CLAIMS

1. An isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl comprises:

i) a heavy chain variable domain (V_H) comprising a heavy chain complementarity determining region (HC-CDR) 1 comprising SSGDYWG (SEQ ID NO: 1), or a variant thereof comprising up to about 3 amino acid substitutions; an HC-CDR2 comprising SIHNX$_1$GSTYYNPSLKG (SEQ ID NO: 213), or a variant thereof comprising up to about 3 amino acid substitutions, wherein X_1 is S, K, or Q; and an HC-CDR3 comprising QFGSETYYX$_1$GIX$_2$P (SEQ ID NO: 190), or a variant thereof comprising up to about 3 amino acid substitutions, wherein X_1 is N, S, V, T, or P, X_2 is D, Y, C, H, S, R, A, E, G, K, W, V, or Q;

and a light chain variable domain (V_L) comprising a light chain complementarity determining region (LC-CDR) 1 comprising RSSQSLLHSX$_1$GYNYLD (SEQ ID NO: 184), or a variant thereof comprising up to about 3 amino acid substitutions, wherein X_1 is N, A, V, F, R, G, H, Q, W, or P; an LC-CDR2 comprising LGSNRAS (SEQ ID NO: 51), or a variant thereof comprising up to about 3 amino acid substitutions; and an LC-CDR3 comprising MQALQTPX$_1$T (SEQ ID NO: 214), wherein X_1 is R or Y, or a variant thereof comprising up to about 3 amino acid substitutions; or

ii) a heavy chain variable domain (V_H) comprising a heavy chain complementarity determining region (HC-CDR) 1 comprising SSGDYWG (SEQ ID NO: 1); an HC-CDR2 comprising amino acid sequence selected from the group of SEQ ID NO:13, and SEQ ID NOs:163-164; and an HC-CDR3 comprising amino acid sequence selected from the group of SEQ ID NO: 24, SEQ ID NO: 36, SEQ ID NOs: 170-183, and SEQ ID NOs: 185-188;

and a light chain variable domain (V_L) comprising a light chain complementarity determining region (LC-CDR) 1 comprising amino acid sequence selected from the group of SEQ ID NO: 37, SEQ ID NO: 50, and SEQ ID NOs: 191-198; an LC-CDR2 comprising LGSNRAS (SEQ ID NO: 51); and an LC-CDR3 comprising amino acid sequence selected from the group of SEQ ID NO: 62 and SEQ ID NO: 69.

2. The isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl of claim 1, comprises:

(i) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 13, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 24, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(ii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 170, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(iii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 171, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(iv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 172, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(v) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 173, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(vi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 36, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(vii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 174, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(viii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 175, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(ix) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 176, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(x) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 177, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 178, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 179, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xiii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 180, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xiv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 191, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 192, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xvi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 193, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xvii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xviii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 194, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xix) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 195, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xx) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 196, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 197, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 36, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxiii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 198, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxiv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 13, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 181, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 164, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 24, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxvi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs; or

(xxvii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 13, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 183, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxviii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 164, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 183, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxix) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 13, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 181, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxx) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 185, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxxi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 186, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxxii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 187, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxxiii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 188, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 50, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs; or

(xxxiv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 163, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 182, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 37, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 51, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 69, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs.

3. The isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl of claim 1 or 2, comprises:

(i) a V_H comprising the amino acid sequence of SEQ ID NOs: 79 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO:79, and a V_L comprising the amino acid sequence of SEQ ID NO: 91 or a

variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO:91;

(ii) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 128-139, SEQ ID NOs: 149-151, SEQ ID NOs:154-155 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 128-139, SEQ ID NOs: 149-151, SEQ ID NOs:154-155, and a V_L comprising the amino acid sequence of SEQ ID NO: 91 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 91;

(iii) a V_H comprising the amino acid sequence of SEQ ID NO: 151 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 151, and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 140-148 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 140-148;

(iv) a V_H comprising the amino acid sequence of any one of SEQ ID NO: 132, SEQ ID NO:149, SEQ ID NOs: 152-153, SEQ ID NOs: 156-157 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NO: 132, SEQ ID NO:149, SEQ ID NOs: 152-153, SEQ ID NOs: 156-157, and a V_L comprising the amino acid sequence of SEQ ID NO: 143 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 143; or

(v) a V_H comprising the amino acid sequence of SEQ ID NO: 151 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 151, and a V_L comprising the amino acid sequence of SEQ ID NO: 98 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 98.

4. An isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl comprises:

i) a heavy chain variable domain (V_H) comprising a heavy chain complementarity determining region (HC-CDR) 1 comprising IHSVH (SEQ ID NO: 4), or a variant thereof comprising up to about 3 amino acid substitutions; an HC-CDR2 comprising

TIISSGTTTTYAQSFQD (SEQ ID NO: 16), or a variant thereof comprising up to about 3 amino acid substitutions; and an HC-CDR3 comprising $X_1X_2X_3X_4$ (SEQ ID NO: 189), or a variant thereof comprising up to about 3 amino acid substitutions, wherein X_1 is D, Y or N, X_2 is G, or A, X_3 is D, or T, X_4 is S, A, or T;

and a light chain variable domain (V_L) comprising a light chain complementarity determining region (LC-CDR) 1 comprising RASQGISSWLA (SEQ ID NO: 40), or a variant thereof comprising up to about 3 amino acid substitutions; an LC-CDR2 comprising HASTLES (SEQ ID NO: 54), or a variant thereof comprising up to about 3 amino acid substitutions; and an LC-CDR3 comprising LQAX_1SLPHT (SEQ ID NO: 158), or a variant thereof comprising up to about 3 amino acid substitutions, wherein X_1 is N, D, Y, F, P, G, K, H, A, C, E, Q, R, S, T, V, W or L; or

ii) a heavy chain variable domain (V_H) comprising a heavy chain complementarity determining region (HC-CDR) 1 comprising IHSVH (SEQ ID NO: 4); an HC-CDR2 comprising TIISSGTTTTYAQSFQD (SEQ ID NO: 16); and an HC-CDR3 comprising amino acid sequence selected from a group of SEQ ID NO: 27, SEQ ID NO: 35, and SEQ ID NOs: 165-169;

and a light chain variable domain (V_L) comprising a light chain complementarity determining region (LC-CDR) 1 comprising RASQGISSWLA (SEQ ID NO: 40); an LC-CDR2 comprising HASTLES (SEQ ID NO: 54); and an LC-CDR3 comprising amino acid sequence selected from a group of SEQ ID NO: 65, SEQ ID NOs: 76-78, and SEQ ID NOs: 199-212.

5. The isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl of claim 4, comprises:

(i) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID

NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(ii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 165, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(iii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 166, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(iv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 35, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(v) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16,

and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 167, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(vi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 168, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(vii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 199, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(viii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

200, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(ix) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 76, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(x) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 201, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 202, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 78, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xiii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 203, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xiv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 204, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

205, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xvi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 206, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xvii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 207, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xviii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 208, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xix) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 77, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xx) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 209, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 210, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

211, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxiii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 212, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxiv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 35, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 76, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 35, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 77, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(xxvi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 35, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 78, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs; or

(xxvii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 4, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 16, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 169, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 40, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 65, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs.

6. The isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl of claim 4 or 5, comprises:

(i) a V_H comprising the amino acid sequence of SEQ ID NOs: 82 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NOs: 82, and a V_L comprising the amino acid sequence of SEQ ID NO: 94 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NOs: 94;

(ii) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 105-110 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 105-110, and a V_L comprising the amino acid sequence of SEQ ID NO: 94 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 94;

(iii) a V_H comprising the amino acid sequence of SEQ ID NO: 82 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 82, and a V_L comprising the amino acid sequence of any one of SEQ ID

NO: 111-127 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NO: 111-127;

(iv) a V_H comprising the amino acid sequence of SEQ ID NO: 107 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 107, and a V_L comprising the amino acid sequence of SEQ ID NO: 113 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 113;

(v) a V_H comprising the amino acid sequence of SEQ ID NO: 107 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 107, and a V_L comprising the amino acid sequence of SEQ ID NO: 123 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 123; or

(vi) a V_H comprising the amino acid sequence of SEQ ID NO: 107 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 107, and a V_L comprising the amino acid sequence of SEQ ID NO: 116 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 116.

7. An isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl comprises:

a V_H comprising an HC-CDR1 comprising the amino acid sequence of any one of SEQ ID NOs: 2-3, and 5-12, or a variant thereof comprising up to about 3 amino acid substitutions; an HC-CDR2 comprising the amino acid sequence of any one of SEQ ID NOs: 14-15, and 17-23, or a variant thereof comprising up to about 3 amino acid substitutions; and an HC-CDR3 comprising the amino acid sequence of any one of SEQ ID NOs: 25-26, and 28-34, or a variant thereof comprising up to about 3 amino acid substitutions; and

a V_L comprising an LC-CDR1 comprising the amino acid sequence of any one of SEQ ID NO: 38-39, and 41-49, or a variant thereof comprising up to about 3 amino acid substitutions; an LC-CDR2 comprising the amino acid sequence of any one of SEQ ID NO: 52-53, and 55-61, or a variant thereof comprising up to about 3 amino acid substitutions; and an LC-CDR3 comprising the amino acid sequence of any one of SEQ ID NOs: 63-64, 66-68,

and 70-75, or a variant thereof comprising up to about 3 amino acid substitutions; preferably comprises:

(i) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 2, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 14, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 25, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 38, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 52, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 63, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(ii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 3, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 15, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 26, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 39, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 53, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 64, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(iii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 5, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 17, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 28, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 41, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 52, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 66, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(iv) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 6, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 18, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 29, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 42, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 55, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 67, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(v) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 14, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 25, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 43, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 56, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 68, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(vi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 8, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 19, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 30, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 44, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 57, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 70, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(vii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 3, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 15, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 26, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 45, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 58, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

71, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(viii) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 9, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 20, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 31, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 46, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 52, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 72, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(ix) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 10, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 21, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 32, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 47, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 59, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 73, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs;

(x) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 11, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 22, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 33, or a variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 48, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 60, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 74, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs; or

(xi) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 12, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 23, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 34, or a

variant thereof comprising up to about 5 amino acid substitutions in the HC-CDRs; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 49, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 61, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 75, or a variant thereof comprising up to about 5 amino acid substitutions in the LC-CDRs.

8. The isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl of claim 7, comprises: a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 80-81, 83-90, and 159 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 80-81, 83-90, and 159; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 92-93, 95-97, and 99-104 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 92-93, 95-97, and 99-104, preferably comprises:
   (i) a V_H comprising the amino acid sequence of SEQ ID NO: 80 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 80 and a V_L comprising the amino acid sequence of SEQ ID NO: 92 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 92;
   (ii) a V_H comprising the amino acid sequence of SEQ ID NO: 81 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 81 and a V_L comprising the amino acid sequence of SEQ ID NO: 93 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 93;
   (iii) a V_H comprising the amino acid sequence of SEQ ID NO: 83 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 83 and a V_L comprising the amino acid sequence of SEQ ID NO: 95 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 95;
   (iv) a V_H comprising the amino acid sequence of SEQ ID NO: 84 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 84 and a V_L comprising the amino acid sequence of SEQ ID NO: 96 or a

variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 96;

(v) a V_H comprising the amino acid sequence of SEQ ID NO: 85 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 85 and a V_L comprising the amino acid sequence of SEQ ID NO: 97 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 97;

(vi) a V_H comprising the amino acid sequence of SEQ ID NO: 86 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 86 and a V_L comprising the amino acid sequence of SEQ ID NO: 99 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 99;

(vii) a V_H comprising the amino acid sequence of SEQ ID NO: 81 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 81 and a V_L comprising the amino acid sequence of SEQ ID NO: 100 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 100;

(viii) a V_H comprising the amino acid sequence of SEQ ID NO: 87 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 87 and a V_L comprising the amino acid sequence of SEQ ID NO: 101 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 101;

(ix) a V_H comprising the amino acid sequence of SEQ ID NO: 88 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 88 and a V_L comprising the amino acid sequence of SEQ ID NO: 102 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 102;

(x) a V_H comprising the amino acid sequence of SEQ ID NO: 89 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 89 and a V_L comprising the amino acid sequence of SEQ ID NO: 103 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 103;

(xi) a V_H comprising the amino acid sequence of SEQ ID NO: 90 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 90 and a V_L comprising the amino acid sequence of SEQ ID NO: 104 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 104; or

(xii) a V_H comprising the amino acid sequence of SEQ ID NO: 159 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 159 and a V_L comprising the amino acid sequence of SEQ ID NO: 95 or a variant thereof having at least about 90% sequence identity to the amino acid sequence of SEQ ID NO: 95.

9. An isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl competitively with the isolated antibody or antigen binding fragment of any one of claims 1-8, or specifically binds to the same epitope as the isolated antibody or antigen binding fragment of any one of claims 1-8.

10. The isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl according to any one of claims 1-9, wherein:
i) the antibody or antigen binding fragment comprises an Fc fragment, preferably, wherein the antibody or antigen binding fragment is a full-length IgG antibody, further preferably, wherein the antibody or antigen binding fragment is a full-length IgG1 or IgG4 antibody;
ii) the antibody or antigen binding fragment is chimeric, human, or humanized; or
iii) the antibody or antigen binding fragment is selected from the group consisting of a Fab, a Fab', a F(ab)'2, a Fab'-SH, a single-chain Fv (scFv), an Fv fragment, a dAb, a Fd, or a diabody.

11. An isolated nucleic acid molecule that encodes the isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl according to any one of claims 1-10.

12. A vector comprising the nucleic acid molecule of claim 11.

13. An isolated host cell comprising the isolated antibody or antigen binding fragment of any one of claims 1-10, the isolated nucleic acid of claim 11, or the vector of claim 12.

14. A method of producing an isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl, comprising:

a) culturing the host cell of claim 13 under conditions effective to express the anti-Psl antibody or antigen binding fragment; and

b) obtaining the expressed anti-Psl antibody or antigen binding fragment from the host cell.

15. A pharmaceutical composition comprising the isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl according to any one of claims 1-10, the nucleic acid of claim 11, the vector of claim 12, or the isolated host cell of claim 13, and a pharmaceutically acceptable carrier.

16. Use of the isolated antibody or antigen binding fragment thereof which specially binds to *Pseudomonas* Psl according to any one of claims 1-10, the nucleic acid of claim 11, the vector of claim 12, the isolated host cell of claim 13, the isolated antibody or antigen binding fragment thereof produced by the method of claim 14, or the pharmaceutical composition of claim 15 in the manufacture of a medicament for treating a disease or condition in an individual.

17. The use of claim 16, wherein,

i) the disease or condition is a pathogenic infection, preferably, wherein the infection is a gram-negative bacterial infection, further preferably, wherein bacterium causing the gram-negative bacterial infection is *Pseudomonas aeruginosa*; and/or

ii) the disease or condition comprises one or more symptoms caused by *Pseudomonas aeruginosa* infection, preferably, wherein the symptom comprises one or more of fever, chills, fatigues, muscle and joint pain, swelling of joints, headache, diarrhea, skin rashes, pus in wounds, bacteremia, acute pneumonia, intraperitoneal infection, respiratory tract infections, septic shock, suppurative arthritis, enteritis, skin and soft tissue infections, urinary

tract infections, intestinal infections, ulcerative keratitis, chronic suppurative otitis media, mastoiditis, sinusitis, or endocarditis; and/or

iii) the medicament further comprises one or more therapeutic agents, wherein at least one of the therapeutic agents is an antibiotic, further preferably, wherein the antibiotic is one or more of Imipenem, Tobramycin, Ciprofloxacin, Meropenem or Aztreonam.