRQAPGKGLEWVSVI YTGGTTYADSVKGRFTISRDNKNTL YLQMNSLRAEDTAVYYCARDYGDSFD YWGGGTLVTVSS SEQ ID NO. 31	QAGLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSNRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTKSNTLVFGGGTKVTVL SEQ ID NO. 32
OIB1	QVQLVQSGGGVVPGRSLRLSCAAS GFTVSSNYMSWVRQAPGKGLEWVSV IYSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYYCARDWGYD KGDWGGGTLVTVSS SEQ ID NO. 33	LPVLTQPPSLSVAPGKTARITCG GNNIDSTGVHWYQQKAGQAPV LVVYDDSDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQ VWDSSSDHVVFGGGTKLTVL SEQ ID NO. 34
OIB11	QVQLVQSGGGGLIQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYYCARDYGDYF DYWGGGTLVTVSS SEQ ID NO. 35	SYELMQPPSASGTPGQRTISC SGSSSNIGSNYVDWYQQLPGTA PKLLIYSNNRPSGVPDRFSGSK SGTSASLAISGLRSEDEADYYCA AWDDSLSGYVFGTGTKVTVL SEQ ID NO. 36

OIB12	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYMHVWRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTTRDTST STVYMELSSLRSEDTAVYYCASSPGA YSSGWYDYWGQGTLLTVSS SEQ ID NO. 37	QPVLTQPPSVSVAPGAAARITC GGNNIGSQIVHWYRQKPGQAPV LVLYYDTERPSGIPERFSGSNSG NTATLTVSRVEAGDEADYFCQV WDLSDHDPGWLFGGGTKLTVL SEQ ID NO. 38
OIB2	QVQLVESGGGLIQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRADTAIVYYCAREGGEHF DYWGQGTLLTVSS SEQ ID NO. 39	QAVLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEGDY YCFSTSSSTLVFGGGTKLTVL SEQ ID NO. 40
OIB3	EVQLVESGAEVKKPGASVKVSCKASG YTFTSYGISWVRQAPGQGLEWMGI SAYNGNTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARDYYYG SGTANDYYYYGMDVWGQGTLLTVSS SEQ ID NO. 41	LPVLTQPPSASGTPGQRVTISCS GSSSNIGNNPVNWYQQVPGTA PKLLIHSSNQRPSPGVDRFSGS KSGASASLAISGLQSEDEADYY CAAWDDILNGLVFGGGTKLTVL SEQ ID NO. 42
OIB8	QVQLVQSGGGLVQPGESLRLSCAAS GFTVSSNHMAWVRQAPGKGLEWVSL IYNGDSTYYPDSVKGRFTISRDNKNA LYLQMNSLRADTAIVYYCARDWGYD TADWGQGTLLTVSS SEQ ID NO. 43	QPVLTQPASVSGSPGQSITISCT GTSSDVGAYNYVSWYQQHPGK APKLMYDVSNRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSNSTLYVFGTGKTVL SEQ ID NO. 44
OIB9	QVQLVQSGAEVKKPGASVKVSCKAS GDTFTGQYMNWVRQAPGQGLEWMG WINPNSGFTNYAQKFQGRVTMTWDT SISTAYMELSLRSDDTAVYYCARDS WDYYSYYGMDVWGQGTLLTVSS SEQ ID NO. 45	DIQLTQSPSFLSASVGDRVTITC RASQDITSYLAWYQQKPGKAPK LLVYAASLTQSGVPSRFSGSGS GTDFTLTISLQPEDFATYYCQQ SYGTPYTFGQGTCKLEIK SEQ ID NO. 46
OIC1	EVQLVESGGGLVQPGGSLRLSCAAS GFTGSNNYMSWVRQAPGKGLEWVSII YSGGNAYYADSVKGRFTISRDNKNI YFQMNSLRVEDTAIVYYCAEGYGGVD YWGGQGTLLTVSS SEQ ID NO. 47	QAGLTQPASVSGSPGQSITISCT GTSSDIGAYNFVSWYQQHAGK GPKLLIYDVNTNRPSGVSDRFSG SKSGNTASLTISGLQADDEADYF CASYTATTTLGYYVFGTGKTVL SEQ ID NO. 48
OIC3	EVQLVQSGGGLVQPGGSLRLSCAAS GFTVNSNHMSWVRQAPGKGLEWVSL IYNGDNTYYADSVKGRFTISRDNPKNT LYLQMNRLRDEDTAVYYCARDWGYN VGDWGQGTLLTVSS SEQ ID NO. 49	LPVLTQPRSVSGSPGQSITISCT GTSDDVGFYNYVSWYQQHPGK APKLLIYDVTKRPSGVDRFSGS KSGNTASLTISGLQAEDEADYY CSSYGGSNFVIFGGGTKTVL SEQ ID NO. 50
OIC6	QVQLVESGGGLVQPGGSLRLSCAAS FTFSRYPMWVRQAPGKGLEWVSSIS GGGDTTYYADSVKGRFAIARDNSKNT VSLEMISLRADTAIVYYCAKDWLYRG GPWGQGTLLTVSS SEQ ID NO. 51	QPVLTQPASVSGSPGQPITISCT GTSSDVGGYNHVSWSYQQYPGE APKVMIFDVSKRPSGVSNRFSG SKSGNTASLTISGLQADDEADYY CNSLTSSGYVFGTGKTVL SEQ ID NO. 52

OIC9	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYGISWVRQAPGQGLEWMGW ISAYNGNTNYAQKLQGRVTMTTDTST STAYMELRSLRSDDTAVYYCARDWG ENEYWGQGTLVTVSS SEQ ID NO. 53	QPVLTQPASVSGSPGQSITISCT GTSSDIGGYNYVSWYQQHPDK APKLMIYDVSSRPSGVSNRFSG SKSGSTASLTISGLQPEDEADYY CISYTNSNIFGGYVFGTGTKLTV L SEQ ID NO. 54
OID1	QVQLVQSGAEVKKPGASVKVSCKTS GYTFTGYMHWRQVPGQGFWMG WISPKTGDNTSPQTFHGRVTMTIDTSI NTAYMEMNRLRSDDTAVYYCAREALI EDAFDIWGQGTMTVTVSS SEQ ID NO. 55	QSVLTQPPSVSGAPGQRVTISC TGSSSNIGAAYDVHWYQQLPGT APKLLIYRNSNRPSGVPDRFSG SKSGTSASLAISGLRSEDEADYY CAAWDDSLSDVVFVGGGTGKLTVL SEQ ID NO. 56
OID10	EVQLVQSGGGGLIQPGGSLRLSCAASG FLVSSKYMSWVRQAPGKGLEWVSVIY TDGSTYYADSVKGRFTISRDNKSNAL YLQMNSLRAEDTAVYYCARDWGYDT ADWGQGTLVTVSS SEQ ID NO. 57	QSVVTQPPSVSAAPGQKISISCS GSSSNVGNVYVSWYQQLPGTA PKLLIFDNNKRPSGIPDRFSGSK SGTSATLGISGLQTGDEADYYC GTWDTSLRALVFGGGTKLTVL SEQ ID NO. 58
OID12	EVQLLES GGGLVQPGRSLRLSCTASG FTFGDYAMSWFRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRHNKNT LYLQMNSLRAEDTAVYYCARGYGIDY WGQGTLVTVSS SEQ ID NO. 59	QSVVTQPPSVSAAPGQRVTISC SGSSSNIENNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSGSK SGTSATLGITGLQTGDEADYYC GTWDSSLSTEVFGGGTKLTVL SEQ ID NO. 60
OID3	EVQLVQSGGGGLVQPGGSLRLSCAAS GFTVSSNHMAWVRQAPGKGLEWVSL IYNGDSTYYPDSVKGRFTISRDNKNA LYLQMNSLRAEDTAVYYCARDWGYD TADWGQGTLVTVSS SEQ ID NO. 61	QSVLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMIYDVTNRPSGVSNRFSG SKSGNAASLTISGLQAEDEADYY CSSYTGSSTLVFGGGTKVTVL SEQ ID NO. 62
OID4	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYMHWRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTTRDTST STVYMELSSLRSED TAVYYCARDRLY GDYFDYWQGQTLVTVSS SEQ ID NO. 63	QSVVTQPPSVSAAPGQKVTISC SGSSSNIGNNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSASK SGTSASLAISGLRSEDEADYYCA AWDDSLSGNWWVFGGGTKLTVL SEQ ID NO. 64
OID5	QVQLVESGGGLIQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYYCASGYGDYE DYWGQGTLVTVSS SEQ ID NO. 65	QSVLTQPPSASGSPGQSVTISC TGTSRDVGGYNYVSWYQQHPG KAPKLMIYDVSKRPSGVSNRFS ASKSGNTASLTISALQAEDEADY YCTSYTGSSPPYVFGTGTKVTV L SEQ ID NO. 66
OID6	EVQLVESGGGLIQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRAEDTAVYYCASGYGDYE DYWGQGTLVTVSS SEQ ID NO. 67	QSVLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMIYDVTKWPSGASNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSTRTYVYGTGTKVTVL SEQ ID NO. 68

OID8	QVQLVQSGAEVKKPGSSVKVSCKAS GGTFSSYAIWVRQAPGQGLEWMGE IPIFGTTNYAQKFQGRVTIIADESTSTA YMESSLRPDDTAVYYCASASSWYE WYFDVWGRGTLTVSS SEQ ID NO. 69	QSVLTQPRSVSGSPGQSVTISC TGTSSDVGGYNYVSWYQQHPG KAPKLMYDVGKRPSGVPDRFS GSKSGNTASLTISGLQAEDEAD YYCSSYTSSGTQVFGTGTKLTV L SEQ ID NO. 70
OIE12	EVQLLES GGGLVQPGRSLRLSCTASG FTFGDYAMSWFRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRHNKNT LYLQMNSLR AEDTAVYYCARGYGIDY WGQGT LTVSS SEQ ID NO. 71	QSVVTQPPSVSAAPGQRTVISC SGSSSNIENNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSGSK SGTSATLGITGLQTGDEADYYC GTWDSLSSTEVFGGGTKLTVL SEQ ID NO. 72
OIE3	QVQLVESGGGLVKPGGSLRLSCAAS GFKFSDNYMTWVRQAPGKGLEWVS ISGSGKTTHFADSVRGRFTISRDN AKNSVDLQMNSLRVEDTAMYYCARWE VG VDAFDIWGQGTMTVTVSS SEQ ID NO. 73	LLVLTQSPSVSVAPGKTARITCG GNNIGSKSVHWYQQKPGQAPV LVVYDDSDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQ VWDSSSDHPVFGGGTKLTVL SEQ ID NO. 74
OIE9	QVQLQQWGAGLLKPSETLSLTCAVYG GPFRSYYWSWIRQPPGKGLEWIGEIN HSGSTNYPNPSLKSRVTISVDRSKNQF SLKLTSVTAADTAVYYCAREGDHEAF DIWGQGTMTVTVSS SEQ ID NO. 75	QPVLTQPPSVSAAPGQKVTISC SGSSSNIGNNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSGSK SGTSATLGITGLQTGDEADYYC GTWDSLSLSSLVFGGGTKLTVL SEQ ID NO. 76
OIF10	QVQLVQSGGGGLVQPGGSLRLSCAAS GFTVNSNHMSWVRQAPGKGLEWVSL IYNGDNTYYADSVKGRFTISRDNPKNT LYLQMNRLRDEDTAVYYCARDWGYN VGDWGQGT LTVSS SEQ ID NO. 77	QSVLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSNRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYAGSNPNPYVFGTGTKVTVL SEQ ID NO. 78
OIF4	EVQLVESGGGLVKPGGSLRLSCAASG FTFSSYRMNWVRQAPGKGLEWVSSI SSDSSDFYYADSVKGRFTISRDNAINS LYLQMNSLR AEDTAVYYCARDWGYD KGDWGQGT LTVSS SEQ ID NO. 79	DIVMTQSPDSLAVSLGERATINC KSSQSLLYNSDNKNYLA WYQQK PGQPPKLLIYWASTRGSGVPDR FSGSGSGTDFTLSSISLQAEDVA VYYCQQYYSTPYTFGQGTKEI K SEQ ID NO. 80
OIF6	QVQLQQWGAGLLKPSETLSLTCAVYG GSFSGYYWSWIRQTPGKGLEWIGEIN HSGSTNYPNPSLKSRVTISADTSRNQF SLRLSSVTAADTAVYYCARGDSGFGV VSSYYFDQWGQGT LTVSS SEQ ID NO. 81	SYELMQPPSESVAPGQTAKITC GGENIGSKSVHWYQQKSGQAP LLVYDDDRDRPSGIPERFFGSN SGDTASLTISGVEAGDEADYYC QVWDSRNDRVVFGGGTKLTVL SEQ ID NO. 82
OIF9	QVQLVESGAEVKKPGASVKVSCKASG YTFTSYGISWVRQAPGQGLEWMGWI SAYNGNTNYAQKLQGRVTMTTDTSTS TAYMELRSLRSDDTAVYYCARELGLD AFDIWGQGTMTVTVSS SEQ ID NO. 83	QSVVTQPPSVSAAPGQKVTISC SGSSSNIGNNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSGSK SGTSATLGITGLQTGDEADYYC GTWDSLS SAVVFGGGTKLTVL SEQ ID NO. 84

OIG1	EVQLVESGAIEVKKPGSSVKVSKASG YTFTNYDINWVRQATGQGLEWMGW MNPNSGNTGYAQKFQGRVTMTRDTS ISTAYMELSSLKSEDTAVYYCARDYY DFDSWGQGTTLTVSS SEQ ID NO. 85	QSVVTQPPSVSAAPGQKVTISC SGSSSNIGKNYVSWYQHFPGTA PKLLIYDNDERPSGIPDRFSGSK SGTSATLGITGLQTGDEADYYC GAWDISLSAWVFGGGTKLTVL SEQ ID NO. 86
OIG11	QVQLVQSGGGLLPGGSLRLSCAAS GFTFSNYDMHWVRQPPGKGLEWVSS IDTAGDTYYEGSAKGRFTISRDNANT LYLQMNSLTTEDTAVYYCAKDRIFWG DFDYWGQGTTLTVSS SEQ ID NO. 87	QAVLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSSSTLYVFGTGTKLTVL SEQ ID NO. 88
OIG12	QVQLVQSGGGLVQPGGSLRLSCAAS GFTFSSYEMNWVRQAPGKGLEWVS ISSSGSTIYYADSVKGRFTISRDN SLYLQMNSLRAEDTAVYYCAREGQLL WAPFDYWGGTTLTVSS SEQ ID NO. 89	QAVLTQPPSVSGAPGQRTVISC TGSNSNIGAGYDVHWYQQLPGT APKLLIYGNTNRPSGVPDRFSG SKSGTSASLAITGLQAEDEADYY CQSYDSRLSAVFGGGTKVTVL SEQ ID NO. 90
OIG2	QVQLVQSGGGLVQPGGSLRLSCAAS GFTVNSNHMSWVRQAPGKGLEWVSL IYNGDNTYYADSVKGRFTISRDNPKNT LYLQMNRLRDEDTAVYYCARDWGYN VGDWGGGTMTVTSS SEQ ID NO. 91	QSALTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSSSTPHYVFGTGTKVTV L SEQ ID NO. 92
OIG5	QMQLVQSGAIEVKKPGASVKVSKAS GYTFTSYMHWRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTRDTST STVYMELNSLRSEDTAVYYCAREYLD YFDYWGGTTLTVSS SEQ ID NO. 93	QAGLTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMYDVSNRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSSSTLRYVFGTGTKLTVL SEQ ID NO. 94
OIG7	QVQLVESGGGLVQPGGSLRLSCAAS GFTFSSYEMNWVRQAPGKGLEWVS ISSSGSTIYYADSVKGRFTISRDN SLYLQMNSLRAEDTAVYYCARVQQW PDDAFDIWGQGTTLTVSS SEQ ID NO. 95	QSVLTQPPSASGAPGQRTVISC SGSSSNIGSDTLDWYQQLPGTA PKLLIYSNNQRPSGVPDRFSGS KSGTSASLAISGLQSEDEANYC AAWDASLNGWVFGGGTKLTVL SEQ ID NO. 96
OIG8	QITLKESGGGVVRPGGSLRLSCAASG FTFDDYGMSWVRQAPGKGLEWVS GSSARNIYYADSVKGRFSISRDN LYLQVNSLRDEDTAVYYCARGAYMD VWNGGTTVTSS SEQ ID NO. 97	AIRMTQSPSSLSASVGRVTITC QASQDISNYLNWYQQKPGKAPK LLIYDASNLETGVPSRFSGSGSG TDFTLTISLQPEDFATYYCLQH NSYPRTFGQGTKVEIK SEQ ID NO. 98
OIG9	QVQLVESGAIEVKKPGASVKVSKASG YTFTSYGISWVRQAPGQGLEWMGI SAYNGNTNYAQKLQGRVTMTTDTST TAYMELRSLRSDDTAVYYCARDLWDT DAFDIWGGGTMTVTSS SEQ ID NO. 99	QAVLTQPPSVSAAPGQKVTISC SGSSSNIGNNYVSWYQQLPGTA PKLLIYDNNKRPSGIPDRFSGSK SGTSATLGITGLQTGDEADYYC GTWDSSLSAYVFGTGTKVTVL SEQ ID NO. 100

OIH10	EVQLVESGGGLVQPGGSLRLSCAAS GFTGSNNYMSWVRQAPGKGLEWVSII YSGGNAYYADSVKGRFTISRDN SKNIL YFQMNSLRVEDTAVYYCAEGYGGVD YWGQGTLVTVSS SEQ ID NO. 101	QSVVTQPPSVSAAPGQKVTISC SGSSSNIGSNSVSWFQHLPGTA PKLLIYDNNQRPSNIPDRFSGSK SGASATLGITGLQTGDEADYYC GTWDHRLNTYVFGTGTKVTVL SEQ ID NO. 102
OIH11	EVQLVQSGGGLVQPGGSLRLSCAAS GFTVSSNHMAWVRQAPGKGLEWVSL IYNGDSTYYPDSVKGRFTISRDN SKNA LYLQMNSLRAEDTAVYYCARDWGYD TADWGQGT LTVTVSS SEQ ID NO. 103	SYELMQPPSASGTPGQRVTISC SGSSSNIGSNTVNWYQQLPGTA PKLLIYSYDQRPSGVPDRFSGS KSGTSASLAISGLQSEDEADYYC AAWDDSLNGYVFGTGTKVTVL SEQ ID NO. 104
OIH12	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYMHVVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTRDTST STVYMELSSLRSED TAVYYCAREYLD YFDYWGGQGT LTVTVSS SEQ ID NO. 105	QSVVTQPASVSGSPGQSITISCT GTSSDVGGYNYVSWYQQHPGK APKLMIYDVSKRPSGVSNRFSG SKSGNTASLTISGLQAEDEADYY CSSYTSSSTYVFGTGTKVTVL SEQ ID NO. 106
OIH3	QVQLVQSGGGLVQPGGSLRLSCAAS GFTVSSNHMAWVRQAPGKGLEWVSL IYNGDSTYYPDSVKGRFTISRDN SKNA LYLQMNSLRAEDTAVYYCARDWGYD TADWGQGT LTVTVSS SEQ ID NO. 107	QPVLTQPASVSGSPGQSIAISCS GTSSDIGTYDSVSWYQQHPGKA PKVIIYEVDKRPSPGVPDRFSGSK SGNTASLT VSGLQAEDEADYYC SSYAGSNNFVFGTGTKLTVL SEQ ID NO. 108
OIH5	QVQLVQSGGGLVQPGGSLRLSCAAS GFTVNSNHMSWVRQAPGKGLEWVSL IYNGDNTYYADSVKGRFTISRDN PKNT LYLQMNRLRDEDTAVYYCARDWGYN VGDWGQGT LTVTVSS SEQ ID NO. 109	QSVLTQPPSASGTPGQRVTISC SGSNSNIGTNTVNWYQQVPGTA PKLLIHGNDQRPSGVPDRFSGS KSDTSASLAITGLQSDDDADYYC SAWDDSLNADVFGGGTKLTVL SEQ ID NO. 110
OIH6	EVQLVQSGAEVKKPGASVKVSCKASG YTFTGYMHVVRQAPGQGLEWMGW INPNSGGTNYAQKFQGRVTMTRDTSI STAYMELSRLRSDDTAVYYCVRSGSY SDFDYWGQGT LTVTVSS SEQ ID NO. 111	SYELMQPPSVSVAPGQTARITC GGNNIGSKSVHWYQQKPGQAPI LVIYYDDDRPSGIPERFSGSKSG NTATLTISGVEAGDEADYYCQV WDSYTYHVVFGGGTKLTVL SEQ ID NO. 112

Sequence Listing
OprF (epitope 8)-binding Antibodies

	Heavy chain variable domain region	Light chain variable domain region
FEA2	EVQLVESGGGLVQPGGSLRLSCAGS GFTFSSYDMNWVRQAPGKGLEWISYI SSSGSAIFYADSVKGRFTISRDNAGNS VYLQMNSLRAEDTAIYYCARRFDYWG QGTLVTVSS SEQ ID NO. 113	DIVMTQTPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWLQQR PGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLNITRVETDDVG IYYCMQGTHWPPFTFGPGTKVD

		IK SEQ ID NO. 114
FEA3	QVQLVESGGGVFQPGRSLRLSCSTS GFTFSSYDMNWVRQAPGKGLEWLSY ISSSGSAMFYADSVKGRFTISRDTAKN SLYLQMNSLRDEDTAVYYCARQFDQ WGQGTTLTVSS SEQ ID NO. 115	DIVMTQSPLSLPVALGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKVSHRDSGVPDR FSGSGSGTDFTLTISRVEAEDLG IYYCAQGTHWPPFTFGQGTKLEI K SEQ ID NO. 116
FEA4	QVQLVQSGGGVVPGRSLRLSCAAS GFTFSSYGMHWVRQAPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARDGRFL PYPGGMDVWGQGTTLTVSS SEQ ID NO. 117	QPVLTQPPSASVAPGQRVTISC SGTTSNIEYNSVHWYQQPLGAA PKLLIYNTDKRPPGIPDRFSASK SGTSASLAISGLRSEDEATYYCA TWDDSLSVMLFGGGTKVTVL SEQ ID NO. 118
FEA7	QVQLVQSGGGLVQPGGSLRLSCAAS GFTFNNYDMNWVRQAPGKGLEWVSY ISSSGSTIYYADSVKGRFTISRDSA EKS LYLQMNSLRAEDTAVYYCARRIDSWG QGTLTVSS SEQ ID NO. 119	DIVMTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLKISRVEAEDV GVYYCMQGTHWPPYTFGQGTK LEIK SEQ ID NO. 120
FEA12	QVQLVESGGGLVQPGGSLRLSCAAS GFTFSSYDMNWVRQAPGKGLEWLSY ISSSGSAMFYADSVKGRFTISRDTAKN SLYLQMNSLRDEDTAVYYCARQFDQ WGQGTTLTVSS SEQ ID NO. 121	DIVMTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKISNRDSGVPDRF SGSGSGTDFTLRISRVEAEDVG VYYCMQGSHPPPFTFGPGTKV DIK SEQ ID NO. 122
FEC2	QVQLVQSGGGLVQPGGSLRLSCAAS GFTVSNNYMSWVRQAPGKGLEWVSV IYGGGSTFYANSVKGRFTISRDNSENT LYLQMNSLRSED TAVYYCARD SGYGD FDYWGGQGTTLTVSS SEQ ID NO. 123	DVVMQTSPSSLSASVGDRVTIT CRASQSISSYLNWYQQKPGKAP KLLIYDAYNLQSGVPSKFSGSGS GTDFTLTISSLPEDFATYYCQQ SYSNPLTFGGGKLEIK SEQ ID NO. 124
FEC4	EVQLVESGAEVKKPGASVKVCKTSG YTFTGHYMDWVRQAPGQGLEWMGGI NPKSGD TDYAQKFQGRVTMTRDTSIS TVYIELNSLTSDDTAMYYCARD FHYW GQGTTLTVSS SEQ ID NO. 125	DIVMTQSPLSLPVTLGQPASISC KSSQSLLHSDGDTYLNWLLQRP GQSPRRLIYKVSSRD SGVPDRF SGSGSGTDFTLKISRVEAD DVG VYYCMQGSHPPPITFGQGT RLE IK SEQ ID NO. 126
FEC10	EVQLVESGGGLIQPGGSLRLSCAASG FTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDN SKNT LYLQMNSLRAEDTAVYYCARD DSYGA FDIWGGQGTMTVTVSS SEQ ID NO. 127	DIVMTQTPSSLSASVGDRVTITC QASQDINNYLNWYQQKPGKAP KLLIYDASNLETGVPSRVSGSGS GTDFTFISSLQPEDIGTYYCQQY DNLPTYFGQGTKVEIK SEQ ID NO. 128

FED2	EVQLVESGGGLVQPGRSLRLSCTASG FTFGDYAMSWFRQAPGKGLEWVGFI RSKAYGGTTEYAASVKGRFTISRDDS KSIAYLQMNSLKTEDTAVYYCSSETGR IDYWGQGTTVTVSS SEQ ID NO. 129	DIVMTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYQVSNRDSGVPDR FSGSGSGTDFTLKISRVEAEDV GVYYCMQGSHPWPITFGQGTR LEIK SEQ ID NO. 130
FED5	EVQLVESGRGVVQPGTSLRLSCAASG FTFSRFDMMHWVRQAPGKGLEWVAFIS YDATKKYYADSVRGRFTISRDNKNT FYLQMNSLRGEDITAVYYCARDYGEFD NWGQGTTLTVSS SEQ ID NO. 131	DVVMQTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLKISRVEAEDV GVYYCMQGTHWPPITFGQGTR VEIK SEQ ID NO. 132
FED8	EVQLVESGGGLVQPGGSLRLSCAAS GFIFGSYEMHWVRQAPGKGLEWVSYI SGSGSKIYYADSVKGRFTISRDNKNS VYLQMNSLGAEDTAVYYCAGSLDYW GQGTTLTVSS SEQ ID NO. 133	DVVMQTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKVSNRDSGVPDR FSGSGSGTDFTLKISRVEAEDV GVYYCMQGTHWPPITFGQGTRL EIK SEQ ID NO. 134
FEE10	QVQLVQSGGGLVKPGGSLRLSCAAS GFTFSSYEMNWVRQAPGKGLEWVSY ISSSGSTIYYADSVKGRFTISRDNKNT LYLQMNSLTAEDTAVYYCASFSKHAH WGQGTTLTVSS SEQ ID NO. 135	DVVMQTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFQQR PGQSPRRLIYKVSNRDSGVPDR SGSGSGTDFTLKISRVEAEDV GVYYCMQGTHWPPITFGQGTRL EIK SEQ ID NO. 136
FEF8	QVQLVESGGGLVQPGGSLRLSCAAS GFTFSNYWMAWVRQAPGKGLEWVA NIKEDGSEKYYVDSVKGRFTISRDNK NSVYLQMNSLRAEDTGVYYCAGRIFDI WGQGTMTVTSS SEQ ID NO. 137	QSVVTQPPSVSAAPGQRVTISC SGSTSNIGTNYVSWFQHLPGAA PKLLIYDNSEPSGIPDRFSASK SGASATLGITGLQTGDEADYYC GTWDDSLSAGVFGGGTKVTVL SEQ ID NO. 138
FEH3	QVQLVQSGAEVKKPGASVKVSCKAS GYTLSSYHMHWRQAPGQGLEWMG LIDPSDDTTVYAQKFQGRVTMTSDTS TSTVYMHLSLRPEDTAVYFCARDLG NFWGQGTTLTVSS SEQ ID NO. 139	DIVMTQSPLSLPVTLGQPASISC RSSQSLVHSDGNTYLNWFHQR PGQSPRRLIYQVSNRDSGVPDR FSGSGSGTDFTLKISRVEADDV GIYYCMQGTHWPPITFGGGTKV EIK SEQ ID NO. 140
FEH7	EVQLVESGGGLVQPGGSLRLSCAAS GFTVSSNYMSWVRQAPGKGLEWVSV IYSGGSTYYADSVKGRFTISRDNKNT LYLQMNSLRGEDITAVYYCARGLRDSS GYHWGSFDPWGQGTTLTVSS SEQ ID NO. 141	SSELTQDPAVSVALGQTVRITCQ GDSLRFYFASWYQQRPGQAPR LVIYGENERPSGIPDRFSASTSG NTASLTIAQAQAEDEGDYYCNS RDNDQHYVFGSGTKLTVL SEQ ID NO. 142

We claim:

1. A fully human antibody of an IgG class that binds to an OprF and OprI epitope that has a heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3,
5 SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55,
10 SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID
15 NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO. 2,
20 SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO.
25 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108,
30 SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof.

2. The fully human antibody of claim 1, wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2 (called OFA1 herein), SEQ ID NO. 3/SEQ ID NO. 4 (called OFC7 herein), SEQ ID NO. 5/SEQ ID NO. 6 (called OFC10 herein), SEQ ID NO. 7/SEQ ID NO. 8 (called OFF7 herein), SEQ ID NO. 9/SEQ ID NO. 10 (called OFF8 herein), SEQ ID NO. 11/SEQ ID NO. 12 (called OFG5 herein), SEQ ID NO. 13/SEQ ID NO. 14 (called OFH10 herein), SEQ ID NO. 15/SEQ ID NO. 16 (called OIA1 herein), SEQ ID NO. 17/SEQ ID NO. 18 (called OIA10 herein), SEQ ID NO. 19/SEQ ID NO. 20 (called OIA2 herein), SEQ ID NO. 21/SEQ ID NO. 22 (called OIA4 herein), SEQ ID NO. 23/SEQ ID NO. 24 (called OIA5 herein), SEQ ID NO. 25/SEQ ID NO. 26 (called OIA6 herein), SEQ ID NO. 27/SEQ ID NO. 28 (called OIA7 herein), SEQ ID NO. 29/SEQ ID NO. 30 (called OIA8 herein), SEQ ID NO. 31/SEQ ID NO. 32 (called OIA9 herein), SEQ ID NO. 33/SEQ ID NO. 34 (called OIB1 herein), SEQ ID NO. 35/SEQ ID NO. 36 (called OIB11 herein), SEQ ID NO. 37/SEQ ID NO. 38 (called OIB12 herein), SEQ ID NO. 39/SEQ ID NO. 40 (called OIB2 herein), SEQ ID NO. 41/SEQ ID NO. 42 (called OIB3 herein), SEQ ID NO. 43/SEQ ID NO. 44 (called OIB8 herein), SEQ ID NO. 45/SEQ ID NO. 46 (called OIB9 herein), SEQ ID NO. 47/SEQ ID NO. 48 (called OIC1 herein), SEQ ID NO. 49/SEQ ID NO. 50 (called OIC3 herein), SEQ ID NO. 51/SEQ ID NO. 52 (called OIC6 herein), SEQ ID NO. 53/SEQ ID NO. 54 (called OIC9 herein), SEQ ID NO. 55/SEQ ID NO. 56 (called OID1 herein), SEQ ID NO. 57/SEQ ID NO. 58 (called OID10 herein), SEQ ID NO. 59/SEQ ID NO. 60 (called OID12 herein), SEQ ID NO. 61/SEQ ID NO. 62 (called OID3 herein), SEQ ID NO. 63/SEQ ID NO. 64 (called OID3 herein), SEQ ID NO. 65/SEQ ID NO. 66 (called OID5 herein), SEQ ID NO. 67/SEQ ID NO. 68 (called OID6 herein), SEQ ID NO. 69/SEQ ID NO. 70 (called OID8 herein), SEQ ID NO. 71/SEQ ID NO. 72 (called OIE12 herein), SEQ ID NO. 73/SEQ ID NO. 74 (called OIE3 herein), SEQ ID NO. 75/SEQ ID NO. 76 (called OIE9 herein), SEQ ID NO. 77/SEQ ID NO. 78 (called OIF10 herein), SEQ ID NO. 79/SEQ ID NO. 80 (called OIF4 herein), SEQ ID NO. 81/SEQ ID NO. 82 (called OIF6 herein), SEQ ID NO. 83/SEQ ID NO. 84 (called OIF9 herein), SEQ ID NO. 85/SEQ ID NO. 86 (called OIG1 herein), SEQ ID NO. 87/SEQ ID NO. 88 (called OIG11 herein), SEQ ID NO. 89/SEQ ID NO. 90 (called OIG12 herein), SEQ ID NO. 91/SEQ ID NO. 92 (called OIG2 herein), SEQ ID NO. 93/SEQ ID NO. 94 (called OIG5 herein), SEQ ID NO. 95/SEQ ID NO. 96 (called OIG7 herein), SEQ ID NO. 97/SEQ ID NO. 98 (called OIG8 herein), SEQ ID NO. 99/SEQ ID NO. 100 (called OIG9 herein), SEQ ID NO. 101/SEQ ID NO. 102 (called OIH10 herein), SEQ ID NO. 103/SEQ ID NO. 104 (called OIH11 herein), SEQ ID NO. 105/SEQ ID NO. 106 (called OIH12 herein),

SEQ ID NO. 107/SEQ ID NO. 108 (called OIH3 herein), SEQ ID NO. 109/SEQ ID NO. 110 (called OIH5 herein), SEQ ID NO. 111/SEQ ID NO. 112 (called OIH6 herein), SEQ ID NO. 113/SEQ ID NO. 114 (called FEA2 herein), SEQ ID NO. 115/SEQ ID NO. 116 (called FEA3 herein), SEQ ID NO. 117/SEQ ID NO. 118 (called FEA4 herein), SEQ ID NO. 119/SEQ ID NO. 120 (called FEA7 herein), SEQ ID NO. 121/SEQ ID NO. 122 (called FEA12 herein), SEQ ID NO. 123/SEQ ID NO. 124 (called FEC2 herein), SEQ ID NO. 125/SEQ ID NO. 126 (called FEC4 herein), SEQ ID NO. 127/SEQ ID NO. 128 (called FEC10 herein), SEQ ID NO. 129/SEQ ID NO. 130 (called FED2 herein), SEQ ID NO. 131/SEQ ID NO. 132 (called FED5 herein), SEQ ID NO. 133/SEQ ID NO. 134 (called FED8 herein), SEQ ID NO. 135/SEQ ID NO. 136 (called FEE10 herein), SEQ ID NO. 137/SEQ ID NO. 138 (called FEF8 herein), SEQ ID NO. 139/SEQ ID NO. 140 (called FEH2 herein), SEQ ID NO. 141/SEQ ID NO. 142 (called FEH7 herein), and combinations thereof.

3. A Fab fully human antibody fragment, having a variable domain region from a heavy chain and a variable domain region from a light chain, wherein the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ

ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof.

4. The fully human antibody Fab fragment of claim 3, wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO.

115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

5. A single chain human antibody, having a variable domain region from a heavy chain and a variable domain region from a light chain and a peptide linker connection the heavy chain and light chain variable domain regions, wherein the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ

ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof.

6. The fully human single chain antibody of claim 5, wherein the single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO.

138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

7. The fully human single chain antibody of claim 5, wherein the fully human single chain antibody has both a heavy chain variable domain region and a light chain variable domain region, wherein the single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

8. A method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections, comprising administering an effective amount of an anti-OprF and anti-OprI polypeptide, wherein the anti-OprF and anti-OprI polypeptide is selected from the group consisting of a fully human antibody of an IgG class that binds to an OprF and OprI epitope with a binding affinity of at least 10^{-6} M, a Fab fully human antibody fragment, having a variable domain region from a heavy chain and a variable domain region from a light chain, a single chain human antibody, having a variable domain region from a heavy chain and a variable domain region from a light chain and a peptide linker connection the heavy chain and light chain variable domain regions, and combinations thereof;

wherein the fully human antibody has a heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has a light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO.

84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof;

wherein the Fab fully human antibody fragment has the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has the light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ

ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and

5 combinations thereof; and

wherein the single chain human antibody has the heavy chain variable domain sequence that is at least 95% identical to the amino acid sequences selected from the group consisting of SEQ ID NO. 1, SEQ ID NO. 3, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 9, SEQ ID NO. 11, SEQ ID NO. 13, SEQ ID NO. 15, SEQ ID NO. 17, SEQ ID NO. 19, SEQ ID NO. 21, SEQ ID NO. 23, SEQ ID NO. 25, SEQ ID NO. 27, SEQ ID NO. 29, SEQ ID NO. 31, SEQ ID NO. 33, SEQ ID NO. 35, SEQ ID NO. 37, SEQ ID NO. 39, SEQ ID NO. 41, SEQ ID NO. 43, SEQ ID NO. 45, SEQ ID NO. 47, SEQ ID NO. 49, SEQ ID NO. 51, SEQ ID NO. 53, SEQ ID NO. 55, SEQ ID NO. 57, SEQ ID NO. 59, SEQ ID NO. 61, SEQ ID NO. 63, SEQ ID NO. 65, SEQ ID NO. 67, SEQ ID NO. 69, SEQ ID NO. 71, SEQ ID NO. 73, SEQ ID NO. 75, SEQ ID NO. 77, SEQ ID NO. 79, SEQ ID NO. 81, SEQ ID NO. 83, SEQ ID NO. 85, SEQ ID NO. 87, SEQ ID NO. 89, SEQ ID NO. 91, SEQ ID NO. 93, SEQ ID NO. 95, SEQ ID NO. 97, SEQ ID NO. 99, SEQ ID NO. 101, SEQ ID NO. 103, SEQ ID NO. 105, SEQ ID NO. 107, SEQ ID NO. 109, SEQ ID NO. 111, SEQ ID NO. 113, SEQ ID NO. 115, SEQ ID NO. 117, SEQ ID NO. 119, SEQ ID NO. 121, SEQ ID NO. 123, SEQ ID NO. 125, SEQ ID NO. 127, SEQ ID NO. 129, SEQ ID NO. 131, SEQ ID NO. 133, SEQ ID NO. 135, SEQ ID NO. 137, SEQ ID NO. 139, SEQ ID NO. 141, and combinations thereof, and that has the light chain variable domain sequence that is at least 95% identical to the amino acid sequence consisting of SEQ ID NO. 2, SEQ ID NO. 4, SEQ ID NO. 6, SEQ ID NO. 8, SEQ ID NO. 10, SEQ ID NO. 12, SEQ ID NO. 14, SEQ ID NO. 16, SEQ ID NO. 18, SEQ ID NO. 20, SEQ ID NO. 22, SEQ ID NO. 24, SEQ ID NO. 26, SEQ ID NO. 28, SEQ ID NO. 30, SEQ ID NO. 32, SEQ ID NO. 34, SEQ ID NO. 36, SEQ ID NO. 38, SEQ ID NO. 40, SEQ ID NO. 42, SEQ ID NO. 44, SEQ ID NO. 46, SEQ ID NO. 48, SEQ ID NO. 50, SEQ ID NO. 52, SEQ ID NO. 54, SEQ ID NO. 56, SEQ ID NO. 58, SEQ ID NO. 60, SEQ ID NO. 62, SEQ ID NO. 64, SEQ ID NO. 66, SEQ ID NO. 68, SEQ ID NO. 70, SEQ ID NO. 72, SEQ ID NO. 74, SEQ ID NO. 76, SEQ ID NO. 78, SEQ ID NO. 80, SEQ ID NO. 82, SEQ ID NO. 84, SEQ ID NO. 86, SEQ ID NO. 88, SEQ ID NO. 90, SEQ ID NO. 92, SEQ ID NO. 94, SEQ ID NO. 96, SEQ ID NO. 98, SEQ ID NO. 100, SEQ ID NO. 102, SEQ ID NO. 104, SEQ ID NO. 106, SEQ ID NO. 108, SEQ ID NO. 110, SEQ ID NO. 112, SEQ ID NO. 114, SEQ ID NO. 116, SEQ ID NO. 118, SEQ ID NO. 120, SEQ ID NO. 122, SEQ

ID NO. 124, SEQ ID NO. 126, SEQ ID NO. 128, SEQ ID NO. 130, SEQ ID NO. 132, SEQ ID NO. 134, SEQ ID NO. 136, SEQ ID NO. 138, SEQ ID NO. 140, SEQ ID NO. 142, and combinations thereof.

9. The method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections of claim 8, wherein the fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

10. The method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections of claim 8, wherein the fully human antibody Fab fragment has both a heavy chain variable domain region and a light chain variable domain region wherein the antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO. 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

11. The method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections of claim 8, wherein the fully human single chain antibody has both a heavy chain variable domain region and a light chain variable domain region, wherein the

single chain fully human antibody has a heavy chain/light chain variable domain sequence selected from the group consisting of SEQ ID NO. 1/SEQ ID NO. 2, SEQ ID NO. 3/SEQ ID NO. 4, SEQ ID NO. 5/SEQ ID NO. 6, SEQ ID NO. 7/SEQ ID NO. 8, SEQ ID NO. 9/SEQ ID NO. 10, SEQ ID NO. 11/SEQ ID NO. 12, SEQ ID NO. 13/SEQ ID NO. 14, SEQ ID NO.

5 15/SEQ ID NO. 16, SEQ ID NO. 17/SEQ ID NO. 18, SEQ ID NO. 19/SEQ ID NO. 20, SEQ ID NO. 21/SEQ ID NO. 22, SEQ ID NO. 23/SEQ ID NO. 24, SEQ ID NO. 25/SEQ ID NO. 26, SEQ ID NO. 27/SEQ ID NO. 28, SEQ ID NO. 29/SEQ ID NO. 30, SEQ ID NO. 31/SEQ ID NO. 32, SEQ ID NO. 33/SEQ ID NO. 34, SEQ ID NO. 35/SEQ ID NO. 36, SEQ ID NO. 37/SEQ ID NO. 38, SEQ ID NO. 39/SEQ ID NO. 40, SEQ ID NO. 41/SEQ ID NO. 42, SEQ ID NO. 43/SEQ ID NO. 44, SEQ ID NO. 45/SEQ ID NO. 46, SEQ ID NO. 47/SEQ ID NO. 48, SEQ ID NO. 49/SEQ ID NO. 50, SEQ ID NO. 51/SEQ ID NO. 52, SEQ ID NO. 53/SEQ ID NO. 54, SEQ ID NO. 55/SEQ ID NO. 56, SEQ ID NO. 57/SEQ ID NO. 58, SEQ ID NO. 59/SEQ ID NO. 60, SEQ ID NO. 61/SEQ ID NO. 62, SEQ ID NO. 63/SEQ ID NO. 64, SEQ ID NO. 65/SEQ ID NO. 66, SEQ ID NO. 67/SEQ ID NO. 68, SEQ ID NO. 69/SEQ ID NO. 70, SEQ ID NO. 71/SEQ ID NO. 72, SEQ ID NO. 73/SEQ ID NO. 74, SEQ ID NO. 75/SEQ ID NO. 76, SEQ ID NO. 77/SEQ ID NO. 78, SEQ ID NO. 79/SEQ ID NO. 80, SEQ ID NO. 81/SEQ ID NO. 82, SEQ ID NO. 83/SEQ ID NO. 84, SEQ ID NO. 85/SEQ ID NO. 86, SEQ ID NO. 87/SEQ ID NO. 88, SEQ ID NO. 89/SEQ ID NO. 90, SEQ ID NO. 91/SEQ ID NO. 92, SEQ ID NO. 93/SEQ ID NO. 94, SEQ ID NO. 95/SEQ ID NO. 96, SEQ ID NO. 97/SEQ ID NO. 98, SEQ ID NO. 99/SEQ ID NO. 100, SEQ ID NO. 101/SEQ ID NO. 102, SEQ ID NO. 103/SEQ ID NO. 104, SEQ ID NO. 105/SEQ ID NO. 106, SEQ ID NO. 107/SEQ ID NO. 108, SEQ ID NO. 109/SEQ ID NO. 110, SEQ ID NO. 111/SEQ ID NO. 112, SEQ ID NO. 113/SEQ ID NO. 114, SEQ ID NO. 115/SEQ ID NO. 116, SEQ ID NO. 117/SEQ ID NO. 118, SEQ ID NO. 119/SEQ ID NO. 120, SEQ ID NO. 121/SEQ ID NO. 122, SEQ ID NO. 123/SEQ ID NO. 124, SEQ ID NO. 125/SEQ ID NO. 126, SEQ ID NO. 127/SEQ ID NO. 128, SEQ ID NO. 129/SEQ ID NO. 130, SEQ ID NO. 131/SEQ ID NO. 132, SEQ ID NO. 133/SEQ ID NO. 134, SEQ ID NO. 135/SEQ ID NO. 136, SEQ ID NO. 137/SEQ ID NO. 138, SEQ ID NO. 139/SEQ ID NO. 140, SEQ ID NO. 141/SEQ ID NO. 142, and combinations thereof.

30 12. The method for treating or preventing a disease caused by *Pseudomonas aeruginosa* infections of claim 8, wherein the disease is selected from the group consisting of burns, surgical site infections, diabetic foot ulcers, infected wounds, and cystic fibrosis.

Figure 1

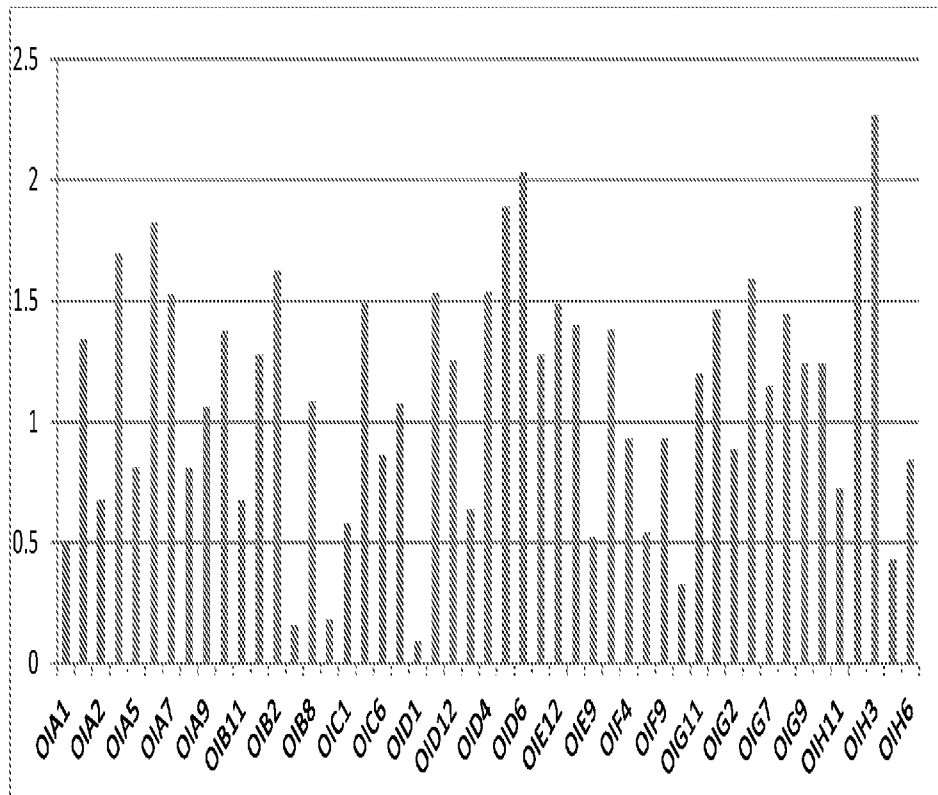


Figure 2

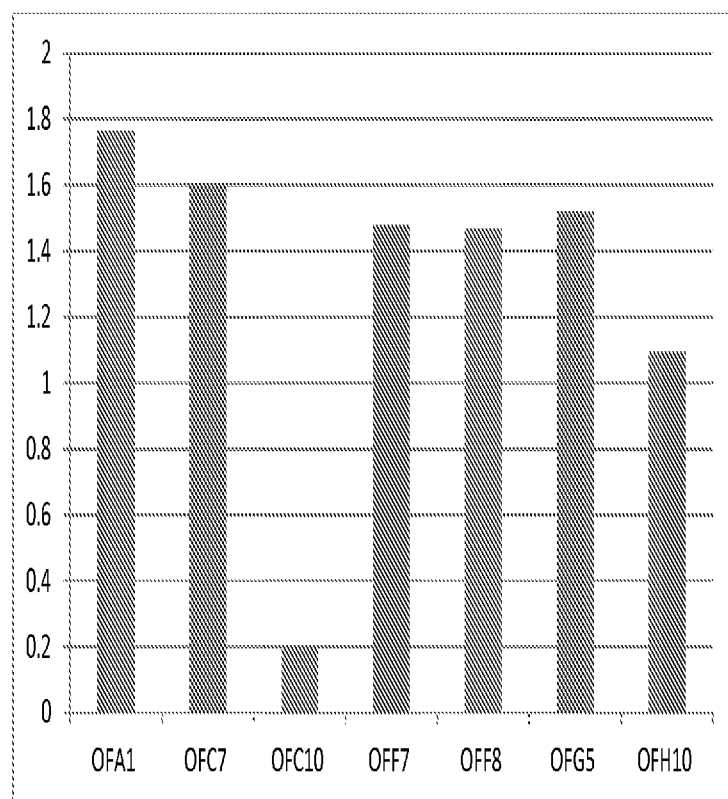


Figure 3

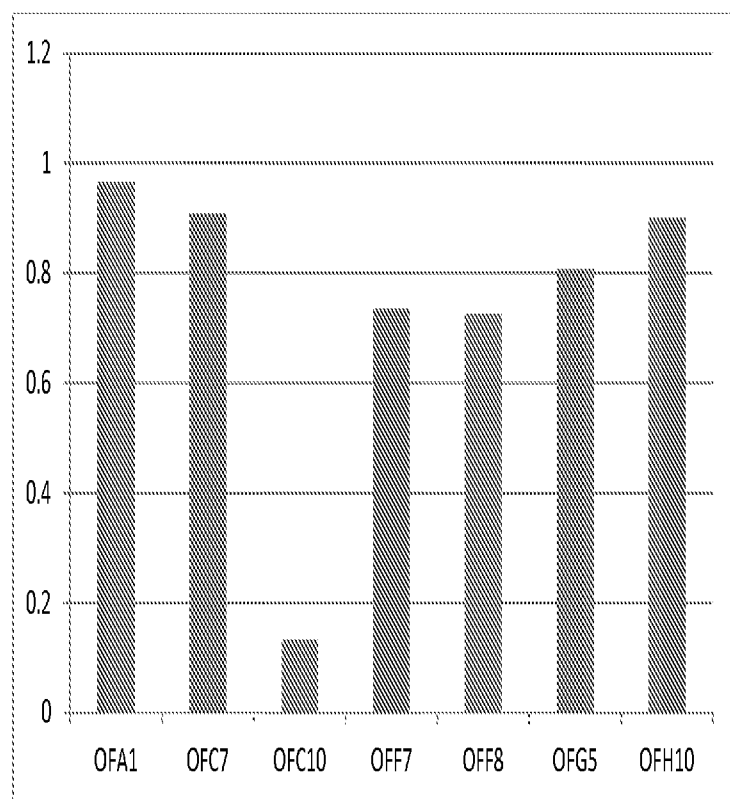


Figure 4

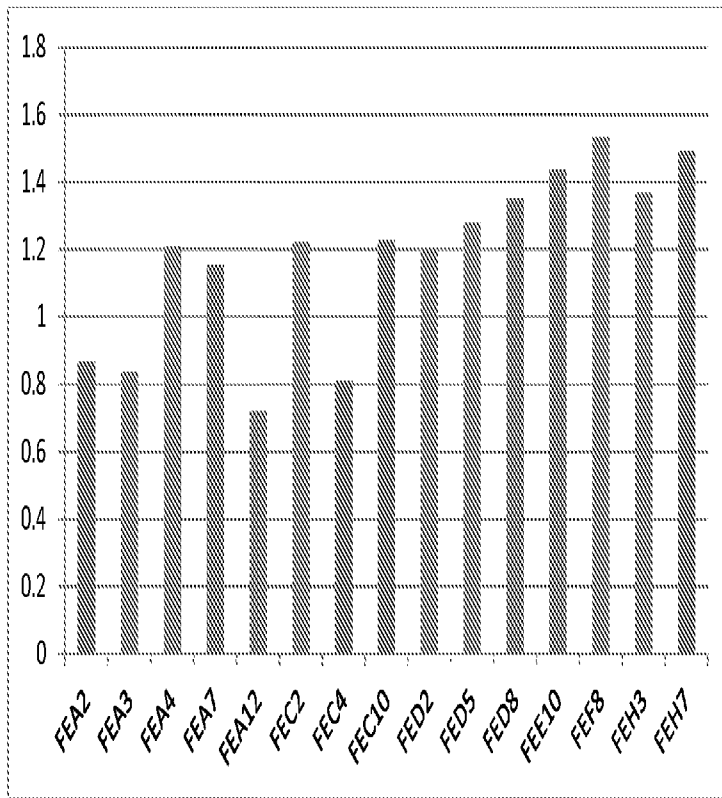


Figure 6

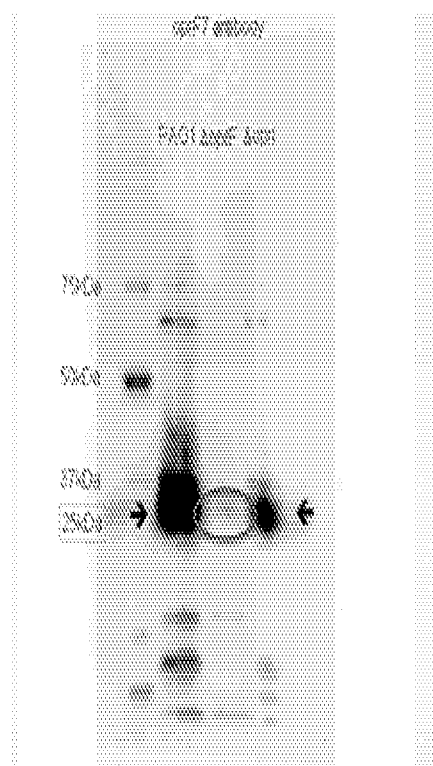


Figure 7



Figure 8A

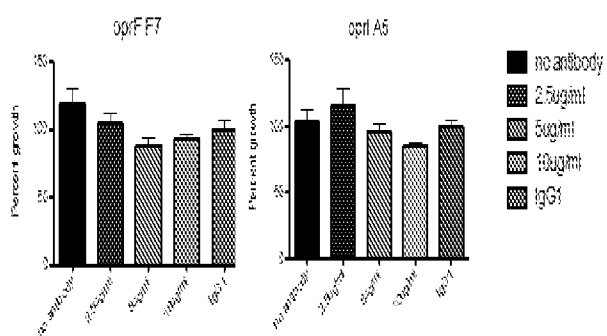


Figure 8B

