Claims

1. A method for delivering a single domain antibody or a therapeutic molecule from an apical surface of a polymeric immunoglobulin receptor (pIgR)-expressing cell to a basolateral surface of the pIgR-expressing cell comprising contacting the pIgR-expressing cell with the single domain antibody or the therapeutic molecule, wherein the single domain antibody binds to pIgR and the therapeutic molecule comprises an agent and the single domain antibody.

2. A method for transporting a therapeutic molecule to a basolateral surface of the pIgR-expressing cell of a subject, the therapeutic molecule comprising an agent and a single domain antibody that binds to pIgR; wherein optionally, the therapeutic molecule is to be administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.

3. A method for transporting a therapeutic molecule to systemic circulation of a subject, the therapeutic molecule comprising an agent and a single domain antibody that binds to pIgR, wherein the therapeutic molecule is to be administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.

4. A method for transporting a therapeutic molecule to lamina propria or gastrointestinal tract of a subject, the therapeutic molecule comprising an agent and a single domain antibody that binds to pIgR, wherein the therapeutic molecule is to be administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.

5. The method of any one of claims 2 to 4, wherein:
   a) the therapeutic agent is transported from an apical surface of a pIgR-expressing cell to a basolateral surface of the pIgR-expressing cell in the subject;
   b) the single domain antibody or the therapeutic molecule comprising the agent and the single domain antibody is capable of being transported from the basolateral surface of the pIgR-expressing cell to the apical surface of the pIgR-expressing cell; or
   c) the pIgR-expressing cell is an epithelial cell; wherein optionally, epithelial cell is an intestinal lumen cell or an airway epithelial cell.

6. The method of any one of claims 1 to 5, wherein the agent is a:

a) diabetes medication; optionally wherein the diabetes medication is selected from a group consisting of insulin, glucagon-like-peptide-1, insulin-mimic peptides, and glucagon-like-peptide-1-mimic peptides;

b) peptide or an antibody or a fragment thereof; optionally wherein the antibody or fragment thereof is selected from a group consisting of an anti-TNF-alpha antibody or a fragment thereof, an anti-IL23 antibody or a fragment thereof, an antibody or a fragment thereof that binds to a receptor of IL23, or an inhibitor of the receptor of IL23; or

c) vaccine; optionally wherein the vaccine is for preventing an infection selected from a group consisting of Vibrio, Cholera, Typhoid, Rotavirus, Tuberculosis, HIV, Flu, Ebola, and Sendai.

7. The method of any one of claims 1 to 6, wherein the single domain antibody

a) binds to an:

i) extracellular domain 1, an extracellular domain 2, an extracellular domain 1-2, an extracellular domain 3, an extracellular domain 2-3, an extracellular domain 4-5, or an extracellular domain 5 of pIgR;

ii) extracellular domain 1 of pIgR;

iii) extracellular domain 2 of pIgR;

iv) extracellular domain 1-2 of pIgR;

v) extracellular domain 3 of pIgR;

vi) extracellular domain 2-3 of pIgR;

vii) extracellular domain 4-5 of pIgR; or

viii) extracellular domain 5 of pIgR;

b) competes with IgA binding to the pIgR; or

c) promotes IgA binding to the pIgR.

8. The method of any one of claims 1 to 7, wherein:

a) the K_D of the binding of the single domain antibody to pIgR:

i) is from about 4 to about 525 nM;

ii) is less than about 50 nM; or

iii) is from about 4 to about 34 nM;

b) the T_m of the single domain antibody:

i) is from about 53 to about 77 °C; or

ii) is from 53.9 to 76.4 °C;

c) pIgR is

i) human pIgR; or

ii) mouse pIgR;

or

d) the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

9. The method of any one of claims 1 to 8, wherein the single domain antibody comprises:

a) a CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60), TTVLTDPRVLNEYAT (SEQ ID NO: 61), DVFGSSGYVETY (SEQ ID NO: 62), PLTAR (SEQ ID NO: 63), DPFNQGY (SEQ ID NO: 64), PLTSR (SEQ ID NO: 65), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66), DQRGY (SEQ ID NO: 67), QRGY (SEQ ID NO: 271), DPFNQGY (SEQ ID NO: 68), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69), ARYYVSGTYFPANY (SEQ ID NO: 70), GSIDLNWYGGMDY (SEQ ID NO: 71), SIDLNWYGGMD (SEQ ID NO: 272), TTVLTDPRVLNEYAT (SEQ ID NO: 72), TVLTDPRVLNEYA (SEQ ID NO: 273), DVFGSSGYVETY (SEQ ID NO: 73), VFGSSGYVET (SEQ ID NO: 274), PLTAR (SEQ ID NO: 74), LTA (SEQ ID NO: 275), DPFNQGY (SEQ ID NO: 75), PFNQG (SEQ ID NO: 276), PLTSR (SEQ ID NO: 76), LTS (SEQ ID NO: 277), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278), DQRGY (SEQ ID NO: 78), RG (SEQ ID NO: 279), DPFNQGY (SEQ ID NO: 79), PFNQG (SEQ ID NO: 280), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80), LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281), ARYYVSGTYFPANY (SEQ ID NO: 81), RYYVSGTYFPAN (SEQ ID NO: 282), CAAGSIDLNWYGGMDY (SEQ ID NO: 82), AAGSIDLNWYGGMDY (SEQ ID NO: 283), CAATTVLTDPRVLNEYAT (SEQ ID NO: 83), AATTVLTDPRVLNEYAT (SEQ ID NO: 284), KADVFGSSGYVETY (SEQ ID NO:

84), NHPLTAR (SEQ ID NO: 85), AADPFNQGY (SEQ ID NO: 86), NHPLTSR (SEQ ID NO: 87), ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRGY (SEQ ID NO: 89), AADPFNQGY (SEQ ID NO: 90), AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91), AAARYYVSGTYFPANY (SEQ ID NO: 92), GSIDLNWYGGMDY (SEQ ID NO: 214), TTVLTDPRVLNEYAT (SEQ ID NO: 215), DVFGSSGYVETY (SEQ ID NO: 216), PLTAR (SEQ ID NO: 217), DPFNQGY (SEQ ID NO: 218), PLTSR (SEQ ID NO: 219), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220), QRGY (SEQ ID NO: 221), DPFNQGY (SEQ ID NO: 222), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223), ARYYVSGTYFPANY (SEQ ID NO: 224), AAGSIDLNWYGGMD (SEQ ID NO: 225), AATTVLTDPRVLNEYA (SEQ ID NO: 226), KADVFGSSGYVET (SEQ ID NO: 227), NHPLTA (SEQ ID NO: 228), AADPFNQG (SEQ ID NO: 229), NHPLTS (SEQ ID NO: 230), ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRG (SEQ ID NO: 232), AADPFNQG (SEQ ID NO: 233), AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234), AAARYYVSGTYFPAN (SEQ ID NO: 235), GSIDLNWYGGMDY (SEQ ID NO: 236), TTVLTDPRVLNEYAT (SEQ ID NO: 237), DVFGSSGYVETY (SEQ ID NO: 238), PLTAR (SEQ ID NO: 239), DPFNQGY (SEQ ID NO: 240), PLTSR (SEQ ID NO: 241), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242), QRGY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246);

b) a CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYYADSVKG (SEQ ID NO: 33), FISGGGTTTYADSVKG (SEQ ID NO: 34), RITGGGSTHYAESVKG (SEQ ID NO: 35), AISWSGGSTTYADPVKG (SEQ ID NO: 36), AISWSGSSAGYGDSVKG (SEQ ID NO: 37), AIRWSGGRTLYADSVKG (SEQ ID NO: 38), SITWNGGSTSYADSVKG (SEQ ID NO: 39), DWNGRGTYY (SEQ ID NO: 40), WNGRGTY (SEQ ID NO: 260), NGGGI (SEQ ID NO: 41), GGG (SEQ ID NO: 261), DRIAT (SEQ ID NO: 42), RIA (SEQ ID NO: 262), TWNGGT (SEQ ID NO: 43), WNGG (SEQ ID NO: 263), SGGGT (SEQ ID NO: 44), GGG (SEQ ID NO: 264), TGGGS (SEQ ID NO: 45), GGG (SEQ ID NO: 265), SWSGGS (SEQ ID NO: 46), WSGG (SEQ ID NO: 266), SWSGSS (SEQ ID NO: 47), WSGS (SEQ ID NO: 267), RWSGGR (SEQ ID NO: 48), WSGG (SEQ ID NO: 268), TWNGGS (SEQ ID NO: 49), WNGG (SEQ

ID NO: 269), IDWNGRGTYY (SEQ ID NO: 50), IDWNGRGTYYR (SEQ ID NO: 270), INGGGIT (SEQ ID NO: 51), IDRIATT (SEQ ID NO: 52), ITWNGGTT (SEQ ID NO: 53), ISGGGTT (SEQ ID NO: 54), ITGGGST (SEQ ID NO: 55), ISWSGGST (SEQ ID NO: 56), ISWSGSSA (SEQ ID NO: 57), IRWSGGRT (SEQ ID NO: 58), ITWNGGST (SEQ ID NO: 59), AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYYADSVKG (SEQ ID NO: 187), FISGGGTTTYADSVKG (SEQ ID NO: 188), RITGGGSTHYAESVKG (SEQ ID NO: 189), AISWSGGSTTYADPVKG (SEQ ID NO: 190), AISWSGSSAGYGDSVKG (SEQ ID NO: 191), AIRWSGGRTLYADSVKG (SEQ ID NO: 192), SITWNGGSTSYADSVKG (SEQ ID NO: 193), FVAAIDWNGRGTYYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIDRIATTT (SEQ ID NO: 196), FVAAITWNGGTTY (SEQ ID NO: 197), WVAFISGGGTTT (SEQ ID NO: 198), LVARITGGGSTH (SEQ ID NO: 199), FVAAISWSGGSTT (SEQ ID NO: 200), FVAAISWSGSSAG (SEQ ID NO: 201), FVAAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), AIDWNGRGTYYRY (SEQ ID NO: 204), RINGGGITH (SEQ ID NO: 205), FIDRIATTT (SEQ ID NO: 206), AITWNGGTTY (SEQ ID NO: 207), FISGGGTTT (SEQ ID NO: 208), RITGGGSTH (SEQ ID NO: 209), AISWSGGSTT (SEQ ID NO: 210), AISWSGSSAG (SEQ ID NO: 211), AIRWSGGRTL (SEQ ID NO: 212), or SITWNGGSTS (SEQ ID NO: 213);

c) a CDR1 sequence of SYRMG (SEQ ID NO: 1), INVMG (SEQ ID NO: 2), SNAMG (SEQ ID NO: 3), SYAMG (SEQ ID NO: 4), SDAMG (SEQ ID NO: 5), INVMG (SEQ ID NO: 6), TYRMG (SEQ ID NO: 7), RYAMG (SEQ ID NO: 8), FTTYRMG (SEQ ID NO: 258), TYRMG (SEQ ID NO: 259), FNTYAMG (SEQ ID NO: 9), GLTFSSY (SEQ ID NO: 10), GSIFSIN (SEQ ID NO: 11), GTSVSSN (SEQ ID NO: 12), GRTFSSY (SEQ ID NO: 13), GSSVSSD (SEQ ID NO: 14), RSIGSIN (SEQ ID NO: 15), GRTFSTY (SEQ ID NO: 16), GFTFTRY (SEQ ID NO: 17), GRTFTTY (SEQ ID NO: 18), GRTLSFNTY (SEQ ID NO: 19), GLTFSSYR (SEQ ID NO: 20), GSIFSINV (SEQ ID NO: 21), GTSVSSNA (SEQ ID NO: 22), GRTFSSYA (SEQ ID NO: 23), GSSVSSDA (SEQ ID NO: 24), RSIGSINV (SEQ ID NO: 25), GRTFSTYR (SEQ ID NO: 26), GFTFTRYA (SEQ ID NO: 27), GRTFTTYR (SEQ ID NO: 28), GRTLSFNTYA (SEQ ID NO: 29), GLTFSSYRMG (SEQ ID NO: 154),

GSIFSINVMG (SEQ ID NO: 155), GTSVSSNAMG (SEQ ID NO: 156), GRTFSSYAMG (SEQ ID NO: 157), GSSVSSDAMG (SEQ ID NO: 158), RSIGSINVMG (SEQ ID NO: 159), GRTFSTYRMG (SEQ ID NO: 160), GFTFTRYAMG (SEQ ID NO: 161), GRTFTTYRMG (SEQ ID NO: 162), GRTLSFNTYAMG (SEQ ID NO: 163), SSYRMG (SEQ ID NO: 164), SINVMG (SEQ ID NO: 165), SSNAMG (SEQ ID NO: 166), SSYAMG (SEQ ID NO: 167), SSDAMG (SEQ ID NO: 168), SINVMG (SEQ ID NO: 169), STYRMG (SEQ ID NO: 170), TRYAMG (SEQ ID NO: 171), TTYRMG (SEQ ID NO: 172), SFNTYAMG (SEQ ID NO: 173), GLTFSSYRMG (SEQ ID NO: 174), GSIFSINVMG (SEQ ID NO: 175), GTSVSSNAMG (SEQ ID NO: 176), GRTFSSYAMG (SEQ ID NO: 177), GSSVSSDAMG (SEQ ID NO: 178), RSIGSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182), or GRTLSFNTYAMG (SEQ ID NO: 183);

d) a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence selected from the group consisting of:

i) VHH1:

1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60);
2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYY (SEQ ID NO: 40) or WNGRGTY (SEQ ID NO: 260), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 71) or SIDLNWYGGMD (SEQ ID NO: 272);
3) the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYY (SEQ ID NO: 50) or IDWNGRGTYYR (SEQ ID NO: 270), and the CDR3 sequence of CAAGSIDLNWYGGMDY (SEQ ID NO: 82) or AAGSIDLNWYGGMDY (SEQ ID NO: 283);
4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);

5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYYRY (SEQ ID NO: 194), and the CDR3 sequence of AAGSIDLNWYGGMD (SEQ ID NO: 225); or
6) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYYRY (SEQ ID NO: 204), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 236);

ii) VHH2:
1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 61);
2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYY (SEQ ID NO: 40) or WNGRGTY (SEQ ID NO: 260), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 72) or TVLTDPRVLNEYA (SEQ ID NO: 273);
3) the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYY (SEQ ID NO: 50) or IDWNGRGTYYR (SEQ ID NO: 270), and the CDR3 sequence of CAATTVLTDPRVLNEYAT (SEQ ID NO: 83) or AATTVLTDPRVLNEYAT (SEQ ID NO: 284);
4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);
5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYYRY (SEQ ID NO: 194), and the CDR3 sequence of AATTVLTDPRVLNEYA (SEQ ID NO: 226); or
6) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYYRY (SEQ ID NO: 204), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 237);

iii) VHH3:
1) the CDR1 sequence of INVMG (SEQ ID NO: 2), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 31), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 62);

2) the CDR1 sequence of GSIFSIN (SEQ ID NO: 11), the CDR2 sequence of NGGGI (SEQ ID NO: 41) or GGG (SEQ ID NO: 261), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 73) or VFGSSGYVET (SEQ ID NO: 274);
3) the CDR1 sequence of GSIFSINV (SEQ ID NO: 21), the CDR2 sequence of INGGGIT (SEQ ID NO: 51), and the CDR3 sequence of KADVFGSSGYVETY (SEQ ID NO: 84);
4) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 155), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 185), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 216);
5) the CDR1 sequence of SINVMG (SEQ ID NO: 165), the CDR2 sequence of LVARINGGGITH (SEQ ID NO: 195), and the CDR3 sequence of KADVFGSSGYVET (SEQ ID NO: 227); or
6) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 175), the CDR2 sequence of RINGGGITH (SEQ ID NO: 205), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 238);

iv) VHH4:

1) the CDR1 sequence of SNAMG (SEQ ID NO: 3), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), and the CDR3 sequence of PLTAR (SEQ ID NO: 63);
2) the CDR1 sequence of GTSVSSN (SEQ ID NO: 12), the CDR2 sequence of DRIAT (SEQ ID NO: 42) or RIA (SEQ ID NO: 262), and the CDR3 sequence of PLTAR (SEQ ID NO: 74) or LTA (SEQ ID NO: 275);
3) the CDR1 sequence of GTSVSSNA (SEQ ID NO: 22), the CDR2 sequence of IDRIATT (SEQ ID NO: 52), and the CDR3 sequence of NHPLTAR (SEQ ID NO: 85);
4) the CDR1 sequence of GTSVSSNAMG (SEQ ID NO: 156), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 186), and the CDR3 sequence of PLTAR (SEQ ID NO: 217);
5) the CDR1 sequence of SSNAMG (SEQ ID NO: 166), the CDR2 sequence of WVGFIDRIATTT (SEQ ID NO: 196), and the CDR3 sequence of NHPLTA (SEQ ID NO: 228); or

6) the CDR1 sequence of GTSVSSNAMG (SEQ ID NO: 176), the CDR2 sequence of FIDRIATTT (SEQ ID NO: 206), and the CDR3 sequence of PLTAR (SEQ ID NO: 239);

v) VHH5:

1) the CDR1 sequence of SYAMG (SEQ ID NO: 4), the CDR2 sequence of AITWNGGTTYYADSVKG (SEQ ID NO: 33), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 64);
2) the CDR1 sequence of GRTFSSY (SEQ ID NO: 13), the CDR2 sequence of TWNGGT (SEQ ID NO: 43) or WNGG (SEQ ID NO: 263), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 75) or PFNQG (SEQ ID NO: 276);
3) the CDR1 sequence of GRTFSSYA (SEQ ID NO: 23), the CDR2 sequence of ITWNGGTT (SEQ ID NO: 53), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 86);
4) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 157), the CDR2 sequence of AITWNGGTTYYADSVKG (SEQ ID NO: 187), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 218);
5) the CDR1 sequence of SSYAMG (SEQ ID NO: 167), the CDR2 sequence of FVAAITWNGGTTY (SEQ ID NO: 197), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 229); or
6) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 177), the CDR2 sequence of AITWNGGTTY (SEQ ID NO: 207), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 240);

vi) VHH6:

1) the CDR1 sequence of SDAMG (SEQ ID NO: 5), the CDR2 sequence of FISGGGTTTYADSVKG (SEQ ID NO: 34), and the CDR3 sequence of PLTSR (SEQ ID NO: 65);
2) the CDR1 sequence of GSSVSSD (SEQ ID NO: 14), the CDR2 sequence of SGGGT (SEQ ID NO: 44) or GGG (SEQ ID NO: 264), and the CDR3 sequence of PLTSR (SEQ ID NO: 76) or LTS (SEQ ID NO: 277);

3) the CDR1 sequence of GSSVSSDA (SEQ ID NO: 24), the CDR2 sequence of ISGGGTT (SEQ ID NO: 54), and the CDR3 sequence of NHPLTSR (SEQ ID NO: 87);
4) the CDR1 sequence of GSSVSSDAMG (SEQ ID NO: 158), the CDR2 sequence of FISGGGTTTYADSVKG (SEQ ID NO: 188), and the CDR3 sequence of PLTSR (SEQ ID NO: 219);
5) the CDR1 sequence of SSDAMG (SEQ ID NO: 168), the CDR2 sequence of WVAFISGGGTTT (SEQ ID NO: 198), and the CDR3 sequence of NHPLTS (SEQ ID NO: 230); or
6) the CDR1 sequence of GSSVSSDAMG (SEQ ID NO: 178), the CDR2 sequence of FISGGGTTT (SEQ ID NO: 208), and the CDR3 sequence of PLTSR (SEQ ID NO: 241);

vii) VHH7:

1) the CDR1 sequence of INVMG (SEQ ID NO: 6), the CDR2 sequence of RITGGGSTHYAESVKG (SEQ ID NO: 35), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66);
2) the CDR1 sequence of RSIGSIN (SEQ ID NO: 15), the CDR2 sequence of TGGGS (SEQ ID NO: 45) or GGG (SEQ ID NO: 265), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77) or VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278);
3) the CDR1 sequence of RSIGSINV (SEQ ID NO: 25), the CDR2 sequence of ITGGGST (SEQ ID NO: 55), and the CDR3 sequence of ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88);
4) the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 159), the CDR2 sequence of RITGGGSTHYAESVKG (SEQ ID NO: 189), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220);
5) the CDR1 sequence of SINVMG (SEQ ID NO: 169), the CDR2 sequence of LVARITGGGSTH (SEQ ID NO: 199), and the CDR3 sequence of ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231); or

6) the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 179), the CDR2 sequence of RITGGGSTH (SEQ ID NO: 209), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242);

viii) VHH8:

1) the CDR1 sequence of TYRMG (SEQ ID NO: 7), the CDR2 sequence of AISWSGGSTTYADPVKG (SEQ ID NO: 36), and the CDR3 sequence of DQRGY (SEQ ID NO: 67) or QRGY (SEQ ID NO: 271);
2) the CDR1 sequence of GRTFSTY (SEQ ID NO: 16), the CDR2 sequence of SWSGGS (SEQ ID NO: 46) or WSGG (SEQ ID NO: 266), and the CDR3 sequence of DQRGY (SEQ ID NO: 78) or RG (SEQ ID NO: 279);
3) the CDR1 sequence of GRTFSTYR (SEQ ID NO: 26), the CDR2 sequence of ISWSGGST (SEQ ID NO: 56), and the CDR3 sequence of NDQRGY (SEQ ID NO: 89);
4) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 160), the CDR2 sequence of AISWSGGSTTYADPVKG (SEQ ID NO: 190), and the CDR3 sequence of QRGY (SEQ ID NO: 221);
5) the CDR1 sequence of STYRMG (SEQ ID NO: 170), the CDR2 sequence of FVAAISWSGGSTT (SEQ ID NO: 200), and the CDR3 sequence of NDQRG (SEQ ID NO: 232); or
6) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 180), the CDR2 sequence of AISWSGGSTT (SEQ ID NO: 210), and the CDR3 sequence of QRGY (SEQ ID NO: 243);

ix) VHH9:

1) the CDR1 sequence of RYAMG (SEQ ID NO: 8), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 37), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 68);
2) the CDR1 sequence of GFTFTRY (SEQ ID NO: 17), the CDR2 sequence of SWSGSS (SEQ ID NO: 47) or WSGS (SEQ ID NO: 267), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 79) or PFNQG (SEQ ID NO: 280);

3) the CDR1 sequence of GFTFTRYA (SEQ ID NO: 27), the CDR2 sequence of ISWSGSSA (SEQ ID NO: 57), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 90);
4) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 161), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 191), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 222);
5) the CDR1 sequence of TRYAMG (SEQ ID NO: 171), the CDR2 sequence of FVAAISWSGSSAG (SEQ ID NO: 201), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 233); or
6) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 181), the CDR2 sequence of AISWSGSSAG (SEQ ID NO: 211), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 244);

x) VHH10:
1) the CDR1 sequence of FTTYRMG (SEQ ID NO: 258) or TYRMG (SEQ ID NO: 259), the CDR2 sequence of AIRWSGGRTLYADSVKG (SEQ ID NO: 38), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69);
2) the CDR1 sequence of GRTFTTY (SEQ ID NO: 18), the CDR2 sequence of RWSGGR (SEQ ID NO: 48) or WSGG (SEQ ID NO: 268), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80) or LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281);
3) the CDR1 sequence of GRTFTTYR (SEQ ID NO: 28), the CDR2 sequence of IRWSGGRT (SEQ ID NO: 58), and the CDR3 sequence of AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91);
4) the CDR1 sequence of GRTFTTYRMG (SEQ ID NO: 162), the CDR2 sequence of AIRWSGGRTLYADSVKG (SEQ ID NO: 192), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223);
5) the CDR1 sequence of TTYRMG (SEQ ID NO: 172), the CDR2 sequence of FVAAIRWSGGRTL (SEQ ID NO: 202), and the CDR3 sequence of AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234); or

6) the CDR1 sequence of GRTFTTYRMG (SEQ ID NO: 182), the CDR2 sequence of AIRWSGGRTL (SEQ ID NO: 212), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245); and

xi) VHH11:

1) the CDR1 sequence of FNTYAMG (SEQ ID NO: 9), the CDR2 sequence of SITWNGGSTSYADSVKG (SEQ ID NO: 39), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 70);
2) the CDR1 sequence of GRTLSFNTY (SEQ ID NO: 19), the CDR2 sequence of TWNGGS (SEQ ID NO: 49) or WNGG (SEQ ID NO: 269), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 81) or RYYVSGTYFPAN (SEQ ID NO: 282);
3) the CDR1 sequence of GRTLSFNTYA (SEQ ID NO: 29), the CDR2 sequence of ITWNGGST (SEQ ID NO: 59), and the CDR3 sequence of AAARYYVSGTYFPANY (SEQ ID NO: 92);
4) the CDR1 sequence of GRTLSFNTYAMG (SEQ ID NO: 163), the CDR2 sequence of SITWNGGSTSYADSVKG (SEQ ID NO: 193), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 224);
5) the CDR1 sequence of SFNTYAMG (SEQ ID NO: 173), the CDR2 sequence of FVASITWNGGSTS (SEQ ID NO: 203), and the CDR3 sequence of AAARYYVSGTYFPAN (SEQ ID NO: 235); or
6) the CDR1 sequence of GRTLSFNTYAMG (SEQ ID NO: 183), the CDR2 sequence of SITWNGGSTS (SEQ ID NO: 213), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 246);

e) a framework derived from the framework of any of the single domain antibodies comprising the sequences of QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW NGRGTYYRYYADSVKGRSTISRDNAKNTMYLQMNSLKPEDTAVYYCAAGSIDL NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93), EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW NGRGTYYRYYADSVKGRSTISRDNAKNTVYLQMNSLKPEDTAVYYCAATTVLT DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG GITHYAESVKGRFTISRDNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET YWGQGTQVTVSS (SEQ ID NO: 95),
EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR IATTTIATSVKGRFAITRDNAKNTVYLQMSGLKPEDTAVYYCNHPLTARWGQGT QVTVSS (SEQ ID NO: 96),
QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITW NGGTTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCAADPFNQGY WGQGTQVTVSS (SEQ ID NO: 97),
EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG GGTTTYADSVKGRFTISRDNTKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG TQVTVSS (SEQ ID NO: 98),
EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG GGSTHYAESVKGRFTISRDNAKNTVYLQMNSLEPEDTAVYYCASMVNPIITAWG TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW SGGSTTYADPVKGRFTISRDNAKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG TLVTVSS (SEQ ID NO: 100),
EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW SGSSAGYGDSVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW GQGTQVTVSS (SEQ ID NO: 101),
EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW SGGRTLYADSVKGRFTISRDNAKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREFVASIT WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

f) a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of SEQ ID NOS: 93-103; or

g) a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of SEQ ID NOS: 93-103.

10. The method of any one of claims 1 to 9, wherein the single domain antibody is

a) genetically fused to the agent;

b) chemically conjugated to the agent; or

c) non-covalently bound to the agent.

11. The method of claim 10, further comprising a linker between the single domain antibody and the agent; wherein optionally, the linker:

a) is a polypeptide; or

b) is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQPQLQPQPNPTTESKSPK (SEQ ID NO: 130), (EAAAK)n (SEQ ID NO: 147), (GGGGS)n (SEQ ID NO: 148) and (GGGS)n (SEQ ID NO: 149), wherein n is an integer from 1 to 20.

12. The method of any one of claims 1 to 11, wherein the method does not inhibit pIgR-mediated transcytosis of IgA.

13. The method of claim 12, wherein the single domain antibody comprises:

a) a CDR1 sequence of SNAMG (SEQ ID NO: 3), INVMG (SEQ ID NO: 6), TYRMG (SEQ ID NO: 7), RYAMG (SEQ ID NO: 8), FTTYRMG (SEQ ID NO: 258), TYRMG (SEQ ID NO: 259), FNTYAMG (SEQ ID NO: 9), GTSVSSN (SEQ ID NO: 12), GRTFSSY (SEQ ID NO: 13), RSIGSIN (SEQ ID NO: 15), GRTFSTY (SEQ ID NO: 16), GFTFTRY (SEQ ID NO: 17), GRTFTTY (SEQ ID NO: 18), GRTLSFNTY (SEQ ID NO: 19), GTSVSSNA (SEQ ID NO: 22), RSIGSINV (SEQ ID NO: 25), GRTFSTYR (SEQ ID NO: 26), GFTFTRYA (SEQ ID NO: 27), GRTFTTYR (SEQ ID NO: 28), GRTLSFNTYA (SEQ ID NO: 29), GTSVSSNAMG (SEQ ID NO: 156), RSIGSINVMG (SEQ ID NO: 159), GRTFSTYRMG (SEQ ID NO: 160), GFTFTRYAMG (SEQ ID NO: 161), GRTFTTYRMG (SEQ ID NO: 162), GRTLSFNTYAMG (SEQ ID NO: 163), SSNAMG (SEQ ID NO: 166), SINVMG (SEQ ID NO: 169), STYRMG (SEQ ID NO: 170),

TRYAMG (SEQ ID NO: 171), TTYRMG (SEQ ID NO: 172), SFNTYAMG (SEQ ID NO: 173), GTSVSSNAMG (SEQ ID NO: 176), RSIGSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182), or GRTLSFNTYAMG (SEQ ID NO: 183);

b) a CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), RITGGGSTHYAESVKG (SEQ ID NO: 35), AISWSGGSTTYADPVKG (SEQ ID NO: 36), AISWSGSSAGYGDSVKG (SEQ ID NO: 37), AIRWSGGRTLYADSVKG (SEQ ID NO: 38), SITWNGGSTSYADSVKG (SEQ ID NO: 39), DRIAT (SEQ ID NO: 42), RIA (SEQ ID NO: 262), TGGGS (SEQ ID NO: 45), GGG (SEQ ID NO: 265), SWSGGS (SEQ ID NO: 46), WSGG (SEQ ID NO: 266), SWSGSS (SEQ ID NO: 47), WSGS (SEQ ID NO: 267), RWSGGR (SEQ ID NO: 48), WSGG (SEQ ID NO: 268), TWNGGS (SEQ ID NO: 49), WNGG (SEQ ID NO: 269), IDRIATT (SEQ ID NO: 52), ITGGGST (SEQ ID NO: 55), ISWSGGST (SEQ ID NO: 56), ISWSGSSA (SEQ ID NO: 57), IRWSGGRT (SEQ ID NO: 58), ITWNGGST (SEQ ID NO: 59), FIDRIATTTIATSVKG (SEQ ID NO: 186), RITGGGSTHYAESVKG (SEQ ID NO: 189), AISWSGGSTTYADPVKG (SEQ ID NO: 190), AISWSGSSAGYGDSVKG (SEQ ID NO: 191), AIRWSGGRTLYADSVKG (SEQ ID NO: 192), SITWNGGSTSYADSVKG (SEQ ID NO: 193), WVGFIDRIATTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVAAISWSGGSTT (SEQ ID NO: 200), FVAAISWSGSSAG (SEQ ID NO: 201), FVAAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), FIDRIATTT (SEQ ID NO: 206), RITGGGSTH (SEQ ID NO: 209), AISWSGGSTT (SEQ ID NO: 210), AISWSGSSAG (SEQ ID NO: 211), AIRWSGGRTL (SEQ ID NO: 212), or SITWNGGSTS (SEQ ID NO: 213); or

c) a CDR3 sequence of PLTAR (SEQ ID NO: 63), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66), DQRGY (SEQ ID NO: 67), QRGY (SEQ ID NO: 271), DPFNQGY (SEQ ID NO: 68), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69), ARYYVSGTYFPANY (SEQ ID NO: 70), PLTAR (SEQ ID NO: 74), LTA (SEQ ID NO: 275), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278), DQRGY (SEQ ID NO: 78), RG (SEQ ID NO: 279), DPFNQGY (SEQ ID NO: 79), PFNQG (SEQ ID NO: 280), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80), LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281), ARYYVSGTYFPANY (SEQ ID NO: 81), RYYVSGTYFPAN (SEQ ID NO: 282), NHPLTAR (SEQ ID NO: 85),

ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRGY (SEQ ID NO: 89), AADPFNQGY (SEQ ID NO: 90), AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91), AAARYYVSGTYFPANY (SEQ ID NO: 92), PLTAR (SEQ ID NO: 217), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220), QRGY (SEQ ID NO: 221), DPFNQGY (SEQ ID NO: 222), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223), ARYYVSGTYFPANY (SEQ ID NO: 224), NHPLTA (SEQ ID NO: 228), ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRG (SEQ ID NO: 232), AADPFNQG (SEQ ID NO: 233), AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234), AAARYYVSGTYFPAN (SEQ ID NO: 235), PLTAR (SEQ ID NO: 239), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242), QRGY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246).

14. A process for providing a molecule to a subject, comprising the molecule comprising an agent and a single domain antibody that binds to polymeric immunoglobulin receptor (pIgR) to be administered to the subject, wherein the molecule is to be administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.

15. The process of claim 14, wherein:

a) the molecule:
   i) is capable of being provided to a basolateral surface of a pIgR-expressing cell from an apical surface of the pIgR-expressing cell in the subject; or
   ii) is capable of being provided to an apical surface of the pIgR-expressing cell from a basolateral surface of an pIgR-expressing cell in the subject;
b) the pIgR-expressing cell is an epithelial cell; wherein optionally, the epithelial cell is an intestinal lumen cell or an airway epithelial cell; or
c) the agent is a:
   i) diabetes medication, wherein the diabetes medication is selected from a group consisting of insulin, glucagon-like-peptide-1, insulin-mimic peptides, and glucagon-like-peptide-1-mimic peptides;

ii) peptide or an antibody or a fragment thereof, wherein the antibody or fragment thereof is selected from a group consisting of an anti-TNF-alpha antibody or a fragment thereof, an anti-IL23 antibody or a fragment thereof, and an antibody that binds to a receptor of IL23 or a fragment thereof; or

iii) vaccine, wherein the vaccine is for preventing an infection selected from a group consisting of Vibrio, Cholera, Typhoid, Rotavirus, Tuberculosis, HIV, Flu, Ebola, and Sendai.

16. The process of claim 14 or claim 15, wherein the single domain antibody:

a) binds to:

i) an extracellular domain 1, an extracellular domain 2, an extracellular domain 1-2, an extracellular domain 3, an extracellular domain 2-3, an extracellular domain 4-5, or an extracellular domain 5 of pIgR;

ii) an extracellular domain 1 of pIgR;

iii) an extracellular domain 2 of pIgR;

iv) an extracellular domain 1-2 of pIgR;

v) an extracellular domain 3 of pIgR;

vi) an extracellular domain 2-3 of pIgR;

vii) an extracellular domain 4-5 of pIgR; or

viii) an extracellular domain 5 of pIgR;

b) competes with IgA binding to the pIgR; or

c) promotes IgA binding to the pIgR.

17. The process of any one of claims 14 to 16, wherein:

a) the K_D of the binding of the single domain antibody to pIgR:

i) is from about 4 to about 525 nM;

ii) is less than about 50 nM; or

iii) is from about 4 to about 34 nM;

b) the T_m of the single domain antibody:

i) is from about 53 to about 77 °C; or

ii) is from 53.9 to 76.4 °C;

c) the pIgR is

i) human pIgR; or

ii) mouse pIgR;

or

d) the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

18. The process of any one of claims 14 to 17, wherein the single domain antibody comprises:

a) a CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60), TTVLTDPRVLNEYAT (SEQ ID NO: 61), DVFGSSGYVETY (SEQ ID NO: 62), PLTAR (SEQ ID NO: 63), DPFNQGY (SEQ ID NO: 64), PLTSR (SEQ ID NO: 65), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66), DQRGY (SEQ ID NO: 67), QRGY (SEQ ID NO: 271), DPFNQGY (SEQ ID NO: 68), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69), ARYYVSGTYFPANY (SEQ ID NO: 70), GSIDLNWYGGMDY (SEQ ID NO: 71), SIDLNWYGGMD (SEQ ID NO: 272), TTVLTDPRVLNEYAT (SEQ ID NO: 72), TVLTDPRVLNEYA (SEQ ID NO: 273), DVFGSSGYVETY (SEQ ID NO: 73), VFGSSGYVET (SEQ ID NO: 274), PLTAR (SEQ ID NO: 74), LTA (SEQ ID NO: 275), DPFNQGY (SEQ ID NO: 75), PFNQG (SEQ ID NO: 276), PLTSR (SEQ ID NO: 76), LTS (SEQ ID NO: 277), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278), DQRGY (SEQ ID NO: 78), RG (SEQ ID NO: 279), DPFNQGY (SEQ ID NO: 79), PFNQG (SEQ ID NO: 280), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80), LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281), ARYYVSGTYFPANY (SEQ ID NO: 81), RYYVSGTYFPAN (SEQ ID NO: 282), CAAGSIDLNWYGGMDY (SEQ ID NO: 82), AAGSIDLNWYGGMDY (SEQ ID NO: 283), CAATTVLTDPRVLNEYAT (SEQ ID NO: 83), AATTVLTDPRVLNEYAT (SEQ ID NO: 284), KADVFGSSGYVETY (SEQ ID NO: 84), NHPLTAR (SEQ ID NO: 85), AADPFNQGY (SEQ ID NO: 86), NHPLTSR (SEQ ID NO: 87), ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRGY (SEQ ID NO: 89), AADPFNQGY (SEQ ID NO: 90), AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91), AAARYYVSGTYFPANY (SEQ ID NO: 92), GSIDLNWYGGMDY (SEQ ID NO: 214), TTVLTDPRVLNEYAT (SEQ ID NO: 215), DVFGSSGYVETY (SEQ ID

NO: 216), PLTAR (SEQ ID NO: 217), DPFNQGY (SEQ ID NO: 218), PLTSR (SEQ ID NO: 219), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220), QRGY (SEQ ID NO: 221), DPFNQGY (SEQ ID NO: 222), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223), ARYYVSGTYFPANY (SEQ ID NO: 224), AAGSIDLNWYGGMD (SEQ ID NO: 225), AATTVLTDPRVLNEYA (SEQ ID NO: 226), KADVFGSSGYVET (SEQ ID NO: 227), NHPLTA (SEQ ID NO: 228), AADPFNQG (SEQ ID NO: 229), NHPLTS (SEQ ID NO: 230), ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRG (SEQ ID NO: 232), AADPFNQG (SEQ ID NO: 233), AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234), AAARYYVSGTYFPAN (SEQ ID NO: 235), GSIDLNWYGGMDY (SEQ ID NO: 236), TTVLTDPRVLNEYAT (SEQ ID NO: 237), DVFGSSGYVETY (SEQ ID NO: 238), PLTAR (SEQ ID NO: 239), DPFNQGY (SEQ ID NO: 240), PLTSR (SEQ ID NO: 241), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242), QRGY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246);

b) a CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYYADSVKG (SEQ ID NO: 33), FISGGGTTTYADSVKG (SEQ ID NO: 34), RITGGGSTHYAESVKG (SEQ ID NO: 35), AISWSGGSTTYADPVKG (SEQ ID NO: 36), AISWSGSSAGYGDSVKG (SEQ ID NO: 37), AIRWSGGRTLYADSVKG (SEQ ID NO: 38), SITWNGGSTSYADSVKG (SEQ ID NO: 39), DWNGRGTYY (SEQ ID NO: 40), WNGRGTY (SEQ ID NO: 260), NGGGI (SEQ ID NO: 41), GGG (SEQ ID NO: 261), DRIAT (SEQ ID NO: 42), RIA (SEQ ID NO: 262), TWNGGT (SEQ ID NO: 43), WNGG (SEQ ID NO: 263), SGGGT (SEQ ID NO: 44), GGG (SEQ ID NO: 264), TGGGS (SEQ ID NO: 45), GGG (SEQ ID NO: 265), SWSGGS (SEQ ID NO: 46), WSGG (SEQ ID NO: 266), SWSGSS (SEQ ID NO: 47), WSGS (SEQ ID NO: 267), RWSGGR (SEQ ID NO: 48), WSGG (SEQ ID NO: 268), TWNGGS (SEQ ID NO: 49), WNGG (SEQ ID NO: 269), IDWNGRGTYY (SEQ ID NO: 50), IDWNGRGTYYR (SEQ ID NO: 270), INGGGIT (SEQ ID NO: 51), IDRIATT (SEQ ID NO: 52), ITWNGGTT (SEQ ID NO: 53), ISGGGTT (SEQ ID NO: 54), ITGGGST (SEQ ID NO: 55), ISWSGGST (SEQ ID NO: 56), ISWSGSSA (SEQ ID NO: 57), IRWSGGRT (SEQ ID NO: 58), ITWNGGST (SEQ ID NO: 59), AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184),

RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYYADSVKG (SEQ ID NO: 187), FISGGGTTTYADSVKG (SEQ ID NO: 188), RITGGGSTHYAESVKG (SEQ ID NO: 189), AISWSGGSTTYADPVKG (SEQ ID NO: 190), AISWSGSSAGYGDSVKG (SEQ ID NO: 191), AIRWSGGRTLYADSVKG (SEQ ID NO: 192), SITWNGGSTSYADSVKG (SEQ ID NO: 193), FVAAIDWNGRGTYYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIDRIATTT (SEQ ID NO: 196), FVAAITWNGGTTY (SEQ ID NO: 197), WVAFISGGGTTT (SEQ ID NO: 198), LVARITGGGSTH (SEQ ID NO: 199), FVAAISWSGGSTT (SEQ ID NO: 200), FVAAISWSGSSAG (SEQ ID NO: 201), FVAAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), AIDWNGRGTYYRY (SEQ ID NO: 204), RINGGGITH (SEQ ID NO: 205), FIDRIATTT (SEQ ID NO: 206), AITWNGGTTY (SEQ ID NO: 207), FISGGGTTT (SEQ ID NO: 208), RITGGGSTH (SEQ ID NO: 209), AISWSGGSTT (SEQ ID NO: 210), AISWSGSSAG (SEQ ID NO: 211), AIRWSGGRTL (SEQ ID NO: 212), or SITWNGGSTS (SEQ ID NO: 213);

c) a CDR1 sequence of SYRMG (SEQ ID NO: 1), INVMG (SEQ ID NO: 2), SNAMG (SEQ ID NO: 3), SYAMG (SEQ ID NO: 4), SDAMG (SEQ ID NO: 5), INVMG (SEQ ID NO: 6), TYRMG (SEQ ID NO: 7), RYAMG (SEQ ID NO: 8), FTTYRMG (SEQ ID NO: 258), TYRMG (SEQ ID NO: 259), FNTYAMG (SEQ ID NO: 9), GLTFSSY (SEQ ID NO: 10), GSIFSIN (SEQ ID NO: 11), GTSVSSN (SEQ ID NO: 12), GRTFSSY (SEQ ID NO: 13), GSSVSSD (SEQ ID NO: 14), RSIGSIN (SEQ ID NO: 15), GRTFSTY (SEQ ID NO: 16), GFTFTRY (SEQ ID NO: 17), GRTFTTY (SEQ ID NO: 18), GRTLSFNTY (SEQ ID NO: 19), GLTFSSYR (SEQ ID NO: 20), GSIFSINV (SEQ ID NO: 21), GTSVSSNA (SEQ ID NO: 22), GRTFSSYA (SEQ ID NO: 23), GSSVSSDA (SEQ ID NO: 24), RSIGSINV (SEQ ID NO: 25), GRTFSTYR (SEQ ID NO: 26), GFTFTRYA (SEQ ID NO: 27), GRTFTTYR (SEQ ID NO: 28), GRTLSFNTYA (SEQ ID NO: 29), GLTFSSYRMG (SEQ ID NO: 154), GSIFSINVMG (SEQ ID NO: 155), GTSVSSNAMG (SEQ ID NO: 156), GRTFSSYAMG (SEQ ID NO: 157), GSSVSSDAMG (SEQ ID NO: 158), RSIGSINVMG (SEQ ID NO: 159), GRTFSTYRMG (SEQ ID NO: 160), GFTFTRYAMG (SEQ ID NO: 161), GRTFTTYRMG (SEQ ID NO: 162), GRTLSFNTYAMG (SEQ ID NO: 163), SSYRMG (SEQ ID NO: 164), SINVMG (SEQ ID NO: 165), SSNAMG (SEQ ID NO: 166),

SSYAMG (SEQ ID NO: 167), SSDAMG (SEQ ID NO: 168), SINVMG (SEQ ID NO: 169), STYRMG (SEQ ID NO: 170), TRYAMG (SEQ ID NO: 171), TTYRMG (SEQ ID NO: 172), SFNTYAMG (SEQ ID NO: 173), GLTFSSYRMG (SEQ ID NO: 174), GSIFSINVMG (SEQ ID NO: 175), GTSVSSNAMG (SEQ ID NO: 176), GRTFSSYAMG (SEQ ID NO: 177), GSSVSSDAMG (SEQ ID NO: 178), RSIGSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182), or GRTLSFNTYAMG (SEQ ID NO: 183);

d) a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence selected from the group consisting of:

i) VHH1:

1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60);
2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYY (SEQ ID NO: 40) or WNGRGTY (SEQ ID NO: 260), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 71) or SIDLNWYGGMD (SEQ ID NO: 272);
3) the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYY (SEQ ID NO: 50) or IDWNGRGTYYR (SEQ ID NO: 270), and the CDR3 sequence of CAAGSIDLNWYGGMDY (SEQ ID NO: 82) or AAGSIDLNWYGGMDY (SEQ ID NO: 283);
4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);
5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYYRY (SEQ ID NO: 194), and the CDR3 sequence of AAGSIDLNWYGGMD (SEQ ID NO: 225); or
6) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYYRY (SEQ ID NO: 204), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 236);

ii) VHH2:

1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 61);
2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYY (SEQ ID NO: 40) or WNGRGTY (SEQ ID NO: 260), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 72) or TVLTDPRVLNEYA (SEQ ID NO: 273);
3) the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYY (SEQ ID NO: 50) or IDWNGRGTYYR (SEQ ID NO: 270), and the CDR3 sequence of CAATTVLTDPRVLNEYAT (SEQ ID NO: 83) or AATTVLTDPRVLNEYAT (SEQ ID NO: 284);
4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);
5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYYRY (SEQ ID NO: 194), and the CDR3 sequence of AATTVLTDPRVLNEYA (SEQ ID NO: 226); or
6) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYYRY (SEQ ID NO: 204), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 237);

iii) VHH3:

1) the CDR1 sequence of INVMG (SEQ ID NO: 2), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 31), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 62);
2) the CDR1 sequence of GSIFSIN (SEQ ID NO: 11), the CDR2 sequence of NGGGI (SEQ ID NO: 41) or GGG (SEQ ID NO: 261), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 73) or VFGSSGYVET (SEQ ID NO: 274);
3) the CDR1 sequence of GSIFSINV (SEQ ID NO: 21), the CDR2 sequence of INGGGIT (SEQ ID NO: 51), and the CDR3 sequence of KADVFGSSGYVETY (SEQ ID NO: 84);

4) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 155), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 185), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 216);
5) the CDR1 sequence of SINVMG (SEQ ID NO: 165), the CDR2 sequence of LVARINGGGITH (SEQ ID NO: 195), and the CDR3 sequence of KADVFGSSGYVET (SEQ ID NO: 227); or
6) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 175), the CDR2 sequence of RINGGGITH (SEQ ID NO: 205), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 238);

iv) VHH4:

1) the CDR1 sequence of SNAMG (SEQ ID NO: 3), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), and the CDR3 sequence of PLTAR (SEQ ID NO: 63);
2) the CDR1 sequence of GTSVSSN (SEQ ID NO: 12), the CDR2 sequence of DRIAT (SEQ ID NO: 42) or RIA (SEQ ID NO: 262), and the CDR3 sequence of PLTAR (SEQ ID NO: 74) or LTA (SEQ ID NO: 275);
3) the CDR1 sequence of GTSVSSNA (SEQ ID NO: 22), the CDR2 sequence of IDRIATT (SEQ ID NO: 52), and the CDR3 sequence of NHPLTAR (SEQ ID NO: 85);
4) the CDR1 sequence of GTSVSSNAMG (SEQ ID NO: 156), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 186), and the CDR3 sequence of PLTAR (SEQ ID NO: 217);
5) the CDR1 sequence of SSNAMG (SEQ ID NO: 166), the CDR2 sequence of WVGFIDRIATTT (SEQ ID NO: 196), and the CDR3 sequence of NHPLTA (SEQ ID NO: 228); or
6) the CDR1 sequence of GTSVSSNAMG (SEQ ID NO: 176), the CDR2 sequence of FIDRIATTT (SEQ ID NO: 206), and the CDR3 sequence of PLTAR (SEQ ID NO: 239);

v) VHH5:

1) the CDR1 sequence of SYAMG (SEQ ID NO: 4), the CDR2 sequence of AITWNGGTTYYADSVKG (SEQ ID NO: 33), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 64);
2) the CDR1 sequence of GRTFSSY (SEQ ID NO: 13), the CDR2 sequence of TWNGGT (SEQ ID NO: 43) or WNGG (SEQ ID NO: 263), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 75) or PFNQG (SEQ ID NO: 276);
3) the CDR1 sequence of GRTFSSYA (SEQ ID NO: 23), the CDR2 sequence of ITWNGGTT (SEQ ID NO: 53), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 86);
4) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 157), the CDR2 sequence of AITWNGGTTYYADSVKG (SEQ ID NO: 187), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 218);
5) the CDR1 sequence of SSYAMG (SEQ ID NO: 167), the CDR2 sequence of FVAAITWNGGTTY (SEQ ID NO: 197), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 229); or
6) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 177), the CDR2 sequence of AITWNGGTTY (SEQ ID NO: 207), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 240);

vi) VHH6:

1) the CDR1 sequence of SDAMG (SEQ ID NO: 5), the CDR2 sequence of FISGGGTTTYADSVKG (SEQ ID NO: 34), and the CDR3 sequence of PLTSR (SEQ ID NO: 65);
2) the CDR1 sequence of GSSVSSD (SEQ ID NO: 14), the CDR2 sequence of SGGGT (SEQ ID NO: 44) or GGG (SEQ ID NO: 264), and the CDR3 sequence of PLTSR (SEQ ID NO: 76) or LTS (SEQ ID NO: 277);
3) the CDR1 sequence of GSSVSSDA (SEQ ID NO: 24), the CDR2 sequence of ISGGGTT (SEQ ID NO: 54), and the CDR3 sequence of NHPLTSR (SEQ ID NO: 87);
4) the CDR1 sequence of GSSVSSDAMG (SEQ ID NO: 158), the CDR2 sequence of FISGGGTTTYADSVKG (SEQ ID NO: 188), and the CDR3 sequence of PLTSR (SEQ ID NO: 219);

5) the CDR1 sequence of SSDAMG (SEQ ID NO: 168), the CDR2 sequence of WVAFISGGGTTT (SEQ ID NO: 198), and the CDR3 sequence of NHPLTS (SEQ ID NO: 230); or

6) the CDR1 sequence of GSSVSSDAMG (SEQ ID NO: 178), the CDR2 sequence of FISGGGTTT (SEQ ID NO: 208), and the CDR3 sequence of PLTSR (SEQ ID NO: 241);

vii) VHH7:

1) the CDR1 sequence of INVMG (SEQ ID NO: 6), the CDR2 sequence of RITGGGSTHYAESVKG (SEQ ID NO: 35), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66);

2) the CDR1 sequence of RSIGSIN (SEQ ID NO: 15), the CDR2 sequence of TGGGS (SEQ ID NO: 45) or GGG (SEQ ID NO: 265), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77) or VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278);

3) the CDR1 sequence of RSIGSINV (SEQ ID NO: 25), the CDR2 sequence of ITGGGST (SEQ ID NO: 55), and the CDR3 sequence of ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88);

4) the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 159), the CDR2 sequence of RITGGGSTHYAESVKG (SEQ ID NO: 189), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220);

5) the CDR1 sequence of SINVMG (SEQ ID NO: 169), the CDR2 sequence of LVARITGGGSTH (SEQ ID NO: 199), and the CDR3 sequence of ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231); or

6) the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 179), the CDR2 sequence of RITGGGSTH (SEQ ID NO: 209), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242);

viii) VHH8:

1) the CDR1 sequence of TYRMG (SEQ ID NO: 7), the CDR2 sequence of AISWSGGSTTYADPVKG (SEQ ID NO: 36), and the CDR3 sequence of DQRGY (SEQ ID NO: 67) or QRGY (SEQ ID NO: 271);

2) the CDR1 sequence of GRTFSTY (SEQ ID NO: 16), the CDR2 sequence of SWSGGS (SEQ ID NO: 46) or WSGG (SEQ ID NO: 266), and the CDR3 sequence of DQRGY (SEQ ID NO: 78) or RG (SEQ ID NO: 279);
3) the CDR1 sequence of GRTFSTYR (SEQ ID NO: 26), the CDR2 sequence of ISWSGGST (SEQ ID NO: 56), and the CDR3 sequence of NDQRGY (SEQ ID NO: 89);
4) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 160), the CDR2 sequence of AISWSGGSTTYADPVKG (SEQ ID NO: 190), and the CDR3 sequence of QRGY (SEQ ID NO: 221);
5) the CDR1 sequence of STYRMG (SEQ ID NO: 170), the CDR2 sequence of FVAAISWSGGSTT (SEQ ID NO: 200), and the CDR3 sequence of NDQRG (SEQ ID NO: 232); or
6) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 180), the CDR2 sequence of AISWSGGSTT (SEQ ID NO: 210), and the CDR3 sequence of QRGY (SEQ ID NO: 243);

ix) VHH9:
1) the CDR1 sequence of RYAMG (SEQ ID NO: 8), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 37), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 68);
2) the CDR1 sequence of GFTFTRY (SEQ ID NO: 17), the CDR2 sequence of SWSGSS (SEQ ID NO: 47) or WSGS (SEQ ID NO: 267), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 79) or PFNQG (SEQ ID NO: 280);
3) the CDR1 sequence of GFTFTRYA (SEQ ID NO: 27), the CDR2 sequence of ISWSGSSA (SEQ ID NO: 57), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 90);
4) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 161), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 191), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 222);
5) the CDR1 sequence of TRYAMG (SEQ ID NO: 171), the CDR2 sequence of FVAAISWSGSSAG (SEQ ID NO: 201), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 233); or

6) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 181), the CDR2 sequence of AISWSGSSAG (SEQ ID NO: 211), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 244);

x) VHH10:

1) the CDR1 sequence of FTTYRMG (SEQ ID NO: 258) or TYRMG (SEQ ID NO: 259), the CDR2 sequence of AIRWSGGRTLYADSVKG (SEQ ID NO: 38), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69);
2) the CDR1 sequence of GRTFTTY (SEQ ID NO: 18), the CDR2 sequence of RWSGGR (SEQ ID NO: 48) or WSGG (SEQ ID NO: 268), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80) or LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281);
3) the CDR1 sequence of GRTFTTYR (SEQ ID NO: 28), the CDR2 sequence of IRWSGGRT (SEQ ID NO: 58), and the CDR3 sequence of AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91);
4) the CDR1 sequence of GRTFTTYRMG (SEQ ID NO: 162), the CDR2 sequence of AIRWSGGRTLYADSVKG (SEQ ID NO: 192), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223);
5) the CDR1 sequence of TTYRMG (SEQ ID NO: 172), the CDR2 sequence of FVAAIRWSGGRTL (SEQ ID NO: 202), and the CDR3 sequence of AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234); or
6) the CDR1 sequence of GRTFTTYRMG (SEQ ID NO: 182), the CDR2 sequence of AIRWSGGRTL (SEQ ID NO: 212), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245); and

xi) VHH11:

1) the CDR1 sequence of FNTYAMG (SEQ ID NO: 9), the CDR2 sequence of SITWNGGSTSYADSVKG (SEQ ID NO: 39), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 70);
2) the CDR1 sequence of GRTLSFNTY (SEQ ID NO: 19), the CDR2 sequence of TWNGGS (SEQ ID NO: 49) or WNGG (SEQ ID NO: 269), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 81) or RYYVSGTYFPAN (SEQ ID NO: 282);

3) the CDR1 sequence of GRTLSFNTYA (SEQ ID NO: 29), the CDR2 sequence of ITWNGGST (SEQ ID NO: 59), and the CDR3 sequence of AAARYYVSGTYFPANY (SEQ ID NO: 92);
4) the CDR1 sequence of GRTLSFNTYAMG (SEQ ID NO: 163), the CDR2 sequence of SITWNGGSTSYADSVKG (SEQ ID NO: 193), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 224);
5) the CDR1 sequence of SFNTYAMG (SEQ ID NO: 173), the CDR2 sequence of FVASITWNGGSTS (SEQ ID NO: 203), and the CDR3 sequence of AAARYYVSGTYFPAN (SEQ ID NO: 235); or
6) the CDR1 sequence of GRTLSFNTYAMG (SEQ ID NO: 183), the CDR2 sequence of SITWNGGSTS (SEQ ID NO: 213), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 246);

e) a framework derived from the framework of any of the single domain antibodies comprising the sequences of QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW NGRGTYYRYYADSVKGRSTISRDNAKNTMYLQMNSLKPEDTAVYYCAAGSIDL NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93), EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW NGRGTYYRYYADSVKGRSTISRDNAKNTVYLQMNSLKPEDTAVYYCAATTVLT DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94), QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG GITHYAESVKGRFTISRDNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET YWGQGTQVTVSS (SEQ ID NO: 95), EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR IATTTIATSVKGRFAITRDNAKNTVYLQMSGLKPEDTAVYYCNHPLTARWGQGT QVTVSS (SEQ ID NO: 96), QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITW NGGTTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCAADPFNQGY WGQGTQVTVSS (SEQ ID NO: 97), EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG GGTTTYADSVKGRFTISRDNTKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG

TQVTVSS (SEQ ID NO: 98),
EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNAKNTVYLQMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
SGGSTTYADPVKGRFTISRDNAKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),
EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
SGSSAGYGDSVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),
EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
SGGRTLYADSVKGRFTISRDNAKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

f) a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of SEQ ID NOS: 93-103; or

g) a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of SEQ ID NOS: 93-103.

19. The process of any one of claims 14 to 18, wherein the single domain antibody is:

a) genetically fused to the agent;

b) chemically conjugated to the agent; or

c) non-covalently bound to the agent.

20. The process of claim 19, further comprising a linker between the single domain antibody and the agent; wherein optionally, the linker:

a) is a polypeptide; or

b) is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQPQLQPQPNPTTESKSPK (SEQ ID NO: 130), (EAAAK)n (SEQ ID NO: 147), (GGGGS)n (SEQ ID NO: 148) and (GGGS)n (SEQ ID NO: 149), wherein n is an integer from 1 to 20.

21. The process of any one of claims 14 to 20, wherein the process does not inhibit pIgR-mediated transcytosis of IgA.

22. The process of claim 21, wherein the single domain antibody comprises:

a) a CDR1 sequence of SNAMG (SEQ ID NO: 3), INVMG (SEQ ID NO: 6), TYRMG (SEQ ID NO: 7), RYAMG (SEQ ID NO: 8), FTTYRMG (SEQ ID NO: 258), TYRMG (SEQ ID NO: 259), FNTYAMG (SEQ ID NO: 9), GTSVSSN (SEQ ID NO: 12), GRTFSSY (SEQ ID NO: 13), RSIGSIN (SEQ ID NO: 15), GRTFSTY (SEQ ID NO: 16), GFTFTRY (SEQ ID NO: 17), GRTFTTY (SEQ ID NO: 18), GRTLSFNTY (SEQ ID NO: 19), GTSVSSNA (SEQ ID NO: 22), RSIGSINV (SEQ ID NO: 25), GRTFSTYR (SEQ ID NO: 26), GFTFTRYA (SEQ ID NO: 27), GRTFTTYR (SEQ ID NO: 28), GRTLSFNTYA (SEQ ID NO: 29), GTSVSSNAMG (SEQ ID NO: 156), RSIGSINVMG (SEQ ID NO: 159), GRTFSTYRMG (SEQ ID NO: 160), GFTFTRYAMG (SEQ ID NO: 161), GRTFTTYRMG (SEQ ID NO: 162), GRTLSFNTYAMG (SEQ ID NO: 163), SSNAMG (SEQ ID NO: 166), SINVMG (SEQ ID NO: 169), STYRMG (SEQ ID NO: 170), TRYAMG (SEQ ID NO: 171), TTYRMG (SEQ ID NO: 172), SFNTYAMG (SEQ ID NO: 173), GTSVSSNAMG (SEQ ID NO: 176), RSIGSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182) or GRTLSFNTYAMG (SEQ ID NO: 183);

b) a CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), RITGGGSTHYAESVKG (SEQ ID NO: 35), AISWSGGSTTYADPVKG (SEQ ID NO: 36), AISWSGSSAGYGDSVKG (SEQ ID NO: 37), AIRWSGGRTLYADSVKG (SEQ ID NO: 38), SITWNGGSTSYADSVKG (SEQ ID NO: 39), DRIAT (SEQ ID NO: 42), RIA (SEQ ID NO: 262), TGGGS (SEQ ID NO: 45), GGG (SEQ ID NO: 265), SWSGGS (SEQ ID NO: 46), WSGG (SEQ ID NO: 266), SWSGSS (SEQ ID NO: 47), WSGS (SEQ ID NO: 267), RWSGGR (SEQ ID NO: 48), WSGG (SEQ ID NO: 268), TWNGGS (SEQ ID NO:

49), WNGG (SEQ ID NO: 269), IDRIATT (SEQ ID NO: 52), ITGGGST (SEQ ID NO: 55), ISWSGGST (SEQ ID NO: 56), ISWSGSSA (SEQ ID NO: 57), IRWSGGRT (SEQ ID NO: 58), ITWNGGST (SEQ ID NO: 59), FIDRIATTTIATSVKG (SEQ ID NO: 186), RITGGGSTHYAESVKG (SEQ ID NO: 189), AISWSGGSTTYADPVKG (SEQ ID NO: 190), AISWSGSSAGYGDSVKG (SEQ ID NO: 191), AIRWSGGRTLYADSVKG (SEQ ID NO: 192), SITWNGGSTSYADSVKG (SEQ ID NO: 193), WVGFIDRIATTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVAAISWSGGSTT (SEQ ID NO: 200), FVAAISWSGSSAG (SEQ ID NO: 201), FVAAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), FIDRIATTT (SEQ ID NO: 206), RITGGGSTH (SEQ ID NO: 209), AISWSGGSTT (SEQ ID NO: 210), AISWSGSSAG (SEQ ID NO: 211), AIRWSGGRTL (SEQ ID NO: 212), SITWNGGSTS (SEQ ID NO: 213); or

c) a CDR3 sequence of PLTAR (SEQ ID NO: 63), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66), DQRGY (SEQ ID NO: 67), QRGY (SEQ ID NO: 271), DPFNQGY (SEQ ID NO: 68), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69), ARYYVSGTYFPANY (SEQ ID NO: 70), PLTAR (SEQ ID NO: 74), LTA (SEQ ID NO: 275), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278), DQRGY (SEQ ID NO: 78), RG (SEQ ID NO: 279), DPFNQGY (SEQ ID NO: 79), PFNQG (SEQ ID NO: 280), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80), LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281), ARYYVSGTYFPANY (SEQ ID NO: 81), RYYVSGTYFPAN (SEQ ID NO: 282), NHPLTAR (SEQ ID NO: 85), ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRGY (SEQ ID NO: 89), AADPFNQGY (SEQ ID NO: 90), AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91), AAARYYVSGTYFPANY (SEQ ID NO: 92), PLTAR (SEQ ID NO: 217), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220), QRGY (SEQ ID NO: 221), DPFNQGY (SEQ ID NO: 222), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223), ARYYVSGTYFPANY (SEQ ID NO: 224), NHPLTA (SEQ ID NO: 228), ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRG (SEQ ID NO: 232), AADPFNQG (SEQ ID NO: 233), AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234), AAARYYVSGTYFPAN (SEQ ID NO: 235), PLTAR (SEQ ID NO: 239), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242), QRGY (SEQ ID NO: 243),

DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246).

23. A process comprising steps for providing a molecule to a subject; wherein optionally, the molecule comprises an agent and a single domain antibody that binds to pIgR.

24. The process of claim 23, wherein:

a) the agent is an antibody or fragment thereof, a peptide, a vaccine, a small molecule, a polynucleotide, a radioisotope, a toxin, an enzyme, an anticoagulant, a hormone, a cytokine, an anti-inflammatory molecule, an RNAi, an antibiotic, or an antibody-antibiotic conjugate; or
b) the single domain antibody is genetically fused or chemically conjugated to the agent.

25. A system for providing a molecule to lamina propria of a subject, comprising a molecule suitable to be administered to the subject, the molecule comprising an agent and a single domain antibody that binds to pIgR, wherein the molecule is to be administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery, or a combination thereof.

26. The system of claim 25, wherein the agent is a:

a) diabetes medication; optionally wherein the diabetes medication is selected from a group consisting of insulin, glucagon-like-peptide-1, insulin-mimic peptides, and glucagon-like-peptide-1-mimic peptides;
b) peptide or an antibody or a fragment thereof; optionally wherein the antibody or fragment thereof is selected from a group consisting of an anti-TNF-alpha antibody or a fragment thereof, an anti-IL23 antibody or a fragment thereof, and an antibody that binds to a receptor of IL23 or a fragment thereof; or
c) vaccine; optionally wherein the vaccine is for preventing an infection selected from a group consisting of Vibrio, Cholera, Typhoid, Rotavirus, Tuberculosis, HIV, Flu, Ebola, and Sendai.

27. The system of claim 25 or claim 26, wherein the single domain antibody:

a) binds to:
   i) an extracellular domain 1, an extracellular domain 2, an extracellular domain 1-2, an extracellular domain 3, an extracellular domain 2-3, an extracellular domain 4-5, or an extracellular domain 5 of pIgR;
   ii) an extracellular domain 1 of pIgR;
   iii) an extracellular domain 2 of pIgR;
   iv) an extracellular domain 1-2 of pIgR;
   v) an extracellular domain 3 of pIgR;
   vi) an extracellular domain 2-3 of pIgR;
   vii) an extracellular domain 4-5 of pIgR; or
   viii) an extracellular domain 5 of pIgR;
b) competes with IgA binding to the pIgR; or
c) promotes IgA binding to the pIgR.

28. The system of any one of claims 25 to 27, wherein:
a) the K_D of the binding of the single domain antibody to pIgR:
   i) is from about 4 to about 525 nM;
   ii) is less than about 50 nM; or
   iii) is from about 4 to about 34 nM;
b) the T_m of the single domain antibody:
   i) is from about 53 to about 77 °C; or
   ii) is from 53.9 to 76.4 °C;
c) pIgR is:
   i) human pIgR; or
   ii) mouse pIgR;
   or
d) the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

29. The system of any one of claims 25 to 28, wherein the single domain antibody comprises:

a) a CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60), TTVLTDPRVLNEYAT (SEQ ID NO: 61), DVFGSSGYVETY (SEQ ID NO: 62), PLTAR (SEQ ID NO: 63), DPFNQGY (SEQ ID NO: 64), PLTSR (SEQ ID NO: 65), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66), DQRGY (SEQ ID NO: 67), QRGY (SEQ ID NO: 271), DPFNQGY (SEQ ID NO: 68), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69), ARYYVSGTYFPANY (SEQ ID NO: 70), GSIDLNWYGGMDY (SEQ ID NO: 71), SIDLNWYGGMD (SEQ ID NO: 272), TTVLTDPRVLNEYAT (SEQ ID NO: 72), TVLTDPRVLNEYA (SEQ ID NO: 273), DVFGSSGYVETY (SEQ ID NO: 73), VFGSSGYVET (SEQ ID NO: 274), PLTAR (SEQ ID NO: 74), LTA (SEQ ID NO: 275), DPFNQGY (SEQ ID NO: 75), PFNQG (SEQ ID NO: 276), PLTSR (SEQ ID NO: 76), LTS (SEQ ID NO: 277), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278), DQRGY (SEQ ID NO: 78), RG (SEQ ID NO: 279), DPFNQGY (SEQ ID NO: 79), PFNQG (SEQ ID NO: 280), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80), LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281), ARYYVSGTYFPANY (SEQ ID NO: 81), RYYVSGTYFPAN (SEQ ID NO: 282), CAAGSIDLNWYGGMDY (SEQ ID NO: 82), AAGSIDLNWYGGMDY (SEQ ID NO: 283), CAATTVLTDPRVLNEYAT (SEQ ID NO: 83), AATTVLTDPRVLNEYAT (SEQ ID NO: 284), KADVFGSSGYVETY (SEQ ID NO: 84), NHPLTAR (SEQ ID NO: 85), AADPFNQGY (SEQ ID NO: 86), NHPLTSR (SEQ ID NO: 87), ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRGY (SEQ ID NO: 89), AADPFNQGY (SEQ ID NO: 90), AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91), AAARYYVSGTYFPANY (SEQ ID NO: 92), GSIDLNWYGGMDY (SEQ ID NO: 214), TTVLTDPRVLNEYAT (SEQ ID NO: 215), DVFGSSGYVETY (SEQ ID NO: 216), PLTAR (SEQ ID NO: 217), DPFNQGY (SEQ ID NO: 218), PLTSR (SEQ ID NO: 219), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220), QRGY (SEQ ID NO: 221), DPFNQGY (SEQ ID NO: 222), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223), ARYYVSGTYFPANY (SEQ ID NO: 224), AAGSIDLNWYGGMD (SEQ ID NO: 225), AATTVLTDPRVLNEYA (SEQ ID NO: 226), KADVFGSSGYVET (SEQ ID NO: 227), NHPLTA (SEQ ID NO: 228), AADPFNQG (SEQ ID NO: 229), NHPLTS (SEQ ID NO: 230), ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRG (SEQ ID NO: 232), AADPFNQG (SEQ ID NO: 233), AADLAEYSGTYSSPADSPAGYD (SEQ ID NO:

234), AAARYYVSGTYFPAN (SEQ ID NO: 235), GSIDLNWYGGMDY (SEQ ID NO: 236), TTVLTDPRVLNEYAT (SEQ ID NO: 237), DVFGSSGYVETY (SEQ ID NO: 238), PLTAR (SEQ ID NO: 239), DPFNQGY (SEQ ID NO: 240), PLTSR (SEQ ID NO: 241), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242), QRGY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246);

b) a CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYYADSVKG (SEQ ID NO: 33), FISGGGTTTYADSVKG (SEQ ID NO: 34), RITGGGSTHYAESVKG (SEQ ID NO: 35), AISWSGGSTTYADPVKG (SEQ ID NO: 36), AISWSGSSAGYGDSVKG (SEQ ID NO: 37), AIRWSGGRTLYADSVKG (SEQ ID NO: 38), SITWNGGSTSYADSVKG (SEQ ID NO: 39), DWNGRGTYY (SEQ ID NO: 40), WNGRGTY (SEQ ID NO: 260), NGGGI (SEQ ID NO: 41), GGG (SEQ ID NO: 261), DRIAT (SEQ ID NO: 42), RIA (SEQ ID NO: 262), TWNGGT (SEQ ID NO: 43), WNGG (SEQ ID NO: 263), SGGGT (SEQ ID NO: 44), GGG (SEQ ID NO: 264), TGGGS (SEQ ID NO: 45), GGG (SEQ ID NO: 265), SWSGGS (SEQ ID NO: 46), WSGG (SEQ ID NO: 266), SWSGSS (SEQ ID NO: 47), WSGS (SEQ ID NO: 267), RWSGGR (SEQ ID NO: 48), WSGG (SEQ ID NO: 268), TWNGGS (SEQ ID NO: 49), WNGG (SEQ ID NO: 269), IDWNGRGTYY (SEQ ID NO: 50), IDWNGRGTYYR (SEQ ID NO: 270), INGGGIT (SEQ ID NO: 51), IDRIATT (SEQ ID NO: 52), ITWNGGTT (SEQ ID NO: 53), ISGGGTT (SEQ ID NO: 54), ITGGGST (SEQ ID NO: 55), ISWSGGST (SEQ ID NO: 56), ISWSGSSA (SEQ ID NO: 57), IRWSGGRT (SEQ ID NO: 58), ITWNGGST (SEQ ID NO: 59), AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYYADSVKG (SEQ ID NO: 187), FISGGGTTTYADSVKG (SEQ ID NO: 188), RITGGGSTHYAESVKG (SEQ ID NO: 189), AISWSGGSTTYADPVKG (SEQ ID NO: 190), AISWSGSSAGYGDSVKG (SEQ ID NO: 191), AIRWSGGRTLYADSVKG (SEQ ID NO: 192), SITWNGGSTSYADSVKG (SEQ ID NO: 193), FVAAIDWNGRGTYYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIDRIATTT (SEQ ID NO: 196), FVAAITWNGGTTY (SEQ ID NO: 197), WVAFISGGGTTT (SEQ ID NO: 198), LVARITGGGSTH (SEQ ID NO: 199),

FVAAISWSGGSTT (SEQ ID NO: 200), FVAAISWSGSSAG (SEQ ID NO: 201), FVAAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), AIDWNGRGTYYRY (SEQ ID NO: 204), RINGGGITH (SEQ ID NO: 205), FIDRIATTT (SEQ ID NO: 206), AITWNGGTTY (SEQ ID NO: 207), FISGGGTTT (SEQ ID NO: 208), RITGGGSTH (SEQ ID NO: 209), AISWSGGSTT (SEQ ID NO: 210), AISWSGSSAG (SEQ ID NO: 211), AIRWSGGRTL (SEQ ID NO: 212), or SITWNGGSTS (SEQ ID NO: 213);

c) a CDR1 sequence of SYRMG (SEQ ID NO: 1), INVMG (SEQ ID NO: 2), SNAMG (SEQ ID NO: 3), SYAMG (SEQ ID NO: 4), SDAMG (SEQ ID NO: 5), INVMG (SEQ ID NO: 6), TYRMG (SEQ ID NO: 7), RYAMG (SEQ ID NO: 8), FTTYRMG (SEQ ID NO: 258), TYRMG (SEQ ID NO: 259), FNTYAMG (SEQ ID NO: 9), GLTFSSY (SEQ ID NO: 10), GSIFSIN (SEQ ID NO: 11), GTSVSSN (SEQ ID NO: 12), GRTFSSY (SEQ ID NO: 13), GSSVSSD (SEQ ID NO: 14), RSIGSIN (SEQ ID NO: 15), GRTFSTY (SEQ ID NO: 16), GFTFTRY (SEQ ID NO: 17), GRTFTTY (SEQ ID NO: 18), GRTLSFNTY (SEQ ID NO: 19), GLTFSSYR (SEQ ID NO: 20), GSIFSINV (SEQ ID NO: 21), GTSVSSNA (SEQ ID NO: 22), GRTFSSYA (SEQ ID NO: 23), GSSVSSDA (SEQ ID NO: 24), RSIGSINV (SEQ ID NO: 25), GRTFSTYR (SEQ ID NO: 26), GFTFTRYA (SEQ ID NO: 27), GRTFTTYR (SEQ ID NO: 28), GRTLSFNTYA (SEQ ID NO: 29), GLTFSSYRMG (SEQ ID NO: 154), GSIFSINVMG (SEQ ID NO: 155), GTSVSSNAMG (SEQ ID NO: 156), GRTFSSYAMG (SEQ ID NO: 157), GSSVSSDAMG (SEQ ID NO: 158), RSIGSINVMG (SEQ ID NO: 159), GRTFSTYRMG (SEQ ID NO: 160), GFTFTRYAMG (SEQ ID NO: 161), GRTFTTYRMG (SEQ ID NO: 162), GRTLSFNTYAMG (SEQ ID NO: 163), SSYRMG (SEQ ID NO: 164), SINVMG (SEQ ID NO: 165), SSNAMG (SEQ ID NO: 166), SSYAMG (SEQ ID NO: 167), SSDAMG (SEQ ID NO: 168), SINVMG (SEQ ID NO: 169), STYRMG (SEQ ID NO: 170), TRYAMG (SEQ ID NO: 171), TTYRMG (SEQ ID NO: 172), SFNTYAMG (SEQ ID NO: 173), GLTFSSYRMG (SEQ ID NO: 174), GSIFSINVMG (SEQ ID NO: 175), GTSVSSNAMG (SEQ ID NO: 176), GRTFSSYAMG (SEQ ID NO: 177), GSSVSSDAMG (SEQ ID NO: 178), RSIGSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182), or GRTLSFNTYAMG (SEQ ID NO: 183);

d) a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence selected from the group consisting of:

i) VHH1:

1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60);
2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYY (SEQ ID NO: 40) or WNGRGTY (SEQ ID NO: 260), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 71) or SIDLNWYGGMD (SEQ ID NO: 272);
3) the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYY (SEQ ID NO: 50) or IDWNGRGTYYR (SEQ ID NO: 270), and the CDR3 sequence of CAAGSIDLNWYGGMDY (SEQ ID NO: 82) or AAGSIDLNWYGGMDY (SEQ ID NO: 283);
4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);
5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYYRY (SEQ ID NO: 194), and the CDR3 sequence of AAGSIDLNWYGGMD (SEQ ID NO: 225); or
6) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYYRY (SEQ ID NO: 204), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 236);

ii) VHH2:

1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 61);
2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYY (SEQ ID NO: 40) or WNGRGTY (SEQ ID NO: 260), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 72) or TVLTDPRVLNEYA (SEQ ID NO: 273);

3) the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYY (SEQ ID NO: 50) or IDWNGRGTYYR (SEQ ID NO: 270), and the CDR3 sequence of CAATTVLTDPRVLNEYAT (SEQ ID NO: 83) or AATTVLTDPRVLNEYAT (SEQ ID NO: 284);
4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);
5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYYRY (SEQ ID NO: 194), and the CDR3 sequence of AATTVLTDPRVLNEYA (SEQ ID NO: 226); or
6) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYYRY (SEQ ID NO: 204), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 237);

iii) VHH3:

1) the CDR1 sequence of INVMG (SEQ ID NO: 2), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 31), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 62);
2) the CDR1 sequence of GSIFSIN (SEQ ID NO: 11), the CDR2 sequence of NGGGI (SEQ ID NO: 41) or GGG (SEQ ID NO: 261), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 73) or VFGSSGYVET (SEQ ID NO: 274);
3) the CDR1 sequence of GSIFSINV (SEQ ID NO: 21), the CDR2 sequence of INGGGIT (SEQ ID NO: 51), and the CDR3 sequence of KADVFGSSGYVETY (SEQ ID NO: 84);
4) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 155), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 185), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 216);
5) the CDR1 sequence of SINVMG (SEQ ID NO: 165), the CDR2 sequence of LVARINGGGITH (SEQ ID NO: 195), and the CDR3 sequence of KADVFGSSGYVET (SEQ ID NO: 227); or

6) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 175), the CDR2 sequence of RINGGGITH (SEQ ID NO: 205), and the CDR3 sequence of DVFGSSGYVETY (SEQ ID NO: 238);

iv) VHH4:

1) the CDR1 sequence of SNAMG (SEQ ID NO: 3), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), and the CDR3 sequence of PLTAR (SEQ ID NO: 63);
2) the CDR1 sequence of GTSVSSN (SEQ ID NO: 12), the CDR2 sequence of DRIAT (SEQ ID NO: 42) or RIA (SEQ ID NO: 262), and the CDR3 sequence of PLTAR (SEQ ID NO: 74) or LTA (SEQ ID NO: 275);
3) the CDR1 sequence of GTSVSSNA (SEQ ID NO: 22), the CDR2 sequence of IDRIATT (SEQ ID NO: 52), and the CDR3 sequence of NHPLTAR (SEQ ID NO: 85);
4) the CDR1 sequence of GTSVSSNAMG (SEQ ID NO: 156), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 186), and the CDR3 sequence of PLTAR (SEQ ID NO: 217);
5) the CDR1 sequence of SSNAMG (SEQ ID NO: 166), the CDR2 sequence of WVGFIDRIATTT (SEQ ID NO: 196), and the CDR3 sequence of NHPLTA (SEQ ID NO: 228); or
6) the CDR1 sequence of GTSVSSNAMG (SEQ ID NO: 176), the CDR2 sequence of FIDRIATTT (SEQ ID NO: 206), and the CDR3 sequence of PLTAR (SEQ ID NO: 239);

v) VHH5:

1) the CDR1 sequence of SYAMG (SEQ ID NO: 4), the CDR2 sequence of AITWNGGTTYYADSVKG (SEQ ID NO: 33), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 64);
2) the CDR1 sequence of GRTFSSY (SEQ ID NO: 13), the CDR2 sequence of TWNGGT (SEQ ID NO: 43) or WNGG (SEQ ID NO: 263), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 75) or PFNQG (SEQ ID NO: 276);

3) the CDR1 sequence of GRTFSSYA (SEQ ID NO: 23), the CDR2 sequence of ITWNGGTT (SEQ ID NO: 53), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 86);
4) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 157), the CDR2 sequence of AITWNGGTTYYADSVKG (SEQ ID NO: 187), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 218);
5) the CDR1 sequence of SSYAMG (SEQ ID NO: 167), the CDR2 sequence of FVAAITWNGGTTY (SEQ ID NO: 197), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 229); or
6) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 177), the CDR2 sequence of AITWNGGTTY (SEQ ID NO: 207), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 240);

vi) VHH6:
1) the CDR1 sequence of SDAMG (SEQ ID NO: 5), the CDR2 sequence of FISGGGTTTYADSVKG (SEQ ID NO: 34), and the CDR3 sequence of PLTSR (SEQ ID NO: 65);
2) the CDR1 sequence of GSSVSSD (SEQ ID NO: 14), the CDR2 sequence of SGGGT (SEQ ID NO: 44) or GGG (SEQ ID NO: 264), and the CDR3 sequence of PLTSR (SEQ ID NO: 76) or LTS (SEQ ID NO: 277);
3) the CDR1 sequence of GSSVSSDA (SEQ ID NO: 24), the CDR2 sequence of ISGGGTT (SEQ ID NO: 54), and the CDR3 sequence of NHPLTSR (SEQ ID NO: 87);
4) the CDR1 sequence of GSSVSSDAMG (SEQ ID NO: 158), the CDR2 sequence of FISGGGTTTYADSVKG (SEQ ID NO: 188), and the CDR3 sequence of PLTSR (SEQ ID NO: 219);
5) the CDR1 sequence of SSDAMG (SEQ ID NO: 168), the CDR2 sequence of WVAFISGGGTTT (SEQ ID NO: 198), and the CDR3 sequence of NHPLTS (SEQ ID NO: 230); or
6) the CDR1 sequence of GSSVSSDAMG (SEQ ID NO: 178), the CDR2 sequence of FISGGGTTT (SEQ ID NO: 208), and the CDR3 sequence of PLTSR (SEQ ID NO: 241);

vii) VHH7:

1) the CDR1 sequence of INVMG (SEQ ID NO: 6), the CDR2 sequence of RITGGGSTHYAESVKG (SEQ ID NO: 35), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66);
2) the CDR1 sequence of RSIGSIN (SEQ ID NO: 15), the CDR2 sequence of TGGGS (SEQ ID NO: 45) or GGG (SEQ ID NO: 265), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77) or VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278);
3) the CDR1 sequence of RSIGSINV (SEQ ID NO: 25), the CDR2 sequence of ITGGGST (SEQ ID NO: 55), and the CDR3 sequence of ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88);
4) the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 159), the CDR2 sequence of RITGGGSTHYAESVKG (SEQ ID NO: 189), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220);
5) the CDR1 sequence of SINVMG (SEQ ID NO: 169), the CDR2 sequence of LVARITGGGSTH (SEQ ID NO: 199), and the CDR3 sequence of ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231); or
6) the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 179), the CDR2 sequence of RITGGGSTH (SEQ ID NO: 209), and the CDR3 sequence of MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242);

viii) VHH8:

1) the CDR1 sequence of TYRMG (SEQ ID NO: 7), the CDR2 sequence of AISWSGGSTTYADPVKG (SEQ ID NO: 36), and the CDR3 sequence of DQRGY (SEQ ID NO: 67) or QRGY (SEQ ID NO: 271);
2) the CDR1 sequence of GRTFSTY (SEQ ID NO: 16), the CDR2 sequence of SWSGGS (SEQ ID NO: 46) or WSGG (SEQ ID NO: 266), and the CDR3 sequence of DQRGY (SEQ ID NO: 78) or RG (SEQ ID NO: 279);
3) the CDR1 sequence of GRTFSTYR (SEQ ID NO: 26), the CDR2 sequence of ISWSGGST (SEQ ID NO: 56), and the CDR3 sequence of NDQRGY (SEQ ID NO: 89);

4) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 160), the CDR2 sequence of AISWSGGSTTYADPVKG (SEQ ID NO: 190), and the CDR3 sequence of QRGY (SEQ ID NO: 221);
5) the CDR1 sequence of STYRMG (SEQ ID NO: 170), the CDR2 sequence of FVAAISWSGGSTT (SEQ ID NO: 200), and the CDR3 sequence of NDQRG (SEQ ID NO: 232); or
6) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 180), the CDR2 sequence of AISWSGGSTT (SEQ ID NO: 210), and the CDR3 sequence of QRGY (SEQ ID NO: 243);

ix) VHH9:

1) the CDR1 sequence of RYAMG (SEQ ID NO: 8), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 37), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 68);
2) the CDR1 sequence of GFTFTRY (SEQ ID NO: 17), the CDR2 sequence of SWSGSS (SEQ ID NO: 47) or WSGS (SEQ ID NO: 267), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 79) or PFNQG (SEQ ID NO: 280);
3) the CDR1 sequence of GFTFTRYA (SEQ ID NO: 27), the CDR2 sequence of ISWSGSSA (SEQ ID NO: 57), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 90);
4) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 161), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 191), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 222);
5) the CDR1 sequence of TRYAMG (SEQ ID NO: 171), the CDR2 sequence of FVAAISWSGSSAG (SEQ ID NO: 201), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 233); or
6) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 181), the CDR2 sequence of AISWSGSSAG (SEQ ID NO: 211), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 244);

x) VHH10:

1) the CDR1 sequence of FTTYRMG (SEQ ID NO: 258) or TYRMG (SEQ ID NO: 259), the CDR2 sequence of AIRWSGGRTLYADSVKG (SEQ ID NO: 38), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69);
2) the CDR1 sequence of GRTFTTY (SEQ ID NO: 18), the CDR2 sequence of RWSGGR (SEQ ID NO: 48) or WSGG (SEQ ID NO: 268), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80) or LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281);
3) the CDR1 sequence of GRTFTTYR (SEQ ID NO: 28), the CDR2 sequence of IRWSGGRT (SEQ ID NO: 58), and the CDR3 sequence of AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91);
4) the CDR1 sequence of GRTFTTYRMG (SEQ ID NO: 162), the CDR2 sequence of AIRWSGGRTLYADSVKG (SEQ ID NO: 192), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223);
5) the CDR1 sequence of TTYRMG (SEQ ID NO: 172), the CDR2 sequence of FVAAIRWSGGRTL (SEQ ID NO: 202), and the CDR3 sequence of AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234); or
6) the CDR1 sequence of GRTFTTYRMG (SEQ ID NO: 182), the CDR2 sequence of AIRWSGGRTL (SEQ ID NO: 212), and the CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245); and

xi) VHH11:
1) the CDR1 sequence of FNTYAMG (SEQ ID NO: 9), the CDR2 sequence of SITWNGGSTSYADSVKG (SEQ ID NO: 39), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 70);
2) the CDR1 sequence of GRTLSFNTY (SEQ ID NO: 19), the CDR2 sequence of TWNGGS (SEQ ID NO: 49) or WNGG (SEQ ID NO: 269), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 81) or RYYVSGTYFPAN (SEQ ID NO: 282);
3) the CDR1 sequence of GRTLSFNTYA (SEQ ID NO: 29), the CDR2 sequence of ITWNGGST (SEQ ID NO: 59), and the CDR3 sequence of AAARYYVSGTYFPANY (SEQ ID NO: 92);

4) the CDR1 sequence of GRTLSFNTYAMG (SEQ ID NO: 163), the CDR2 sequence of SITWNGGSTSYADSVKG (SEQ ID NO: 193), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 224);
5) the CDR1 sequence of SFNTYAMG (SEQ ID NO: 173), the CDR2 sequence of FVASITWNGGSTS (SEQ ID NO: 203), and the CDR3 sequence of AAARYYVSGTYFPAN (SEQ ID NO: 235); or
6) the CDR1 sequence of GRTLSFNTYAMG (SEQ ID NO: 183), the CDR2 sequence of SITWNGGSTS (SEQ ID NO: 213), and the CDR3 sequence of ARYYVSGTYFPANY (SEQ ID NO: 246);

e) a framework derived from the framework of any of the single domain antibodies comprising the sequences of QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW NGRGTYYRYYADSVKGRSTISRDNAKNTMYLQMNSLKPEDTAVYYCAAGSIDL NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93), EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW NGRGTYYRYYADSVKGRSTISRDNAKNTVYLQMNSLKPEDTAVYYCAATTVLT DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94), QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG GITHYAESVKGRFTISRDNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET YWGQGTQVTVSS (SEQ ID NO: 95), EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR IATTTIATSVKGRFAITRDNAKNTVYLQMSGLKPEDTAVYYCNHPLTARWGQGT QVTVSS (SEQ ID NO: 96), QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITW NGGTTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCAADPFNQGY WGQGTQVTVSS (SEQ ID NO: 97), EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG GGTTTYADSVKGRFTISRDNTKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG TQVTVSS (SEQ ID NO: 98), EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG GGSTHYAESVKGRFTISRDNAKNTVYLQMNSLEPEDTAVYYCASMVNPIITAWG

TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
SGGSTTYADPVKGRFTISRDNAKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),
EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
SGSSAGYGDSVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),
EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
SGGRTLYADSVKGRFTISRDNAKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

f) a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of SEQ ID NOS: 93-103; or
g) a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of SEQ ID NOS: 93-103.

30. The system of any one of claims 25 to 29, wherein the single domain antibody:

a) is genetically fused to the agent;
b) is chemically conjugated to the agent; or
c) is non-covalently bound to the agent.

31. The system of claim 30, further comprising a linker between the single domain antibody and the agent; wherein optionally, the linker:

a) is a polypeptide; or
b) is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQPQLQPQPNPTTESKSPK (SEQ ID NO: 130), (EAAAK)n (SEQ ID NO: 147), (GGGGS)n (SEQ ID NO: 147) and (GGGS)n (SEQ ID NO: 149), wherein n is an integer from 1 to 20.

32. The system of any one of claims 25 to 31, wherein the system does not inhibit pIgR-mediated transcytosis of IgA.

33. The system of claim 32, wherein the single domain antibody comprises:

a) a CDR1 sequence of SNAMG (SEQ ID NO: 3), INVMG (SEQ ID NO: 6), TYRMG (SEQ ID NO: 7), RYAMG (SEQ ID NO: 8), FTTYRMG (SEQ ID NO: 258), TYRMG (SEQ ID NO: 259), FNTYAMG (SEQ ID NO: 9), GTSVSSN (SEQ ID NO: 12), GRTFSSY (SEQ ID NO: 13), RSIGSIN (SEQ ID NO: 15), GRTFSTY (SEQ ID NO: 16), GFTFTRY (SEQ ID NO: 17), GRTFTTY (SEQ ID NO: 18), GRTLSFNTY (SEQ ID NO: 19), GTSVSSNA (SEQ ID NO: 22), RSIGSINV (SEQ ID NO: 25), GRTFSTYR (SEQ ID NO: 26), GFTFTRYA (SEQ ID NO: 27), GRTFTTYR (SEQ ID NO: 28), GRTLSFNTYA (SEQ ID NO: 29), GTSVSSNAMG (SEQ ID NO: 156), RSIGSINVMG (SEQ ID NO: 159), GRTFSTYRMG (SEQ ID NO: 160), GFTFTRYAMG (SEQ ID NO: 161), GRTFTTYRMG (SEQ ID NO: 162), GRTLSFNTYAMG (SEQ ID NO: 163), SSNAMG (SEQ ID NO: 166), SINVMG (SEQ ID NO: 169), STYRMG (SEQ ID NO: 170), TRYAMG (SEQ ID NO: 171), TTYRMG (SEQ ID NO: 172), SFNTYAMG (SEQ ID NO: 173), GTSVSSNAMG (SEQ ID NO: 176), RSIGSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182) or GRTLSFNTYAMG (SEQ ID NO: 183);

b) a CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), RITGGGSTHYAESVKG (SEQ ID NO: 35), AISWSGGSTTYADPVKG (SEQ ID NO: 36), AISWSGSSAGYGDSVKG (SEQ ID NO: 37), AIRWSGGRTLYADSVKG (SEQ ID NO: 38), SITWNGGSTSYADSVKG (SEQ ID NO: 39), DRIAT (SEQ ID NO: 42), RIA (SEQ ID NO: 262), TGGGS (SEQ ID NO: 45), GGG (SEQ ID NO: 265), SWSGGS (SEQ ID NO: 46), WSGG (SEQ ID NO: 266), SWSGSS (SEQ ID NO: 47), WSGS (SEQ ID NO: 267), RWSGGR (SEQ ID NO: 48), WSGG (SEQ ID NO: 268), TWNGGS (SEQ ID NO: 49), WNGG (SEQ ID NO: 269), IDRIATT (SEQ ID NO: 52), ITGGGST (SEQ ID NO: 55), ISWSGGST (SEQ ID NO: 56), ISWSGSSA (SEQ ID NO: 57), IRWSGGRT (SEQ ID NO: 58), ITWNGGST (SEQ ID NO: 59), FIDRIATTTIATSVKG (SEQ ID NO: 186), RITGGGSTHYAESVKG (SEQ ID NO: 189), AISWSGGSTTYADPVKG (SEQ ID NO:

190), AISWSGSSAGYGDSVKG (SEQ ID NO: 191), AIRWSGGRTLYADSVKG (SEQ ID NO: 192), SITWNGGSTSYADSVKG (SEQ ID NO: 193), WVGFIDRIATTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVAAISWSGGSTT (SEQ ID NO: 200), FVAAISWSGSSAG (SEQ ID NO: 201), FVAAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), FIDRIATTT (SEQ ID NO: 206), RITGGGSTH (SEQ ID NO: 209), AISWSGGSTT (SEQ ID NO: 210), AISWSGSSAG (SEQ ID NO: 211), AIRWSGGRTL (SEQ ID NO: 212), SITWNGGSTS (SEQ ID NO: 213); or

c) a CDR3 sequence of PLTAR (SEQ ID NO: 63), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 66), DQRGY (SEQ ID NO: 67), QRGY (SEQ ID NO: 271), DPFNQGY (SEQ ID NO: 68), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 69), ARYYVSGTYFPANY (SEQ ID NO: 70), PLTAR (SEQ ID NO: 74), LTA (SEQ ID NO: 275), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPIITAWGTIGVREIPDYD (SEQ ID NO: 278), DQRGY (SEQ ID NO: 78), RG (SEQ ID NO: 279), DPFNQGY (SEQ ID NO: 79), PFNQG (SEQ ID NO: 280), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80), LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281), ARYYVSGTYFPANY (SEQ ID NO: 81), RYYVSGTYFPAN (SEQ ID NO: 282), NHPLTAR (SEQ ID NO: 85), ASMVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRGY (SEQ ID NO: 89), AADPFNQGY (SEQ ID NO: 90), AADLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 91), AAARYYVSGTYFPANY (SEQ ID NO: 92), PLTAR (SEQ ID NO: 217), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 220), QRGY (SEQ ID NO: 221), DPFNQGY (SEQ ID NO: 222), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 223), ARYYVSGTYFPANY (SEQ ID NO: 224), NHPLTA (SEQ ID NO: 228), ASMVNPIITAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRG (SEQ ID NO: 232), AADPFNQG (SEQ ID NO: 233), AADLAEYSGTYSSPADSPAGYD (SEQ ID NO: 234), AAARYYVSGTYFPAN (SEQ ID NO: 235), PLTAR (SEQ ID NO: 239), MVNPIITAWGTIGVREIPDYDY (SEQ ID NO: 242), QRGY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246).

34. A system comprising a means for providing a molecule to lamina propria of a subject; optionally wherein:

a) the molecule comprises an agent and a single domain antibody that binds to pIgR;
b) the agent is an antibody or fragment thereof, a peptide, a vaccine, a small molecule, a polynucleotide, a radioisotope, a toxin, an enzyme, an anticoagulant, a hormone, a cytokine, an anti-inflammatory molecule, an RNAi, an antibiotic, or an antibody-antibiotic conjugate; or
c) the single domain antibody is genetically fused or chemically conjugated to the agent.