

Claims

1. A VHH domain that binds to an extracellular domain of polymeric immunoglobulin receptor (pIgR).
2. The VHH domain of claim 1, wherein
 - a) the VHH domain binds to an:
 - i) extracellular domain 1 of pIgR;
 - ii) extracellular domain 2 of pIgR;
 - iii) extracellular domain 1-2 of pIgR;
 - iv) extracellular domain 3 of pIgR;
 - v) extracellular domain 2-3 of pIgR;
 - vi) extracellular domain 4-5 of pIgR; or
 - vii) extracellular domain 5 of pIgR;
 - b) the VHH domain competes with IgA binding to the pIgR; or
 - c) the VHH domain promotes IgA binding to the pIgR.
3. The VHH domain of claim 1 or claim 2, wherein:
 - a) pIgR is human pIgR;
 - b) pIgR is mouse pIgR; or
 - c) the VHH domain does not detectably bind to the amino acid sequence of:
EKAVADTRDQADGSRASVDSGSSEEQGGSSR (SEQ ID NO: 143);
EREIQNVGDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 144); or
EREIQNVRDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 145).
4. The VHH domain of any one of claims 1 to 3, wherein:
 - a) the K_D of the binding of the VHH domain to pIgR:
 - i) is from about 4 to about 525 nM;
 - ii) is less than about 50 nM; or
 - iii) from about 4 to about 34 nM;or
 - b) T_m of the VHH domain:

- i) is from about 53 to about 77 °C; or
- ii) is from 53.9 to 76.4 °C.

5. The VHH domain of any one of claims 1 to 4, wherein the VHH domain 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), AAARYYYVSGTYFPANY (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),

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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYADSVKG (SEQ ID NO: 33), FISGGGTTYADSVKG (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), DWNGRGTY (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), IDWNGRGTY (SEQ ID NO: 50), IDWNGRGTYR (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), AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (SEQ ID NO: 187), FISGGGTTYADSVKG (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), FVAAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTT (SEQ ID NO: 196), FVAATWNGGTTY (SEQ ID NO: 197), WVAISGGGTTT (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), AIDWNGRGTYRY (SEQ ID NO: 204), RINGGGITH (SEQ ID NO: 205), FIATTT (SEQ ID NO: 206), ATWNGGTTY (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), GRTLSTY (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), GRTLSTYA (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), GRTLSTYAMG (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), STYAMG (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 GRTLSTFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

- 1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYYYRYADSVKG (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 FVAAIDWNGRGTYYYRY (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 AIDWNGRGTYYYRY (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 AIDWNGRGTYYYRYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRLNEYAT (SEQ ID NO: 61);

- 2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTTY (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 IDWNGRGTTY (SEQ ID NO: 50) or IDWNGRGTTYR (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 AIDWNGRGTTYRYADSVKG (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 FVAIDWNGRGTTYRY (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 AIDWNGRGTTYRY (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 WVGFIATTTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 FISGGGTTYADSVKG (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 FISGGGTTYADSVKG (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 SWSGGGS (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 FVAIRWSGGRTL (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 GRTL SFNTY (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 GRTL SFNTYA (SEQ ID NO: 29), the CDR2 sequence of ITWNGGST (SEQ ID NO: 59), and the CDR3 sequence of AAARYYYVSGTYFPANY (SEQ ID NO: 92);

- 4) the CDR1 sequence of GRTLSTFNTYAMG (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 GRTLSTFNTYAMG (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 VHH domains comprising the sequences of
- QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYRYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWyGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYRYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVLT
DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
- QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWQGTQVTVSS (SEQ ID NO: 95),
- EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
IATTTIATSVKGRFAITRDNAKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),
- QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),
- EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98),
- EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG

TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
 SGGSTTYADPVKGRFTISRDNANKNTVYLRMNSLKPEDTAVYYCNDQRGYWGGG
 TLVTVSS (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
 SGSSAGYGDSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
 GQGTQVTVSS (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
 SGGRTLYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
 YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKEREFVASIT
 WNGGSTSYADSVKGRFTITRDNANKNTATLRMNSLQPDDTAVYYCAAARYYVSG
 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.

6. An isolated nucleic acid molecule encoding:

- a) the VHH domain of any of claims 1 to 5; or
- b) the VHH domain having a sequence with at least 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the sequence of:

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNANKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93);
 EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNANKNTVYLRMNSLKPEDTAVYYCAATTVL
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94);
 QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
 GITHYAESVKGRFTISRDNANKNTVYLRMNSLKPEDTAAYYCKADVFGSSGYVET

YWGQGTQVTVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRI
IATTTIATSVKGRFAITRDNAKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITW
NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98);

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99);

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISW
SGGSTTYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISW
SGSSAGYGDSVKGRFTISRDNKNTLYLMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
SGGRTLYADSVKGRFTISRDNKNTAYLMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

optionally wherein, the nucleic acid molecule comprises a sequence with at least 85%,
90%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to the polynucleotide
sequence of any one of SEQ ID NOS: 133-142.

7. A vector comprising the nucleic acid molecule of claim 6.

8. A cell expressing the nucleic acid molecule of claim 6.

9. A pharmaceutical composition comprising the VHH domain of any of claims 1 to 6 and a pharmaceutically acceptable excipient.

10. A pharmaceutical composition comprising:

- a) a means for delivering a molecule to a mucosal lumen of a subject, and a pharmaceutically acceptable carrier;
- b) a means for delivering a molecule into systemic circulation in a subject, and a pharmaceutically acceptable carrier;
- c) a means for delivering a molecule into lamina propria of a subject, and a pharmaceutically acceptable carrier;
- d) a means for delivering a molecule to an organ of a subject, and a pharmaceutically acceptable carrier; or
- e) a means for delivering a molecule to a pIgR-expressing cell, and a pharmaceutically acceptable carrier;

optionally wherein, the molecule is an antibody or fragment thereof, a peptide, a vaccine, a small molecule, a polynucleotide, a molecule comprising a radioactive isotope, a toxin, an enzyme, an anticoagulant, a hormone, a cytokine, an anti-inflammatory molecule, an RNAi, an mRNA, a self-replicating RNA, an antibiotic, or an antibody-antibiotic conjugate.

11. A therapeutic molecule comprising an agent and a VHH domain that binds to an extracellular domain of polymeric immunoglobulin receptor (pIgR).

12. The therapeutic molecule of claim 11, wherein:

- a) the VHH domain binds to an:
 - i) extracellular domain 1 of pIgR;
 - ii) extracellular domain 2 of pIgR;
 - iii) extracellular domain 1-2 of pIgR;
 - iv) extracellular domain 3 of pIgR;
 - v) extracellular domain 2-3 of pIgR;

- vi) extracellular domain 4-5 of pIgR; or
- vii) extracellular domain 5 of pIgR;
- b) pIgR is:
 - i) human pIgR; or
 - ii) mouse pIgR;
- c) the VHH domain does not detectably bind to the amino acid sequence of:
 - i) EKAVADTRDQADGSRASVDSGSSEEQGGSSR (SEQ ID NO: 143);
 - ii) EREIQNVGDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 144); or
 - iii) EREIQNVRDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 145);
- d) the VHH domain competes with IgA binding to the pIgR;
- e) the VHH domain promotes IgA binding to the pIgR;
- f) the K_D of the binding of the VHH domain 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;
 or
- g) the T_m of the VHH domain:
 - i) is from about 53 to about 77 °C; or
 - ii) is from 53.9 to 76.4 °C.

13. The therapeutic molecule of claim 11 or claim 12, wherein the VHH domain 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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYADSVKG (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), DWNGRGTY (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), IDWNGRGTY (SEQ ID NO: 50), IDWNGRGTYR (SEQ ID NO: 270), INGGGIT (SEQ ID NO: 51), IDRIATT (SEQ ID NO: 52), ITWNGGTT (SEQ ID NO: 53), ISGGGT (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), AIDWNGRGTYRYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (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), FVAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTT (SEQ ID NO: 196), FVAITWNGGTTY (SEQ ID NO: 197), WVAFISGGGTTT (SEQ ID NO: 198), LVARITGGGSTH (SEQ ID NO: 199), FVAISWSGGSTT (SEQ ID NO: 200), FVAISWSGSSAG (SEQ ID NO: 201), FVAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), AIDWNGRGTYRY (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), GRTL SFNTY (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), GRTL SFNTYA (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), GRTL SFNTYAMG (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 GRTL SFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

- 1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYRYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTTY (SEQ ID NO: 50) or IDWNGRGTTYR (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 AIDWNGRGTTYRYYADSVKG (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 FVAAIDWNGRGTTYRY (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 AIDWNGRGTTYRY (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 AIDWNGRGTTYRYYADSVKG (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 DWNGRGTTY (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 IDWNGRGTTY (SEQ ID NO: 50) or IDWNGRGTTYR (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 AIDWNGRGTTYRYYADSVKG (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 FVAAIDWNGRGTTYRY (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 AIDWNGRGTYRY (SEQ ID NO: 204), and the CDR3 sequence of TTVLTDPRLNEYAT (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 WVGFIATTTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 ISGGGT (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 GRTL SFNTY (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 GRTL SFNTYA (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 GRTL SFNTYAMG (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 GRTL SFNTYAMG (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 VHH domains comprising the sequences of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYYYRYADSVKGRSTISRDNNAKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
 EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYYYRYADSVKGRSTISRDNNAKNTVYLMNSLKPEDTAVYYCAATTVL
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
 QLQLVESGGGLVQPGGSLRLSCAASGSISSINVMGWYRQAPGKQRELVARINGG
 GITHYAESVKGRFTISRDNNAKNTVYLMNSLKPEDTAAYYCKADVFGSSGYVET
 YWGQGTQVTVSS (SEQ ID NO: 95),
 EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
 IATTTIATSVKGRFAITRDNNAKNTVYLMNSLKPEDTAVYYCNHPLTARWGQGT
 QVTVSS (SEQ ID NO: 96),
 QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKREFVAAITW
 NGGTTYADSVKGRFTISRDNNAKNTVYLMNSLKPEDTAVYYCAADPFNQGY
 WGQGTQVTVSS (SEQ ID NO: 97),
 EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
 GGTTYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
 TQVTVSS (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
 GGSTHYAESVKGRFTISRDNNAKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG
 TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
 SGGSTTYADPVKGRFTISRDNNAKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
 TLVTVSS (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
 SGSSAGYGDSVKGRFTISRDNNAKNTLYLMNSLKPEDTAVYYCAADPFNQGYW
 GQGTQVTVSS (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKREFVAAIRW
 SGGRTLYADSVKGRFTISRDNNAKNTAYLMNNLRPEDTAVYYCAADLAEYSGT
 YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKREFVASIT

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.

14. The therapeutic molecule of any one of claims 11 to 13, 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;
- b) the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine;
or
- c) the VHH domain is:
 - i) genetically fused to the agent;
 - ii) chemically conjugated to the agent; or
 - iii) non-covalently bound to the agent.

15. The therapeutic molecule of claim 14, further comprising a linker between the VHH domain and the agent; optionally wherein, the linker:

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

16. A pharmaceutical composition comprising the therapeutic molecule of any of claims 11 to 15 and a pharmaceutically acceptable carrier.

17. A method of delivering a therapeutic molecule to a mucosal lumen of a subject, the therapeutic molecule of any of claims 11 to 15 is to be administered to the subject; optionally wherein:

- a) the therapeutic molecule is to be delivered to the mucosal lumen via forward transcytosis from the basolateral surface of a mucosal epithelial cell to the apical surface of the mucosal epithelial cell;
- b) the mucosal epithelial cell is at or adjacent to the mucosal lumen;
- c) the mucosal lumen is in the lung or in the gastrointestinal tract of the subject;
- d) the mucosal epithelial cell is a cancer cell, wherein the cancer cell is a lung cancer cell, an esophageal cancer cell, a stomach cancer cell, a duodenal cancer cell, a liver cancer cell, a bladder cancer cell, a sinus cancer cell, a nasal cavity cancer cell, an endometrial cancer cell or a colorectal cancer cell; or
- e) the cell is in a subject.

18. A method of delivering a therapeutic molecule to an organ of a subject, the therapeutic molecule of any of claims 11 to 15 is to be administered to the subject; optionally wherein:

- a) the organ is selected from the group consisting of gastrointestinal track, small intestine, large intestine, stomach, esophagus, salivary gland, lung, vagina, uterus, and lacrimal gland;
- b) the organ is lung;
- c) the agent is an antibody or fragment thereof, a peptide, a vaccine, a small molecule, a polynucleotide, a molecule comprising a radioactive isotope, a toxin, an enzyme, an anticoagulant, a hormone, a cytokine, an anti-inflammatory molecule, an RNAi, an mRNA, a self-replicating RNA, an antibiotic, or an antibody-antibiotic conjugate;
- d) the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine, wherein the antibiotic is selected from the group consisting of a macrolide antibiotic, a fluoroquinolone, a tetracycline, amoxicillin, ceftriaxone, penicillin G, linezolid, moxifloxacin, and azithromycin;
- e) the therapeutic molecule is to be administered to the bloodstream of the subject; or
- f) the molecule is to be administered intravenously or subcutaneously.

19. A method of delivering a therapeutic molecule into systemic circulation in a subject, the therapeutic molecule of any of claims 11 to 15 is to be administered to the subject; optionally wherein:

- a) the therapeutic molecule is to be delivered into the systemic circulation via reverse transcytosis from the apical surface of an epithelial cell to the basolateral surface of the epithelial cell;
- b) the therapeutic molecule is to be delivered by oral delivery, buccal delivery, nasal delivery or inhalation delivery; or
- c) the agent is a peptide, an antibody or fragment thereof or a vaccine.

20. A method of delivering a therapeutic molecule into lamina propria of a subject, the therapeutic molecule of any of claims 11 to 15 is to be administered to the subject; optionally wherein:

- a) the therapeutic molecule is to be delivered into the lamina propria via reverse transcytosis from the apical surface of an epithelial cell to the basolateral surface of the epithelial cell;
- b) the therapeutic molecule is to be delivered by oral delivery or buccal delivery; or
- c) the agent is a peptide or an antibody or fragment thereof.

21. A method of increasing the rate of pIgR-mediated transcytosis across an epithelial cell comprising contacting the cell with (i) a VHH domain that binds to 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 polymeric immunoglobulin receptor (pIgR) or (ii) a therapeutic molecule comprising an agent and the VHH domain; optionally wherein, the transcytosis is forward transcytosis or reverse transcytosis.

22. A method of modulating a function of pIgR in a cell comprising contacting the cell with (i) a VHH domain that binds to 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 polymeric immunoglobulin receptor (pIgR) or (ii) a therapeutic molecule comprising an agent and the VHH domain; optionally wherein, modulating the function of pIgR in the cell is activating said function of pIgR in said cell or inhibiting said function of pIgR in said cell.

23. A method of delivery to a pIgR-expressing cell comprising contacting the cell with a VHH domain or a therapeutic molecule, wherein the VHH domain binds to 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 polymeric immunoglobulin receptor (pIgR), and wherein the therapeutic molecule comprises an agent and the VHH domain.

24. The method of claim 23, wherein:

- a) the method of delivery is oral delivery, buccal delivery, nasal delivery or inhalation delivery;
- b) the VHH domain:
 - i) competes with IgA binding to the pIgR; or
 - ii) promotes IgA binding to the pIgR;
- c) the K_D of the binding of the VHH domain 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;
- d) the T_m of the VHH domain:
 - i) is from about 53 to about 77 °C; or
 - ii) is from 53.9 to 76.4 °C;
- e) the VHH domain binds to the:
 - i) extracellular domain 1 of pIgR;
 - ii) extracellular domain 2 of pIgR;
 - iii) extracellular domain 1-2 of pIgR;
 - iv) extracellular domain 3 of pIgR;
 - v) extracellular domain 2-3 of pIgR;
 - vi) extracellular domain 4-5 of pIgR; or
 - vii) extracellular domain 5 of pIgR;
- f) the pIgR is human pIgR or mouse pIgR; or

- g) the VHH domain does not detectably bind to the amino acid sequence of:
 EKAVADTRDQADGSRASVDSGSSEEQGGSSR (SEQ ID NO: 143);
 EREIQNVGDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 144); or
 EREIQNVRDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 145).

25. The method of any one of claims 21 to 24, wherein the VHH domain 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),

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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYADSVKG (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), DWNGRGTTY (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), IDWNGRGTTY (SEQ ID NO: 50), IDWNGRGTYR (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), AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (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), FVAAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTT (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), AIDWNGRGTYRY (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), GRTLSENTY (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), GRTLSENTYA (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), GRTLSENTYAMG (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 GRTLSEFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

- 1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYYYRYADSVKG (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 FVAAIDWNGRGTYYYRY (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 AIDWNGRGTYYYRY (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 AIDWNGRGTYYYRYYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYYYRYYADSVKG (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 FVAAIDWNGRGTYYYRY (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 AIDWNGRGTYYYRY (SEQ ID NO: 204), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 237);
- iii) VHH3:
- 1) the CDR1 sequence of INVMMG (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 WVG FIDRIATTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 FISGGGTTTTYADSVKG (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 FISGGGTTTTYADSVKG (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 GRTLSEFNTY (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 VHH domains comprising the sequences of
- QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVL
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
- QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
 GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
 YWGQGTQVTVSS (SEQ ID NO: 95),
- EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
 IATTTIATSVKGRFAITRDNKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
 QVTVSS (SEQ ID NO: 96),
- QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
 NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
 WGQGTQVTVSS (SEQ ID NO: 97),
- EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
 GGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG

TQVTVSS (SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNANTVYLLQMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
SGGSTTYADPVKGRFTISRDNANTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
SGSSAGYGDSVKGRFTISRDNANTLYLQMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
SGGRTLYADSVKGRFTISRDNANTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNANTATLRMNSLQPDDTAVYYCAAARYYVSG
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.

26. The method of any one of claims 21 to 25, 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 mRNA, a self-replicating RNA, an antibiotic, or an antibody-antibiotic conjugate;
- b) the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine;
- c) the VHH domain is:
 - i) genetically fused to the agent;
 - ii) chemically conjugated to the agent; or

- iii) non-covalently bound to the agent; or
- d) the method does not inhibit pIgR-mediated transcytosis of IgA.

27. The method of claim 26, further comprising a linker between the VHH domain and the agent; optionally wherein, the linker:

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

28. The method of claim 26, wherein the VHH domain 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), GRTLSEFNTY (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), GRTLSEFNTYA (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), GRTLSEFNTYAMG (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 GRTLSEFNTYAMG (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: 43), or RIA (SEQ ID NO: 44);

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), WVG FIDRIATTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVA AISWSGGSTT (SEQ ID NO: 200), FVA AISWSGSSAG (SEQ ID NO: 201), FVA AIRWSGGRTL (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).

29. A method to diagnose a disease or condition comprising detecting the amount of VHH domain in a tissue of a subject, wherein the subject is to be administered with (i) a VHH domain that binds to 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 polymeric immunoglobulin receptor (pIgR), or (ii) a therapeutic molecule comprising an agent and the VHH domain prior to the detecting of the amount of VHH domain in the tissue of the subject, the tissue comprises a diseased cell, and comparing the amount of VHH domain in the tissue of the subject with a reference amount of VHH domain in the tissue of a comparable healthy subject.

30. The method of claim 29, wherein:

- a) the tissue comprises a mucosal cell or a mucosal lumen;
- b) the VHH domain competes with IgA binding to the pIgR or promotes IgA binding to the pIgR;
- c) the K_D of the binding of the VHH domain 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;
- d) the T_m of the VHH domain:
 - i) is from about 53 to about 77 °C; or
 - ii) is from 53.9 to 76.4 °C;
- e) the VHH domain binds to the:
 - i) extracellular domain 1 of pIgR;
 - ii) extracellular domain 2 of pIgR;
 - iii) extracellular domain 1-2 of pIgR;
 - iv) extracellular domain 3 of pIgR;

- v) extracellular domain 2-3 of pIgR;
 - vi) extracellular domain 4-5 of pIgR; or
 - vii) extracellular domain 5 of pIgR;
- f) the pIgR is human pIgR or mouse pIgR; or
- g) the VHH domain does not detectably bind to the amino acid sequence of:
 EKAVADTRDQADGSRASVDSGSSEEQGGSSR (SEQ ID NO: 143);
 EREIQNVGDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 144); or
 EREIQNVRDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 145).

31. The method of claim 29 or 30, wherein the VHH domain 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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTTYADSVKG (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), DWNGRGTY (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), IDWNGRGTY (SEQ ID NO: 50), IDWNGRGTYR (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), AIDWNGRGTYRYYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (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), FVAAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVG FIDRIATTT (SEQ ID NO: 196), FVAAITWNGGTTY (SEQ ID NO: 197), WVA FISGGGTTT (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), AIDWNGRGTYRY (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), GRTL SFNTY (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), GRTL SFNTYA (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), GRTLSEFNTYAMG (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), GSIFSSINVMG (SEQ ID NO: 175), GTSVSSNAMG (SEQ ID NO: 176), GRTFSSYAMG (SEQ ID NO: 177), GSSVSSDAMG (SEQ ID NO: 178), RSIGSSINVMG (SEQ ID NO: 179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182), or GRTLSEFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYRYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYRYRYADSVKG (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 FVAAIDWNGRGTYRY (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 AIDWNGRGTYRY (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 AIDWNGRGTYRYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYRYRYADSVKG (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 FVAIDWNGRGTYRY (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 AIDWNGRGTYRY (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 WVG FIDRIATTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 FISGGGTTTTYADSVKG (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 FVA AIRWSGGRTL (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 VHH domains comprising the sequences of
- QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVL
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
- QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
 GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
 YWGQGTQVTVSS (SEQ ID NO: 95),
- EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
 IATTTIATSVKGRFAITRDNKNTVYLMQMSGLKPEDTAVYYCNHPLTARWGQGT
 QVTVSS (SEQ ID NO: 96),
- QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKEREFVAAITW

NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
 WGQGTQVTVSS (SEQ ID NO: 97),
 EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
 GGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
 TQVTVSS (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
 GGSTHYAESVKGRFTISRDNKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG
 TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISW
 SGGSTTYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
 TLVTVSS (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISW
 SGSSAGYGDSVKGRFTISRDNKNTLYLMNSLKPEDTAVYYCAADPFNQGYW
 GQGTQVTVSS (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKERE FVA AIRW
 SGGRTLYADSVKGRFTISRDNKNTAYLMNNLRPEDTAVYYCAADLA EYSGT
 YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKERE FVASIT
 WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAA RYYYVSG
 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.

32. The method of any one of claims 29 to 31, 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 mRNA, a self-replicating RNA, an antibiotic, or an antibody-antibiotic conjugate;

- b) the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine;
- c) the VHH domain is:
 - i) genetically fused to the agent;
 - ii) chemically conjugated to the agent; or
 - iii) non-covalently bound to the agent;
- d) the VHH domain comprises a radioisotope; optionally wherein, the radioisotope is zirconium-89;
- e) the disease is:
 - i) lung cancer, and wherein the tissue is lung;
 - ii) endometrial cancer, and wherein the tissue is the uterus;
 - iii) colon cancer, and wherein the tissue is the colon;
 - iv) an inflammatory disease, and wherein the tissue is lamina propria;
 - v) inflammatory bowel disease; or
 - vi) Crohn's disease or ulcerative colitis;
- f) the diseased cell expresses an antigen, and wherein the therapeutic molecule is coupled to an antibody that specifically recognizes the antigen; or
- g) the antigen is specific to the diseased cell.

33. The method of claim 32, wherein a linker is between the VHH domain and the agent; optionally wherein, the linker:

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

34. A method for:

- a) 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;
- b) transporting a therapeutic molecule to a basolateral surface of the pIgR-expressing cell of a subject, wherein the therapeutic molecule comprises an agent and a single domain antibody that binds to pIgR, wherein the therapeutic molecule is to be administered to a subject; optionally wherein, the therapeutic molecule is to be administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery;
 - c) transporting a therapeutic molecule to systemic circulation of a subject, wherein the therapeutic molecule comprises 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; or
 - d) transporting a therapeutic molecule to lamina propria or gastrointestinal tract of a subject, wherein the therapeutic molecule comprises 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.

35. The method of claim 34, wherein the therapeutic agent is to be transported from an apical surface of a pIgR-expressing cell to a basolateral surface of the pIgR-expressing cell in the subject.

36. The method of claim 34 or 35, wherein:

- a) 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;
- b) the pIgR-expressing cell is an epithelial cell;
- c) the epithelial cell is an intestinal lumen cell or an airway epithelial cell;
- d) the agent is a 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;
- e) the agent is a peptide or an antibody or a fragment thereof;

- f) 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;
- g) the agent is a 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;
- h) the single domain antibody 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;
- i) the single domain antibody competes with IgA binding to the pIgR or promotes IgA binding to the pIgR;
- j) 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;
- k) 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
- l) pIgR is human pIgR or mouse pIgR; or
- m) the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

37. The method of any one of claims 34 to 36, 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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYADSVKG (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), DWNGRGTY (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), IDWNGRGTY (SEQ ID NO: 50), IDWNGRGTYR (SEQ ID NO: 270), INGGGIT (SEQ ID NO: 51), IDRIATT (SEQ ID NO: 52), ITWNGGTT (SEQ ID NO: 53), ISGGGT (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), AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (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), FVAAIDWNGRGTYRY (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), AIDWNGRGTYRY (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), GRTLSTY (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), GRTLSTY (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), GRTLSTYAMG (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), STYAMG (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);

179), GRTFSTYRMG (SEQ ID NO: 180), GFTFTRYAMG (SEQ ID NO: 181), GRTFTTYRMG (SEQ ID NO: 182), or GRTLSEFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

- 1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYYYRYADSVKG (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 FVAAIDWNGRGTYYYRY (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 AIDWNGRGTYYYRY (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 AIDWNGRGTYYYRYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRLNEYAT (SEQ ID NO: 61);
- 2) the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYRYADSVKG (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 FVAAIDWNGRGTYRY (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 AIDWNGRGTYRY (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 DVFGSSGYVETV (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 WVGFIATTTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 FISGGGTTYADSVKG (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 FISGGGTTYADSVKG (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 GRTL SFNTY (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 GRTL SFNTYA (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 GRTLSTFNTYAMG (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 GRTLSTFNTYAMG (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 VHH domains comprising the sequences of
- QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNNAKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNNAKNTVYLQMNSLKPEDTAVYYCAATTVLT
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
- QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
 GITHYAESVKGRFTISRDNNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
 YWGQGTQVTVSS (SEQ ID NO: 95),
- EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
 IATTTIATSVKGRFAITRDNAKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
 QVTVSS (SEQ ID NO: 96),
- QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
 NGGTTYADSVKGRFTISRDNNAKNTVYLMNSLKPEDTAVYYCAADPFNQGY
 WGQGTQVTVSS (SEQ ID NO: 97),
- EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
 GGTTYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
 TQVTVSS (SEQ ID NO: 98),
- EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
 GGSTHYAESVKGRFTISRDNNAKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG

TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
 SGGSTTYADPVKGRFTISRDNANKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
 TLVTVSS (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
 SGSSAGYGDSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
 GQGTQVTVSS (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
 SGGRTLYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
 YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKEREFVASIT
 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.

38. The method of any one of claims 34 to 37, wherein:

- a the single domain antibody is:
 - i) genetically fused to the agent;
 - ii) chemically conjugated to the agent; or
 - iii) non-covalently bound to the agent;
 or
- b) the method does not inhibit pIgR-mediated transcytosis of IgA.

39. The method of claim 38, further comprising a linker between the single domain antibody and the agent; optionally wherein, 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.

40. The method of claim 38, 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), GRTLSTFNTY (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), GRTLSTFNTYA (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), GRTLSTFNTYAMG (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 GRTLSTFNTYAMG (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), WVG FIDRIATTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVA AISWSGGSTT (SEQ ID NO: 200), FVA AISWSGSSAG (SEQ ID NO: 201), FVA AIRWSGGRTL (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).

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

42. The process of claim 41, wherein:

- a) the molecule is capable of being provided to a basolateral surface of an pIgR-expressing cell from an apical surface of the pIgR-expressing cell in the subject;
- b) the molecule 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;
- c) the pIgR-expressing cell is an epithelial cell;
- d) the epithelial cell is an intestinal lumen cell or an airway epithelial cell;
- e) the agent is a 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;
- f) wherein the agent is a 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;
- g) the agent is a 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;
- h) the single domain antibody 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;
- i) the single domain antibody competes with IgA binding to the pIgR or promotes IgA binding to the pIgR;

- j) 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;
 - k) 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.
 - l) pIgR is human pIgR or mouse pIgR;
- or
- m) the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

43. The process of claim 41 or claim 42, wherein the single domain antibody comprises:

- a) a CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60), TTVLTDPRLNEYAT (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), TTVLTDPRLNEYAT (SEQ ID NO: 72), TVLTDPRLNEYA (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), CAATTVLTDPRLNEYAT (SEQ ID NO: 83), AATTVLTDPRLNEYAT (SEQ ID NO: 284), KADVFGSSGYVETY (SEQ ID NO: 285),

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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYADSVKG (SEQ ID NO: 33), FISGGGTTTTYADSVKG (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), DWNGRGTTY (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), IDWNGRGTY (SEQ ID NO: 50), IDWNGRGTYR (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), AIDWNGRGTYRYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (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), FVAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTTT (SEQ ID NO: 196), FVAITWNGGTTY (SEQ ID NO: 197), WVAFISGGGTTT (SEQ ID NO: 198), LVARITGGGSTH (SEQ ID NO: 199), FVAISWSGGSTT (SEQ ID NO: 200), FVAISWSGSSAG (SEQ ID NO: 201), FVAIRWSGGRTL (SEQ ID NO: 202), FVASITWNGGSTS (SEQ ID NO: 203), AIDWNGRGTYRY (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), GRTLSTFNTY (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), GRTLSTFNTYA (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), GRTLSEFNTYAMG (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), SEFNTYAMG (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 GRTLSEFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

- 1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYRYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYRYRYADSVKG (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 FVAAIDWNGRGTYRY (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 AIDWNGRGTYRY (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 AIDWNGRGTYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYRYADSVKG (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 FVAAIDWNGRGTYRY (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 AIDWNGRGTYRY (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 WVG FIDRIATTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 FISGGGTTTTYADSVKG (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 ISGGGT (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 FVA AIRWSGGRTL (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 GRTL SFNTY (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 GRTL SFNTYA (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 GRTL SFNTYAMG (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 GRTL SFNTYAMG (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 VHH domains comprising the sequences of
- QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDN AKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDN AKNTVYLQMNSLKPEDTAVYYCAATTVL
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGSLRLSCAASGFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDIR
IATTTIATSVKGRFAITRDNKNTVYLQMNSLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKREFVAAITW
NGGTTYADSVKGRFTISRDNKNTVYLQMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNKNTVYLQMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
SGGSTTYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
SGSSAGYGDSVKGRFTISRDNKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKREFVAAIRW
SGGRTLYADSVKGRFTISRDNKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKREFVASIT
WNGGSTSYADSVKGRFTITRDNKNTATLRMNSLQPDDTAVYYCAAARYYVSG
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.

44. The process of any one of claims 41 to 43, wherein:

- a) the single domain antibody is:
 - i) genetically fused to the agent;
 - ii) chemically conjugated to the agent; or
 - iii) non-covalently bound to the agent; or
- b) the process does not inhibit pIgR-mediated transcytosis of IgA.

45. The process of claim 44, further comprising a linker between the single domain antibody and the agent; optionally wherein, the linker:

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

46. The process of claim 44, 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), GRTLSTFNTY (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), GRTLSTFNTYA (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), GRTLSTFNTYAMG (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 GRTLSTFNTYAMG (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), WVG FIDRIATTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVA AISWSGGSTT (SEQ ID NO: 200), FVA AISWSGSSAG (SEQ ID NO: 201), FVA AIRWSGGRTL (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).

47. A process comprising steps for providing a molecule to 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;
 - c) the agent is an antibody or fragment thereof, a peptide, or a vaccine; or
 - d) the single domain antibody is genetically fused or chemically conjugated to the agent.
48. 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.
49. The system of claim 48, wherein:
- a) 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;
- b) the single domain antibody 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;
- c) the single domain antibody competes with IgA binding to the pIgR;
- d) the single domain antibody promotes IgA binding to the pIgR;
- e) 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;
- f) 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;
- g) the pIgR is:
 - i) human pIgR; or

ii) mouse pIgR;

or

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

50. The system of claim 48 or claim 49, 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 AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYADSVKG (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), DWNGRGTTY (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), IDWNGRGTTY (SEQ ID NO: 50), IDWNGRGTYR (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), AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 184), RINGGGITHYAESVKG (SEQ ID NO: 185), FIDRIATTTIATSVKG (SEQ ID NO: 186), AITWNGGTTYADSVKG (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), FVAAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTT (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), AIDWNGRGTYRY (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), GRTLSENTY (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), GRTLSENTYA (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), GRTLSENTYAMG (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 GRTLSEFNTYAMG (SEQ ID NO: 183);

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

i) VHH1:

- 1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYYYRYADSVKG (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 FVAAIDWNGRGTYYYRY (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 AIDWNGRGTYYYRY (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 AIDWNGRGTYYYRYYADSVKG (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 DWNGRGTY (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 IDWNGRGTY (SEQ ID NO: 50) or IDWNGRGTYR (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 AIDWNGRGTYYYRYYADSVKG (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 FVAAIDWNGRGTYYYRY (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 AIDWNGRGTYYYRY (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 WVG FIDRIATTT (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 AITWNGGTTYADSVKG (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 AITWNGGTTYADSVKG (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 FISGGGTTTTYADSVKG (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 ISGGGT (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 FISGGGTTTTYADSVKG (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 FVA AISWSGGSTT (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 FVA AISWSGSSAG (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 GRTL SFNTY (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 GRTLSEFNTYA (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 GRTLSEFNTYAMG (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 SEFNTYAMG (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 GRTLSEFNTYAMG (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 VHH domains comprising the sequences of
- QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
 NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
 NGRGTYRYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVL
 DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
- QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
 GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
 YWGQGTQVTVSS (SEQ ID NO: 95),
- EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
 IATTTIATSVKGRFAITRDNKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
 QVTVSS (SEQ ID NO: 96),
- QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
 NGGTTYADSVKGRFTISRDNKNTVYLQMNSLKPEDTAVYYCAADPFNQGY
 WGQGTQVTVSS (SEQ ID NO: 97),
- EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
 GGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG

TQVTVSS (SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNANTVYLMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISW
SGGSTTYADPVKGRFTISRDNANTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISW
SGSSAGYGDSVKGRFTISRDNANTLYLMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
SGGRTLYADSVKGRFTISRDNANTAYLMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNANTATLRMNSLQPDDTAVYYCAAARYYVSG
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.

51. The system of any one of claims 48 to 50, wherein:

- a) the single domain antibody:
 - i) is genetically fused to the agent;
 - ii) chemically conjugated to the agent; or
 - iii) non-covalently bound to the agent; or
- b) the system does not inhibit pIgR-mediated transcytosis of IgA.

52. The system of claim 51, further comprising a linker between the single domain antibody and the agent; optionally wherein, the linker:

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

53. The system of claim 52, 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), GRTLSEFNTY (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), GRTLSEFNTYA (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), GRTLSEFNTYAMG (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), SEFNTYAMG (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 GRTLSEFNTYAMG (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), WSGGSS (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),

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), WVG FIDRIATTT (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).

54. A system comprising a means for providing a molecule to lamina propria of a subject.

55. The system of claim 54, wherein the molecule comprises an agent and a single domain antibody that binds to pIgR; optionally 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;
- b) the agent is an antibody or fragment thereof, a peptide, or a vaccine; or
- c) the single domain antibody is genetically fused or chemically conjugated to the agent.