

~~WHAT IS CLAIMED:~~

Claims

1. A VHH domain that binds to an extracellular domain of polymeric immunoglobulin receptor (pIgR).

2. The VHH domain of claim 1, wherein ~~the VHH domain binds to an extracellular domain 1 of~~ pIgR.

~~3. 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;~~

~~4. The VHH domain of claim 1, wherein the VHH domain binds to an iii) _____ extracellular domain 1-2 of pIgR;~~

~~5. The VHH domain of claim 1, wherein the VHH domain binds to an iv) _____ extracellular domain 3 of pIgR;~~

~~6. The VHH domain of claim 1, wherein the VHH domain binds to an v) _____ extracellular domain 2-3 of pIgR;~~

~~7. The VHH domain of claim 1, wherein the VHH domain binds to an extracellular domain 4-5 of pIgR.~~

~~8. The VHH domain of claim 1, wherein the VHH domain binds to an vi) _____ extracellular domain 4-5 of pIgR; or~~

9. The VHH^{vii}) extracellular domain 5 of any one of claims 1 to 8, wherein pIgR is human pIgR;

~~10. The VHH domain of any one of claims 1 to 8, wherein pIgR is mouse pIgR.~~

~~11. The VHH domain of any one of claims 1 to 8, wherein the VHH domain does not detectably bind to the amino acid sequence of EKAVADTRDQADGSRASVDSCGSSEEQGGSSR (SEQ ID NO: 143), EREIQNVGDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 144), or EREIQNVRDQAQENRASGDAGSADGQSRSSSSK (SEQ ID NO: 145).~~

12. The VHH domain of claim 1, wherein b) the VHH domain competes with IgA binding to the pIgR; or

~~13. The VHH domain of claim 1, wherein c) the VHH domain promotes IgA binding to the pIgR.~~

~~143. 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:

EKAVADTRDQADGSRASVDSCGSSEEQGGSSR (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 13, wherein the K_D of the binding of the VHH domain to pIgR is from about 4 to about 525 nM.~~

~~15. The VHH domain of any one of claims 1 to 143, 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

~~16. The VHH domain of any one of claims 1 to 15, wherein the K_D of the binding of the VHH domain to pIgR is iii) _____ from about 4 to about 34 nM;~~

~~17. The VHH domain of any one of claims 1 to 16, wherein the or~~

b) T_m of the VHH domain;

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

~~18. The VHH domain of any one of claims 1 to 17, wherein the T_m of the VHH domain ii) _____ is from 53.9 to 76.4 °C.~~

~~195.~~ The VHH domain of any one of claims 1 to ~~184~~, 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);

~~20. The VHH domain of any one of claims 1 to 9, wherein the VHH domain comprises b)~~
 _____ a CDR2 sequence of AIDWNGRGTYRYADSVKG (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), 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), IDWNGRGTTY (SEQ ID NO: 50), IDWNGRGTTYR (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), AIDWNGRGTTYRYADSVKG (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), FVAAIDWNGRGTTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTTT (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), AIDWNGRGTTYRY (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)-);

21. ~~The VHH domain of any one of claims 1 to 10, wherein the VHH domain comprises 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), GRTLSEFNTY (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), GRTLSEFNTYA (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), 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);

~~22. The VHH domain of any one of claims 1 to 10, wherein the VHH domain comprises d)~~
 _____ a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence of the VHH domain selected from the group consisting of:

ai) VHH1:

———i1) 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);

ii2) 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);

- ~~iii~~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);
- ~~iv~~4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTTYRYRYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);
- ~~v~~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
- ~~vi~~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);
- ~~b~~ii) VHH2:
 - ~~i~~1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTTYRYRYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 61);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTTYRYRYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);
 - ~~v~~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

- ~~iii~~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);
- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- ~~ev~~) VHH5:
 - ~~i~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);

—fvi) VHH6:

——i1) 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);

——ii2) 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);

——iii3) 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);

——iv4) 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);

——v5) 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

——vi6) 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);

——gvii) VHH7:

————i1) 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);

————ii2) 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);

————iii3) 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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- h) ~~VHH9:~~
- ~~iviii)~~ 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);
- i) ~~VHH10:~~
- ~~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);
- ~~ii~~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);
- ~~iii~~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);
- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- ~~j)~~ ~~VHH11:~~
- ~~ix)~~ 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);
 - ~~ii~~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);
 - ~~iii~~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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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
- ~~k~~) VHH12:
- ~~ix~~i) 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~5) the CDR1 sequence of SFNTYAMG (SEQ ID NO: 173), the CDR2 sequence of FVASITWNGGSTS (SEQ ID NO: 203), and the CDR3 sequence of AAARYYYVSGTYFPAN (SEQ ID NO: 235); or
 - ~~vi~~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)-);

23. The VHH domain of any one of claims 1 to 22, wherein the VHH domain comprises e)

_____ a framework derived from the framework of any of the VHH domains comprising the sequences of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYYYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWyGGMDYWGQGTQVTVSS (SEQ ID NO: 93),

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYYYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVL
TDPRLNEYATWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFD
RIATTTIATSVKGRFAITRDNKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),

QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTYADSVKGRFTISRDNKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
SGGSTTYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
SGSSAGYGDSVKGRFTISRDNKNTLYLMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKREFVAAIRW

SGGRTLYADSVKGRFTISRDNANTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNANTATLRMNSLQPDDTAVYYCAAARYYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

24. ~~The VHH domain of any one of claims 1 to 22, wherein the VHH domain comprises a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of~~

~~QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TTYRYYADSVKGRSTISRDNANTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93),~~

~~EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TTYRYYADSVKGRSTISRDNANTVYLMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94),~~

~~QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGGITHY
AESVKGRFTISRDNANTVYLMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95),~~

~~EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNANTVYLMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96),~~

~~QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITWNGGTT
YYADSVKGRFTISRDNANTVYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97),~~

~~EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98),~~

~~EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDVLRITGGGSTH
YAESVKGRFTISRDNANTVYLMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99),~~

~~QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST~~

TYADPVKGRFTISRDNANKNTVYLRMNSLKPEDTAVYYCNDQRCYWGQGTQVTVSS
(SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTTRYAMGWFRQAPGKERSFVAAISWSGSSA
GYGDSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRWSGGRT
LYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKEREFVASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

25. The VHH domain of any one of claims 1 to 24, wherein the VHH domain is comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANKNTVYLRMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
AESVKGRFTISRDNANKNTVYLRMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYLRMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRTFTSYAMGWFRQAPGKEREFVAAITWNGGTT
YYADSVKGRFTISRDNANKNTVYLRMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
 TYADSVKGRFTISRDN TKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
 (SEQ ID NO: 98);

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
 YAESVKGRFTISRDN AKNTVY LQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
 DYWGQGTQVTVSS (SEQ ID NO: 99);

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
 TYADPVKGRFTISRDN AKNTVY LRMNSLKPEDTAVYYCNDQRCYWGQGT LTVTVSS
 (SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
 GYGDSVKGRFTISRDN AKNTLY LQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKERE FVA AIRWSGGRT
 LYADSVKGRFTISRDN AKNTAY LQMNNLRPEDTAVYYCAADLA EYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKERE FVASITWNG
 GSTSYADSVKGRFTITRDN AKNTAT LRMNSLPDDTAVYYCAAARYV VSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

26f) 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 the VHH domain of any of claims 1 to 25.:

27. 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
NGRGTYRYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYRYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVLT
DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFI
IATTTIATSVKGRFAITRDNAKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKEREVFAAITW
NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98);

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99);

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
SGGSTTYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
SGSSAGYGDSVKGRFTISRDNKNTLYLMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVFAAIRW
SGGRTLADSVKGRFTISRDNKNTAYLMNNLRPEDTAVYYCAADLAEYSGT

YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSEFNTYAMGWFRQAPGKEREFVASIT
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.

~~287.~~ A vector comprising the nucleic acid molecule of claim ~~26 or claim 276.~~

~~298.~~ A cell expressing the nucleic acid molecule of claim ~~26 or claim 276.~~

~~309.~~ A pharmaceutical composition comprising the VHH domain of any of claims 1 to ~~256~~
and a pharmaceutically acceptable excipient.

~~3110.~~ A pharmaceutical composition comprising:

a) a means for delivering a molecule to a mucosal lumen of a subject, and a pharmaceutically
acceptable carrier;

~~32. A pharmaceutical composition comprising b)~~ a means for delivering a molecule
into systemic circulation in a subject, and a pharmaceutically acceptable carrier;

~~33. A pharmaceutical composition comprising c)~~ a means for delivering a molecule
into lamina propria of a subject, and a pharmaceutically acceptable carrier;

~~34. A pharmaceutical composition comprising d)~~ a means for delivering a molecule to
an organ of a subject, and a pharmaceutically acceptable carrier; or

~~35. A pharmaceutical composition comprising e)~~ a means for delivering a molecule to
a pIgR-expressing cell, and a pharmaceutically acceptable carrier;

~~36. The pharmaceutical composition of any one of claims 31 to 35, wherein 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.

~~37~~11. A therapeutic molecule comprising an agent and a VHH domain that binds to an extracellular domain of polymeric immunoglobulin receptor (pIgR).

~~38~~12. The therapeutic molecule of claim ~~37~~11, wherein:

a) the VHH domain binds to an:

i) extracellular domain 1 of pIgR;

~~39. The therapeutic molecule of claim 37, wherein the VHH domain binds to an ii)~~
extracellular domain 2 of pIgR;

~~40. The therapeutic molecule of claim 37, wherein the VHH domain binds to an iii)~~
extracellular domain 1-2 of pIgR;

~~41. The therapeutic molecule of claim 37, wherein the VHH domain binds to an iv)~~
extracellular domain 3 of pIgR;

~~42. The therapeutic molecule of claim 37, wherein the VHH domain binds to an v)~~
extracellular domain 2-3 of pIgR;

~~43. The therapeutic molecule of claim 37, wherein the VHH domain binds to an vi)~~
extracellular domain 4-5 of pIgR; or

- ~~44. The therapeutic molecule of claim 37, wherein the VHH domain binds to an vii) extracellular domain 5 of pIgR;~~
- ~~45. The therapeutic molecule of any one of claims 37 to 44, wherein b) pIgR is:~~
~~i) human pIgR; or~~
- ~~46. The therapeutic molecule of any one of claims 37 to 44, wherein pIgR is mouse pIgR.~~
- ~~47. The therapeutic molecule of any one of claims 37 to 44, wherein 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);~~
- ~~48. The therapeutic molecule of claim 37, wherein d) the VHH domain competes with IgA binding to the pIgR;~~
- ~~49. The therapeutic molecule of claim 37, wherein e) the VHH domain promotes IgA binding to the pIgR;~~
- ~~50. The therapeutic molecule of any one of claims 37 to 49, wherein f) the K_D of the binding of the VHH domain to pIgR;~~
~~i) is from about 4 to about 525 nM;~~
- ~~51. The therapeutic molecule of any one of claims 37 to 50, wherein the K_D of the binding of the VHH domain to pIgR ii) is less than about 50 nM; or~~

~~52. The therapeutic molecule of any one of claims 37 to 51, wherein the K_D of the binding of the VHH domain to pIgR-iii) is from about 4 to about 34 nM;~~

~~53. The therapeutic molecule of any one of claims 37 to 52, wherein or~~
g) the T_m of the VHH domain-;
i) is from about 53 to about 77 °C; or

~~54. The therapeutic molecule of any one of claims 37 to 53, wherein the T_m of the VHH domain-ii) is from 53.9 to 76.4 °C.~~

~~55~~13. The therapeutic molecule of ~~any one of claims 37 to 54~~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);

~~56. The therapeutic molecule of any one of claims 37 to 55, wherein the VHH domain comprises b) a CDR2 sequence of AIDWNGRGTYRYADSVKG (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), IDWNGRGTTYR (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), AIDWNGRGTTYRYADSVKG (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), FVAAIDWNGRGTTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTTT (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), AIDWNGRGTTYRY (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)-);

57. ~~The therapeutic molecule of any one of claims 37 to 56, wherein the VHH domain comprises 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), GRTLSTNTY

(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), GRTLSEFNTYA (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);

~~58. The therapeutic molecule of any one of claims 37 to 57, wherein the VHH domain comprises d) a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence of the VHH domain selected from the group consisting of:~~

ai) VHH1:

——i1) 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);

ii2) 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);

——iii3) 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);

———~~iv~~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);

———~~v~~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

———~~vi~~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);

——~~b~~ii) VHH2:

———~~i~~1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 61);

———~~ii~~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);

———~~iii~~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);

———~~iv~~4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);

———~~v~~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

- ~~iii~~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);
- ~~iv~~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);
- ~~v~~5) the CDR1 sequence of SSNAMG (SEQ ID NO: 166), the CDR2 sequence of WVGFI~~DRI~~ATTT (SEQ ID NO: 196), and the CDR3 sequence of NHPLTA (SEQ ID NO: 228); or
- ~~vi~~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);
- ~~ev~~) VHH5:
 - ~~i~~1) the CDR1 sequence of SYAMG (SEQ ID NO: 4), the CDR2 sequence of AITWNGGTTY~~Y~~ADSVKG (SEQ ID NO: 33), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 64);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~4) the CDR1 sequence of GRTFSSYAMG (SEQ ID NO: 157), the CDR2 sequence of AITWNGGTTY~~Y~~ADSVKG (SEQ ID NO: 187), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 218);
 - ~~v~~5) the CDR1 sequence of SSYAMG (SEQ ID NO: 167), the CDR2 sequence of FVA~~A~~ITWNGGTTY (SEQ ID NO: 197), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 229); or
 - ~~vi~~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);

—fvi) VHH6:

- i1) 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);
- ii2) 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);
- iii3) 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);
- iv4) 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);
- v5) 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
- vi6) 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);
- gvii) VHH7:
 - i1) 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);
 - ii2) 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);
 - iii3) 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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- h) ~~VHH9:~~
- ~~iviii)~~ 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);
- i) ~~VHH10:~~
- ~~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);
- ii) 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);
- iii) 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);
- iv) 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);
- v) 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
- vi) 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);
- j) VHH11:
- ix) 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);
 - ii) 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);
 - iii) 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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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
- ~~k~~) VHH12:
- ~~ix~~i) 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~5) the CDR1 sequence of SFNTYAMG (SEQ ID NO: 173), the CDR2 sequence of FVASITWNGGSTS (SEQ ID NO: 203), and the CDR3 sequence of AAARYYYVSGTYFPAN (SEQ ID NO: 235); or
 - ~~vi~~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)-);

59. ~~The therapeutic molecule of any one of claims 37 to 58, wherein the VHH domain~~

~~comprises e)~~ a framework derived from the framework of any of the VHH domains comprising the sequences of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYYYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWyGGMDYWGQGTQVTVSS (SEQ ID NO: 93),

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYYYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVL
TDPRLNEYATWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDIR
IATTTIATSVKGRFAITRDNKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),

QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
NGGTTYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTYADSVKGRFTISRDNKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG
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),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKREFVAAIRW

SGGRTLYADSVKGRFTISRDNANTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREVASIT
WNGGSTSYADSVKGRFTITRDNANTATLRMNSLQPDDTAVYYCAAARYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

~~60. The therapeutic molecule of any one of claims 37 to 58, wherein the VHH domain comprises a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of~~

~~QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TTYRYYADSVKGRSTISRDNANTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93),~~

~~EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TTYRYYADSVKGRSTISRDNANTVYLMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94),~~

~~QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
AESVKGRFTISRDNANTVYLMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95),~~

~~EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDRIATTT
IATSVKGRFAITRDNANTVYLMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96),~~

~~QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFAAITWNGGTT
YYADSVKGRFTISRDNANTVYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97),~~

~~EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98),~~

~~EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDVLRITGGGSTH
YAESVKGRFTISRDNANTVYLMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99),~~

~~QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAASWSGGST~~

TYADPVKGRFTISRDNNAKNTVYLRMNSLKPEDTAVYYCNDQRCYWGQGTQVTVSS
(SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTTRYAMGWFRQAPGKERSFVAAISWSGSSA
GYGDSVKGRFTISRDNNAKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRWSGGRT
LYADSVKGRFTISRDNNAKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKEREFVASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

61. The therapeutic molecule of any one of claims 37 to 60, wherein the VHH domain is
comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or
100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNNAKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNNAKNTVYLQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
AESVKGRFTISRDNNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRTFTSSYAMGWFRQAPGKEREFVAAITWNGGTT
YYADSVKGRFTISRDNNAKNTVYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
 TYADSVKGRFTISRDN TKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
 (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
 YAESVKGRFTISRDN AKNTVY LQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
 DYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
 TYADPVKGRFTISRDN AKNTVY LRMNSLKPEDTAVYYCNDQRCYWGQGT LTVTVSS
 (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
 GYGDSVKGRFTISRDN AKNTLY LQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKERE FVA AIRWSGGRT
 LYADSVKGRFTISRDN AKNTAY LQMNNLRPEDTAVYYCAADLA EYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKERE FVA SITWNG
 GSTSYADSVKGRFTITRDN AKNTAT LRMNSLPDDTAVYYCAAARYYVSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

62. The therapeutic molecule of any one of claims 37 to 61, wherein
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;

~~63. The therapeutic molecule of claim 62, wherein b) the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine;~~

~~64. The therapeutic molecule of claim 62 or claim 63, wherein~~

~~c) the VHH domain is:~~

~~i) genetically fused ~~or to the agent~~;~~

~~ii) chemically conjugated to the agent; or~~

~~65iii) non-covalently bound to the agent.~~

~~15. The therapeutic molecule of claim 64, further comprising a linker between the VHH domain and the agent;~~

~~66. The therapeutic molecule of claim 65, optionally wherein, the linker:~~

~~a) is a polypeptide; or~~

~~67. The therapeutic molecule of claim 66, wherein the linker b) is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQQLQPQNPTTESKSPK (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.~~

~~68. The therapeutic molecule of any one of claims 37 to 67, wherein the VHH domain is chemically conjugated to the agent.~~

~~69. The therapeutic molecule of any one of claims 37 to 67, wherein the VHH domain is non-covalently bound to the agent.~~

~~70~~16. A pharmaceutical composition comprising the therapeutic molecule of any of claims ~~37~~11 to ~~69~~15 and a pharmaceutically acceptable carrier.

~~71~~17. A method of delivering a therapeutic molecule to a mucosal lumen of a subject, the ~~method comprising administering~~therapeutic molecule of any of claims 11 to 15 is to be administered to the subject-; optionally wherein:

a) _____ the therapeutic molecule ~~of any of claims 37~~is to ~~69~~.

~~72. The method of claim 71, wherein the therapeutic molecule is~~b ~~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-;~~

~~73. The method of claim 71, wherein~~b) ~~the mucosal epithelial cell is at or adjacent to the mucosal lumen-;~~

~~74. The method of claim 72 or 73, wherein~~c) ~~the mucosal lumen is in the lung or in the gastrointestinal tract of the subject-;~~

~~75. The method of any one of claims 72 to 73, wherein~~d) ~~the mucosal epithelial cell is a cancer cell-~~

~~76. The method of claim 75, 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

~~77. The method of any one of claims 72 to 76, wherein~~e) ~~the cell is in a subject.~~

~~78~~18. A method of delivering a therapeutic molecule to an organ of a subject, ~~the method comprising administering to the subject the therapeutic molecule of any of claims 37 to 67,~~11 to 15 is to be administered to the subject; optionally wherein:

~~79. The method of claim 78, 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;_i

~~80. The method of claim 79, wherein b)~~ the organ is lung;_i

~~81. The method of any one of claims 71 to 80, wherein 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;_i

~~82. The method of claim 81, wherein d)~~ the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine;

~~83. The method of claim 82, 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;~~_i

~~84. The method of any one of claims 71 to 83, wherein e)~~ the therapeutic molecule is to be administered to the bloodstream of the subject;_i or

~~85. The method of any one of claims 71 to 83, wherein f) _____ the molecule is to be administered intravenously or subcutaneously.~~

86

19. A method of delivering a therapeutic molecule into systemic circulation in a subject, the ~~method comprising administering to the subject the therapeutic molecule of any of claims 3711 to 15 is to~~ be administered to the subject; optionally wherein:

~~87. The method of claim 86, 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;~~

~~88. The method of claim 86, wherein b) _____ the therapeutic molecule is to be delivered by oral delivery, buccal delivery, nasal delivery or inhalation delivery; or~~

~~89. The method of any one of claims 86 to 88, wherein c) _____ the agent is a peptide, an antibody or fragment thereof or a vaccine.~~

~~9020.~~ A method of delivering a therapeutic molecule into lamina propria of a subject, the ~~method comprising administering to the subject the therapeutic molecule of any of claims 3711 to 15 is to~~ be administered to the subject; optionally wherein:

~~91. The method of claim 90, 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;~~

~~92. The method of claim 90, wherein b) _____ the therapeutic molecule is to be delivered by oral delivery or buccal delivery; or~~

~~93. The method of any one of claims 90 to 92, wherein c) _____ the agent is a peptide or an antibody or fragment thereof.~~

~~94~~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.

~~95. The method of claim 94, wherein the transcytosis is forward transcytosis.~~

~~96. The method of claim 94, wherein the transcytosis is reverse transcytosis.~~

~~97~~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.

~~98. The method of claim 97, wherein the modulating the function of pIgR in the cell is activating said function of pIgR in said cell.~~

~~99. The method of claim 97, wherein the modulating the function of pIgR in the cell is inhibiting said function of pIgR in said cell.~~

~~100~~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.

~~101~~24. The method of claim ~~98~~23, wherein:

a) the method of delivery is oral delivery, buccal delivery, nasal delivery or inhalation delivery;

~~102. The method of any one of claims 94 to 100, wherein b) the VHH domain:~~

i) competes with IgA binding to the pIgR; or

~~103. The method of any one of claims 94 to 100, wherein the VHH domain ii)~~

promotes IgA binding to the pIgR;

~~104. The method of any one of claims 94 to 103, wherein c) the K_D of the binding of the VHH domain to pIgR:~~

i) is from about 4 to about 525 nM;

~~105. The method of any one of claims 94 to 104, wherein the K_D of the binding of the~~

~~VHH domain to pIgR ii) is less than about 50 nM; or~~

~~106. The method of any one of claims 94 to 105, wherein the K_D of the binding of the~~

~~VHH domain to pIgR iii) is from about 4 to about 34 nM;~~

~~107. The method of any one of claims 94 to 106, wherein d) the T_m of the VHH domain:~~

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

- ~~108. The method of any one of claims 94 to 107, wherein the T_m of the VHH domain ii)
 is from 53.9 to 76.4 °C;~~
- ~~109. The method of any one of claims 94 to 108, wherein e) the VHH domain binds to the
:
i) extracellular domain 1 of pIgR;~~
- ~~110. The method of any one of claims 94 to 108, wherein the VHH domain binds to the
ii) extracellular domain 2 of pIgR;~~
- ~~111. The method of any one of claims 94 to 108, wherein the VHH domain binds to the
iii) extracellular domain 1-2 of pIgR;~~
- ~~112. The method of any one of claims 94 to 108, wherein the VHH domain binds to the
iv) extracellular domain 3 of pIgR;~~
- ~~113. The method of any one of claims 94 to 108, wherein the VHH domain binds to the
v) extracellular domain 2-3 of pIgR;~~
- ~~114. The method of any one of claims 94 to 108, wherein the VHH domain binds to the
vi) extracellular domain 4-5 of pIgR; or~~
- ~~115. The method of any one of claims 94 to 108, wherein the VHH domain binds to the
vii) extracellular domain 5 of pIgR;~~
- ~~116. The method of any one of claims 94 to 115, wherein f) the pIgR is human pIgR-~~

~~117. The method of any one of claims 94 to 115, wherein pIgR is or mouse pIgR; or~~

~~118. The method of any one of claims 94 to 115, wherein 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).~~

~~119~~25. The method of any one of claims ~~94~~21 to ~~118~~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), 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);

~~120. The method of any one of claims 94 to 119, wherein the VHH domain comprises 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), IDWNGRGTTYR (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), AIDWNGRGTTYRYYADSVKG (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), FVAAIDWNGRGTTYRY (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), AIDWNGRGTTYRY (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);

~~121. The method of any one of claims 94 to 120, wherein the VHH domain comprises 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), GRTLSEFNTY (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), GRTLSEFNTYA (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);

~~122. The method of any one of claims 94 to 121, wherein the VHH domain comprises d)~~

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

ai) VHH1:

———~~i~~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);

~~ii~~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);

———~~iii~~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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- ~~b~~ii) VHH2:
 - ~~i~~1) the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 61);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTYYYRYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);
 - ~~v~~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
 - ~~vi~~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);
- ~~e~~iii) VHH3:

- i1) the CDR1 sequence of INVMG (SEQ ID NO: 2), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 31), and the CDR3 sequence of DVFGSSSGYVETY (SEQ ID NO: 62);
- ii2) 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 DVFGSSSGYVETY (SEQ ID NO: 73) or VFGSSSGYVET (SEQ ID NO: 274);
- iii3) the CDR1 sequence of GSIFSINV (SEQ ID NO: 21), the CDR2 sequence of INGGGIT (SEQ ID NO: 51), and the CDR3 sequence of KADVFGSSSGYVETY (SEQ ID NO: 84);
- iv4) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 155), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 185), and the CDR3 sequence of DVFGSSSGYVETY (SEQ ID NO: 216);
- v5) the CDR1 sequence of SINVMG (SEQ ID NO: 165), the CDR2 sequence of LVARINGGGITH (SEQ ID NO: 195), and the CDR3 sequence of KADVFGSSSGYVET (SEQ ID NO: 227); or
- vi6) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 175), the CDR2 sequence of RINGGGITH (SEQ ID NO: 205), and the CDR3 sequence of DVFGSSSGYVETY (SEQ ID NO: 238);
- div) VHH4:
 - i1) 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);
 - ii2) 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);
 - iii3) 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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- ~~ev~~5) VHH5:
 - ~~i~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~5) the CDR1 sequence of SSYAMG (SEQ ID NO: 167), the CDR2 sequence of FVA AITWNGGTTY (SEQ ID NO: 197), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 229); or
 - ~~vi~~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);
- ~~fvi~~6) VHH6:

- i1) 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);
- ii2) 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);
- iii3) 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);
- iv4) 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);
- v5) 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
- vi6) 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);
- gvii) VHH7:
 - i1) 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);
 - ii2) 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);
 - iii3) 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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- h) ~~VHH9:~~
- ~~iviii)~~ 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);
- i) ~~VHH10:~~
- ~~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);
- ii) 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);
- iii) 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);
- iv) 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);
- v) 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
- vi) 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);
- j) VHH11:
- ix) 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);
 - ii) 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);
 - iii) 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);

- ~~iv~~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);
- ~~v~~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
- ~~vi~~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
- ~~k~~) VHH12:
 - ~~ix~~i) 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~5) the CDR1 sequence of SFNTYAMG (SEQ ID NO: 173), the CDR2 sequence of FVASITWNGGSTS (SEQ ID NO: 203), and the CDR3 sequence of AAARYYYVSGTYFPAN (SEQ ID NO: 235); or
 - ~~vi~~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)-);

123. ~~The method of any one of claims 94 to 121, wherein the VHH domain comprises e)~~

_____ a framework derived from the framework of any of the VHH domains comprising the sequences of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYYYRYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWyGGMDYWGQGTQVTVSS (SEQ ID NO: 93),

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYYYRYADSVKGRSTISRDNKNTVYLQMNSLKPEDTAVYYCAATTVL
TDPRLNEYATWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDIR
IATTTIATSVKGRFAITRDNKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
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),

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

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

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKREFVAAIRW

SGGRTLYADSVKGRFTISRDNANTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNANTATLRMNSLQPDDTAVYYCAAARYYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

124. The method of any one of claims 94 to 121, wherein the VHH domain comprises a
framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%,
99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93),

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANTVYLMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
AESVKGRFTISRDNANTVYLMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNANTVYLMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96),

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITWNGGTT
YYADSVKGRFTISRDNANTVYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDVLRITGGGSTH
YAESVKGRFTISRDNANTVYLMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISWSGGST

TYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRCYWGQGTQVTVSS
(SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTTRYAMGWFRQAPGKERSFVAAISWSGSSA
GYGDSVKGRFTISRDNKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRWSGGRT
LYADSVKGRFTISRDNKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKEREFVASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

125. The method of any one of claims 94 to 124, wherein the VHH domain is comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNKNTVYLRMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
AESVKGRFTISRDNKNTVYLRMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDRIATTT
IATSVKGRFAITRDNAKNTVYLRMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRTFTSYAMGWFRQAPGKEREFVAAITWNGGTT
YYADSVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
 TYADSVKGRFTISRDN TKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
 (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
 YAESVKGRFTISRDN AKNTVY LQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
 DYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
 TYADPVKGRFTISRDN AKNTVY LRMNSLKPEDTAVYYCNDQRCYWGQGT LTVTVSS
 (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
 GYGDSVKGRFTISRDN AKNTLY LQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKERE FVA AIRWSGGRT
 LYADSVKGRFTISRDN AKNTAY LQMNNLRPEDTAVYYCAADLA EYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKERE FVA SITWNG
 GSTSYADSVKGRFTITRDN AKNTAT LRMNSLPDDTAVYYCAAARYYVSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

~~126. The method of any one of claims 94 to 125, wherein 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;

~~127. The method of claim 126, wherein b)~~ the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine;

~~128. The method of any one of claims 125 to 127, wherein c)~~ the VHH domain is:

i) ~~genetically fused to the agent;~~

ii) ~~chemically conjugated to the agent; or~~

~~129.iii) non-covalently bound to the agent; or~~

~~d) the method does not inhibit pIgR-mediated transcytosis of IgA.~~

~~27. The method of claim 128~~26, further comprising a linker between the VHH domain and the agent;

~~130. The method of claim 129; optionally wherein, the linker:~~

a) ~~is a polypeptide; or~~

~~131. The method of claim 130, wherein the linker 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.

~~132. The method of any one of claims 125 to 131, wherein the VHH domain is chemically conjugated to the agent.~~

~~133. The method of any one of claims 125 to 131, wherein the VHH domain is non-covalently bound to the agent.~~

~~134. The method of any one of claims 94 to 133, wherein the method does not inhibit pIgR-mediated transcytosis of IgA.~~

~~135~~28. The method of claim ~~134~~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)-;

~~136. The method of claim 134 or claim 135, wherein the VHH domain comprises 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), 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

~~137. The method of any one of claims 134 to 136, wherein the VHH domain comprises 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).

~~138~~29. A method to diagnose a disease or condition comprising ~~administering to~~ 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 subject, the method comprising detecting of the amount of VHH domain in the tissue of the subject, ~~wherein~~ 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.

~~139~~30. The method of claim ~~138~~29, wherein:

a) the tissue comprises a mucosal cell;

~~140. The method of claim 138, wherein the tissue comprises or a mucosal lumen;~~

~~141. The method of claim 138, wherein b) the VHH domain competes with IgA binding to the pIgR;~~

~~142. The method of claim 138, wherein the VHH domain or promotes IgA binding to the pIgR;~~

~~143. The method of any one of claims 138 to 142, wherein c) the K_D of the binding of the VHH domain to pIgR;~~

i) is from about 4 to about 525 nM;

- ~~144. The method of any one of claims 138 to 143, wherein the K_D of the binding of the VHH domain to pIgR-ii) is less than about 50 nM; or~~
- ~~145. The method of any one of claims 138 to 144, wherein the K_D of the binding of the VHH domain to pIgR-iii) is from about 4 to about 34 nM;~~
- ~~146. The method of any one of claims 138 to 145, wherein the d) _____ the T_m of the VHH domain;~~
i) _____ is from about 53 to about 77 °C; or
- ~~147. The method of any one of claims 138 to 146, wherein the T_m of the VHH domain-ii) _____ is from 53.9 to 76.4 °C;~~
- ~~148. The method of any one of claims 138 to 147, wherein e) _____ the VHH domain binds to the _____~~
i) _____ extracellular domain 1 of pIgR;
- ~~149. The method of any one of claims 138 to 147, wherein the VHH domain binds to the ii) _____ extracellular domain 2 of pIgR;~~
- ~~150. The method of any one of claims 138 to 147, wherein the VHH domain binds to the iii) _____ extracellular domain 1-2 of pIgR;~~
- ~~151. The method of any one of claims 138 to 147, wherein the VHH domain binds to the iv) _____ extracellular domain 3 of pIgR;~~
- ~~152. The method of any one of claims 138 to 147, wherein the VHH domain binds to the v) _____ extracellular domain 2-3 of pIgR;~~

~~153. The method of any one of claims 138 to 147, wherein the VHH domain binds to the~~
~~vi extracellular domain 4-5 of pIgR; or~~

~~154. The method of any one of claims 138 to 147, wherein the VHH domain binds to the~~
~~vii extracellular domain 5 of pIgR;~~

~~155. The method of any one of claims 138 to 154, wherein f) _____ the pIgR is human pIgR-~~

~~156. The method of any one of claims 138 to 154, wherein pIgR is or mouse pIgR; or~~

~~157. The method of any one of claims 138 to 154, wherein the 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).~~

~~158~~31. The method of ~~any one of claims 138 to 157~~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);

~~159. The method of any one of claims 138 to 158, wherein the VHH domain comprises 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), 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), GRTLSEFNTY (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), GRTLSEFNTYA (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 DWNGRGTYRY (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 AIRWSGGRTL YADSVKG (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
NGRGTYYYRYADSVKGRSTISRDNNAKNTVYLQMNSLKPEDTAVYYCAATTVL
DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),
EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
IATTTIATSVKGRFAITRDNNAKNTVYLMNSGLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),
QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREVFAAITW
NGGTTYADSVKGRFTISRDNNAKNTVYLQMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),
EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98),
EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDVLRITG
GGSTHYAESVKGRFTISRDNNAKNTVYLMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISW
SGGSTTYADPVKGRFTISRDNNAKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),
EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISW
SGSSAGYGDSVKGRFTISRDNNAKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
GQGTQVTVSS (SEQ ID NO: 101),
EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVFAAIRW
SGGRTLYADSVKGRFTISRDNNAKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKEREVFAISIT

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.

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 EPKTPKPQPQQLQPQNPTTESKSPK (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), INGGIT (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), FVAAIDWNGRGTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTTT (SEQ ID NO: 196), FVAAITWNGGTTY (SEQ ID NO: 197), WVAIFISGGGTTT (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);

160. The method of any one of claims 138 to 159, wherein the VHH domain comprises 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), GRTLSEFNTYA (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)-);

~~161. The method of any one of claims 138 to 160, wherein the VHH domain comprises d)~~

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

ai) VHH1:

———~~i~~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);

~~ii~~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);

———~~iii~~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);

————— iv) — 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);
 ————— v) — the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYRYRY (SEQ ID NO: 194), and the CDR3 sequence of AAGSIDLNWYGGMD (SEQ ID NO: 225); or
 ————— vi) — the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYRYRY (SEQ ID NO: 204), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 236);
 ————— b) — VHH2:
 ————— i) — 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);
 ————— ii) — the CDR1 sequence of GLTFSSY (SEQ ID NO: 10), the CDR2 sequence of DWNGRGTYRY (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);
 ————— iii) — the CDR1 sequence of GLTFSSYR (SEQ ID NO: 20), the CDR2 sequence of IDWNGRGTYRY (SEQ ID NO: 50) or IDWNGRGTYRYR (SEQ ID NO: 270), and the CDR3 sequence of CAATTVLTDPRVLNEYAT (SEQ ID NO: 83) or AATTVLTDPRVLNEYAT (SEQ ID NO: 284);
 ————— iv) — 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);
 ————— v) — the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAAIDWNGRGTYRYRY (SEQ ID NO: 194), and the CDR3 sequence of AATTVLTDPRVLNEYA (SEQ ID NO: 226); or
 ————— vi) — the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 174), the CDR2 sequence of AIDWNGRGTYRYRY (SEQ ID NO: 204), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 237);
 ————— c) — VHH3:

————— i) ————— 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);

————— ii) ————— 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);

————— iii) ————— 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);

————— iv) ————— 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);

————— v) ————— 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

————— vi) ————— 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);

————— d) ————— VHH4:

————— i) ————— the CDR1 sequence of SNAMEG (SEQ ID NO: 3), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 32), and the CDR3 sequence of PLTAR (SEQ ID NO: 63);

————— ii) ————— 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);

————— iii) ————— 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);

————— iv) ————— the CDR1 sequence of GTSVSSNAMEG (SEQ ID NO: 156), the CDR2 sequence of FIDRIATTTIATSVKG (SEQ ID NO: 186), and the CDR3 sequence of PLTAR (SEQ ID NO: 217);

—————v)————the CDR1 sequence of SSNAMG (SEQ ID NO: 166), the CDR2 sequence of WVGFIDRIATTT (SEQ ID NO: 196), and the CDR3 sequence of NHPLTA (SEQ ID NO: 228); or

—————vi)————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);

—————e)————VHH5:

—————i)————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);

—————ii)————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);

—————iii)————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);

—————iv)————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);

—————v)————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

—————vi)————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);

—————f)————VHH6:

—————i)————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);

————— ii) ——— 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);

————— iii) ——— 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);

————— iv) ——— 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);

————— v) ——— 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

————— vi) ——— 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);

————— g) ——— VHH7:

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

————— ii) ——— 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 MVNPHITAWGTIGVREIPDYDY (SEQ ID NO: 77) or VNPHTAWGTIGVREIPDYD (SEQ ID NO: 278);

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

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

_____v) _____ the CDR1 sequence of SINVMG (SEQ ID NO: 169), the CDR2 sequence of LVARITGGGTH (SEQ ID NO: 199), and the CDR3 sequence of ASMVNPHTAWGTIGVREIPDYD (SEQ ID NO: 231); or
 _____vi) _____ the CDR1 sequence of RSIGSINVMG (SEQ ID NO: 179), the CDR2 sequence of RITGGGTH (SEQ ID NO: 209), and the CDR3 sequence of MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 242);
 _____h) _____ VHH9:
 _____i) _____ 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);
 _____ii) _____ 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);
 _____iii) _____ 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);
 _____iv) _____ 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);
 _____v) _____ the CDR1 sequence of STYRMG (SEQ ID NO: 170), the CDR2 sequence of FVAAISWSGGSTT (SEQ ID NO: 200), and the CDR3 sequence of NDQRG (SEQ ID NO: 232); or
 _____vi) _____ 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);
 _____i) _____ VHH10:
 _____i) _____ 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);

————— ii) — the CDR1 sequence of GFTTFTRY (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 PFNQC (SEQ ID NO: 280);

————— iii) — the CDR1 sequence of GFTTFTRYA (SEQ ID NO: 27), the CDR2 sequence of ISWSGSSA (SEQ ID NO: 57), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 90);

————— iv) — the CDR1 sequence of GFTTFTRYAMG (SEQ ID NO: 161), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 191), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 222);

————— v) — 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

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

————— j) — VHH11:

————— i) — 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);

————— ii) — 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);

————— iii) — 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);

————— iv) — 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);

————v)——— 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
 ————vi)——— 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
 ————k)——— VHH12:
 ————i)——— 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);
 ————ii)——— 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);
 ————iii)——— 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);
 ————iv)——— 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);
 ————v)——— 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
 ————vi)——— 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).

162. The method of any one of claims 138 to 161, wherein the VHH domain comprises a framework derived from the framework of any of the VHH domains comprising the sequences of QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG TYYRYYADSVKGRSTISRDN AKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD

YWGQGTQVTVSS (SEQ ID NO: 93),
EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANKNTVYVLQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94),
QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGGITHY
AESVKGRFTISRDNANKNTVYVLQMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95),
EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYVLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96),
QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREVFAAITWNGGTT
YYADSVKGRFTISRDNANKNTVYVLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97),
EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNANKNTVYVLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98),
EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDVLRITGGGSTH
YAESVKGRFTISRDNANKNTVYVLQMNSLEPEDTAVYYCASMVNPHTAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99),
QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISWSGGST
TYADPVKGRFTISRDNANKNTVYVLRMNSLKPEDTAVYYCNDQRCGYWGQGTQVTVSS
(SEQ ID NO: 100),
EVQVVESGGGLVQAGGSLRLSCAASGFTFTTRYAMGWFRQAPGKERSFVAAISWSGSSA
GYGDSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 101),
EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVFAAIRWSGGRT
LYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKEREVFAITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDETAVYYCAAARYYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

163. The method of any one of claims 138 to 162, wherein the VHH domain comprises a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNAKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNAKNTVYLMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGGITHY
AESVKGRFTISRDNAKNTVYLMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYLMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRFTFSSYAMGWFRQAPGKREFVAAITWNGGTT
YYADSVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98);

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
YAESVKGRFTISRDNAKNTVYLMNSLEPEDTAVYYCASMVNPIITAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99);

QVQLVESGGGLVQAGGSLRLSCAVSGRFTFSTYRMGWFRQAPGKERSFVA AISWSGGST
TYADPVKGRFTISRDNAKNTVYLMNSLKPEDTAVYYCNDQRCGYWGQGTQVTVSS
(SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
GYGDSVKGRFTISRDNAKNTLYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFFVAAIRWSGGRT
LYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSTFYAMGWFRQAPGKEREFFVASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQDDTAVYYCAAARYVVSQTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

164. The method of any one of claims 138 to 163, wherein the VHH domain is comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93);
EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANKNTVYLQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94);
QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGGITHY
AESVKGRFTISRDNANKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95);
EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);
QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFFVAITWNGGTT
YYADSVKGRFTISRDNANKNTVYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97);
EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNNTKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98);
EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
YAESVKGRFTISRDNANKNTVYLQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY

DYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISWSGGST
 TYADPVKGRFTISRDNANKNTVYLRMNSLKPEDTAVYYCNDQRCYWGQGTQVTVSS
 (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISWSGSSA
 GYGDSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYYCAADPFNQCYWGQGTQVTVSS
 (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRWSGGRT
 LYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKEREFVASITWNG
 GSTSYADSVKGRFTITRDNAKNTATLRMNSLQDDTAVYYCAAARYVSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

165. The method of any one of claims 138 to 164, wherein 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.

166. The method of claim 165, wherein the agent is an antibiotic, an antibody or fragment thereof, a peptide or a vaccine.

167. The method of any one of claims 138 to 166, wherein the VHH domain is genetically fused or chemically conjugated to the agent.

168. The method of claim 167, wherein a linker is between the VHH domain and the agent.

~~169. The method of claim 168, wherein the linker is a polypeptide.~~

~~170. The method of claim 169, wherein the linker is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQPQLQPQPNPTTESKSPK (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.~~

~~171. The method of any one of claims 138 to 170, wherein the VHH domain is chemically conjugated to the agent.~~

~~172. The method of any one of claims 138 to 171, wherein the VHH domain is non-covalently bound to the agent.~~

~~173. The method of any one of claims 138 to 172, wherein the VHH domain comprises a radioisotope.~~

~~174. The method of claim 173, wherein the radioisotope is zirconium-89.~~

~~175. The method of any of claims 138 to 174, wherein the disease is lung cancer, and wherein the tissue is lung.~~

~~176. The method of any of claims 138 to 174, wherein the disease is endometrial cancer, and wherein the tissue is the uterus.~~

177. The method of any of claims 138 to 174, wherein the disease is colon cancer, and wherein the tissue is the colon.

178. The method of any of claims 138 to 174, wherein the disease is an inflammatory disease, and wherein the tissue is lamina propria.

179. The method of claim 178, wherein the inflammatory disease is inflammatory bowel disease.

180. The method of claim 179, wherein the inflammatory disease is Crohn's disease or ulcerative colitis.

181. The method of any one of claims 138 to 180, wherein the diseased cell expresses an antigen, and wherein the therapeutic molecule is coupled to an antibody that specifically recognizes the antigen.

182. The method of claim 181, wherein the antigen is specific to the diseased cell.

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

184. A method for transporting a therapeutic molecule to a basolateral surface of the pIgR-expressing cell of a subject, comprising administering to the subject the therapeutic molecule comprising an agent and a single domain antibody that binds to pIgR.

~~185. The method of claim 184, wherein the therapeutic molecule is administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.~~

~~186. A method for transporting a therapeutic molecule to systemic circulation of a subject, comprising administering to the subject a therapeutic molecule comprising an agent and a single domain antibody that binds to pIgR, wherein the therapeutic molecule is administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.~~

~~187. A method for transporting a therapeutic molecule to lamina propria or gastrointestinal tract of a subject, comprising administering to the subject a therapeutic molecule comprising an agent and a single domain antibody that binds to pIgR, wherein the therapeutic molecule is administered to the subject via oral delivery, buccal delivery, nasal delivery or inhalation delivery.~~

~~188. The method of any one of claims 184 to 187, wherein the therapeutic agent is transported from an apical surface of a pIgR-expressing cell to a basolateral surface of the pIgR-expressing cell in the subject.~~

~~189. The method of claim 183 or claim 188, wherein 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.~~

~~190. The method of any one of claims 183 to 189, wherein the pIgR-expressing cell is an epithelial cell.~~

191. The method of claim 190, wherein the epithelia cell is an intestinal lumen cell or an airway epithelial cell.

192. The method of any one of claims 183 to 191, wherein the agent is a diabetes medication.

193. The method of claim 192, 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.

194. The method of any one of claims 183 to 191, wherein the agent is a peptide or an antibody or a fragment thereof.

195. The method of claim 194, wherein the antibody or fragment thereof is selected from a group consisting of an anti TNF alpha antibody or a fragment thereof, an anti IL23 antibody or a fragment thereof, an antibody or a fragment thereof that binds to a receptor of IL23, or an inhibitor of the receptor of IL23.

196. The method of any one of claims 183 to 191, wherein the agent is a vaccine.

197. The method of claim 196, wherein the vaccine is for preventing an infection selected from a group consisting of Vibrio, Cholera, Typhoid, Rotavirus, Tuberculosis, HIV, Flu, Ebola, and Sendai.

198. The method of any one of claims 183 to 197, wherein the single domain antibody 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 pIgR.

199. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 1 of pIgR.

200. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 2 of pIgR.

201. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 1-2 of pIgR.

202. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 3 of pIgR.

203. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 2-3 of pIgR.

204. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 4-5 of pIgR.

205. The method of any one of claims 183 to 197, wherein the single domain antibody binds to an extracellular domain 5 of pIgR.

206. The method of any one of claims 183 to 205, wherein the single domain antibody competes with IgA binding to the pIgR.

207. The method of any one of claims 183 to 205, wherein the single domain antibody promotes IgA binding to the pIgR.

208. The method of any one of claims 183 to 207, wherein the K_D of the binding of the single domain antibody to pIgR is from about 4 to about 525 nM.

209. The method of any one of claims 183 to 207, wherein the K_D of the binding of the single domain antibody to pIgR is less than about 50 nM.

210. The method of any one of claims 183 to 207, wherein the K_D of the binding of the single domain antibody to pIgR is from about 4 to about 34 nM.

211. The method of any one of claims 183 to 210, wherein the T_m of the single domain antibody is from about 53 to about 77 °C.

212. The method of any one of claims 183 to 210, wherein the T_m of the single domain antibody is from 53.9 to 76.4 °C.

213. The method of any one of claims 183 to 212, wherein pIgR is human pIgR.

214. The method of any one of claims 183 to 212, wherein pIgR is mouse pIgR.

215. The method of any one of claims 183 to 212, wherein the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

216. The method of any one of claims 183 to 215, wherein the single domain antibody comprises 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), MVNPHTAWGTIGVREIPDYDY (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), MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPHTAWGTIGVREIPDYD (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), ASMVNPHTAWGTIGVREIPDYDY (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), MVNPHTAWGTIGVREIPDYDY (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), ASMVNPHTAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRC (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), MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 242), QRCY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246).

217. The method of any one of claims 183 to 216, wherein the single domain antibody comprises 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), 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), INGGIT (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), FISGGGTTTTYADSVKG (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).

218. The method of any one of claims 183 to 217, wherein the single domain antibody comprises 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), GRTLSEFNTY (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), GRTLSEFNTYA (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), 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).~~

~~219. The method of any one of claims 183 to 218, wherein the single domain antibody comprises a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence of the single domain antibody selected from the group consisting of:~~

~~—— a) —— VHH1:~~

~~—— i) —— the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60);~~

~~—— ii) —— 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);~~

~~—— iii) —— 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);~~

~~—— iv) —— 4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTYYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);~~

~~—— v) —— 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~~

~~—— vi) —— 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);~~

~~—— bii) VHH2:~~

- i1) 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);
- ii2) 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);
- iii3) 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);
- iv4) 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);
- v5) the CDR1 sequence of SSYRMG (SEQ ID NO: 164), the CDR2 sequence of FVAIDWNGRGTYYYRY (SEQ ID NO: 194), and the CDR3 sequence of AATTVLTDPRVLNEYA (SEQ ID NO: 226); or
- vi6) 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);
- eiii) VHH3:
 - i1) 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);
 - ii2) 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);
 - iii3) 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);

- ~~iv~~4) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 155), the CDR2 sequence of RINGGGITHYAESVKG (SEQ ID NO: 185), and the CDR3 sequence of DVFGSSSGYVETY (SEQ ID NO: 216);
- ~~v~~5) the CDR1 sequence of SINVMG (SEQ ID NO: 165), the CDR2 sequence of LVARINGGGITH (SEQ ID NO: 195), and the CDR3 sequence of KADVFGSSSGYVET (SEQ ID NO: 227); or
- ~~vi~~6) the CDR1 sequence of GSIFSINVMG (SEQ ID NO: 175), the CDR2 sequence of RINGGGITH (SEQ ID NO: 205), and the CDR3 sequence of DVFGSSSGYVETY (SEQ ID NO: 238);
- ~~div~~v) VHH4:
 - ~~i~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~5) the CDR1 sequence of SSNAMG (SEQ ID NO: 166), the CDR2 sequence of WVGFIIDRIATTT (SEQ ID NO: 196), and the CDR3 sequence of NHPLTA (SEQ ID NO: 228); or
 - ~~vi~~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);
- ~~ev~~v) VHH5:

- i1) 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);
- ii2) 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);
- iii3) 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);
- iv4) 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);
- v5) 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
- vi6) 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);
- fvi)VHH6:
 - i1) 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);
 - ii2) 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);
 - iii3) 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);
 - iv4) 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);

- ~~v~~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
- ~~vi~~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);
- ~~g~~vii) VHH7:
 - ~~i~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);
- ~~h~~) VHH9:
 - ~~iviii~~) VHH8:
 - 1) the CDR1 sequence of TYRMG (SEQ ID NO: 7), the CDR2 sequence of AISWGGSTTYADPVKG (SEQ ID NO: 36), and the CDR3 sequence of DQRGY (SEQ ID NO: 67) or QRGY (SEQ ID NO: 271);

- ~~ii~~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);
- ~~iii~~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);
- ~~iv~~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);
- ~~v~~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
- ~~vi~~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);
- ~~i~~) ~~VHH10~~:
- ~~ii~~x) ~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);

- ~~v~~5) the CDR1 sequence of TRYAMG (SEQ ID NO: 171), the CDR2 sequence of FVAAISWSGSSAG (SEQ ID NO: 201), and the CDR3 sequence of AADPFNQG (SEQ ID NO: 233); or
- ~~vi~~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);
- j) VHH11:
 - ~~ix~~i) 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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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
- k) VHH12:
 - ~~ixi~~i) VHH11:

- i) 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);
- ~~ii~~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);
- ~~iii~~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);
- ~~iv~~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);
- ~~v~~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
- ~~vi~~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)-i;

~~220. The method of any one of claims 183 to 219, wherein the single domain antibody~~

~~comprises e)~~ a framework derived from the framework of any of the ~~single domain antibodies~~ 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),
 EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRI
 IATTTIATSVKGRFAITRDNAKNTVYQLQMSGLKPEDTAVYYCNHPLTARWGQGT
 QVTVSS (SEQ ID NO: 96),
 QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREVFAAITW
 NGGTTYADSVKGRFTISRDNKNTVYQLQMNSLKPEDTAVYYCAADPFNQGY
 WGQGTQVTVSS (SEQ ID NO: 97),
 EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
 GGTTYADSVKGRFTISRDNKNTVYQLHMNSLKPEDTAVYYCNHPLTSRWGQG
 TVTVSS (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
 GGSTHYAESVKGRFTISRDNKNTVYQLQMNSLEPEDTAVYYCASMVNPIITAWG
 TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISW
 SGGSTTYADPVKGRFTISRDNKNTVYQLRMNSLKPEDTAVYYCNDQRGYWGQG
 TLVTVSS (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISW
 SGSSAGYGDSVKGRFTISRDNKNTLYQLQMNSLKPEDTAVYYCAADPFNQGYW
 GQGTQVTVSS (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVFAAIRW
 SGGRTLYADSVKGRFTISRDNKNTAYQLQMNNLRPEDTAVYYCAADLAEYSGT
 YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSENTYAMGWFRQAPGKEREVFAISIT
 WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG
 TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

~~221. The method of any one of claims 183 to 219, wherein the single domain antibody comprises a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of~~
 QVQLVESGGGLVQAGGSLRLACAAPGLTFSSYRMGWFRQAPGQEREVFAAIDWNGRG
 TYYRYYADSVKGRSTISRDNKNTMYQLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD

YWGQGTQVTVSS (SEQ ID NO: 93),
EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNANKNTVYVLQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94),
QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGGITHY
AESVKGRFTISRDNANKNTVYVLQMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95),
EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYVLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96),
QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITWNGGTT
YYADSVKGRFTISRDNANKNTVYVLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97),
EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNNTKNTVYVLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98),
EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQORDLVARITGGGSTH
YAESVKGRFTISRDNANKNTVYVLQMNSLEPEDTAVYYCASMVNPHTAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99),
QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISWSGGST
TYADPVKGRFTISRDNANKNTVYVLRMNSLKPEDTAVYYCNDQRCGYWGQGTTLTVTVSS
(SEQ ID NO: 100),
EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISWSGSSA
GYGDSVKGRFTISRDNANKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 101),
EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRWSGGRT
LYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102), or
QVQLVETGGGLVQAGDSLRLSCAASGRTLSENTYAMGWFRQAPGKEREFVASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

222. The method of any one of claims 183 to 221, wherein the single domain antibody is comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNAKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
YWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
TYYRYYADSVKGRSTISRDNAKNTVYLLQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
TWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSISSINVMGWYRQAPGKQRELVARINGGGGITHY
AESVKGRFTISRDNAKNTVYLLQMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYLLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRFTFSSYAMGWFRQAPGKREFVAAITWNGGTT
YYADSVKGRFTISRDNAKNTVYLLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNKNTVYLLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98);

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
YAESVKGRFTISRDNAKNTVYLLQMNSLEPEDTAVYYCASMVNPIITAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99);

QVQLVESGGGLVQAGGSLRLSCAVSGRFTFSTYRMGWFRQAPGKERSFVA AISWSGGST
TYADPVKGRFTISRDNAKNTVYLLRMNSLKPEDTAVYYCNDQRCGYWGQGTQVTVSS
(SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
GYGDSVKGRFTISRDNAKNTLYLLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
S (SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFFVAAIRWSGGRT
 LYADSVKGRFTISRDNANKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTFYAMGWFRQAPGKEREFFVASITWNG
 GSTSYADSVKGRFTITRDNAKNTATLRMNSLPDDTAVYYCAAARYYVSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

223. The method of any one of claims 183 to 222, wherein the single domain antibody is 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

~~224~~iii) non-covalently bound to the agent;

or

b) the method does not inhibit pIgR-mediated transcytosis of IgA.

39. The method of claim ~~223~~38, further comprising a linker between the single domain antibody
 and the agent-

~~225. The method of claim 224;~~ optionally wherein, the linker-

a) is a polypeptide-; or

~~226. The method of claim 225, wherein the linker 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), (GGGS)_n (SEQ ID NO: 148) and (GGGS)_n (SEQ ID NO: 149), wherein n is an integer from 1 to 20.~~

~~227. The method of any one of claims 223 to 226, wherein the single domain antibody is chemically conjugated to the agent.~~

~~228. The method of any one of claims 223 to 226, wherein the single domain antibody is non-covalently bound to the agent.~~

~~229. The method of any one of claims 183 to 228, wherein the method does not inhibit pIgR-mediated transcytosis of IgA.~~

~~230~~40. The method of claim ~~229~~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), GRTL SFNTY (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), GRTL SFNTYA (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), GRTL SFNTYAMG (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 GRTL SFNTYAMG (SEQ ID NO: 183)-);

~~231. The method of claim 229 or claim 230, wherein the single domain antibody comprises 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), WVGFIATTTT (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~~ or

~~232. The method of any one of claims 229 to 231, wherein the single domain antibody comprises~~
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).

~~233-41.~~ A process for providing a molecule to a subject, ~~comprising administering to the subject wherein~~ the molecule ~~comprising~~ 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.

~~234~~42. The process of claim ~~233~~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;

~~235. The process of claim 233 or claim 234, wherein 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;

~~236. The process of any one of claims 233 to 235, wherein c)~~ the pIgR-expressing cell is an epithelial cell;

~~237. The process of claim 236, wherein d) _____ the epitheliaepithelial cell is an intestinal lumen cell or an airway epithelial cell-;~~

~~238. The process of any one of claims 233 to 237, wherein e) _____ the agent is a diabetes medication-~~

~~239. The process of claim 238, 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-;~~

~~240. The process of any one of claims 233 to 237, f) wherein the agent is a peptide or an antibody or a fragment thereof-~~

~~241. The process of claim 240, 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-;~~

~~242. The process of any one of claims 233 to 237, wherein g) _____ the agent is a vaccine-~~

~~243. The process of claim 242,; 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-;~~

~~244. The process of any one of claims 233 to 243, wherein 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;

~~245. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an ii) extracellular domain 1 of pIgR;~~

~~246. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an iii) extracellular domain 2 of pIgR;~~

~~247. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an iv) extracellular domain 1-2 of pIgR;~~

~~248. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an v) extracellular domain 3 of pIgR;~~

~~249. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an vi) extracellular domain 2-3 of pIgR;~~

~~250. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an vii) extracellular domain 4-5 of pIgR; or~~

~~251. The process of any one of claims 233 to 243, wherein the single domain antibody binds to an viii) extracellular domain 5 of pIgR;~~

~~252. The process of any one of claims 233 to 251, wherein i) the single domain antibody competes with IgA binding to the pIgR-~~

- ~~253. The process of any one of claims 233 to 251, wherein the single domain antibody or promotes IgA binding to the pIgR-;~~
- ~~254. The process of any one of claims 233 to 253, wherein j) the K_D of the binding of the single domain antibody to pIgR-;~~
- ~~i) is from about 4 to about 525 nM-;~~
- ~~255. The process of any one of claims 233 to 253, wherein the K_D of the binding of the single domain antibody to pIgR- ii) is less than about 50 nM-; or~~
- ~~256. The process of any one of claims 233 to 253, wherein the K_D of the binding of the single domain antibody to pIgR- iii) is from about 4 to about 34 nM-;~~
- ~~257. The process of any one of claims 233 to 256, wherein k) the T_m of the single domain antibody-;~~
- ~~i) is from about 53 to about 77 °C-; or~~
- ~~258. The process of any one of claims 233 to 256, wherein the T_m of the single domain antibody- ii) is from 53.9 to 76.4 °C.~~
- ~~259. The process of any one of claims 233 to 258, wherein l) pIgR is human pIgR-~~
- ~~260. The process of any one of claims 233 to 258, wherein pIgR is or mouse pIgR-;~~
- ~~261. The process of any one of claims 233 to 258, wherein or~~
- ~~m) the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.~~

~~262~~43. The process of ~~any one of claims 233 to 261~~claim 41 or claim 42, 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), 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), 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);

~~263. The process of any one of claims 233 to 262, wherein the single domain antibody comprises 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), WVGFDRIATTT (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)-);

264. ~~The process of any one of claims 233 to 263, wherein the single domain antibody comprises 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), GRTLSEFNTY (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), GRTLSEFNTYA (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), 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).~~

~~265. The process of any one of claims 233 to 264, wherein the single domain antibody comprises a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence of the single domain antibody selected from the group consisting of:~~

~~—— a) —— VHH1:~~

~~—— i) —— the CDR1 sequence of SYRMG (SEQ ID NO: 1), the CDR2 sequence of AIDWNGRGTYYYRYYADSVKG (SEQ ID NO: 30), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 60);~~

~~—— ii) —— 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);~~

~~—— iii) —— 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);~~

~~—— iv) —— the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTYYYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);~~

~~—— v) —— 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~~

~~—— vi) —— 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);~~

~~—— b) —— VHH2:~~

————— i) ——— 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);

————— ii) ——— 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);

————— iii) ——— 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);

————— iv) ——— 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);

————— v) ——— 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

————— vi) ——— 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);

————— c) ——— VHH3:

————— i) ——— 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);

————— ii) ——— 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);

————— iii) ——— 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);

—————iv)———— 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);

—————v)———— 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

—————vi)———— 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);

—————d)———— VHH4:

—————i)———— 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);

—————ii)———— 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);

—————iii)———— 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);

—————iv)———— 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);

—————v)———— 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

—————vi)———— 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);

—————e)———— VHH5:

- i) ——— 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);
- ii) ——— 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);
- iii) ——— 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);
- iv) ——— 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);
- v) ——— 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
- vi) ——— 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);
- f) ——— VHH6:
 - i) ——— 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);
 - ii) ——— 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);
 - iii) ——— 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);
 - iv) ——— 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);

—————v)————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

—————vi)————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);

—————g)————VHH7:

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

—————ii)————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 MVNPHITAWGTIGVREIPDYDY (SEQ ID NO: 77) or VNPITAWGTIGVREIPDYD (SEQ ID NO: 278);

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

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

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

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

—————h)————VHH9:

—————i)————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);

————— ii) ————— 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);

————— iii) ————— 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);

————— iv) ————— 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);

————— v) ————— 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

————— vi) ————— 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);

————— i) ————— VHH10:

————— i) ————— 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);

————— ii) ————— 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);

————— iii) ————— 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);

————— iv) ————— 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);

————— v) ————— 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

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

—————j) — VHH11:

—————i) — 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);

—————ii) — 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);

—————iii) — 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);

—————iv) — 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);

—————v) — 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

—————vi) — 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

—————k) — VHH12:

—————i) — 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);

—————ii) — 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);

———— iii) ——— 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);
 ———— iv) ——— 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);
 ———— v) ——— 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
 ———— vi) ——— 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).

266. The process of any one of claims 233 to 265, wherein the single domain antibody comprises a framework derived from the framework of any of the single domain antibody comprising the sequences of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
 TYYRYYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
 YWGQGTQVTVSS (SEQ ID NO: 93);

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
 TYYRYYADSVKGRSTISRDNKNTVYLMNSLKPEDTAVYYCAATTVLTPRVLNEYA
 TWGQGTQVTVSS (SEQ ID NO: 94);

QLQLVESGGGLVQPGGSLRLSCAASGSISSINVMGWYRQAPGKQRELVARINGGGITHY
 AESVKGRFTISRDNKNTVYLMNSLKPEDTAAYYCKADVFGSSGYVETWYWGQGTQV
 TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDRIATTT
 IATSVKGRFAITRDNKNTVYLMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
 (SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREFVAAITWNGGTT
 YYADSVKGRFTISRDNKNTVYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
 TYADSVKGRFTISRDN TKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
 (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
 YAESVKGRFTISRDN AKNTVY LQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
 DYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
 TYADPVKGRFTISRDN AKNTVY LRMNSLKPEDTAVYYCNDQRCYWGQGT LTVTVSS
 (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
 GYGDSVKGRFTISRDN AKNTLY LQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKERE FVA AIRWSGGRT
 LYADSVKGRFTISRDN AKNTAY LQMNNLRPEDTAVYYCAADLA EYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKERE FVA SITWNG
 GSTSYADSVKGRFTITRDN AKNTAT LRMNSLQ PDDTAVYYCAAARYV VSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

267. The process of any one of claims 233 to 265, wherein the single domain antibody comprises a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQERE FVA AIDWNGRG
 TYYRYYADSVKGRSTISRDN AKNTMY LQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
 YWGQGTQVTVSS (SEQ ID NO: 93),
 EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQERE FVA AIDWNGRG
 TYYRYYADSVKGRSTISRDN AKNTVY LQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
 TWGQGTQVTVSS (SEQ ID NO: 94),
 QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
 AESVKGRFTISRDN AKNTVY LQMNSLKPEDTA AYYCKADVFGSSGYVETYWGQGTQV

TVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYVLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96),

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREVAAITWNGGTT
YYADSVKGRFTISRDNKNTVYVLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNKNTVYVLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
YAESVKGRFTISRDNKNTVYVLQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
TYADPVKGRFTISRDNKNTVYVLRMNSLKPEDTAVYYCNDQRCYWGQGTQVTVSS
(SEQ ID NO: 100),

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
GYGDSVKGRFTISRDNKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 101),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVAAIRWSGGRT
LYADSVKGRFTISRDNKNTAYLQMNNLRPEDTAVYYCAADLA EYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102), or

QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKEREV ASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

268. The process of any one of claims 233 to 267, wherein the single domain antibody is
comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or
100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREVAAIDWNGRG

TYYRYYADSVKGRSTISRDNNAKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
 YWGQGTQVTVSS (SEQ ID NO: 93);
 EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
 TYYRYYADSVKGRSTISRDNNAKNTVYLMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
 TWGQGTQVTVSS (SEQ ID NO: 94);
 QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGGITHY
 AESVKGRFTISRDNNAKNTVYLMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
 TVSS (SEQ ID NO: 95);
 EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
 IATSVKGRFAITRDNAKNTVYLMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
 (SEQ ID NO: 96);
 QVQLVESGGGLVQAGGSLRLSCAASGRFTFSSYAMGWFRQAPGKREFVAAITWNGGTT
 YYADSVKGRFTISRDNNAKNTVYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 97);
 EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
 TYADSVKGRFTISRDNNTKNTVYLMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
 (SEQ ID NO: 98);
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
 YAESVKGRFTISRDNNAKNTVYLMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
 DYWGQGTQVTVSS (SEQ ID NO: 99);
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
 TYADPVKGRFTISRDNNAKNTVYLRMNSLKPEDTAVYYCNDQRCGYWGQGTTLTVSS
 (SEQ ID NO: 100);
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTTRYAMGWFRQAPGKERSFVA AISWSGSSA
 GYGDSVKGRFTISRDNNAKNTLYLMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 101);
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKREFVAAIRWSGGRT
 LYADSVKGRFTISRDNNAKNTAYLMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102); or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTNTYAMGWFRQAPGKREFVASITWNG

GSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

269. The process of any one of claims 233 to 268, wherein the single domain antibody is genetically fused or chemically conjugated to the agent.

270. The process of claim 269, further comprising a linker between the single domain antibody and the agent.

271. The process of claim 270, wherein the linker is a polypeptide.

272. The process of claim 271, wherein the linker is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQPQLQPQPNPTTESKSPK (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.

273. The process of any one of claims 269 to 272, wherein the single domain antibody is chemically conjugated to the agent.

274. The process of any one of claims 269 to 272, wherein the single domain antibody is non-covalently bound to the agent.

275. The process of any one of claims 233 to 274, wherein the process does not inhibit pIgR-mediated transcytosis of IgA.

276. The process of claim 275, wherein the single domain antibody comprises 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).~~

277. The process of claim 275 or claim 276, wherein the single domain antibody comprises 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), WVGFIATTTT (SEQ ID NO: 196), LVARITGGGSTH (SEQ ID NO: 199), FVA AISWSGGSTT (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).~~

~~278. The process of any one of claims 275 to 277, wherein the single domain antibody comprises a CDR3 sequence of PLTAR (SEQ ID NO: 63), MVNPHTAWGTIGVREIPDYDY (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), MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 77), VNPHTAWGTIGVREIPDYD (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), ASMVNPHTAWGTIGVREIPDYDY (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), MVNPHTAWGTIGVREIPDYDY (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), ASMVNPHTAWGTIGVREIPDYD (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), MVNPHTAWGTIGVREIPDYDY (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).~~

~~279. A process comprising steps for providing a molecule to a subject.~~

280. The process of claim 279, wherein the molecule comprises an agent and a single domain antibody that binds to pIgR.

281. The process of claim 280, wherein 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.

282. The process of any one of claims 279 to 281, wherein the agent is an antibody or fragment thereof, a peptide, or a vaccine.

283. The process of any one of claims 280 to 282, wherein the single domain antibody is genetically fused or chemically conjugated to the agent.

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

285. The system of claim 284, wherein the agent is a diabetes medication.

286. The system of claim 285, 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.

287. The system of claim 284, wherein the agent is a peptide or an antibody or a fragment thereof.

288. The system of claim 287, 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.

289. The system of claim 284, wherein the agent is a vaccine.

290. The system of claim 289, wherein the vaccine is for preventing an infection selected from a group consisting of Vibrio, Cholera, Typhoid, Rotavirus, Tuberculosis, HIV, Flu, Ebola, and Sendai.

291. The system of any one of claims 284 to 290, wherein the single domain antibody 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 pIgR.

292. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 1 of pIgR.

293. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 2 of pIgR.

294. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 1-2 of pIgR.

295. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 3 of pIgR.

296. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 2-3 of pIgR.

297. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 4-5 of pIgR.

298. The system of any one of claims 284 to 290, wherein the single domain antibody binds to an extracellular domain 5 of pIgR.

299. The system of any one of claims 284 to 298, wherein the single domain antibody competes with IgA binding to the pIgR.

300. The system of any one of claims 284 to 298, wherein the single domain antibody promotes IgA binding to the pIgR.

301. The system of any one of claims 284 to 300, wherein the K_D of the binding of the single domain antibody to pIgR is from about 4 to about 525 nM.

302. The system of any one of claims 284 to 300, wherein the K_D of the binding of the single domain antibody to pIgR is less than about 50 nM.

303. The system of any one of claims 284 to 300, wherein the K_D of the binding of the single domain antibody to pIgR is from about 4 to about 34 nM.

304. The system of any one of claims 284 to 303, wherein the T_m of the single domain antibody is from about 53 to about 77 °C.

305. The system of any one of claims 284 to 303, wherein the T_m of the single domain antibody is from 53.9 to 76.4 °C.

306. The system of any one of claims 284 to 305, wherein pIgR is human pIgR.

307. The system of any one of claims 284 to 305, wherein pIgR is mouse pIgR.

308. The system of any one of claims 284 to 305, wherein the single domain antibody does not bind to a stalk sequence of human pIgR and/or a stalk sequence of mouse pIgR.

309. The system of any one of claims 284 to 308, wherein the single domain antibody comprises 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), MVNPHTAWGTIGVREIPDYDY (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), MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 77),

~~VNPHTAWGTIGVREIPDYD (SEQ ID NO: 278), DQRCY (SEQ ID NO: 78), RC (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), ASMVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 88), NDQRCY (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), MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 220), QRCY (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), ASMVNPHTAWGTIGVREIPDYD (SEQ ID NO: 231), NDQRC (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), MVNPHTAWGTIGVREIPDYDY (SEQ ID NO: 242), QRCY (SEQ ID NO: 243), DPFNQGY (SEQ ID NO: 244), DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 245), or ARYYVSGTYFPANY (SEQ ID NO: 246).~~

310. The system of any one of claims 284 to 309, wherein the single domain antibody comprises a CDR2 sequence of ~~AIDWNGRGTYRYRYADSVKG (SEQ ID NO: 30), RINGGGITHYAESVKG (SEQ ID NO: 31), FIDRIATTTIATSVKG (SEQ ID NO: 32), AITWNGGTTYRYADSVKG (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), IDWNGRGTTY (SEQ ID NO: 50), IDWNGRGTTYR (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), AIDWNGRGTTYRYRYADSVKG (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), FVAAIDWNGRGTTYRY (SEQ ID NO: 194), LVARINGGGITH (SEQ ID NO: 195), WVGFIATTTT (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), AIDWNGRGTTYRY (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).~~

311. ~~The system of any one of claims 284 to 310, wherein the single domain antibody comprises 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 GRTLSENTYAMG (SEQ ID NO: 183);

~~312. The system of any one of claims 284 to 311, wherein the single domain antibody comprises d) a CDR1 sequence, a CDR2 sequence, and a CDR3 sequence of the single VHH domain antibody selected from the group consisting of:~~

ai) VHH1:

——i1) 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);

- ii₂) 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);
- iii₃) 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);
- iv₄) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR 2 sequence of AIDWNGRGTYRYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of GSIDLNWYGGMDY (SEQ ID NO: 214);
- v₅) 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
- vi₆) 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);
- bii) VHH2:
 - i₁) 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);
 - ii₂) 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);
 - iii₃) 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);

- ~~iv~~4) the CDR1 sequence of GLTFSSYRMG (SEQ ID NO: 154), the CDR2 sequence of AIDWNGRGTYRYYADSVKG (SEQ ID NO: 184), and the CDR3 sequence of TTVLTDPRVLNEYAT (SEQ ID NO: 215);
- ~~v~~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
- ~~vi~~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);
- ~~e~~iii) VHH3:
 - ~~i~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);
- ~~d~~iv) VHH4:

- i1) 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);
- ii2) 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);
- iii3) 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);
- iv4) 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);
- v5) 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
- vi6) 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);
- ev) VHH5:
 - i1) 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);
 - ii2) 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);
 - iii3) 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);
 - iv4) 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);

- ~~v~~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
- ~~vi~~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);
- ~~f~~vi) VHH6:
 - ~~i~~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);
 - ~~ii~~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);
 - ~~iii~~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);
 - ~~iv~~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);
 - ~~v~~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
 - ~~vi~~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);
- ~~g~~vii) VHH7:
 - ~~i~~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);
 - ~~ii~~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);

———~~iii~~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);

———~~iv~~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);

———~~v~~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

———~~vi~~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);

———h) VHH9:

———~~iviii~~) 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);

———~~ii~~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);

———~~iii~~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);

———~~iv~~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);

———~~v~~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

CDR3 sequence of DLAEYSGTYSSPADSPAGYDY (SEQ ID NO: 80) or
LAEYSGTYSSPADSPAGYD (SEQ ID NO: 281);

———~~iii~~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);

———~~iv~~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);

———~~v~~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

———~~vi~~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

———k) ~~VHH12:~~

———~~ixi~~) 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);

———~~ii~~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);

———~~iii~~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);

———~~iv~~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);

—v5) 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

—vi6) 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)-);

~~313. The system of any one of claims 284 to 312, wherein the single domain antibody~~

~~comprises e) a framework derived from the framework of any of the single domain antibodies~~
VHH domains comprising the sequences of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYRYRYADSVKGRSTISRDN AKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),

EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYRYRYADSVKGRSTISRDN AKNTVYLQMNSLKPEDTAVYYCAATTVL
DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),

QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDN AKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVG FIDR
IATTTIATSVKGRFAITRDNAKNTVYLQMSG LKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKREFVAAITW
NGGTTYADSVKGRFTISRDN AKNTVYLQMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTTTYADSVKGRFTISRDN TKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98),

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDN AKNTVYLQMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISW
 SGGSTTYADPVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
 TLVTVSS (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISW
 SGSSAGYGDSVKGRFTISRDNKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW
 GQGTQVTVSS (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVFAAIRW
 SGGRTLYADSVKGRFTISRDNKNTAYLQMNNLRPEDTAVYYCAADLAEYSGT
 YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTLSTYAMGWFRQAPGKEREVFAISIT
 WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG
 TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

314. The system of any one of claims 284 to 312, wherein the single domain antibody comprises a framework comprising sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
 TYYRYYADSVKGRSTISRDNKNTMYLQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
 YWGQGTQVTVSS (SEQ ID NO: 93),
 EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDWNGRG
 TYYRYYADSVKGRSTISRDNKNTVYLRMNSLKPEDTAVYYCAATTVLTPRVLNEYA
 TWGQGTQVTVSS (SEQ ID NO: 94),
 QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
 AESVKGRFTISRDNKNTVYLRMNSLKPEDTAAYYCKADVFGSSGYVETYWGQGTQV
 TVSS (SEQ ID NO: 95),
 EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
 IATSVKGRFAITRDNAKNTVYLRMNSLKPEDTAVYYCNHPLTARWGQGTQVTVSS
 (SEQ ID NO: 96),
 QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREVFAAITWNGGTT
 YYADSVKGRFTISRDNKNTVYLRMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 97),

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
 TYADSVKGRFTISRDN TKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
 (SEQ ID NO: 98),
 EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
 YAESVKGRFTISRDN AKNTVY LQMNSLEPEDTAVYYCASMVNPHITAWGTIGVREIPDY
 DYWGQGTQVTVSS (SEQ ID NO: 99),
 QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISWSGGST
 TYADPVKGRFTISRDN AKNTVY LRMNSLKPEDTAVYYCNDQRCYWGQGT LTVTVSS
 (SEQ ID NO: 100),
 EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISWSGSSA
 GYGDSVKGRFTISRDN AKNTLY LQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVS
 S (SEQ ID NO: 101),
 EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKERE FVA AIRWSGGRT
 LYADSVKGRFTISRDN AKNTAY LQMNNLRPEDTAVYYCAADLA EYSGTYSSPADSPAG
 YDYWGQGTQVTVSS (SEQ ID NO: 102), or
 QVQLVETGGGLVQAGDSLRLSCAASGRTL SFNTYAMGWFRQAPGKERE FVA SITWNG
 GSTSYADSVKGRFTITRDN AKNTAT LRMNSLQ PDDTAVYYCAAARYV VSGTYFPANY
 WGQGTQVTVSS (SEQ ID NO: 103).

315. The system of any one of claims 284 to 314, wherein the single domain antibody is
 comprised of a sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or
 100% sequence identity with the sequence of

QVQLVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQERE FVA AIDWNGRG
 TYYRYYADSVKGRSTISRDN AKNTMY LQMNSLKPEDTAVYYCAAGSIDLNWYGGMD
 YWGQGTQVTVSS (SEQ ID NO: 93),
 EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQERE FVA AIDWNGRG
 TYYRYYADSVKGRSTISRDN AKNTVY LQMNSLKPEDTAVYYCAATTVLTDPRVLNEYA
 TWGQGTQVTVSS (SEQ ID NO: 94),
 QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGGGITHY
 AESVKGRFTISRDN AKNTVY LQMNSLKPEDTA AYYCKADVFGSSGYVETYWGQGTQV

TVSS (SEQ ID NO: 95);

EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFDRIATTT
IATSVKGRFAITRDNAKNTVYVLQMSGLKPEDTAVYYCNHPLTARWGQGTQVTVSS
(SEQ ID NO: 96);

QVQLVESGGGLVQAGGSLRLSCAASGRTFSSYAMGWFRQAPGKEREVAAITWNGGTT
YYADSVKGRFTISRDNKNTVYVLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 97);

EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISGGGTT
TYADSVKGRFTISRDNKNTVYVLHMNSLKPEDTAVYYCNHPLTSRWGQGTQVTVSS
(SEQ ID NO: 98);

EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITGGGSTH
YAESVKGRFTISRDNKNTVYVLQMNSLEPEDTAVYYCASMVNPHTAWGTIGVREIPDY
DYWGQGTQVTVSS (SEQ ID NO: 99);

QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVAAISWSGGST
TYADPVKGRFTISRDNKNTVYVLRMNSLKPEDTAVYYCNDQRCGYWGQGTQVTVSS
(SEQ ID NO: 100);

EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVAAISWSGSSA
GYGDSVKGRFTISRDNKNTLYLQMNSLKPEDTAVYYCAADPFNQGYWGQGTQVTVSS
(SEQ ID NO: 101);

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREVAAIRWSGGRT
LYADSVKGRFTISRDNKNTAYLQMNNLRPEDTAVYYCAADLAEYSGTYSSPADSPAG
YDYWGQGTQVTVSS (SEQ ID NO: 102); or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSENTYAMGWFRQAPGKEREVASITWNG
GSTSYADSVKGRFTITRDNAKNTATLRMNSLQDDTAVYYCAAARYYVSGTYFPANY
WGQGTQVTVSS (SEQ ID NO: 103).

316. The system of any one of claims 284 to 315, wherein the single domain antibody is 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

317iii) non-covalently bound to the agent; or

b) the process does not inhibit pIgR-mediated transcytosis of IgA.

45. The ~~system~~process of claim 31644, further comprising a linker between the single domain antibody and the agent:

318. The system of claim 317; optionally wherein, the linker:

a) is a polypeptide; or

319. The system of claim 318, wherein the linker b) is a flexible linker comprising a sequence selected from the group consisting of EPKTPKPQPQQLQPQNPPTTESKSPK (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.

32046. The system of any one of claims 316 to 319, wherein the single domain antibody is chemically conjugated to the agent.

321. The system of any one of claims 316 to 319, wherein the single domain antibody is non-covalently bound to the agent.

~~322. The system of any one of claims 284 to 321, wherein the system does not inhibit pIgR-mediated transcytosis of IgA.~~

~~323. The system~~process of claim ~~322~~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), 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);~~);~~

~~324. The system of claim 322 or claim 323, wherein the single domain antibody comprises-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), 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

325. ~~The system of any one of claims 322c)~~ 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), AAARYYYVSGTYFPANY (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), AAARYYYVSGTYFPAN (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 324a 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), 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), 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), 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), WVGFIATTTT (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), AISWSGSAG (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), GRTLSTY (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 GRTLSTY (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 AIDWNGRGTYYYRYYADSVKG (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 AIDWNGRGTYYYRYYADSVKG (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 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 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 WVGFI DRIATTT (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
FVAAISWSGGSTT (SEQ ID NO: 200), and the CDR3 sequence of NDQRG
(SEQ ID NO: 232); or

6) the CDR1 sequence of GRTFSTYRMG (SEQ ID NO: 180), the CDR2 sequence of AISWSGGSTT (SEQ ID NO: 210), and the CDR3 sequence of QRGY (SEQ ID NO: 243);

ix) VHH9:

- 1) the CDR1 sequence of RYAMG (SEQ ID NO: 8), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 37), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 68);
- 2) the CDR1 sequence of GFTFTRY (SEQ ID NO: 17), the CDR2 sequence of SWSGSS (SEQ ID NO: 47) or WSGS (SEQ ID NO: 267), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 79) or PFNQG (SEQ ID NO: 280);
- 3) the CDR1 sequence of GFTFTRYA (SEQ ID NO: 27), the CDR2 sequence of ISWSGSSA (SEQ ID NO: 57), and the CDR3 sequence of AADPFNQGY (SEQ ID NO: 90);
- 4) the CDR1 sequence of GFTFTRYAMG (SEQ ID NO: 161), the CDR2 sequence of AISWSGSSAGYGDSVKG (SEQ ID NO: 191), and the CDR3 sequence of DPFNQGY (SEQ ID NO: 222);
- 5) the CDR1 sequence of TRYAMG (SEQ ID NO: 171), the CDR2 sequence of 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 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
NGRGTYRYRYADSVKGRSTISRDNNAKNTMYLQMNSLKPEDTAVYYCAAGSIDL
NWYGGMDYWGQGTQVTVSS (SEQ ID NO: 93),
- EVQVVESGGGLVQAGGSLKLACAAPGLTFSSYRMGWFRQAPGQEREFVAAIDW
NGRGTYRYRYADSVKGRSTISRDNNAKNTVYLQMNSLKPEDTAVYYCAATTVL
DPRVLNEYATWGQGTQVTVSS (SEQ ID NO: 94),
- QLQLVESGGGLVQPGGSLRLSCAASGSIFSINVMGWYRQAPGKQRELVARINGG
GITHYAESVKGRFTISRDNNAKNTVYLQMNSLKPEDTAAYYCKADVFGSSGYVET
YWGQGTQVTVSS (SEQ ID NO: 95),
- EVQVVESGGGLVQAGGSLRLSCAVSGTSVSSNAMGWYRQAPGKQREWVGFIDR
IATTTIATSVKGRFAITRDNAKNTVYLQMSGSLKPEDTAVYYCNHPLTARWGQGT
QVTVSS (SEQ ID NO: 96),
- QVQLVESGGGLVQAGGSLRLSCAASGRFTSSYAMGWFRQAPGKREFVAAITW
NGGTTYADSVKGRFTISRDNNAKNTVYLQMNSLKPEDTAVYYCAADPFNQGY
WGQGTQVTVSS (SEQ ID NO: 97),
- EVQLVESGGGLVQAGGSLRLSCAVSGSSVSSDAMGWYRQAPGNQRAWVAFISG
GGTTTYADSVKGRFTISRDNNTKNTVYLHMNSLKPEDTAVYYCNHPLTSRWGQG
TQVTVSS (SEQ ID NO: 98),
- EVQVVESGGGLVQAGGSLRLACVASRSIGSINVMGWYRQAPGKQRDLVARITG
GGSTHYAESVKGRFTISRDNNAKNTVYLQMNSLEPEDTAVYYCASMVNPIITAWG
TIGVREIPDYDYWGQGTQVTVSS (SEQ ID NO: 99),
- QVQLVESGGGLVQAGGSLRLSCAVSGRTFSTYRMGWFRQAPGKERSFVA AISW
SGGSTTYADPVKGRFTISRDNNAKNTVYLRMNSLKPEDTAVYYCNDQRGYWGQG
TLVTVSS (SEQ ID NO: 100),
- EVQVVESGGGLVQAGGSLRLSCAASGFTFTRYAMGWFRQAPGKERSFVA AISW
SGSSAGYGDSVKGRFTISRDNNAKNTLYLQMNSLKPEDTAVYYCAADPFNQGYW

GQGTQVTVSS (SEQ ID NO: 101),

EVQVVESGGGLVQAGGSLRLSCAASGRTFTTYRMGWFRQAPGKEREFVAAIRW
SGGRTL YADSVKGRFTISRDN AKNTAYLQMNLRPEDTAVYYCAADLAEYSGT
YSSPADSPAGYDYWGQGTQVTVSS (SEQ ID NO: 102), or

QVQLVETGGGLVQAGDSLRLSCAASGRTLSFNTYAMGWFRQAPGKEREFVASIT
WNGGSTSYADSVKGRFTITRDNAKNTATLRMNSLQPDDTAVYYCAAARYYVSG
TYFPANYWGQGTQVTVSS (SEQ ID NO: 103);

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

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 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.

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), 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), WVGFIATTT (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), FIDRIATT (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).

32654. A system comprising a means for providing a molecule to lamina propria of a subject.

32755. The system of claim 32654, wherein the molecule comprises an agent and a single domain antibody that binds to pIgR-

328. The system of claim 327, 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;

~~329. The system of any one of claims 326 to 328, wherein b) the agent is an antibody or fragment thereof, a peptide, or a vaccine; or~~

~~330. The system of any one of claims 327 to 329, wherein c) the single domain antibody is genetically fused or chemically conjugated to the agent.~~