[0010] In one aspect, provided herein, are therapeutic agents that bind to an antigen expressed on a target cell, such as a diseased cell, for example, a cancer cell. Binding of the therapeutic agents to a target antigen on a target cell can initiate the process of destruction of the target cell. In some embodiments, the therapeutic agent is a recombinant nucleic acid that can be expressed in a cell of a subject, such as a mammalian cell, a human cell, a myeloid cell or a monocyte. In some embodiments, the therapeutic agent is a recombinant protein that can bind to a target antigen on a target cell. In some embodiments, the therapeutic agent is a cell, for example, a mammalian cell, a human cell, a myeloid cell or a monocyte, wherein the cell comprises a recombinant nucleic acid, and/or expresses a recombinant protein, such that the myeloid cell can be targeted to a diseased cell, expressing the target antigen on the surface of the cell; and the myeloid cell lyses or phagocytizes the diseased cell.

[0010a] In one aspect, provided herein is a composition comprising a recombinant polynucleic acid encapsulated by a nanoparticle delivery vehicle, wherein the recombinant polynucleic acid comprises a sequence encoding a chimeric fusion protein (CFP), the CFP comprising: (a) an extracellular domain comprising an anti-GPC3 binding domain, and (b) a transmembrane domain operatively linked to the extracellular domain, wherein the transmembrane domain is a transmembrane domain from a protein that dimerizes with endogenous FcR-gamma receptors; wherein the CFP is expressed on the surface of myeloid cells that express the endogenous FcR-gamma receptors.

[0010b] In another aspect, provided herein is a pharmaceutical composition comprising the composition as described herein, and a pharmaceutically acceptable excipient.

[0010c] In another aspect, provided herein is the use of the composition as described herein in the manufacture of a medicament for treating a subject having cancer.

[0010d] In another aspect, provided herein is the composition as described herein for use as a medicament.

[0011] In one aspect, provided herein is a recombinant nucleic acid encoding a chimeric fusion protein comprising (a) a transmembrane domain and (b) an intracellular domain operably linked to the transmembrane domain, wherein the chimeric fusion protein responds to an extracellular cue, wherein the intracellular domain influences the intracellular mechanism of action and activation of the myeloid cell upon receiving the extracellular cue. In one embodiment, the chimeric fusion protein is a chimeric receptor, having an extracellular antigen binding domain in addition to (a) a transmembrane domain and (b) an intracellular domain operably linked to the transmembrane domain, and engagement of the extracellular antigen binding domain of the chimeric fusion protein to the target antigen that the extracellular binding domain binds to provides the extracellular cue to the receptor and for the receptor mediated activation of the myeloid cell.

[0012] In one aspect, provided herein is a recombinant nucleic acid encoding a chimeric fusion protein comprising (a) a transmembrane domain and (b) an intracellular domain operably linked to the transmembrane domain, wherein the intracellular domain comprises an intracellular signaling domain

with a Xaa1-Leu-Xaa3-Iso-Ser motif, wherein Xaa1 is a hydrophilic amino acid, and Xaa3 is any amino acid. In some embodiments, the Ser of Xaa1-Leu-Xaa3-Iso-Ser is a phosphorylation site.

[0013] In some embodiments, Xaa1 is serine, threonine, tyrosine, histidine, asparagine, aspartic acid, glutamine, glutamic acid, lysine or arginine. In some embodiments, Xaa1 is serine. In some embodiments, Xaa1 is threonine. In some embodiments, Xaa1 is tyrosine. In some embodiments, Xaa1 is histidine. In some embodiments, Xaa1 is asparagine, aspartic acid, glutamine, glutamic acid, lysine or arginine. In some embodiments, Xaa1 is asparagine. In some embodiments, Xaa1 is aspartic acid. In some embodiments, Xaa1 is glutamine. In some embodiments, Xaa1 is glutamic acid. In some embodiments, Xaa1 is lysine. In some embodiments, Xaa1 is arginine.

[0014] In some embodiments, Xaa1 is histidine, asparagine, aspartic acid, glutamine, glutamic acid, lysine or arginine. In some embodiments, Xaa1 is histidine. In some embodiments, Xaa1 is asparagine, aspartic acid, glutamine, glutamic acid, lysine or arginine. In some embodiments, Xaa1 is asparagine. In some embodiments, Xaa1 is aspartic acid. In some embodiments, Xaa1 is glutamine. In some

embodiments, Xaa1 is glutamic acid. In some embodiments, Xaa1 is lysine. In some embodiments, Xaa1 is arginine. In some embodiments, Xaa1 is not serine. In some embodiments, Xaa1 is not threonine. In some embodiments, Xaa1 is not tyrosine.

[0015] In some embodiments, Xaa1 is serine, asparagine, aspartic acid, glutamine, glutamic acid, lysine or arginine. In some embodiments, Xaa1 is serine. In some embodiments, Xaa1 is asparagine. In some embodiments, Xaa1 is aspartic acid. In some embodiments, Xaa1 is glutamine. In some embodiments, Xaa1 is glutamic acid. In some embodiments, Xaa1 is lysine. In some embodiments, Xaa1 is arginine. In some embodiments, Xaa1 is not histidine. In some embodiments, Xaa1 is not threonine. In some embodiments, Xaa1 is not tyrosine.

[0016] In some embodiments, Xaa1 is asparagine, aspartic acid, glutamine, glutamic acid, lysine or arginine. In some embodiments, Xaa1 is asparagine. In some embodiments, Xaa1 is aspartic acid. In some embodiments, Xaa1 is glutamine. In some embodiments, Xaa1 is glutamic acid. In some embodiments, Xaa1 is lysine. In some embodiments, Xaa1 is arginine. In some embodiments, Xaa1 is not serine. In some embodiments, Xaa1 is not threonine. In some embodiments, Xaa1 is not tyrosine. In some embodiments, Xaa1 is not histidine.

[0017] In some embodiments, Xaa1-Leu-Xaa3-Iso-Ser is SLHIS (SEQ ID NO: 108).

[0018] In some embodiments, Xaa1-Leu-Xaa3-Iso-Ser is NLEIS (SEQ ID NO: 109).

[0019] In some embodiments, Xaa1-Leu-Xaa3-Iso-Ser is DLAIS (SEQ ID NO: 110).

[0020] In some embodiments, Xaa1-Leu-Xaa3-Iso-Ser is ELLIS (SEQ ID NO: 111).

[0021] In some aspects, the chimeric fusion protein further comprises an extracellular domain comprising an antigen binding domain, wherein the transmembrane domain is operably linked with the extracellular domain. In some embodiments, the intracellular domain comprises at least one additional intracellular signaling domain. In some embodiments, the at least one additional intracellular signaling domain is derived form an intracellular PI3-kinase recruitment domain, a phagocytosis receptor intracellular domain, a pattern recognition receptor intracellular domain, a CD40 intracellular domain, an FcR intracellular domain, or a cytokine or chemokine receptor intracellular domain. In some embodiments, intracellular signaling domain comprises an amino acid sequence derived from a cytosolic adaptor protein, a mitochondrial membrane protein or an endoplasmic reticulum membrane protein. In one aspect, the intracellular signaling domain of the chimeric fusion protein comprises an amino acid sequence derived from a TRIF protein. In some embodiments, intracellular signaling domain comprises a truncated TRIF intracellular domain. In some embodiments, the sequence of the truncated TRIF intracellular domain is about 150 to 300 amino acids in length, about 150 to 270 amino acids in length, or about 150-250 amino acids in length. In some embodiments, intracellular signaling domain comprises an amino acid sequence having at least 80% sequence identity to SEQ ID NO: 36. In some embodiments, intracellular signaling domain comprises an amino acid sequence having at least 80% sequence identity to SEQ ID NO: 37. In some

In some embodiments, the antigen is an antigen of fibronectin, vitronectin, collagen, or laminin. In some embodiments, the antigen binding domain can bind to two or more different antigens.

[00211] In some embodiments, the antigen binding domain comprises a sequence of an antigen binding domain provided herein, such as a sequence of an antigen binding domain in a Table provided herein.

[00212] In some embodiments, the target protein is CD70. In some embodiments, the antigen binding domain comprises an anti-CD70 antibody or binding fragment thereof, wherein the antigen binding domain comprises a heavy chain variable domain (VH) comprising a heavy chain complementarity determining region 3 (HC CDR3) that is the HC CDR3 of any one of the VH sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYADSVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 112) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO: 113). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 1 (HC CDR1) that is the HC CDR1 of any one of the VH sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYADSVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 112) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO: 113). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 2 (HC CDR2) that is the HC CDR2 of any one of the VH sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYADSVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 112) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO: 113). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof comprises with 70-100% sequence identity to any one of the sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYADSVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 112) and

QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADS VKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO: 113) In some embodiments, the VH is a single domain antibody domain. In some embodiments, the VH is a VHH.

[00213] In some embodiments the target protein is GPC3. In some embodiments, the antigen binding domain comprises an anti-GPC3 antibody or binding fragment thereof, wherein the antigen binding domain comprises a heavy chain variable domain (VH) comprising a heavy chain complementarity

determining region 3 (HC CDR3) of any one of the sequences selected from the group consisting of ATACADTTQYAYDY (SEQ ID NO: 114), ATACADTTLYEYDY (SEQ ID NO: 115), ATACVDTTQYEYDY (SEQ ID NO: 116), ATACADATQHEYDY (SEQ ID NO: 117), ATACADTTQYDYDY (SEQ ID NO: 118), ATACADTTQYEYDY (SEQ ID NO: 119), ATACADTTHYEYDY (SEQ ID NO: 120), ATACVITTLYEYDY (SEQ ID NO: 121), ATACAETTLYEYDY (SEQ ID NO: 122), ATACADTTQHEYDY (SEQ ID NO: 123), ATACVDTTHYEYDY (SEQ ID NO: 124), ATACASTTLYEYDY (SEQ ID NO: 125), ATACVVTTLYEYDY (SEQ ID NO: 126), ATACGGATGPYDY (SEQ ID NO: 127), ATACAGAIGPYDY (SEQ ID NO: 128), ATACVVVGDQNDY (SEQ ID NO: 129), ATACVVVGDRNDY (SEQ ID NO: 130), ATDCAGGTSTPYDY (SEQ ID NO: 131), ATDCAGGTATPYDY (SEQ ID NO: 132), ATACVVADRNEYDY (SEQ ID NO: 133), ATSCVVVTKNEYDY (SEQ ID NO: 134), ATACSGLTHEYDY (SEQ ID NO: 135), ATTCSGLTHEYDY (SEQ ID NO: 136), ATACANWSSLGPYDY (SEQ ID NO: 137), ATACANWSTLGPYDY (SEQ ID NO: 138), ATACSDPRVYEYDY (SEQ ID NO: 139), ATTCASPEKYEYDY (SEQ ID NO: 140), ATHCGGTSWGTSYDY (SEQ ID NO: 141), ATHCGGSSWSNEYDY (SEQ ID NO: 142), YARYSGRTY (SEQ ID NO: 143), ASSAWPAGPKHQVEYDY (SEQ ID NO: 144), ATACGSLVGMYDY (SEQ ID NO: 145), ATACGSAVHEYDY (SEQ ID NO: 146), ATDCVGFGSNWFDY (SEQ ID NO: 147), ATACASPVIYEYDY (SEQ ID NO: 148), ATDCAGGVGHEYDY (SEQ ID NO: 149), ATDCSLHGSDYPYDY (SEQ ID NO: 150) and AVRIYSGSFDNTLAYDY (SEQ ID NO: 151). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 1 (HC CDR1) of any one of the sequences selected from the group consisting of SEQ ID NOs: GFPLAYYA (SEQ ID NO: 152), GFSLDYYA (SEQ ID NO: 153), GFPLDYYA (SEQ ID NO: 154), GFTLDYYA (SEQ ID NO: 155), GFSLNYYA (SEQ ID NO: 156), GFTLAYYA (SEQ ID NO: 157), GFTLGYYA (SEQ ID NO: 158), GFPLNYYA (SEQ ID NO: 159), GFPLHYYA (SEQ ID NO: 160), GFSLGYYA (SEQ ID NO: 161), GFPLGYYA (SEQ ID NO: 162), GFPLEYYA (SEQ ID NO: 163), GSDFRADA (SEQ ID NO: 164), GRTFSSYG (SEQ ID NO: 165), GFSLAYYA (SEQ ID NO: 166) and GLTFRSVG (SEQ ID NO: 167). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 2 (HC CDR2) of any one of the sequences selected from the group consisting of SEQ ID NOs: ISNSDGST (SEQ ID NO: 168), ISASDGST (SEQ ID NO: 169), ISSSDGST (SEQ ID NO: 170), ISSSDGNT (SEQ ID NO: 171), ISSADGST (SEQ ID NO: 172), ISSSGGST (SEQ ID NO: 173), ISSGDGST (SEQ ID NO: 174), ISAGDGNT (SEQ ID NO: 175), ISSSDDST (SEQ ID NO: 176), ISSNDGST (SEQ ID NO: 177), ISSPDGST (SEQ ID NO: 178), ISSRTGGT (SEQ ID NO: 179), ISAGDGSST (SEQ ID NO: 180), ISSSDGSSSDGNT (SEQ ID NO: 181), ISSGDGNT (SEQ ID NO: 182), ISSGDGKT (SEQ ID NO: 183), ISSSDGGT (SEQ ID NO: 184), ISSRTGST (SEQ ID NO: 185), ISSRTGNT (SEQ ID NO: 186), ISSSDGHSST (SEQ ID NO: 187), ISSSSDGNT (SEQ ID NO: 188), ISASNGNT (SEQ ID NO: 189), ISSGSDGNT (SEQ ID NO: 190), ISASDGNT (SEQ ID NO:

191), IDSITSI (SEQ ID NO: 192), ISWSGGSTIAASVGST (SEQ ID NO: 193), ISSSDGSDGNT (SEQ ID NO: 194) and ASPSGVIT (SEQ ID NO: 195). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof comprises with 70-100% sequence identity to any one of the sequences selected from the group consisting of QVQLQESGGGLVHSGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ ID NO: 196),
QVQLQESGGGLVHSGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSVKGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 197),
QVQLQESGGGLVHSGGSLRLSCAASGFTLDYYAIGWFRRAPGKEREGVSCISSGDGKTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACAGAIGPYDYWGQGTQVTVSS (SEQ ID NO: 198),
QVQLQESGGGLVPPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSVKGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 199),
QVQLQESGGGLVQAGGSLRLSCAASGFSLGYYAIGWFRQAPGKEREGVSCISSSDGHSSTYYADSVKGRFTISRDNAKNTVYLQMNNLKPEDTAVYYCATDCAGGTATPYDYWGQGTQVTVSS (SEQ ID NO: 200),
QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYGMGWFRQAPGKEREFVAAISWSGGSTYYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCASSAWPAGPKHQVEYDYWGQGTQVTVSS (SEQ ID NO: 201),
QVQLQESGGGLVQAGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVACISSRTGSTYYADSVKGRFTISRDNAKNTVALQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 202),

QVQLQESGGGLVQDGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACAETTLYEYDYWGQGTQVTVSS (SEQ ID
NO: 203),
QVQLQESGGGLVQPGESLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACANWSTLGPYDYWGQGTQVTVSS (SEQ
ID NO: 204),
QVQLQESGGGLVQPGESLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADSV
KGRFTISRDNAKNTVYLQMNRLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ
ID NO: 205),
QVQLQESGGGLVQPGGSLKLSCAASGSDFRADAMGWYRQAPGKEREPVAIDSITSIYYVDSVEG
RFTISRDNTKNTVYLQMTSLKPEDTAVYYCYARYSGRTYWGRGTQVTVSS (SEQ ID NO: 206),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLRPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS (SEQ ID
NO: 207),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV
KGRFAISRDNAKNTVYLQMNSLKPEDTAVYYCATACSDPRVYEYDYWGQGTQVTVSS (SEQ ID
NO: 208),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ
ID NO: 209),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTHYEYDYWGQGTQVTVSS (SEQ
ID NO: 210),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADATQHEYDYWGQGTQVTVSS (SEQ
ID NO: 211),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ
ID NO: 212),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ
ID NO: 213),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID
NO: 214),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRRAPGKEREGVSCISSSDGNTYYADAV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ
ID NO: 215),

QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISAGDGSSTYYADS
VKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACASTTLYEYDYWGQGTQVTVSS (SEQ
ID NO: 216),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV
KGRFTISRDNAKNAVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ
ID NO: 217),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ
ID NO: 218),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS (SEQ
ID NO: 219),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSPDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS (SEQ
ID NO: 220),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSSDGSDGNTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCSLHGSDYPYDYWGQGTQVTVSS
(SEQ ID NO: 221),

QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 222),
QVQLQESGGGLVQPGGSLRLSCAASGFPLEYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACSDPRVYEYDYWGQGTQVTVSS (SEQ ID NO: 223),
QVQLQESGGGLVQPGGSLRLSCAASGFPLGYYAIGWFRQAPGKEREGVSCISSSDDSTYYADSV KGRFTISRDNDKNTVYLQMNSLKPEDTAVYYCATDCAGGTSTPYDYWGQGTQVTVSS (SEQ ID NO: 224),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSGDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATSCVVVTKNEYDYWGQGTQVTVSS (SEQ ID NO: 225),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 226),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVVADRNEYDYWGQGTQVTVSS (SEQ ID NO: 227),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLRPEDTAVYYCATACVVADRNEYDYWGQGTQVTVSS (SEQ ID NO: 228),
QVQLQESGGGLVQPGGSLRLSCAASGFPLNYYAIGWFRQAPGKEREGVSCISASDGNTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATTCASPEKYEYDYWGQGTQVTVSS (SEQ ID NO: 229),
QVQLQESGGGLVQPGGSLRLSCAASGFPLNYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFIISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 230),
QVQLQESGGGLVQPGGSLRLSCAASGFPLNYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGSAVHEYDYWGQGTQVTVSS (SEQ ID NO: 231),
QVQLQESGGGLVQPGGSLRLSCAASGFSLAYYAIGWFRQAPGKEREGVSCIAASVGSTYYADSV KGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATDCAGGVGHEYDYWGQGTQVTVSS (SEQ ID NO: 232),
QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNAVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 233),
QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNAVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS (SEQ

ID NO: 234),
QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCAGGTSTPYDYWGQGTQVTVSS (SEQ ID
NO: 235),
QVQLQESGGGLVQPGGSLRLSCAASGFSLNYYAIGWFRQAPGKEREGVSCISAGDGNTYYADS
VKGRFTISRDNAANTVSLQMDSLKPEDTAVYYCATACVITTLYEYDYWGQGTQVTVSS (SEQ
ID NO: 236),
QVQLQESGGGLVQPGGSLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ
ID NO: 237),
QVQLQESGGGLVQPGGSLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ
ID NO: 238),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVACISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID
NO: 239),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVACISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPQDTAVYYCATACGSLVGMYDYWGQGTQVTVSP (SEQ ID
NO: 240),

QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISASDGNTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATTCASPEKYEYDYWGQGTQVTVSS (SEQ ID
NO: 241),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISASNGNTYYADSV
KGRFTISRDSAKNTVYLQMNSLKPEDTAVYYCATTCSGLTHEYDYWGQGTQVTVSS (SEQ ID
NO: 242),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSGDGNTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID
NO: 243),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSGDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATHCGGSSWSNEYDYWGQGTQVTVSS (SEQ
ID NO: 244),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSNDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ
ID NO: 245),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGGTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID
NO: 246),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSSSDGNTY
YADSVKGRFTISRDNAKNTVYLQMNNLKPEDTAVYYCATACVVTTLYEYDYWGQGTQVTVSS
(SEQ ID NO: 247),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSP (SEQ
ID NO: 248),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID
NO: 249),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSGGSTYYADSV
KGRFTISRDNAKNTVYLQMNMLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ
ID NO: 250),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSGGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACASPVIYEYDYWGQGTQVTVSS (SEQ ID
NO: 251),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSGGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCAGGTSTPYDYWGQGTQVTVSS (SEQ ID
NO: 252),
QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ

ID NO: 253),
QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACANWSSLGPYDYWGQGTQVTVSS (SEQ
ID NO: 254),
QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTGVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID
NO: 255),
QVQLQESGGGLVQPGGSLRLSCEGSGFSLDYYAIGWFRQAPGKEREGVSCISSGDGNTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCVGFGSNWFDYWGQGTQVTVSS (SEQ
ID NO: 256),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVACISSRTGSTYYADSV
KGRFTISRDNAKNTVALQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID
NO: 257),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGGTYYADSV
KGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDRNDYWGQGTQVTVSS (SEQ ID
NO: 258),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGGTYYADSV

KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 259),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGGTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 260),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGNTYYADSV KGRFTISRDDAKNMVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 261),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 262),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQALGKEREGVSCISSRTGSTYYADSV KGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 263),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFAISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 264),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 265),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 266),
QVQLQESGGGLVQPGGSLRLSCVASGFPLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 267),
QVQLQESGGGLVQPGGSLRLSCVASGFSLDYYAIGWFRQAPGKEREGVSCISNSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYAYDYWGQGTQVTVSS (SEQ ID NO: 268),
QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSGSDGNTYYADS VKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACSGLTHEYDYWGQGTQVTVSS (SEQ ID NO: 269),
QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSSDDSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 270),
QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSSSDGNTYYADS VKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATTCSGLTHEYDYWGQGTQVTVSS (SEQ ID NO: 271),

QVQLQESGGGLVQPGGSLRLSCVASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 272),
QVQLQESGGGLVQPGGSLRLSCVGSGFTLDYYAIGWFRQAPGKEREGVSCISSNDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 273),
QVQLQESGGGLVQSGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACAETTLYEYDYWGQGTQVTVSS (SEQ ID NO: 274),
QVQLQESGGGLVQTGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 275),
QVQLQESGGGMVQAGESLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADS VKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADATQHEYDYWGQGTQVTVSS (SEQ ID NO: 276),
QVQLQESGGGSVQPGESLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS (SEQ ID NO: 277),
QVQLQESGGGSVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSGDGSTYYADSV

KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTHYEYDYWGQGTQVTVSS (SEQ ID NO: 278),
QVQLQESGGGSVQSGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 279),
QVQLQESGGGSVRPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV KGRFTISRDNAKNAVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ ID NO: 280),
QVQLQESGGGVAQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS (SEQ ID NO: 281),
QVQLQESGGGVVQAGGSLKLSCAASGSDFRADAMGWYRQAPGKEREPVAIDSITSIYYVDSVE GRFTISRDNTKNTVYLQMTSLKPEDTAVYYCYARYSGRTYWGRGTQVTVSS (SEQ ID NO: 282),
QVQLQESGGGVVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSGDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATHCGGTSWGTSYDYWGQGTQVTVSS (SEQ ID NO: 283),
QVQLQESGGGVVQPGGSLRLSCAASGLTFRSVGMGWFRRAPGKEREFVATASPSGVITYYADS VKGRFTISRDNAKNTVYLEMNSLKPEDTAVYYCAVRIYSGSFDNTLAYDYWGQGTQVTVSS (SEQ ID NO: 284),
QVQLQESGGGVVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 285), and
QVQLQESGGGVVQSGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV KGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 286). In some embodiments, the VH is a single domain antibody domain. In some embodiments, the VH is a VHH.

[00214] In some embodiments, the antigen binding domain comprises an autoantigen or fragment thereof, such as Dsg1 or Dsg3. In some embodiments, the antigen binding domain comprises a receptor domain or an antibody domain wherein the antibody domain binds to an auto antigen, such as Dsg1 or Dsg3.

[00215] In some embodiments, the transmembrane domain and the antigen binding domain are operatively linked through a linker. In some embodiments, the transmembrane domain and the antigen binding domain are operatively linked through a linker such as a hinge region of CD8α, IgG1 or IgG4.

[00216] In some embodiments, the extracellular domain comprises a multimerization scaffold.

[00217] In some embodiments, the transmembrane domain comprises a CD8 transmembrane domain. In some embodiments, the transmembrane domain comprises a CD28 transmembrane domain. In some embodiments, the transmembrane domain comprises a CD68 transmembrane

domain. In some embodiments, the transmembrane domain comprises a CD2 transmembrane domain. In some embodiments, the transmembrane domain comprises an FcR transmembrane domain. In some embodiments, the transmembrane domain comprises an FcRγ transmembrane domain. In some embodiments, the transmembrane domain comprises an FcRα transmembrane domain. In some embodiments, the transmembrane domain comprises an FcRβ transmembrane domain. In some embodiments, the transmembrane domain comprises an FcRε transmembrane domain. In some embodiments, the transmembrane domain comprises a transmembrane domain from a syntaxin, such as syntaxin 3 or syntaxin 4 or syntaxin 5. In some embodiments, the transmembrane domain

native intracellular adaptor protein domain, without compromising the effectiveness of the chimeric protein. In some embodiments, such effectiveness is referred to as the enhanced phagocytic potential compared to an identical cell that does not express a chimeric protein. In some embodiments, such effectiveness is referred to as the enhanced inflammatory potential compared to an identical cell that does not express a chimeric protein. In some embodiments, such effectiveness is referred to as the enhanced NF-kappa B activation, or interferon activation in the cell expressing the chimeric protein, compared to an identical cell that does not express a chimeric protein.

[00235] In some embodiments, the myeloid cells are specifically targeted for delivery. Myeloid cells can be targeted using specialized biodegradable polymers, such as PLGA (poly(lactic-co-glycolic) acid and/or polyvinyl alcohol (PVA). In some embodiments, one or more compounds can be selectively incorporated in such polymeric structures to affect the myeloid cell function. In some embodiments, the targeting structures are multilayered, e.g., of one or more PLGA and one or more PVA layers. In some embodiments, the targeting structures are assembled in an order for a layered activity. In some embodiments, the targeted polymeric structures are organized in specific shaped components, such as labile structures that can adhere to a myeloid cell surface and deliver one or more components such as growth factors and cytokines, such as to maintain the myeloid cell in a microenvironment that endows a specific polarization. In some embodiments, the polymeric structures are such that they are not phagocytosed by the myeloid cell, but they can remain adhered on the surface. In some embodiments the one or more growth factors may be M1 polarization factors, such as a cytokine. In some embodiments the one or more growth factors may be an M2 polarization factor, such as a cytokine. In some embodiments, the one or more growth factors may be a macrophage activating cytokine, such as IFNγ. In some embodiments the polymeric structures are capable of sustained release of the one or more growth factors in an in vivo environment, such as in a solid tumor.

[00236] In some embodiments, the recombinant nucleic acid comprises a sequence encoding a homeostatic regulator of inflammation. In some embodiments, the homeostatic regulator of inflammation is a sequence in an untranslated region (UTR) of an mRNA. In some embodiments, the sequence in the UTR is a sequence that binds to an RNA binding protein. In some embodiments, translation is inhibited or prevented upon binding of the RNA binding protein to the sequence in an untranslated region (UTR). In some embodiments, the sequence in the UTR comprises a consensus sequence of WWWU(AUUUA)UUUW, wherein W is A or U (SEQ ID NO: 287). In some embodiments, the recombinant nucleic acid is expressed on a bicistronic vector.

[00237] In some embodiments, the target cell is a mammalian cell. In some embodiments, the target cell is a human cell. In some embodiments, the target cell comprises a cell infected with a pathogen. In some embodiments, the target cell is a cancer cell. In some embodiments, the target cell is a cancer cell that is a lymphocyte. In some embodiments, the target cell is a cancer cell that is an ovarian cancer cell. In some embodiments, the target cell is a cancer cell that is a breast cell. In some embodiments,