

elution buffer solution from a buffer source to the polypeptide binding column, via the first holding coil, and through a second holding coil downstream of the polypeptide binding column, thereby eluting polypeptides bound to the polypeptide binding column and moving an elution/polypeptide mixture comprising the elution buffer solution and the eluted polypeptides to the second holding coil; (d) moving the elution/polypeptide mixture from the second holding coil to a reaction chamber; (e) incubating the polypeptides in the elution/polypeptide mixture in the reaction chamber, resulting in denatured polypeptides; (f) moving a reducing reagent that cleaves disulfide bond crosslinks to the reaction chamber via the first holding coil after (e); (g) incubating the denatured polypeptides with the reducing reagent in the reaction chamber, resulting in denatured and reduced polypeptides; (h) moving an alkylating reagent that alkylates sulfhydryls to the reaction chamber after (g); (i) incubating the denatured and reduced polypeptides with the alkylating reagent in the reaction chamber, thereby alkylating the denatured and reduced polypeptides; (j) moving the denatured, reduced, and alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to a desalting column via the first holding coil, the desalting column equilibrated with a proteolysis buffer; (k) applying the denatured, reduced, and alkylated polypeptides to the desalting column, thereby separating the denatured, reduced, and alkylated polypeptides from the reducing and alkylating reagents, and resulting in desalted polypeptides; (l) moving the desalted polypeptides to a proteolytic enzyme column downstream of the desalting column; (m) digesting the desalted polypeptides in the third polypeptide column, resulting in digested polypeptides; and (n) moving the digested polypeptides to an analytical device for analysis of the digested polypeptides. One aspect of the present disclosure provides a method for performing a real-time assay. The method includes the steps of: (a) moving a sample of a product containing polypeptides to a polypeptide-binding column via a first holding coil; (b) binding the polypeptides in the sample to the polypeptide binding column, thereby separating the polypeptides in the sample from a remainder of the sample; (c) moving an elution buffer solution from a buffer source to the polypeptide binding column, via the first holding coil, and through a second holding coil downstream of the polypeptide

binding column, thereby eluting polypeptides bound to the polypeptide binding column and moving an elution/polypeptide mixture comprising the elution buffer solution and the eluted polypeptides to the second holding coil; (d) moving the elution/polypeptide mixture from the second holding coil to a reaction chamber; (e) incubating the polypeptides in the elution/polypeptide mixture in the reaction chamber, resulting in denatured polypeptides; (f) moving a reducing reagent that cleaves disulfide bond crosslinks to the reaction chamber via the first holding coil after (e); (g) incubating the denatured polypeptides with the reducing reagent in the reaction chamber, resulting in denatured and reduced polypeptides; (h) moving an alkylating reagent that alkylates sulfhydryls to the reaction chamber after (g); (i) incubating the denatured and reduced polypeptides with the alkylating reagent in the reaction chamber, thereby alkylating the denatured and reduced polypeptides; (j) moving the denatured, reduced, and alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to a desalting column via the first holding coil, the desalting column equilibrated with a proteolysis buffer; (k) applying the denatured, reduced, and alkylated polypeptides to the desalting column, thereby separating the denatured, reduced, and alkylated polypeptides from the reducing and alkylating reagents, and resulting in desalted polypeptides; (l) moving the desalted polypeptides to a proteolytic enzyme column downstream of the desalting column; (m) digesting the desalted polypeptides in the proteolytic enzyme column, resulting in digested polypeptides; and (n) moving the digested polypeptides to an analytical device for analysis of the digested polypeptides.

[0008] Another aspect of the present disclosure provides a method for performing a real-time assay using a closed system including a multi-port valve, a first holding coil upstream of the multi-port valve, a polypeptide binding column fluidly coupled to and downstream of a first port of the multi-port valve, a second holding coil fluidly coupled to and downstream of the polypeptide binding column, a reaction chamber fluidly coupled to and downstream of second and third ports of the multi-port valve, a desalting column fluidly coupled to and downstream of a fourth port of the multi-port valve, and a proteolytic enzyme column downstream of the desalting column. The method includes:

(a) moving, via a controller communicatively coupled to the closed system, a sample of a product containing polypeptides to the first holding coil; (b) positioning, via the controller, the multi-port valve in a first position in which the first holding coil is connected to the polypeptide binding column via the first port of the multi-port valve, such that the sample flows to the first column, whereby polypeptides in the sample bind to the polypeptide binding column; (c) when the multi-port valve is in the first position, moving, via the controller, an elution buffer solution from a source of elution buffer solution to the second holding coil via the polypeptide binding column, such that the elution buffer solution elutes substantially all of the polypeptides bound to the polypeptide binding column; (d) moving, via the controller, the multi-port valve to a second position in which the second holding coil is connected to the reaction chamber via the second port of the multi-port valve; (e) when the multi-port valve is in the second position, moving, via the controller, an elution/polypeptide mixture comprising the elution buffer solution and the eluted polypeptides to the reaction chamber, whereby the polypeptides in the elution/polypeptide mixture are denatured; (f) moving, via the controller, the multi-port valve to a third position in which the first holding coil is connected to the reaction chamber via the third port of the multi-port valve; (g) after (f), moving, via the controller, a reducing reagent that cleaves disulfide bond crosslinks to the first holding coil, and moving, via the controller, the reducing reagent from the first holding coil to the reaction chamber via the third port of the multi-port valve, thereby reducing the denatured polypeptides; (h) after (g), moving, via the controller, an alkylating reagent that alkylates sulfhydryl groups to the first holding coil, and moving, via the controller, the alkylating reagent from the first holding coil to the reaction chamber via the third port, thereby alkylating the denatured and reduced polypeptides; (i) moving, via the controller, the alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to the first holding coil via the third port; (j) moving, via the controller, the multi-port valve to a fourth position in which the first holding coil is connected to the desalting column via the

CLAIMS

What is claimed is:

1. A method for performing a real-time assay, the method comprising the steps of:
 - (a) moving a sample of a product containing polypeptides to a polypeptide-binding column via a first holding coil;
 - (b) binding the polypeptides in the sample to the polypeptide binding column, thereby separating the polypeptides in the sample from a remainder of the sample;
 - (c) moving an elution buffer solution from a buffer source to the polypeptide binding column, via the first holding coil, and through a second holding coil downstream of the polypeptide binding column, thereby eluting polypeptides bound to the polypeptide binding column and moving an elution/polypeptide mixture comprising the elution buffer solution and the eluted polypeptides to the second holding coil;
 - (d) moving the elution/polypeptide mixture from the second holding coil to a reaction chamber;
 - (e) incubating the polypeptides in the elution/polypeptide mixture in the reaction chamber, resulting in denatured polypeptides;
 - (f) moving a reducing reagent that cleaves disulfide bond crosslinks to the reaction chamber via the first holding coil after (e);
 - (g) incubating the denatured polypeptides with the reducing reagent in the reaction chamber, resulting in denatured and reduced polypeptides;
 - (h) moving an alkylating reagent that alkylates sulfhydryls to the reaction chamber after (g);
 - (i) incubating the denatured and reduced polypeptides with the alkylating reagent in the reaction chamber, thereby alkylating the denatured and reduced polypeptides;
 - (j) moving the denatured, reduced, and alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to a desalting column via the first holding coil, the desalting column equilibrated with a proteolysis buffer;

(k) applying the denatured, reduced, and alkylated polypeptides to the desalting column, thereby separating the denatured, reduced, and alkylated polypeptides from the reducing and alkylating reagents, and resulting in desalted polypeptides;

(l) moving the desalted polypeptides to a proteolytic enzyme column downstream of the desalting column;

(m) digesting the desalted polypeptides in the proteolytic enzyme column, resulting in digested polypeptides; and

(n) moving the digested polypeptides to an analytical device for analysis of the digested polypeptides.

2. The method of claim 1, wherein one or more of (a), (c), (d), (f), (h), (i), (l), and (n) are performed automatically; and/or wherein (a) through (n) are performed in a closed system.

3. The method of claim 1 or 2, wherein (a) comprises positioning a multi-port valve in a first position in which the first holding coil and the polypeptide binding column are fluidly coupled via a first port of the multi-port valve, optionally wherein (d) comprises positioning the multi-port valve in a second position in which the second holding coil and the reaction chamber are fluidly coupled via a second port of the multi-port valve.

4. The method of claim 2 or 3, wherein (f) and (h) each comprises positioning the multi-port valve in a third position in which the first holding coil and the reaction chamber are fluidly coupled via a third port of the multi-port valve, optionally wherein (j) comprises:

moving the denatured, reduced, and alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to the desalting column via the third port of the multi-port valve; and

positioning the multi-port valve in a fourth position in which the first holding coil and the desalting column are fluidly coupled via a fourth port of the multi-port valve.

5. The method of any one of claims 1 to 4, further comprising:
prior to or during (d), moving a first valve fluidly coupled to and located downstream of the reaction chamber to a first position in which the first valve directs contents received from the first holding coil in excess of a volume of the reaction chamber to a waste chamber, optionally, wherein the method further comprises after (i), moving the first valve from the first position to a second position in which the first valve directs air into the reaction chamber; and/or
after (k) and before (l), (o) moving a second valve fluidly coupled to and located between the desalting and proteolytic enzyme columns from a first position, in which the second valve directs contents received from the desalting column to a waste chamber, to a second position, in which the second valve directs contents received from the desalting column to the proteolytic enzyme column, and/or
wherein (a) comprises moving the sample of the product from a vessel containing the polypeptides to the polypeptide-binding column via the first holding coil, and/or
prior to (d), at least partially filling the reaction chamber with a denaturing reagent, and wherein (e) comprises incubating the polypeptides in the elution/polypeptide mixture with the denaturing reagent in the reaction chamber, optionally wherein at least partially filling the reaction chamber with the denaturing reagent comprises moving the denaturing reagent from a denaturing buffer source to the reaction chamber via the first holding coil or wherein (j) further comprises moving the denaturing reagent from the reaction chamber to the desalting column via the first holding coil, and wherein (k) further separates the denatured, reduced, and alkylated polypeptides from the denaturing reagent; and/or
applying heat to the reaction chamber.

6. A method for performing a real-time assay using a closed system comprising a multi-port valve, a first holding coil upstream of the multi-port valve, a polypeptide binding column fluidly coupled to and downstream of a first port of the multi-port valve, a second holding coil fluidly coupled to and downstream of the polypeptide binding column, a reaction chamber fluidly coupled to and downstream of second and third ports of the multi-port valve, a desalting column fluidly coupled to and

downstream of a fourth port of the multi-port valve, and a proteolytic enzyme column downstream of the desalting column, the method comprising:

(a) moving, via a controller communicatively coupled to the closed system, a sample of a product containing polypeptides to the first holding coil;

(b) positioning, via the controller, the multi-port valve in a first position in which the first holding coil is connected to the polypeptide binding column via the first port of the multi-port valve, such that the sample flows to the first column, whereby polypeptides in the sample bind to the polypeptide binding column;

(c) when the multi-port valve is in the first position, moving, via the controller, an elution buffer solution from a source of elution buffer solution to the second holding coil via the polypeptide binding column, such that the elution buffer solution elutes substantially all of the polypeptides bound to the polypeptide binding column;

(d) moving, via the controller, the multi-port valve to a second position in which the second holding coil is connected to the reaction chamber via the second port of the multi-port valve;

(e) when the multi-port valve is in the second position, moving, via the controller, an elution/polypeptide mixture comprising the elution buffer solution and the eluted polypeptides to the reaction chamber, whereby the polypeptides in the elution/polypeptide mixture are denatured;

(f) moving, via the controller, the multi-port valve to a third position in which the first holding coil is connected to the reaction chamber via the third port of the multi-port valve;

(g) after (f), moving, via the controller, a reducing reagent that cleaves disulfide bond crosslinks to the first holding coil, and moving, via the controller, the reducing reagent from the first holding coil to the reaction chamber via the third port of the multi-port valve, thereby reducing the denatured polypeptides;

(h) after (g), moving, via the controller, an alkylating reagent that alkylates sulfhydryl groups to the first holding coil, and moving, via the controller, the alkylating reagent from the first holding coil to the reaction chamber via the third port, thereby alkylating the denatured and reduced polypeptides;

(i) moving, via the controller, the alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to the first holding coil via the third port;

(j) moving, via the controller, the multi-port valve to a fourth position in which the first holding coil is connected to the desalting column via the fourth port of the multi-port valve, and, when the multi-port valve is in the fourth position, moving the alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the first holding coil to the desalting column, whereby the denatured, reduced, and alkylated polypeptides are applied to the desalting column, thus separating the denatured, reduced, and alkylated polypeptides from the reducing and alkylating reagents, resulting in desalted polypeptides;

(k) moving, via the controller, the desalted polypeptides to the proteolytic enzyme column, whereby the desalted polypeptides are digested; and

(l) passing, via the controller, the digested polypeptides to an analytical device, whereby the digested polypeptides are analyzed.

7. The method of claim 6, wherein (a) comprises moving, via the controller, the sample from a vessel containing the polypeptides to the first holding coil and/or wherein (k) comprises passing the digested polypeptides to an analytical device selected from the group consisting of a liquid chromatography device, a high-performance liquid chromatography device, an ultra high-performance liquid chromatography device, a mass spectrometry device, and a glycan analysis device, or a combination thereof.

8. The method of any one of claim 6 or 7, further comprising, prior to (e), moving, via the controller, the multi-port valve to the third position, and moving, via the controller, a denaturing reagent to the reaction chamber.

9. The method of claim 8, wherein moving the denaturing reagent to the reaction chamber comprises: moving, via the controller, the denaturing reagent from a denaturing buffer source to the first holding coil via a pump, and moving, via the

controller, the denaturing reagent from the first holding coil to the reaction chamber via the third port of the multi-port valve.

10. The method of claim 8 or 9, wherein (i) further comprises moving the denaturing reagent from the reaction chamber to the first holding coil via the third port, and wherein (j) further comprises moving the denaturing reagent from the first holding coil to the desalting column, and whereby when the denatured, reduced, and alkylated polypeptides are applied to the desalting column, the denatured, reduced, and alkylated polypeptides are further separated from the denaturing reagent.

11. A closed system for performing an online, real-time assay, the system comprising:

- a first holding coil fluidly arranged to receive a sample of a product containing polypeptides;

- a multi-port valve fluidly coupled to and located downstream of the first holding coil;

- a polypeptide binding column fluidly coupled to the multi-port valve and arranged to receive the sample from the first holding coil via a first port of the multi-port valve, the polypeptide binding column configured to bind the polypeptides from the sample,

- a buffer source fluidly coupled to the multi-port valve and arranged to supply elution buffer solution to a second holding coil located downstream of the polypeptide binding column, such that the elution buffer solution is adapted to elute substantially all of the polypeptides from the polypeptide binding column;

- a reaction chamber fluidly coupled to the multi-port valve and arranged downstream of the polypeptide binding column, the reaction chamber adapted to receive a mixture from the polypeptide binding column via a second port of the multi-port valve, the mixture comprising the elution buffer solution and the eluted polypeptides, wherein the polypeptides of the mixture are denatured in the reaction chamber, wherein the reaction chamber is arranged to receive a reducing reagent that cleaves disulfide bond crosslinks via the first holding coil and a third port of the multi-port valve, the reducing reagent reduces the denatured polypeptides, and wherein the reaction chamber is further

arranged to receive an alkylating reagent that alkylates sulfhydryls via the first holding coil and the third port of the multi-port valve, wherein the alkylating reagent alkylates the denatured and reduced polypeptides in the reaction chamber;

a desalting column fluidly coupled to the multi-port valve and arranged to receive the denatured, reduced, and alkylated polypeptides, the elution buffer solution, and the alkylating reagent from the reaction chamber, the desalting column configured to separate the denatured, reduced, and alkylated polypeptides from the elution buffer solution, the reducing reagent, and the alkylating reagent; and

a proteolytic enzyme column fluidly coupled to and arranged downstream of the second polypeptide column to obtain the separated polypeptides from the desalting column, the proteolytic enzyme column configured to digest the desalted polypeptides.

12. A closed system for performing a real-time assay, the system comprising:
- a multi-port valve;
 - a first holding coil upstream of the multi-port valve;
 - a polypeptide binding column fluidly coupled to and downstream of a first port of the multi-port valve;
 - a second holding coil fluidly coupled to and downstream of the polypeptide binding column;
 - a reaction chamber fluidly coupled to and downstream of second and third ports of the multi-port valve;
 - a desalting column fluidly coupled to and downstream of a fourth port of the multi-port valve;
 - a proteolytic enzyme column downstream of the desalting column; and
 - a controller communicatively coupled to the multi-port valve and comprising a memory, a processor, and logic stored on the memory and executable by the processor to:
 - (a) move a sample of a product containing polypeptides to the first holding coil;
 - (b) position the multi-port valve in a first position in which the first holding coil is connected to the polypeptide binding column via the first port of the multi-

port valve, such that the sample flows to the first column, whereby polypeptides in the sample bind to the polypeptide binding column;

(c) when the multi-port valve is in the first position, move an elution buffer solution from a source of elution buffer solution to the second holding coil via the polypeptide binding column, such that the elution buffer solution elutes substantially all of the polypeptides bound to the polypeptide binding column;

(d) move the multi-port valve to a second position in which the second holding coil is connected to the reaction chamber via the second port of the multi-port valve;

(e) when the multi-port valve is in the second position, move an elution/polypeptide mixture comprising the elution buffer solution and the eluted polypeptides to the reaction chamber, whereby the polypeptides in the elution/polypeptide mixture are denatured;

(f) move the multi-port valve to a third position in which the first holding coil is connected to the reaction chamber via the third port of the multi-port valve;

(g) after (f), move a reducing reagent that cleaves disulfide bonds to the first holding coil, and move the reducing reagent from the first holding coil to the reaction chamber via the third port of the multi-port valve, thereby reducing the denatured polypeptides;

(h) after (g), move an alkylating reagent that alkylates sulfhydryls to the first holding coil, and move the alkylating reagent from the first holding coil to the reaction chamber via the third port, thereby alkylating the denatured and reduced polypeptides;

(i) move the denatured, reduced, and alkylated polypeptides, the elution buffer solution, the reducing reagent, and the alkylating reagent from the reaction chamber to the first holding coil via the third port;

(j) move the multi-port valve to a fourth position in which the first holding coil is connected to the desalting column via the fourth port of the multi-port valve, and, when the multi-port valve is in the fourth position, move the denatured, reduced, and alkylated polypeptides, the elution buffer solution, the reducing reagent, and the

alkylating reagent from the first holding coil to the desalting column, whereby the denatured, reduced, and alkylated polypeptides are de-salted;

(k) move the desalted polypeptides to the proteolytic enzyme column, whereby the desalted polypeptides are digested; and

(l) pass the digested polypeptides to a glycan analysis device, whereby the digested polypeptides are separated and quantified.

13. The method of claims 1-10 or the system of claims 11-12, wherein the polypeptide of the product is a therapeutic polypeptide, optionally, wherein the therapeutic polypeptide is selected from the group consisting of an antibody or antigen-binding fragment thereof, a derivative of an antibody or antibody fragment, and a fusion polypeptide.

14. The method or system of claim 13, wherein the antibody is selected from the group consisting of infliximab, bevacizumab, ranibizumab, cetuximab, ranibizumab, palivizumab, abagovomab, abciximab, actoxumab, adalimumab, afelimomab, afutuzumab, alacizumab, alacizumab pegol, ald518, alemtuzumab, alirocumab, alemtuzumab, altumomab, amatuximab, anatumomab mafenatox, anrukinzumab, apolizumab, arcitumomab, aselizumab, altinumab, atlizumab, atorolimumab, tocilizumab, bapineuzumab, basiliximab, bavituximab, bectumomab, belimumab, benralizumab, bertilimumab, besilesomab, bevacizumab, bezlotoxumab, biciromab, bivatzumab, bivatzumab mertansine, blinatumomab, blosozumab, brentuximab vedotin, briakinumab, brodalumab, canakinumab, cantuzumab mertansine, cantuzumab mertansine, caplacizumab, capromab pendetide, carlumab, catumaxomab, cc49, cedelizumab, certolizumab pegol, cetuximab, citatuzumab bogatox, cixutumumab, clazakizumab, clenoliximab, clivatuzumab tetraxetan, conatumumab, crenezumab, cr6261, dacetuzumab, daclizumab, dalotuzumab, daratumumab, demcizumab, denosumab, detumomab, dorlimomab aritox, drozitumab, duligotumab, dupilumab, ecomeximab, eculizumab, edobacomab, edrecolomab, efalizumab, efungumab, elotuzumab, elsilimomab, enavatuzumab, enlimomab pegol, enokizumab, enokizumab, enoticumab, enoticumab, ensituximab, epitumomab cituxetan, epratuzumab, erlizumab,

ertumaxomab, etaracizumab, etrolizumab, exbivirumab, exbivirumab, fanolesomab, faralimomab, farletuzumab, fasinumab, fbta05, felvizumab, fezakinumab, ficlatuzumab, figitumumab, flanvotumab, fontolizumab, foralumab, foravirumab, fresolimumab, fulranumab, futuximab, galiximab, ganitumab, gantenerumab, gavilimumab, gentuzumab ozogamicin, gevokizumab, girentuximab, glembatumumab vedotin, golimumab, gomiliximab, gs6624, ibalizumab, ibritumomab tiuxetan, icrucumab, igovomab, imciromab, imgatuzumab, inclacumab, indatuximab ravtansine, infliximab, intetumumab, inolimumab, inotuzumab ozogamicin, ipilimumab, iratumumab, itolizumab, ixekizumab, keliximab, labetuzumab, lebrikizumab, lemalesomab, lerdelimomab, lexatumumab, libivirumab, ligelizumab, lintuzumab, lirilumab, lorvotuzumab mertansine, lucatumumab, lumiliximab, mapatumumab, maslimomab, mavrilimumab, matuzumab, mepolizumab, metelimomab, milatuzumab, minretumomab, mitumomab, mogamulizumab, morolimumab, motavizumab, moxetumomab pasudotox, muromonab-cd3, nacolomab tafenatox, namilumab, naptumomab estafenatox, narnatumab, natalizumab, nebacumab, necitumumab, nerelimomab, nesvacumab, nimotuzumab, nivolumab, nofetumomab merpentan, ocaratuzumab, ocrelizumab, odulimumab, ofatumumab, olaratumab, olokizumab, omalizumab, onartuzumab, oportuzumab monatox, oregovomab, orticumab, otelixizumab, oxelumab, ozanezumab, ozoralizumab, pagibaximab, palivizumab, panitumumab, panobacumab, parsatuzumab, pascolizumab, pateclizumab, patritumab, pemtumomab, perakizumab, pertuzumab, pexelizumab, pidilizumab, pintumomab, placulumab, ponezumab, priliximab, pritumumab, PRO 140, quilizumab, racotumomab, radretumab, rafivirumab, ramucirumab, ranibizumab, raxibacumab, regavirumab, reslizumab, rilotumumab, rituximab, robatumumab, roledumab, romosozumab, rontalizumab, rovelizumab, ruplizumab, samalizumab, sarilumab, satumomab pendetide, secukinumab, sevirumab, sibrotuzumab, sifalimumab, siltuximab, simtuzumab, siplizumab, sirukumab, solanezumab, solitomab, sonepcizumab, sontuzumab, stamulumab, sulesomab, suvizumab, tabalumab, tacatuzumab tetraxetan, tadocizumab, talizumab, tanezumab, taplitumomab paptox, tefibazumab, telimomab aritox, tenatumomab, tefibazumab, telimomab aritox, tenatumomab, teneliximab, teplizumab, teprotumumab, tezepelumab, TGN1412, tremelimomab, ticilimumab, tildrakizumab, tigatuzumab, TNX-650,

tocilizumab, toralizumab, tositumomab, tralokinumab, trastuzumab, TRBS07, tregalizumab, tremelimumab, tucotuzumab celmoleukin, tuvirumab, ublituximab, urelumab, urtoxazumab, ustekinumab, vapaliximab, vatelizumab, vedolizumab, veltuzumab, vepalimomab, vesencumab, visilizumab, volociximab, vorsetuzumab mafodotin, votumumab, zalutumumab, zanolimumab, zatuximab, ziralimumab, zolimomab aritox, and those antibodies shown in Table 1.

15. The method or system of claim 13, wherein the therapeutic polypeptide is a polypeptide selected from the group consisting of a glycoprotein, CD polypeptide, a HER receptor polypeptide, a cell adhesion polypeptide, a growth factor polypeptide, an insulin polypeptide, an insulin-related polypeptide, a coagulation polypeptide, a coagulation-related polypeptide, albumin, IgE, a blood group antigen, a colony stimulating factor, a receptor, a neurotrophic factor, an interferon, an interleukin, a viral antigen, a lipoprotein, calcitonin, glucagon, atrial natriuretic factor, lung surfactant, tumor necrosis factor-alpha and -beta, enkephalinase, mouse gonadotropin-associated peptide, DNase, inhibin, activating, an integrin, protein A, protein D, a rheumatoid factor, an immunotoxin, a bone morphogenetic protein, a superoxide dismutase, a surface membrane polypeptide, a decay accelerating factor, an AIDS envelope, a transport polypeptide, a homing receptor, an addressin, a regulatory polypeptide, an immunoadhesin, a myostatin, a TALL polypeptide, an amyloid polypeptide, a thymic stromal lymphopoietin, a RANK ligand, a c-kit polypeptide, a TNF receptor, and an angiopoietin, and biologically active fragments, analogs or variants thereof.