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(54) Title: BINDING PROTEINS 1

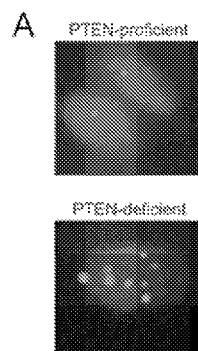
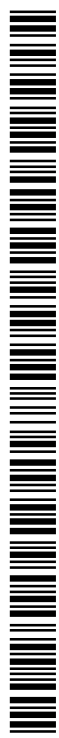


FIGURE 8

(57) Abstract: The present disclosure relates to cell penetrating anti-DNA binding proteins. Compositions comprising these binding proteins may be useful for delivering agents to cells and treating diseases such as cancer.



BINDING PROTEINS 1**FIELD OF THE INVENTION**

- The present disclosure relates to cell penetrating anti-DNA binding proteins.
- 5 Compositions comprising these binding proteins may be useful for delivering agents to cells and treating diseases such as cancer.

BACKGROUND OF THE INVENTION

- Development of cell penetrating anti-DNA binding proteins as therapeutic
- 10 agents for human diseases has great clinical potential, in particular because of their ability to selectively impair DNA repair pathways and/or deliver various therapeutic payloads to target cells.

Accordingly, improved cell penetrating anti-DNA binding proteins are required.

15 **SUMMARY OF THE INVENTION**

The present inventors have identified cell penetrating anti-DNA binding protein modifications that surprisingly increase nuclear penetration. In some cases, these modifications may also improve physical stability and reduce immunogenicity.

- Accordingly, in a first example, the present disclosure relates to a cell
- 20 penetrating anti-DNA binding protein having an antigen binding domain, wherein the antigen binding domain binds to or specifically binds to DNA and comprises a heavy chain variable region (V_H) having a complementarity determining region (CDR) 1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a light chain variable region (V_L) having a
- 25 CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In this example, the CDRs have been defined using Kabat.

- In another example, the present disclosure relates to a cell penetrating anti-DNA binding protein having an antigen binding domain, wherein the antigen binding domain
- 30 binds to or specifically binds to DNA and comprises:

- a heavy chain variable region (V_H) having a complementarity determining region (CDR) 1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12;
 - a light chain variable region (V_L) having a CDR1 as shown in SEQ ID
- 35 NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In this example, the CDRs have been defined using IMGT.

In another example, binding proteins according to the present disclosure comprise:

- (i) a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23;
- 5 (ii) a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29; or
- (iii) a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For
- 10 example, the binding protein may comprise a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23. In another example, the binding protein may comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. In another example, the binding protein may comprise a V_H comprising a sequence at least 95% identical to the
- 15 sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29.

In another example, the V_H and a V_L are separated by a linker. For example, the linker may be comprise (Gly₄Ser)₃. In another example the linker comprises an amino

20 acid sequence as shown in SEQ ID NO: 30.

In an example, the V_H and V_L are in a single polypeptide chain. For example, the binding protein may be:

- (i) a single chain Fv fragment (scFv);
- (ii) a dimeric scFv (di-scFv);
- 25 (iii) a trimeric scFv (tri-scFv);
- (iv) any one of (i), (ii) or (iii) linked to a constant region of an antibody, Fc or a heavy chain constant domain C_{H2} and/or C_{H3} . For example, the binding protein may be a di-scFv. In this example, the scFv's may be separated by a linker. For example, the linker may comprise an amino acid sequence as shown in SEQ ID NO: 31.

30 In another example, the V_H and V_L are in separate polypeptide chains. For example, the binding protein may be:

- (i) a diabody;
- (ii) a triabody;
- (iii) a tetrabody;
- 35 (iv) a Fab;
- (v) a F(ab')₂;

- (vi) a Fv;
- (vii) one of (i) to (vi) linked to a constant region of an antibody, Fc or a heavy chain constant domain C_H2 and/or C_H3; or,
- (viii) an intact antibody.

5 Thus, the V_H and V_L of an Fv can be formed of a single peptide chain (e.g. scFv), or can be formed of two separate peptide chains.

In an example, the binding protein is humanized.

In another example, the present disclosure relates to a cell penetrating anti-DNA Fv fragment having an antigen binding domain, wherein the antigen binding domain
10 binds to or specifically binds to DNA and comprises at least one of:

- a V_H having a CDR 1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3, a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8;
15
- a V_H having a CDR 1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11, a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16;
20
- a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29.

25 In this example, the Fv fragment may be a di-scFv. In an example, the Fv fragment may comprise an amino acid sequence as shown in any one of SEQ ID NOs: 32 – 47. For example, the Fv fragment may comprise an amino acid sequence as shown in SEQ ID NO: 41.

In some embodiments, the Fv is naked. In another example, the Fv fragment
30 may be conjugated to another compound.

In an example, the Fv is humanized. For example, the Fv may be a humanized di-scFv.

In another example, the present disclosure relates to a nucleic acid sequence encoding an above referenced binding proteins. Exemplary nucleic acid sequences are
35 shown in SEQ ID NOs: 51 – 66. The disclosed nucleic acid sequences can be codon-optimized to increase levels of expression for synthesizing the proteins. In another

example, the present disclosure relates to an expression vector comprising a nucleic acid sequence according to the present disclosure. For example, the expression vector may comprise a nucleic acid sequences are shown in any one of SEQ ID NOs: 51 – 66 or a codon optimized sequence thereof.

5 In another example, the present disclosure relates to a host cell comprising an above referenced binding protein, nucleic acid or vector, or codon optimized sequence thereof.

 In another example, the present disclosure relates to a method of treating cancer. For example, a method of treating cancer comprising administering to a subject an Fv
10 fragment comprising an amino acid sequence as shown in any one of SEQ ID NOs: 32, 36, 41 or 43. For example, an Fv fragment comprising an amino acid sequence as shown in SEQ ID NOs: 32 may be administered to a subject. In another example, an Fv fragment comprising an amino acid sequence as shown in SEQ ID NOs: 36 may be administered to a subject. In another example, an Fv fragment comprising an amino
15 acid sequence as shown in SEQ ID NOs: 41 may be administered to a subject. In another example, an Fv fragment comprising an amino acid sequence as shown in SEQ ID NOs: 43 may be administered to a subject. In an example, the cancer is colon cancer, brain cancer, prostate cancer, ovarian cancer, endometrial cancer, breast cancer, or pancreatic cancer. For example, the cancer may be colon cancer or brain cancer. In
20 an example, the cancer is brain cancer. In an example, the brain cancer is glioblastoma.

 In another example, the present disclosure relates to use of a binding protein such as an Fv fragment, composition, vector or host cell according to the present disclosure in the manufacture of a medicament for treating cancer. In another example, the present disclosure relates to a binding protein such as an Fv fragment, composition,
25 vector or host cell according to the present disclosure for use in treating cancer.

 The experimental results below also illustrate that binding proteins disclosed herein can work with poly (ADP-ribose) polymerase (PARP) inhibitors to kill cancer cells. Accordingly, in another example, the present disclosure relates to a method of treating cancer in a subject in need thereof, the method comprising administering to the
30 subject a binding protein or Fv fragment defined herein and a PARP inhibitor.

 In an example, the PARP inhibitor is olaparib.

 In an example, the cancer is substantially HDR deficient. In another example, the cancer is substantially BRCA2 deficient. In another example, the cancer is substantially PTEN deficient. In an example, the cancer is colon cancer, brain cancer,
35 prostate cancer, ovarian cancer, endometrial cancer, breast cancer, or pancreatic cancer. For example, the cancer may be colon cancer or brain cancer. In an example, the

cancer is brain cancer. In an example, the brain cancer is glioblastoma. In an example, the cancer is resistant to PARP inhibition. For example, the cancer may be resistant to treatment with olaparib. In another example, the cancer is triple negative breast cancer.

In another example, the present disclosure relates to a therapeutic combination comprising a binding protein or Fv fragment defined herein and a PARP inhibitor, the combination being provided for simultaneous or sequential administration. In another example, the present disclosure relates to a therapeutic combination comprising:

- a binding protein or Fv comprising the CDRs of SEQ ID NOs: 41; or,
- a binding protein comprising the amino acid sequence shown in SEQ ID NO: 41;

and, a PARP inhibitor, the combination being provided for simultaneous or sequential administration. For example, the binding protein or Fv can comprise heavy chain CDRs as shown in SEQ ID NOs: 1, 3 and 4 and light chain CDRs as shown in SEQ ID NOs: 6, 7 and 8. In these examples, the therapeutic combination may be used for treating cancer.

Furthermore, in these examples, the PARP inhibitor may be olaparib.

In another example, the present disclosure relates to a cell penetrating anti-DNA binding protein having an antigen binding domain, wherein the antigen binding domain binds to DNA and comprises: (i) a heavy chain variable region (V_H) and a light chain variable region (V_L), wherein the V_H has a complementarity determining region (CDR) 1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and the V_L has a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8; or, (ii) a V_H and a V_L, wherein the V_H has a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and the V_L has a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

Any example herein shall be taken to apply *mutatis mutandis* to any other example unless specifically stated otherwise.

The present disclosure is not to be limited in scope by the specific examples described herein, which are intended for the purpose of exemplification only. Functionally-equivalent products, compositions and methods are clearly within the scope of the disclosure, as described herein.

Throughout this specification, unless specifically stated otherwise or the context requires otherwise, reference to a single step, composition of matter, group of steps or group

of compositions of matter shall be taken to encompass one and a plurality (i.e. one or more) of those steps, compositions of matter, groups of steps or group of compositions of matter.

The disclosure is hereinafter described by way of the following non-limiting Examples and with reference to the accompanying drawings.

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it existed before the priority date of each of the appended claims.

Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

BRIEF DESCRIPTION OF THE ACCOMPANYING DRAWINGS

Figure 1. Images illustrating the results of SDS-PAGE analysis of reduced and denatured variants.

Figure 2. Images illustrating the results of SDS-PAGE analysis of non-reduced variants.

- Figure 3.** Images illustrating the results of Alkaline phosphatase-based survey of nuclear penetration.
- Figure 4.** Plots showing Quantitative analysis of the alkaline phosphatase-based survey of nuclear penetration.
- 5 **Figure 5.** Histograms of Quantitative analysis of the alkaline phosphatase-based survey of nuclear penetration.
- Figure 6.** Images illustrating the results of Immunofluorescence-based survey of nuclear penetration.
- Figure 7.** Plots showing Quantitative analysis of the immunofluorescence-based
10 survey of nuclear penetration.
- Figure 8, Panel A.** Exemplary images showing Accumulation of DNA damage in PTEN-proficient and PTEN-deficient cancer cells.
- Figure 8, Panel B.** Histogram showing Accumulation of DNA damage in PTEN-proficient and PTEN-deficient cancer cells.
- 15 **Figure 9.** Histogram showing Cell viability of PTEN-deficient cancer cells.
- Figure 10, Panel A.** Exemplary images showing Accumulation of DNA damage in BRCA2-proficient and BRCA2-deficient cancer cells.
- Figure 10, Panel B.** Histogram showing Accumulation of DNA damage in BRCA2-proficient and BRCA2-deficient cancer cells.
- 20 **Figure 11.** di-scFv (SEQ ID NO: 41) penetrates HDR deficient DLD-1 colon cancer cell nuclei.
- Figure 12.** di-scFv (SEQ ID NO: 41) penetrates HDR deficient MCF-7 breast cancer cell nuclei.
- Figure 13.** More than additive cell death mediated by di-scFv (SEQ ID NO: 41) and
25 PARP inhibitor in HDR deficient cancer cells (* $p < 0.05$ compared to olaparib or the di-scFv alone).
- Figure 14.** di-scFv (SEQ ID NO: 41) kills primary human glioblastoma cells.
- Figure 15.** di-scFv (SEQ ID NO: 41) penetrates human glioblastoma spheres (A) and reduces sphere volume in a time-dependent (B) and dose-dependent (C) manner.
- 30 **Figure 16.** *In-vivo* assessment of di-scFv (SEQ ID NO: 41) in a orthotopic mouse model of glioblastoma. a) Representative H&E stained brain sections from mice treated with control or di-scFv (SEQ ID NO: 41) and corresponding quantification of area. (* $P < 0.04$, $n = 3$). b) Representative micrographs of TUNEL staining, and corresponding percentage of TUNEL-positive cells. * denotes a $P \leq 0.05$ as determined
35 by a one-way ANOVA test. c) Protein L-based immunostaining for comparison of di-scFv (SEQ ID NO: 41) in tumour and adjacent brain tissue. d) Body weight (grams)

profile for mice in the survival study (n=7). e) Survival data for control PBS versus di-scFv (SEQ ID NO: 41) treatment arms (n=7, P=0.02, Mantel-Cox test).

Figure 17. Effect of di-scFv (SEQ ID NO: 41) on Foci Accumulation. The percentage of P53BP1-positive cells increased in HDR-deficient DLD1 and U251 cells following
 5 24 hour PAT-DX1 and combination treatment(s).

KEY TO SEQUENCE LISTING

- SEQ ID NO: 1 – Heavy Chain CDR1 KABAT
- SEQ ID NO: 2 – Heavy Chain CDR2 (variants 2 – 4, 6 – 8, 10 - 12) KABAT
- 10 SEQ ID NO: 3 – Heavy Chain CDR2 (variants 13 – 19) KABAT
- SEQ ID NO: 4 – Heavy Chain CDR3 KABAT
- SEQ ID NO: 5 – Light Chain CDR1 (variants 2 – 4, 6 – 8, 10 - 12) KABAT
- SEQ ID NO: 6 – Light Chain CDR1 (variants 13 – 19) KABAT
- SEQ ID NO: 7 – Light Chain CDR2 KABAT
- 15 SEQ ID NO: 8 – Light Chain CDR3 KABAT
- SEQ ID NO: 9 – Heavy Chain CDR1 IMGT
- SEQ ID NO: 10 – Heavy Chain CDR2 (variants 2 – 4, 6 – 8, 10 - 12) IMGT
- SEQ ID NO: 11 – Heavy Chain CDR2 (variants 13 – 19) IMGT
- SEQ ID NO: 12 – Heavy Chain CDR3 IMGT
- 20 SEQ ID NO: 13 – Light Chain CDR1 (variants 2 – 4, 6 – 8, 10 - 12) IMGT
- SEQ ID NO: 14 – Light Chain CDR1 (variants 13 – 19) IMGT
- SEQ ID NO: 15 – Light Chain CDR2 IMGT
- SEQ ID NO: 16 – Light Chain CDR3 IMGT
- SEQ ID NO: 17 – Heavy Chain variable region (variants 2, 6 and 10)
- 25 SEQ ID NO: 18 – Heavy Chain variable region (variants 3, 7 and 11)
- SEQ ID NO: 19 – Heavy Chain variable region (variants 4, 8 and 12)
- SEQ ID NO: 20 – Heavy Chain variable region (variants 6 and 10)
- SEQ ID NO: 21 – Heavy Chain variable region (variants 13, 16 and 19)
- SEQ ID NO: 22 – Heavy Chain variable region (variants 14 and 17)
- 30 SEQ ID NO: 23 – Heavy Chain variable region (variants 15 and 18)
- SEQ ID NO: 24 – Light Chain variable region (variants 2, 3 and 4)
- SEQ ID NO: 25 – Light Chain variable region (variants 6, 7 and 8)
- SEQ ID NO: 26 – Light Chain variable region (variants 10, 11 and 12)
- SEQ ID NO: 27 – Light Chain variable region (variants 13, 14 and 15)
- 35 SEQ ID NO: 28 – Light Chain variable region (variants 16, 17 and 18)
- SEQ ID NO: 29 – Light Chain variable region (variant 19)

- SEQ ID NO: 30 – Linker sequence 1
SEQ ID NO: 31 – Linker sequence 2
SEQ ID NO: 32 – Variant 2
SEQ ID NO: 33 – Variant 3
5 SEQ ID NO: 34 – Variant 4
SEQ ID NO: 35 – Variant 6
SEQ ID NO: 36 – Variant 7
SEQ ID NO: 37 – Variant 8
SEQ ID NO: 38 – Variant 10
10 SEQ ID NO: 39 – Variant 11
SEQ ID NO: 40 – Variant 12
SEQ ID NO: 41 – Variant 13
SEQ ID NO: 42 – Variant 14
SEQ ID NO: 43 – Variant 15
15 SEQ ID NO: 44 – Variant 16
SEQ ID NO: 45 – Variant 17
SEQ ID NO: 46 – Variant 18
SEQ ID NO: 47 – Variant 19
SEQ ID NO: 48 – Heavy Chain variable region murine (D31N) anti-DNA binding
20 antibody
SEQ ID NO: 49 – Light Chain variable region murine (D31N) anti-DNA binding
antibody
SEQ ID NO: 50 – (D31N) murine prototype produced from *P. pastoris*
SEQ ID NO: 51 – DNA sequence Variant 2
25 SEQ ID NO: 52 – DNA sequence Variant 3
SEQ ID NO: 53 – DNA sequence Variant 4
SEQ ID NO: 54 – DNA sequence Variant 6
SEQ ID NO: 55 – DNA sequence Variant 7
SEQ ID NO: 56 – DNA sequence Variant 8
30 SEQ ID NO: 57 – DNA sequence Variant 10
SEQ ID NO: 58 – DNA sequence Variant 11
SEQ ID NO: 59 – DNA sequence Variant 12
SEQ ID NO: 60 – DNA sequence Variant 13
SEQ ID NO: 61 – DNA sequence Variant 14
35 SEQ ID NO: 62 – DNA sequence Variant 15
SEQ ID NO: 63 – DNA sequence Variant 16

- SEQ ID NO: 64 – DNA sequence Variant 17
 SEQ ID NO: 65 – DNA sequence Variant 18
 SEQ ID NO: 66 – DNA sequence Variant 19
 SEQ ID NO: 67 - (GGGGS)₃ linker
 5 SEQ ID NO: 68 – 3E10 human IgG1 L2345A/L235A heavy chain full length sequence
 SEQ ID NO: 69 - 3E10 human IgG1 constant heavy region 1
 SEQ ID NO: 70 - 3E10 human IgG1 hinge region
 SEQ ID NO: 71 - 3E10 human IgG1 L2345A/L235A constant heavy region 2
 SEQ ID NO: 72 - 3E10 human IgG1 constant heavy region 3
 10 SEQ ID NO: 73 - 3E10 human IgG1 N297D heavy chain full length sequence
 SEQ ID NO: 74 - 3E10 human IgG1 N297D constant heavy region 2
 SEQ ID NO: 75 - 3E10 human IgG1 L2345A/L235A/N297D heavy chain full length sequence
 SEQ ID NO: 76 - 3E10 human IgG1 L2345A/L235A/N297D constant heavy region 2
 15 SEQ ID NO: 77 – Unmodified constant heavy region 2
 SEQ ID NO: 78 – Light chain full length sequence

DETAILED DESCRIPTION OF THE INVENTION

General Techniques and Selected Definitions

- 20 Unless specifically defined otherwise, all technical and scientific terms used herein shall be taken to have the same meaning as commonly understood by one of ordinary skill in the art (e.g., molecular biology, biochemistry, antibodies, antibody fragments such as single chain fragment variable and clinical studies).

- The term "cell-penetrating" is used in the context of the present disclosure to refer to an anti-DNA binding protein such as an antigen binding fragment that is transported into the nucleus of living mammalian cells and binds DNA (e.g., single-stranded and/or double-stranded DNA). In an example, a cell-penetrating anti-DNA binding protein is transported into the nucleus of a cell without the aid of a carrier or conjugate.

- 30 The term "anti-DNA binding protein" is used in the context of the present disclosure to refer to proteins capable of binding DNA. Exemplary binding proteins include immunoglobulin, antibodies and antigenic binding fragments. Other examples of binding proteins are discussed below.

- The term "immunoglobulin" will be understood to include any anti-DNA binding protein comprising an immunoglobulin domain. Exemplary immunoglobulins are antibodies. Additional proteins encompassed by the term "immunoglobulin"

include domain antibodies, camelid antibodies and antibodies from cartilaginous fish (i.e., immunoglobulin new antigen receptors (IgNARs)). Generally, camelid antibodies and IgNARs comprise a V_H , however lack a V_L and are often referred to as heavy chain immunoglobulins. Other "immunoglobulins" include T cell receptors.

5 The term "antibody" is used in the context of the present disclosure to refer to immunoglobulin molecules immunologically reactive with a particular antigen and includes both polyclonal and monoclonal antibodies. The term also includes genetically engineered forms such as chimeric antibodies (e.g., humanized murine antibodies) and heteroconjugate antibodies (e.g., bispecific antibodies). The term
10 "antibody" also includes antigen binding forms of antibodies, including fragments with antigen-binding capability (e.g., Fab', F(ab')₂, Fab, Fv and rIgG as discussed in Pierce Catalogue and Handbook, 1994-1995 (Pierce Chemical Co., Rockford, Ill.); Kuby, J., Immunology, 3rd Ed., W.H. Freeman & Co., New York (1998). The term is also used to refer to recombinant single chain Fv fragments (scFv) as well as divalent (di-scFv)
15 and trivalent (tri-scFV) forms thereof. The term antibody also includes bivalent or bispecific molecules, diabodies, triabodies, and tetrabodies. Examples of bivalent and bispecific molecules are described in Kostelny et al. (1992) J Immunol 148:1547; Pack and Pluckthun (1992) Biochemistry 31:1579; Hollinger et al., 1993, supra, Gruber et al. (1994) J. Immunol.:5368, Zhu et al. (1997) Protein Sci 6:781, Hu et al. (1996) Cancer
20 Res. 56:3055, Adams et al. (1993) Cancer Res. 53:4026, and McCartney, et al. (1995) Protein Eng. 8:301.

An "antigen binding fragment" of an antibody comprises one or more variable regions of an intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂ and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules
25 and multispecific antibodies formed from antibody fragments. For example, the term antigen binding fragment may be used to refer to recombinant single chain Fv fragments (scFv) as well as divalent (di-scFv) and trivalent (tri-scFV) forms thereof. Such fragments can be produced via various methods known in the art. For example, di-scFv encompassed by the present disclosure can be produced and purified by the
30 methods described in Example 1 below.

The terms "full-length antibody", "intact antibody" or "whole antibody" are used interchangeably to refer to an antibody in its substantially intact form, as opposed to an antigen binding fragment of an antibody. Specifically, whole antibodies include those with heavy and light chains including an Fc region. The constant domains may
35 be wild-type sequence constant domains (e.g., human wild-type sequence constant domains) or amino acid sequence variants thereof.

As used herein, “variable region” refers to the portions of the light and/or heavy chains of an antibody as defined herein that specifically binds to an antigen and, for example, includes amino acid sequences of CDRs; i.e., CDRL1, CDR2, and CDR3, and framework regions (FRs). For example, the variable region comprises three or four FRs (e.g., FR1, FR2, FR3 and optionally FR4) together with three CDRs. V_H refers to the variable region of the heavy chain. V_L refers to the variable region of the light chain.

As used herein, the term “complementarity determining regions” (syn. CDRs; i.e., CDRL1, CDR2, and CDR3) refers to the amino acid residues of an antibody variable region the presence of which are major contributors to specific antigen binding. Each variable region typically has three CDR regions identified as CDRL1, CDR2 and CDR3. In one example, the amino acid positions assigned to CDRs and FRs are defined according to Kabat Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda, Md., 1987 and 1991 (also referred to herein as “the Kabat numbering system” or “Kabat”).

Other conventions that include corrections or alternate numbering systems for variable domains include IMGT (Lefranc, et al. (2003), Dev Comp Immunol 27: 55-77), Chothia (Chothia C, Lesk AM (1987), J Mol Biol 196: 901-917; Chothia, et al. (1989), Nature 342: 877-883) and AHO (Honegger A, Plückthun A (2001) J Mol Biol 309: 657-670). For convenience, examples of binding proteins of the present disclosure may also be labelled according to IMGT. These examples are expressly indicated as such. For example, see SEQ ID NO: 9 – 16.

“Framework regions” (Syn. FR) are those variable domain residues other than the CDR residues.

The term “constant region” as used herein, refers to a portion of heavy chain or light chain of an antibody other than the variable region. In a heavy chain, the constant region generally comprises a plurality of constant domains and a hinge region, e.g., a IgG constant region comprises the following linked components, a constant heavy C_H1, a linker, a C_H2 and a C_H3. In a heavy chain, a constant region comprises a Fc. In a light chain, a constant region generally comprise one constant domain (a CL1).

The term “fragment crystallizable” or “Fc” or “Fc region” or “Fc portion” (which can be used interchangeably herein) refers to a region of an antibody comprising at least one constant domain and which is generally (though not necessarily) glycosylated and which is capable of binding to one or more Fc receptors and/or components of the complement cascade. The heavy chain constant region can be selected from any of the five isotypes: α, δ, ε, γ, or μ. Exemplary heavy chain constant regions are gamma 1 (IgG1), gamma 2 (IgG2) and gamma 3 (IgG3), or hybrids thereof.

A "constant domain" is a domain in an antibody the sequence of which is highly similar in antibodies/antibodies of the same type, e.g., IgG or IgM or IgE. A constant region of an antibody generally comprises a plurality of constant domains, e.g., the constant region of γ , α or δ heavy chain comprises two constant domains.

5 The term "naked" is used to refer to binding proteins of the present disclosure that are not conjugated to another compound, e.g., a toxic compound or radiolabel. For example, the term "naked" can be used to refer to binding proteins such as di-scFv that are not conjugated to another compound. Accordingly, in one example, the binding proteins of the present disclosure are "naked". Put another way, the binding proteins of
10 the present disclosure can be un-conjugated.

In contrast, the term "conjugated" is used in the context of the present disclosure to refer to binding proteins of the present disclosure that are conjugated to another compound, e.g., a toxic compound such as a cytotoxic agent or radiolabel. Accordingly, in one example, the binding proteins of the present disclosure are
15 "conjugated".

The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents a cellular function and/or causes cell death or destruction. Cytotoxic agents include, but are not limited to, radioactive isotopes (e.g., At^{211} , ^{131}I , ^{125}I , ^{90}Y , ^{186}Re , ^{188}Re , ^{153}Sm , Bi, P, Pb and radioactive isotopes of Lu), chemotherapeutic agents or
20 drugs (e.g., methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents); growth inhibitory agents; enzymes and fragments thereof such as nucleolytic enzymes; antibiotics; toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or
25 variants thereof; and the various antitumor or anticancer agents disclosed below.

Terms such as "host cell," "host cell line," and "host cell culture" are used interchangeably in the context of the present disclosure to refer to cells into which exogenous nucleic acid has been introduced, including the progeny of such cells. Host cells include "transformants" and "transformed cells," which include the primary
30 transformed cell and progeny derived therefrom without regard to the number of passages. Progeny may not be completely identical in nucleic acid content to a parent cell, but may contain mutations. Mutant progeny that have the same function or biological activity as screened or selected for in the originally transformed cell are included herein.

35 An "isolated nucleic acid" according to the present disclosure is a nucleic acid molecule that has been separated from a component of its natural environment. An

isolated nucleic acid includes a nucleic acid molecule contained in cells that ordinarily contain the nucleic acid molecule, but the nucleic acid molecule is present extrachromosomally or at a chromosomal location that is different from its natural chromosomal location.

5 "Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative
10 substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill of those practicing in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences,
15 including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

As used herein, the term "binds" in reference to the interaction of a binding protein and an antigen means that the interaction is dependent upon the presence of a particular structure (e.g., an antigenic determinant or epitope) on the antigen. For
20 example, a binding protein recognizes and binds to a specific antigen structure rather than to antigens generally. For example, if a binding protein binds to epitope "A", the presence of a molecule containing epitope "A" (or free, unlabeled "A"), in a reaction containing labeled "A" and the binding protein, will reduce the amount of labeled "A" bound to the binding protein.

25 As used herein, the term "specifically binds" shall be taken to mean that the binding interaction between a binding protein and DNA is dependent on detection of the DNA by the binding protein. Accordingly, the binding protein preferentially binds or recognizes DNA even when present in a mixture of other molecules or organisms.

In one example, the binding protein reacts or associates more frequently, more
30 rapidly, with greater duration and/or with greater affinity with DNA than it does with alternative antigens or cells. It is also understood by reading this definition that, for example, a binding protein specifically binds to DNA may or may not specifically bind to a second antigen. As such, "specific binding" does not necessarily require exclusive binding or non-detectable binding of another antigen. The term "specifically binds"
35 can be used interchangeably with "selectively binds" herein. Generally, reference herein to binding means specific binding, and each term shall be understood to provide

explicit support for the other term. Methods for determining specific binding will be apparent to the skilled person. For example, a binding protein of the disclosure is contacted with DNA or an alternative antigen. Binding of the binding protein to DNA or alternative antigen is then determined and a binding protein that binds as set out
5 above to the DNA rather than the alternative antigen is considered to specifically bind to DNA.

Binding proteins according to the present disclosure and compositions comprising the same can be administered to a subject to treat various indications. Terms such as "subject", "patient" or "individual" are terms that can, in context, be
10 used interchangeably in the present disclosure. In an example, the subject is a mammal. The mammal may be a companion animal such as a dog or cat, or a livestock animal such as a horse or cow. In one example, the subject is a human. For example, the subject can be an adult. In another example, the subject can be a child. In another example, the subject can be an adolescent.

15 As used herein, the term "treatment" refers to clinical intervention designed to alter the natural course of the individual or cell being treated during the course of clinical pathology. Desirable effects of treatment include decreasing the rate of disease progression, ameliorating or palliating the disease state, and remission or improved prognosis. An individual is successfully "treated", for example, if one or more
20 symptoms associated with a disease are mitigated or eliminated.

As used herein, the term "prevention" includes providing prophylaxis with respect to occurrence or recurrence of a disease in an individual. An individual may be predisposed to or at risk of developing the disease or disease relapse but has not yet been diagnosed with the disease or the relapse.

25 The term "treatment" is used in the context of the present specification to refer to the medical management of a patient with the intent to cure, ameliorate or stabilize a disease, pathological condition, or disorder. The term "treatment" includes active treatment, that is, treatment directed specifically toward the improvement of a disease, pathological condition, or disorder, and also includes causal treatment, that is, treatment
30 directed toward removal of the cause of the associated disease, pathological condition, or disorder. In addition, the term "treatment" includes palliative treatment, that is, treatment designed for the relief of symptoms rather than the curing of the disease, pathological condition, or disorder; prophylactic treatment, that is, treatment directed to minimizing or partially or completely inhibiting the development of the associated
35 disease, pathological condition, or disorder; and supportive treatment, that is, treatment

employed to supplement another specific therapy directed toward the improvement of the associated disease, pathological condition, or disorder.

An "effective amount" refers to at least an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result. An effective amount can be provided in one or more administrations. In some examples of the present disclosure, the term "effective amount" is meant an amount necessary to effect treatment of a disease or condition described below. The effective amount may vary according to the disease or condition to be treated and also according to the weight, age, racial background, sex, health and/or physical condition and other factors relevant to the subject being treated. Typically, the effective amount will fall within a relatively broad range (e.g. a "dosage" range) that can be determined through routine trial and experimentation by a medical practitioner. The effective amount can be administered in a single dose or in a dose repeated once or several times over a treatment period.

A "therapeutically effective amount" is at least the minimum concentration required to effect a measurable improvement of a particular disorder (e.g. cancer). A therapeutically effective amount herein may vary according to factors such as the disease state, age, sex, and weight of the patient, and the ability of the binding protein to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the binding protein are outweighed by the therapeutically beneficial effects. In the case of cancer, the therapeutically effective amount of the binding protein may reduce the number of cancer cells; reduce the primary tumor size; inhibit (i.e., slow to some extent and, in some examples, stop) cancer cell infiltration into peripheral organs; inhibit (i.e., slow to some extent and, in some examples, stop) tumor metastasis; inhibit or delay, to some extent, tumor growth or tumor progression; and/or relieve to some extent one or more of the symptoms associated with the cancer. To the extent the binding protein may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. For cancer therapy, efficacy *in vivo* can, for example, be measured by assessing the duration of survival, time to disease progression (TTP), the response rates (RR), duration of response, and/or quality of life.

Deimmunized, Chimeric, Humanized, Synhumanized, Primatized and Human Antibodies or Antigen Binding Fragments

Monoclonal antibodies are one exemplary form of binding protein contemplated by the present disclosure. The term "monoclonal antibody" or "MAb" refers to a

homogeneous antibody population capable of binding to the same antigen(s), for example, to the same epitope within the antigen. This term is not intended to be limited as regards to the source of the antibody or the manner in which it is made.

In an example, binding proteins encompassed by the present disclosure may be
5 “humanized”. A “humanized antibody” is an immunoglobulin molecule which contains minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit
10 having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two,
15 variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. In an example, the humanized antibody will also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., Nature 321:522-525 (1986); Riechmann et al., Nature 332:323-329 (1988); and
20 Presta, Curr. Op. Struct. Biol. 2:593-596 (1992)).

In an example, “human” binding proteins of the present disclosure can include amino acid residues not encoded by human sequences, e.g. mutations introduced by random or site directed mutations *in vitro* (in particular mutations which involve
25 conservative substitutions or mutations in a small number of residues of the protein, e.g. in 1, 2, 3, 4 or 5 of the residues of the protein). These “human antibodies” do not necessarily need to be generated as a result of an immune response of a human, rather, they can be generated using recombinant means (e.g., screening a phage display library) and/or by a transgenic animal (e.g., a mouse) comprising nucleic acid encoding
30 human antibody constant and/or variable regions and/or using guided selection (e.g., as described in or U.S. Patent No. 5,565,332). This term also encompasses affinity matured forms of such antibodies.

In another example, binding proteins encompassed by the present disclosure may be synhumanized. The term “synhumanized” refers to an antibody prepared by a
35 method described in WO2007/019620. A synhumanized antibody includes a variable region of an antibody, wherein the variable region comprises FRs from a New World

primate antibody variable region and CDRs from a non-New World primate antibody variable region.

In another example, a binding protein of the present disclosure may be primatized. A “primatized antibody” comprises variable region(s) from an antibody generated following immunization of a non-human primate (e.g., a cynomolgus macaque). In an example, the variable regions of the non-human primate antibody are linked to human constant regions to produce a primatized antibody. Exemplary methods for producing primatized antibodies are described in U.S. Patent No. 6,113,898.

10 In one example, a binding protein of the disclosure is a chimeric antibody or fragment. The term “chimeric antibody” or “chimeric antigen binding fragment” refers to an antibody or fragment in which one or more of the variable domains is from a particular species (e.g., murine, such as mouse or rat) or belonging to a particular antibody class or subclass, while the remainder of the antibody or fragment is from another species (such as, for example, human or non-human primate) or belonging to another antibody class or subclass. In one example, a chimeric antibody comprising a V_H and/or a V_L from a non-human antibody (e.g., a murine antibody) and the remaining regions of the antibody are from a human antibody.

The present disclosure also contemplates a deimmunized antibody or antigen binding fragment thereof, e.g., as described in WO2000/34317 and WO2004/108158. De-immunized antibodies and fragments have one or more epitopes, e.g., B cell epitopes or T cell epitopes removed (i.e., mutated) to thereby reduce the likelihood that a subject will raise an immune response against the antibody or protein. For example, an antibody of the disclosure is analyzed to identify one or more B or T cell epitopes and one or more amino acid residues within the epitope is mutated to thereby reduce the immunogenicity of the antibody.

Antibody Fragments

Single-Domain Antibodies

30 In some examples, a binding protein of the disclosure is or comprises a single-domain antibody (which is used interchangeably with the term “domain antibody” or “dAb”). A single-domain antibody is a single polypeptide chain comprising all or a portion of the heavy chain variable domain of an antibody.

Single Chain Fv (scFv) Fragments

One of skill in the art will be aware that scFv's comprise V_H and V_L regions in a single polypeptide chain and a polypeptide linker between the V_H and V_L which enables the scFv to form the desired structure for antigen binding (i.e., for the V_H and V_L of the single polypeptide chain to associate with one another to form a Fv). Single-chain variable fragments lack the constant Fc region found in complete antibody molecules and therefore can have reduced immunogenicity. Exemplary linkers comprise in excess of 12 amino acid residues with (Gly₄Ser)₃ being one of the more favoured linkers for a scFv. Another example of a suitable linker is provided in SEQ ID NO: 31.

The present disclosure also contemplates a disulfide stabilized Fv (or diFv or dsFv), in which a single cysteine residue is introduced into a FR of V_H and a FR of V_L and the cysteine residues linked by a disulfide bond to yield a stable Fv.

In another example, the present disclosure encompasses a dimeric scFv (di-scFv), i.e., a protein comprising two scFv molecules linked by a non-covalent or covalent linkage, e.g., by a leucine zipper domain (e.g., derived from Fos or Jun) or trimeric scFv (tri-scFv). In another example, two scFv's are linked by a peptide linker of sufficient length to permit both scFv's to form and to bind to an antigen, e.g., as described in U.S. Published Application No. 20060263367.

Diabodies, Triabodies, Tetrabodies

In some examples, an antigen binding fragment of the disclosure is or comprises a diabody, triabody, tetrabody or higher order protein complex such as those described in WO98/044001 and/or WO94/007921.

For example, a diabody is a protein comprising two associated polypeptide chains, each polypeptide chain comprising the structure V_L-X-V_H or V_H-X-V_L, wherein X is a linker comprising insufficient residues to permit the V_H and V_L in a single polypeptide chain to associate (or form an Fv) or is absent, and wherein the V_H of one polypeptide chain binds to a V_L of the other polypeptide chain to form an antigen binding site, i.e., to form a Fv molecule capable of specifically binding to one or more antigens. The V_L and V_H can be the same in each polypeptide chain or the V_L and V_H can be different in each polypeptide chain so as to form a bispecific diabody (i.e., comprising two Fv's having different specificity).

Other Antibodies and Antibody Fragments

Other examples of binding proteins encompassed by the present disclosure include:

- (i) “key and hole” bispecific proteins as described in U.S. Patent No. 5,731,168;
- 5. (ii) heteroconjugate proteins, e.g., as described in U.S. Patent No. 4,676,980;
- (iii) heteroconjugate proteins produced using a chemical cross-linker, e.g., as described in U.S. Patent No. 4,676,980; and
- (iv) Fab₃ (e.g., as described in EP19930302894).

10 Immunoglobulins and Immunoglobulin Fragments

An example of a binding protein of the present disclosure is a protein (e.g., an antibody mimetic) comprising a variable region of an immunoglobulin, such as a T cell receptor or a heavy chain immunoglobulin (e.g., an IgNAR, a camelid antibody).

15 *V-Like Proteins*

An example of a binding protein of the disclosure is a T-cell receptor. T cell receptors have two V-domains that combine into a structure similar to the Fv module of an antibody. Novotny et al., Proc Natl Acad Sci USA 88: 8646-8650, 1991 describes how the two V-domains of the T-cell receptor (termed alpha and beta) can be fused and
20 expressed as a single chain polypeptide and, further, how to alter surface residues to reduce the hydrophobicity directly analogous to an antibody scFv. Other publications describing production of single-chain T-cell receptors or multimeric T cell receptors comprising two V-alpha and V-beta domains include WO1999/045110 or WO2011/107595.

25 Other non-antibody proteins comprising antigen binding domains include proteins with V-like domains, which are generally monomeric. Examples of proteins comprising such V-like domains include CTLA-4, CD28 and ICOS. Further disclosure of proteins comprising such V-like domains is included in WO1999/045110.

30 *Affibodies*

In a further example, a binding protein of the disclosure is an affibody. An affibody is a scaffold derived from the Z domain (antigen binding domain) of Protein A of *Staphylococcus aureus* which can be engineered to bind to antigen. The Z domain consists of a three-helical bundle of approximately 58 amino acids. Libraries have been
35 generated by randomization of surface residues. For further details see EP1641818.

Avimers

- In a further example, a binding protein of the disclosure is an Avimer. Avimers are multidomain proteins derived from the A-domain scaffold family. The native domains of approximately 35 amino acids adopt a defined disulfide bonded structure.
- 5 Diversity is generated by shuffling of the natural variation exhibited by the family of A-domains. For further details see WO2002/088171.

Binding Proteins

- In one example, anti-DNA binding proteins according to the present disclosure
- 10 comprise a heavy chain variable region (V_H) having a CDR 1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4. For example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4. In another example, an anti-DNA binding protein can
- 15 comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4.

- In another example, the anti-DNA binding proteins comprise a light chain variable region (V_L) having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. For
- 20 example, an anti-DNA binding protein can comprise a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an anti-DNA binding protein can comprise a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

- 25 In another example, the anti-DNA binding proteins comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. For example, an anti-DNA binding protein can comprise a V_H
- 30 having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in
- 35 SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an

anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

Above exemplified binding proteins may also have CDRs assigned using the IMGT system. Accordingly, in another example, the anti-DNA binding protein comprises a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12. For example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12. In another example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12.

In another example, the anti-DNA binding protein comprises a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. For example, an anti-DNA binding protein can comprise a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an anti-DNA binding protein can comprise a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16.

In another example, the anti-DNA binding proteins comprises a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. For example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 14, a

CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an anti-DNA binding protein can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16.

10 In another example, the anti-DNA binding proteins comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23. For example, an anti-DNA binding protein can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 18. In another example, an anti-DNA binding protein can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 23. In another example, the anti-DNA binding proteins comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an anti-DNA binding protein can comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 25. In another example, an anti-DNA binding protein can comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In another example, the anti-DNA binding proteins comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an anti-DNA binding protein can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 18 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 25. In another example, an anti-DNA binding protein can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In these examples, the V_H and/or V_L can be at least 96%, at least 97%, at least 98% or at least 99% identical to the recited SEQ ID NO.

In another example, the anti-DNA binding proteins comprise a V_H comprising a sequence as shown in any one of SEQ ID NOs: 17 to 23. For example, an anti-DNA binding protein can comprise a V_H comprising a sequence as shown in SEQ ID NO: 18. In another example, an anti-DNA binding protein can comprise a V_H comprising a

sequence as shown in SEQ ID NO: 23. In another example, the anti-DNA binding proteins comprise a V_L comprising a sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an anti-DNA binding protein can comprise a V_L comprising a sequence as shown in SEQ ID NO: 25. In another example, an anti-DNA binding protein can comprise a V_L comprising a sequence as shown in SEQ ID NO: 27. In another example, the anti-DNA binding proteins comprise a V_H comprising a sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an anti-DNA binding protein can comprise a V_H comprising a sequence as shown in SEQ ID NO: 18 and a V_L comprising a sequence as shown in SEQ ID NO: 25. In another example, an anti-DNA binding protein can comprise a V_H comprising a sequence as shown in SEQ ID NO: 23 and a V_L comprising a sequence as shown in SEQ ID NO: 27.

In an example, the anti-DNA binding protein can be a cell penetrating anti-DNA Fv fragment having an antigen binding domain, wherein the antigen binding domain binds to or specifically binds to DNA. For example, the Fv can bind the same epitope as a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv can bind the same epitope as a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50. In an example, the Fv comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4. For example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4.

In another example, the Fv comprises a V_L having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. For example, an Fv can comprise a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an anti-DNA binding protein can comprise a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

In another example, the Fv comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. For

example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

Above exemplified Fv may also have CDRs assigned using the IMGT system. Accordingly, in another example, the Fv comprises a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12. For example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12.

In another example, the Fv comprises a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. For example, an Fv can comprise a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an Fv can comprise a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16.

In another example, the Fv comprises a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. For example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15

and a CDR3 as shown in SEQ ID NO: 16. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an Fv can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16.

In another example, the Fv comprises a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23. For example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 18. In another example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 21. In another example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 23. In another example, the Fv comprises a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an Fv can comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 25. In another example, an Fv can comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In another example, the Fv comprises a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 18 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 25. In another example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 21 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In another example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In these examples, the V_H and/or V_L can be at least 96%, at least 97%, at least 98%

or at least 99% identical to the recited SEQ ID NO. In these examples, the Fv can have an above referenced combination of CDRs. For example, an Fv can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 21 and a V_L comprising a sequence at least 95% identical to the sequence as shown in
5 SEQ ID NO: 27, wherein the V_H has a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and the V_L has a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

In another example, the Fv comprises a V_H comprising a sequence as shown in
10 any one of SEQ ID NOs: 17 to 23. For example, an Fv can comprise a V_H comprising a sequence as shown in SEQ ID NO: 18. In another example, an Fv can comprise a V_H comprising a sequence as shown in SEQ ID NO: 21. In another example, an Fv can comprise a V_H comprising a sequence as shown in SEQ ID NO: 23. In another example, the Fv comprises a V_L comprising a sequence as shown in any one of SEQ ID
15 NOs: 24 to 29. For example, an Fv can comprise a V_L comprising a sequence as shown in SEQ ID NO: 25. In another example, an Fv can comprise a V_L comprising a sequence as shown in SEQ ID NO: 27. In another example, the Fv comprises a V_H comprising a sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an
20 Fv can comprise a V_H comprising a sequence as shown in SEQ ID NO: 18 and a V_L comprising a sequence as shown in SEQ ID NO: 25. In another example, an Fv can comprise a V_H comprising a sequence as shown in SEQ ID NO: 21 and a V_L comprising a sequence as shown in SEQ ID NO: 27. In another example, an Fv can comprise a V_H comprising a sequence as shown in SEQ ID NO: 23 and a V_L
25 comprising a sequence as shown in SEQ ID NO: 27.

In another example, the Fv has improved manufacturability compared to a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv has improved manufacturability compared to a di-scFv having
30 an amino acid sequence as shown in SEQ ID NO: 50.

Improved manufacturability encompasses post translational modifications or increased chemical stability relating to reduced numbers of deamidation sites, aspartate isomerization sites, oxidation sites such as methionine and tryptophan, free-cysteine thiol groups, N & O-glycosylation sites, the presence of C-terminal lysine and/or
35 isoelectric point.

In an example, the Fv comprises less asparagine in the V_H and/or V_L compared with a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv comprises less asparagine in the V_H and/or V_L compared with a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50.

In an example, the Fv comprises less methionine in the V_H and/or V_L compared with a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv comprises less methionine in the V_H and/or V_L compared with a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50.

In an example, the Fv comprises less tryptophan in the V_H and/or V_L compared with a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv comprises less tryptophan in the V_H and/or V_L compared with a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50.

In an example, the Fv comprises less aspartic acid in the V_H and/or V_L compared with a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv comprises less aspartic acid in the V_H and/or V_L compared with a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50.

In an example, the physical stability of the Fv is greater than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the physical stability of the Fv is greater than a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50.

Physical stability can include propensity for aggregation in solution. The term "aggregation" is used in the context of the present disclosure to refer to protein self-association, which can occur in multiple environments, from cell culture and fermentation, to isolation, purification and formulation processes. For example, the term "aggregation" can be used when describing the formation of inclusions; the accumulation of protein in "insoluble" fractions following cell fractionation; the appearance of turbidity, protein precipitation or formation of particles in samples; or the formation of small soluble oligomers amongst others.

Accordingly, in the above referenced examples, the physical stability of a Fv can be based on its physical stability in solution, wherein precipitation of the Fv from solution indicates that the Fv has become unstable. To assess physical stability,

solutions comprising a Fv according to the present disclosure or either a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 or a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 can be incubated at
5 4°C and assessed visually for precipitation at two weeks, four weeks, 12 weeks, six months and 12 months.

In an example, the physical stability of an Fv according to the present disclosure is greater than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in
10 SEQ ID NO: 49 or a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 when the Fv remains in solution at 4°C for at least four weeks. In an example, the physical stability of an Fv according to the present disclosure is greater than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 or a
15 di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 when the Fv remains in solution at 4°C for at least six months.

In another example, the Fv has reduced immunogenicity in a human subject compared to a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in
20 SEQ ID NO: 49. For example, an Fv can have reduced immunogenicity compared to a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 when immunogenicity is measure via enzyme-linked immunosorbent assay (ELISA). In another example, an Fv can have reduced immunogenicity compared to a binding
25 protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 when immunogenicity is measure via Surface Plasmon Resonance.

In another example, the capacity of the Fv to penetrate cells is greater than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID
30 NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the capacity of the Fv to penetrate cells is greater than a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50. In another example, the capacity of the Fv to penetrate cell nuclei is greater than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising
35 an amino acid sequence as shown in SEQ ID NO: 49. In another example, the capacity of the Fv to penetrate cell nuclei is greater than a di-scFv having an amino acid

sequence as shown in SEQ ID NO: 50. For example, the di-scFv can comprise an amino acid sequence as shown in SEQ ID NO: 36. In another example, the di-scFv can comprise an amino acid sequence as shown in SEQ ID NO: 41. In another example, the di-scFv can comprise an amino acid sequence as shown in SEQ ID NO: 43. In the
5 above referenced examples, the capacity of a binding protein to penetrate cells or cell nuclei can be measured using a colorimetric assay. For example, cells can be treated with control media, a binding protein according to the present disclosure or either a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 or a
10 di-scFv having an amino acid sequence as shown in SEQ ID NO: 50 for one hour. Cells are then washed, fixed, blocked with 1% BSA-TBST, and then probed with protein L for one hour. Cells are then washed and incubated with an anti-protein L primary antibody for one hour. After another round of washing, cells are incubated with an alkaline phosphatase-conjugated secondary antibody for one hour. Finally,
15 cells are washed and signal is developed by addition of NBT/BCIP. Signal development is stopped by removal of NBT/BCIP and washing once distinct nuclear stain is identifiable in any of the samples. Nuclear and or cellular staining is then measured using Image J.

In an example, an Fv providing nuclear staining having reciprocal intensity of at
20 least 190 absorbance units (au) has greater capacity to penetrate cell nuclei. In an example, an Fv providing nuclear staining having reciprocal intensity of at least 200 au has greater capacity to penetrate cell nuclei. In an example, an Fv providing nuclear staining having reciprocal intensity of at least 210 au has greater capacity to penetrate cell nuclei. In an example, an Fv providing nuclear staining having reciprocal intensity
25 of at least 220 au has greater capacity to penetrate cell nuclei. In another example, the capacity of an Fv to penetrate cell nuclei can be assessed by measuring florescence in individual cells. In an example, an Fv providing nuclear staining having reciprocal intensity of at least 190 au in at least 20 cells has greater capacity to penetrate cell nuclei. In another example, an Fv providing nuclear staining having reciprocal
30 intensity of at least 190 au in at least 30 cells has greater capacity to penetrate cell nuclei. In another example, an Fv providing nuclear staining having reciprocal intensity of at least 190 au in at least 40 cells has greater capacity to penetrate cell nuclei. In another example, an Fv providing nuclear staining having reciprocal intensity of at least 200 au in at least 20 cells has greater capacity to penetrate cell
35 nuclei. In another example, an Fv providing nuclear staining having reciprocal intensity of at least 200 au in at least 30 cells has greater capacity to penetrate cell

nuclei. In another example, an Fv providing nuclear staining having reciprocal intensity of at least 200 au in at least 50 cells has greater capacity to penetrate cell nuclei. In another example, an Fv providing nuclear staining having reciprocal intensity of at least 200 au in at least 70 cells has greater capacity to penetrate cell
5 nuclei. In another example, an Fv providing nuclear staining having reciprocal intensity of at least 200 au in at least 80 cells has greater capacity to penetrate cell nuclei.

In another example, the Fv has higher specificity for DNA than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48
10 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv has higher specificity for DNA than a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50.

In another example, the Fv has lower cross-reactivity (i.e. the ability of an Fv to react with similar antigenic sites on different proteins) compared to a binding protein
15 having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv has lower cross-reactivity with other targets compared to a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50. In this example, cross-reactivity of an Fv can be measured using various methods. In an example, cross-reactivity is
20 assessed via ELISA.

In another example, the Fv has higher binding affinity for DNA than a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the Fv has higher binding affinity for DNA than a di-scFv having an amino
25 acid sequence as shown in SEQ ID NO: 50.

In the above referenced examples, the affinity of an Fv for DNA can be measured using various methods. In an example, the dissociation constant (K_D) or association constant (K_A) or equilibrium constant (K_D) of a binding protein for DNA is determined. These constants for a binding protein are, in one example, measured by a
30 radiolabeled or fluorescently-labelled DNA-binding assay. This assay equilibrates the binding protein with a minimal concentration of labelled DNA (or a soluble form thereof, e.g., comprising an extracellular region of DNA fused to an Fc region) in the presence of a titration series of unlabelled DNA. Following washing to remove unbound DNA, the amount of label is determined.

35 Affinity measurements can be determined by standard methodology for antibody reactions, for example, immunoassays, surface plasmon resonance (SPR) (Rich and

Myszka *Curr. Opin. Biotechnol* 11:54, 2000; Englebienne *Analyst* 123: 1599, 1998), isothermal titration calorimetry (ITC) or other kinetic interaction assays known in the art.

In one example, the constants are measured by using surface plasmon resonance assays, e.g., using BIAcore surface plasmon resonance (BIAcore, Inc., Piscataway, NJ) with immobilized DNA. Exemplary SPR methods are described in U.S. Patent No. 7,229,619.

In some embodiments, the binding affinity for DNA of the Fv is between about 5nM and about 100pM, 10pM, 1pM, 100fM, 10fM, or 1 fM.

In an example, Fv encompassed by the present disclosure have a binding affinity for DNA comparable to about 5nM or less, or about 4.9 nM, or about 4.8 nM, or about 4.7 nM, or about 4.6 nM, or about 4.7 nM, or about 4.6 nM, or about 4.5 nM, or about 4.4 nM, or about 4.3 nM, or about 4.2 nM, or about 4.1 nM, or about 4.0 nM, or about 3.9 nM, or about 3.8 nM, or about 3.7 nM, or about 3.6 nM, or about 3.5 nM, or about 3.4 nM, or about 3.3 nM, or about 3.2 nM, or about 3.1 nM, or about 3.0 nM.

In other examples, subject Fv can have a binding affinity for DNA comparable to about 100 pM, or about 150 pM, or about 200 pM, or about 250 pM, or about 300 pM, or about 350 pM, or about 400 pM, or about 450 pM, or about 466 pM as measured by surface plasmon resonance (e.g. using a BIAcore 3000 instrument).

In the other examples, the affinity of a binding protein for DNA can be measured using Isothermal Titration Microcalorimetry.

In an example, the Fv comprises a linker. Various suitable linkers and methods for their design have been described previously (e.g. U.S. Patent No. 4,946,778; WO 1994/012520; and U.S. Patent No. 4,704,692). In an example, the Fv comprises a glycine-serine (GS) linker. For example, the GS linker can comprise (GGGGS)₃ (SEQ ID NO: 67). In an example, the Fv comprises a linker having the sequence shown in SEQ ID NO: 30. In another example, the Fv comprises a linker having the sequence shown in SEQ ID NO: 31. In another example, the Fv comprises linkers having the sequences shown in SEQ ID NO: 30 and SEQ ID NO: 31.

In an example, the V_H and V_L of the Fv can be in a single polypeptide chain. In another example, the Fv lacks an Fc region. For example, the Fv can be a single chain Fv fragment (scFv), a dimeric scFv (di-scFv), a trimeric scFv (tri-scFv). In an example, the Fv is an scFv. In another example, the Fv is a di-scFv. In another example, the Fv is a tri-scFv.

In another example, the scFv, di-scFv or tri-scFv can be linked to a constant region of an antibody, Fc or a heavy chain constant domain C_H2 and/or C_H3.

In an example, the present disclosure encompasses a cell penetrating di-scFv having an antigen binding domain, wherein the antigen binding domain binds to or specifically binds to DNA.

In an example, a di-scFv according to the present disclosure comprises an amino acid sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 32 to 47. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 32. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 33. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 34. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 35. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 36. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 37. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 38. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 39. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 40. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 41. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 42. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 43. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 44. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 45. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 46. In an example, the di-scFv comprises an amino acid sequence at least 95% identical to the sequence shown in SEQ ID NO: 47. For example, the di-scFv comprises an amino acid sequence at least 95% identical to the amino acid sequence shown in any one of SEQ ID NOs: 32, 36, 41 or 43. In these examples, amino acid sequences can be at least 96%, at least 97%, at least 98% or at least 99% identical to the recited SEQ ID NO.

In an example, a di-scFv according to the present disclosure comprises an amino acid sequence as shown in any one of SEQ ID NOs: 32 to 47. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 32. In an example,

the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 33. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 34. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 35. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 36. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 37. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 38. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 39. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 40. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 41. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 42. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 43. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 44. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 45. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 46. In an example, the di-scFv comprises an amino acid sequence as shown in SEQ ID NO: 47. For example, the di-scFv can comprise an amino acid sequence as shown in any one of SEQ ID NOs: 32, 36, 41 and 43.

In another example, the V_H and V_L of the binding protein are in a separate polypeptide chain. For example, the binding protein can be a diabody, triabody, tetrabody, Fab, $F(ab')_2$. In another example, the binding protein can be an Fv which comprises a V_H and V_L in separate polypeptide chains. In these examples, the binding proteins may be linked to a constant region of an antibody, Fc or a heavy chain constant domain C_H2 and/or C_H3 . In another example, the binding protein can be an intact antibody. Accordingly, in an example, the present disclosure encompasses an antibody having an antigen binding domain, wherein the antigen binding domain binds to or specifically binds to DNA. For example, the antibody can bind the same epitope as a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. In another example, the antibody can bind the same epitope as a di-scFv having an amino acid sequence as shown in SEQ ID NO: 50. In an example, the antibody comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4. For example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4. In another example, an antibody

can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4.

In another example, the antibody comprises a V_L having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. For example, an antibody can comprise a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an anti-DNA binding protein can comprise a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

10 In another example, the antibody comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 or SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5 or SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. For example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

Above exemplified antibodies may also have CDRs assigned using the IMGT system. Accordingly, in another example, the antibody comprises a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12. For example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12.

In another example, the antibody comprises a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. For example, an antibody can comprise a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an antibody can comprise a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16.

In another example, the antibody comprises a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 or SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13 or SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. For example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 10 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 13, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16. In another example, an antibody can comprise a V_H having a CDR1 as shown in SEQ ID NO: 9, a CDR2 as shown in SEQ ID NO: 11 and a CDR3 as shown in SEQ ID NO: 12 and a V_L having a CDR1 as shown in SEQ ID NO: 14, a CDR2 as shown in SEQ ID NO: 15 and a CDR3 as shown in SEQ ID NO: 16.

In another example, the antibody comprises a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23. For example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 18. In another example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 21. In another example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 23. In another example, the antibody comprises a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an antibody can comprise a V_L comprising a sequence at least 95% identical to the

sequence as shown in SEQ ID NO: 25. In another example, an antibody can comprise a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In another example, the antibody comprises a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 18 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 25. In another example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 21 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In another example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27. In these examples, the V_H and/or V_L can be at least 96%, at least 97%, at least 98% or at least 99% identical to the recited SEQ ID NO. In these examples, the antibody can have an above referenced combination of CDRs. For example, an antibody can comprise a V_H comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 21 and a V_L comprising a sequence at least 95% identical to the sequence as shown in SEQ ID NO: 27, wherein the V_H has a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and the V_L has a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.

In another example, the antibody comprises a V_H comprising a sequence as shown in any one of SEQ ID NOs: 17 to 23. For example, an antibody can comprise a V_H comprising a sequence as shown in SEQ ID NO: 18. In another example, an antibody can comprise a V_H comprising a sequence as shown in SEQ ID NO: 21. In another example, an antibody can comprise a V_H comprising a sequence as shown in SEQ ID NO: 23. In another example, the antibody comprises a V_L comprising a sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an antibody can comprise a V_L comprising a sequence as shown in SEQ ID NO: 25. In another example, an antibody can comprise a V_L comprising a sequence as shown in SEQ ID NO: 27. In another example, the antibody comprises a V_H comprising a sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence as shown in any one of SEQ ID NOs: 24 to 29. For example, an antibody can comprise a V_H comprising a sequence as shown in SEQ ID NO: 18 and a V_L comprising a sequence as

shown in SEQ ID NO: 25. In another example, an antibody can comprise a V_H comprising a sequence as shown in SEQ ID NO: 21 and a V_L comprising a sequence as shown in SEQ ID NO: 27. In another example, an antibody can comprise a V_H comprising a sequence as shown in SEQ ID NO: 23 and a V_L comprising a sequence as shown in SEQ ID NO: 27.

In another example, an above referenced antibody can comprise a constant heavy region 1 comprising a sequence as shown in SEQ ID NO: 69. In another example, an above referenced antibody can comprise a constant heavy region 3 comprising a sequence as shown in SEQ ID NO: 72. In another example, an above referenced antibody can comprise a hinge region comprising a sequence as shown in SEQ ID NO: 70. In these examples, the antibody can comprise a V_L comprising the amino acid sequence shown in SEQ ID NO: 27. For example, the antibody can comprise the amino acid sequence shown in SEQ ID NO: 78.

In another example, an above referenced antibody can comprise a constant heavy region 1 comprising a sequence as shown in SEQ ID NO: 69, a constant heavy region 3 comprising a sequence as shown in SEQ ID NO: 72, a hinge region comprising a sequence as shown in SEQ ID NO: 70 and a constant heavy region 2 comprising a sequence as shown in any one of SEQ ID NOs: 71, 74, 76. In this example, the antibody can comprise a V_L comprising the amino acid sequence shown in SEQ ID NO: 27. For example, the antibody can comprise the amino acid sequence shown in SEQ ID NO: 78.

In another example, the antibody has an amino acid sequence shown in SEQ ID NO: 68. In another example, the antibody has an amino acid sequence shown in SEQ ID NO: 73. In another example, the antibody has an amino acid sequence shown in SEQ ID NO: 75. In another example, the antibody has an amino acid sequence shown in any one of SEQ ID NOs: 68, 73 or 75.

As known in the art, antibodies can come in different isotypes such as IgA, IgD, IgE, IgG, and IgM. In an example, antibodies encompassed by the present disclosure are IgG. In another example, antibodies encompassed by the present disclosure are IgM.

In an example, the physical stability of an antibody according to the present disclosure is greater than an Fv such as a scFv or a di-scFv having corresponding V_H and V_L sequences. In an example, the physical stability of an antibody according to the present disclosure is greater than a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 when the antibody remains in solution at 4°C for at least four weeks. In an example, the physical stability of an antibody according to the present

disclosure is greater than a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 when the antibody remains in solution at 4°C for at least six months.

In another example, the antibody has reduced immunogenicity in a human subject compared to a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49. For example, an antibody can have reduced immunogenicity compared to a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 when immunogenicity is measure via enzyme-linked immunosorbent assay (ELISA). In another example, an antibody can have reduced immunogenicity compared to a binding protein having a V_H comprising an amino acid sequence as shown in SEQ ID NO: 48 and a V_L comprising an amino acid sequence as shown in SEQ ID NO: 49 when immunogenicity is measure via Surface Plasmon Resonance.

In another example, the antibody has reduced immunogenicity in a human subject compared to a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50. For example, an antibody can have reduced immunogenicity compared to a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 when immunogenicity is measure via enzyme-linked immunosorbent assay (ELISA). In another example, an antibody can have reduced immunogenicity compared to a di-scFv comprising an amino acid sequence as shown in SEQ ID NO: 50 when immunogenicity is measure via Surface Plasmon Resonance.

In an example, the antibody has a modified Fc region. For example, the antibody Fc region can comprise an amino acid sequence as shown in SEQ ID NO: 71. In another example, the antibody Fc region comprises an amino acid sequence as shown in SEQ ID NO: 74. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 76. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in any one of SEQ ID NOs: 71, 74 or 76. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with three amino acid substitutions. In this example, the two of the amino acid substations are between amino acid 1 and 10 of SEQ ID NO: 77. In another example, the two of the amino acid substations are between amino acid 5 and 10 of SEQ ID NO: 77. In another example, the two amino acid substitutions are at positions 7 and 8 of SEQ ID NO: 77. In these examples, the third amino acid substitution is between amino acid 65 and 75 of SEQ ID NO: 77. In another example, the third amino acid substitution is between amino acid 68 and 72 of SEQ ID NO: 77. In another example, the third amino acid

substitution is between amino acid 65 and 75 of SEQ ID NO: 77. In an example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with a L7A mutation. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with a L8A mutation. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with a N70D mutation. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with L7A and L8A mutations. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with L7A and N70D mutations. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with L8A and N70D mutations. In another example, the antibody comprises an Fc region comprising an amino acid sequence as shown in SEQ ID NO: 77 with L7A, L8A and N70D mutations.

Although variation in the disclosed sequences including heavy and light chain polypeptide sequences, and CDRs thereof, is generally provided above with at least 95% sequence identity to the reference sequence, variants with less identity are also expressly disclosed. Thus, in some examples, a DNA binding protein includes a polypeptide at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, or at least 94% identical to the amino acid sequence of the polypeptide of any of SEQ ID NOS: 32-47. In some embodiments, a DNA binding protein includes a variable heavy chain and/or light chain having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, or at least 94% identical to the amino acid sequence of the heavy and/or light chain of any of SEQ ID NOS: 32-47 (e.g., any of SEQ ID NO: 17-29). In some embodiments, a DNA binding protein includes one or more CDRs having least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, or at least 94% identical to the amino acid sequence of the CDRs of any of SEQ ID NOS: 32-47 (e.g., any of SEQ ID NO: 1-16).

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Binding Protein Production

Recombinant Expression

In one example, a binding protein as described herein is a peptide or polypeptide (e.g., is an antibody or antigen binding fragment thereof). In one example, the binding protein is recombinant.

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In the case of a recombinant peptide or polypeptide, nucleic acid encoding same can be cloned into expression vectors, which are then transfected into host cells, such as *E. coli* cells, yeast cells, insect cells, or mammalian cells, such as simian COS cells, Chinese Hamster Ovary (CHO) cells, human embryonic kidney (HEK) cells, or myeloma cells that do not otherwise produce immunoglobulin or antibody protein.

Suitable molecular cloning techniques are known in the art and described, for example in Ausubel *et al.*, (editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present) or Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press (1989). A wide variety of cloning and *in vitro* amplification methods are suitable for the construction of recombinant nucleic acids. Methods of producing recombinant antibodies are also known in the art. See U.S. Patent No. 4,816,567 or U.S. Patent No. 5,530,101.

Following isolation, the nucleic acid is inserted operably linked to a promoter in an expression construct or expression vector for further cloning (amplification of the DNA) or for expression in a cell-free system or in cells. Thus, another example of the disclosure provides an expression construct that comprises an isolated nucleic acid of the disclosure and one or more additional nucleotide sequences. Suitably, the expression construct is in the form of, or comprises genetic components of, a plasmid, bacteriophage, a cosmid, a yeast or bacterial artificial chromosome as are understood in the art. Expression constructs may be suitable for maintenance and propagation of the isolated nucleic acid in bacteria or other host cells, for manipulation by recombinant DNA technology and/or for expression of the nucleic acid or a binding protein of the disclosure.

Many vectors for expression in cells are available. The vector components generally include, but are not limited to, one or more of the following: a signal sequence, a sequence encoding the binding protein (e.g., derived from the information provided herein), an enhancer element, a promoter, and a transcription termination sequence. Exemplary signal sequences include prokaryotic secretion signals (e.g., pelB, alkaline phosphatase, penicillinase, Ipp, or heat-stable enterotoxin II), yeast secretion signals (e.g., invertase leader, α factor leader, or acid phosphatase leader) or mammalian secretion signals (e.g., herpes simplex gD signal).

Exemplary promoters active in mammalian cells include cytomegalovirus immediate early promoter (CMV-IE), human elongation factor 1- α promoter (EF1), small nuclear RNA promoters (U1a and U1b), α -myosin heavy chain promoter, Simian virus 40 promoter (SV40), Rous sarcoma virus promoter (RSV), Adenovirus major late

promoter, β -actin promoter; hybrid regulatory element comprising a CMV enhancer/ β -actin promoter or an immunoglobulin or antibody promoter or active fragment thereof. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture; baby hamster kidney cells (BHK, ATCC CCL 10); or Chinese hamster ovary cells (CHO).

Typical promoters suitable for expression in yeast cells such as for example a yeast cell selected from the group comprising *Pichia pastoris*, *Saccharomyces cerevisiae* and *S. pombe*, include, but are not limited to, the *ADHI* promoter, the *GALI* promoter, the *GAL4* promoter, the *CUP1* promoter, the *PHO5* promoter, the *nmf* promoter, the *RPR1* promoter, or the *TEF1* promoter.

Means for introducing the isolated nucleic acid or expression construct comprising same into a cell for expression are known to those skilled in the art. The technique used for a given cell depends on the known successful techniques. Means for introducing recombinant DNA into cells include microinjection, transfection mediated by DEAE-dextran, transfection mediated by liposomes such as by using lipofectamine (Gibco, MD, USA) and/or cellfectin (Gibco, MD, USA), PEG-mediated DNA uptake, electroporation and microparticle bombardment such as by using DNA-coated tungsten or gold particles (Agracetus Inc., WI, USA) amongst others.

The host cells used to produce the binding protein (e.g., antibody or antigen binding fragment) may be cultured in a variety of media, depending on the cell type used. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing mammalian cells. Media for culturing other cell types discussed herein are known in the art.

The skilled artisan will understand from the foregoing description that the present disclosure also provides an isolated nucleic acid encoding a binding protein (e.g., a peptide or polypeptide binding protein or an antibody or antigen binding fragment thereof) of the present disclosure.

The present disclosure also provides an expression construct comprising an isolated nucleic acid of the disclosure operably linked to a promoter. In one example, the expression construct is an expression vector.

In one example, the expression construct of the disclosure comprises a nucleic acid encoding a polypeptide (e.g., comprising a V_H) operably linked to a promoter and a nucleic acid encoding another polypeptide (e.g., comprising a V_L) operably linked to a promoter.

The disclosure also provides a host cell comprising an expression construct according to the present disclosure.

- The present disclosure also provides an isolated cell expressing a binding protein of the disclosure or a recombinant cell genetically-modified to express the binding protein.

Isolation of Proteins

Methods for purifying binding proteins according to the present disclosure are known in the art and/or described herein. An example is provided in Example 1 below.

- 10 Where a peptide or polypeptide is secreted into the medium, supernatants from such expression systems can be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of
15 adventitious contaminants.

The binding protein prepared from cells can be purified using, for example, ion exchange, hydroxyapatite chromatography, hydrophobic interaction chromatography, gel electrophoresis, dialysis, affinity chromatography (e.g., protein A affinity chromatography or protein G chromatography), or any combination of the foregoing.

- 20 These methods are known in the art and described, for example in WO99/57134 or Ed Harlow and David Lane (editors) Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, (1988).

Conjugates

In one example, a binding protein of the present disclosure is conjugated to another compound. The binding protein can be directly or indirectly bound to the compound (e.g., can comprise a linker in the case of indirect binding). Examples of
 5 compounds include, a radioisotope (e.g., iodine-131, yttrium-90 or indium-111), a detectable label (e.g., a fluorophore or a fluorescent nanocrystal or quantum dot), a therapeutic compound (e.g., a chemotherapeutic or an anti-inflammatory), a colloid (e.g., gold), a toxin (e.g., ricin or tetanus toxoid), a nucleic acid, a peptide (e.g., a serum albumin binding peptide), a protein (e.g., a protein comprising an antigen
 10 binding domain of an antibody or serum albumin), an agent that increases the half-life of the compound in a subject (e.g., polyethylene glycol or other water soluble polymer having this activity) and mixtures thereof.

Methods for attaching a drug or other small molecule pharmaceutical to an antibody are well known and can include use of bifunctional chemical linkers such as
 15 N-succinimidyl (4-iodoacetyl)-aminobenzoate; sulfosuccinimidyl(4-iodoacetyl)-aminobenzoate; 4-succinimidyl-oxycarbonyl--(2-pyridyldithio) toluene; sulfosuccinimidyl-6-[α -methyl- $\forall$ -(pyridyldithiol)-toluamido] hexanoate; N-succinimidyl-3-(-(2-pyridyldithio)-propionate; succinimidyl-6-[3 (-(2-pyridyldithio)-propionamido] hexanoate; sulfosuccinimidyl-6-[3 (-(2-pyridyldithio)-propionamido]
 20 hexanoate; 3-(2-pyridyldithio)-propionyl hydrazide, Ellman's reagent, dichlorotriazinic acid, S-(2-thiopyridyl)-L-cysteine, and the like. Further bifunctional linking molecules are discussed in, for example, U.S. Patent Nos. 5,349,066, 5,618,528, 4,569,789, 4,952,394, and 5,137,877.

The linker can be cleavable or noncleavable. Highly stable linkers can reduce the
 25 amount of payload that falls off in circulation, thus improving the safety profile, and ensuring that more of the payload arrives at the target cell. Linkers can be based on chemical motifs including disulfides, hydrazones or peptides (cleavable), or thioethers (noncleavable) and control the distribution and delivery of the active agent to the target cell. Cleavable and noncleavable types of linkers have been proven to be safe in
 30 preclinical and clinical trials (see, e.g., Brentuximab vedotin which includes an enzyme-sensitive linker cleavable by cathepsin; and Trastuzumab emtansine, which includes a stable, non-cleavable linker). In particular embodiments, the linker is a peptide linker cleavable by Edman degradation (Bachor, et al., *Molecular diversity*, 17 (3): 605–11 (2013)).

35 A non-cleavable linker can keep the active agent within the cell or the target microenvironment. As a result, the entire antibody, linker and active agent enter the

targeted cell where the antibody is degraded to the level of an amino acid. The resulting complex between the amino acid of the antibody, the linker and the active agent becomes the active drug. In contrast, cleavable linkers are catalyzed by enzymes in the target cell or microenvironment where it releases the active agent. Once cleaved, the
5 payload can escape from the targeted cell and attack neighboring cells (also referred to as “bystander killing”). In the case of the disclosed binding proteins, cleavage of the linker can lead to two active agents, the antibody itself and its payload, which can have different mechanisms of action in the target cell or microenvironment.

In some embodiments, there is one or more additional molecules, between the
10 active agent and the cleavage site. Other considerations include site-specific conjugation (TDCs) (Axup, *Proceedings of the National Academy of Sciences*, 109 (40): 16101–6 (2012) and conjugation techniques such as those described in Lyon, et al., *Bioconjugate Chem.*, 32 (10): 1059–1062 (2014), and Kolodych, et al., *Bioconjugate Chem.*, 26 (2): 197–200 (2015) which can improve stability and
15 therapeutic index, and α emitting immunoconjugates (Wulbrand, et al., Multhoff, Gabriele, ed., *PLoS ONE*. 8 (5): e64730 (2013)).

In an example, the binding protein is conjugated to nanoparticles or microparticles (for example as reviewed in Kogan *et al.*, *Nanomedicine (Lond)*. 2: 287–306, 2007). The nanoparticles may be metallic nanoparticles. The particles can be
20 polymeric particles, liposomes, micelles, microbubbles, and other carriers and delivery vehicles known in the art.

If the delivery vehicle is a polymeric particle, the binding protein can be coupled directly to the particle or to an adaptor element such as a fatty acid which is incorporated into the polymer. Ligands may be attached to the surface of polymeric
25 particles via a functional chemical group (carboxylic acids, aldehydes, amines, sulfhydryls and hydroxyls) present on the surface of the particle and present on the ligand to be attached. Functionality may be introduced post-particle preparation, by crosslinking of particles and ligands with homo- or heterobifunctional crosslinkers. This procedure may use a suitable chemistry and a class of crosslinkers (CDT, EDAC,
30 glutaraldehydes, etc. as discussed in more detail below) or any other crosslinker that couples ligands to the particle surface via chemical modification of the particle surface after preparation.

Binding proteins may also be attached to polymeric particles indirectly through adaptor elements which interact with the polymeric particle. Adaptor elements may be
35 attached to polymeric particles in at least two ways. The first is during the preparation of the micro- and nanoparticles, for example, by incorporation of stabilizers with

functional chemical groups during emulsion preparation of microparticles. For example, adaptor elements, such as fatty acids, hydrophobic or amphiphilic peptides and polypeptides can be inserted into the particles during emulsion preparation. In a second embodiment, adaptor elements may be amphiphilic molecules such as fatty acids or lipids which may be passively adsorbed and adhered to the particle surface, thereby introducing functional end groups for tethering to binding proteins. Adaptor elements may associate with micro- and nanoparticles through a variety of interactions including, but not limited to, hydrophobic interactions, electrostatic interactions and covalent coupling.

Suitable polymers include ethylcellulose and other natural or synthetic cellulose derivatives. Polymers which are slowly soluble and form a gel in an aqueous environment, such as hydroxypropyl methylcellulose or polyethylene oxide may also be suitable as materials for particles. Other polymers include, but are not limited to, polyanhydrides, poly (ester anhydrides), polyhydroxy acids, such as polylactide (PLA), polyglycolide (PGA), poly(lactide-co-glycolide) (PLGA), poly-3-hydroxybutyrate (PHB) and copolymers thereof, poly-4-hydroxybutyrate (P4HB) and copolymers thereof, polycaprolactone and copolymers thereof, and combinations thereof.

Some exemplary compounds that can be conjugated to a binding protein of the present disclosure are listed in Table 1.

Table 1. Compounds useful in conjugation.

Group	Detail
Radioisotopes (either directly or indirectly)	^{123}I, ^{125}I, ^{130}I, ^{133}I, ^{135}I, ^{47}Sc, ^{72}As, ^{72}Sc, ^{90}Y, ^{88}Y, ^{97}Ru, ^{100}Pd, $^{101\text{m}}\text{Rh}$, $^{101\text{m}}\text{Rh}$, ^{119}Sb, ^{128}Ba, ^{197}Hg, ^{211}At, ^{212}Bi, ^{153}Sm, ^{169}Eu, ^{212}Pb, ^{109}Pd, ^{111}In, ^{67}Cu, ^{68}Cu, ^{67}Cu, ^{75}Br, ^{76}Br, ^{77}Br, $^{99\text{m}}\text{Tc}$, ^{11}C, ^{13}N, ^{15}O, ^{18}I, ^{188}Re, ^{203}Pb, ^{64}Cu, ^{105}Rh, ^{198}Au, ^{199}Ag or ^{177}Lu
Half-life extenders	- Polyethylene glycol - Glycerol - Glucose
Fluorescent probes	- Phycoerythrin (PE) - Allophycocyanin (APC) - Alexa Fluor 488 - Cy5.5
Biologics	- fluorescent proteins such as Renilla luciferase, GFP - immune modulators or proteins, such as cytokines, e.g., an interferon

Group	Detail
	• toxins • an immunoglobulin or antibody or antibody variable region • half-life extenders such as albumin or antibody variable regions or peptides that bind to albumin
Chemotherapeutics	• Taxol • 5-FU • Doxorubicin • Idarubicin

In one example, a binding protein of the disclosure is conjugated to a chemotherapy agent.

In one example, a binding protein of the disclosure is conjugated to a
5 maytansinoid, e.g., DM1 or DM4.

In another example, a binding protein of the disclosure is conjugated to an auristatin, e.g., MMAE or MMAD.

In another example, a binding protein of the disclosure is conjugated to and
enzyme, e.g., MTM1, GAA or AGL.

10 In another example, a binding protein of the disclosure is conjugated to MBNL.

In another example, a binding protein of the disclosure is conjugated to a heat shock protein (HSP). In various examples, a binding protein of the disclosure is conjugated to a HSP from family HSP33, HSP70, HSP90, HSP100, small HSP (sHSP) or a combination thereof. For example, a binding protein of the disclosure can be
15 conjugated to HSP72. Accordingly, in an example, the present disclosure encompasses an Fv conjugated to a HSP from HSP70 family. In another example, the present disclosure encompasses an Fv conjugated to HSP72.

In another example, a binding protein of the disclosure is conjugated to a PARP inhibitor disclosed herein. For example, a binding protein of the disclosure can be
20 conjugated to olaparib.

In one aspect of the above examples, binding protein conjugates can be used to deliver conjugated payloads to a cell. Exemplary cells include cardiac cells such as cardiomyocytes, lung cells such as alveolar cells and neural cells such as neurons. Other exemplary cells include cancerous cells or virally infected cells.

In some embodiments, one or more the foregoing compounds are expressly excluded from being conjugated to the disclosed binding proteins. For example, the binding protein can be naked.

Compositions

Suitably, in compositions or methods for administration of a binding protein according to the present disclosure to a subject, the binding protein is combined with a pharmaceutically acceptable carrier as is understood in the art. In one example, the present disclosure provides a composition (e.g., a pharmaceutical composition) comprising a binding protein of the disclosure combined with a pharmaceutically acceptable carrier. In another example, the disclosure provides a kit comprising a pharmaceutically acceptable carrier suitable for combining or mixing with a binding protein prior to administration to the subject. In this example, the kit may further comprise instructions for use.

In general terms, "carrier" is used to refer to a solid or liquid filler, binder, diluent, encapsulating substance, emulsifier, wetting agent, solvent, suspending agent, coating or lubricant that may be safely administered to a subject, e.g., a human subject. Depending upon the particular route of administration, a variety of acceptable carriers, known in the art may be used, as for example described in Remington's Pharmaceutical Sciences (Mack Publishing Co. N.J. USA, 1991).

For example, suitable carriers may be selected from a group including sugars (e.g. sucrose, maltose, trehalose, glucose), starches, cellulose and its derivatives, malt, gelatine, talc, calcium sulfate, oils inclusive of vegetable oils, synthetic oils and synthetic mono- or di-glycerides, lower alcohols, polyols, alginic acid, phosphate buffered solutions, lubricants such as sodium or magnesium stearate, isotonic saline and pyrogen-free water. In an example, the carrier is not H₂O.

In an example, the carrier is compatible with, or suitable for, parenteral administration. Parenteral administration includes any route of administration that is not through the alimentary canal. Examples of parenteral administration include injection, infusion and the like. Examples of administration by injection include intravenous, intra-arterial, intramuscular and subcutaneous injection. In another example, compositions can be delivered via a depot or slow-release formulation which may be delivered intradermally, intramuscularly or subcutaneously.

In some embodiments, the binding protein is encapsulated or incorporated in nanoparticle, microparticle, or other delivery vehicle such as, but not limited to, those discussed above.

In some embodiments, a DNA binding protein is utilized detecting site or sites of cancer, tissue damage, injury, infection, or ischemia. The method typically including administering to a subject in need thereof an effective amount an agent that is detectable using diagnostic imaging or nuclear medicine techniques, and detecting the

agent. In such methods, the agent is typically conjugated to the DNA binding protein or encapsulated in a delivery vehicle conjugated with the DNA binding protein. The diagnostic imaging or nuclear medicine technique can be, for example, PET-CT, bone scan, MRI, CT, echocardiography, ultrasound, and x-ray.

5 In an example, binding proteins and compositions comprising the same can be used in the manufacture of a medicament for the treatment of a condition. In another example, the present disclosure relates to a binding protein or compositions comprising the same for use in the treatment of a condition. Examples of conditions to be treated are discussed below.

10 The methods and uses typically include administering a subject in need there of an effective amount of a binding protein. In some embodiments, the subject has cancer or virally infected or transformed cells. In some embodiments, the subject has a disease or disorder characterized by exogenous or extracellular DNA, including but not limited to, ischemia, tissue damage, injury, or an infection. The methods and uses can
15 include a combination therapy with a second, third, or more additional active agents. For example, the disclosed binding proteins can be used in combination with standard chemotherapy, radiation therapy, and other anti-cancer treatments. Radiation therapy (a.k.a. radiotherapy) is the medical use of ionizing radiation as part of cancer treatment to control malignant cells.

20

Combination Therapy

 Data compiled by the present inventors indicates that the disclosed binding proteins work with poly (ADP-ribose) polymerase (PARP) inhibitors to kill cancer cells. For example, more than additive cell death was observed in HDR-deficient
25 cancer cells treated with di-scFv and PARP inhibitor.

 Accordingly, in another example, the present disclosure encompasses a method of treating cancer in a subject in need thereof, the method comprising administering to the subject a binding protein disclosed herein and a PARP inhibitor. In another example, the present disclosure relates to a therapeutic combination comprising a
30 binding protein disclosed herein and a PARP inhibitor, the combination being provided for simultaneous or sequential administration. In another example, the present disclosure relates to a therapeutic combination comprising a binding protein disclosed herein and a PARP inhibitor for use in treating cancer.

 In an example, the PARP inhibitor is selected from the group consisting of
35 olaparib, niraparib, veliparib, rucaparib, talazoparib and BGB-290. For example, the PARP inhibitor can be olaparib.

Examples of binding proteins suitable for administration with a PARP inhibitor are provided above. In one example, the binding protein comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, the binding protein comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, the binding protein comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In another example, the binding protein comprises a V_H having a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and a V_L having a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8. In these examples, the binding protein can be an Fv. In an example, the binding protein can be a di-scFv.

Subjects having one or more of the conditions discussed below may be treated by administering a binding protein disclosed herein and a PARP inhibitor. In an example, the subject has pancreatic cancer. In another example, the subject has colon cancer. In an example, the subject has a cancer that is substantially BRCA2 deficient.

In another example, an above referenced combination therapy can be used to treat subjects with cancer resistant to PARP inhibitor therapy.

In an example, the binding protein and PARP inhibitor are administered as a single composition.

In another example, the binding protein and PARP inhibitor are administered as separate compositions. For example, the binding protein and PARP inhibitor can be administered simultaneously. In another example, binding protein and PARP inhibitor can be administered sequentially. In this example, administration of the binding protein and PARP inhibitor is carried out over a defined time period (usually minutes, hours or days). In an example, the period between sequential administration can be several days, provided that there is still sufficient levels of the first therapeutic to provide or add to the therapeutic benefit of the second therapeutic when it is administered. In one example, administration of a binding protein is followed by sequential administration of a PARP inhibitor. In another example, administration of a PARP inhibitor is followed by sequential administration of a binding protein.

Therapeutic combinations according to the present disclosure can be administered via various routes. Exemplary routes of administration include intravenous administration as a bolus or by continuous infusion over a period of time, intramuscular, intraperitoneal, intracerebrospinal, intrathecal, oral routes.

5 In an example, the binding protein and PARP inhibitor are administered via the same route. For example, both the binding protein and PARP inhibitor can be administered intravenously via continuous infusion. In another example, the binding protein and PARP inhibitor are administered via different routes. For example, the binding protein can administered intravenously via continuous infusion and the PARP
10 inhibitor can be administered orally.

In some examples, administration of a binding protein or Fv fragment defined herein and a PARP inhibitor achieves a result greater than when the binding protein or Fv fragment and the PARP inhibitor are administered alone or in isolation. For example, the result achieved by the combination can be more than additive of the
15 results achieved by the individual components alone.

In an example, administration of the combination of a binding protein or Fv fragment defined herein and a PARP inhibitor is effective to reduce cancer cell proliferation or viability in a subject with cancer to a greater degree than administering to the subject the same amounts of the individual components alone. For example, the
20 reduction in cancer cell proliferation or viability in the subject with cancer can be more than the additive of the results achieved by the individual components alone. In some examples, in subjects with cancer, the combination is effective to reduce tumour burden, reduce tumour progression, or a combination thereof, which may also be more than additive of the results achieved by the individual components alone.

25

Conditions to be Treated

In an example, binding proteins according to the present disclosure can be administered to a subject to treat various conditions.

In some examples of the disclosure, a method described herein is for the
30 treatment of a cancer. The term "cancer" refers to or describes the physiological condition in mammals that is typically characterized by unregulated cell growth/proliferation. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include, but are not limited to, squamous cell
35 cancer (e.g. , epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous

carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer and gastrointestinal stromal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, cancer of the urinary tract, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, superficial spreading melanoma, lentigo maligna melanoma, acral lentiginous melanomas, nodular melanomas, multiple myeloma and B-cell lymphoma (including low grade/follicular non-Hodgkin's lymphoma (NHL); mantle cell lymphoma; AIDS-related lymphoma; and Waldenstrom's Macroglobulinemia); chronic lymphocytic leukemia (CLL); acute lymphoblastic leukemia (ALL); hairy cell leukemia; chronic myeloblastic leukemia; and post-transplant lymphoproliferative disorder (PTLD), as well as abnormal vascular proliferation associated with phakomatoses, edema (such as that associated with brain tumors), Meigs' syndrome, brain, as well as head and neck cancer, and associated metastases. In another example, the term "cancer" encompasses triple negative breast cancer. Accordingly, in an example, the present disclosure relates to a method of treating breast, ovarian, colon, prostate, lung, brain, skin, liver, stomach, pancreatic or blood based cancer. In another example, the present disclosure relates to treating glioblastoma. In this example, glioblastoma may be treated by administering a binding protein disclosed herein such as a di-scFv having SEQ ID NO: 41 or an antibody having the heavy and light chain variable regions defined in SEQ ID NO: 41.

In other examples, a method described herein is used to treat cancers that are linked to mutations in BRCA1, BRCA2, PALB2, OR RAD51B, RAD51C, RAD51D or related genes. In other examples, a method described herein is used to treat cancers that are linked to mutations in genes associated with DNA mismatch repair, such as MSH2, MLH1, PMS2, and related genes. In other examples, a method described herein is used to treat cancers with silenced DNA repair genes, such as BRCA1, MLH1, OR RAD51B, RAD51C, OR RAD51D.

In another example, a method described herein is used to kill cells with impaired DNA repair processes. For example, cells with impaired DNA repair may aberrantly express a gene involved in DNA repair, DNA synthesis, or homologous recombination. Exemplary genes include XRCC1, ADPRT (PARP-1), ADPRTL2, (PARP-2), POLYMERASE BETA, CTPS, MLH1, MSH2, FANCD2, PMS2, p53, p21, PTEN, RPA, RPA1, RPA2, RPA3, XPD, ERCC1, XPF, MMS19, RAD51, RAD51B, RAD51C, RAD51D, DMC1, XRCCR, XRCC3, BRCA1, BRCA2, PALB2, RAD52,

RAD54, RAD50, MREU, NB51, WRN, BLM, KU70, KU80, ATM, ATR, CIPK1, CHK2, FANCA, FANCB, FANCC, FANCD1, FANCD2, FANCE, FANCF, FANCG, FANCC, FANCD1, FANCD2, FANCE, FANCF, FANCG, RAD1, and RAD9. In an example, a method described herein can be used to kill HDR deficient cells. In another example, a method described herein is used to kill cells with a mutant tumor suppressor gene. For example, cells can have one or more mutations in BRCA1 or BRCA2. For example, cells can be BRCA2 deficient colon cancer cells.

In an example, a method described herein is for the treatment of a cancer that is substantially HDR deficient. In an example, a method described herein is for the treatment of a cancer that is substantially BRCA2 deficient. For example, a BRCA2 deficient colon cancer may be treated. In another example, a method described herein is for the treatment of a cancer that is substantially PTEN deficient. For example, a PTEN deficient brain cancer may be treated. In another example, a method described herein is for the treatment of a cancer that is resistant to PARP inhibition.

In other examples of the disclosure, a method described herein is used to treat virally transformed cells, such as cells infected with an oncovirus. The term "oncovirus" is used in the context of the present disclosure to refer to viruses that are able to replicate in and reduce growth of tumour cells. In an example, the oncovirus virus is able to naturally replicate in and reduce growth of tumour cells. Examples of such viruses include Newcastle disease virus, vesicular stomatitis, myxoma, reovirus, sindbis, measles and coxsackievirus. In another example, the oncovirus virus is engineered to replicate in and reduce growth of tumour cells. Exemplary viruses suitable for such engineering include adenovirus, herpes simplex virus (HSV), lentivirus, vaccina and vesicular stomatitis virus (VSV).

Other exemplary oncoviruses include Human papillomaviruses (HPV), Hepatitis B (HBV), Hepatitis C (HCV), Human T-lymphotropic virus (HTLV), Kaposi's sarcoma-associated herpesvirus (HHV-8), Merkel cell polyomavirus, Epstein-Barr virus (EBV), Human immunodeficiency virus (HIV), and Human cytomegalovirus (CMV).

In other examples of the disclosure, a method described herein is used to kill cells transformed with a latent virus. Exemplary latent viruses include CMV, EBV, Herpes simplex virus (type 1 and 2), and Varicella zoster virus.

In other examples of the disclosure, a method described herein is used to treat active viral infections due to viruses that give rise to cancer, immunodeficiency, hepatitis, encephalitis, pneumonitis or respiratory illness. Exemplary viruses include above referenced oncovirus, parvovirus, poxvirus, herpes virus.

In other examples of the disclosure, a method described herein is used to treat Colorado Tick Fever (caused by Coltivirus, RNA virus), West Nile Fever (encephalitis, caused by a flavivirus that primarily occurs in the Middle East and Africa), Yellow Fever, Rabies (caused by a number of different strains of neurotropic viruses of the family Rhabdoviridae), viral hepatitis, gastroenteritis (viral)-acute viral gastroenteritis caused by Norwalk and Norwalk-like viruses, rotaviruses, caliciviruses, and astroviruses, poliomyelitis, influenza (flu), caused by orthomyxoviruses that can undergo frequent antigenic variation, measles (rubeola), paramyxoviridae, mumps, respiratory syndromes including viral pneumonia and acute respiratory syndromes including croup caused by a variety of viruses collectively referred to as acute respiratory viruses, and respiratory illness caused by the respiratory syncytial virus.

In other examples of the disclosure, a method described herein is used to treat a nucleotide repeat disorder or an exon splicing disorder. In other examples of the disclosure, a method described herein is used to treat a disorder associated with aberrant microsatellite expansion, such as myotonic dystrophy. For example, the methods of the present disclosure may be used to treat Myotonic dystrophy. Examples of Myotonic dystrophy type 1 (DM1; trinucleotide (CTG)_n expansion of n=50 to >3000 in the 3'-untranslated region of the Dystrophia myotonica-protein kinase (DMPK) gene) and type 2 (DM2; tetranucleotide (CCTG)_n expansion of n=75 to about 11,000 in the first intron of zinc finger protein 9 (ZNF9) gene. In other examples of the disclosure, a method described herein is used to treat neurofibromatosis. In other examples of the disclosure, a method described herein is used to treat Huntington's Disease. In other examples of the disclosure, a method described herein is used to treat myotubular myopathy. In other examples of the disclosure, a method described herein is used to treat a glycogen storage disorder. In other examples of the disclosure, a method described herein is used to treat Pompe Disease. In other examples of the disclosure, a method described herein is used to treat Forbes-Cori Disease. In other examples of the disclosure, a method described herein is used to treat Lafora Disease.

In other examples of the disclosure, a method described herein is used to increase Muscleblind-like (MBNL) activity in a cell *in vitro* or in a subject by administering a binding protein according to the present disclosure conjugated to an MBNL polypeptide. In other examples of the disclosure, a method described herein is used for enzyme or protein replacement therapy.

In other examples of the disclosure, a method described herein is used to increase HSP activity in a cell *in vitro* or in a subject by administering a binding protein according to the present disclosure conjugated to a HSP from HSP70 family. In other

examples of the disclosure, a method described herein is used to increase HSP72 activity in a cell *in vitro* or in a subject by administering a binding protein according to the present disclosure conjugated to an HSP72 polypeptide.

5 **EXAMPLES**

EXAMPLE 1 – Expression and Purification of di-scFV variants

Single gene GS vectors (using Lonza's GS Xceed™ Gene Expression System) were established, sequenced, linearized and used to generate a stable pool for each variant. Following cryopreservation the propagated stable pools were expanded to 200
10 mL culture volume each and subjected to an abridged fed batch overgrow with a single bolus feed on day 4 and harvested on day 8. Supernatant titre was determined by Protein L Octet. Clarified supernatant for ion exchange purification was obtained by centrifugation followed by filter sterilisation using a 0.22 µm filter. An ion exchange purification method was developed using the dimer version of the murine antibody as a
15 reference.

Clarified supernatant was purified using a pre-packed 5 mL HiTrap Capto S column (GE Healthcare, 17-544122) on an AKTA purifier (run at 5 mL/min). The column was equilibrated with 50 mM Sodium Phosphate pH 6 before and after sample loading and the product was eluted with a linear gradient from 0-1 M NaCl.
20 Quantification of bound and unbound material by Protein L Octet showed that approximately 57% of material remained in the unbound fraction. Repeating the chromatography using the unbound fraction again resulted in approximately 64% of the starting material remaining in the unbound fraction.

Purification of the remaining supernatants was performed using two sequential
25 steps of ion exchange chromatography with a linear elution gradient from 0-1 M NaCl. Following purification, the products were quantified and concentrated to approximately 1 mg/mL by ultrafiltration using Amicon Ultra-15 filters (Millipore, UFC903024).

Duplicate samples were analysed by SE-HPLC on an Agilent 1200 series HPLC system, using a Zorbax GF-250 9.4 mm ID x 25 cm column (Agilent) and by SDS-
30 PAGE analysis. Yields and titres of expression cultures are summarised in Table 1. SDS-PAGE analysis of variants is shown in Figures 1 and 2.

Table 1. Yields and titres of expression cultures.

Product	Estimated Titre (mg/L)	Final concentration (mg/mL)	Volume (mL)	Final Yeild (mg)	Monomer (%)
var_2	393.4	1.079	3.2	3.5	84.08
var_3	436.8	1.156	1.5	1.7	80.61
var_4	445.0	1.090	2.5	2.7	84.26
var_6	275.7	1.214	1.6	1.9	93.02
var_7	288.4	0.829	1.5	1.2	79.16
var_8	373.7	1.024	2.0	2.0	81.71
var_10	325.2	0.767	5.6	4.3	85.17
var_11	349.7	1.181	6.2	7.3	81.86
var_12	396.1	1.169	4.0	4.7	80.86
var_13	459.1	0.803	5.0	4.0	86.13
var_14	527.5	0.799	4.0	3.2	82.72
var_15	584.2	1.003	3.2	3.2	86.34
var_16	391.9	0.842	5.6	4.7	85.53
var_17	315.6	1.106	1.8	2.0	85.79
var_18	460.3	1.118	4.5	5.0	85.37
var_19	318.9	0.401	3.1	1.2	84.47
tri_L1H2	251.4	1.091	3.2	3.5	95.47
Di_scFv_B72.3	55.7		0.0	0.0	
di_scFv_D31N	270.7	1.027	6.6	6.8	95.36
tri_scFv_D31N	40.2	0.658	2.5	1.6	93.34

EXAMPLE 2 – Nuclear Penetration of Variants**5 Alkaline phosphatase-based survey of nuclear penetration**

- DLD1 colon cancer cells were treated with control media or each of the indicated variants for one hour. Cells were then washed, fixed, blocked with 1% BSA-TBST, and then probed with protein L for one hour. Cells were then washed and incubated with an anti-protein L primary antibody for one hour. After another round of
- 10 washing cells were incubated with an alkaline phosphatase-conjugated secondary antibody for one hour. Finally, cells were washed and signal was developed by addition of NBT/BCIP. Representative images are shown in Figure 3. Dark stain indicates location of the variants.

Raw integrated density values reflecting nuclear alkaline phosphatase staining in the DLD1 cells from the experiment in Figure 3 were obtained by analysis using ImageJ. Boxplots of distributions of values are presented for each variant in Figure 4.

Histogram plots of cell counts versus nuclear staining intensity (represented as reciprocal intensity in arbitrary units) are shown in Figure 5. Most of the variants, other than variants 12 and 14, showed improved nuclear penetration relative to the yeast prototype, which is demonstrated by right shift of histogram peak. In addition, the narrowing of distributions observed in the histograms for most of the humanized variants shows improved uniformity of nuclear penetration relative to the yeast prototype. Variants 13 and 15 in particular showed notable right shift and narrowing of distributions relative to the yeast prototype.

Immunofluorescence-based survey of nuclear penetration

DLD1 colon cancer cells were treated with control media or each of the indicated variants for one hour. Cells were then washed, fixed, blocked with 1% BSA-TBST, and then probed with protein L for one hour. Cells were then washed and incubated with an anti-protein L primary antibody for one hour. After another round of washing cells were incubated with an Alexa488-conjugated secondary antibody for one hour. Finally, cells were washed and signal was visualized by fluorescence microscopy. Representative images are shown in Figure 6. Green signal indicates location of the variants.

Raw integrated density values reflecting Alexa488 fluorescence signal in the DLD1 cells from the experiment in Figure 6 were obtained by analysis using ImageJ. Boxplots of distributions of values are presented for each variant in Figure 7.

EXAMPLE 2 – Accumulation of DNA damage

A matched pair of PTEN-proficient and deficient U251 human glioma cells were treated with control media or media containing Variant 10, 11, 13, 15, or 16 for twenty-four hours. Cells were then washed, fixed, blocked, and then probed with an anti-phospho-53BP1 antibody overnight. Cells were then washed and incubated with an AlexaFluor555-conjugated secondary antibody. Finally, cells were washed, counterstained with DAPI, and visualized under a fluorescence microscope. Images were saved and evaluated by CellProfiler to determine mean number of phospho-53BP1 foci per cell. The new variants increased the number of foci in the PTEN-deficient cells, but not the PTEN-proficient cells. Representative images are shown in

Figure 8, Panel A, and quantitative analysis by CellProfiler is shown in Figure 8, Panel B.

Cell viability of PTEN-deficient U87 human glioma cells was also assessed following treatment with control media or media containing Variants 10, 13, 15, or 16. Cell viability was determined 7 days after treatment using Trypan blue exclusion assay and by direct visualization of cell morphology by light microscopy. All variants caused reductions in cell viability relative to control treated cells (Figure 9).

Next, a matched pair of BRCA2-proficient and deficient DLD1 colon cancer cells was treated with control media or media containing Variants 10, 13, 15, or 16. Cell viability was determined 7 days later by Trypan blue exclusion assay and by direct visualization of cell morphology by light microscopy. The variants were not toxic to the BRCA2-proficient cells, but the BRCA2-deficient cells were killed by the variants. These data indicate that variants are able to selectively kill cancer cells with impaired DNA repair. Moreover, these data indicate that the variants will be able to discriminate between cancerous cells with impaired DNA repair and healthy cells to selectively kill cancer cells. Representative light microscope images shown the changes in morphology in the BRCA2-deficient cancer cells treated with the variants are shown in Figure 10, Panel A. Quantitative analysis of the cell survival by Trypan blue exclusion assay is shown in Figure 10, Panel B.

20

EXAMPLE 3 – Di-scFv co-administration with PARP inhibition in HDR deficient cancer cells

DLD-1 and MCF-7 cells were treated with control or di-scFv (SEQ ID NO: 41), and nuclear penetration was evaluated by protein L immunostain of fixed cells. The di-scFv successfully penetrated DLD-1 and MCF-7 cell nuclei (Figures 11 and 12).

Homology-directed repair (HDR) deficient BRCA2- DLD1 cells and PTEN-U251 cells were treated with control, 5 nM olaparib, 10 μ M di-scFv, or 10 μ M di-scFv + 5 nM olaparib. Surviving fraction was determined by colony formation assay. Surprisingly, more than additive cell death was observed in HDR-deficient cancer cells treated with di-scFv and the PARP inhibitor (Figure 13).

It was then determined whether the combination of di-scFv and olaparib is simply universally cytotoxic, regardless of DNA repair status. To evaluate this possibility, HDR-proficient DLD1 cells were treated with the above regimen to confirm selectivity of combination therapy to HDR-deficient malignant cells. No effect on cell death was observed for the di-scFv alone or in combination with PARP

35

inhibitor. These findings demonstrate that HDR-proficient cells remain resistant to the effects of both the di-scFv and olaparib, even when used in combination.

EXAMPLE 4 – Effect of Di-scFv (SEQ ID NO: 41) on primary human glioblastoma (GBM) cells

Primary human glioblastoma (GBM) cancer cells extracted from primary human GBM tumours from patients were treated with control or di-scFv (SEQ ID NO: 41), and percentage of live cells was evaluated by trypan blue staining. Five of the seven glioblastoma tumour explants treated with di-scFv (SEQ ID NO: 41) showed significant cancer cell death (Figure 14).

GBM cancer stem cells extracted from primary human GBM tumours from patients and grown as spheres were treated with control or di-scFv (SEQ ID NO: 41), and the effect of dose and incubation time on reduction of sphere volume was evaluated by confocal micrographs of DX1-rhodamine cellular penetration into GBM cells. Tumour spheres are recognised as a useful tool for pre-clinical studies as they retain tumour heterogeneity and more closely represent the original patient tumour. Treatment of human GBM cancer stem cells (CSCs) grown as tumour spheres with di-scFv (SEQ ID NO: 41) demonstrated cellular penetration in GBM spheres and reduced sphere volume in dose-dependent and time-dependant manner (Figure 15).

EXAMPLE 5 - Evaluation of the effect of di-scFv (SEQ ID NO: 41) on human GBM cells in an orthotopic mouse model

An orthotopic mouse model of GBM was generated by intracranial injection of GBM cells extracted from human GBM tumours. Once the tumours developed in the brain, mice were treated by tail vein injection of control or di-scFv variant 13 (SEQ ID NO: 41), and effect of di-scFv on reduction of tumour volume was evaluated by extraction of tumours. Evaluation of brain sections showed that the glioblastoma tumours in mice treated with di-scFv were more than 40% smaller than the comparable tumours in control mice (Figure 16A). TUNEL staining also demonstrated increased incidence of apoptosis in di-scFv-treated tumours (Figure 16B). The observed reduction in tumour size and increased TUNEL staining in the di-scFv-treated GBM tumours suggested that di-scFv variant 13 (SEQ ID NO: 41) successfully crossed the blood brain barrier to localize in and impact GBM tumour growth. To confirm this, tumours and normal brain were probed for di-scFv by protein L immunostaining. As shown in Figure 16C, the di-scFv was detected in the nuclei of GBM tumour cells, but was not evident in surrounding adjacent normal brain cells.

Additionally, a group of 7 mice was evaluated for the survival benefit and mice treated with di-scFv showed a median survival of 87 days, more than 20% longer than controls (median 72 days). Mean survival data reflected these trends (83 days $\pm$ 3.2 days for di-scFv treated mice, 71 days $\pm$ 1.2 days for controls) (Figure 16E). Statistical analysis indicated a significant difference between the two groups, with P value = 0.004. No toxicity or weight loss associated with di-scFv treatments was observed (Figure 16D).

EXAMPLE 6 - The Effect of PAT-DX1 on Foci Accumulation

10 A matched pair of BRCA2-proficient and deficient DLD1 colon cancer cells and PTEN-proficient and deficient U251 human glioma cells were treated with control media or media containing 10 μ M di-scFv variant 13 (SEQ ID NO: 41), 5nM olaparib, or combination treatment. Phospho-53BP1 antibody staining was evaluated by Cell Profiler to determine mean number of phospho-53BP1 foci per cell. di-scFv variant 13
15 (SEQ ID NO: 41) treatment alone and in combination with olaparib increased the number of phospho-53BP1 foci in both the BRCA2-deficient DLD1 and the PTEN-deficient U251 cells, but not in proficient cells (Figure 17).

20 It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the disclosure as shown in the specific embodiments without departing from the spirit or scope of the disclosure as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

25 All publications discussed above are incorporated herein in their entirety. Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is solely for the purpose of providing a context for the present disclosure. It is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field
30 relevant to the present disclosure as it existed before the priority date of each claim of this application.

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CLAIMS

1. A cell penetrating anti-DNA binding protein having an antigen binding domain, wherein the antigen binding domain binds to DNA and comprises:
- 5 (i) a heavy chain variable region (V_H) and a light chain variable region (V_L), wherein the V_H has a complementarity determining region (CDR) 1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3 and a CDR3 as shown in SEQ ID NO: 4 and the V_L has a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8; or,
- 10 (ii) a V_H and a V_L , wherein the V_H has a CDR1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 2 and a CDR3 as shown in SEQ ID NO: 4 and the V_L has a CDR1 as shown in SEQ ID NO: 5, a CDR2 as shown in SEQ ID NO: 7 and a CDR3 as shown in SEQ ID NO: 8.
- 15 2. The binding protein of claim 1 comprising:
- (i) a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23;
- (ii) a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29; or
- 20 (iii) a V_H comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 17 to 23 and a V_L comprising a sequence at least 95% identical to the sequence as shown in any one of SEQ ID NOs: 24 to 29.
- 25 3. The binding protein according to claim 1 or 2, wherein the V_H and a V_L are separated by a linker.
4. The binding protein of claim 3, wherein the linker comprises the sequence shown in SEQ ID NO: 30.
- 30 5. The binding protein of any one of claims 1 to 4, wherein, the V_H and V_L are in a single polypeptide chain.
6. The binding protein of claim 5, which is:
- 35 (i) a single chain Fv fragment (scFv);
- (ii) a dimeric scFv (di-scFv);
- (iii) a trimeric scFv (tri-scFv);

- (iv) any one of (i), (ii) or (iii) linked to a constant region of an antibody, Fc or a heavy chain constant domain C_H2 and/or C_H3.
- 5 7. The binding protein of claim 6, which is a scFv.
8. The binding protein of claim 6, which is a di-scFv.
9. The binding protein according to any one of claims 1 to 4, wherein, the V_H and V_L are in a separate polypeptide chain.
- 10 10. The binding protein of claim 9, which is:
- (i) a diabody;
- (ii) a triabody;
- (iii) a tetrabody;
- 15 (iv) a Fab;
- (v) a F(ab')₂;
- (vi) a Fv;
- (vii) one of (i) to (vi) linked to a constant region of an antibody, Fc or a heavy chain constant domain C_H2 and/or C_H3; or,
- 20 (viii) an intact antibody.
11. The binding protein of claim 10, which is an antibody.
12. The binding protein according to any one of claims 1 to 11, which comprises an amino acid sequence as shown in any one of SEQ ID NOs: 41 – 47.
- 25 13. The binding protein according to any one of claims 1 to 12, which is conjugated to another compound.
- 30 14. The binding protein according to any one of claims 1 to 13, wherein the V_H has a complementarity determining region (CDR) 1 as shown in SEQ ID NO: 1, a CDR2 as shown in SEQ ID NO: 3, and a CDR3 as shown in SEQ ID NO: 4; and the V_L has a CDR1 as shown in SEQ ID NO: 6, a CDR2 as shown in SEQ ID NO: 7, and a CDR3 as shown in SEQ ID NO: 8.

15. The binding protein according to any one of claims 1 to 14, wherein the VH comprises a sequence at least 99% identical to the sequence as shown in SEQ ID NO: 21 and the VL comprises a sequence at least 99% identical to the sequence as shown in SEQ ID NO: 27.
- 5 16. The binding protein according to any one of claims 1 to 15, wherein the VH comprises the sequence shown in SEQ ID NO: 21 and the VL comprises the sequence shown in SEQ ID NO: 27.
- 10 17. A nucleic acid encoding a binding protein defined by any one of claims 1 to 16.
18. An expression construct comprising a nucleic acid defined by claim 17.
- 15 19. A method of treating cancer in a subject, the method comprising administering to the subject and effective amount of a binding protein according to any one of claims 1 to 16.
- 20 20. The method according to claim 19, wherein the binding protein is provided with a PARP inhibitor.
21. The method of claim 20, wherein the PARP inhibitor is olaparib.
22. Use of a binding protein according to any one of claims 1 to 16 in the manufacture of a medicament for treating cancer.
- 25 23. The method according any one of claims 19 to 21, or the use according to claim 22, wherein the cancer is:
- 30 (i) HDR deficient; resistant to PARP inhibition; BRCA2 deficient; and/or PTEN deficient; or
- (ii) wherein the cancer is colon cancer, brain cancer, prostate, ovarian, breast, endometrial, melanoma, or pancreatic cancer.
24. The method or use according to claim 23, wherein the cancer is a triple negative breast cancer or glioblastoma.

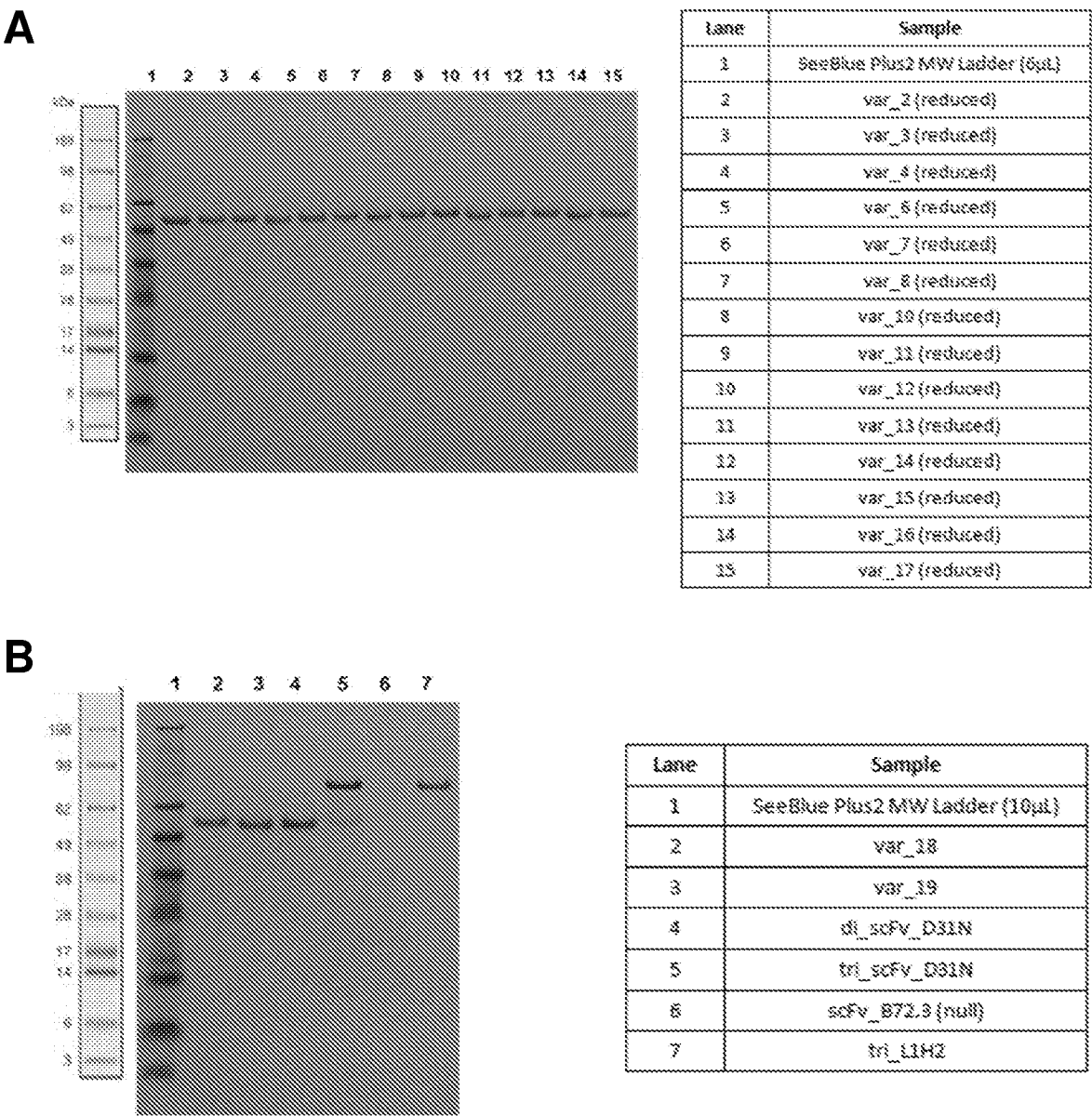


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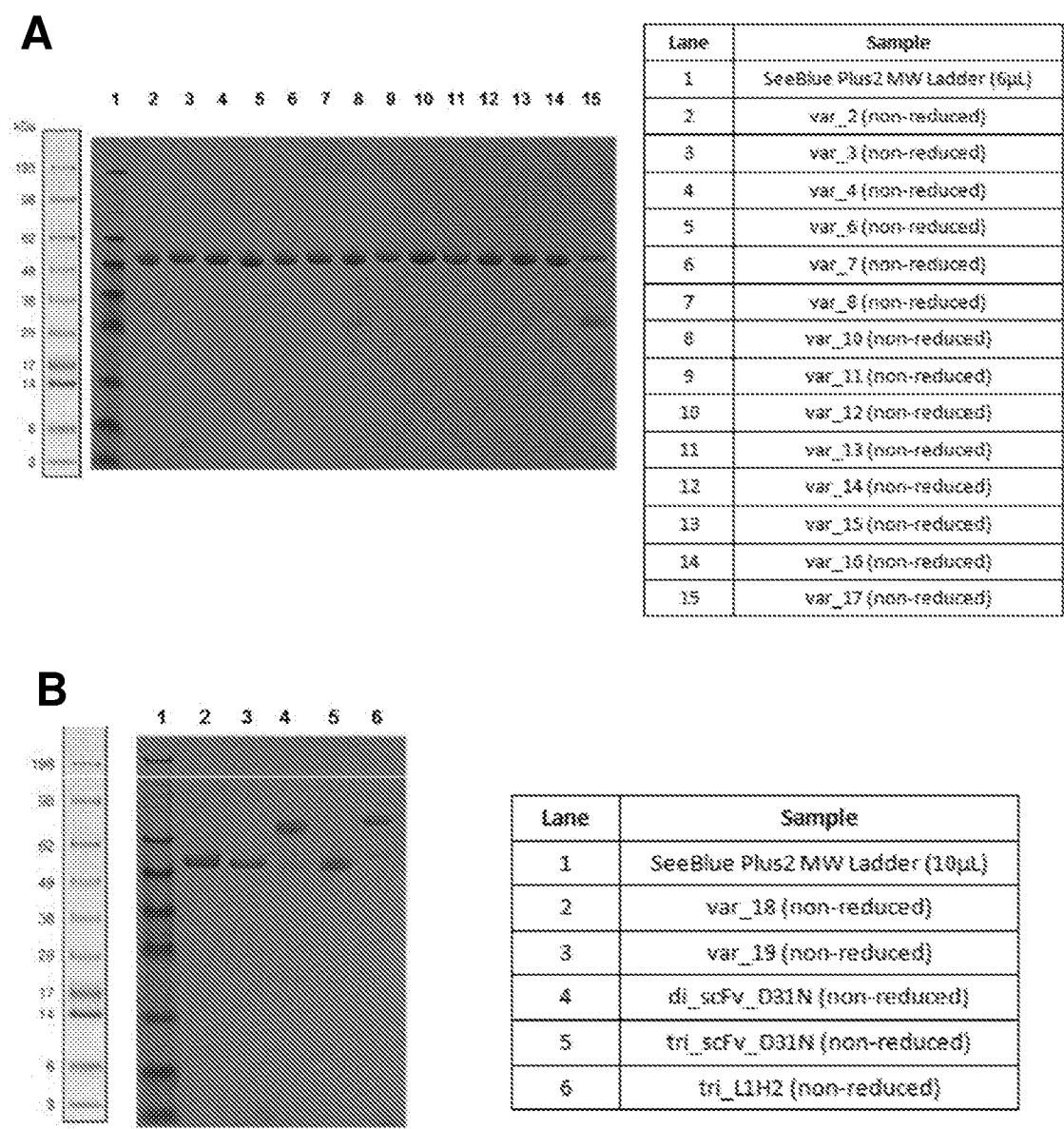


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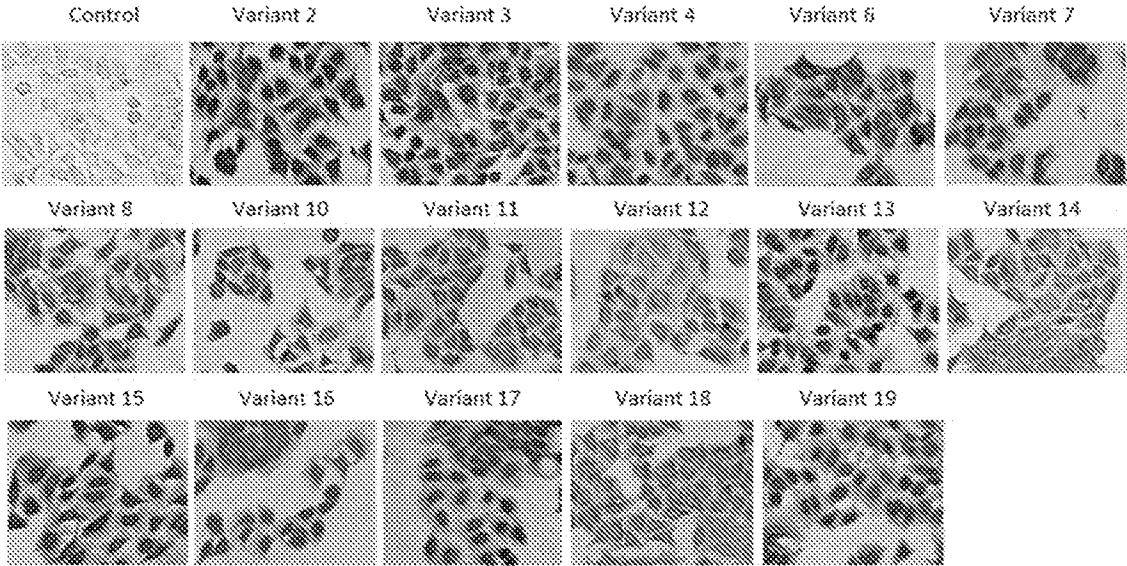


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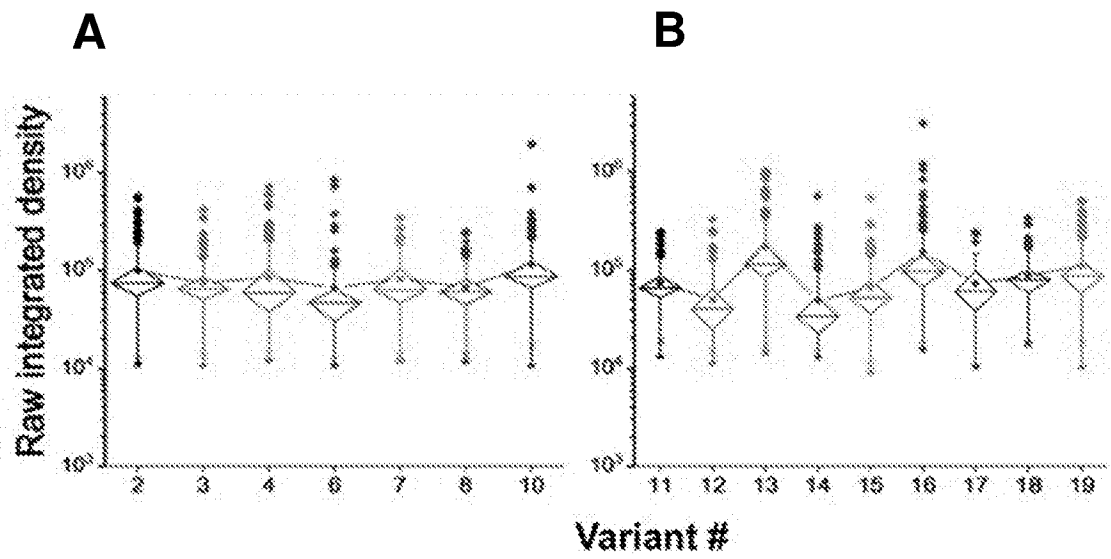
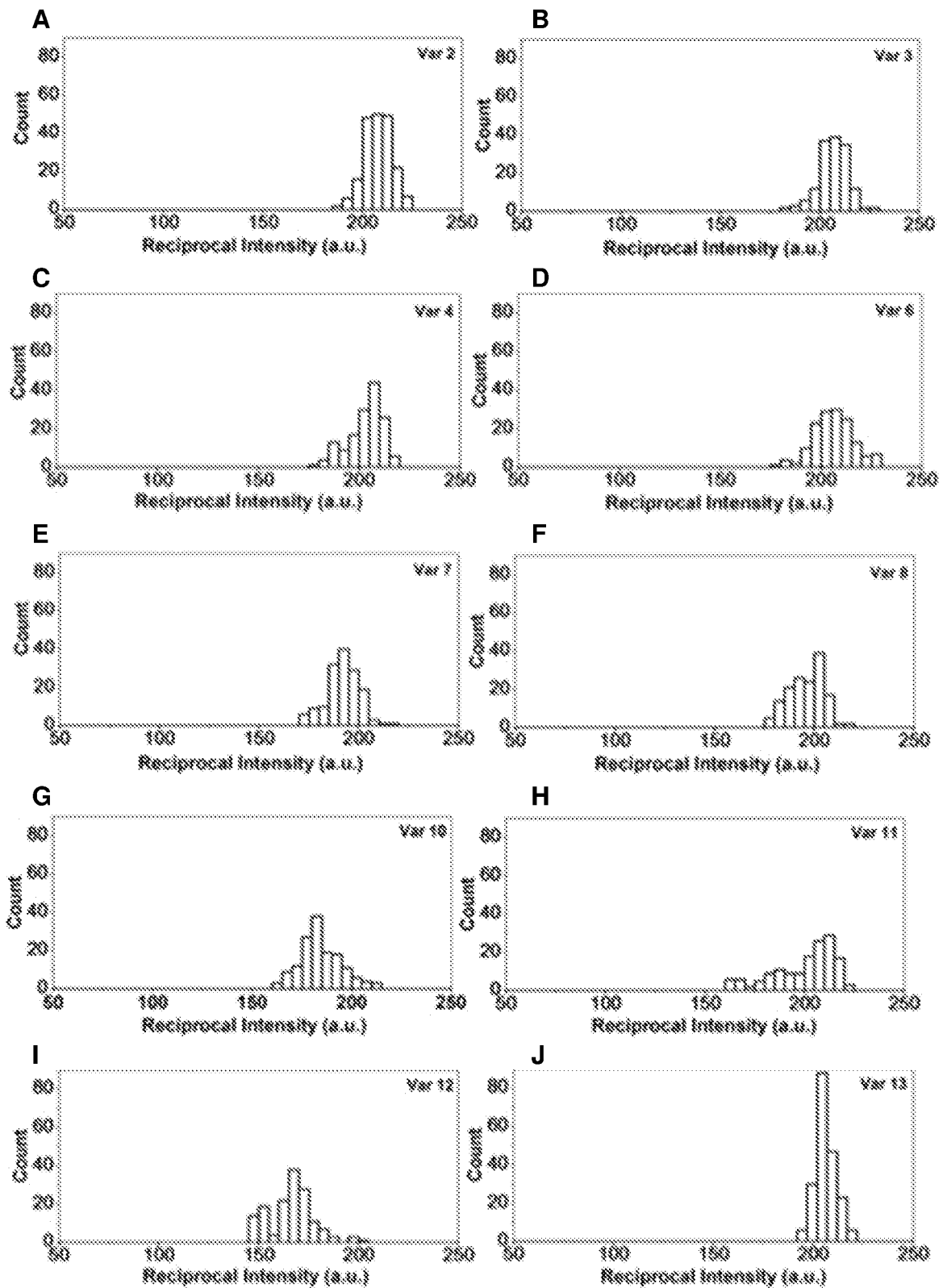


FIGURE 4

5/18

**FIGURE 5 (Part 1)**

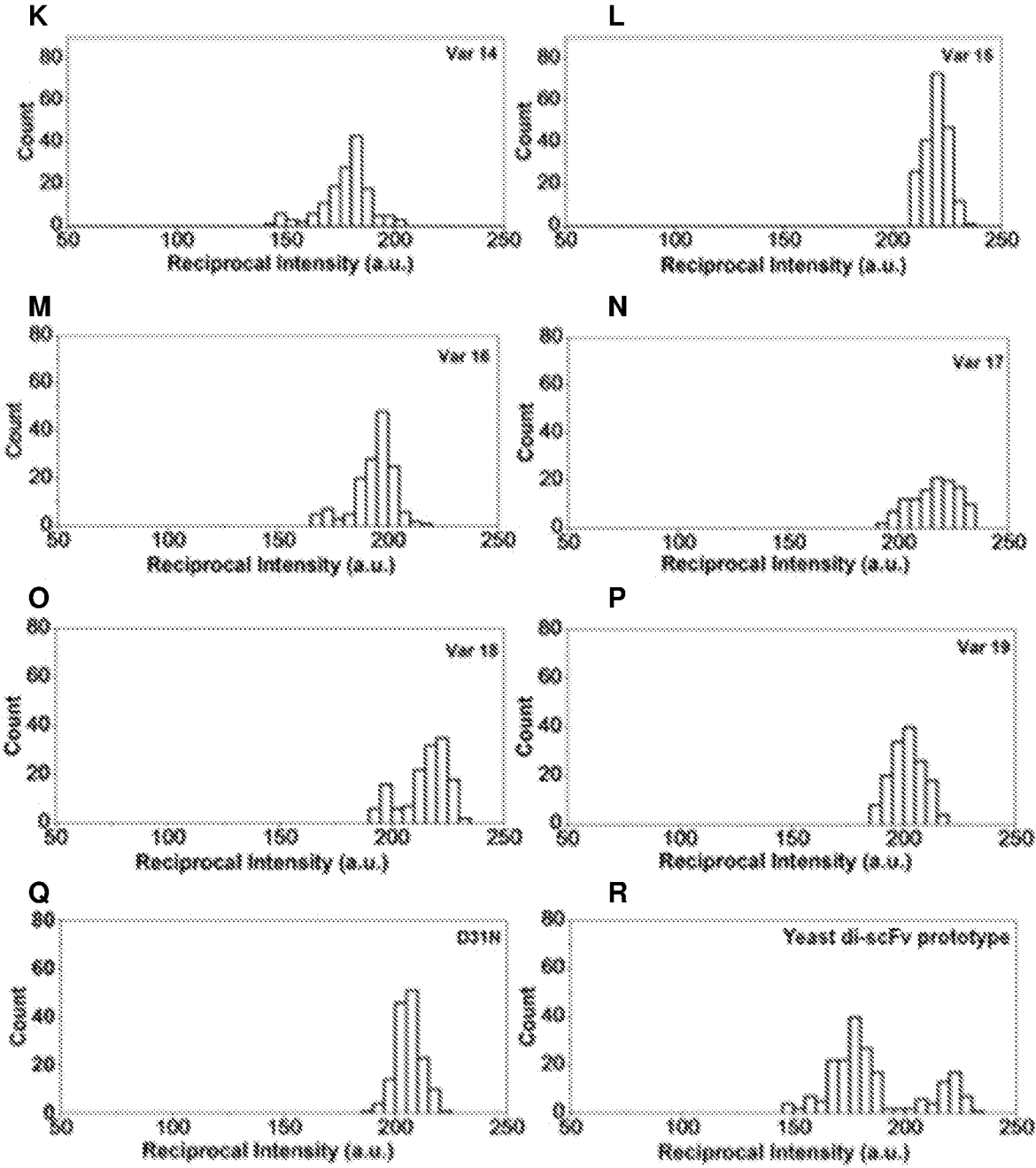


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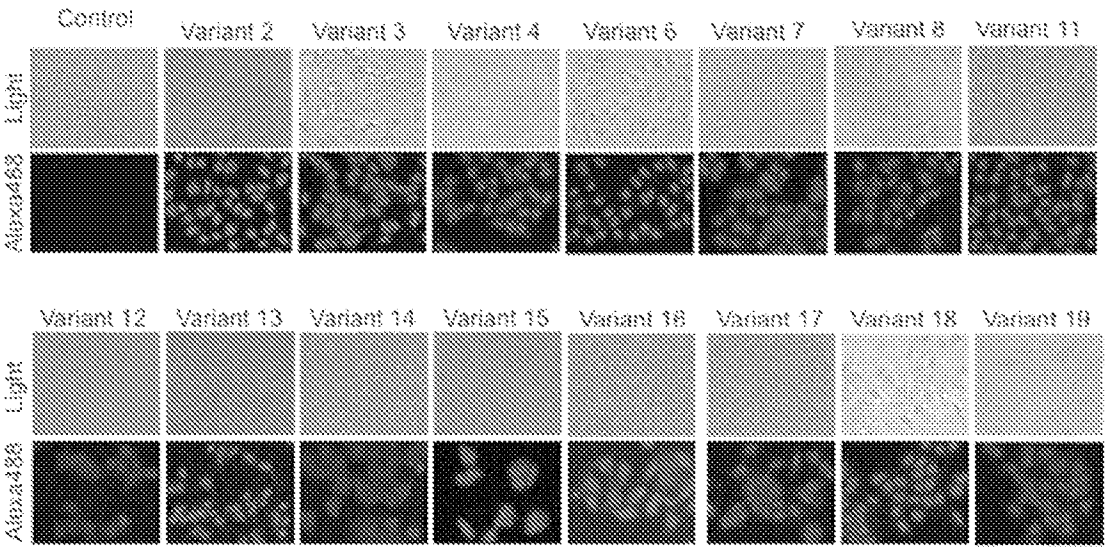


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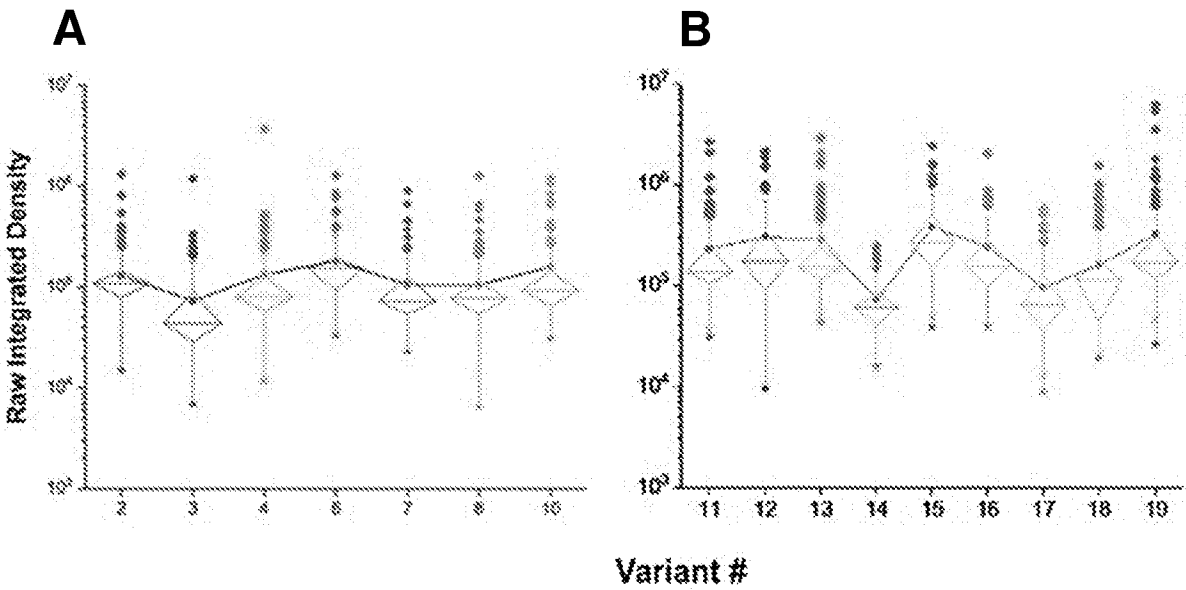


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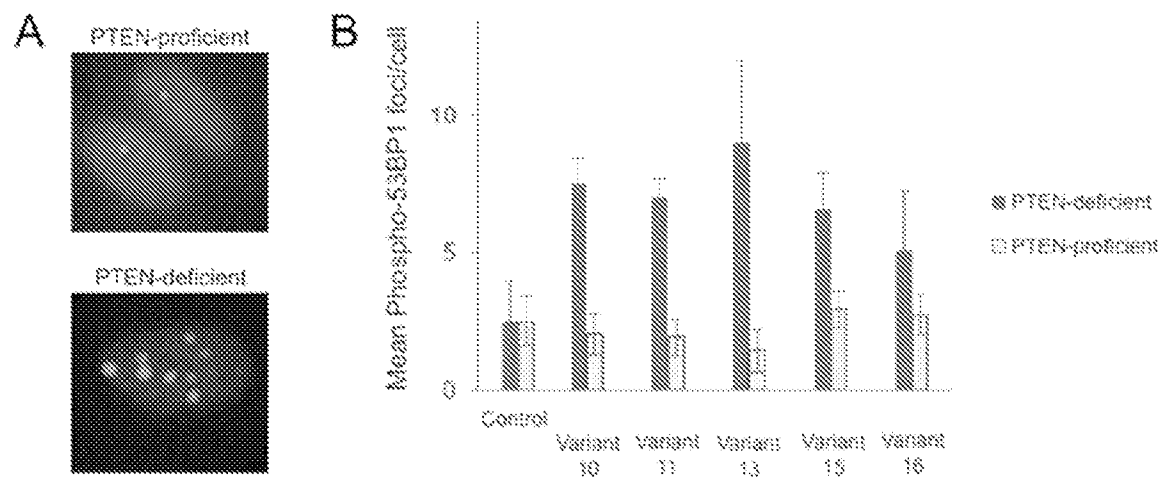


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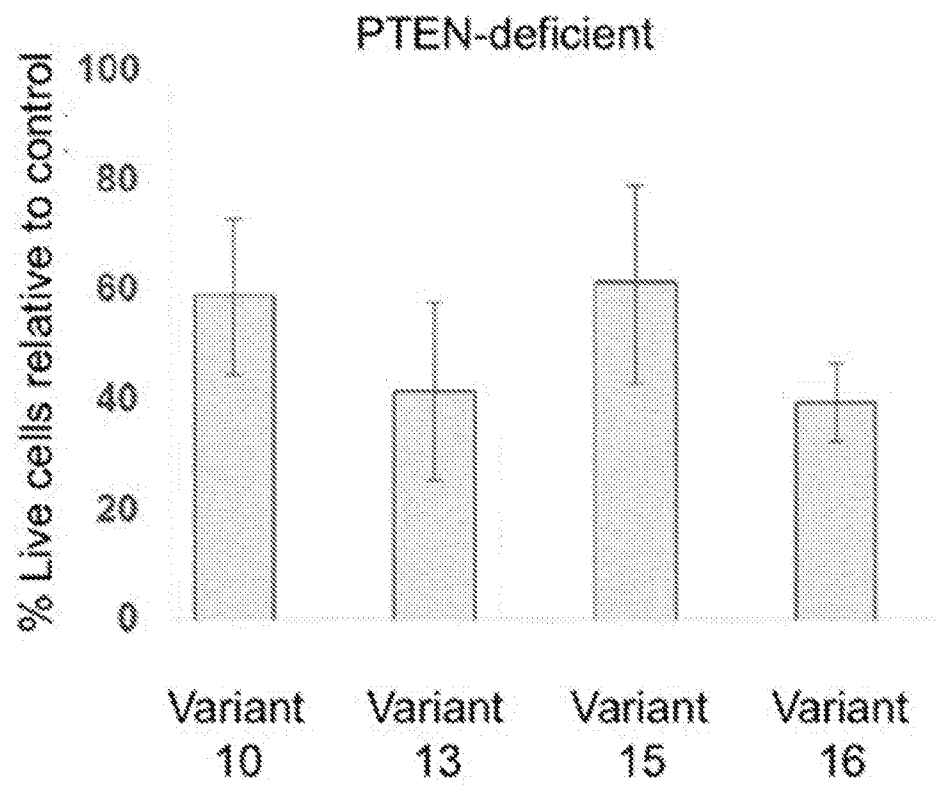


FIGURE 9

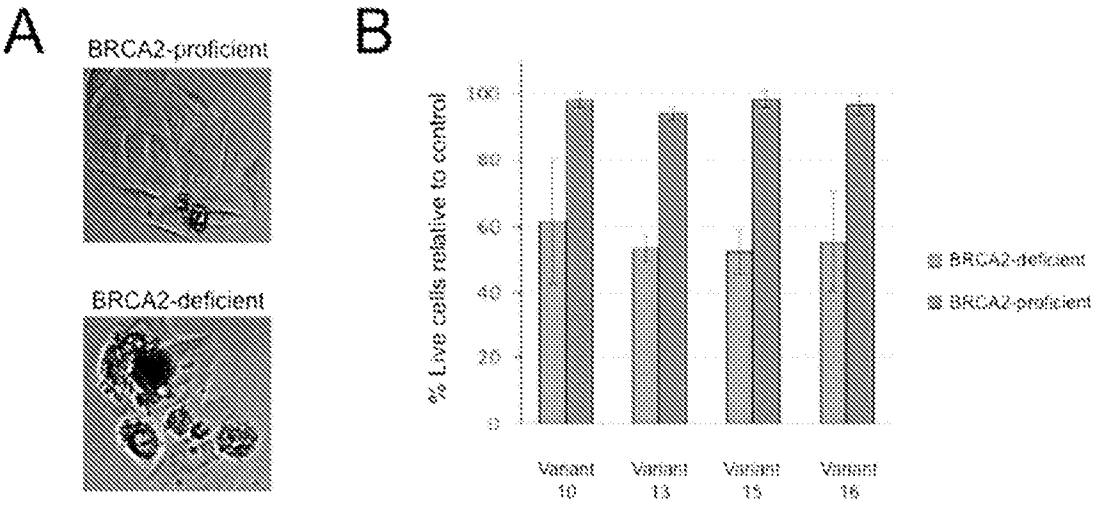


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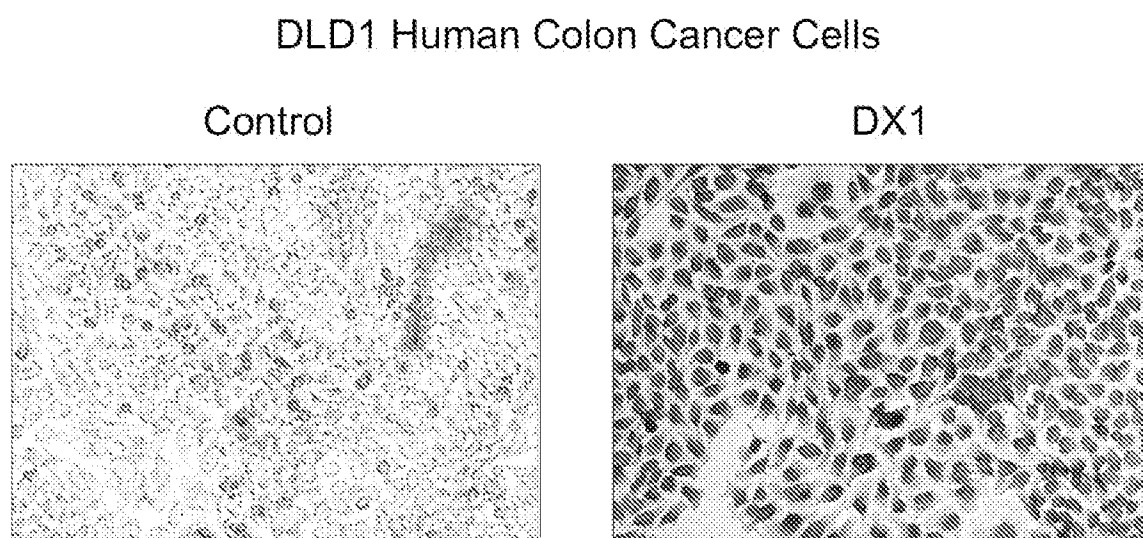
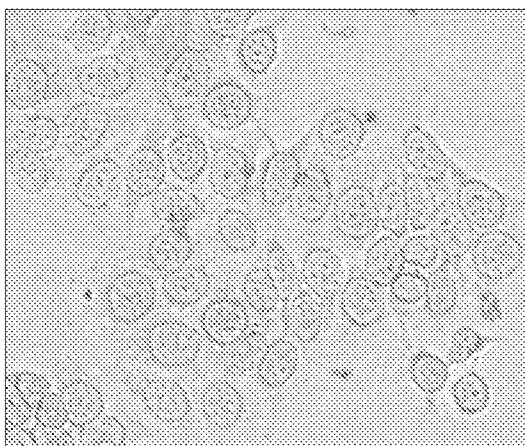


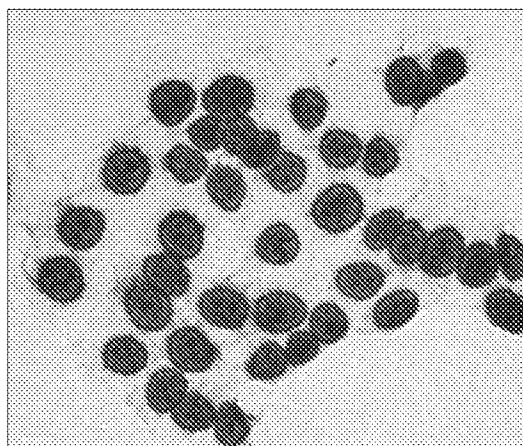
FIGURE 11

MCF-7 Human Breast Cancer Cells

Control



DX1

**FIGURE 12**

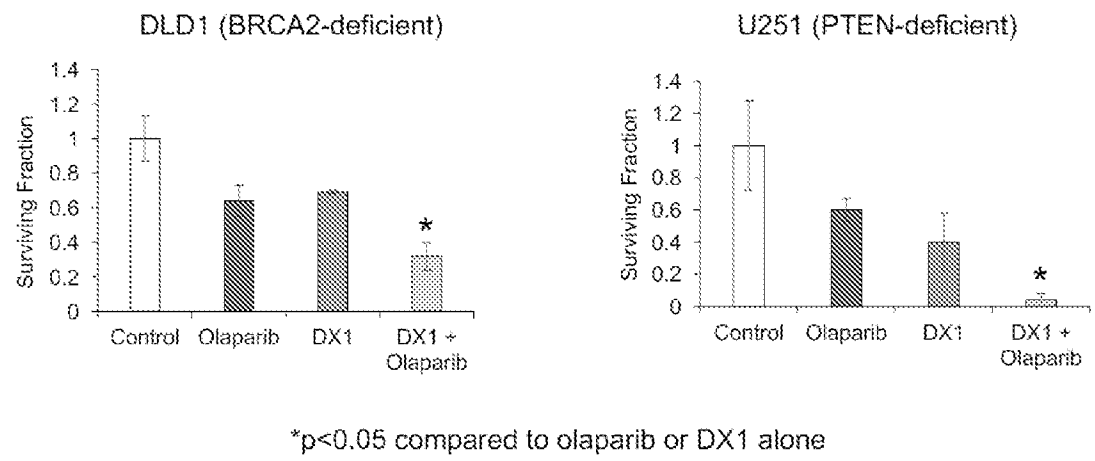


FIGURE 13

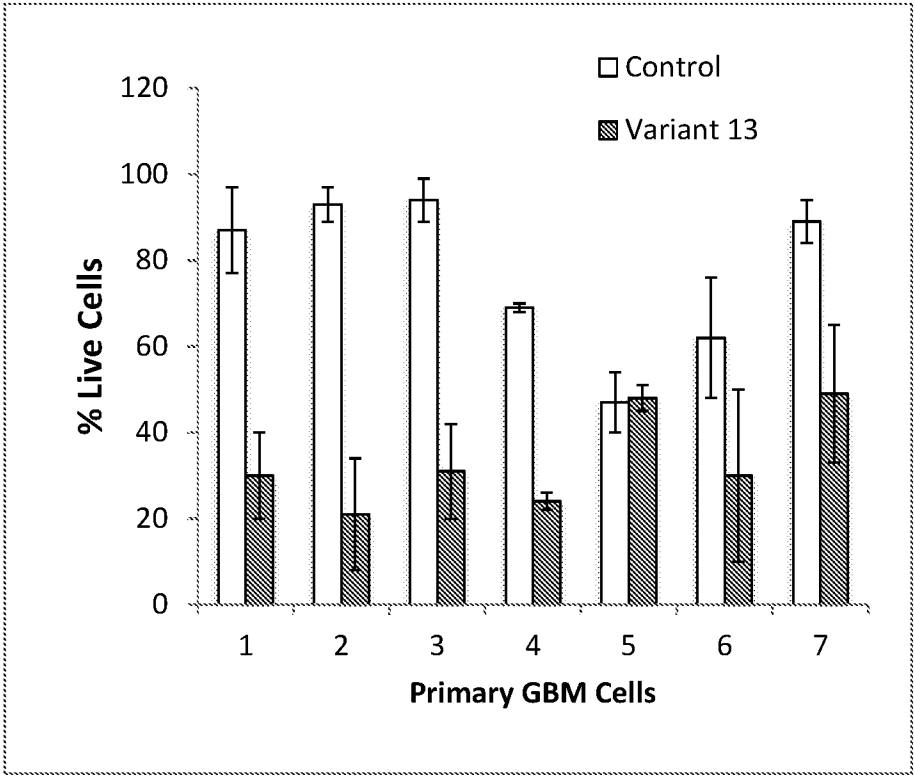


FIGURE 14

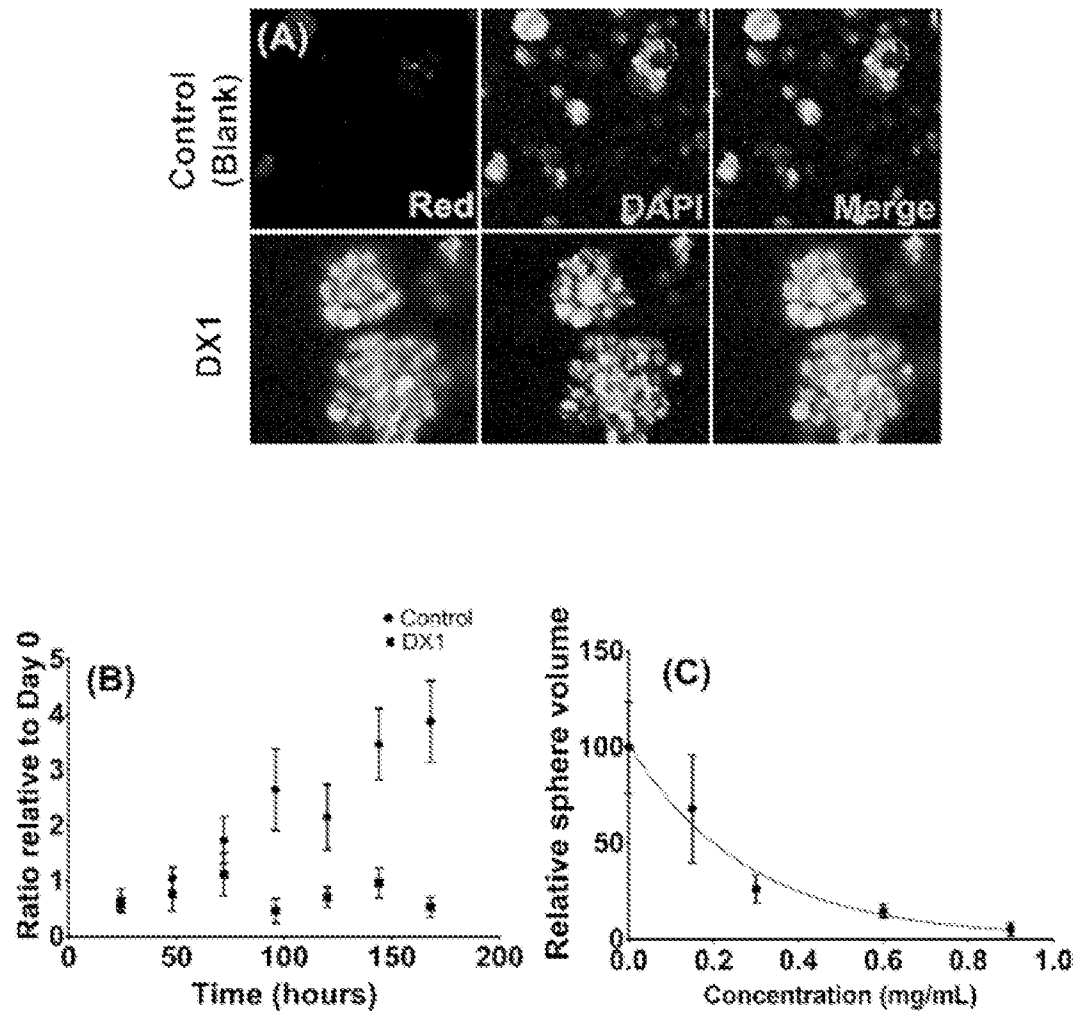


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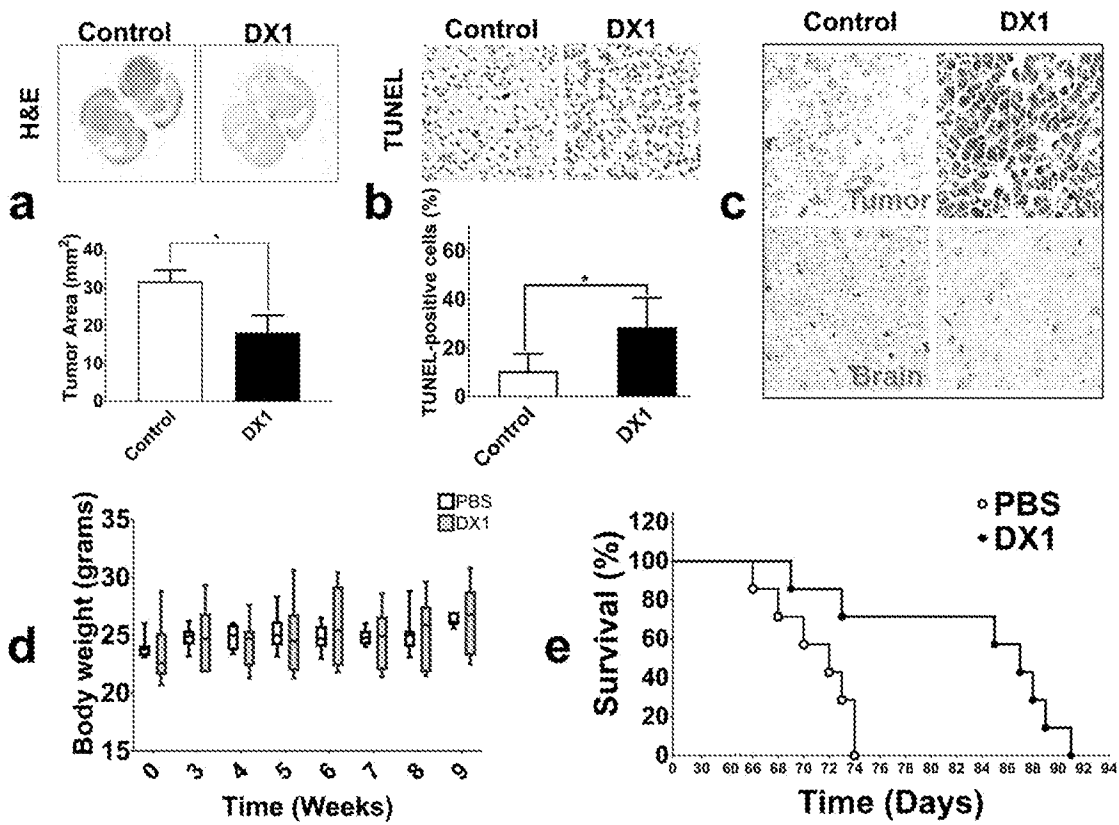


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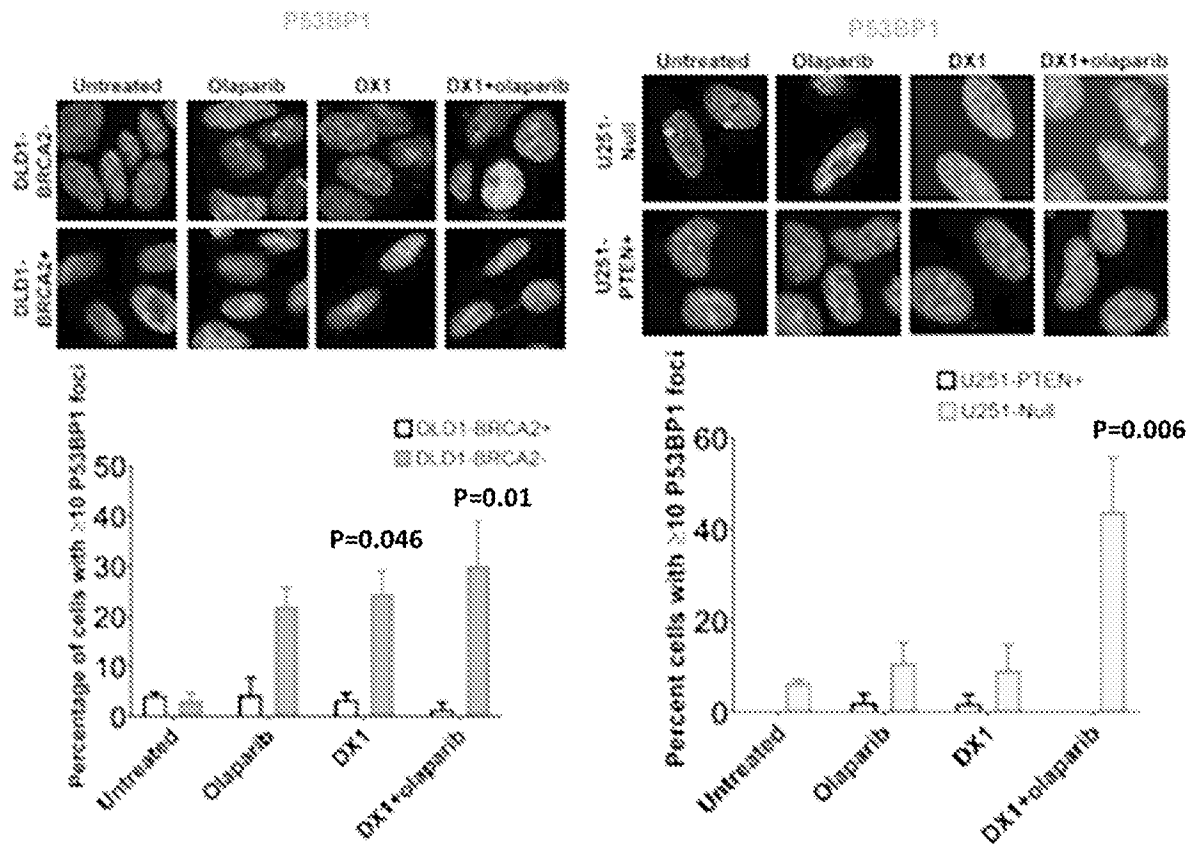


FIGURE 17

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Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 22

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain variable region (variants 14 and 17)

<400> 22

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

RICE-203W01_Sequence_listing_ST25.txt

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

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

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 23

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain variable region (variants 15 and 18)

<400> 23

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val Lys Pro Gly Gly
1 5 10 15

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

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

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

RICE-203W01_Sequence_listing_ST25.txt

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

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

Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 24
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain variable region (variants 2, 3 and 4)

<400> 24

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

RICE-203W01_Sequence_listing_ST25.txt

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 25
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain variable region (variants 6, 7 and 8)

<400> 25

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 26
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain variable region (variants 10, 11 and 12)

<400> 26

RICE-203W01_Sequence_listing_ST25.txt

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 27

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain variable region (variants 13, 14 and 15)

<400> 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

RICE-203W01_Sequence_listing_ST25.txt

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 28

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain variable region (variants 16, 17 and 18)

<400> 28

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

RICE-203W01_Sequence_listing_ST25.txt

<210> 29

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Light Chain variable region (variant 19)

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 30

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker sequence 1

<400> 30

Arg Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

RICE-203W01_Sequence_listing_ST25.txt

Gly Gly Gly Gly Ser
20

<210> 31
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker sequence 2

<400> 31

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Leu Glu Ser
1 5 10 15

Ser Gly Ser

<210> 32
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 2

<400> 32

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

RICE-203W01_Sequence_listing_ST25.txt

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
195 200 205

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

RICE-203W01_Sequence_listing_ST25.txt

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
 290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Lys
 305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 340 345 350

Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
 355 360 365

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
 370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
 420 425 430

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 435 440 445

Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
 450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 485 490 495

RICE-203W01_Sequence_listing_ST25.txt

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 33
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 3

<400> 33

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
130 135 140

RICE-203W01_Sequence_listing_ST25.txt

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

RICE-203W01_Sequence_listing_ST25.txt

Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 34
<211> 515
<212> PRT
<213> Artificial Sequence

<220>

RICE-203W01_Sequence_listing_ST25.txt

<223> Variant 4

<400> 34

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val
130 135 140

Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

RICE-203W01_Sequence_listing_ST25.txt

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

RICE-203W01_Sequence_listing_ST25.txt

Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val Lys Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 35
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 6

<400> 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

RICE-203W01_Sequence_listing_ST25.txt

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
195 200 205

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

RICE-203W01_Sequence_listing_ST25.txt

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

RICE-203W01_Sequence_listing_ST25.txt

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 36
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 7

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

RICE-203W01_Sequence_listing_ST25.txt

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

RICE-203W01_Sequence_listing_ST25.txt

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

RICE-203W01_Sequence_listing_ST25.txt

Val Ser Ser
515

<210> 37
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 8

<400> 37

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val
130 135 140

Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

RICE-203W01_Sequence_listing_ST25.txt

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

RICE-203W01_Sequence_listing_ST25.txt

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val Lys Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 38
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 10

<400> 38

RICE-203W01_Sequence_listing_ST25.txt

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
195 200 205

RICE-203W01_Sequence_listing_ST25.txt

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
405 410 415

RICE-203W01_Sequence_listing_ST25.txt

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 39
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 11

<400> 39

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

RICE-203W01_Sequence_listing_ST25.txt

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

RICE-203W01_Sequence_listing_ST25.txt

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

RICE-203W01_Sequence_listing_ST25.txt

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 40
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 12

<400> 40

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

RICE-203W01_Sequence_listing_ST25.txt

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val
130 135 140

Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

RICE-203W01_Sequence_listing_ST25.txt

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val Lys Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

RICE-203W01_Sequence_listing_ST25.txt

<210> 41

<211> 515

<212> PRT

<213> Artificial Sequence

<220>

<223> Variant 13

<400> 41

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

RICE-203W01_Sequence_listing_ST25.txt

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
195 200 205

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

RICE-203W01_Sequence_listing_ST25.txt

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 42
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 14

<400> 42

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

RICE-203W01_Sequence_listing_ST25.txt

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

RICE-203W01_Sequence_listing_ST25.txt

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

RICE-203W01_Sequence_listing_ST25.txt

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 43
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 15

<400> 43

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

RICE-203W01_Sequence_listing_ST25.txt

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val
130 135 140

Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

RICE-203W01_Sequence_listing_ST25.txt

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val Lys Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

RICE-203W01_Sequence_listing_ST25.txt

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 44
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 16

<400> 44

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

RICE-203W01_Sequence_listing_ST25.txt

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
195 200 205

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

RICE-203W01_Sequence_listing_ST25.txt

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 45
<211> 515
<212> PRT
<213> Artificial Sequence

RICE-203W01_Sequence_listing_ST25.txt

<220>

<223> Variant 17

<400> 45

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

RICE-203W01_Sequence_listing_ST25.txt

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

RICE-203W01_Sequence_listing_ST25.txt

Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 46
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 18

<400> 46

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

RICE-203W01_Sequence_listing_ST25.txt

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val
130 135 140

Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
195 200 205

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

RICE-203W01_Sequence_listing_ST25.txt

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Asp Val Lys Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu Glu Trp Val Ser
435 440 445

RICE-203W01_Sequence_listing_ST25.txt

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

Val Ser Ser
515

<210> 47
<211> 515
<212> PRT
<213> Artificial Sequence

<220>
<223> Variant 19

<400> 47

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg
85 90 95

RICE-203W01_Sequence_listing_ST25.txt

Glu Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
130 135 140

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
145 150 155 160

Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly
165 170 175

Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr
180 185 190

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys
195 200 205

Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
210 215 220

Val Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln
225 230 235 240

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
245 250 255

Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp Ile Gln Met Thr
260 265 270

Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Ala Thr Ile
275 280 285

Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser Ser Tyr Ser Tyr Met
290 295 300

RICE-203W01_Sequence_listing_ST25.txt

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile Lys
305 310 315 320

Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
325 330 335

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
340 345 350

Asp Phe Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Phe Pro Trp Thr
355 360 365

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala Pro
370 375 380

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
385 390 395 400

Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
405 410 415

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr Gly
420 425 430

Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
435 440 445

Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val Lys
450 455 460

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
465 470 475 480

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
485 490 495

Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr
500 505 510

RICE-203W01_Sequence_listing_ST25.txt

Val Ser Ser
515

<210> 48
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy Chain variable region murine 3E10 (D31N)

<400> 48

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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

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

Ala Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Thr Val
50 55 60

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

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

Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Leu
100 105 110

Thr Val Ser Ser
115

<210> 49
<211> 111
<212> PRT
<213> Artificial Sequence

RICE-203W01_Sequence_listing_ST25.txt

<220>

<223> Light Chain variable region murine 3E10 (D31N)

<400> 49

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala
50 55 60

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 50

<211> 541

<212> PRT

<213> Artificial Sequence

<220>

<223> 3E10 (D31N) murine prototype produced from P. pastoris

<400> 50

Ala Gly Ile His Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
1 5 10 15

Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser
20 25 30

RICE-203W01_Sequence_listing_ST25.txt

Val Ser Thr Ser Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro
35 40 45

Gly Gln Pro Pro Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser
50 55 60

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
65 70 75 80

Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
85 90 95

Gln His Ser Arg Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu
100 105 110

Glu Ile Lys Arg Ala Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
130 135 140

Gly Gly Leu Val Lys Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala
145 150 155 160

Ser Gly Phe Thr Phe Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala
165 170 175

Pro Glu Lys Gly Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Ser Ser
180 185 190

Thr Ile Tyr Tyr Ala Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg
195 200 205

Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser
210 215 220

Glu Asp Thr Ala Met Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp
225 230 235 240

RICE-203W01_Sequence_listing_ST25.txt

Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys
245 250 255

Gly Pro Ser Val Phe Pro Leu Ala Pro Leu Glu Ser Ser Gly Ser Asp
260 265 270

Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
275 280 285

Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Ser
290 295 300

Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys
305 310 315 320

Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ala Arg
325 330 335

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro
340 345 350

Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu
355 360 365

Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala
370 375 380

Asp Ala Ala Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
385 390 395 400

Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
405 410 415

Pro Gly Gly Ser Arg Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
420 425 430

Ser Asn Tyr Gly Met His Trp Val Arg Gln Ala Pro Glu Lys Gly Leu
435 440 445

RICE-203W01_Sequence_listing_ST25.txt

Glu Trp Val Ala Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala
450 455 460

Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
465 470 475 480

Thr Leu Phe Leu Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Met
485 490 495

Tyr Tyr Cys Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly
500 505 510

Thr Thr Leu Thr Val Ser Ser Leu Glu Gln Lys Leu Ile Ser Glu Glu
515 520 525

Asp Leu Asn Ser Ala Val Asp His His His His His His
530 535 540

<210> 51
<211> 1555
<212> DNA
<213> Artificial Sequence

<220>
<223> Variant 2

<400> 51
gacatccaga tgaccagtc tccatcctct ctgtctgctt ccctgggcga cagagccacc 60
atcacctgta gagcctcaa gtccgtgtcc acctcctct actcctacat gcactggtat 120
cagcagaagc ccggccagcc tcctaagctg ctgattaagt acgcctccta cctggaatcc 180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc 240
agcctgcagc ctgaggatgc cgctacctac tactgccagc actccagaga gttcccttgg 300
acctttggcg gaggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga 360
ggaagcggag gcggaggttc tgggtggtgg ggatctgaag tgcagctggg ggaatctggc 420
ggaggattgg ttcagcctgg cggctctctg agactgtctt gtgccgcttc tggcttcacc 480
ttctccaact acggcatgca ttgggtccga caggcccctg gcaaaggact ggaatgggtg 540
tcctacatct cctccagctc ctccaccatc tactacgccg actccgtgaa gggcagattc 600

RICE-203W01_Sequence_listing_ST25.txt

accatctcca gagacaacgc caagaactcc ctgtacctgc agatgaacag cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggcacaacag tgaccgtgtc ctctgcttcc accaaggagc cctctgtgtt ccctctggct	780
cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtccgcc	840
tctctgggag atagagctac aatcacatgc cgggccagca agtctgtgtc taccagcagc	900
tacagctata tgcatgtgta tcaacaaaaa cctgggcagc caccaaaaact gctgatcaaa	960
tacgctagct acctcgagag cggcgtgcc aagcagatttt ctggctccgg cagcggcaca	1020
gactttacac tcaccattag ctccctgcaa ccagaggagc ctgccaccta ttattgtcag	1080
cactcccgcg aatttccatg gaccttcgga ggccggcaca aagtcgagat caagcgggct	1140
gatgctgcac caggtggcgg cggtagtggg ggccggaggaa gtggcggagg cggatctgaa	1200
gtccaattgg ttgaaagcgg cggtggcctt gtgcaaccgc gtggaagtct gagactctcc	1260
tgcgctgcct ccggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
ggcaaaggct tggagtgggt ttcctatatc agctcctcta gcagcaccat ctattatgct	1380
gacagcgtga aaggccggtt taccatcagc cgggataatg ccaagaatag cctgtatctc	1440
caaatgaact ctctccgcgc tgaggatata gctgtgtact attgcgcccg cagaggactc	1500
ctgctcgatt actggggaca gggaactacc gtgacagtgt ctagctgatg aattc	1555

<210> 52
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 3

<400> 52 gacatccaga tgaccagtc tccatcctct ctgtctgctt ccctgggcga cagagccacc	60
atcacctgta gagcctcaa gtccgtgtcc acctcctct actcctacat gcactggtat	120
cagcagaagc ccggccagcc tcctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
agcctgcagc ctgaggatgc cgctacctac tactgccagc actccagaga gttcccttgg	300

RICE-203W01_Sequence_listing_ST25.txt

acctttggcg gaggcaccaa ggtggaaatc aagagagctg acgtgctcc tggcggcgga	360
ggaagcggag gcggaggttc tgggtggtggt ggatctgaag tgcagctggt ggaatcaggt	420
ggcggagttg ttcagcctgg cggctctctg agactgtctt gtgccgcttc tggcttcacc	480
ttctccaact acggcatgca ttgggtccga caggcccctg agaaaggcct ggaatgggtg	540
tcctacatct cctccagctc ctccaccatc tactacgccg actccgtgaa gggcagattc	600
accatctctc gggacaactc caagaacacc ctgtacctgc agatgaactc cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggcacaacag tgaccgtgtc ctctgcttcc accaaggagc cctctgtgtt ccctctggct	780
cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtccgcc	840
tctctgggag atagagctac aatcacatgc cgggccagca agtctgtgtc taccagcagc	900
tacagctata tgcatgtgta tcaacaaaaa cctgggcagc caccaaaact gctgatcaaa	960
tacgctagct acctcgagag cggcgtgcc aagcagatttt ctggctccgg cagcggcaca	1020
gactttacac tcaccattag ctccctgcaa ccagaggacg ctgccaccta ttattgtcag	1080
cactcccgcg aatttccatg gaccttcgga ggcggcacaa aagtcgagat caagcgggct	1140
gatgctgcac caggtggcgg cggatctggt ggcggaggct ctggcggagg cggtagtga	1200
gttcagttgg tcgagtcagg cgggtggcggt gtgcaacctg gtggtagtct gaggctgtcc	1260
tgcgctgcct ccggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
gagaagggac ttgagtgggt ttcctatatc agctccagca gctctaccat ctattatgct	1380
gacagcgtga aaggccggtt taccatcagc cgggataaca gcaagaatac tctgtatctc	1440
caaatgaata gcctgcgcgc cgaggataca gctgtgtatt attgcgccag acggggactc	1500
ctgctggatt actggggaca aggtactacc gtgacagtgt ccagctgatg aattc	1555

<210> 53
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 4

RICE-203W01_Sequence_listing_ST25.txt

<400> 53

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atcacctgta gagcctccaa gtccgtgtcc acctcctcct actcctacat gcactggtat	120
cagcagaagc ccggccagcc tcctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
agcctgcagc ctgaggatgc cgctacctac tactgccagc actccagaga gttcccttgg	300
acctttggcg gaggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga	360
ggaagcggag gcggaggttc tgggtggtggt ggatctgaag tgcagctggt ggaatctggc	420
ggtggcgacg tgaaacctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc	480
ttctccaact acggcatgca ttgggtccga caggcccctg agaaaggcct ggaatgggtg	540
tcctacatct cctccagctc ctccaccatc tactacgccg actccgtgaa gggcagattc	600
accatctctc gggacaactc caagaacacc ctgtacctgc agatgaactc cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
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cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtccgcc	840
tctctgggag atagagctac aatcacatgc cgggccagca agtctgtgtc taccagcagc	900
tacagctata tgcatttgta tcaacaaaaa cctgggcagc caccaaaaact gctgatcaaa	960
tacgctagct acctcagagc cggcgtgcca agcagatttt ctggctccgg cagcggcaca	1020
gactttacac tcaccattag ctccctgcaa ccagaggacg ctgccaccta ttattgtcag	1080
cactcccgcg aatttccatg gaccttcggt ggcggaacaa aggtcgagat caagcgggct	1140
gatgcagcac ctggcggagg cggttcaggt ggcggaggat caggcggtagg cggtagttaa	1200
gttcagttgg ttgagtccgg cggaggggat gttaagcctg gcggtagcct gagactctcc	1260
tgcgctgctt ccggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
gagaagggac ttgagtgggt ttcctatatc agctccagca gctctaccat ctattatgct	1380
gacagcgtga aaggccggtt taccatcagc cgggataaca gcaagaatac tctgtatctc	1440
caaatgaaca gcctgcgcgc cgaggataca gctgtgtatt attgcgccag acggggactc	1500
ctgctggatt actggggaca aggtactacc gtgacagtgt ccagctgatg aattc	1555

RICE-203W01_Sequence_listing_ST25.txt

<210> 54
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 6

<400> 54
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 atcacctgta gagcctccaa gtccgtgtcc acctcctcct actcctacat gcaactggtat 120
 cagcagaagc ccggccaggc tcctaagctg ctgattaagt acgcctccta cctggaatcc 180
 ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc 240
 agcctgcagc ctgaggactt cgccacctac tactgccagc actccagaga gttcccttgg 300
 acctttggcc agggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga 360
 ggatctggcg gaggtggaag cggaggcggt ggatctgaag tgcagctggt tgagagtgggt 420
 ggcggattgg ttcagcctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc 480
 ttctccaact acggcatgca ttgggtccga caggccccctg gcaaaggact ggaatgggtg 540
 tcctacatct cctccagctc ctccaccatc tactacgccg actccgtgaa gggcagattc 600
 accatctcca gagacaacgc caagaactcc ctgtacctgc agatgaacag cctgagagcc 660
 gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag 720
 ggaacaaccg tgaccgtgtc ctctgcttcc acaaagggcc cctctgtgtt ccctctggct 780
 cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtccgcc 840
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 tacagctata tgcataggta tcaacaaaaa cccgggcaag ccccaaagct cctgatcaaa 960
 tacgccagct atctggaaag cggcgtgcca tctcggtttt ctggctccgg aagcggcaca 1020
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 catagccgcg agtttccatg gacattcgga cagggaacta aggtcgagat caagcgggcc 1140
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 gttcagttgg tcgagtcagg cggcggactt gttcaaccag gtggtagcct gagactgagc 1260

RICE-203W01_Sequence_listing_ST25.txt

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ggcaaaggct tggagtgggt ttcctatata agctcctcta gctctaccat ctattatgcc	1380
gatagcgtga aaggccggtt taccatcagc cgggataatg ccaagaatag cctgtatctc	1440
caaatgaact ctctccgcgc tgaggataacc gctgtgtatt attgcgcccg cagaggactc	1500
ctgctcgatt actggggaca gggcactaca gtgacagtgt ctagctgatg aattc	1555

<210> 55
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 7

<400> 55 gacatccaga tgaccagtc tccatcctct ctgtctgctt ccctgggcga cagagccacc	60
atcacctgta gagcctccaa gtccgtgtcc acctcctcct actcctacat gcactggtat	120
cagcagaagc ccggccaggc tcctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
agcctgcagc ctgaggactt cgccacctac tactgccagc actccagaga gttcccttgg	300
acctttggcc agggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga	360
ggatctggcg gaggtggaag cggaggcggg ggatctgaag tgcagctggg tgagagtggg	420
ggcggagttg ttcagcctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc	480
ttctccaact acggcatgca ttgggtccga caggcccctg agaaaggcct ggaatgggtg	540
tcctacatct cctccagctc ctccaccatc tactacgccg actccgtgaa gggcagattc	600
accatctctc gggacaactc caagaacacc ctgtacctgc agatgaactc cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggaacaaccg tgaccgtgtc ctctgcttcc acaaagggcc cctctgtgtt ccctctggct	780
cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtccgcc	840
tctctgggag atagagctac aatcacatgc cgggccagca agtctgtgtc taccagcagc	900
tacagctata tgcattggta tcaacaaaaa cccgggcaag ccccaaagct cctgatcaaa	960

RICE-203W01_Sequence_listing_ST25.txt

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catagccgcg agttttccatg gacattcgga cagggaacta aggtcgagat caagcgggcc	1140
gatgctgcac ctggcggagg cggttcaggt ggtggtggat cagggtggcgg aggcagtga	1200
gtccagttgg tggaatcagg cgggtggcgtt gtgcaacctg gtggaagtct gaggctgtcc	1260
tgcgctgctt ccggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
gagaaggac ttgagtgggt ttcctatatc agctccagca gctctaccat ctattatgct	1380
gacagcgtga aaggccggtt taccatcagc cgggataaca gcaagaatac tctgtatctc	1440
caaatgaata gcctgcgcgc cgaggataca gctgtgtatt attgcgccag acggggactc	1500
ctgctggatt actggggaca aggcactaca gtgacagtgt ccagctgatg aattc	1555

<210> 56
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 8

<400> 56	
gacatccaga tgaccagtc tccatcctct ctgtctgctt ccctgggcga cagagccacc	60
atcacctgta gagcctcaa gtccgtgtcc acctcctct actcctacat gcactggtat	120
cagcagaagc ccggccaggc tcctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
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acctttggcc agggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga	360
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<210> 57
 <211> 1555
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 <213> Artificial Sequence

<220>
 <223> Variant 10

<400> 57	
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RICE-203W01_Sequence_listing_ST25.txt

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<210> 58
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 11

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RICE-203W01_Sequence_listing_ST25.txt

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RICE-203W01_Sequence_listing_ST25.txt

<210> 59

<211> 1555

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant 12

<400> 59

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RICE-203W01_Sequence_listing_ST25.txt

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<210> 60
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 13

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tacagctata tgcatggta tcaacaaaaa cctgggcagc caccaaaact gctgatcaaa	960
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RICE-203W01_Sequence_listing_ST25.txt

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<210> 61
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 14

<400> 61	
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RICE-203W01_Sequence_listing_ST25.txt

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<210> 62
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 15

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RICE-203W01_Sequence_listing_ST25.txt

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<210> 63

<211> 1555

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant 16

<400> 63

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RICE-203W01_Sequence_listing_ST25.txt

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<210> 64
<211> 1555

RICE-203W01_Sequence_listing_ST25.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Variant 17

<400> 64

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acctttggcc agggcaccaa ggtggaaatc aagagagctg acgtgctcc tggcggcgga	360
ggatctggcg gaggtggaag cggaggcggt ggatctgaag tgcagctggg tgagagtggg	420
ggcggagttg ttcagcctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc	480
ttctccaact acggcatgca ttgggtccga caggcccctg agaaaggcct ggaatgggtg	540
tcctacatct cctccggctc ctccaccatc tactacgccg actctgtgaa gggcagattc	600
accatcagcc gggacaactc caagaacacc ctgtacctgc agatgaactc cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggaacaaccg tgaccgtgtc tagcgcttcc acaaagggcc cctctgtgtt ccctctggct	780
cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtctgct	840
tccgtgggag atcgcgtgac aatcacatgc agagccagca agacagtgtc taccagcagc	900
tacagctata tgcattggta tcaacaaaaa cccgggaaag ctccaagct cctgatcaaa	960
tacgccagct atctggaaag cggcgtgcca tctcggtttt ccggaagcgg ctctggaaca	1020
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catagccgcg agtttccatg gacattcgga cagggaacta aggtcgagat caagcgggcc	1140
gatgctgcac ctggcggagg cggttcaggt ggtggtggat caggtggcgg aggcagtgaa	1200
gtccagttgg tggaatcagg cgggtggcgtt gtgcaacctg gtggaagtct gaggctgtcc	1260
tgcgctgctt ccggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
gagaagggac ttgagtgggt ttcctatatc agctccggca gcagcaccat ctattatgct	1380

RICE-203W01_Sequence_listing_ST25.txt

gacagcgtga aaggccggtt caccatctcc agagacaaca gcaagaatac tctgtatctc	1440
caaatgaata gcctgcgcgc cgaggataca gctgtgtatt attgcgccag acgggggactc	1500
ctgctggatt actggggaca aggcactaca gtgacagtgt cctcctgatg aattc	1555

<210> 65
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 18

<400> 65	
gacatccaga tgaccagtc tccatcctct ctgtccgcct ctgtgggcga cagagtgacc	60
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cagcagaagc ccggcaaggc ccctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
agcctgcagc ctgaggactt cgccacctac tactgccagc actccagaga gttcccttgg	300
acctttggcc agggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga	360
ggatctggcg gaggtggaag cggaggcggt ggatctgaag tgcagctggg tgagagtggc	420
ggaggcgacg tgaaacctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc	480
ttctccaact acggcatgca ttgggtccga caggcccctg agaaaggcct ggaatgggtg	540
tcctacatct cctccggctc ctccaccatc tactacgccg actctgtgaa gggcagattc	600
accatcagcc gggacaactc caagaacacc ctgtacctgc agatgaactc cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggaacaaccg tgaccgtgtc tagcgcttcc acaaagggcc cctctgtgtt ccctctggct	780
cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtctgct	840
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tacagctata tgcatgtgta tcaacaaaaa cccgggaaag ctcccaagct cctgatcaaa	960
tacgccagct atctggaaag cggcgtgcc a tctcggtttt ccggaagcgg ctctggaaca	1020
gactttacac tcaccattag ctccctccag ccagaggatt ttgctaccta ttattgccag	1080

RICE-203W01_Sequence_listing_ST25.txt

catagccgcg agtttccatg gacattcggg caggggaacta aggtcgagat caagcggggcc	1140
gatgctgcac caggcgggtg tggttcaggc ggaggcggta gcggcggagg cggctctgaa	1200
gttcaattgg tggaatcagg tggcggggat gtcaagcctg gtggaagtct gagactcagc	1260
tgtgccgcca gcggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
gagaagggac ttgagtgggt ttcctatatc agctccggca gcagcaccat ctattatgct	1380
gacagcgtga aaggccggtt caccatctcc agagacaaca gcaagaatac tctgtatctc	1440
caaatgaaca gcctgcgcgc cgaggataca gctgtgtatt attgcgccag acggggactc	1500
ctgctggatt actggggaca aggcactaca gtgacagtgt cctcctgatg aattc	1555

<210> 66
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 19

<400> 66 gacatccaga tgaccagtc tccatcctct ctgtctgctt ccctgggcga cagagccacc	60
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cagcagaagc ccggccaggc tcctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
agcctgcagc ctgaggactt cgccacctac tactgccagc actccagaga gttcccttgg	300
acctttggcc agggcaccaa ggtggaaatc aagagagctg acgctgctcc tggcggcgga	360
ggatctggcg gaggtggaag cggaggcggg ggatctgaag tgcagctggt tgagagtggg	420
ggcggattgg ttcagcctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc	480
ttctccaact acggcatgca ttgggtccga caggccccctg gcaaaggact ggaatgggtg	540
tcctacatct cctccggctc ctccaccatc tactacgccg actctgtgaa gggcagattc	600
accatctctc gggacaacgc caagaactcc ctgtacctgc agatgaacag cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggaacaaccg tgaccgtgtc tagcgcttcc acaaagggcc cctctgtgtt ccctctggct	780

RICE-203W01_Sequence_listing_ST25.txt

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tacagctata tgcattggta tcaacaaaaa cccgggcaag ccccaaagct cctgatcaaa	960
tacgccagct atctggaaag cggcgtgcc a tctcggtttt ccggaagcgg ctctggaaca	1020
gactttacac tcaccattag ctccctccag ccagaggatt ttgctaccta ttattgccag	1080
catagccgcg agtttccatg gacattcgg a cagggaacta aggtcgagat caagcgggcc	1140
gatgctgcac ctggcggagg cggttcaggt ggcggaggca gcggtggcgg cggtagtga	1200
gttcagttgg tcgagtcagg cggcggactt gttcaaccag gtggtagcct gagactgagc	1260
tgtgctgctt ccggctttac cttcagcaat tacggaatgc actgggttcg ccaagctcca	1320
ggcaaaggct tggagtgggt ttcatatatc tccagcggca gcagcaccat ctattatgct	1380
gacagcgtga aaggccggtt caccatcagc agagataatg ccaagaacag cctctacctc	1440
caaatgaact cactgcgcgc tgaggatacc gctgtgtatt attgcgcccg cagaggactc	1500
ctgctcgatt actggggaca gggcactaca gtgacagtgt cctcctgatg aattc	1555

<210> 67
 <211> 1555
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Variant 19

<400> 67	
gacatccaga tgaccagtc tccatcctct ctgtctgctt ccctgggcga cagagccacc	60
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cagcagaagc ccggccaggc tcctaagctg ctgattaagt acgcctccta cctggaatcc	180
ggcgtgccct ctagattctc cggctctggc tctggcaccg actttaccct gacaatctcc	240
agcctgcagc ctgaggactt cgccacctac tactgccagc actccagaga gttcccttgg	300
acctttggcc agggcaccaa ggtggaaatc aagagagctg acgtgctcc tggcggcgga	360
ggatctggcg gaggtggaag cggaggcggt ggatctgaag tgcagctggt tgagagtgg	420
ggcggattgg ttcagcctgg cggatctctg agactgtctt gtgccgcctc tggcttcacc	480

RICE-203W01_Sequence_listing_ST25.txt

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accatctctc gggacaacgc caagaactcc ctgtacctgc agatgaacag cctgagagcc	660
gaggacaccg ccgtgtacta ctgtgctaga agaggcctgc tgctggacta ttggggccag	720
ggaacaaccg tgaccgtgtc tagcgcttcc acaaagggcc cctctgtgtt ccctctggct	780
cctctggaat cttccggctc cgatattcag atgacacaga gcccttccag cctgtccgcc	840
tctctgggag atagagctac aatcacatgc cgggccagca agacagtgtc taccagcagc	900
tacagctata tgcattggta tcaacaaaaa cccgggcaag ccccaaagct cctgatcaaa	960
tacgccagct atctggaaag cggcgtgcc a tctcggtttt ccggaagcgg ctctggaaca	1020
gactttacac tcaccattag ctccctccag ccagaggatt ttgctaccta ttattgccag	1080
catagccgcg agtttccatg gacattcgg a cagggaacta aggtcgagat caagcgggcc	1140
gatgctgcac ctggcggagg cggttcaggt ggcggaggca gcggtggcgg cggtagtga a	1200
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gacagcgtga aaggccggtt caccatcagc agagataatg ccaagaacag cctctacctc	1440
caaatgaact cactgcgcgc tgaggatacc gctgtgtatt attgcgccc g cagaggactc	1500
ctgctcgatt actggggaca gggcactaca gtgacagtgt cctcctgatg aattc	1555

<210> 68

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Full length heavy chain

<400> 68

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

RICE-203W01_Sequence_listing_ST25.txt

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

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

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

RICE-203W01_Sequence_listing_ST25.txt

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

RICE-203W01_Sequence_listing_ST25.txt

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 69
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 constant heavy region 1

<400> 69

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> 70
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 hinge region

<400> 70

RICE-203W01_Sequence_listing_ST25.txt

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
1 5 10

<210> 71
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1 L2345A/L235A constant heavy region 2

<400> 71

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys

<210> 72
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> IgG1 constant heavy region 3

<400> 72

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
1 5 10 15

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 73

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1 N297D heavy chain full length sequence

<400> 73

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

RICE-203W01_Sequence_listing_ST25.txt

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

RICE-203W01_Sequence_listing_ST25.txt

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asp Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 74
<211> 113

RICE-203W01_Sequence_listing_ST25.txt

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1 N297D constant heavy region 2

<400> 74

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Tyr Asp Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys

<210> 75

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1 L2345A/L235A/N297D heavy chain full length sequence

<400> 75

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

RICE-203W01_Sequence_listing_ST25.txt

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

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

Ser Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Arg Gly Leu Leu Leu Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

RICE-203W01_Sequence_listing_ST25.txt

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Tyr Asp Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

RICE-203W01_Sequence_listing_ST25.txt

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440 445

<210> 76
 <211> 113
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1 L2345A/L235A/N297D constant heavy region 2

<400> 76

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
 1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 50 55 60

Arg Glu Glu Gln Tyr Asp Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 100 105 110

Lys

<210> 77
 <211> 113
 <212> PRT
 <213> Artificial Sequence

RICE-203W01_Sequence_listing_ST25.txt

<220>

<223> Unmodified constant heavy region 2

<400> 77

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys

<210> 78

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain full length sequence

<400> 78

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

RICE-203W01_Sequence_listing_ST25.txt

Asp Arg Ala Thr Ile Thr Cys Arg Ala Ser Lys Thr Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser
50 55 60

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

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

Glu Phe Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215