

RECOMBINANT VECTORS COMPRISING POLYCISTRONIC EXPRESSION CASSETTES AND METHODS OF USE THEREOF

1. FIELD

[0001] The instant disclosure relates to polycistronic vectors comprising at least three cistrons and methods of using the same.

2. BACKGROUND

[0002] Co-expression of multiple genes in each cell of a population is critical for a wide variety of biomedical applications. A standard strategy for multigene expression is to incorporate the transgenes into multiple vectors and introduce each vector into the cell. However, the use of multiple vectors often produces a substantially heterogeneous population of engineered cells, wherein not all cells express each of the transgenes or do not express each of the transgenes to a similar degree. Such heterogeneity leads to several problems, particularly for therapeutic applications, including e.g., diminished persistence of the desired engineered cell phenotype *in vivo*, complex manufacturing and purification requirements, and lot-to-lot variability of the engineered cell product.

[0003] Given the problems associated with the use of multiple vectors to co-express multiple genes in single cells, there is an unmet need for single polycistronic vectors capable of not only expressing a plurality of transgenes in a single cell, but also of expressing some or all transgenes to a similar degree across a cell population, resulting in an engineered cell population optimized for therapeutic use.

3. SUMMARY

[0004] The instant disclosure provides recombinant vectors comprising a polycistronic expression cassette comprising a transcriptional regulatory element operably linked to a polycistronic polynucleotide.

[0005] Provided herein is a recombinant vector comprising a polycistronic expression cassette, wherein the polycistronic expression cassette comprises a transcriptional regulatory element operably linked to a polycistronic polynucleotide that comprises: a first polynucleotide sequence that encodes a T cell receptor (TCR) alpha chain comprising an alpha chain variable ($V\alpha$) region and an alpha chain constant ($C\alpha$) region; a second polynucleotide sequence that comprises a first 2A element; a third polynucleotide sequence that encodes a TCR beta chain comprising a beta

chain variable (V β) region and a beta chain constant (C β) region; a fourth polynucleotide sequence that comprises a second 2A element; and a fifth polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof.

[0006] In some embodiments, either or both of the first 2A element and the second 2A element, independently, is a P2A element, a T2A element, an F2A element, or an E2A element.

[0007] In some embodiments, the first 2A element is a P2A element.

[0008] In some embodiments, the P2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 18 or 20, or the amino acid sequence of SEQ ID NO: 18 or 20 comprising 1, 2, or 3 amino acid modifications.

[0009] In some embodiments, the P2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 19 or 21.

[0010] In some embodiments, the second 2A element is a T2A element.

[0011] In some embodiments, the T2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 22 or 24, or the amino acid sequence of SEQ ID NO: 22 or 24 comprising 1, 2, or 3 amino acid modifications.

[0012] In some embodiments, the T2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 23 or 25.

[0013] In some embodiments, either or both of the second polynucleotide sequence and the fourth polynucleotide sequence, independently, encode a furin recognition site.

[0014] In some embodiments, the furin recognition site comprises the amino acid sequence of SEQ ID NO: 2 or 4, or the amino acid sequence of SEQ ID NO: 2 or 4 comprising 1, 2, or 3 amino acid modifications.

[0015] In some embodiments, the furin recognition site is encoded by the polynucleotide sequence of SEQ ID NO: 3 or 5 or the polynucleotide sequence of SEQ ID NO: 3 or 5 comprising 1, 2, or 3 nucleotide modifications.

[0016] In some embodiments, the second polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 10, or the amino acid sequence of SEQ ID NO: 10 comprising 1, 2, or 3 amino acid modifications.

[0017] In some embodiments, the second polynucleotide sequence comprises a polynucleotide

sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 11.

[0018] In some embodiments, the fourth polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 12, or the amino acid sequence of SEQ ID NO: 12 comprising 1, 2, or 3 amino acid modifications.

[0019] In some embodiments, the fourth polynucleotide sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 13.

[0020] In some embodiments, the IL-15, or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 76.

[0021] In some embodiments, the IL-15, or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 77.

[0022] In some embodiments, the IL-15R α , or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 78.

[0023] In some embodiments, the IL-15R α , or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 79.

[0024] In some embodiments, the IL-15, or functional fragment or functional variant thereof, is operably linked to the IL-15R α , or functional fragment or functional variant thereof, via a peptide linker.

[0025] In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 81, or the amino acid sequence of SEQ ID NO: 81 comprising 1, 2, or 3 amino acid modifications.

[0026] In some embodiments, the peptide linker is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 82.

[0027] In some embodiments, the fusion protein is membrane bound.

[0028] In some embodiments, the fusion protein comprises an amino acid sequence at least

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 70 or 73.

[0029] In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 71 or 74.

[0030] In some embodiments, the C α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 40-49.

[0031] In some embodiments, the C α region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 55, 57, or 58.

[0032] In some embodiments, the C β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 50-54 or 60.

[0033] In some embodiments, the C β region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 56 or 59.

[0034] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.

[0035] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.

[0036] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.

[0037] In some embodiments, the first polynucleotide sequence and the second polynucleotide

sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.

[0038] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 181.

[0039] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.

[0040] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 252.

[0041] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.

[0042] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.

[0043] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.

[0044] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; and the third polynucleotide sequence, the second

polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.

[0045] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; and the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 183.

[0046] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.

[0047] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 255.

[0048] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.

[0049] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; or the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164.

[0050] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; or the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238.

[0051] In some embodiments, the first polynucleotide sequence, the second polynucleotide

sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[0052] In some embodiments, the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 184 or 214; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[0053] In some embodiments, the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.

[0054] In some embodiments, the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 258 or 278; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[0055] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.

[0056] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165.

[0057] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the

twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241.

[0058] In some embodiments, the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[0059] In some embodiments, the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 185 or 215; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[0060] In some embodiments, the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.

[0061] In some embodiments, the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 261 or 281; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[0062] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.

[0063] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.

[0064] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.

[0065] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.

[0066] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 187 or 217.

[0067] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; and the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.

[0068] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; and the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 259 or 279.

[0069] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.

[0070] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.

[0071] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.

[0072] In some embodiments, the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; and the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.

[0073] In some embodiments, the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; and the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 189 or 219.

[0074] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.

[0075] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 256 or 276.

[0076] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.

[0077] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; or the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170.

[0078] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the sixth combination polynucleotide sequence

comprises the polynucleotide sequence of SEQ ID NO: 235; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; or the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242.

[0079] In some embodiments, the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[0080] In some embodiments, the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 190; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[0081] In some embodiments, the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[0082] In some embodiments, the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 262; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[0083] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.

[0084] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination

polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171.

[0085] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243.

[0086] In some embodiments, the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[0087] In some embodiments, the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 191; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[0088] In some embodiments, the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[0089] In some embodiments, the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 263; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[0090] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.

[0091] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.

[0092] In some embodiments, the fourth combination polynucleotide sequence comprises the

polynucleotide sequence of SEQ ID NO: 233; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.

[0093] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[0094] In some embodiments, the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 222; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[0095] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.

[0096] In some embodiments, the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[0097] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.

[0098] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.

[0099] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; or the eighth combination polynucleotide sequence

comprises the polynucleotide sequence of SEQ ID NO: 237.

[00100] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.

[00101] In some embodiments, the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 223; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.

[00102] In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59. In some embodiments, the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

[00103] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.

[00104] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.

[00105] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.

[00106] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[00107] In some embodiments, the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 222; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[00108] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[00109] In some embodiments, the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[00110] In some embodiments, the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.

[00111] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.

[00112] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237.

[00113] In some embodiments, the third polynucleotide sequence and the second

polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.

[00114] In some embodiments, the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 223; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

[00115] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.

[00116] In some embodiments, the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.

[00117] In some embodiments, the polycistronic polynucleotide further comprises a sixth polynucleotide sequence that comprises a third 2A element; and a seventh polynucleotide sequence that comprises a marker protein.

[00118] In some embodiments, the third 2A element is a P2A element, a T2A element, an F2A element, or an E2A element.

[00119] In some embodiments, the marker protein comprises domain III of HER1, or a functional fragment or functional variant thereof; an N-terminal portion of domain IV of HER1; and a transmembrane domain of CD28, or a functional fragment or functional variant thereof.

[00120] In some embodiments, the domain III of HER1, or a functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 104.

[00121] In some embodiments, the N-terminal portion of domain IV of HER1 comprises amino acids 1-40, 1-39, 1-38, 1-37, 1-36, 1-35, 1-34, 1-33, 1-32, 1-31, 1-30, 1-29, 1-28, 1-27, 1-26, 1-25,

1-24, 1-23, 1-22, 1-21, 1-20, 1-19, 1-18, 1-17, 1-16, 1-15, 1-14, 1-13, 1-12, 1-11, or 1-10 of SEQ ID NO: 105.

[00122] In some embodiments, the N-terminal portion of domain IV of HER1 comprises amino acids 1-21 of SEQ ID NO: 105.

[00123] In some embodiments, the N-terminal portion of domain IV of HER1 comprises the amino acid sequence of SEQ ID NO: 106, or the amino acid sequence of SEQ ID NO: 106, comprising 1, 2, or 3 amino acid modifications.

[00124] In some embodiments, the transmembrane region of CD28 comprises the amino acid sequence of SEQ ID NO: 107, or the amino acid sequence of SEQ ID NO: 107, comprising 1, 2, or 3 amino acid modifications.

[00125] In some embodiments, the marker protein comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, or 112.

[00126] In some embodiments, the V α region comprises complementarity determining region 1 α (CDR1 α), CDR2 α , and CDR3 α , comprising the amino acid sequences of SEQ ID NO: 1001 + 10n, 1002 + 10n, and 1003 + 10n, respectively, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00127] In some embodiments, the V β region comprises CDR1 β , CDR2 β , and CDR3 β , comprising the amino acid sequences of SEQ ID NO: 2001 + 10n, 2002 + 10n, and 2003 + 10n, respectively, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00128] In some embodiments, the V α region comprises the CDR1 α , CDR2 α , and CDR3 α from a V α region comprising the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00129] In some embodiments, the V β region comprises the CDR1 β , CDR2 β , and CDR3 β from a V β region comprising the amino acid sequence of SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00130] In some embodiments, the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00131] In some embodiments, the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence

of SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00132] In some embodiments, the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2004 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1005 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2005 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1006 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2006 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1007 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2007 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00133] In some embodiments, the TCR alpha chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1008 + 10n, wherein n is an integer from 0 to 79. In some embodiments, the TCR alpha chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1009 + 10n, wherein n is an integer from 0 to 79.

[00134] In some embodiments, the TCR alpha chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1010 + 10n, wherein n is an integer from 0 to 79.

[00135] In some embodiments, the TCR beta chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid

sequence of SEQ ID NO: 2008 + 10n, wherein n is an integer from 0 to 79. In some embodiments, n=0.

[00136] In some embodiments, the TCR beta chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2009 + 10n, wherein n is an integer from 0 to 79.

[00137] In some embodiments, the TCR beta chain comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2010 + 10n, wherein n is an integer from 0 to 79.

[00138] In some embodiments, transcriptional regulatory element comprises a promoter.

[00139] In some embodiments, the promoter is a human elongation factor 1-alpha (hEF-1 α) hybrid promoter.

[00140] In some embodiments, the promoter comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:150.

[00141] In some embodiments, the recombinant vector further comprises a polyA sequence at the 3' end of the polycistronic expression cassette.

[00142] In some embodiments, the polyA sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:151.

[00143] In some embodiments, the recombinant vector further comprises a Left inverted terminal repeat (ITR) and a Right ITR, wherein the Left ITR and the Right ITR flank the polycistronic expression cassette.

[00144] In some embodiments, the recombinant vector comprises, in order from 5' to 3': the Left ITR; the transcriptional regulatory element; the first polynucleotide sequence; the second polynucleotide sequence; the third polynucleotide sequence; the fourth polynucleotide sequence; the fifth polynucleotide sequence; and the Right ITR.

[00145] In some embodiments, the recombinant vector is a non-viral vector.

[00146] In some embodiments, the non-viral vector is a plasmid.

[00147] In some embodiments, the recombinant vector is a viral vector.

[00148] In some embodiments, the recombinant vector is a polynucleotide.

[00149] Also provided herein is a polynucleotide encoding an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid

sequence selected from the group consisting of SEQ ID NOs: 161, 163, 164, 165, 167, 169, 170, and 171.

[00150] Also provided herein is a polynucleotide comprising a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 232, 235, 236, 238, 239, 241, 242, and 243.

[00151] Also provided herein is a population of cells that comprises any recombinant vector provided herein, or any polynucleotide provided herein.

[00152] In some embodiments, the recombinant vector or the polynucleotide is integrated into the genome of the population of cells.

[00153] In some embodiments, the cells are immune effector cells.

[00154] In some embodiments, the immune effector cells are selected from the group consisting of T cells, natural killer (NK) cells, B cells, mast cells, and myeloid-derived phagocytes.

[00155] In some embodiments, the immune effector cells are T cells.

[00156] In some embodiments, the T cells are selected from the group consisting of naïve T cells (CD4⁺ or CD8⁺); killer CD8⁺ T cells; cytotoxic CD4⁺ T cells; helper CD4⁺ T cells; CD4⁺ T cells corresponding to Th1, Th2, Th9, Th17, Th22, follicular helper (T_{fh}), regulatory (T_{reg}) lineages; tumor infiltrating lymphocytes (TILs); and memory T cells (central memory, effector memory, stem cell memory, stem cell-like memory).

[00157] In some embodiments, the population of cells comprises alpha/beta T cells, gamma/delta T cells, or natural killer T (NKT) cells.

[00158] In some embodiments, the population of cells comprises CD4⁺ T cells, CD8⁺ T cells, or both CD4⁺ T cells and CD8⁺ T cells.

[00159] In some embodiments, the cells are *ex vivo*.

[00160] In some embodiments, the cells are human.

[00161] In some embodiments, the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA⁺CD45RO⁻CD62L⁺CD95⁺ cells.

[00162] In some embodiments, the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA⁺CD45RO⁺CD62L⁺CD95⁺ cells.

[00163] Also provided herein is a population of cells comprising a polycistronic expression cassette comprising a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α ,

or a functional fragment or functional variant thereof; a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95+ cells.

[00164] Also provided herein is a population of cells comprising a polycistronic expression cassette comprising a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof; a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95+ cells.

[00165] Also provided herein is a method of producing a population of engineered cells, comprising introducing into a population of cells any recombinant vector provided herein, and a DNA transposase or a polynucleotide encoding a DNA transposase; and culturing the population of cells under conditions wherein the transposase integrates the polycistronic expression cassette into the genome of the population of cells, thereby producing the population of engineered cells.

[00166] In some embodiments, the Left ITR and the Right ITR are ITRs of a DNA transposon selected from the group consisting of a *Sleeping Beauty* transposon, a piggyBac transposon, a TcBuster transposon, and a Tol2 transposon.

[00167] In some embodiments, the DNA transposon is the *Sleeping Beauty* transposon.

[00168] In some embodiments, the transposase is a *Sleeping Beauty* transposase.

[00169] In some embodiments, the *Sleeping Beauty* transposase is selected from the group consisting of SB11, SB10, SB100X, hSB110, and hSB81.

[00170] In some embodiments, the *Sleeping Beauty* transposase is SB11.

[00171] In some embodiments, the SB11 comprises an amino acid sequence at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 300.

[00172] In some embodiments, the SB11 is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 301.

[00173] In some embodiments, the polynucleotide encoding the DNA transposase is a DNA vector or an RNA vector.

[00174] In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290 or 291; and the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292, 293 or 294.

[00175] In some embodiments, the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation, sonication, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, or mechanical deformation by passage through a microfluidic device, or a colloidal dispersion system.

[00176] In some embodiments, the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation.

[00177] In some embodiments, the method is completed within 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.

[00178] In some embodiments, wherein the method is completed in less than 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.

[00179] In some embodiments, the population of cells is cryopreserved and thawed before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

[00180] In some embodiments, the population of cells is rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

[00181] In some embodiments, the population of cells is not rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

[00182] In some embodiments, the population of cells comprises expanded human *ex vivo* cells.

[00183] In some embodiments, the population of cells is not activated *ex vivo*.

[00184] In some embodiments, the population of cells comprises T cells.

[00185] Also provided herein is a method of treating cancer in a subject in need thereof comprising administering to the subject a therapeutically effective amount of any of the populations of cells provided herein, thereby treating the cancer.

[00186] In some embodiments, the cancer is selected from lung, cholangiocarcinoma, pancreatic, colorectal, gynecological, and ovarian cancer.

[00187] Also provided herein is a method of treating an autoimmune disease or disorder in a subject in need thereof comprising administering to the subject a therapeutically effective amount any of the populations of cells provided herein, thereby treating the autoimmune disease or disorder.

4. BRIEF DESCRIPTION OF THE RAWINGS

[00188] The accompanying drawings which are incorporated in and constitute a part of this specification, illustrate exemplary embodiments of the present disclosure and, together with the description, serve to explain principles of the present disclosure.

[00189] **FIG. 1** is a set of schematics of the structures of TCR α (A), TCR β (B), and mbIL15 (15), shown from N terminus (left) to C terminus (right).

[00190] **FIG. 2A** is a set of schematics of the ORFs of tricistronic Cassettes APBT15, ATBP15, AP15TB, AT15PB, BPAT15, BTAP15, BP15TA, and BT15PA. **FIG. 2B** is a set of schematics of the ORFs of control Cassettes 15, APB, and BPA.

[00191] **FIG. 3** is a schematic diagram depicting double transposition and single transposition approaches using a *Sleeping Beauty* transposon/transposase system to generate T cells expressing TCR α /TCR β and mbIL15.

[00192] **FIG. 4** is a set of 2-parameter flow plots showing transgene co-expression as assessed after electroporation and overnight incubation for each of Groups 1-14.

[00193] **FIG. 5A** is a set of 2-parameter flow plots showing representative TCR transgene expression in CD3⁺ cells after overnight incubation for each of Groups 1-14. **FIG. 5B** provides TCR expression data from three donors presented as % mTCR⁺ cells out of CD3⁺ cells.

[00194] **FIG. 6A-6C** shows TCR and mbIL15 expression after first phase expansion (Day 13). **FIG. 6A** provides representative TCR and mbIL15 expression data from each of Groups 1-14. **FIG. 6B** provides TCR expression data from three donors presented as % mTCR⁺ cells out of CD3⁺ cells. **FIG. 6C** provides TCR and mbIL15 co-expression data from three donors presented as % TCR⁺mbIL15⁺ cells out of CD3⁺ cells.

[00195] **FIG. 7A-7B** shows total numbers of TCR⁺ and TCR⁺mbIL15⁺ cells after first phase expansion (Day 13). **FIG. 7A** provides TCR expression data from three donors presented as total

number of mTCR⁺ T cells. **FIG. 7B** provides total number of TCR+mbIL15⁺ T cells from three donors.

[00196] **FIG. 8A-8B** shows cell viability after electroporation (Day 1; **FIG. 8A**) and after first phase expansion (Day 13; **FIG. 8B**) for each of Groups 1-14.

[00197] **FIG. 9A-9B** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 1-14 after first phase expansion (Day 13) with wild-type or mutant neoantigen pulsed T2 cells. Data is presented as % 4-1BB positive cells of CD8⁺ cells at increasing concentrations of neoantigen peptide.

[00198] **FIG. 10** shows phosphorylated STAT5 levels in transposed CD3⁺ T cells from each of Groups 1-14 after first phase expansion (Day 13). Isotype negative control and IL-15 treated positive control was included for comparison. (dTp = double transposed with separate mbIL15 and TCR vectors).

[00199] **FIG. 11** shows apoptosis levels in transposed T cells from each of Groups 2-14 after being expanded for 13 days and then activated for 9 days with CD3/CD28 Dynabeads® (ThermoFisher).

[00200] **FIG. 12** is a set of schematics illustrating the differences between the S version and N version of the TCR only and mbIL15 TCR constructs shown from N terminus (left) to C terminus (right).

[00201] **FIG. 13A-13B** shows TCR expression on CD3⁺ cells (**FIG. 13A**) the day after electroporation (Day 1) and after the first phase expansion prior to enrichment (Day 11 Pre-enrichment) as well as (**FIG. 13B**) after the first phase expansion following enrichment (Day 11 Post-enrichment) and at the end of the second phase expansion. Data from four donors are presented.

[00202] **FIG. 14A-14B** shows TCR and mbIL15 co-expression on CD3⁺ T cells (**FIG. 14A**) the day after electroporation (Day 1) and after the first phase expansion prior to enrichment (Day 11 Pre-enrichment) as well as after the first phase expansion following enrichment (Day 11 Post-enrichment) and at the end of the second phase expansion. Data from four donors are presented.

[00203] **FIG. 15** is a set of 2-parameter flow plots showing representative TCR and mbIL15 transgenes expression in CD3⁺ cells after the second phase expansion.

[00204] **FIG. 16A-16B** shows the fold expansion of cells (**FIG. 16A**) after the first expansion phase and (**FIG. 16B**) after the second expansion phase. Data from four donors are presented.

[00205] **FIG. 17A-17B** shows the absolute count of TCR expressing cells in culture (**FIG. 17A**) after the first expansion phase and (**FIG. 17B**) after the second expansion phase. Data from four donors are presented.

[00206] **FIG. 18** shows phosphorylated STAT5 levels after second phase expansion (Day 27) in CD3⁺ T cells transposed with different versions of polycistronic plasmids encoding TCR001. Some containing non-cysteine substituted TCR constant regions (N version) or that are optionally further codon-optimized (NU version). Non-transposed (NT) = NT (Group 2.1); BPA (Group 2.2); BPA-N (Group 2.3); AP15TB (Group 2.4); AP15TB-N (Group 2.5); AP15TB-NU (Group 2.6); BP15TA (Group 2.7); BP15TA-N (Group 2.8); and BP15TA-NU (Group 2.9).

[00207] **FIG. 19A-19B** shows functional data from transposed T cells co-cultured with neoantigen pulsed dendritic cells. **FIG. 19A** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 2.1-2.9 after second phase expansion (Day 27) with wild-type or mutant neoantigen peptide pulsed dendritic cells. Data is presented as % 4-1BB positive cells of CD8⁺ cells at increasing concentrations of neoantigen peptide. **FIG. 19B** shows interferon- γ (IFN- γ) secretion after overnight co-culture of transposed T cells from each of Groups 2.1-2.9 after second phase expansion (Day 27) with wild-type or mutant neoantigen pulsed dendritic cells.

[00208] **FIG. 20A-20B** shows TCR expression and cell survival after 4 weeks of long-term cytokine withdrawal (LTWD) incubation in transposed cells from each of Groups 2.2-2.9. **FIG. 20A** shows the expression of mTCR detected on CD3⁺ gated population with mouse TCR beta antibody and **FIG. 20B** shows cell survival as the percent of live cells recovered relative to initial input number of cells at the beginning of the LTWD.

[00209] **FIG. 21A-21B** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 2.2-2.9 after 4 weeks of LTWD incubation with wild-type or mutant neoantigen (10 μ g/ml) pulsed dendritic cells.

[00210] **FIG. 22A-22B** shows IFN- γ secretion after overnight co-culture of transposed T cells from each of Groups 2.2-2.9 after 4 weeks of LTWD incubation with wild-type or mutant neoantigen (10 μ g/ml) pulsed dendritic cells.

[00211] **FIG. 23A-23C** is a set of pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-expansion (**FIG. 23A**), day 22 post-expansion (**FIG. 23B**), and after 4 weeks of LTWD culture (**FIG. 23C**) in cells transposed with the tested plasmids (Groups 2.2-2.9).

[00212] **FIG. 24** is a set of 2-parameter flow plots showing representative TCR and mbIL15 transgene co-expression in CD3⁺ cells after overnight incubation (Day 1), after first phase expansion (Day 11, pre- and post-enrichment) and after second phase expansion (Day 22) for each of Groups 3.2-3.4 expressing TCR001 +/- mbIL15 (BPA-N, AP15TB-NU, and BP15TA-NU).

[00213] **FIG. 25A-25C** shows TCR⁺ population changes during the first expansion phase (Day 1 vs. Day 11 pre-enrichment) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00214] **FIG. 26A-26C** shows TCR⁺ population changes during the second expansion phase (Day 11 post-enrichment vs. Day 22) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00215] **FIG. 27A-27C** shows TCR⁺/mbIL15⁺ population changes during the first expansion phase (Day 1 vs. Day 11 pre-enrichment) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00216] **FIG. 28A-28C** shows TCR⁺/mbIL15⁺ population changes during the second expansion phase (Day 11 post-enrichment vs. Day 22) for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30). Each graph presents data from a separate TCR; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00217] **FIG. 29A-29I** shows specific induction of activation marker, 4-1BB, after overnight co-culture of transposed T cells from each of Groups 3.1-3.30 after second phase expansion (Day 27) with wild-type (WT) or mutant (Mut) neoantigen pulsed dendritic cells. Data is presented as % 4-1BB positive cells of total CD3⁺, CD4⁺ or CD8⁺ T cells at increasing concentrations of neoantigen peptide. NT = non-transposed; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00218] **FIG. 30A-30I** shows IFN- γ secretion after overnight co-culture of transposed T cells from each of Groups 3.1-3.30 after second phase expansion (Day 27) with wild-type (WT) or mutant (Mut) neoantigen pulsed dendritic cells. Data is presented as IFN- γ level (pg/mL) at increasing concentrations of neoantigen peptide. NT = non-transposed; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00219] **FIG. 31** shows the specific lysis of negative control (Mut+HLA-) tumor cell line AU565 and target tumor cell line TYK-nu (Mut+HLA+) by T cells expressing TCR001 +/- mbIL15. NT = non-transposed; TCR001 only = BPA-N, TCR001 with mbIL15 = AP15TB-NU or BP15TA-NU.

[00220] **FIG. 32A-32B** shows the specific lysis of a tumor cell line by T cells expressing (**FIG. 32A**) TCR022 +/- mbIL15 or (**FIG. 32B**) TCR075 +/- mbIL15. Tumor cell line was transfected with the appropriate HLA-expression plasmid and pulsed with either wild type (WT) or mutant (Mut) peptides and co-cultured with T cells. NT = non-transposed; TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00221] **FIG. 33** shows TCR+ population for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD). TCR only = BPA-N, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00222] **FIG. 34A-34C** shows cell survival for cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD). BPA-N (IL2) = TCR only cultured with IL2, NT = non-transposed, BPA-N = TCR only, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00223] **FIG. 35A-35I** shows specific induction of activation marker, 4-1BB, after overnight co-culture of cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD) with wild-type or mutant neoantigen pulsed dendritic cells. Data are presented as % 4-1BB+ of either CD3+, CD4+, or CD8+ T cells. BPA-N (IL2) = TCR only cultured with IL2, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00224] **FIG. 36A-36C** shows IFN- γ secretion after overnight co-culture of cells transposed with various TCRs +/- mbIL15 (Groups 3.1-3.30) after long-term cytokine withdrawal (LTWD) with wild-type or mutant neoantigen pulsed dendritic cells. BPA-N (IL2) = TCR only cultured with IL2, TCR with mbIL15 = AP15TB-NU or BP15TA-NU.

[00225] **FIG. 37A-37I** shows a comparison of 4-1BB induction in cells transposed with various TCRs + mbIL15 (Groups 3.1-3.30) pre- and post-LTWD culture after overnight co-culture with wild-type or mutant neoantigen pulsed dendritic cells. Data are presented as % 4-1BB+ of either CD3+, CD4+, or CD8+ T cells.

[00226] **FIG. 38** is a set of representative pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-expansion of cells transposed with TCR001 expressed from either BPA-N or with mbIL15 from either AP15TB-NU or BP15TA-NU.

[00227] **FIG. 39** is a set of representative pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets at day 22 post-expansion of cells transposed with TCR001 expressed from either BPA-N or with mbIL15 from either AP15TB-NU or BP15TA-NU.

[00228] **FIG. 40A-40E** is a set of pie charts showing the mean frequency of live CD3⁺ T cell memory and effector subsets of in cells transposed with the tested plasmids (Groups 3.1-3.30) after 4 weeks of LTWD culture.

5. DETAILED DESCRIPTION

[00229] The instant disclosure provides recombinant polycistronic nucleic acid vectors comprising at least three cistrons, wherein the first cistron encodes an α chain of an artificial T-cell receptor (TCR), the second cistron encodes a β chain of an artificial TCR, and the third cistron encodes a fusion protein that comprises IL-15 and IL-15R α (e.g., mbIL15), or a functional fragment or functional variant thereof. In some embodiments, the polycistronic nucleic acid further comprises a fourth cistron that encodes a marker protein (e.g., HER1t). In some embodiments, the cistrons are separated by polynucleotide sequence that comprise 2A elements. Also provided are immune effector cells comprising these vectors, immune effector cells engineered *ex vivo* utilizing the vectors to express the three proteins encoded by the vectors, pharmaceutical compositions comprising these vectors or engineered immune effector cells made utilizing these vectors, and methods of treating a subject using these vectors or engineered immune effector cells made utilizing these vectors.

[00230] The polycistronic vectors described herein are particularly useful in methods of manufacturing populations of engineered cells (e.g., immune effector cells) that are substantially homogeneous compared to the prior art systems that utilized at least two vectors for the expression of three proteins.

5.1 Definitions

[00231] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the claimed subject matter belongs. It is to be understood that the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of any subject matter claimed. In this application, the use of the singular includes the plural unless specifically stated otherwise. It must be noted that, as used in the specification and the appended claims, the singular

forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. In this application, the use of “or” means “and/or” unless stated otherwise. Furthermore, use of the term “including” as well as other forms, such as “include,” “includes,” and “included,” is not limiting. The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[00232] As used herein, the terms “about” and “approximately,” when used to modify a numeric value or numeric range, indicate that deviations of 5% to 10% above (*e.g.*, up to 5% to 10% above) and 5% to 10% below (*e.g.*, up to 5% to 10% below) the value or range remain within the intended meaning of the recited value or range.

[00233] As used herein, the terms “T cell receptor” and “TCR” are used interchangeably and refer to molecules comprising CDRs or variable regions from $\alpha\beta$ T cell receptors. Examples of TCRs include, but are not limited to, full-length TCRs, antigen-binding fragments of TCRs, soluble TCRs lacking transmembrane and cytoplasmic regions, single-chain TCRs containing variable regions of TCRs attached by a flexible linker, TCR chains linked by an engineered disulfide bond, single TCR variable domains, single peptide-MHC-specific TCRs, multi-specific TCRs (including bispecific TCRs), TCR fusions, TCRs comprising co-stimulatory regions, human TCRs, humanized TCRs, chimeric TCRs, recombinantly produced TCRs, and synthetic TCRs. In certain embodiments, the TCR is a full-length TCR comprising a full-length α chain and a full-length β chain. In certain embodiments, the TCR is a soluble TCR lacking transmembrane and/or cytoplasmic region(s). In certain embodiments, the TCR is a single-chain TCR (scTCR) comprising $V\alpha$ and $V\beta$ linked by a peptide linker, such as a scTCR having a structure as described in PCT Publication No.: WO 2003/020763, WO 2004/033685, or WO 2011/044186, each of which is incorporated by reference herein in its entirety. In certain embodiments, the TCR comprises a transmembrane region. In certain embodiments, the TCR comprises a co-stimulatory signaling region.

[00234] As used herein, the term “full-length TCR” refers to a TCR comprising a dimer of a first and a second polypeptide chain, each of which comprises a TCR variable region and a TCR constant region comprising a TCR transmembrane region and a TCR cytoplasmic region. In certain embodiments, the full-length TCR comprises one or two unmodified TCR chains, *e.g.*, unmodified α or β TCR chains. In certain embodiments, the full-length TCR comprises one or two altered TCR chains, such as chimeric TCR chains and/or TCR chains comprising one or more amino acid substitutions, insertions, or deletions relative to an unmodified TCR chain. In certain

embodiments, the full-length TCR comprises a mature, full-length TCR α chain and a mature, full-length TCR β chain.

[00235] As used herein, the term “TCR variable region” refers to the portion of a mature TCR polypeptide chain (*e.g.*, a TCR α chain or β chain) which is not encoded by the TRAC gene for TCR α chains, either the TRBC1 or TRBC2 genes for TCR β chains, or the TRDC gene for TCR δ chains. In some embodiments, the TCR variable region of a TCR α chain encompasses all amino acids of a mature TCR α chain polypeptide which are encoded by a TRAV and/or TRAJ gene, and the TCR variable region of a TCR β chain encompasses all amino acids of a mature TCR β chain polypeptide which are encoded by a TRBV, TRBD, and/or TRBJ gene (see, *e.g.*, Lefranc and Lefranc, (2001) “T cell receptor FactsBook.” *Academic Press*, ISBN 0-12-441352-8, which is incorporated by reference herein in its entirety). TCR variable regions generally comprise framework regions (FR) 1, 2, 3, and 4 and complementarity determining regions (CDR) 1, 2, and 3.

[00236] As used herein, the terms “ α chain variable region” and “V α ” are used interchangeably and refer to the variable region of a TCR α chain.

[00237] As used herein, the terms “ β chain variable region” and “V β ” are used interchangeably and refer to the variable region of a TCR β chain.

[00238] As used herein in the context of a TCR, the term “CDR” or “complementarity determining region” means the noncontiguous antigen combining sites found within the variable regions of a TCR chain (*e.g.*, an α chain or a β chain). These regions have been described in Lefranc, (1999) *The Immunologist* 7: 132-136; Lefranc *et al.*, (1999) *Nucleic Acids Res* 27: 209-212; Lefranc (2001) “T cell receptor FactsBook.” *Academic Press*, ISBN 0-12-441352-8; Lefranc *et al.*, (2003) *Dev Comp Immunol.* 27(1):55-77; and in Kabat *et al.*, (1991) “Sequences of protein of immunological interest,” each of which is herein incorporated by reference in its entirety. In certain embodiments, CDRs are determined according to the IMGT numbering system described in Lefranc (1999) *supra*. In certain embodiments, CDRs are defined according to the Kabat numbering system described in Kabat *supra*. In certain embodiments, CDRs are defined empirically, *e.g.*, based upon a structural analysis of the interaction of a TCR with a cognate antigen (*e.g.*, a peptide or a peptide-MHC complex). In certain embodiments, the α chain and β chain CDRs of a TCR are defined according to different conventions (*e.g.*, according to the Kabat or IMGT numbering systems, or empirically based upon structural analysis).

[00239] As used herein, the term “framework amino acid residues” refers to those amino acids in the framework region of a TCR chain (*e.g.*, an α chain or a β chain). The term “framework region” or “FR” as used herein includes the amino acid residues that are part of the TCR variable region, but are not part of the CDRs.

[00240] As used herein, the term “constant region” with respect to a TCR refers to the portion of a TCR that is encoded by the TRAC gene (for TCR α chains) or either the TRBC1 or TRBC2 gene (for TCR β chains), optionally lacking all or a portion of a transmembrane region and/or all or a portion of a cytoplasmic region. In certain embodiments, a TCR constant region lacks a transmembrane region and a cytoplasmic region. A TCR constant region does not include amino acids encoded by a TRAV, TRAJ, TRBV, TRBD, TRBJ, TRDV, TRDD, TRDJ, TRGV, or TRGJ gene (*see, e.g.*, “T cell receptor FactsBook,” *supra*).

[00241] As used herein, the terms “major histocompatibility complex” and “MHC” are used interchangeably and refer to an MHC class I molecule and/or an MHC class II molecule.

[00242] As used herein, the term “MHC class I” refers to a dimer of an MHC class I α chain and a β 2 microglobulin chain and the term “MHC class II” refers to a dimer of an MHC class II α chain and an MHC class II β chain.

[00243] As used herein, the terms “human leukocyte antigen” and “HLA” are used interchangeably and can also refer to the proteins encoded by the MHC genes. HLA-A, HLA-B, HLA-C, HLA-E, HLA-F, and HLA-G refer to major and minor gene products of MHC class I genes. HLA-DP, HLA-DQ, and HLA-DR refer to gene products of MHC class II genes, which are expressed on antigen-presenting cells, B cells, and T cells.

[00244] As used herein, the term “peptide-MHC complex” refers to an MHC molecule (MHC class I or MHC class II) with a peptide bound in the art-recognized peptide binding pocket of the MHC. In some embodiments, the MHC molecule is a membrane-bound protein expressed on the cell surface. In some embodiments, the MHC molecule is a soluble protein lacking transmembrane or cytoplasmic regions.

[00245] As used herein, the term “extracellular” with respect to a recombinant transmembrane protein refers to the portion or portions of the recombinant transmembrane protein that are located outside of a cell.

[00246] As used herein, the term “transmembrane” with respect to a recombinant transmembrane protein refers to the portion or portions of the recombinant transmembrane protein that are embedded in the plasma membrane of a cell.

[00247] As used herein, the term “cytoplasmic” with respect to a recombinant transmembrane protein refers to the portion or portions of the recombinant transmembrane protein that are located in the cytoplasm of a cell.

[00248] As used herein, the term “co-stimulatory signaling region” refers to the intracellular portion of a co-stimulatory molecule that is responsible for mediating intracellular signaling events.

[00249] “Binding affinity” generally refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (*e.g.*, a TCR) and its binding partner (*e.g.*, a peptide-MHC complex). Unless indicated otherwise, as used herein, “binding affinity” refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (*e.g.*, a TCR and a peptide-MHC complex). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_D). Affinity can be measured and/or expressed in a number of ways known in the art, including, but not limited to, equilibrium dissociation constant (K_D) and equilibrium association constant (K_A). The K_D is calculated from the quotient of k_{off}/k_{on} , whereas K_A is calculated from the quotient of k_{on}/k_{off} . K_{on} refers to the association rate constant and k_{off} refers to the dissociation rate constant. The k_{on} and k_{off} can be determined by techniques known to one of ordinary skill in the art, such as use of BIAcore® or KinExA. As used herein, a “lower affinity” refers to a larger K_D .

[00250] “Avidity” generally refers to the affinity of binding molecule (*e.g.*, a TCR) and its binding partner (*e.g.*, a peptide-MHC complex). Binding molecules described herein are able to bind antigen via two (or more) sites in which the multiple interactions synergize to enhance the “apparent” affinity. Avidity is the measure of the strength of binding between the binding molecule described herein (*e.g.*, a TCR) and the pertinent antigens (*e.g.*, a peptide-MHC complex). Avidity is related to both the affinity between an antigenic determinant and its antigen binding site on the antigen-binding molecule and the number of pertinent binding sites present on the antigen-binding molecules.

[00251] For example, “specifically binds to” may be used to refer to the ability of a TCR to preferentially bind to a particular antigen (*e.g.*, a specific peptide or a specific peptide-MHC complex combination) as such binding is understood by one skilled in the art. For example, a TCR that specifically binds to an antigen can bind to other antigens, generally with lower affinity as determined by, *e.g.*, BIAcore®, or other immunoassays known in the art (*see, e.g.*, Savage *et al.*, (1999) *Immunity*. 10(4):485-92, which is incorporated by reference herein in its entirety). In a

specific embodiment, a TCR that specifically binds to an antigen binds to the antigen with an association constant (K_a) that is at least 2-fold, 5-fold, 10-fold, 50-fold, 100-fold, 500-fold, 1,000-fold, 5,000-fold, or 10,000-fold greater than the K_a when the TCR binds to another antigen.

[00252] As used herein, an “epitope” is a term in the art and refers to a localized region of an antigen (*e.g.*, a peptide or a peptide-MHC complex) to which a TCR can bind. In certain embodiments, the epitope to which a TCR binds can be determined by, *e.g.*, NMR spectroscopy, X-ray diffraction crystallography studies, ELISA assays, hydrogen/deuterium exchange coupled with mass spectrometry (*e.g.*, liquid chromatography electrospray mass spectrometry), flow cytometry analysis, mutagenesis mapping (*e.g.*, site-directed mutagenesis mapping), and/or structural modeling. For X-ray crystallography, crystallization may be accomplished using any of the known methods in the art (*e.g.*, Giegé R *et al.*, (1994) *Acta Crystallogr D Biol Crystallogr* 50(Pt 4): 339-350; McPherson A, (1990) *Eur J Biochem* 189: 1-23; Chayen NE, (1997) *Structure* 5: 1269-1274; McPherson A, (1976) *J Biol Chem* 251: 6300-6303, each of which is herein incorporated by reference in its entirety). TCR:antigen crystals may be studied using well-known X-ray diffraction techniques and may be refined using computer software such as X-PLOR (Yale University, 1992, distributed by Molecular Simulations, Inc.; *see, e.g.*, *Meth Enzymol* (1985) volumes 114 & 115, eds Wyckoff H. W., *et al.*; U.S. 2004/0014194); and BUSTER (Bricogne G, (1993) *Acta Crystallogr D Biol Crystallogr* 49(Pt 1): 37-60; Bricogne G, (1997) *Meth Enzymol* 276A: 361-423, ed Carter CW; and Roversi P *et al.*, (2000) *Acta Crystallogr D Biol Crystallogr* 56(Pt 10): 1316-1323), each of which is herein incorporated by reference in its entirety. Mutagenesis mapping studies may be accomplished using any method known to one of skill in the art. *See, e.g.*, Champe M *et al.*, (1995) *J Biol Chem* 270: 1388-1394 and Cunningham BC & Wells J A, (1989) *Science* 244: 1081-1085, each of which is herein incorporated by reference in its entirety, for a description of mutagenesis techniques, including alanine scanning mutagenesis techniques. In a specific embodiment, the epitope of an antigen is determined using alanine scanning mutagenesis studies. In a specific embodiment, the epitope of an antigen is determined using hydrogen/deuterium exchange coupled with mass spectrometry. In certain embodiments, the antigen is a peptide-MHC complex. In certain embodiments, the antigen is a peptide presented by an MHC molecule.

[00253] As used herein, the terms “treat,” “treating,” and “treatment” refer to therapeutic or preventative measures described herein. In some embodiments, the methods of “treatment” employ administration of a TCR or a cell expressing a TCR to a subject having a disease or disorder, or

predisposed to having such a disease or disorder, in order to prevent, cure, delay, reduce the severity of, or ameliorate one or more symptoms of the disease or disorder or recurring disease or disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

[00254] As used herein, the term “effective amount” in the context of the administration of a therapy to a subject refers to the amount of a therapy that achieves a desired prophylactic or therapeutic effect.

[00255] As used herein, the term “subject” includes any human or non-human animal. In one embodiment, the subject is a human or non-human mammal. In one embodiment, the subject is a human.

[00256] The determination of “percent identity” between two sequences (*e.g.*, amino acid sequences or nucleic acid sequences) can be accomplished using a mathematical algorithm. A specific, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin S & Altschul S F, (1990) *PNAS* 87: 2264-2268, modified as in Karlin S & Altschul SF, (1993) *PNAS* 90: 5873-5877, each of which is herein incorporated by reference in its entirety. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul SF *et al.*, (1990) *J Mol Biol* 215: 403, which is herein incorporated by reference in its entirety. BLAST nucleotide searches can be performed with the NBLAST nucleotide program parameters set, *e.g.*, at score=100, wordlength=12 to obtain nucleotide sequences homologous to a nucleic acid molecule described herein. BLAST protein searches can be performed with the XBLAST program parameters set, *e.g.*, at score=50, wordlength=3 to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul S F *et al.*, (1997) *Nuc Acids Res* 25: 3389-3402, which is herein incorporated by reference in its entirety. Alternatively, PSI BLAST can be used to perform an iterated search which detects distant relationships between molecules. *Id.* When utilizing BLAST, Gapped BLAST, and PSI BLAST programs, the default parameters of the respective programs (*e.g.*, of XBLAST and NBLAST) can be used (*see, e.g.*, National Center for Biotechnology Information (NCBI) on the worldwide web, ncbi.nlm.nih.gov). Another specific, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17, which is herein incorporated by reference in its entirety. Such an algorithm is incorporated in the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package.

When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.

[00257] The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically only exact matches are counted.

[00258] As used herein, the terms “antibody” and “antibodies” include full-length antibodies, antigen-binding fragments of full-length antibodies, and molecules comprising antibody CDRs, VH regions, or VL regions. Examples of antibodies include monoclonal antibodies, recombinantly produced antibodies, monospecific antibodies, multi-specific antibodies (including bispecific antibodies), human antibodies, humanized antibodies, chimeric antibodies, immunoglobulins, synthetic antibodies, tetrameric antibodies comprising two heavy chain and two light chain molecules, an antibody light chain monomer, an antibody heavy chain monomer, an antibody light chain dimer, an antibody heavy chain dimer, an antibody light chain-antibody heavy chain pair, intrabodies, heteroconjugate antibodies, antibody-drug conjugates, single domain antibodies, monovalent antibodies, single chain antibodies or single-chain Fvs (scFv), camelized antibodies, affibodies, Fab fragments, F(ab')₂ fragments, disulfide-linked Fvs (sdFv), anti-idiotypic (anti-Id) antibodies (including, *e.g.*, anti-anti-Id antibodies), and antigen-binding fragments of any of the above. In certain embodiments, antibodies described herein refer to polyclonal antibody populations. Antibodies can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA, or IgY), any class (*e.g.*, IgG₁, IgG₂, IgG₃, IgG₄, IgA₁ or IgA₂), or any subclass (*e.g.*, IgG_{2a} or IgG_{2b}) of immunoglobulin molecule. In certain embodiments, antibodies described herein are IgG antibodies, or a class (*e.g.*, human IgG₁ or IgG₄) or subclass thereof. In a specific embodiment, the antibody is a humanized monoclonal antibody. In another specific embodiment, the antibody is a human monoclonal antibody.

[00259] As used herein, the term “cistron” refers to a polynucleotide sequence from which a transgene product can be produced.

[00260] As used herein, the term “polycistronic vector” refers to a polynucleotide vector that comprises a polycistronic expression cassette.

[00261] As used herein, the term “polycistronic expression cassette” refers to a polynucleotide sequence wherein the expression of three or more transgenes is regulated by common transcriptional regulatory elements (*e.g.*, a common promoter) and can simultaneously express three or more separate proteins from the same mRNA. Exemplary polycistronic vectors, without

limitation, include tricistronic vectors (containing three cistrons) and tetracistronic vectors (containing four cistrons).

[00262] As used herein, the term “polycistronic polynucleotide” refers to a polynucleotide that comprises three or more cistrons.

[00263] As used herein, the term “transcriptional regulatory element” refers to a polynucleotide sequence that mediates regulation of transcription of another polynucleotide sequence. Exemplary transcriptional regulatory elements include, but are not limited to, promoters and enhancers.

[00264] As used herein, a “furin recognition site” refers to an amino acid sequence, or a nucleotide sequence encoding the amino acid sequence, which can be cleaved by the furin enzyme. The furin enzyme is also known as PACE. In some embodiments, the furin recognition site comprises the amino acid sequence RXXR (SEQ ID NO: 1), wherein X at position 2 is any amino acid and X at position 3 is arginine or lysine. In some embodiments, the furin recognition site comprises the sequences shown below in Table 1.

[00265] **Table 1. Amino acid sequences of exemplary furin recognition sites and polynucleotide sequences encoding same.**

Description	Sequence	SEQ ID NO:
Furin recognition site	RAKR	2
Furin recognition site polynucleotide coding sequence	CGGGCGAAACGC	3
Furin recognition site (alternative)	RAKRSGSG	4
Furin recognition site (alternative) polynucleotide coding sequence	CGGGCGAAACGCTCTGGAAGCGGA	5

[00266] In some embodiments, the furin recognition site comprises an amino acid sequence that is identical to the amino acid sequence of SEQ ID NO: 2 or 4, or comprises 1, 2, or 3 amino acid modifications, relative to SEQ ID NO: 2 or 4; or is encoded by a polynucleotide sequence 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 3 or 5. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the furin recognition site is capable of mediating the cleavage (via furin) of the first protein from the second protein, resulting in two distinct polypeptides from the same mRNA molecule.

[00267] Responsive to recognition of the furin recognition site by the furin enzyme, the furin enzyme induces cleavage of a given polypeptide on the C-terminal side of the furin recognition site or a portion thereof. Accordingly, polypeptides produced by furin-mediated cleavage at a furin recognition site may retain all or a portion of the furin recognition site on their C-terminus. For example, the C-terminus of a first polypeptide of the present disclosure may comprise the amino acid sequence RAKR (SEQ ID NO: 2) or RA.

[00268] As used herein, a “2A element” refers to a polynucleotide sequence which, when expressed in an mRNA, can induce ribosomal skipping during translation of the mRNA in a cell. Thus, two separate polypeptides may be produced from a single mRNA molecule. An amino acid sequence encoded by a 2A element is referred to as a “self-cleaving peptide.” 2A elements may be viral in origin. Exemplary 2A elements include T2A elements, P2A elements, E2A elements, and F2A elements.

[00269] As used herein, the term “P2A element” refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 19, or 21; (ii) encodes the amino acid sequence of SEQ ID NO: 18, or 20; or (iii) encodes the amino acid sequence of SEQ ID NO: 18, or 20, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the P2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the P2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the P2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the P2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the P2A element can be termed an “fP2A element.” In some embodiments, a fP2A element refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 11; (ii) encodes the amino acid sequence of SEQ ID NO: 10; or (iii) encodes the amino acid sequence of SEQ ID NO: 10, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the P2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 20 and 21).

[00270] As used herein, the term “T2A element” refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 23, or 25; (ii) encodes the amino acid sequence of SEQ ID NO: 22, or 24; or (iii) encodes the amino acid sequence of SEQ ID NO: 22, or 24, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the T2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide

bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the T2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the T2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the T2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the T2A element can be termed an "fT2A element." In some embodiments, an fT2A element refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 13; (ii) encodes the amino acid sequence of SEQ ID NO: 12; or (iii) encodes the amino acid sequence of SEQ ID NO: 12, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the T2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 24 and 25).

[00271] As used herein, the term "F2A element" refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 27, or 29; (ii) encodes the amino acid sequence of SEQ ID NO: 26, or 28; or (iii) encodes the amino acid sequence of SEQ ID NO: 26, or 28, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the F2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the F2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the F2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the F2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the F2A element can be termed an "fF2A element." In some embodiments, a fF2A element refers to a polynucleotide that (i) comprises a polynucleotide

sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 15; (ii) encodes the amino acid sequence of SEQ ID NO: 14; or (iii) encodes the amino acid sequence of SEQ ID NO: 14, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the F2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 28 and 29).

[00272] As used herein, the term “E2A element” refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 31, or 33; (ii) encodes the amino acid sequence of SEQ ID NO: 30, or 32; or (iii) encodes the amino acid sequence of SEQ ID NO: 30, or 32, comprising 1, 2, or 3 amino acid modifications. In some embodiments, when positioned in a vector between a first polynucleotide sequence encoding a first protein and a second polynucleotide sequence encoding a second protein, the E2A element is capable of mediating the translation of the first polynucleotide sequence and the second polynucleotide sequence as two distinct polypeptides from the same mRNA molecule by preventing the synthesis of a peptide bond, *e.g.*, between the penultimate residue (*e.g.*, glycine) and the ultimate residue (*e.g.*, proline) at the C terminus of the translation product of the E2A element, *e.g.*, such that the penultimate residue (*e.g.*, glycine) becomes the C-terminal residue of the first protein and the ultimate residue (*e.g.*, proline) becomes the N-terminal residue of the second protein. In some embodiments, the E2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKR (SEQ ID NO: 2). In some embodiments, the E2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a furin recognition site, *e.g.*, RAKRSGSG (SEQ ID NO: 4), and the E2A element can be termed an “fE2A element.” In some embodiments, a fE2A element refers to a polynucleotide that (i) comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 17; (ii) encodes the amino acid sequence of SEQ ID NO: 16; or (iii) encodes the amino acid sequence of SEQ ID NO: 16, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the E2A element additionally comprises, at its 5' end, a polynucleotide sequence that encodes a GSG (*e.g.*, SEQ ID Nos: 32 and 33).

[00273] Examples of 2A elements comprising furin recognition sites at their N-terminal/5' ends are found below in Table 2. The 2A sites themselves are broken out in Table 3.

Table 2. Polynucleotide sequences of exemplary furin-2A elements and amino acid sequences of translations thereof.

Description	Sequence	SEQ ID NO:
Translation of Furin-P2A element	RAKRSGSGATNFSLLKQAGDVEENPGP	10
Furin-P2A element	CGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGC TGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	11
Translation of Furin-T2A element	RAKRSGSGEGRGSLTTCGDVEENPGP	12
Furin-T2A element	CGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTC TAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	13
Translation of Furin-F2A element	RAKRSGSGVKQTLNFDLLKLAGDVESNPGP	14
Furin-F2A element	CGGGCGAAACGCTCTGGAAGCGGAGTGAAGCAGACCCTGAATT TCGACCTGCTGAAGCTGGCCGGGACGTGGAGAGCAACCCTGG CCCC	15
Translation of Furin-E2A element	RAKRSGSQCTNYALLKLAGDVESNPGP	16
Furin-E2A element	CGGGCGAAACGCTCTGGAAGCGGACAGTGTACTAATTATGCTC TCTTGAAATTGGCTGGAGATGTTGAGAGCAACCCAGGTCCC	17

Table 3. Amino acid and polynucleotide sequences of exemplary 2A elements.

Description	Amino Acid Sequence	SEQ ID NO:
P2A (exemplary amino acid sequence)	ATNFSLLKQAGDVEENPGP	18
P2A (exemplary nucleotide sequence)	GCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGATGTGGAGG AGAACCCTGGCCCA	19
P2A (with flanking residues) (exemplary amino acid sequence)	GSGATNFSLLKQAGDVEENPGP	20
P2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCG ATGTGGAGGAGAACCCTGGCCCA	21
T2A (exemplary amino acid sequence)	EGRGSLTTCGDVEENPGP	22
T2A (exemplary nucleotide sequence)	GAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGA ATCCCGGCCCT	23
T2A (with flanking residues) (exemplary amino acid sequence)	GSGEGRGSLTTCGDVEENPGP	24
T2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACG TGGAGGAGAATCCCGGCCCT	25
F2A (exemplary amino acid sequence)	VKQTLNFDLLKLAGDVESNPGP	26
F2A (exemplary nucleotide sequence)	GTGAAGCAGACCCTGAATTTTCGACCTGCTGAAGCTGGCCGGG ACGTGGAGAGCAACCCTGGCCCC	27
F2A (with flanking residues) (exemplary amino acid sequence)	GSGVKQTLNFDLLKLAGDVESNPGP	28
F2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGAGTGAAGCAGACCCTGAATTTTCGACCTGCTGAAGC TGGCCGGGACGTGGAGAGCAACCCTGGCCCC	29
E2A (exemplary amino acid sequence)	QCTNYALLKLAGDVESNPGP	30
E2A (exemplary nucleotide sequence)	CAGTGTACTAATTATGCTCTCTTGAAATTGGCTGGAGATGTTG AGAGCAACCCAGGTCCC	31
E2A (with flanking residues) (exemplary amino acid sequence)	GSGQCTNYALLKLAGDVESNPGP	32

Description	Amino Acid Sequence	SEQ ID NO:
E2A (with flanking residues) (exemplary nucleotide sequence)	GGCTCCGGACAGTGTACTAATTATGCTCTCTTGAAATTGGCTG GAGATGTTGAGAGCAACCCAGGTCCC	33

[00274] As used herein, the terms “inverted terminal repeat,” “ITR,” “inverted repeat/direct repeat,” and “IR/DR” are used interchangeably and refer to a polynucleotide sequence, *e.g.*, of about 230 nucleotides (*e.g.*, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, or 240 nucleotides), flanking (*e.g.*, with or without an intervening polynucleotide sequence) one end of an expression cassette (*e.g.*, a polycistronic expression cassette) that can be cleaved by a transposase polypeptide when used in combination with a corresponding, *e.g.*, reverse-complementary (*e.g.*, perfectly or imperfectly reverse-complementary) polynucleotide sequence, *e.g.*, of about 230 nucleotides (*e.g.*, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, or 240 nucleotides), flanking (*e.g.*, with or without an intervening polynucleotide sequence) the opposite end of the expression cassette (*e.g.*, a polycistronic expression cassette) (*e.g.*, as described in Cui *et al.*, *J. Mol. Biol.* 2002;318(5):1221-35, the contents of which are incorporated by reference in their entirety herein). In some embodiments, an ITR, *e.g.*, an ITR of a DNA transposon (*e.g.*, a *Sleeping Beauty* transposon, a piggyBac transposon, a TcBuster transposon, and a Tol2 transposon) contains two direct repeats (“DRs”), *e.g.*, imperfect direct repeats, *e.g.*, of about 30 nucleotides (*e.g.*, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35 nucleotides), located at each end of the ITR. The terms “ITR” and “DR,” when used in reference to a single- or double-stranded DNA vector, refer to the DNA sequence of the sense strand. A transposase polypeptide may recognize the sense strand and/or the antisense strand of DNA.

[00275] As used herein, the term “Left ITR,” when used in reference to a linear single- or double-stranded DNA vector, refers to the ITR positioned 5’ of the polycistronic expression cassette. As used herein, the term “Right ITR,” when used in reference to a linear single- or double-stranded DNA vector, refers to the ITR positioned 3’ of the polycistronic expression cassette. When a circular vector is used, the Left ITR is closer than the Right ITR to the 5’ end of the polycistronic expression cassette, and the Right ITR is closer than the Left ITR to the 3’ end of the polycistronic expression cassette.

[00276] As used herein, the term “operably linked” refers to a linkage of polynucleotide sequence elements or amino acid sequence elements in a functional relationship. For example, a

polynucleotide sequence is operably linked when it is placed into a functional relationship with another polynucleotide sequence. In some embodiments, a transcription regulatory polynucleotide sequence *e.g.*, a promoter, enhancer, or other expression control element is operably linked to a polynucleotide sequence that encodes a protein if it affects the transcription of the polynucleotide sequence that encodes the protein.

[00277] The term “polynucleotide” as used herein refers to a polymer of DNA or RNA. The polynucleotide sequence can be single-stranded or double-stranded; contain natural, non-natural, or altered nucleotides; and contain a natural, non-natural, or altered internucleotide linkage, such as a phosphoroamidate linkage or a phosphorothioate linkage, instead of the phosphodiester found between the nucleotides of an unmodified polynucleotide sequence. Polynucleotide sequences include, but are not limited to, all polynucleotide sequences which are obtained by any means available in the art, including, without limitation, recombinant means, *e.g.*, the cloning of polynucleotide sequences from a recombinant library or a cell genome, using ordinary cloning technology and polymerase chain reaction, and the like, and by synthetic means.

[00278] The terms “protein” and “polypeptide” are used interchangeably herein and refer to a polymer of amino acids connected by one or more peptide bonds. As used herein, “amino acid sequence” refers to the information describing the relative order and identity of amino acid residues which make up a polypeptide.

[00279] The term “functional variant” as used herein in reference to a protein or polypeptide refers to a protein that comprises at least one amino acid modification (*e.g.*, a substitution, deletion, addition) compared to the amino acid sequence of a reference protein, that retains at least one particular function. In some embodiments, the reference protein is a wild type protein. For example, a functional variant of an IL-15 protein can refer to an IL-15 protein comprising an amino acid substitution compared to a wild type IL-15 protein that retains the ability to bind the IL-15 receptor α chain (IL-15R α). Not all functions of the reference wild type protein need be retained by the functional variant of the protein. In some instances, one or more functions are selectively reduced or eliminated.

[00280] The term “functional fragment” as used herein in reference to a protein or polypeptide refers to a fragment of a reference protein that retains at least one particular function. For example, a functional fragment of an IL-15 protein can refer to a fragment of the protein that retains the ability to specifically bind IL-15R α . Not all functions of the reference protein need be retained by a functional fragment of the protein. In some instances, one or more functions are selectively

reduced or eliminated.

[00281] As used herein, the term “modification,” with reference to a polynucleotide sequence, refers to a polynucleotide sequence that comprises at least one substitution, alteration, inversion, addition, or deletion of nucleotide compared to a reference polynucleotide sequence. As used herein, the term “modification,” with reference to an amino acid sequence, refers to an amino acid sequence that comprises at least one substitution, alteration, inversion, addition, or deletion of an amino acid residue compared to a reference amino acid sequence.

[00282] As used herein, the term “derived from,” with reference to a polynucleotide sequence, refers to a polynucleotide sequence that has at least 85% sequence identity to a reference naturally occurring nucleic acid sequence from which it is derived. The term “derived from,” with reference to an amino acid sequence, refers to an amino acid sequence that has at least 85% sequence identity to a reference naturally occurring amino acid sequence from which it is derived. The term “derived from” as used herein does not denote any specific process or method for obtaining the polynucleotide or amino acid sequence. For example, the polynucleotide or amino acid sequence can be chemically synthesized.

[00283] As used herein, the term “linked to” refers to covalent or noncovalent binding between two molecules or moieties. The skilled worker will appreciate that when a first molecule or moiety is linked to a second molecule or moiety, the linkage need not be direct, but instead, can be via an intervening molecule or moiety.

[00284] As used herein, the term “cytokine” refers to a molecule that mediates and/or regulates a biological or cellular function or process (*e.g.*, immunity, inflammation, and hematopoiesis). As used herein, cytokines include, but are not limited to, lymphokines, chemokines, monokines, and interleukins. The term cytokine as used herein also encompasses functional variants and functional variants of wild type cytokines.

[00285] As used herein, the term “marker protein” or “marker polypeptide” are used interchangeably and refer to a protein or polypeptide that can be expressed on the surface of a cell, which can be utilized to mark or deplete cells expressing the marker protein or polypeptide. In some embodiments, depletion of cells expressing the marker protein or polypeptide is performed through the administration of a molecule that specifically binds the marker protein or polypeptide (*e.g.*, an antibody that mediates antibody dependent cellular cytotoxicity).

[00286] As used herein, the term “immune effector cell” refers to a cell that is involved in the promotion of an immune effector function. Examples of immune effector cells include, but are not

limited to, T cells (*e.g.*, alpha/beta T cells and gamma/delta T cells, CD4⁺ T cells, CD8⁺ T cells, natural killer T (NKT) cells), natural killer (NK) cells, B cells, mast cells, and myeloid-derived phagocytes.

[00287] As used herein, the term, “immune stem cell” refers to a cell that is pluripotent and can differentiate into one or more types of immune cells, including immune effector cells. Immune stem cells include, but are not limited to, bone marrow stem cells, hematopoietic stem cells, embryonic stem cells, induced pluripotent stem cells, umbilical blood stem cells, lymphocyte progenitor cells, stem cell memory T cells, and stem cell memory-like T cells. In certain embodiments, the immune stem cell is isolated and/or enriched from adult and fetal bone marrow, umbilical cord blood, or peripheral blood.

[00288] As used herein, the term “immune effector function” refers to a specialized function of an immune effector cell. The effector function of any given immune effector cell can be different. For example, an effector function of a CD8⁺ T cell is cytolytic activity, and an effector function of a CD4⁺ T cell is secretion of a cytokine.

5.2 T cell Receptors

[00289] In one aspect, the instant disclosure provides TCRs that can be expressed via a polycistronic expression cassette of the present disclosure. In certain embodiments, the TCR comprises a T cell receptor (TCR) alpha chain comprising an alpha chain variable (V α) region and an alpha chain constant (C α) region and a TCR beta chain comprising a beta chain variable (V β) region and a beta chain constant (C β). The amino acid sequences of constant domains comprised in the TCRs disclosed herein are shown in Tables 4 and 5 below.

Table 4. Amino acid sequences of TCR C α regions.

Description	Sequence	SEQ ID NO:
C α (murine, degenerate)	XIQNPEPAVYQLKDPRSQDSTLCLEFTDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	40

Description	Sequence	SEQ ID NO:
C α (murine, degenerate) (exemplary nucleotide sequence)	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTC AGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCC TAAACAATGGAGTCCGGCACCTTCATCACCACAAGNNNGTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACAT CTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTC TGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATG AACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTGCTGCTGA AGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTCC NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	57
C α (murine, cysteine- and LIV-substituted)	NIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	41
C α (murine, cysteine- and LIV-substituted) (exemplary nucleotide sequence)	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTC AGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCC TAAACAATGGAGTCCGGCACCTTCATCACCACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACAT CTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTC TGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATG AACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGA AGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTCC	55
C α (murine, LIV substituted)	NIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	42
C α (murine, LIV substituted) (exemplary nucleotide sequence)	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTC AGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCC TAAACAATGGAGTCCGGCACCTTCATCACCACAAGACCGTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACAT CTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTC TGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATG AACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGA AGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTCC	58
C α (murine, cysteine-substituted)	NIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	43
C α (murine, wild type)	NIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKTVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	44
C α (human, degenerate)	XIQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDSDVYITDKXVLDM RSMDFKSNASAVWSNKSDFACANAFNNSIIPEDTFFPSPSSCDVKLVEKSF ETDTNLNFQNLXVXXFRILLKLVAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr X at position 48 is Thr or Cys; X at position 116 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 118 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 119 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	45

Description	Sequence	SEQ ID NO:
C α (human, cysteine- and LIV-substituted; degenerate at position 1)	XIQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDSVYITDKCVLDM RSMDFKSN SAVAWSNKSD FACANAFNNSIIPEDTFFPSP ESSCDVKLVEKSF ETDTNLNFQNL LVIVFRILLK VAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	46
C α (human, LIV-substituted; degenerate at position 1)	XIQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDSVYITDKTVLDM RSMDFKSN SAVAWSNKSD FACANAFNNSIIPEDTFFPSP ESSCDVKLVEKSF ETDTNLNFQNL LVIVFRILLK VAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	47
C α (human, cysteine-substituted; degenerate at position 1)	XIQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDSVYITDKCVLDM RSMDFKSN SAVAWSNKSD FACANAFNNSIIPEDTFFPSP ESSCDVKLVEKSF ETDTNLNFQNL SVIGFRILLK VAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	48
C α (human, wild type; degenerate at position 1)	XIQNPDPVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKSDSVYITDKTVLDM RSMDFKSN SAVAWSNKSD FACANAFNNSIIPEDTFFPSP ESSCDVKLVEKSF ETDTNLNFQNL SVIGFRILLK VAGFNLLMTLRLWSS X at position 1 is Asn, Asp, His, or Tyr	49

Table 5. Amino acid sequences of TCR C β regions.

Description	Sequence	SEQ ID NO:
C β (murine, degenerate)	EDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNS X at position 57 is Ser or Cys	50
C β (murine, degenerate) (exemplary nucleotide sequence)	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCA AGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGGGG CTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTG CACTCTGGCGTGNNNACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCG GAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAA TGGCCTGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGT GGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAGGGCGTGCT GTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCG GTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAACTCT NNN at positions 169-171 make up a codon that encodes Ser or Cys	59
C β (murine, cysteine-substituted)	EDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNS	51
C β (murine, cysteine-substituted) (exemplary nucleotide sequence)	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCA AGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGGGG CTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTG CACTCTGGCGTGTCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCG GAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAA TGGCCTGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGT GGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAGGGCGTGCT GTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCG GTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAACTCT	56
C β (murine, wild type)	EDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEV HSGVSTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNS	52
C β (human, degenerate)	EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEV HSGVXTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLS ENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKA TLYAVLV SALVLMAMVKRKDSRG X at position 57 is Ser or Cys	53
C β (human, cysteine-substituted)	EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEV HSGVCTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLS ENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKA TLYAVLV SALVLMAMVKRKDSRG	54
C β (human, wild type)	EDLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEV HSGVSTDPQPLKEQPALNDSRYCLSSRLRVSATFWQNP RNHFRCQVQFYGLS ENDEWTQDRAKPVTQIVSAEAWGRADCGFTSESYQQGVLSATILYEILLGKA TLYAVLV SALVLMAMVKRKDSRG	60

[00290] As used herein, “LIV-substituted” refers to a C α sequence disclosed herein which, relative to SEQ ID NO: 40, comprises a leucine residue at position 112, an isoleucine residue at

position 114, and a valine residue at position 115. See, for example, SEQ ID Nos: 41 and 42. In some embodiments, and independent of the LIV-substitutions a Ca sequence disclosed herein can comprise a cysteine at position 48, replacing the threonine residue. (Compare SEQ ID Nos: 40-44). In some embodiments, the C β sequence disclosed herein has a substitution of the serine at residue 57 with cysteine. This is shown in SEQ ID Nos: 50 and 51.

[00291] Tumor Protein p53 (also referred to as “p53”) acts as a tumor suppressor by, for example, regulating cell division. In some embodiments, wild type full-length p53 has the amino acid sequence of SEQ ID NO: 340, shown below.

```
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAMDDLMLSPDDIEQWFTEDPGP
DEAPRMPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRGLHSGTAK
SVTCTYSPALNKMFCQLAKTQPVQLWVDSTPPPQTRVRAMAIYKQSQHMTQVVRRCPHHE
RCSDSDGLAPPQHLIRVEGNLRVEYLLDRNTFRHSVVVPYEPPEVGSDDCTTIHNYMCNS
SCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGDRDRTEENLRKKGEPPHHELP
PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG
GSAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD (SEQ ID NO: 340)
```

[00292] Kirsten rat sarcoma viral oncogene homolog (KRAS), also referred to as GTPase Kras, V-Ki-Ras2 Kirsten rat sarcoma viral oncogene, or KRAS2, is a member of the small GTPase superfamily. There are two transcript variants of KRAS: KRAS variant A and KRAS variant B. Hereinafter, references to “KRAS” (mutated or unmutated) refer to both variant A and variant B, unless specified otherwise. In some embodiments, wild type KRAS variant A has the amino acid sequence of SEQ ID NO: 341 and wild type KRAS variant B has the amino acid sequence of SEQ ID NO: 342, both shown below.

```
MTEYKLVVVGAGGVGKSALTIQLIQNHVFDEYDPTIEDSYRKQVVIDGETCLLDILDITAG
QEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSQVPMVLVGNKCDL
PSRTVDTKQAQDLARSYGIPFIETSAKTRQVRDAFYTLVREIRQYRLKKISKEEKTGPG
VKIKKCIIM (SEQ ID NO: 341)
```

```
MTEYKLVVVGAGGVGKSALTIQLIQNHVFDEYDPTIEDSYRKQVVIDGETCLLDILDITAG
QEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSQVPMVLVGNKCDL
PSRTVDTKQAQDLARSYGIPFIETSAKTRQGVDDAFYTLVREIRKHKEKMSKDGKKKKKK
SKTKCVIM (SEQ ID NO: 342)
```

[00293] EGFR (also referred to as ERBB1 or HER1) is a transmembrane glycoprotein that belongs to the receptor tyrosine kinase (RTK) super-family of cell surface receptors, which mediate cell signaling by extra-cellular growth factors. Examples of wild type (WT), unmutated human EGFR amino acid sequences include those disclosed in GenBank Accession Nos. NP_001333826.1 (isoform e precursor), NP_001333827.1 (isoform f precursor), NP_001333828.1 (isoform g precursor), NP_001333829.1 (isoform h precursor), NP_001333870.1 (isoform i precursor), NP_005219.2 (isoform a precursor), NP_958439.1 (isoform b precursor), NP_958440.1 (isoform c

precursor), and NP_958441.1 (isoform d precursor). In some embodiments, wild type EGFR has the amino acid sequence of SEQ ID NO: 343

MRPSGTAGAAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFNCEV
VLGNLEITYVQRNYDLFLKTIQEVAGYVLIALNTVERIPLNLQIIRGNMYENSYALA
VLSNYDANKTGLKELPMRNLQEIILHGA VRFSNNPALCNVESIQWRDIVSSDFLSNMMSDF
QNLHLSGCKQCDPSCPNWSCWGAGEENCQKLTKIIICAQQCSGRCRGKSPSDCCHNQCAAGC
TGPRESDCLVCRKFRDEATCKDTCPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYV
VTDHGSCVRACGADSYEMEEDGVRKCKCEGPCRKVCNIGIGIGEFKDSLSINATNIKHF
NCTSIISGLHLILPVAFRGDSFTHTPPLDPQELDLKTVKEITGFLLIQAWPENRTDLHAF
ENLEIIRGRKQHGQFSLAVVSLNITSLGLRSLKEISDGDVVISGNKNLCYANTINWKKL
FGTSGQKTKIISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGECVDKCN
LLEGEPRFVENSECIIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTC PAGVM
GENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCP TNGPKIPSIATGMVGALLLLLVV
ALGIGLFMRRRHIVRKRTLRLRLQERELVEPLTPSGEAPNQALLRLKETEFKKIKVLGS
GAFGTVYKGLWIPGEKVKIPVAIKELREATSPKANKEILDEAYVMASVDNPHVCRLGI
CLTSTVQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRLVHRDLAA
RNVLVKTPQHVKITDFGLAKLLGAEKEYHAEGGKVPKWMMALESILHRIYTHQSDVWSY
GVTVWELMTFGSKPYDGI PASEISSILEKGERLPQPPICTIDVYIMVVKCWMIDADSRPK
FRELIIIEFSKMARDPQRYLVIQGDERMHLPSPTDSNFYRALMDEEDMDVVDAD EYLI PQ
QGFFSSPSTSRTPLLSSLSATSNNSTVACIDRNLQSCPIKEDSFLQRYSSDPTGALTED
SIDDTFLPVPEYINQSVKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPEYLN
TVQPTCVNSTFDS PAHWAQKGS HQISLDNPDYQQDFFPEAKPNGIFKGSTAENAEYLRV
APQSSEFIGA (SEQ ID NO: 343)

[00294] The amino acid sequences of exemplary TCRs are set forth in Table 6 herein.

Table 6A. Amino acid sequences of TCR001.

Description	Sequence	SEQ ID NO:
CDR1 α	NYSPAY	1001
CDR2 α	IRENEKE	1002
CDR3 α	ALDIYPHDMR	1003
V α without signal peptide (SignalP)	QKIEQNSEALNIQEGKTATLTCNYTNYS PAYLQWYRQDPGRGPVFLLLIREN EKEKRKERLKVTFDTTLKQSLFHITASQPADSATYLCALDIYPHDMRFGAGT RLTVKP	1004
V α without signal peptide (IMGT)	SQKIEQNSEALNIQEGKTATLTCNYTNYS PAYLQWYRQDPGRGPVFLLLIRE NEKEKRKERLKVTFDTTLKQSLFHITASQPADSATYLCALDIYPHDMRFGAG TRLTVKP	1005
V α	MXSFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYS PAY LQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITASQPAD SATYLCALDIYPHDMRFGAGTRLTVKP (X = any amino acid)	1006
		1007
α chain with WT signal peptide, C α (substituted)	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYS PAY LQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITASQPAD SATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRS QDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVIVLRILLKLVAGFNLL MTLRLWSS	1008
α chain with alternative signal peptide, C α (substituted)	MASFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYS PAY LQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITASQPAD SATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRS QDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVIVLRILLKLVAGFNLL MTLRLWSS	1009

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) with signal C α	MHSFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPGRGPVFLLLIRENEKEKRERLKVTFDTLTKQSLFHITASQPADSATYLCALDIYPHDMRFAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1010
CDR1 β	SGHAT	2001
CDR2 β	FQNNGV	2002
CDR3 β	ASSLDPGDTGELF	2003
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVL	2004
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVL	2005
V β	MXTRLWCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVL (X = any amino acid)	2006
		2007
β chain with WT signal peptide, (substituted) C β	MGTRLWCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2008
β chain with alternative signal peptide, C β (substituted)	MATRLWCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2009
β chain with alternative signal peptide, C β (substituted)	MHTRLWCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2010

[00295] In some embodiments, TCR001 interacts with and/or is specific for a peptide from the tumor protein p53 (p53). In some embodiments, the peptide is from a neoantigen of p53 and has the amino acid change R175H (in which position 175 of the p53 protein is mutated from Arg to His). In some embodiments, TCR001 interacts with and/or is specific for the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6B. Amino acid sequences of TCR002.

Description	Sequence	SEQ ID NO:
CDR1 α	DSASNY	1011
CDR2 α	IRSNVGE	1012
CDR3 α	AASKSAIMVVLQTSSSL	1013
V α without signal peptide (SignalP)	ENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQV	1014
V α without signal peptide (IMGT)	GENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTS SLELALCLLSSQV	1015
V α	MXSIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQV (X = any amino acid)	1016
		1017
α chain with WT signal peptide, (substituted) C α	MTSIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQVNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVLVIRILLKLVAGFNLLMTLRLWSS	1018
α chain with alternative signal peptide, (substituted) C α	MASIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQVNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVLVIRILLKLVAGFNLLMTLRLWSS	1019
α chain with alternative signal peptide, (substituted) C α	MHSIRAVFI FLWLQLDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASKSAIMVVLQTSSSLELALCLLSSQVNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNNGAIAWSNQTSTFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVLVIRILLKLVAGFNLLMTLRLWSS	1020
CDR1 β	MNHEY	2011
CDR2 β	SMNVEV	2012
CDR3 β	ASSIQQGADTQY	2013
V β without signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL	2014
V β without signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL	2015
V β	MXPQLLGYYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVL (X = any amino acid)	2016
		2017
β chain with WT signal peptide, (substituted) C β	MGPQLLGYYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES P SPNQTSLYFCASSIQQGADTQYFGPGTRLTVLLEDLRNVT PKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2018

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAPQLLGYYVLCCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILIESPSPNQ TSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2019
β chain with alternative signal peptide, C β (substituted)	MHPQLLGYYVLCCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILIESPSPNQ TSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2020

[00296] In some embodiments, TCR002 interacts with and/or is specific for a peptide from p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR002 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6C. Amino acid sequences of TCR003.

Description	Sequence	SEQ ID NO:
CDR1 α	NSAFQY	1021
CDR2 α	TYSSGN	1022
CDR3 α	AMSGLKEDSSYKLI	1023
V α w/o signal peptide (SignalP)	QQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTY SSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMSGLKEDSSYKLI FGSGTRLLVRP	1024
V α w/o signal peptide (IMGT)	QKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMSGLKEDSSYKLIF GSGTRLLVRP	1025
V α	MXKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMSGLKEDSSYKLIFGSGTRLLVRP (X = any amino acid)	1026
		1027
α chain w/WT signal peptide, C α (substituted)	MMKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMSGLKEDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPQSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTST CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1028
α chain w/alternative signal peptide, C α (substituted)	MAKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMSGLKEDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPQSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTST CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1029

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIKSDQPS DSATYLCAMSGLKEDSSYKLI FGSGTRLLVRPNIQNPEPAVYQLKDPKSDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPDATLTKESFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1030
CDR1 β	MNHEY	2021
CDR2 β	SMNVEV	2022
CDR3 β	ASSIQQGADTQY	2023
V β w/o signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEV TDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASSIQQGADTQYFGP GTRLTVL	2024
V β w/o signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNV EVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASSIQQGADTQYF GPGTRLTVL	2025
V β	MXPQLLGYYVLCCLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQ TSLYFCASSIQQGADTQYFGPGTRLTVL (X = any amino acid)	2026
		2027
β chain w/WT signal peptide, C β (substituted)	MGPQLLGYYVLCCLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQ TSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2028
β chain w/alternative signal peptide, C β (substituted)	MAPQLLGYYVLCCLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQ TSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2029
β chain w/alternative signal peptide, C β (substituted)	MHPQLLGYYVLCCLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQ TSLYFCASSIQQGADTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2030

[00297] In some embodiments, TCR003 interacts with and/or is specific for a peptide from p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR003 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6D. Amino acid sequences of TCR004.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASQS	1031

Description	Sequence	SEQ ID NO:
CDR2 α	VYSSGN	1032
CDR3 α	VVQPGGYQKVT	1033
V α w/o signal peptide (SignalP)	QRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIP	1034
V α w/o signal peptide (IMGT)	RKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIP	1035
V α	MXSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIP (X = any amino acid)	1036
		1037
α chain w/WT signal peptide, C α (substituted)	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIPNIQNPEPAVYQLKDPRSQDSTLCCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKLVAGFNLL MTLRLWSS	1038
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIPNIQNPEPAVYQLKDPRSQDSTLCCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKLVAGFNLL MTLRLWSS	1039
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVVQPGGYQKVTFGTGTKLQVIPNIQNPEPAVYQLKDPRSQDSTLCCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKLVAGFNLL MTLRLWSS	1040
CDR1 β	MNHNS	2031
CDR2 β	SASEGT	2032
CDR3 β	ASSEGLWQVGDEQY	2033
V β w/o signal peptide (SignalP)	GVTQTTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAASEGTTDKGEVPNGYNVSRNLKREFSLRLESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVT	2034
V β w/o signal peptide (IMGT)	NAGVTQTTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAASEGTTDKGEVPNGYNVSRNLKREFSLRLESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVT	2035
V β	MXIGLLCCVAFSLLWASPVNAGVTQTTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAASEGTTDKGEVPNGYNVSRNLKREFSLRLESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVT (X = any amino acid)	2036
		2037
β chain w/WT signal peptide, C β (substituted)	MSIGLLCCVAFSLLWASPVNAGVTQTTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSAASEGTTDKGEVPNGYNVSRNLKREFSLRLESAAPSQTSVYFCASSEGLWQVGDEQYFGPGTRLTVTDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSAFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2038

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHNMY WYRQDPGMGLRLIYYASASEGTTDKGEVPNGYNVSRNLKREFSLRLESAAPSQ TSVYFCASSEGLWQVGDEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2039
β chain w/alternative signal peptide, C β (substituted)	MHIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHNMY WYRQDPGMGLRLIYYASASEGTTDKGEVPNGYNVSRNLKREFSLRLESAAPSQ TSVYFCASSEGLWQVGDEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2040

[00298] In some embodiments, TCR004 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR004 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6E. Amino acid sequences of TCR005.

Description	Sequence	SEQ ID NO:
CDR1 α	TSENNYY	1041
CDR2 α	QEAYKQQN	1042
CDR3 α	AFMGYSGAGSYQLT	1043
V α w/o signal peptide (SignalP)	QTVTQSQPEMSVQEAEVTLSCTYDTSENNYLFWYKQPPSRQMILVIRQEA YKQQNATENRFSVNFQKAASFSLKISDSQLGDTAMYFCAFMGYSGAGSYQL TFGKGTKLSVIP	1044
V α w/o signal peptide (IMGT)	AQTVTQSQPEMSVQEAEVTLSCTYDTSENNYLFWYKQPPSRQMILVIRQE AYKQQNATENRFSVNFQKAASFSLKISDSQLGDTAMYFCAFMGYSGAGSYQ LTFGKGTKLSVIP	1045
V α	MXRVSLWAVVSTCLESQMAQTVTQSQPEMSVQEAEVTLSCTYDTSENNY YLFYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAASFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTFGKGTKLSVIP (X = any amino acid)	1046
		1047
α chain w/WT signal peptide, C α (substituted)	MTRVSLWAVVSTCLESQMAQTVTQSQPEMSVQEAEVTLSCTYDTSENNY YLFYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAASFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPQRSQ STLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSE TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVLRIILLKV AGFNLLMTLRLWSS	1048
α chain w/alternative signal peptide, C α (substituted)	MARVSLWAVVSTCLESQMAQTVTQSQPEMSVQEAEVTLSCTYDTSENNY YLFYKQPPSRQMILVIRQEAAYKQQNATENRFSVNFQKAASFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPQRSQ STLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSE TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLIVLRIILLKV AGFNLLMTLRLWSS	1049

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHRVSLWAVVSTCLESMAQTVTQSQPEMSVQEAETVTLSCYDTSENYY YLFWYKQPPSRQMILVIRQEAAYKQONATENRFSVNFQKAASFSLKISDSQL GDTAMYFCAFMGYSGAGSYQLTFGKGTKLSVLPNIQNPEPAVYQLKDPRSQD STLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSF TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFPQNLLVILRILLKLV AGFNLLMTLRLWSS	1050
CDR1 β	ENHRY	2041
CDR2 β	SYGVKD	2042
CDR3 β	AISELVTGDSPLH	2043
V β w/o signal peptide (SignalP)	GITQSPRHKTETGTPVTLRCHQTENHRYMYWYRQDPGHGLRLIHYSYGVKD TDKGEVSDGYSVSRKTEDFLLTLESATSSQTSVYFCAISELVTGDSPLHFG NGTRLTVT	2044
V β w/o signal peptide (IMGT)	DAGITQSPRHKTETGTPVTLRCHQTENHRYMYWYRQDPGHGLRLIHYSYGV KTDKGEVSDGYSVSRKTEDFLLTLESATSSQTSVYFCAISELVTGDSPLH FGNGTRLTVT	2045
V β	MXTRLFFYVALCLLWTGHMDAGITQSPRHKTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVT (X = any amino acid)	2046
		2047
β chain w/WT signal peptide, C β (substituted)	MGTRLFFYVALCLLWTGHMDAGITQSPRHKTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVTEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATI IYEILLGKATLYAVLVSTLVVMAMVKKRNS	2048
β chain w/alternative signal peptide, C β (substituted)	MATRLFFYVALCLLWTGHMDAGITQSPRHKTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVTEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATI IYEILLGKATLYAVLVSTLVVMAMVKKRNS	2049
β chain w/alternative signal peptide, C β (substituted)	MHTRLFFYVALCLLWTGHMDAGITQSPRHKTETGTPVTLRCHQTENHRYMY WYRQDPGHGLRLIHYSYGVKDTDKGEVSDGYSVSRKTEDFLLTLESATSSQ TSVYFCAISELVTGDSPLHFGNGTRLTVTEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATI IYEILLGKATLYAVLVSTLVVMAMVKKRNS	2050

[00299] In some embodiments, TCR005 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR005 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6F. Amino acid sequences of TCR006.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1051

Description	Sequence	SEQ ID NO:
CDR2 α	GLKNN	1052
CDR3 α	IVRGSPGAGGTSYGKLT	1053
V α w/o signal peptide (SignalP)	KTTPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNN ETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRGSPGAGGTSYGKLT FGQGTILTVHP	1054
V α w/o signal peptide (IMGT)	DAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLK NNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRGSPGAGGTSYGKL TFGQGTILTVHP	1055
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFGQGTILTVHP (X = any amino acid)	1056
		1057
α chain w/WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFGQGTILTVHPNINPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1058
α chain w/alternative signal peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFGQGTILTVHPNINPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1059
α chain w/alternative signal peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRGSPGAGGTSYGKLTFGQGTILTVHPNINPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1060
CDR1 β	LNHDA	2051
CDR2 β	SQIVND	2052
CDR3 β	ASSIRTEAF	2053
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSIRTEAFFGQGR LTVV	2054
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSIRTEAFFGQ TRLTVV	2055
V β	MXNQVLCCVVLCLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGRTRLTVV (X = any amino acid)	2056
		2057
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVLCLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGRTRLTVVEDLRNVTPPKVSLFEPKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILGKATLYAVLVSTLVVMAMVKRKN	2058

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVKRKN S	2059
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSIRTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRADCGITS ASYQQGVLSATILYEI LLGKATLYAVLVSTLVVMAMVKRKN S	2060

[00300] In some embodiments, TCR006 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR006 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6G. Amino acid sequences of TCR007.

Description	Sequence	SEQ ID NO:
CDR1 α	TTSDR	1061
CDR2 α	LLSNGAV	1062
CDR3 α	AVAHMDSNYQLI	1063
V α w/o signal peptide (SignalP)	ELKVEQNPLFLSMQEGKNTIYCNYSTTSDRLYWYRQDPGKSLES L FVLLSN GAVKQEGRLMASLDTKARLSTLHITA AVHDL SATYFC AVAHMDSNYQLIWGA GTKLI IKP	1064
V α w/o signal peptide (IMGT)	ELKVEQNPLFLSMQEGKNTIYCNYSTTSDRLYWYRQDPGKSLES L FVLLSN GAVKQEGRLMASLDTKARLSTLHITA AVHDL SATYFC AVAHMDSNYQLIWGA GTKLI IKP	1065
V α	MXKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNTIYCNYSTTSDRLYW YRQDPGKSLES L FVLLSNGAVKQEGRLMASLDTKARLSTLHITA AVHDL SAT YFC AVAHMDSNYQLIWGAGTKLI IKP	1066
	(X = any amino acid)	1067
α chain w/WT signal peptide, C α (substituted)	MKKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNTIYCNYSTTSDRLYW YRQDPGKSLES L FVLLSNGAVKQEGRLMASLDTKARLSTLHITA AVHDL SAT YFC AVAHMDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQT SFTCQDI FK ETNATYPSSDVPCDATLTEKS FETDMNLN FQNLLVIVLRILL LK VAGFNLLM TLRLWSS	1068
α chain w/alternative signal peptide, C α (substituted)	MAKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNTIYCNYSTTSDRLYW YRQDPGKSLES L FVLLSNGAVKQEGRLMASLDTKARLSTLHITA AVHDL SAT YFC AVAHMDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQT SFTCQDI FK ETNATYPSSDVPCDATLTEKS FETDMNLN FQNLLVIVLRILL LK VAGFNLLM TLRLWSS	1069

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHKLLAMILWLQLDRLSGELKVEQNPLFLSMQEGKNYTIYCNYSTTSDRLYW YRQDPGKSLESFLVLLSNGAVKQEGRLMASLDTKARLSTLHITAAVHDLSAT YFCAVAHMDSNYQLIWGAGTKLI I KPNIQNPEPAVYQLKDPRSQDSTLCLEF DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLM TLRLWSS	1070
CDR1 β	MNHEY	2061
CDR2 β	SVGEGT	2062
CDR3 β	ASSYAGLAAPREQF	2063
V β w/o signal peptide (SignalP)	GVTQTPKFRVLKTGQSM TLLCAQDMNHEMYWYRQDPGMGLRLIHYSVGEGT TAKGEVPDGYNVSRLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQFF GPGTRLTVL	2064
V β w/o signal peptide (IMGT)	NAGVTQTPKFRVLKTGQSM TLLCAQDMNHEMYWYRQDPGMGLRLIHYSVGE GTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQTSVYFCASSYAGLAAPREQ FFGPGTRLTVL	2065
V β	MXLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASSYAGLAAPREQFFGPGTRLTVL (X = any amino acid)	2066
		2067
β chain w/WT signal peptide, C β (substituted)	MSLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASSYAGLAAPREQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2068
β chain w/alternative signal peptide, C β (substituted)	MALGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASSYAGLAAPREQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2069
β chain w/alternative signal peptide, C β (substituted)	MHLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLKKQNFLLGLESAAPSQ TSVYFCASSYAGLAAPREQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2070

[00301] In some embodiments, TCR007 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR007 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6H. Amino acid sequences of TCR008.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1071

Description	Sequence	SEQ ID NO:
CDR2 α	GLKNN	1072
CDR3 α	IVRARANAGGTSYGKLT	1073
V α w/o signal peptide (SignalP)	KTTPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNN ETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLT FGQGTILTVHP	1074
V α w/o signal peptide (IMGT)	DAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLK NNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLT TFGQGTILTVHP	1075
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHP (X = any amino acid)	1076
		1077
α chain w/WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHPNINPEPAVYQLKDPKSDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1078
α chain w/alternative signal peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHPNINPEPAVYQLKDPKSDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1079
α chain w/alternative signal peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQGTILTVHPNINPEPAVYQLKDPKSDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1080
CDR1 β	LNHDA	2071
CDR2 β	SQIVND	2072
CDR3 β	ASLQFNEQF	2073
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASLQFNEQFFGPGTR LTVL	2074
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASLQFNEQFFGPG TRLTVL	2075
V β	MXMSNQVLCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHD AMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVL (X = any amino acid)	2076
V β (alternative)	MXNQVLCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHD AMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKN PTAFYLCASLQFNEQFFGPGTRLTVL (X = any amino acid)	2077
β chain w/WT signal peptide, C β (substituted)	MSMSNQVLCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHD AMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNP RNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2078

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAMSNQVLCVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDA MYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2079
β chain w/alternative signal peptide, C β (substituted)	MHMSNQVLCVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDA MYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQK NPTAFYLCASLQFNEQFFGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2080

[00302] In some embodiments, TCR008 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR008 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6I. Amino acid sequences of TCR009.

Description	Sequence	SEQ ID NO:
CDR1 α	SSNFYA	1081
CDR2 α	MTLNGDE	1082
CDR3 α	ALITGGGNKLT	1083
V α w/o signal peptide (SignalP)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTL NGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCALITGGGNKLTFGT GTQLKVEL	1084
V α w/o signal peptide (IMGT)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTL NGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCALITGGGNKLTFGT GTQLKVEL	1085
V α	MXKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFGTGTQLKVEL	1086
	(X = any amino acid)	1087
α chain w/WT signal peptide, C α (substituted)	MEKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFTDKCVLDMKAMDSKSNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGF NLLMTLRLWSS	1088
α chain w/alternative signal peptide, C α (substituted)	MAKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFGTGTQLKVELNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFTDKCVLDMKAMDSKSNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGF NLLMTLRLWSS	1089

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHKNPLAAPLLILWFHLCVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNF YALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQP EDSATYLCALITGGGNKLTFTGTQLKVELNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMSGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1090
CDR1 β	MNHEY	2081
CDR2 β	SVGEGT	2082
CDR3 β	ASRLQGWN SPLH	2083
V β w/o signal peptide (SignalP)	GVTQT PKFRVLKTGQSM TLLCAQDMNHEMYWYRQDPGMGLRLIHYSVGEGT TAKGEVPDGYNVSRLLKQNFLLGLESAAPSQTSVYFCASRLQGWN SPLHFGN GTRLTVT	2084
V β w/o signal peptide (IMGT)	NAGVTQT PKFRVLKTGQSM TLLCAQDMNHEMYWYRQDPGMGLRLIHYSVGE GTTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQTSVYFCASRLQGWN SPLHF GNGTRLTVT	2085
V β	MXLGLLCCGAFSLLWAGPVNAGVTQT PKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVT (X = any amino acid)	2086
		2087
β chain w/WT signal peptide, C β (substituted)	MSLGLLCCGAFSLLWAGPVNAGVTQT PKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2088
β chain w/alternative signal peptide, C β (substituted)	MALGLLCCGAFSLLWAGPVNAGVTQT PKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2089
β chain w/alternative signal peptide, C β (substituted)	MHLGLLCCGAFSLLWAGPVNAGVTQT PKFRVLKTGQSM TLLCAQDMNHEMY WYRQDPGMGLRLIHYSVGEGTTAKGEVPDGYNVSRLLKQNFLLGLESAAPSQ TSVYFCASRLQGWN SPLHFGNGTRLTVTEDLRNVTPPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2090

[00303] In some embodiments, TCR009 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR009 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6J. Amino acid sequences of TCR010.

Description	Sequence	SEQ ID NO:
CDR1 α	TTLSN	1091

Description	Sequence	SEQ ID NO:
CDR2 α	LVKSGEV	1092
CDR3 α	AGPGGAGSYQLT	1093
V α w/o signal peptide (SignalP)	QQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQWYKQRPGGHPVFLIQLVKSG EVKKQKRLTFQFGEAKKNSSLHITATQTTDVGT YFCAGPGGAGSYQLTFGKG TKLSVIP	1094
V α w/o signal peptide (IMGT)	GQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQWYKQRPGGHPVFLIQLVKSG EVKKQKRLTFQFGEAKKNSSLHITATQTTDVGT YFCAGPGGAGSYQLTFGKG GTKLSVIP	1095
V α	MXLITSMVLVWMLQSLQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGT YFCAGPGGAGSYQLTFGKGTKLSVIP (X = any amino acid)	1096
		1097
α chain w/WT signal peptide, C α (substituted)	MLLITSMVLVWMLQSLQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGT YFCAGPGGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCLEFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNLLM TLRWSS	1098
α chain w/alternative signal peptide, C α (substituted)	MALITSMVLVWMLQSLQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGT YFCAGPGGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCLEFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNLLM TLRWSS	1099
α chain w/alternative signal peptide, C α (substituted)	MHLITSMVLVWMLQSLQVNGQQVMQIPQYQHVQEGEDFTTYCNSSTTLSNIQW YKQRPGGHPVFLIQLVKSGEVKKQKRLTFQFGEAKKNSSLHITATQTTDVGT YFCAGPGGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCLEFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNLLM TLRWSS	1100
CDR1 β	MNHEY	2091
CDR2 β	SMNVEV	2092
CDR3 β	ASSPFVVGQINEQY	2093
V β w/o signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEV TDKGDVPEGYKVSREKRNFP LILES P SPNQTSLYFCASSPFVVGQINEQY FGPGRRLTVT	2094
V β w/o signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNV EVTDKGDVPEGYKVSREKRNFP LILES P SPNQTSLYFCASSPFVVGQINE QYFGPGRRLTVT	2095
V β	MXPQLLGYYVLCCLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSREKRNFP LILES P SPNQ TSLYFCASSPFVVGQINEQYFGPGRRLTVT (X = any amino acid)	2096
		2097
β chain w/WT signal peptide, C β (substituted)	MGPQLLGYYVLCCLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSREKRNFP LILES P SPNQ TSLYFCASSPFVVGQINEQYFGPGRRLTVTEDLRNVT PPKVSLFEPKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2098

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPQLLGYYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES PPNQ TSLYFCASSPFVVGQINEQYFGPGTRLTVTEDLRNVTPPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELS W W VNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2099
β chain w/alternative signal peptide, C β (substituted)	MHPQLLGYYVVLCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMS WYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVS RKEKRNFP LILES PPNQ TSLYFCASSPFVVGQINEQYFGPGTRLTVTEDLRNVTPPKVSLFEP SKAEI ANKQKATLVCLARGFFPDHVELS W W VNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2100

[00304] In some embodiments, TCR010 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR010 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6K. Amino acid sequences of TCR011.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1101
CDR2 α	GLKNN	1102
CDR3 α	IVRARANAGGTSYGKLT	1103
V α w/o signal peptide (SignalP)	KTTPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNN ETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLT FGQTILTVHP	1104
V α w/o signal peptide (IMGT)	DAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLK NNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKL TFGQTILTVHP	1105
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHP (X = any amino acid)	1106
		1107
α chain w/WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHPNINPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1108
α chain w/alternative signal peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYW YRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYY CIVRARANAGGTSYGKLTFGQTILTVHPNINPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1109

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWYRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSSTLILPHATLRDTAVYYCIVRARANAGGTSYGKLTFGQGTILTVHPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVLVLRILLKLVAGFN LLMTLRLWSS	1110
CDR1 β	LNHDA	2101
CDR2 β	SQIVND	2102
CDR3 β	ATRTGNEAF	2103
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCATRTGNEAFFGQGTRLTVV	2104
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCATRTGNEAFFGQGTRLTVV	2105
V β	MXNQVLCCVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCATRTGNEAFFGQGTRLTVV (X = any amino acid)	2106
		2107
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCATRTGNEAFFGQGTRLTVVEDLRNVTPPKVSLEFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVKRKNS	2108
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCATRTGNEAFFGQGTRLTVVEDLRNVTPPKVSLEFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVKRKNS	2109
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCATRTGNEAFFGQGTRLTVVEDLRNVTPPKVSLEFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVKRKNS	2110

[00305] In some embodiments, TCR011 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR011 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6L. Amino acid sequences of TCR012.

Description	Sequence	SEQ ID NO:
CDR1 α	VSNAYN	1111

Description	Sequence	SEQ ID NO:
CDR2 α	GSKP	1112
CDR3 α	AVEDRRRTALI	1113
V α w/o signal peptide (SignalP)	KDQVFQPSSTVASSEGAVVEIFCNHVSNAYNFFWYLHFGPCAPRLLVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSV SS	1114
V α w/o signal peptide (IMGT)	KDQVFQPSSTVASSEGAVVEIFCNHVSNAYNFFWYLHFGPCAPRLLVKGSKP SQQGRYNMTYERFSSSLILQVREADAAVYYCAVEDRRRTALIFGKGTTLSV SS	1115
V α	MXLQSTLGAVWLGLLLNSLWKVAESKDQVFQPSSTVASSEGAVVEIFCNHVS NAYNFFWYLHFGPCAPRLLVKGSKPSQQGRYNMTYERFSSSLILQVREADA AVYYCAVEDRRRTALIFGKGTTLSVSS (X = any amino acid)	1116
		1117
α chain w/WT signal peptide, C α (substituted)	MALQSTLGAVWLGLLLNSLWKVAESKDQVFQPSSTVASSEGAVVEIFCNHVS NAYNFFWYLHFGPCAPRLLVKGSKPSQQGRYNMTYERFSSSLILQVREADA AVYYCAVEDRRRTALIFGKGTTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVIRILLKLVAGFNLL MTLRLWSS	1118
		1119
α chain w/alternative signal peptide, C α (substituted)	MHLQSTLGAVWLGLLLNSLWKVAESKDQVFQPSSTVASSEGAVVEIFCNHVS NAYNFFWYLHFGPCAPRLLVKGSKPSQQGRYNMTYERFSSSLILQVREADA AVYYCAVEDRRRTALIFGKGTTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVIRILLKLVAGFNLL MTLRLWSS	1120
CDR1 β	SNHLY	2111
CDR2 β	FYNNEI	2112
CDR3 β	ASSEYQSQSNEQF	2113
V β w/o signal peptide (SignalP)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLEDSAMYFCASSEYQSQSNEQ FFGPGTRLTVL	2114
V β w/o signal peptide (IMGT)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLEDSAMYFCASSEYQSQSNEQ FFGPGTRLTVL	2115
V β	MXTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASSEYQSQSNEQFFGPGTRLTVL (X = any amino acid)	2116
		2117
β chain w/WT signal peptide, C β (substituted)	MDTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASSEYQSQSNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2118
β chain w/alternative signal peptide, C β (substituted)	MATWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASSEYQSQSNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2119

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MHTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPISNHLYFY WYRQILGQKVEFLVSFYNNIESEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASSEYQSQSNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCVQVFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2120

[00306] In some embodiments, TCR012 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR012 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6M. Amino acid sequences of TCR013.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGTDY	1121
CDR2 α	GLTSN	1122
CDR3 α	ILRDNNARLM	1123
V α w/o signal peptide (SignalP)	KTTPNSMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSTLILHRATLRDAVYYCILRDNNARLMFGDGTQLV VKP	1124
V α w/o signal peptide (IMGT)	DAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLT SNVNNRMASLAIAEDRKSTLILHRATLRDAVYYCILRDNNARLMFGDGTQ LVVKP	1125
V α	MXLVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSTLILHRATLRDAVYY CILRDNNARLMFGDGTQLVVKP (X = any amino acid)	1126
		1127
α chain w/WT signal peptide, C α (substituted)	MKLVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSTLILHRATLRDAVYY CILRDNNARLMFGDGTQLVVKPNIQNPEPAVYQLKDPQSQDSTLCFLTFDFS QINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNLLMTLRL WSS	1128
α chain w/alternative signal peptide, C α (substituted)	MALVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSTLILHRATLRDAVYY CILRDNNARLMFGDGTQLVVKPNIQNPEPAVYQLKDPQSQDSTLCFLTFDFS QINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNLLMTLRL WSS	1129
α chain w/alternative signal peptide, C α (substituted)	MHLVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSTLILHRATLRDAVYY CILRDNNARLMFGDGTQLVVKPNIQNPEPAVYQLKDPQSQDSTLCFLTFDFS QINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNLLMTLRL WSS	1130
CDR1 β	MNHEY	2121

Description	Sequence	SEQ ID NO:
CDR2 β	SMNVEV	2122
CDR3 β	ASGLVGFNQPH	2123
V β w/o signal peptide (SignalP)	QVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASGLVGFNQPHFGDGTRLSIL	2124
V β w/o signal peptide (IMGT)	EAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASGLVGFNQPHFGDGTRLSIL	2125
V β	MXPQLLGYYVLCCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASGLVGFNQPHFGDGTRLSIL (X = any amino acid)	2126
		2127
β chain w/WT signal peptide, C β (substituted)	MGPQLLGYYVLCCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASGLVGFNQPHFGDGTRLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2128
β chain w/alternative signal peptide, C β (substituted)	MAPQLLGYYVLCCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASGLVGFNQPHFGDGTRLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2129
β chain w/alternative signal peptide, C β (substituted)	MHPQLLGYYVLCCLLGAGPLEAQVTQNPRYLITVTGKKLTVTCSQNMNHEYMSWYRQDPGLGLRQIYYSMNVEVTDKGDVPEGYKVSKEKRNFPILILESPSPNQTSLYFCASGLVGFNQPHFGDGTRLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2130

[00307] In some embodiments, TCR013 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R175H relative to the wild type p53 sequence. In some embodiments, TCR013 interacts with the neoantigen in the context of HLA-DRB1*13:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6N. Amino acid sequences of TCR014

Description	Sequence	SEQ ID NO:
CDR1 α	VSGNPY	1131
CDR2 α	YITGDNLV	1132
CDR3 α	AVRDGSATSGTYKYI	1133
V α w/o signal peptide (SignalP)	QSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLEFWYVQYPNRLGQFLKYYITGDNLVKGSYGFEAEFNKQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVLA	1134

Description	Sequence	SEQ ID NO:
V α w/o signal peptide (IMGT)	AQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVL	1135
V α	MXSAPISMLAMLFLLSGLRAQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVL	1136
	(X = any amino acid)	1137
α chain w/WT signal peptide, C α (substituted)	MASAPISMLAMLFLLSGLRAQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVLANIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPDATLLEKSFETDMNLFQNLVIVLRILLKVA	1138
	GENLLMTLRLWSS	1139
α chain w/alternative signal peptide, C α (substituted)	MHSAPISMLAMLFLLSGLRAQSVAPQEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDGSATSGTYKYIFGTGTRLKVLANIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPDATLLEKSFETDMNLFQNLVIVLRILLKVA	1140
CDR1 β	SEHNR	2131
CDR2 β	FQNEAQ	2132
CDR3 β	ASSPGLAYEQY	2133
V β w/o signal peptide (SignalP)	DTGVSQDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERPFGSFTLEIQRTSQGDSAMYLCASSPGLAYEQYFGPGTRLTVT	2134
V β w/o signal peptide (IMGT)	DTGVSQDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERPFGSFTLEIQRTSQGDSAMYLCASSPGLAYEQYFGPGTRLTVT	2135
V β	MXTSLLCWMALCCLLGADHADTGVSDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERPFGSFTLEIQRTSQGDSAMYLCASSPGLAYEQYFGPGTRLTVT	2136
	(X = any amino acid)	2137
β chain w/WT signal peptide, C β (substituted)	MGTSLLCWMALCCLLGADHADTGVSDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERPFGSFTLEIQRTSQGDSAMYLCASSPGLAYEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2138
β chain w/alternative signal peptide, C β (substituted)	MATSLLCWMALCCLLGADHADTGVSDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERPFGSFTLEIQRTSQGDSAMYLCASSPGLAYEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2139
β chain w/alternative signal peptide, C β (substituted)	MHTSLLCWMALCCLLGADHADTGVSDPRHKITKRGQNVTFRCDPISSEHNRLYWYRQTLGQGPEFLTYFQNEAQLEKSRLLSDRFSAERPFGSFTLEIQRTSQGDSAMYLCASSPGLAYEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2140

[00308] In some embodiments, TCR014 interacts with and/or is specific for p53. In some

embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change Y220C relative to the wild type p53 sequence. In some embodiments, TCR014 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2020/264269, incorporated herein by reference in its entirety.

Table 6O. Amino acid sequences of TCR015.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1141
CDR2 α	IYSNGD	1142
CDR3 α	AWN SGG S NY KLT	1143
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLC A WNSGG S NY KLT FG KGTLLTVNP	1144
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIYS NGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLC A WNSGG S NY KLT FG KGTLLTVNP	1145
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC A WNSGG S NY KLT FG KGTLLTVNP	1146
	(X = any amino acid)	1147
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC A WNSGG S NY KLT FG KGTLLTVNPNIQNPEPAVYQLKDPRS QDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSK SNGAIAWSNQT SFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI VLR I L L L K VAGFN LLMTLRLWSS	1148
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC A WNSGG S NY KLT FG KGTLLTVNPNIQNPEPAVYQLKDPRS QDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSK SNGAIAWSNQT SFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI VLR I L L L K VAGFN LLMTLRLWSS	1149
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQS FFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLC A WNSGG S NY KLT FG KGTLLTVNPNIQNPEPAVYQLKDPRS QDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSK SNGAIAWSNQT SFTCQD I FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI VLR I L L L K VAGFN LLMTLRLWSS	1150
CDR1 β	MNHEY	2141
CDR2 β	SVGEGT	2142
CDR3 β	ASSYSQAWGQPQH	2143
V β w/o signal peptide (SignalP)	GVTQT PKFRVLKTGQSM TLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGEGT TAKGEVPDGYNVSR LKKQNFLLGLESAAPSQTSVYFCASSYSQAWGQPQHFG DGT RLSIL	2144
V β w/o signal peptide (IMGT)	NAGVTQT PKFRVLKTGQSM TLLCAQDMNHEYMYWYRQDPGMGLRLIHYSVGE GTTAKGEVPDGYNVSR LKKQNFLLGLESAAPSQTSVYFCASSYSQAWGQPQH FGDGT RLSIL	2145
V β	MXLGLLCCGAFSLLWAGPVNAGVTQT PKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGT TAKGEVPDGYNVSR LKKQNFLLGLESAAPSQ	2146

Description	Sequence	SEQ ID NO:
	TSVYFCASSYSQAWGQPQHFGDGTRLSIL (X = any amino acid)	2147
β chain w/WT signal peptide, C β (substituted)	MSLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGETTAKGEVPDGYNVSRLKKQN FLLGLESAAAPSQ TSVYFCASSYSQAWGQPQHFGDGTRLSILEDLRNVT PPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2148
β chain w/alternative signal peptide, C β (substituted)	MALGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGETTAKGEVPDGYNVSRLKKQN FLLGLESAAAPSQ TSVYFCASSYSQAWGQPQHFGDGTRLSILEDLRNVT PPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2149
β chain w/alternative signal peptide, C β (substituted)	MHLGLLCCGAFSLLWAGPVNAGVTQTPKFRVLKTGQSM TLLCAQDMNHEYMY WYRQDPGMGLRLIHYSVGEGETTAKGEVPDGYNVSRLKKQN FLLGLESAAAPSQ TSVYFCASSYSQAWGQPQHFGDGTRLSILEDLRNVT PPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPK PVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2150

[00309] In some embodiments, TCR015 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change Y220C relative to the wild type p53 sequence. In some embodiments, TCR015 interacts with the neoantigen in the context of HLA-DRB1*04:01:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6P. Amino acid sequences of TCR016.

Description	Sequence	SEQ ID NO:
CDR1 α	VSGNPY	1151
CDR2 α	YITGDNLV	1152
CDR3 α	AVRVWDYKLS	1153
V α w/o signal peptide (SignalP)	QSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPN RGLQFLLKYITG DNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFC AVRVWDYKLSFGAG TTVTVRA	1154
V α w/o signal peptide (IMGT)	AQSVAQPEDQVNVAEGNPLTVKCTYSVSGNPYLFWYVQYPN RGLQFLLKYIT GDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFC AVRVWDYKLSFGA GTTVTVRA	1155
V α	MXSAPISMLAMLF TSLGLRAQSV AQPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPN RGLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFC AVRVWDYKLSFGAGTTVTVRA	1156
	(X = any amino acid)	1157
α chain w/WT signal peptide, C α	MASAPISMLAMLF TSLGLRAQSV AQPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPN RGLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFC AVRVWDYKLSFGAGTTVTVRANIQNPEPAVYQLKDP RSQDSTLCLF	1158

Description	Sequence	SEQ ID NO:
(substituted)	TDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAS NQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILL LKVAGFNLL MTLRLWSS	1159
α chain w/alternative signal peptide, C α (substituted)	MHSAPISMLAMLF TSLGSLRAQSVAPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRGLQFL LKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFC AVRVDYKLSFGAGTTVTVRANIQNPEPAVYQLKDP RSQDSTLCLF TDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAS NQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILL LKVAGFNLL MTLRLWSS	1160
CDR1 β	LNHDA	2151
CDR2 β	SQIVND	2152
CDR3 β	ASSISAGGDGYT	2153
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSISAGGDGYTFGS GTRLTVV	2154
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSISAGGDGYTF GSGTRLTVV	2155
V β	MXNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSISAGGDGYTFGS GTRLTVV (X = any amino acid)	2156
		2157
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSISAGGDGYTFGS GTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2158
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSISAGGDGYTFGS GTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2159
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSISAGGDGYTFGS GTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFR CQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2160

[00310] In some embodiments, TCR016 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change Y220C relative to the wild type p53 sequence. In some embodiments, TCR016 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6Q. Amino acid sequences of TCR017.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1161
CDR2 α	NVLDGL	1162
CDR3 α	AVKWTGGFKTI	1163
V α w/o signal peptide (SignalP)	QNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVKWTGGFKTIFGAGTR LFVKA	1164
V α w/o signal peptide (IMGT)	GQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVKWTGGFKTIFGAGT RLFVKA	1165
V α	MXGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTRLFVKA (X = any amino acid)	1166
		1167
α chain w/WT signal peptide, C α (substituted)	MWGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLCLETFDFD SQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETN ATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLR LWSS	1168
α chain w/alternative signal peptide, C α (substituted)	MAGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLCLETFDFD SQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETN ATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLR LWSS	1169
α chain w/alternative signal peptide, C α (substituted)	MHGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVKWTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLCLETFDFD SQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETN ATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLR LWSS	1170
CDR1 β	MNHEY	2161
CDR2 β	SVGAGI	2162
CDR3 β	ASSYRESHYGYT	2163
V β w/o signal peptide (SignalP)	GVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGI TDQGEVPNGYNVSRSTEDFPLRLLSAAPSQTSVYFCASSYRESHYGYTFGS GTRLTVV	2164
V β w/o signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGA GITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQTSVYFCASSYRESHYGYTF GSGTRLTVV	2165
V β	MXIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGSGTRLTVV (X = any amino acid)	2166
		2167
β chain w/WT signal peptide, C β (substituted)	MSIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNP RNHFRCQQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2168

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2169
β chain w/alternative signal peptide, C β (substituted)	MHIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQ TSVYFCASSYRESHYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2170

[00311] In some embodiments, TCR017 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR017 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6R. Amino acid sequences of TCR018.

Description	Sequence	SEQ ID NO:
CDR1 α	YGGTVN	1171
CDR2 α	YFSGDPLV	1172
CDR3 α	AVKGDYKLS	1173
V α w/o signal peptide (SignalP)	QSVSQHNHHVILSEAASLELGCNYSYGGTVNLFWYVQYPGQHLQLLLKYFSG DPLVKGIKGFEAEFIKSKFSFNLRKPSVQWSDTAEYFCAVKGDYKLSFGAGT TDTVRA	1174
V α w/o signal peptide (IMGT)	AQSVSQHNHHVILSEAASLELGCNYSYGGTVNLFWYVQYPGQHLQLLLKYFS GDPLVKGIKGFEAEFIKSKFSFNLRKPSVQWSDTAEYFCAVKGDYKLSFGAG TDTVRA	1175
V α	MXLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEAEFIKSKFSFNLRKPSVQWSD TAEYFCAVKGDYKLSFGAGTDTVRA (X = any amino acid)	1176
		1177
α chain w/WT signal peptide, C α (substituted)	MLLLLI PVLGMI FALRDARAQSVSQHNHHVILSEAASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEAEFIKSKFSFNLRKPSVQWSD TAEYFCAVKGDYKLSFGAGTDTVVRANIQNPEPAVYQLKDPRSQDSTLCCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKS FETDMNLFQNLVIVLRILLKLVAGFNLLM TLRLWSS	1178
α chain w/alternative signal peptide, C α (substituted)	MALLLI PVLGMI FALRDARAQSVSQHNHHVILSEAASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEAEFIKSKFSFNLRKPSVQWSD TAEYFCAVKGDYKLSFGAGTDTVVRANIQNPEPAVYQLKDPRSQDSTLCCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFK ETNATYPSSDVPCDATLTEKS FETDMNLFQNLVIVLRILLKLVAGFNLLM TLRLWSS	1179

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHLLLPVLGMI FALRDARAQSVSQHNHHVILSEASLELGCNYSYGGTVNL FWYVQYPGQHLQLLLKYFSGDPLVKGIKGFEAEFIKSKFSFNLKRPSPVQWSD TAEYFCVKGDKLSFGAGTTVTVRANIQNPEPAVYQLKDPRSQDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLM TLRLWSS	1180
CDR1 β	SGHAT	2171
CDR2 β	FQNNGV	2172
CDR3 β	ASSLVNTEAF	2173
V β w/o signal peptide (SignalP)	GVAQSPRYKII EKRSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLVNTEAFFGQG TRLTVV	2174
V β w/o signal peptide (IMGT)	EAGVAQSPRYKII EKRSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNN GVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLVNTEAFFG QGTRLTVV	2175
V β	MXTRLWCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVV (X = any amino acid)	2176
		2177
β chain w/WT signal peptide, C β (substituted)	MGTRLWCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2178
β chain w/alternative signal peptide, C β (substituted)	MATRLWCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2179
β chain w/alternative signal peptide, C β (substituted)	MHTRLWCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLVNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2180

[00312] In some embodiments, TCR018 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR018 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6S. Amino acid sequences of TCR019.

Description	Sequence	SEQ ID NO:
CDR1 α	TRDTTY	1181

Description	Sequence	SEQ ID NO:
CDR2 α	RNSFDEQN	1182
CDR3 α	ALSEGGSNYKLT	1183
V α w/o signal peptide (SignalP)	QKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLT FGKGTLLTVNP	1184
V α w/o signal peptide (IMGT)	AQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLT FGKGTLLTVNP	1185
V α	MXTASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLT FGKGTLLTVNP (X = any amino acid)	1186
		1187
α chain w/WT signal peptide, C α (substituted)	MLTASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLT FGKGTLLTVNPNIQNPEPAVYQLKDPERSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAG FNLLMTLRLWSS	1188
α chain w/alternative signal peptide, C α (substituted)	MATASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLT FGKGTLLTVNPNIQNPEPAVYQLKDPERSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAG FNLLMTLRLWSS	1189
α chain w/alternative signal peptide, C α (substituted)	MHTASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDVCYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEGGSNYKLT FGKGTLLTVNPNIQNPEPAVYQLKDPERSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAG FNLLMTLRLWSS	1190
CDR1 β	LNHNV	2181
CDR2 β	YYDKDF	2182
CDR3 β	ATSRELRGNEQF	2183
V β w/o signal peptide (SignalP)	DAMVIQNPRYQVTQFGKPVTLSQSQT LNHNVMYQYQKSSQAPKLLFHYYDKDFNNEADTPDNFQSRPNTSFCFLDIRSPGLGDAAMYL CATSRELRGNEQFFGPGTRLTVL	2184
V β w/o signal peptide (IMGT)	DAMVIQNPRYQVTQFGKPVTLSQSQT LNHNVMYQYQKSSQAPKLLFHYYDKDFNNEADTPDNFQSRPNTSFCFLDIRSPGLGDAAMYL CATSRELRGNEQFFGPGTRLTVL	2185
V β	MXPGLLHWMALCCLGTGHGDAMVIQNPRYQVTQFGKPVTLSQSQT LNHNVMYQYQKSSQAPKLLFHYYDKDFNNEADTPDNFQSRPNTSFCFLDIRSPGLGDAAMYL CATSRELRGNEQFFGPGTRLTVL (X = any amino acid)	2186
		2187
β chain w/WT signal peptide, C β (substituted)	MGPGLLHWMALCCLGTGHGDAMVIQNPRYQVTQFGKPVTLSQSQT LNHNVMYQYQKSSQAPKLLFHYYDKDFNNEADTPDNFQSRPNTSFCFLDIRSPGLGDAAMYL CATSRELRGNEQFFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRCCQVFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2188

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPGLLHWMALCCLGTGHGDAMVIQNPRYQVTQFGKPVTLSCSQTLNHNVMY WYQQKSSQAPKLLFHYDQDFNNEADTPDNFQSRRPNTSFCFLDIRSPGLGD AAMYLCAATSRELRGNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2189
β chain w/alternative signal peptide, C β (substituted)	MHPGLLHWMALCCLGTGHGDAMVIQNPRYQVTQFGKPVTLSCSQTLNHNVMY WYQQKSSQAPKLLFHYDQDFNNEADTPDNFQSRRPNTSFCFLDIRSPGLGD AAMYLCAATSRELRGNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2190

[00313] In some embodiments, TCR019 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR019 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6T. Amino acid sequences of TCR020.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1191
CDR2 α	IYSNGD	1192
CDR3 α	AVNDAGNMLT	1193
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIY SNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVNDAGNMLTFGGG TRLMVKP	1194
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYS NGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVNDAGNMLTFGGGT RLMVKP	1195
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSD SATYLCAVNDAGNMLTFGGGTRLMVKP (X = any amino acid)	1196
		1197
α chain with WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSD SATYLCAVNDAGNMLTFGGGTRLMVKPNIQNPEPAVYQLKDPRSQDSTLCLE TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1198
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSD SATYLCAVNDAGNMLTFGGGTRLMVKPNIQNPEPAVYQLKDPRSQDSTLCLE TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1199

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNDAGNMLTFGGGTRLMVKPNIQNPEPAVYQLKDPRSQDSTLCCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1200
CDR1 β	DFQATT	2191
CDR2 β	SNEGSKA	2192
CDR3 β	SAAGQANTEAF	2193
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSAAGQA NTEAFFGQGTRLTVV	2194
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSAAGQANTEA FFGQGTRLTVV	2195
V β	MXLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVV (X = any amino acid)	2196
		2197
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVVEDLRNVTTPKVSLEFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2198
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVVEDLRNVTTPKVSLEFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2199
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSAAGQANTEAFFGQGTRLTVVEDLRNVTTPKVSLEFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2200

[00314] In some embodiments, TCR020 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change G245S relative to the wild type p53 sequence. In some embodiments, TCR020 interacts with the neoantigen in the context of HLA-DRB3*02:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6U. Amino acid sequences of TCR021.

Description	Sequence	SEQ ID NO:
CDR1 α	TRDTTTY	1201
CDR2 α	RNSFDEQN	1202
CDR3 α	ALSEVDSGNTPLV	1203
V α without signal peptide (SignalP)	QKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEVDSGNTPLVFGKGTRLSVIA	1204
V α without signal peptide (IMGT)	AQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEVDSGNTPLVFGKGTRLSVIA	1205
V α	MXTASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEVDSGNTPLVFGKGTRLSVIA (X = any amino acid)	1206
		1207
α chain with WT signal peptide, C α (substituted)	MLTASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEVDSGNTPLVFGKGTRLSVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNLVIVLRILLKVA GENLLMTLRLWSS	1208
α chain with alternative signal peptide, C α (substituted)	MATASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEVDSGNTPLVFGKGTRLSVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNLVIVLRILLKVA GENLLMTLRLWSS	1209
α chain with alternative signal peptide, C α (substituted)	MHTASLLRAVIASICVSSMAQKVTQAQTEISVVEKEDVTLDCVYETRDTTYLFWYKQPPSGELVFLIRNRSFDEQNEISGRYSWNFQKSTSSFNFTITASQVVD SAVYFCALSEVDSGNTPLVFGKGTRLSVIANIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLNFQNLVIVLRILLKVA GENLLMTLRLWSS	1210
CDR1 β	SGDLS	2201
CDR2 β	YNGEE	2202
CDR3 β	ASSVGSSSSTDTQY	2203
V β without signal peptide (SignalP)	GVTQTTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVL	2204
V β without signal peptide (IMGT)	DSGVTQTTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVL	2205
V β	MXHFRLLCCVAFCLLGAGPVD SGVTQTTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVL (X = any amino acid)	2206
		2207
β chain with WT signal peptide, C β (substituted)	MGFRLLCCVAFCLLGAGPVD SGVTQTTPKHLITATGQRVTLRCS PRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDSALYFCASSVGSSSSTDTQYFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2208

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSSELGD SALYFCASSVGSSSSTDTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2209
β chain with alternative signal peptide, C β (substituted)	MHFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSSELGD SALYFCASSVGSSSSTDTQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2210

[00315] In some embodiments, TCR021 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR021 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6V. Amino acid sequences of TCR022.

Description	Sequence	SEQ ID NO:
CDR1 α	NTAFDY	1771
CDR2 α	IRPDVSE	1772
CDR3 α	AAEAGNHRG STLGRLY	1773
V α w/o signal peptide (SignalP)	QQKEKSDQQQVKQSPQSLIVQKGGISIINCA YENTAFDYFPWYQQFPKGKPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLHIMDSQPGDSATYFCAAEAGNH RGSTLGRLYFGRGTQLTVWP	1774
V α w/o signal peptide (IMGT)	QQQVKQSPQSLIVQKGGISIINCA YENTAFDYFPWYQQFPKGKPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLHIMDSQPGDSATYFCAAEAGNHRG STLGRLYFGRGTQLTVWP	1775
V α	MXKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISIINCA YENTAFDYFPWYQQFPKGKPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEAGNHRG STLGRLYFGRGTQLTVWP	1776
	(X = any amino acid)	1777
α chain with WT signal peptide, C α (substituted)	MDKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISIINCA YENTAFDYFPWYQQFPKGKPA LLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEAGNHRG STLGRLYFGRGTQLTVWP NIQNPEPAVYQ LKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIV LRILLKLVAGFNLLMTLRWSS	1778

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MAKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISIINCA YENTAFDYFPWYQQFPGKGPALLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEAGNHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQ LKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVIV LRILLKLVAGFNLLMTLRLWSS	1779
α chain with alternative peptide, (substituted) C α	MHKILGASFLVLWLQLCWVSGQQKEKSDQQQVKQSPQSLIVQKGGISIINCA YENTAFDYFPWYQQFPGKGPALLIAIRPDVSEKKEGRFTISFNKSAKQFSLH IMDSQPGDSATYFCAAEAGNHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQ LKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAI AWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVIV LRILLKLVAGFNLLMTLRLWSS	1780
CDR1 β	SGHRS	2771
CDR2 β	YFSETQ	2772
CDR3 β	ASSLAAGGYFNEQF	2773
V β w/o signal peptide (SignalP)	GVTQTTPRYLIKTRGQQVTLSCSPISGHRSSVSWYQQTPGQGLQFLFEYFSETQ RNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFF GPGTRLTVL	2774
V β w/o signal peptide (IMGT)	KAGVTQTTPRYLIKTRGQQVTLSCSPISGHRSSVSWYQQTPGQGLQFLFEYFSE TQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQ FFGPGTRLTVL	2775
V β	MXSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPISGHRSSV WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVL (X = any amino acid)	2776
		2777
β chain with WT signal peptide, (substituted) C β	MGSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPISGHRSSV WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSAFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2778
β chain with alternative signal peptide, C β (substituted)	MASRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPISGHRSSV WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSAFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2779
β chain with alternative signal peptide, C β (substituted)	MHSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPISGHRSSV WYQQTPGQGLQFLFEYFSETQRNKGNFPGRFSGRQFSNSRSEMNVTLELGD SALYLCASSLAAGGYFNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSAFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2780

[00316] In some embodiments, TCR022 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR022 interacts with the neoantigen in the context of HLA-A*11:01, as described in International Publication No. WO 2021/163434, incorporated herein by reference in its entirety.

Table 6W. Amino acid sequences of TCR023.

Description	Sequence	SEQ ID NO:
CDR1 α	NSAFQY	1221
CDR2 α	TYSSGN	1222
CDR3 α	AMTSPYNNNDMR	1223
V α without signal peptide (SignalP)	QQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFG AGTRLTVKP	1224
V α without signal peptide (IMGT)	QKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGA GTRLTVKP	1225
V α	MXKSLRVLLVILWLQLSWWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKP (X = any amino acid)	1226
		1227
α chain with WT signal peptide, C α (substituted)	MCKSLRVLLVILWLQLSWWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGF NLLMTLRLWSS	1228
α chain with alternative signal peptide, C α (substituted)	MAKSLRVLLVILWLQLSWWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGF NLLMTLRLWSS	1229
α chain with alternative signal peptide, C α (substituted)	MHKSRLRVLLVILWLQLSWWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGF NLLMTLRLWSS	1230
CDR1 β	DFQATT	2221
CDR2 β	SNEGSKA	2222
CDR3 β	SGGLEEAARQFI	2223
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSGGLEE AARQFIGPGTRLTVL	2224
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSGGLEEAARQ FIGPGTRLTVL	2225
V β	MXLLLLLLGPGISLLLPGLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVL (X = any amino acid)	2226
		2227

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2228
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2229
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICSGGLEEAARQFIGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2230

[00317] In some embodiments, TCR023 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR023 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6X. Amino acid sequences of TCR024.

Description	Sequence	SEQ ID NO:
CDR1 α	NSAFQY	1231
CDR2 α	TYSSGN	1232
CDR3 α	AMTSPYNNNDMR	1233
V α without signal peptide (SignalP)	QKQVEQDPGPLSVPEGAI VSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTY SSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFG AGTRLTVKP	1234
V α without signal peptide (IMGT)	QKQVEQDPGPLSVPEGAI VSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYS SGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGA GTRLTVKP	1235
V α	MXKSLRVLLVILWLQLSWVWSQKQVEQDPGPLSVPEGAI VSLNCTYSNSAF QYFMWYRQYSRKGPPELLMYTYSNGKEDGRFTAQVDKSSKYISLFIRDSQPS DSATYLCAMTSPYNNNDMRFGAGTRLTVKP	1236
	(X = any amino acid)	1237

Description	Sequence	SEQ ID NO:
α chain with WT signal peptide, (substituted) C α	MCKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGAGTRLTVPKNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1238
α chain with alternative signal peptide, (substituted) C α	MAKSLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGAGTRLTVPKNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1239
α chain with alternative signal peptide, (substituted) C α	MHKSRLRVLLVILWLQLSWVWSQQKEVEQDPGPLSVPEGAIIVSLNCTYSNSAFQYFMWYRQYSRKGPPELLMYTYSSGNKEDGRFTAQVDKSSKYISLFIRDSQPSDSATYLCAMTSPYNNNDMRFGAGTRLTVPKNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1240
CDR1 β	DFQATT	2231
CDR2 β	SNEGSKA	2232
CDR3 β	SGGLEEAARQFI	2233
V β without signal peptide (SignalP)	AVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSGGLEEAARQFIGPGRRLTVL	2234
V β without signal peptide (IMGT)	GAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSGGLEEAARQFIGPGRRLTVL	2235
V β	MXLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSGGLEEAARQFIGPGRRLTVL (X = any amino acid)	2236
		2237
β chain with WT signal peptide, (substituted) C β	MLLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSGGLEEAARQFIGPGRRLTVLEDLRNVTTPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSAFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2238
β chain with alternative signal peptide, (substituted) C β	MALLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSGGLEEAARQFIGPGRRLTVLEDLRNVTTPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSAFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2239
β chain with alternative signal peptide, (substituted) C β	MHLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSGGLEEAARQFIGPGRRLTVLEDLRNVTTPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSAFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2240

[00318] In some embodiments, TCR024 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has

the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR024 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6Y. Amino acid sequences of TCR025.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGNEY	1241
CDR2 α	GLKNN	1242
CDR3 α	IVPNDYKLS	1243
V α without signal peptide (SignalP)	KTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTTVRA	1244
V α without signal peptide (IMGT)	DAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTTVRA	1245
V α	MXLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTTVRA	1246
	(X = any amino acid)	1247
α chain with WT signal peptide, C α (substituted)	MRLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTTVVRANIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRIILLKVAGFNLLMTLRLWSS	1248
α chain with alternative peptide, C α (substituted)	MALVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTTVVRANIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRIILLKVAGFNLLMTLRLWSS	1249
α chain with alternative peptide, C α (substituted)	MHLVARVTVFLTFGTIIDAKTTQPPSMDCAEGRAANLPCNHSTISGNEYVYWRQIHSQGPQYIIHGLKNNETNEMASLIITEDRKSSTLILPHATLRDTAVYYCIVPNDYKLSFGAGTTTVVRANIQNPEPAVYQLKDPQSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRIILLKVAGFNLLMTLRLWSS	1250
CDR1 β	MDHEN	2241
CDR2 β	SYDVKM	2242
CDR3 β	ASSFGTGSIQETQY	2243
V β without signal peptide (SignalP)	SRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQTSMYLCASSFGTGSIQETQYFGPGTRLLVL	2244
V β without signal peptide (IMGT)	DVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQTSMYLCASSFGTGSIQETQYFGPGTRLLVL	2245
V β	MXIRLLCRVAFCLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQTSMYLCASSFGTGSIQETQYFGPGTRLLVL	2246
	(X = any amino acid)	2247

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MGIRLLCRVAFCFLLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILESASTNQ TSMYLCASSFGTGSIQETQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2248
β chain with alternative signal peptide, C β (substituted)	MAIRLLCRVAFCFLLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILESASTNQ TSMYLCASSFGTGSIQETQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2249
β chain with alternative signal peptide, C β (substituted)	MHIRLLCRVAFCFLLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILESASTNQ TSMYLCASSFGTGSIQETQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2250

[00319] In some embodiments, TCR025 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR025 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6Z. Amino acid sequences of TCR026

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1251
CDR2 α	ATKADDK	1252
CDR3 α	ALNPAGGTSYGKLT	1253
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKA DDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALNPAGGTSYGKLT FGQGTILTVHP	1254
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATK ADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALNPAGGTSYGKL TFGQGTILTVHP	1255
V α	MXYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALNPAGGTSYGKLTFGQGTILTVHP	1256
	(X = any amino acid)	1257
α chain with WT signal peptide, C α (substituted)	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALNPAGGTSYGKLTFGQGTILTVHPNIQNPEPAVYQLKDP RSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASNQTSFTC QDIFKETNATYPSSDVPDATLTEKSFETDMNLFQNLVIVLRI LLLKVAG FNLLMTLRWSS	1258

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MAYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALNPNAGGTSYGKLTFGQGTILTVHPNIQNPEPAVYQLKDPERSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFNQNLVIVLRILLKLVAGFNLLMTLRLWSS	1259
α chain with alternative peptide, (substituted) C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALNPNAGGTSYGKLTFGQGTILTVHPNIQNPEPAVYQLKDPERSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFNQNLVIVLRILLKLVAGFNLLMTLRLWSS	1260
CDR1 β	SGHTS	2251
CDR2 β	YDEGEE	2252
CDR3 β	ASSSPGATSGGANTGELF	2253
V β without signal peptide (SignalP)	GVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEEERNRGNFPPRFSGRQFPNYSSELNVNALELEDALYLCASSSPGATSGGANTGELFFGEGSRLTVL	2254
V β without signal peptide (IMGT)	EAGVTQSPTHLIKTRGQQATLRCSPISGHTSVYWYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSSELNVNALELEDALYLCASSSPGATSGGAN TGELFFGEGSRLTVL	2255
V β	MXPRLFWALLCLLGTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVY WYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSSELNVNALELED SALYLCASSSPGATSGGANTGELFFGEGSRLTVL (X = any amino acid)	2256
		2257
β chain with WT signal peptide, (substituted) C β	MGPRLFWALLCLLGTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVY WYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSSELNVNALELED SALYLCASSSPGATSGGANTGELFFGEGSRLTVLEDLRNVT PPKVSLFEP SK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNP RNFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAW GRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVKR KNS	2258
β chain with alternative signal peptide, C β (substituted)	MAPRLFWALLCLLGTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVY WYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSSELNVNALELED SALYLCASSSPGATSGGANTGELFFGEGSRLTVLEDLRNVT PPKVSLFEP SK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNP RNFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAW GRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVKR KNS	2259
β chain with alternative signal peptide, C β (substituted)	MHPRLFWALLCLLGTGPVEAGVTQSPTHLIKTRGQQATLRCSPISGHTSVY WYQQALGLGLQFLLWYDEGEERNRGNFPPRFSGRQFPNYSSELNVNALELED SALYLCASSSPGATSGGANTGELFFGEGSRLTVLEDLRNVT PPKVSLFEP SK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNP RNFRCQVQFHGLSEEDKWPEGSPKPVTQNI SAEAW GRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVKR KNS	2260

[00320] In some embodiments, TCR026 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR026 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AA. Amino acid sequences of TCR027.

Description	Sequence	SEQ ID NO:
CDR1 α	DSSSTY	1261
CDR2 α	IFSNMDM	1262
CDR3 α	AEIPRDSGGGADGLT	1263
V α without signal peptide (SignalP)	EDVEQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSNM DMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEIPRDSGGGADGLTF GKGTHLIIQP	1264
V α without signal peptide (IMGT)	GEDVEQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSN MDMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEIPRDSGGGADGLT FGKGTHLIIQP	1265
V α	MXTFAGFSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQP (X = any amino acid)	1266
		1267
α chain with WT signal peptide, C α (substituted)	MKTFAFGSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1268
α chain with alternative signal peptide, C α (substituted)	MATFAFGSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1269
α chain with alternative signal peptide, C α (substituted)	MHTFAFGSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1270
CDR1 β	DFQATT	2261
CDR2 β	SNEGSKA	2262
CDR3 β	SARDLQRSYEQY	2263
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSARDLQ RSYEQYFGPGTRLTVT	2264
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICSARDLQRSYE QYFGPGTRLTVT	2265
V β	MXLLLLLLPGISLLLPGLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLT TVTSAHPEDSSFYICSARDLQRSYEQYFGPGTRLTVT (X = any amino acid)	2266
		2267

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICARDLQRSYEQYFGPGTRLTVTEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2268
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICARDLQRSYEQYFGPGTRLTVTEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2269
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICARDLQRSYEQYFGPGTRLTVTEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2270

[00321] In some embodiments, TCR027 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR027 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AB. Amino acid sequences of TCR028.

Description	Sequence	SEQ ID NO:
CDR1 α	DSSSTY	1271
CDR2 α	IFSNMMD	1272
CDR3 α	AEIPRDSGGGADGLT	1273
V α without signal peptide (SignalP)	EDVEQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSNM DMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEIPRDSGGGADGLTF GKGTHLIIQP	1274
V α without signal peptide (IMGT)	GEDVEQSLFLSVREGDSSVINCTYTDSSSTYLYWYKQEPGAGLQLLTYIFSN MDMKQDQRLTVLLNKKDKHLSLRIADTQTGDSAIYFCAEIPRDSGGGADGLT FGKGTHLIIQP	1275
V α	MXTFAGFSFLFLWLQLDCMSRGEDVEQSLFLSVREGDSSVINCTYTDSSSTY LYWYKQEPGAGLQLLTYIFSNMDMKQDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQP	1276
	(X = any amino acid)	1277

Description	Sequence	SEQ ID NO:
α chain with WT signal peptide, C α (substituted)	MKTFAFGFSFLFLWLQLDCMSRGEDVEQSLFSLVREGDSSVINCTYTDSSSTY LYWKQEPGAGLQLLTYIFSNMDMKDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1278
α chain with alternative signal peptide, C α (substituted)	MATFAFGFSFLFLWLQLDCMSRGEDVEQSLFSLVREGDSSVINCTYTDSSSTY LYWKQEPGAGLQLLTYIFSNMDMKDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1279
α chain with alternative signal peptide, C α (substituted)	MHTFAFGFSFLFLWLQLDCMSRGEDVEQSLFSLVREGDSSVINCTYTDSSSTY LYWKQEPGAGLQLLTYIFSNMDMKDQRLTVLLNKKDKHLSLRIADTQTGD SAIYFCAEIPRDSGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1280
CDR1 β	DFQATT	2271
CDR2 β	SNEGSKA	2272
CDR3 β	SARDLQRSYEQY	2273
V β without signal peptide (SignalP)	AVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEG SKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYICARDLQRSYEQ YFGPGTRLTVT	2274
V β without signal peptide (IMGT)	GAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYICARDLQRSYEQ YFGPGTRLTVT	2275
V β	MXLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQ FFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDS SFYICARDLQRSYEQYFGPGTRLTVT (X = any amino acid)	2276
		2277
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQ FFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDS SFYICARDLQRSYEQYFGPGTRLTVTEDLRNVTPPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2278
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQ FFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDS SFYICARDLQRSYEQYFGPGTRLTVTEDLRNVTPPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2279
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQ FFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDS SFYICARDLQRSYEQYFGPGTRLTVTEDLRNVTPPKVSLEFESKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2280

[00322] In some embodiments, TCR028 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has

the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR028 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AC. Amino acid sequences of TCR029.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1281
CDR2 α	IRSNMDK	1282
CDR3 α	AEPVGGGLNSGYALN	1283
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTP	1284
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTP	1285
V α	MXGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTP (X = any amino acid)	1286
		1287
α chain with WT signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTPNIQNPEPAVYQLKDRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFNLLVIVLRIILLKVAGFNLLMTLRLWSS	1288
		1289
α chain with alternative signal peptide, C α (substituted)	MHGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEPVGGGLNSGYALNFGKGTSLLVTPNIQNPEPAVYQLKDRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFNLLVIVLRIILLKVAGFNLLMTLRLWSS	1290
CDR1 β	SGHKS	2281
CDR2 β	QYYEKEE	2282
CDR3 β	ASSGGRTSGAYEQF	2283
V β without signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPISGHKSVSWYQQVLGQGPQFIQYYEKEERGRGNFPDRFSARQFPNYSSELNVNALLLGDLSALYLCASSGGRTSGAYEQFFGPGTRLTVL	2284
V β without signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPISGHKSVSWYQQVLGQGPQFIQYYEKEERGRGNFPDRFSARQFPNYSSELNVNALLLGDLSALYLCASSGGRTSGAYEQFFGPGTRLTVL	2285
V β	MXPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPISGHKSVSWYQQVLGQGPQFIQYYEKEERGRGNFPDRFSARQFPNYSSELNVNALLLGDLSALYLCASSGGRTSGAYEQFFGPGTRLTVL (X = any amino acid)	2286
		2287

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MGPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPI SGHKSVS WYQQVLGGQGPQFIFQYYEKEERGRGNFPDRFSARQFPNYSSELNVNALLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2288
β chain with alternative signal peptide, C β (substituted)	MAPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPI SGHKSVS WYQQVLGGQGPQFIFQYYEKEERGRGNFPDRFSARQFPNYSSELNVNALLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2289
β chain with alternative signal peptide, C β (substituted)	MHPGLLCWVLLCLLGAGPVDAGVTQSPTHLIKTRGQQVTLRCSPI SGHKSVS WYQQVLGGQGPQFIFQYYEKEERGRGNFPDRFSARQFPNYSSELNVNALLGD SALYLCASSGGRTSGAYEQFFGPGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2290

[00323] In some embodiments, TCR029 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR029 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AD. Amino acid sequences of TCR030.

Description	Sequence	SEQ ID NO:
CDR1 α	VSGLRG	1291
CDR2 α	LYSAGEE	1292
CDR3 α	AVTAHRGSLGRLY	1293
V α without signal peptide (SignalP)	EDQVTQSPEALRLQEGESSLNCSYTVSGLRGLFWYRQDPGKGPEFLFTLYS AGEEKEKERLKATLTKKESFLHITAPKPEDSATYLCAVTAHRGSLGRLYFG RGTQLTVWP	1294
V α without signal peptide (IMGT)	EDQVTQSPEALRLQEGESSLNCSYTVSGLRGLFWYRQDPGKGPEFLFTLYS AGEEKEKERLKATLTKKESFLHITAPKPEDSATYLCAVTAHRGSLGRLYFG RGTQLTVWP	1295
V α	MXKMLECAFIVLWLQGLWLSGEDQVTQSPEALRLQEGESSLNCSYTVSGLR GLFWYRQDPGKGPEFLFTLYSAGEEKEKERLKATLTKKESFLHITAPKPEDS ATYLCAVTAHRGSLGRLYFGRGTQLTVWP	1296
	(X = any amino acid)	1297
α chain with WT signal peptide, C α (substituted)	MEKMLECAFIVLWLQGLWLSGEDQVTQSPEALRLQEGESSLNCSYTVSGLR GLFWYRQDPGKGPEFLFTLYSAGEEKEKERLKATLTKKESFLHITAPKPEDS ATYLCAVTAHRGSLGRLYFGRGTQLTVWPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQT SFTCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNL LVIVLRILLKLVAGF NLLMTLRLWSS	1298

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MAKMLECAFIVLWLQGLWLSGEDQVTQSPEALRLQEGESSSLNCSYTVSGLR GLFWYRQDPGKGPEFLFTLYSAGEEKEKERLKATLTKKESFLHITAPKPEDS ATYLCVTAHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQLKDRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1299
α chain with alternative peptide, (substituted) C α	MHKMLECAFIVLWLQGLWLSGEDQVTQSPEALRLQEGESSSLNCSYTVSGLR GLFWYRQDPGKGPEFLFTLYSAGEEKEKERLKATLTKKESFLHITAPKPEDS ATYLCVTAHRGSTLGRLYFGRGTQLTVWPNIQNPEPAVYQLKDRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGF NLLMTLRLWSS	1300
CDR1 β	SGHDT	2291
CDR2 β	YEEEE	2292
CDR3 β	ASSRRGGAYNEQF	2293
V β without signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEE RQRGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSRRGGAYNEQFFG PGTRLTVL	2294
V β without signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEE EERQRGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSRRGGAYNEQF FGPTRLTVL	2295
V β	MXPGLLCWALLCCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSRRGGAYNEQFFGPGTRLTVL (X = any amino acid)	2296
		2297
β chain with WT signal peptide, C β (substituted)	MGPGLLCWALLCCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSRRGGAYNEQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPРНHFRСQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2298
β chain with alternative signal peptide, C β (substituted)	MAPGLLCWALLCCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSRRGGAYNEQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPРНHFRСQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2299
β chain with alternative signal peptide, C β (substituted)	MHPGLLCWALLCCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSRRGGAYNEQFFGPGTRLTVLEDLRNVTTPKVSLEFESKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPРНHFRСQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2300

[00324] In some embodiments, TCR030 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR030 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AE. Amino acid sequences of TCR031.

Description	Sequence	SEQ ID NO:
CDR1 α	SSNFYA	1301
CDR2 α	MTLNGDE	1302
CDR3 α	ASVGGGADGLT	1303
V α without signal peptide (SignalP)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLIIQP	1304
V α without signal peptide (IMGT)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLIIQP	1305
V α	MXKNPLAAPLLILWFHLCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLIIQP (X = any amino acid)	1306
		1307
α chain with WT signal peptide, (substituted) C α	MEKNPLAAPLLILWFHLCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1308
α chain with alternative signal peptide, (substituted) C α	MAKNPLAAPLLILWFHLCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1309
α chain with alternative signal peptide, (substituted) C α	MHKNPLAAPLLILWFHLCVSSI LNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRI SATLNTKEGYSYLYIKGSQPEDSATYLCASVGGGADGLTFGKGTHLIIQPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSS	1310
CDR1 β	SGHTA	2301
CDR2 β	FQNSA	2302
CDR3 β	ASTWDRGSYNEQF	2303
V β without signal peptide (SignalP)	GVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQEDSAVYLCASTWDRGSYNEQFFGPGTRLTVL	2304
V β without signal peptide (IMGT)	GAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQEDSAVYLCASTWDRGSYNEQFFGPGTRLTVL	2305
V β	MXTRLLFWVAFCLLGADHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALY WYRQSLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCASTWDRGSYNEQFFGPGTRLTVL (X = any amino acid)	2306
		2307

Description	Sequence	SEQ ID NO:
β chain with WT signal peptide, C β (substituted)	MGTRLLFWVAFCLLGADHTGAGVQSQSPSNKVTEKGDVELRCDPISGHTALY WYRQSLGQGLEFLIYFQGNAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCASWTDRGSYNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2308
β chain with alternative signal peptide, C β (substituted)	MATRLLFWVAFCLLGADHTGAGVQSQSPSNKVTEKGDVELRCDPISGHTALY WYRQSLGQGLEFLIYFQGNAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCASWTDRGSYNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2309
β chain with alternative signal peptide, C β (substituted)	MHTRLLFWVAFCLLGADHTGAGVQSQSPSNKVTEKGDVELRCDPISGHTALY WYRQSLGQGLEFLIYFQGNAPDKSGLPSDRFSAERTGGSVSTLTIQRTQQE DSAVYLCASWTDRGSYNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2310

[00325] In some embodiments, TCR031 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR031 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AF. Amino acid sequences of TCR032.

Description	Sequence	SEQ ID NO:
CDR1 α	NSMFDY	1311
CDR2 α	ISSIKDK	1312
CDR3 α	AANTGNQFY	1313
V α without signal peptide (SignalP)	QQKNDDQVKQNSPSSLVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFL ISISSIKDKNEDGRFTVFLNLSAKHLSLHIVPSQPGDSAVYFCAANTGNQFY FGTGTSLTVIP	1314
V α without signal peptide (IMGT)	DQQVKQNSPSSLVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISS IKDKNEDGRFTVFLNLSAKHLSLHIVPSQPGDSAVYFCAANTGNQFYFGTGT SLTVIP	1315
V α	MXMLLGASVLILWLQPDWVNSQQKNDDQVKQNSPSSLVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISSIKDKNEDGRFTVFLNLSAKHLSLHIV PSQPGDSAVYFCAANTGNQFYFGTGTSLTVIP (X = any amino acid)	1316
		1317
α chain with WT signal peptide, C α (substituted)	MAMLLGASVLILWLQPDWVNSQQKNDDQVKQNSPSSLVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISSIKDKNEDGRFTVFLNLSAKHLSLHIV PSQPGDSAVYFCAANTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPQSQDS TLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSSNGAIAWSNQTST CQDIFKETNATYPSSDVPDATLTKESFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1318
		1319

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISSISKDNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAANTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKVA GFNLLMTLRLWSS	1320
CDR1 β	SGHAT	2311
CDR2 β	FQNGGV	2312
CDR3 β	ASSHLAGEFYNEQF	2313
V β without signal peptide (SignalP)	GVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQFQNGGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSHLAGEFYNEQF FGGPTRLTVL	2314
V β without signal peptide (IMGT)	EAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQFQNGGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSHLAGEFYNEQF FGGPTRLTVL	2315
V β	MXTRLWCWAAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQFQNGGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSHLAGEFYNEQF FGGPTRLTVL (X = any amino acid)	2316
		2317
β chain with WT signal peptide, C β (substituted)	MGTRLWCWAAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQFQNGGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSHLAGEFYNEQF FGGPTRLTVLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRA DCGITSAS YQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2318
β chain with alternative signal peptide, C β (substituted)	MATRLWCWAAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQFQNGGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSHLAGEFYNEQF FGGPTRLTVLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRA DCGITSAS YQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2319
β chain with alternative signal peptide, C β (substituted)	MHTRLWCWAAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGP KLLIQFQNGGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSHLAGEFYNEQF FGGPTRLTVLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRA DCGITSAS YQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2320

[00326] In some embodiments, TCR032 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR032 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AG. Amino acid sequences of TCR033.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFYG	1321
CDR2 α	NALDGL	1322
CDR3 α	AFAYGQNFV	1323
V α without signal peptide (SignalP)	QSLEQPSSEVTAVEGAIVQINCTYQTSGFYGLSWYQQHDGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLQLQELQMKDSASYFCAFAYGQNFVFGPGTRLSVLP	1324
V α without signal peptide (IMGT)	GQSLEQPSSEVTAVEGAIVQINCTYQTSGFYGLSWYQQHDGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLQLQELQMKDSASYFCAFAYGQNFVFGPGTRLSVLP	1325
V α	MXGAFLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSGFYGLSWYQQHDGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLQLQELQMKDSASYFCAFAYGQNFVFGPGTRLSVLP (X = any amino acid)	1326
		1327
α chain with WT signal peptide, (substituted) C α	MWGAFLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSGFYGLSWYQQHDGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLQLQELQMKDSASYFCAFAYGQNFVFGPGTRLSVLPNIQNPEPAVYQLKDRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATALTEKSFETDMNLNFNQNLVIVLRIILLKVAGFNLLMTLRLWSS	1328
α chain with alternative signal peptide, (substituted) C α	MAGAFLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSGFYGLSWYQQHDGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLQLQELQMKDSASYFCAFAYGQNFVFGPGTRLSVLPNIQNPEPAVYQLKDRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATALTEKSFETDMNLNFNQNLVIVLRIILLKVAGFNLLMTLRLWSS	1329
α chain with alternative signal peptide, (substituted) C α	MHGAFLLYVSMKMGGTAGQSLEQPSSEVTAVEGAIVQINCTYQTSGFYGLSWYQQHDGGAPTFLSYNALDGLLEETGRFSSFLSRSDSYGYLLQLQELQMKDSASYFCAFAYGQNFVFGPGTRLSVLPNIQNPEPAVYQLKDRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATALTEKSFETDMNLNFNQNLVIVLRIILLKVAGFNLLMTLRLWSS	1330
CDR1 β	SGDLS	2321
CDR2 β	YNGEE	2322
CDR3 β	ASSPLGDSGNTIY	2323
V β without signal peptide (SignalP)	GVTQTPKHLITATGQRTVLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDLSALYFCASSPLGDSGNTIYFGEGLTVV	2324
V β without signal peptide (IMGT)	DSGVTQTPKHLITATGQRTVLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDLSALYFCASSPLGDSGNTIYFGEGLTVV	2325
V β	MXFRLCCVAFCLLGAGPVDGVTQTPKHLITATGQRTVLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDLSALYFCASSPLGDSGNTIYFGEGLTVV (X = any amino acid)	2326
		2327
β chain with WT signal peptide, (substituted) C β	MGFRLCCVAFCLLGAGPVDGVTQTPKHLITATGQRTVLRCSPRSGDLSVYWYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSLELGDLSALYFCASSPLGDSGNTIYFGEGLTVVVDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRNS	2328

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSSELGD SALYFCASSPLGDSGNTIYFGECSWLT VVEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2329
β chain with alternative signal peptide, C β (substituted)	MHFRLLCCVAFCLLGAGPVD SGVTQTPKHLITATGQRVTLRCS PRSGDLSVY WYQQSLDQGLQFLIQYYNGEERAKGNILERFSAQQFPDLHSELNLSSELGD SALYFCASSPLGDSGNTIYFGECSWLT VVEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2330

[00327] In some embodiments, TCR034 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR034 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AH. Amino acid sequences of TCR034.

Description	Sequence	SEQ ID NO:
CDR1 α	TSINN	1331
CDR2 α	IRSNERE	1332
CDR3 α	ATDAWNNDMR	1333
V α without signal peptide (SignalP)	QQGEEDPQALS IQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIR SNE REKHSGRRLRVTLDT SKKSSLLITASRAADTASYFCATDAWNNDMRFGAGTR LTVKP	1334
V α without signal peptide (IMGT)	SQQGEEDPQALS IQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIR SN EREKHSGRRLRVTLDT SKKSSLLITASRAADTASYFCATDAWNNDMRFGAGT RLTVKP	1335
V α	MXTLLGVSLVILWLQLARVNSQQGEEDPQALS IQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIR SNEREKHSGRRLRVTLDT SKKSSLLITASRAADT ASYFCATDAWNNDMRFGAGTR LTVKP (X = any amino acid)	1336
		1337
α chain with WT signal peptide, C α (substituted)	METLLGVSLVILWLQLARVNSQQGEEDPQALS IQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIR SNEREKHSGRRLRVTLDT SKKSSLLITASRAADT ASYFCATDAWNNDMRFGAGTR LTVKPNIQNPEPAVYQLKDP RSQDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVIIVLRILLK VAGFNLLM TLRLWSS	1338
α chain with alternative signal peptide, C α (substituted)	MATLLGVSLVILWLQLARVNSQQGEEDPQALS IQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIR SNEREKHSGRRLRVTLDT SKKSSLLITASRAADT ASYFCATDAWNNDMRFGAGTR LTVKPNIQNPEPAVYQLKDP RSQDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVIIVLRILLK VAGFNLLM TLRLWSS	1339

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINNL QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDAWNNDMRFGAGTRLTVPKNIQNPEPAVYQLKDPRSQDSTLCLEFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVLRILLKLVAGFNLLM TLRWSS	1340
CDR1 β	MNHNS	2331
CDR2 β	SASEG	2332
CDR3 β	ASSESQGNTEAF	2333
V β without signal peptide (SignalP)	GVTQT PKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSASEGT TDKGEVPNGYNVSRNLNKRFLSLRESAAPSQTSVYFCASSESQGNTEAFFGQ GTRLTVV	2334
V β without signal peptide (IMGT)	NAGVTQT PKFQVLKTGQSMTLQCAQDMNHNSMYWYRQDPGMGLRLIYYSASE GTTDKGEVPNGYNVSRNLNKRFLSLRESAAPSQTSVYFCASSESQGNTEAFF GQGTRLTVV	2335
V β	MXIGLLCCVAFSLLWASPVNAGVTQT PKFQVLKTGQSMTLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRESAAPSQ TSVYFCASSESQGNTEAFFGQGTRLTVV (X = any amino acid)	2336
		2337
β chain with WT signal peptide, C β (substituted)	MSIGLLCCVAFSLLWASPVNAGVTQT PKFQVLKTGQSMTLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRESAAPSQ TSVYFCASSESQGNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2338
β chain with alternative signal peptide, C β (substituted)	MAIGLLCCVAFSLLWASPVNAGVTQT PKFQVLKTGQSMTLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRESAAPSQ TSVYFCASSESQGNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2339
β chain with WT signal peptide, C β (substituted)	MHIGLLCCVAFSLLWASPVNAGVTQT PKFQVLKTGQSMTLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRESAAPSQ TSVYFCASSESQGNTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2340

[00328] In some embodiments, TCR034 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR034 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AI. Amino acid sequences of TCR035.

Description	Sequence	SEQ ID NO:
CDR1 α	VSPFSN	1341
CDR2 α	MTFSENT	1342
CDR3 α	VVSSYKII	1343
V α without signal peptide (SignalP)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWKQDTGRGPVSLTIMTF SENTKSNRGYTATLDADTKQSSLHITASQLSDSASYICVVSSYKIIIFGTGTRLHVFP	1344
V α without signal peptide (IMGT)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWKQDTGRGPVSLTIMTF SENTKSNRGYTATLDADTKQSSLHITASQLSDSASYICVVSSYKIIIFGTGTRLHVFP	1345
V α	MXKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFP	1346
	(X = any amino acid)	1347
α chain with WT signal peptide, C α (substituted)	MAKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFPNIQNPEPAVYQLKDPRSQDSTLCFLT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIEFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLM TRLWSS	1348
α chain with alternative signal peptide, C α (substituted)	MAKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFPNIQNPEPAVYQLKDPRSQDSTLCFLT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIEFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLM TRLWSS	1349
α chain with alternative signal peptide, C α (substituted)	MHKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSSYKIIIFGTGTRLHVFPNIQNPEPAVYQLKDPRSQDSTLCFLT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIEFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLVIVLRILLKLVAGFNLLM TRLWSS	1350
CDR1 β	SGHTA	2341
CDR2 β	FQGNSA	2342
CDR3 β	ASSPIQGENSPLH	2343
V β without signal peptide (SignalP)	GVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGNSA PDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHF GNGTRLTVT	2344
V β without signal peptide (IMGT)	GAGVSQSPSNKVTEKGKDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPL HFGNGTRLTVT	2345
V β	MXTRLFFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGNSAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVT	2346
	(X = any amino acid)	2347
β chain with WT signal peptide, C β (substituted)	MGTRLFFWVAFCLLGAYHTGAGVSQSPSNKVTEKGKDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGNSAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTIEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRNS	2348

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLFVWAFCLLGAYHTGAGVQSPPSNKVTEKGDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGNAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2349
β chain with alternative signal peptide, C β (substituted)	MHTRLLFVWAFCLLGAYHTGAGVQSPPSNKVTEKGDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGNAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2350

[00329] In some embodiments, TCR035 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR035 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AJ. Amino acid sequences of TCR036.

Description	Sequence	SEQ ID NO:
CDR1 α	VSPFSN	1351
CDR2 α	MTFSENT	1352
CDR3 α	VVSSYKLI	1353
V α without signal peptide (SignalP)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIMTF SENTKSNRGYTATLDADTKQSSLHITASQLSDSASYICVVSYYKLI FGTGTR LQVFP	1354
V α without signal peptide (IMGT)	KNQVEQSPQSLIIILEGKNCTLQCNYTVSPFSNLRWYKQDTGRGPVSLTIMTF SENTKSNRGYTATLDADTKQSSLHITASQLSDSASYICVVSYYKLI FGTGTR LQVFP	1355
V α	MXKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSYYKLI FGTGTRLQVFP (X = any amino acid)	1356
		1357
α chain with WT signal peptide, C α (substituted)	MKKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSYYKLI FGTGTRLQVFPNIQNPEPAVYQLKDPQSDSTLCFLT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTCDIFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVLIRILLKLVAGFNLLM TLRLWSS	1358
α chain with alternative signal peptide, C α (substituted)	MAKHLTTFLVILWLIFYRNGNGKNQVEQSPQSLIIILEGKNCTLQCNYTVSPFS NLRWYKQDTGRGPVSLTIMTFSENTKSNRGYTATLDADTKQSSLHITASQLS DSASYICVVSYYKLI FGTGTRLQVFPNIQNPEPAVYQLKDPQSDSTLCFLT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTCDIFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVLIRILLKLVAGFNLLM TLRLWSS	1359

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHKHLTTFVLVLWLIFYRGNGKNQVEQSPQSLIIILEGKNCTLQCNVTVSPFS NLRWYKQDTGRGPVSLTMTFSENTKSNGRYTATLDADTKQSSLHITASQLS DSASYICVVSSYKLI FGTGTRLQVFPNIQNPEPAVYQLKDPRSQDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLM TLRLWSS	1360
CDR1 β	SGHTA	2351
CDR2 β	FQGN SA	2352
CDR3 β	ASSPIQGENSPLH	2353
V β without signal peptide (SignalP)	GVSQSPSNKVTEKGDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SA PDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPLHF GNGTRLTVT	2354
V β without signal peptide (IMGT)	GAGVSQSPSNKVTEKGDVELRCDPISGHTALYWYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQEDSAVYLCASSPIQGENSPL HFGNGTRLTVT	2355
V β	MXTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVT (X = any amino acid)	2356
		2357
β chain with WT signal peptide, C β (substituted)	MGTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVTTPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2358
β chain with alternative signal peptide, C β (substituted)	MATRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVTTPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2359
β chain with alternative signal peptide, C β (substituted)	MHTRLLEFWVAFCLLGAYHTGAGVSQSPSNKVTEKGDVELRCDPISGHTALY WYRQRLGQGLEFLIYFQGN SAPDKSGLPSDRFSAERTGESVSTLTIQRTQQE DSAVYLCASSPIQGENSPLHFGNGTRLTVTEDLRNVTTPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2360

[00330] In some embodiments, TCR036 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR036 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AK. Amino acid sequences of TCR037.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVSVY	1361
CDR2 α	YLSGSTLV	1362
CDR3 α	AVSKGTGAQKLV	1363
V α without signal peptide (SignalP)	QSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINP	1364
V α without signal peptide (IMGT)	AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINP	1365
V α	MXLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINP (X = any amino acid)	1366
		1367
α chain with WT signal peptide, (substituted) C α	MLLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1368
α chain with alternative signal peptide, (substituted) C α	MALLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1369
α chain with alternative signal peptide, (substituted) C α	MHLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSKGTGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1370
CDR1 β	LNHDA	2361
CDR2 β	SQIVND	2362
CDR3 β	ASEAF	2363
V β without signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTVV	2364
V β without signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLT VV	2365
V β	MXNQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTVV (X = any amino acid)	2366
		2367
β chain with WT signal peptide, (substituted) C β	MSNQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNPTASYLCASEAFFGQGTRLTVVEDLRNVTTPKVSLEFPSKAEIANQKATLVC LARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFW HNPRNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNISAEAWGRADCGITSASYQ QGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2368

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MANQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNP TASYLCASEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVC LARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFW HNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQ QGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2369
β chain with alternative signal peptide, C β (substituted)	MHNQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLIVTSAQKNP TASYLCASEAFFGQGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVC LARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFW HNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQ QGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2370

[00331] In some embodiments, TCR037 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR037 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AL. Amino acid sequences of TCR038.

Description	Sequence	SEQ ID NO:
CDR1 α	TISGTDY	1371
CDR2 α	GLTSN	1372
CDR3 α	ILASGAGSYQLT	1373
V α without signal peptide (SignalP)	KTTPNSMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAVYYCILASGAGSYQLTFGKGTK LSVIP	1374
V α without signal peptide (IMGT)	DAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLT SNVNNRMASLAIAEDRKSSTLILHRATLRDAVYYCILASGAGSYQLTFGKG TKLSVIP	1375
V α	MXLVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAVYY CILASGAGSYQLTFGKGTKLSVIP (X = any amino acid)	1376
		1377
α chain with WT signal peptide, C α (substituted)	MKLVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAVYY CILASGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDP RSQDSTLCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTLEKSFETDMNLNFQNL LVI VLRILLKLVAGFNLLMTL RLWSS	1378
α chain with alternative signal peptide, C α (substituted)	MALVTSTITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHW YRQLPSQGPEYVIHGLTSN VNNRMASLAIAEDRKSSTLILHRATLRDAVYY CILASGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDP RSQDSTLCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTLEKSFETDMNLNFQNL LVI VLRILLKLVAGFNLLMTL RLWSS	1379

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHLVTSITVLLSLGIMGDAKTTQPNMESNEEEPVHLPCNHSTISGTDYIHWYRQLPSQGPEYVIHGLTSNVNNRMASLAIAEDRKSSTLILHRATLRDAAVYYCILASGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1380
CDR1 β	LGHD	2371
CDR2 β	YNNKEL	2372
CDR3 β	ASRTIGYNTEAF	2373
V β without signal peptide (SignalP)	QTPKYLVTQMGNDSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETVFNRFSPKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGRLTVV	2374
V β without signal peptide (IMGT)	DTAVSQTPKYLVTQMGNDSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETVFNRFSPKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGRLTVV	2375
V β	MXCRLCCVVFCLLQAGPLDTAVSQTPKYLVTQMGNDSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETVFNRFSPKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGRLTVV (X = any amino acid)	2376
		2377
β chain with WT signal peptide, C β (substituted)	MGCRLCCVVFCLLQAGPLDTAVSQTPKYLVTQMGNDSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETVFNRFSPKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGRLTVVEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVRKNS	2378
β chain with alternative signal peptide, C β (substituted)	MACRLCCVVFCLLQAGPLDTAVSQTPKYLVTQMGNDSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETVFNRFSPKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGRLTVVEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVRKNS	2379
β chain with alternative signal peptide, C β (substituted)	MHCRLCCVVFCLLQAGPLDTAVSQTPKYLVTQMGNDSIKCEQNLGHDTMYWYKQDSKKFLKIMFSYNNKELIINETVFNRFSPKSPDKAHLNLHINSLELGDSAVYFCASRTIGYNTEAFFGQGRLTVVEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVRKNS	2380

[00332] In some embodiments, TCR038 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR038 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AM. Amino acid sequences of TCR039.

Description	Sequence	SEQ ID NO:
CDR1 α	VGISA	1381
CDR2 α	LSSGK	1382
CDR3 α	AALSYNTDKLI	1383
V α without signal peptide (SignalP)	AKNEVEQSPQNLTAEGEFITTINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFP	1384
V α without signal peptide (IMGT)	KNEVEQSPQNLTAEGEFITTINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFP	1385
V α	MXKIRQFLLAILLWLQSLSCVSAKNEVEQSPQNLTAEGEFITTINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFP	1386
	(X = any amino acid)	1387
α chain with WT signal peptide, C α (substituted)	MKKIRQFLLAILLWLQSLSCVSAKNEVEQSPQNLTAEGEFITTINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFPNIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1388
α chain with alternative signal peptide, C α (substituted)	MAKIRQFLLAILLWLQSLSCVSAKNEVEQSPQNLTAEGEFITTINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFPNIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1389
α chain with alternative signal peptide, C α (substituted)	MHKIRQFLLAILLWLQSLSCVSAKNEVEQSPQNLTAEGEFITTINCSYSVGISALHWLQQHPGGGIVSLFMLSSGKKKHGRLIATINIQEKHSSLHITASHPRDSAVYICAALSYNTDKLIFGTGTRLQVFPNIQNPEPAVYQLKDPRSQDSTLCLETFDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1390
CDR1 β	SGHTA	2381
CDR2 β	FQGTGA	2382
CDR3 β	ASSLSGLLQETQY	2383
V β without signal peptide (SignalP)	GVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVL	2384
V β without signal peptide (IMGT)	GAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVL	2385
V β	MXTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVL	2386
	(X = any amino acid)	2387
β chain with WT signal peptide, C β (substituted)	MGTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALYWYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERGDSAVYLCASSLSGLLQETQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2388

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALY WYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERG DSAVYLCASSLSGLLQETQYFGPGTRLLVLEDLRNVTPPKVSLFEPSCAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2389
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGADHTGAGVSQTPSNKVTEKGKYVELRCDPISGHTALY WYRQSLGQGPEFLIYFQGTGAADDSGLPNDRFFAVRPEGSVSTLKIQRTERG DSAVYLCASSLSGLLQETQYFGPGTRLLVLEDLRNVTPPKVSLFEPSCAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2390

[00333] In some embodiments, TCR039 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR039 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AN. Amino acid sequences of TCR040.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1391
CDR2 α	ATKADDK	1392
CDR3 α	ALSHTGSSNTGKLI	1393
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKA DDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIF GQGTRLQVKP	1394
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATK ADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHTGSSNTGKLIF FGQGTRLQVKP	1395
V α	MXYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSHTGSSNTGKLIFGQGTRLQVKP (X = any amino acid)	1396
		1397
α chain with WT signal peptide, C α (substituted)	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSHTGSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLLKVAGF NLLMTLRLWSS	1398
α chain with alternative signal peptide, C α (substituted)	MAYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSHTGSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLLKVAGF NLLMTLRLWSS	1399

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLKATKADDKGSNGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSHGTSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVGAFNLLMTLRLWSS	1400
CDR1 β	SGHAT	2391
CDR2 β	FQNGGV	2392
CDR3 β	ASSTGGGRHQPH	2393
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLIL	2394
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLIL	2395
V β	MXTRLWCWAAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLIL (X = any amino acid)	2396
		2397
β chain with WT signal peptide, C β (substituted)	MGTRLWCWAAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLILEDLRNVTTPKVSLEFESKAEDIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATIILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2398
β chain with alternative signal peptide, C β (substituted)	MATRLWCWAAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLILEDLRNVTTPKVSLEFESKAEDIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATIILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2399
β chain with alternative signal peptide, C β (substituted)	MHTRLWCWAAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLILEDLRNVTTPKVSLEFESKAEDIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATIILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2400

[00334] In some embodiments, TCR040 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR040 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AO. Amino acid sequences of TCR041.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1401
CDR2 α	ATKADDK	1402
CDR3 α	ALSQTGSSKTGKLI	1403
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSKTGKLIFGQGTRLQVKP	1404
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSKTGKLIFGQGTRLQVKP	1405
V α	MXYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSKTGKLIFGQGTRLQVKP	1406
	(X = any amino acid)	1407
α chain with WT signal peptide, (substituted) C α	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSKTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1408
α chain with alternative signal peptide, (substituted) C α	MAYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSKTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1409
α chain with alternative signal peptide, (substituted) C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSKTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1410
CDR1 β	SGHAT	2401
CDR2 β	FQNGV	2402
CDR3 β	ASSTGGGRHQPH	2403
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSIL	2404
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSIL	2405
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSIL	2406
	(X = any amino acid)	2407
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRNS	2408

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCCLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2409
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCCLGAELTEAGVAQSPRYKIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2410

[00335] In some embodiments, TCR041 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR041 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AP. Amino acid sequences of TCR042.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1411
CDR2 α	ATKADDK	1412
CDR3 α	ALSQTGSSNTGKLI	1413
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKA DDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSNTGKLIF GQGTRLQVKP	1414
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATK ADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSNTGKLIF FGQGTRLQVKP	1415
V α	MXYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSQTGSSNTGKLIFGQGTRLQVKP (X = any amino acid)	1416
		1417
α chain with WT signal peptide, C α (substituted)	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSQTGSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAWSNQT SFTCQ DIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVIVLRL ILLKLVAGF NLLMTLRLWSS	1418
α chain with alternative signal peptide, C α (substituted)	MAYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSL FWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDS AVYFCALSQTGSSNTGKLIFGQGTRLQVKPNIQNPEPAVYQLKDP RSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSN GAIAWSNQT SFTCQ DIFKETNATYPSSDVPCDATLTEKS FETDMNLNFQNL LVIVLRL ILLKLVAGF NLLMTLRLWSS	1419

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGQLLLKATKADDKGSNGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSQTGSSNTGKLI FGQGTRLQVKPNIQNPEPAVYQLKDRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVIVLRI LLLKVAGFNLLMTLRLWSS	1420
CDR1 β	SGHAT	2411
CDR2 β	FQNGGV	2412
CDR3 β	ASSTGGGRHQPH	2413
V β without signal peptide (SignalP)	GVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRSL	2414
V β without signal peptide (IMGT)	EAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRSL	2415
V β	MXTRLWCWAAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRSL (X = any amino acid)	2416
		2417
β chain with WT signal peptide, C β (substituted)	MGTRLWCWAAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLILEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2418
β chain with alternative signal peptide, C β (substituted)	MATRLWCWAAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLILEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2419
β chain with alternative signal peptide, C β (substituted)	MHTRLWCWAAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDSSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGRSLILEDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2420

[00336] In some embodiments, TCR042 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR042 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AQ. Amino acid sequences of TCR043.

Description	Sequence	SEQ ID NO:
CDR1 α	ATGYPS	1421
CDR2 α	ATKADDK	1422
CDR3 α	ALSTTGSSNTGKLI	1423
V α without signal peptide (SignalP)	NSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKP	1424
V α without signal peptide (IMGT)	GNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKP	1425
V α	MXYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKP	1426
	(X = any amino acid)	1427
α chain with WT signal peptide, (substituted) C α	MNYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1428
α chain with alternative signal peptide, (substituted) C α	MAYSPGLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1429
α chain with alternative signal peptide, (substituted) C α	MHYSPLVSLILLLLGRTRGNSVTQMEGPVTLSEEAFLTINCTYTATGYPSLFWYVQYPGEGLQLLLKATKADDKGSNKGFEATYRKETTSFHLEKGSVQVSDSAVYFCALSTTGSSNTGKLIFGQGTTLQVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLLMTLRLWSS	1430
CDR1 β	SGHAT	2421
CDR2 β	FQNGV	2422
CDR3 β	ASSTGGGRHQPH	2423
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSIL	2424
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSIL	2425
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSIL	2426
	(X = any amino acid)	2427
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNGVVDVDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2428

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2429
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSTGGGRHQPHFGDGTLSILEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKR KNS	2430

[00337] In some embodiments, TCR043 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR043 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AR. Amino acid sequences of TCR044.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1431
CDR2 α	IYSNGD	1432
CDR3 α	AVSWYSTLT	1433
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQSFFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLCAVSWYSTLT FFGKT MLLVSP	1434
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYS DRGSQSFFWYRQYSGKSP ELIMFIY NGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLCAVSWYSTLT FFGKT MLLVSP	1435
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLCAVSWYSTLT FFGKTMLLVSP	1436
	(X = any amino acid)	1437
α chain with WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLCAVSWYSTLT FFGKTMLLVSPNIQNPEPAVYQLKDPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQT SFTCQDIFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLK VAGFNLLM TLRLWSS	1438
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLCAVSWYSTLT FFGKTMLLVSPNIQNPEPAVYQLKDPRS QDSTLC LFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQT SFTCQDIFK ETNATYPSSDVPCDATLTEKS FETDMNLNFQNLIVIVLRILLK VAGFNLLM TLRLWSS	1439

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCVSWYSTLTFTGKGTMLLVSPNIQNPEPAVYQLKDPRSQDSTLCLFT DFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTCQDIFK ETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLM TLRLWSS	1440
CDR1 β	WSHSY	2431
CDR2 β	SAAADI	2432
CDR3 β	ASSGSRTDTQY	2433
V β without signal peptide (SignalP)	GITQSPRYKITETGRQVTLMCHQTWSHSYMFWYRQDLGHGLRLIYSAADI TDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSGSRTDTQYFGPG TRLTVL	2434
V β without signal peptide (IMGT)	DAGITQSPRYKITETGRQVTLMCHQTWSHSYMFWYRQDLGHGLRLIYSAAD DITDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSGSRTDTQYFG PGTRLTVL	2435
V β	MXTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVL (X = any amino acid)	2436
		2437
β chain with WT signal peptide, C β (substituted)	MGTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2438
β chain with alternative signal peptide, C β (substituted)	MATRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2439
β chain with alternative signal peptide, C β (substituted)	MHTRLFFYVALCCLWAGHRDAGITQSPRYKITETGRQVTLMCHQTWSHSYMF WYRQDLGHGLRLIYSAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSGSRTDTQYFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2440

[00338] In some embodiments, TCR044 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR044 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AS. Amino acid sequences of TCR045.

Description	Sequence	SEQ ID NO:
CDR1 α	SVFSS	1441
CDR2 α	VVTGGEV	1442
CDR3 α	AGEFAGNQFY	1443
V α without signal peptide (SignalP)	QLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQWYRQEPGEGPVLLVTVVTGG EVKKLKRITFQFGDARKDSSLHITAAQPGDTGLYLCAGEFAGNQFYFGTGTSLTVIP	1444
V α without signal peptide (IMGT)	TQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQWYRQEPGEGPVLLVTVVTG GEVKKLKRITFQFGDARKDSSLHITAAQPGDTGLYLCAGEFAGNQFYFGTGTSLTVIP	1445
V α	MXLKFSVSI LWIQLAWVSTQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTGGEVKKLKRITFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIP (X = any amino acid)	1446
		1447
α chain with WT signal peptide, C α (substituted)	MVLKFSVSI LWIQLAWVSTQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTGGEVKKLKRITFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDRSQDSTLCCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTKEFSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1448
α chain with alternative signal peptide, C α (substituted)	MALKFSVSI LWIQLAWVSTQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTGGEVKKLKRITFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDRSQDSTLCCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTKEFSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1449
α chain with alternative signal peptide, C α (substituted)	MHLKFSVSI LWIQLAWVSTQLLEQSPQFLSIQEGENLTVYCNSSSVFSSLQW YRQEPGEGPVLLVTVVTGGEVKKLKRITFQFGDARKDSSLHITAAQPGDTGL YLCAGEFAGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDRSQDSTLCCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTKEFSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1450
CDR1 β	MGHRA	2441
CDR2 β	YSYEKL	2442
CDR3 β	ASSQVGLTYEQY	2443
V β without signal peptide (SignalP)	EVTQTTPKHLVMGMTNKKSLKCEQHMGHARAMYWKQKAKKPELMFVYSYEKL SINESVPSRFSPECNSSLNLHLHALQPEDSALYLCASSQVGLTYEQYFGP GTRLTVT	2444
V β without signal peptide (IMGT)	DTEVTQTTPKHLVMGMTNKKSLKCEQHMGHARAMYWKQKAKKPELMFVYSYE KLSINESVPSRFSPECNSSLNLHLHALQPEDSALYLCASSQVGLTYEQYF GPGTRLTVT	2445
V β	MXCRLCCAVLCLLGAVPIDTEVTQTTPKHLVMGMTNKKSLKCEQHMGHARAMY WKQKAKKPELMFVYSYEKLSINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRLTVT (X = any amino acid)	2446
		2447
β chain with WT signal peptide, C β (substituted)	MGCRLCCAVLCLLGAVPIDTEVTQTTPKHLVMGMTNKKSLKCEQHMGHARAMY WKQKAKKPELMFVYSYEKLSINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRLTVTEDLRNVTPEKVSLEFESKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2448

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MACRLCCAVLCLLGAVPIDTEVTQTPKHLVGMGTNKKSLKCEQHMGHRAMY WYKQKAKKPELMFVYSYEKLSINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2449
β chain with alternative signal peptide, C β (substituted)	MHCRLCCAVLCLLGAVPIDTEVTQTPKHLVGMGTNKKSLKCEQHMGHRAMY WYKQKAKKPELMFVYSYEKLSINESVPSRFSPECNSSLNLHLHALQPED SALYLCASSQVGLTYEQYFGPGTRLTVTEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKNS	2450

[00339] In some embodiments, TCR045 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR045 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AT. Amino acid sequences of TCR046.

Description	Sequence	SEQ ID NO:
CDR1 α	VSGNPY	1451
CDR2 α	YITGDNLV	1452
CDR3 α	AVRDNSGGSNYKLT	1453
V α without signal peptide (SignalP)	QSVAPEDQVNVAEGNPLTVKCTYSVSGNPYLEFWYVQYPNRLQFLLKYITG DNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDNSGGSNYKLT FGKGTLLTVNP	1454
V α without signal peptide (IMGT)	AQSVAPEDQVNVAEGNPLTVKCTYSVSGNPYLEFWYVQYPNRLQFLLKYIT GDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSDSALYFCAVRDNSGGSNYKL TFGKGTLLTVNP	1455
V α	MXSAPISMLAMLFLLSGLRAQSVAPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRDNSGGSNYKLTFGKGTLLTVNP (X = any amino acid)	1456
		1457
α chain with WT signal peptide, C α (substituted)	MASAPISMLAMLFLLSGLRAQSVAPEDQVNVAEGNPLTVKCTYSVSGNPYL FWYVQYPNRLQFLLKYITGDNLVKGSYGFEAEFNKSQTSFHLKKPSALVSD SALYFCAVRDNSGGSNYKLTFGKGTLLTVNPNIQNPEPAVYQLKDPKSDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASWNSQTSFTC QDIFKETNATYPSDDVPCDATLTEKSFETDMNLNFQNLVIVLRIILLKVAG FNLLMTLRLWSS	1458
		1459

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHSAPISMLAMLF T L S G L R A Q S V A Q P E D Q V N V A E G N P L T V K C T Y S V S G N P Y L F W Y V Q Y P N R G L Q F L L K Y I T G D N L V K G S Y G F E A E F N K S Q T S F H L K K P S A L V S D S A L Y F C A V R D N S G G S N Y K L T F G K G T L L T V N P N I Q N P E P A V Y Q L K D P R S Q D S T L C L F T D F D S Q I N V P K T M E S G T F I T D K C V L D M K A M D S K S N G A I A W S N Q T S F T C Q D I F K E T N A T Y P S S D V P C D A T L T E K S F E T D M N L N F Q N L L V I V L R I L L L K V A G F N L L M T L R L W S S	1460
CDR1 β	SGHAT	2451
CDR2 β	FQNNGV	2452
CDR3 β	ASSLGQGQTQY	2453
V β without signal peptide (SignalP)	GVAQSPRYKII EKRSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGQGQTQYFGP GTRLLVL	2454
V β without signal peptide (IMGT)	EAGVAQSPRYKII EKRSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNN GVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGQGQTQYF GPGTRLLVL	2455
V β	MXTRLLCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVL (X = any amino acid)	2456
		2457
β chain with WT signal peptide, C β (substituted)	MGTRLLCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2458
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2459
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCCLGAELTEAGVAQSPRYKII EKRSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGQGQTQYFGPGTRLLVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2460

[00340] In some embodiments, TCR046 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR046 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AU. Amino acid sequences of TCR047.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVSVY	1461
CDR2 α	YLSGSTLV	1462
CDR3 α	AVRGSSGTYKYI	1463
V α without signal peptide (SignalP)	QSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYKYIFGTGTRLKVL	1464
V α without signal peptide (IMGT)	AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYKYIFGTGTRLKVL	1465
V α	MXLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYKYIFGTGTRLKVL (X = any amino acid)	1466
		1467
α chain with WT signal peptide, (substituted) C α	MLLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYKYIFGTGTRLKVLNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1468
α chain with alternative signal peptide, (substituted) C α	MALLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYKYIFGTGTRLKVLNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1469
α chain with alternative signal peptide, (substituted) C α	MHLLLVPFAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYLSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVRGSSGTYKYIFGTGTRLKVLNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1470
CDR1 β	MDHEN	2461
CDR2 β	SYDVKM	2462
CDR3 β	ASKGDQNTAEAF	2463
V β without signal peptide (SignalP)	SRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQTSMYLCASKGDQNTAEAFQGQTRLT V	2464
V β without signal peptide (IMGT)	DVKVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDV KMKEKGD IPEGYSVSREKKERFSLILESASTNQTSMYLCASKGDQNTAEAF GQGTRLT V	2465
V β	MXIRLLCRVAFCFGLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQ TSMYLCASKGDQNTAEAFQGQTRLT V (X = any amino acid)	2466
		2467
β chain with WT signal peptide, (substituted) C β	MGIRLLCRVAFCFGLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQ TSMYLCASKGDQNTAEAFQGQTRLT VVEDLRNVT PKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNP RNHFRCQVQHGLSEEDKWPEGSPKPVTONI SAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2468

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAIRLLCRVAFCFLLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQ TSMYLCASKGDQNTAEAFFGQGTRLTVVEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWSVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2469
β chain with alternative signal peptide, C β (substituted)	MHIRLLCRVAFCFLLAVGLVDVKVTQSSRYLVKRTGEKVFLECVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGDIPGYSVSREKKERFSLILESASTNQ TSMYLCASKGDQNTAEAFFGQGTRLTVVEDLRNVTTPKVSLFEPKAEIANKQ KATLVCLARGFFPDHVELSWSVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2470

[00341] In some embodiments, TCR047 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR047 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AV. Amino acid sequences of TCR048.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1471
CDR2 α	NVLDGL	1472
CDR3 α	AVRDLQTGANNLF	1473
V α without signal peptide (SignalP)	QNIDQPTMTATEGAIVQINCTYQTSFGNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVRDLQTGANNLFFGTG TRLTVIP	1474
V α without signal peptide (IMGT)	GQNIDQPTMTATEGAIVQINCTYQTSFGNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVRDLQTGANNLFFGT GTRLTVIP	1475
V α	MXGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSFGNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVRDLQTGANNLFFGTGTRLTVIP (X = any amino acid)	1476
		1477
α chain with WT signal peptide, C α (substituted)	MWGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSFGNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVRDLQTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPRSQDSTLCFLTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPDCATLTEKSFETDMNLNFQNLIVLRIILLKLVAGFNLLMT LRLWSS	1478

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MAGVFLLYVSMKMGTTGQNIHQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVRDLQGTGANNLFFGTGTRLTVI PNIQNPEPAVYQLKDPQSQDSTLCCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1479
α chain with alternative peptide, (substituted) C α	MHG VFLLYVSMKMGTTGQNIHQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVRDLQGTGANNLFFGTGTRLTVI PNIQNPEPAVYQLKDPQSQDSTLCCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1480
CDR1 β	MDHEN	2471
CDR2 β	SYDVKM	2472
CDR3 β	ASSLTFGTTEAF	2473
V β without signal peptide (SignalP)	SRYLVKRTGEKVFLQCVQDMDHENMFWRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQTSMYLCASSLTFGTTEAFFGQGTRLT VV	2474
V β without signal peptide (IMGT)	DKVTQSSRYLVKRTGEKVFLQCVQDMDHENMFWRQDPGLGLRLIYFSYDV KMKEKGD IPEGYSVSREKKERFSLILESASTNQTSMYLCASSLTFGTTEAFF GQGTRLTVV	2475
V β	MXIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLQCVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVV (X = any amino acid)	2476
		2477
β chain with WT signal peptide, (substituted) C β	MGIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLQCVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVRKNS	2478
β chain with alternative signal peptide, (substituted) C β	MAIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLQCVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVRKNS	2479
β chain with alternative signal peptide, (substituted) C β	MHIRLLCRVAFCF LAVGLVDVKVTQSSRYLVKRTGEKVFLQCVQDMDHENMF WYRQDPGLGLRLIYFSYDVKMKEKGD IPEGYSVSREKKERFSLILESASTNQ TSMYLCASSLTFGTTEAFFGQGTRLTVVEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVVRKNS	2480

[00342] In some embodiments, TCR048 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248Q relative to the wild type p53 sequence. In some embodiments, TCR048 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AW. Amino acid sequences of TCR049.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1481
CDR2 α	NVLDGL	1482
CDR3 α	AFYYGGSQGNLI	1483
V α without signal peptide (SignalP)	QNIDQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKGT KLSVKP	1484
V α without signal peptide (IMGT)	GQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAFYYGGSQGNLIFGKG TKLSVKP	1485
V α	MXGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAFYYGGSQGNLIFGKGTKLSVKP (X = any amino acid)	1486
		1487
α chain with WT signal peptide, (substituted) C α	MWGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAFYYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDPQSQDSTLCCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1488
α chain with alternative signal peptide, (substituted) C α	MAGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAFYYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDPQSQDSTLCCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1489
α chain with alternative signal peptide, (substituted) C α	MHGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAFYYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDPQSQDSTLCCLFTDF DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1490
CDR1 β	SGHVS	2481
CDR2 β	FQNEAQ	2482
CDR3 β	ASSFGSGSTDTQY	2483
V β without signal peptide (SignalP)	GVSQSPRYKVAKRQDVALRCDPISGHVSLFWYQQALGQGPEFLTYFQNEAQ LDKSGLPSDRFFAERPEGSVSTLKIQRTOQEDSAVYLCASSFGSGSTDTQYF GPGTRLTVL	2484
V β without signal peptide (IMGT)	GAGVSQSPRYKVAKRQDVALRCDPISGHVSLFWYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQRTOQEDSAVYLCASSFGSGSTDTQYF GPGTRLTVL	2485
V β	MXTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPISGHVSLF WYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQRTOQE DSAVYLCASSFGSGSTDTQYF GPGTRLTVL (X = any amino acid)	2486
		2487
β chain with WT signal peptide, (substituted) C β	MGTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPISGHVSLF WYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQRTOQE DSAVYLCASSFGSGSTDTQYF GPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2488

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPISGHVSLF WYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQTQQE DSAVYLCASSFGSGSTDYFPGPTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2489
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWVVLGFLGTDHTGAGVSQSPRYKVAKRQDVALRCDPISGHVSLF WYQQALGQGPEFLTYFQNEAQLDKSGLPSDRFFAERPEGSVSTLKIQTQQE DSAVYLCASSFGSGSTDYFPGPTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2490

[00343] In some embodiments, TCR049 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR049 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AX. Amino acid sequences of TCR050.

Description	Sequence	SEQ ID NO:
CDR1 α	VTNFRS	1491
CDR2 α	LTSSGIE	1492
CDR3 α	AGQNYGGSQGNLI	1493
V α without signal peptide (SignalP)	EDKVVQSPLSLVVHEGDTVTLNCSYEVNTNFRSLLWYKQEKKAPTFLFMLTSS GIEKKSGRLSSILDKKELSSILNITATQTGDSAIYLCAGQNYGGSQGNLIFG KGTKLSVKP	1494
V α without signal peptide (IMGT)	EDKVVQSPLSLVVHEGDTVTLNCSYEVNTNFRSLLWYKQEKKAPTFLFMLTSS GIEKKSGRLSSILDKKELSSILNITATQTGDSAIYLCAGQNYGGSQGNLIFG KGTKLSVKP	1495
V α	MXKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVNTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSILDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKP	1496
	(X = any amino acid)	1497
α chain with WT signal peptide, C α (substituted)	MMKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVNTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSILDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGF NLLMTLRLWSS	1498
α chain with alternative signal peptide, C α (substituted)	MAKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVNTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSILDKKELSSILNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDPRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGF NLLMTLRLWSS	1499

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHKCPQALLAIFWLLLSWVSSSEDKVVQSPLSLVVHEGDTVTLNCSYEVTNFR SLLWYKQEKKAPTFLFMLTSSGIEKKSGRLSSI LDKKELSSI LNITATQTGD SAIYLCAGQNYGGSQGNLIFGKGTKLSVKPNIQNPEPAVYQLKDRSQDSTL CLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKVGAF NLLMTLRLWSS	1500
CDR1 β	SNHLY	2491
CDR2 β	FYNNE	2492
CDR3 β	ASRDPAYEQY	2493
V β without signal peptide (SignalP)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLEDSAMYFCASRDPAYEQYFG PGTRLTVT	2494
V β without signal peptide (IMGT)	EPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFYWYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLEDSAMYFCASRDPAYEQYFG PGTRLTVT	2495
V β	MXTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVT (X = any amino acid)	2496
		2497
β chain with WT signal peptide, C β (substituted)	MDTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2498
β chain with alternative signal peptide, C β (substituted)	MATWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2499
β chain with alternative signal peptide, C β (substituted)	MHTWLVCWAI FSLKAGLTEPEVTQTPSHQVTQMGQEVILRCVPI SNHLYFY WYRQILGQKVEFLVSFYNN EISEKSEIFDDQFSVERPDGSNFTLKIRSTKLE DSAMYFCASRDPAYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQ KATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLR VSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGI TSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKNS	2500

[00344] In some embodiments, TCR050 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR050 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AY. Amino acid sequences of TCR051.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1501
CDR2 α	IYSNGD	1502
CDR3 α	AVTLCGGYNKLI	1503
V α without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVTLCGGYNKLI FGA GTRLAVHP	1504
V α without signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVTLCGGYNKLI FGA GTRLAVHP	1505
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVTLCGGYNKLI FGA GTRLAVHP	1506
	(X = any amino acid)	1507
α chain with WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVTLCGGYNKLI FGA GTRLAVHPNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1508
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVTLCGGYNKLI FGA GTRLAVHPNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1509
α chain with alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIIRDSQPSDSATYLCAVTLCGGYNKLI FGA GTRLAVHPNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1510
CDR1 β	LNHDA	2501
CDR2 β	SQIVND	2502
CDR3 β	ASSSRDYEQY	2503
V β without signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2504
V β without signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2505
V β	MXNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2506
	(X = any amino acid)	2507
β chain with WT signal peptide, C β (substituted)	MSNQVLCCVVLCCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVTEDLRNVT PPKVSLFEPKAEIANKQK ATLVLCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2508

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MANQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2509
β chain with alternative signal peptide, C β (substituted)	MHNQVLCCVVLFCFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2510

[00345] In some embodiments, TCR051 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR051 interacts with the neoantigen in the context of HLA-DPA1*03:01/ DPB1*02:01:02, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6AZ. Amino acid sequences of TCR052.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVSVY	1511
CDR2 α	YLSGSTLV	1512
CDR3 α	AVSDLVRDDKII	1513
V α without signal peptide (SignalP)	QSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYL SG STLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSDLVRDDKIIIFG KGTRLHILP	1514
V α without signal peptide (IMGT)	AQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYLFWYVQYPNQGLQLLLKYL S GSTLVESINGFEAEFNKSQTSFHLRKPSVHISDTAEYFCAVSDLVRDDKIIIF GKGTRLHILP	1515
V α	MXLLLVPFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYL SGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRDDKIIIFGKGTRLHILP	1516
	(X = any amino acid)	1517
α chain with WT signal peptide, C α (substituted)	MLLLLVPFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYL SGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRDDKIIIFGKGTRLHILPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVLVIVLRILLKLVAGFN LLMTLRLWSS	1518

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MALLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYLSGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRRDDKIIIFGKGTRLHLIPNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1519
α chain with alternative peptide, (substituted) C α	MHLLLVPAFQVIFTLGGTRAQSVTQLDSQVPVFEEAPVELRCNYSSSVSVYL FWYVQYPNQGLQLLLKYLSGSTLVESINGFEAEFNKSQTSFHLRKPSVHISD TAEYFCAVSDLVRRDDKIIIFGKGTRLHLIPNIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1520
CDR1 β	MNHNS	2511
CDR2 β	SASEGT	2512
CDR3 β	ASIGGFEEAF	2513
V β without signal peptide (SignalP)	GVTQTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSASEGT TDKGEVPNGYNVSRNLNKRFLSLRLESAAPSQTSVYFCASIGGFEEAFFGQGR LTVV	2514
V β without signal peptide (IMGT)	NAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMYWYRQDPGMGLRLIYYSASE GTTDKGEVPNGYNVSRNLNKRFLSLRLESAAPSQTSVYFCASIGGFEEAFFGQG TRLTVV	2515
V β	MXIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGR LTVV (X = any amino acid)	2516
		2517
β chain with WT signal peptide, C β (substituted)	MSIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGR LTVV TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2518
β chain with alternative signal peptide, C β (substituted)	MAIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGR LTVV TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2519
β chain with alternative signal peptide, C β (substituted)	MHIGLLCCVAFSLLWASPVNAGVTQTPKFQVLKTGQSM TLQCAQDMNHNSMY WYRQDPGMGLRLIYYSASEGTTDKGEVPNGYNVSRNLNKRFLSLRLESAAPSQ TSVYFCASIGGFEEAFFGQGR LTVV TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2520

[00346] In some embodiments, TCR052 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR052 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BA. Amino acid sequences of TCR053.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1521
CDR2 α	NVLDGL	1522
CDR3 α	AVYPGGSQGNLI	1523
V α without signal peptide (SignalP)	QNIDQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKGT KLSVKP	1524
V α without signal peptide (IMGT)	GQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYPGGSQGNLIFGKG TKLSVKP	1525
V α	MXGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYPGGSQGNLIFGKGT (X = any amino acid)	1526
		1527
α chain with WT signal peptide, (substituted) C α	MWGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYPGGSQGNLIFGKGT DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1528
α chain with alternative signal peptide, (substituted) C α	MAGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYPGGSQGNLIFGKGT DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1529
α chain with alternative signal peptide, (substituted) C α	MHGVFLLYVSMKMGTTGQNIDQPTMTATEGAIVQINCTYQTSGFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYPGGSQGNLIFGKGT DSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKET NATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTL RLWSS	1530
CDR1 β	SGHAT	2521
CDR2 β	FQNNGV	2522
CDR3 β	ASSLGTGSTDTQY	2523
V β without signal peptide (SignalP)	GVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGTGSTDTQYF GPGTRLTVL	2524
V β without signal peptide (IMGT)	EAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLGTGSTDTQ YFGPTRLTVL	2525
V β	MXTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGTGSTDTQYFGPTRLTVL (X = any amino acid)	2526
		2527
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGTGSTDTQYFGPTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2528

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGTGSTDYFQFPGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2529
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPI SGHATLY WYQQILGQGPKLLIQFQNGGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASSLGTGSTDYFQFPGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2530

[00347] In some embodiments, TCR053 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR053 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BB. Amino acid sequences of TCR054.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1531
CDR2 α	IYSNGD	1532
CDR3 α	AVTLGGYNKLI	1533
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQSFFWYRQYSGKSP ELIMFIY SNGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLCAVTL SGGYNKLIFG AGTRLAVHP	1534
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYS DRGSQSFFWYRQYSGKSP ELIMFIYS NGDKEDGRFTAQLNKASQYVSL LIRDSQPSDSATYLCAVTL SGGYNKLIFGA GTRLAVHP	1535
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLCAVTL SGGYNKLIFGAGTRLAVHP	1536
	(X = any amino acid)	1537
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLCAVTL SGGYNKLIFGAGTRLAVHPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI VLRILLKLVAGFN LLMTLRLWSS	1538
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYS DRGSQ SFFWYRQYSGKSP ELIMFIYSNGDKEDGRFTAQLNKASQYVSL LIRDSQPSD SATYLCAVTL SGGYNKLIFGAGTRLAVHPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVI VLRILLKLVAGFN LLMTLRLWSS	1539

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCVATLSGGYNKLIFFAGTRLAVHPNIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRIILLKVAGFN LLMTLRLWSS	1540
CDR1 β	LNHDA	2531
CDR2 β	SQIVND	2532
CDR3 β	ASSSRDYEQY	2533
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIVND FQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGPGT RLTVT	2534
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSCQNLNHDAMYWYRQDPGQGLRLIYYSQIV NDFQKGDIVEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSSRDYEQYFGP GTRLTVT	2535
V β	MXNQVLCCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVT (X = any amino acid)	2536
		2537
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2538
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2539
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVFLCFLGANTVDGGITQSPKYLFRKEGQNVTLSCQNLNHDAMY WYRQDPGQGLRLIYYSQIVNDFQKGDIVEGYSVSREKKESFPLTVTSAQKNP TAFYLCASSSRDYEQYFGPGTRLTVTEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2540

[00348] In some embodiments, TCR054 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR054 interacts with the neoantigen in the context of DPA1*01:03/DBP1*02:01 as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BC. Amino acid sequences of TCR055.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1541
CDR2 α	IRSNMDK	1542
CDR3 α	AEYIQGAQKLV	1543
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINP	1544
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINP	1545
V α	MXGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINP (X = any amino acid)	1546
		1547
α chain with WT signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNLMTLRLWSS	1548
α chain with alternative signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNLMTLRLWSS	1549
α chain with alternative signal peptide, C α (substituted)	MHGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAEYIQGAQKLVFGQGTRLTINPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNLMTLRLWSS	1550
CDR1 β	LGHNA	2541
CDR2 β	YSLEER	2542
CDR3 β	ASSQEDNEQF	2543
V β without signal peptide (SignalP)	ELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVL	2544
V β without signal peptide (IMGT)	ETGVTQTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVL	2545
V β	MXCRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVL (X = any amino acid)	2546
		2547
β chain with WT signal peptide, C β (substituted)	MGCRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQEDNEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRKN	2548

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, Cβ (substituted)	MACRLCCAVLCLLGAGELVPMETGVTQTFRHLVMGMTNKKSLKCEQHLGHN AMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQEDNEQFFGPGTRTLVLEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2549
β chain with alternative signal peptide, Cβ (substituted)	MHCRLCCAVLCLLGAGELVPMETGVTQTFRHLVMGMTNKKSLKCEQHLGHN AMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQEDNEQFFGPGTRTLVLEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2550

[00349] In some embodiments, TCR055 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR055 interacts with the neoantigen in the context of HLA-C*01:02, as described in International Publication No. WO 2021/163477, incorporated herein by reference in its entirety.

Table 6BD. Amino acid sequences of TCR056.

Description	Sequence	SEQ ID NO:
CDR1α	DRGSQS	1551
CDR2α	IYSNGD	1552
CDR3α	AVNPPVKTSYDKVI	1553
Vα without signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIY SNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVNPPVKTSYDKVI FGPGTSLSVIP	1554
Vα without signal peptide (IMGT)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYS NGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVNPPVKTSYDKVIF GPGTSLSVIP	1555
Vα	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIP	1556
	(X = any amino acid)	1557
α chain with WT signal peptide, Cα (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIPNIQNPEPAVYQLKDPQRSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFC QDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAG FNLLMTLRLWSS	1558
α chain with alternative signal peptide, Cα (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAVNPPVKTSYDKVIFGPGTSLSVIPNIQNPEPAVYQLKDPQRSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFC QDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRI LLLKVAG FNLLMTLRLWSS	1559

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCVNPVPKTSYDKVIFGPGTSLSVIPNIQNPEPAVYQLKDPERSQDST LCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIASNQTSTFTC QDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKLVAG FNLLMTLRLWSS	1560
CDR1 β	SGHVS	2551
CDR2 β	FNYES	2552
CDR3 β	ASSHREPHTGELF	2553
V β without signal peptide (SignalP)	GVSQSPRYKVTKRQDVALRCDPISGHVSLYWRQALGQGPEFLTYFNYESQ QDKSGLPNDRFSAERPEGSISTLTIQRTQORDSAMYRCASSHREPHTGELFF GEGSRLTVL	2554
V β without signal peptide (IMGT)	GAGVSQSPRYKVTKRQDVALRCDPISGHVSLYWRQALGQGPEFLTYFNYES AQDKSGLPNDRFSAERPEGSISTLTIQRTQORDSAMYRCASSHREPHTGEL FFGEGSRLTVL	2555
V β	MXTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNYESAQDKSGLPNDRFSAERPEGSISTLTIQRTQOR DSAMYRCASSHREPHTGELFFGEGSRLTVL (X = any amino acid)	2556
		2557
β chain with WT signal peptide, (substituted) C β	MGTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNYESAQDKSGLPNDRFSAERPEGSISTLTIQRTQOR DSAMYRCASSHREPHTGELFFGEGSRLTVLEDLRNVTTPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPNNHRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2558
β chain with alternative signal peptide, (substituted) C β	MATSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNYESAQDKSGLPNDRFSAERPEGSISTLTIQRTQOR DSAMYRCASSHREPHTGELFFGEGSRLTVLEDLRNVTTPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPNNHRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2559
β chain with alternative signal peptide, (substituted) C β	MHTSLLCWVVLGFLGTDHTGAGVSQSPRYKVTKRQDVALRCDPISGHVSLY WYRQALGQGPEFLTYFNYESAQDKSGLPNDRFSAERPEGSISTLTIQRTQOR DSAMYRCASSHREPHTGELFFGEGSRLTVLEDLRNVTTPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPNNHRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2560

[00350] In some embodiments, TCR056 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR056 interacts with the neoantigen in the context of HLA-A*02:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BE. Amino acid sequences of TCR057.

Description	Sequence	SEQ ID NO:
CDR1 α	TSGFNG	1561

Description	Sequence	SEQ ID NO:
CDR2 α	NVLDGL	1562
CDR3 α	AVYTGGFKTI	1563
V α without signal peptide (SignalP)	QNIDQPTTEMTATEGAIVQINCTYQTS GFNGLFWYQQHAGEAPTFLSYNVLDG LEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYTGGFKTIFGAGTRL FVKA	1564
V α without signal peptide (IMGT)	GQNIDQPTTEMTATEGAIVQINCTYQTS GFNGLFWYQQHAGEAPTFLSYNVLD GLEEKGRFSSFLSRSGYSYLLKELQMKDSASYLCAVYTGGFKTIFGAGTR L FVKA	1565
V α	MXGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKA (X = any amino acid)	1566
		1567
α chain with WT signal peptide, (substituted) C α	MWGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLCFLTFDFS QINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNLLMTLRL WSS	1568
α chain with alternative peptide, (substituted) with signal C α	MAGVFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLCFLTFDFS QINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNLLMTLRL WSS	1569
α chain with alternative peptide, (substituted) with signal C α	MHG VFLLYVSMKMGTTGQNIDQPTTEMTATEGAIVQINCTYQTS GFNGLFWY QQHAGEAPTFLSYNVLDGLEEKGRFSSFLSRSGYSYLLKELQMKDSASYL CAVYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLCFLTFDFS QINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNA TYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNLLMTLRL WSS	1570
CDR1 β	SGHAT	2561
CDR2 β	FQNNGV	2562
CDR3 β	ASNLGGGSTDTQY	2563
V β without signal peptide (SignalP)	GVAQSPRYKII EKQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNNGV VDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASN LGGGSTDTQYF GPGTRLTVL	2564
V β without signal peptide (IMGT)	EAGVAQSPRYKII EKQSVAFWCNPISGHATLYWYQQILGQGPKLLIQFQNN GVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASN LGGGSTDTQ YFGPTRLTVL	2565
V β	MXTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASN LGGGSTDTQYF GPGTRLTVL (X = any amino acid)	2566
		2567
β chain with WT signal peptide, (substituted) C β	MGTRLLCWAALCCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNNGVDDSQLPKDRFSAERLKGVDSTLKI QPAKLE DSAVYLCASN LGGGSTDTQYF GPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2568

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MATRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASNLGGGSTDQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPARNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2569
β chain with alternative signal peptide, C β (substituted)	MHTRLLCWAALCLLGAELTEAGVAQSPRYKIIIEKRQSVAFWCNPISGHATLY WYQQILGQGPKLLIQFQNGVDDSQLPKDRFSAERLKGVDSTLKIQPAKLE DSAVYLCASNLGGGSTDQYFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIA NKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNPARNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2570

[00351] In some embodiments, TCR057 interacts with and/or is specific for p53. In some embodiments, the peptide is from a neoantigen of p53. In some embodiments, the neoantigen has the amino acid change R248W relative to the wild type p53 sequence. In some embodiments, TCR057 interacts with the neoantigen in the context of HLA-A*68:01, as described in International Publication No. WO 2019/067243, incorporated herein by reference in its entirety.

Table 6BF. Amino acid sequences of TCR058.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASQS	1571
CDR2 α	VYSSGN	1572
CDR3 α	AVNPKYTGGFKTI	1573
V α without signal peptide (SignalP)	QRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVY SSGNEDGRFTAHLNRSQYISLLIRDSKLSDSATYLCVAVNPKYTGGFKTIFG AGTRLFVKA	1574
V α without signal peptide (IMGT)	RKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVY SGNEDGRFTAHLNRSQYISLLIRDSKLSDSATYLCVAVNPKYTGGFKTIFGA GTRLFVKA	1575
V α	MXSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGGFKTIFGAGTRLFVKA	1576
	(X = any amino acid)	1577
α chain with WT signal peptide, C α (substituted)	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1578
α chain with alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPQSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFN LLMTLRLWSS	1579

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQ SFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAHLNRSQYISLLIRDSKLSDS ATYLCVAVNPKYTGFKTIFGAGTRLFVKANIQNPEPAVYQLKDPRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQD IFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFN LLMTLRLWSS	1580
CDR1 β	LGHNA	2571
CDR2 β	YSLEER	2572
CDR3 β	ASSQDVTSEWVDTIY	2573
V β without signal peptide (SignalP)	ELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMF VYSLEERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQDVTSEWVDTIYFGEQSWLTVV	2574
V β without signal peptide (IMGT)	ETGVTQTPRHLVMGMTNKKSLKCEQHLGHNAMYWYKQSAKKPLELMFVYSLE ERVENNSVPSRFSPECNSSHFLHLHTLQPEDSALYLCASSQDVTSEWVDTIYFGEQSWLTVV	2575
V β	MXCRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHN AMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGEQSWLTVV (X = any amino acid)	2576
		2577
β chain with WT signal peptide, (substituted) C β	MGCRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHN AMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGEQSWLTVVEDLRNVTTPPKVSLFEPK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNPVPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAW GRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVVRKNS	2578
β chain with alternative signal peptide, (substituted) C β	MACRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHN AMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGEQSWLTVVEDLRNVTTPPKVSLFEPK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNPVPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAW GRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVVRKNS	2579
β chain with alternative signal peptide, (substituted) C β	MHCRLCCAVLCLLGAGELVPMETGVTQTPRHLVMGMTNKKSLKCEQHLGHN AMYWYKQSAKKPLELMFVYSLEERVENNSVPSRFSPECNSSHFLHLHTLQ PEDSALYLCASSQDVTSEWVDTIYFGEQSWLTVVEDLRNVTTPPKVSLFEPK AEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSY CLSSRLRVSATFWHNPVPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAW GRADCGITSASYQQGVLSATILYEIILGKATLYAVLVSTLVVMAMVVRKNS	2580

[00352] In some embodiments, TCR058 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR058 interacts with the neoantigen in the context of HLA-C*01:02, as described in International Publication No. WO 2021/163477, incorporated herein by reference in its entirety.

Table 6BG. Amino acid sequences of TCR059.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASQS	1581

Description	Sequence	SEQ ID NO:
CDR2 α	VYSSGN	1582
CDR3 α	VVDDQTGANNLF	1583
V α without signal peptide (SignalP)	QRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVDDQTGANNLFFGTGTRLTVIP	1584
V α without signal peptide (IMGT)	RKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVDDQTGANNLFFGTGTRLTVIP	1585
V α	MXSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVDDQTGANNLFFGTGTRLTVIP (X = any amino acid)	1586
		1587
α chain with WT signal peptide, C α (substituted)	MISLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVDDQTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLMTLRLWSS	1588
α chain alternative peptide, (substituted) with signal C α	MASLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVDDQTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLMTLRLWSS	1589
α chain alternative peptide, (substituted) with signal C α	MHSLRVLLVILWLQLSWVWSQRKEVEQDPGPFNVPEGATVAFNCTYSNSASQSFFWYRQDCRKEPKLLMSVYSSGNEDGRFTAQLNRSQYISLLIRDSKLSDSATYLCVDDQTGANNLFFGTGTRLTVIPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLMTLRLWSS	1590
CDR1 β	MNHEY	2581
CDR2 β	SVGAGI	2582
CDR3 β	ASRNLGDTQY	2583
V β without signal peptide (SignalP)	GVTQTTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQTSVYFCASRNLGDTQYFGPGTRLTVL	2584
V β without signal peptide (IMGT)	NAGVTQTTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQTSVYFCASRNLGDTQYFGPGTRLTVL	2585
V β	MXIGLLCCAALSLLWAGPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQTSVYFCASRNLGDTQYFGPGTRLTVL (X = any amino acid)	2586
		2587
β chain with WT signal peptide, C β (substituted)	MSIGLLCCAALSLLWAGPVNAGVTQTTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQTSVYFCASRNLGDTQYFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSAFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2588

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MAIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQ TSVYFCASRNLDGTQYFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2589
β chain with alternative signal peptide, C β (substituted)	MHIGLLCCAALSLLWAGPVNAGVTQTPKFQVLKTGQSMTLQCAQDMNHEYMS WYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTEDFPLRLLSAAPSQ TSVYFCASRNLDGTQYFGPGTRLTVLEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2590

[00353] In some embodiments, TCR059 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR059 interacts with the neoantigen in the context of HLA-C*01:02, as described in International Publication No. WO 2021/163477, incorporated herein by reference in its entirety.

Table 6BH. Amino acid sequences of TCR060.

Description	Sequence	SEQ ID NO:
CDR1 α	TSINN	1591
CDR2 α	IRSNERE	1592
CDR3 α	ATDGETSGSRLT	1593
V α without signal peptide (SignalP)	QQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIR SNE REKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEG TQLTVNP	1594
V α without signal peptide (IMGT)	SQQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIR SN EREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGE GTQLTVNP	1595
V α	MXTLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINN LQ WYRQNSGRGLVHLILIR SNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNP (X = any amino acid)	1596
		1597
α chain with WT signal peptide, C α (substituted)	METLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINN LQ WYRQNSGRGLVHLILIR SNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDP RSQDSTLC LF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDI F KETNATYPSSDVPCDATLTEKSFETDMNLFQNL LVIVLRILL LK VAGFNLL MTLRLWSS	1598
α chain with alternative signal peptide, C α (substituted)	MATLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINN LQ WYRQNSGRGLVHLILIR SNEREKHSGRRLRVTLDTSKKSSSLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDP RSQDSTLC LF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQT SFTCQDI F KETNATYPSSDVPCDATLTEKSFETDMNLFQNL LVIVLRILL LK VAGFNLL MTLRLWSS	1599

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHTLLGVSLVILWLQLAVNSQQGEEDPQALSIQEGENATMNC SYKTSINNLO WYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSLLITASRAADTA SYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPRSQDSTLCLEF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1600
CDR1 β	DFQATT	2591
CDR2 β	SNEGSKA	2592
CDR3 β	SASRGATGQPQH	2593
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSASRGA TGQPQHFGDGTRLSIL	2594
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTSTLTVTSAHPEDSSFYICSASRGATGQP QHFGDGTRLSIL	2595
V β	MXLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSIL (X = any amino acid)	2596
		2597
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSILEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NS	2598
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSILEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NS	2599
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSTL TVTSAHPEDSSFYICSASRGATGQPQHFGDGTRLSILEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKRK NS	2600

[00354] In some embodiments, TCR060 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR060 interacts with the neoantigen in the context of an HLA-DPA1*01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

Table 6BI. Amino acid sequences of TCR061.

Description	Sequence	SEQ ID NO:
CDR1 α	SSNFYA	1601
CDR2 α	MTLNGDE	1602
CDR3 α	AFTTGNQFY	1603
V α w/o signal peptide (SignalP)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIP	1604
V α w/o signal peptide (IMGT)	ILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIP	1605
V α	MXKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIP (X = any amino acid)	1606
		1607
α chain w/WT signal peptide, C α (substituted)	MEKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPKSDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNL LMTLRLWSS	1608
α chain w/alternative signal peptide, C α (substituted)	MAKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPKSDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNL LMTLRLWSS	1609
α chain w/alternative signal peptide, C α (substituted)	MHKNPLAAPLLILWFHLDVSSILNVEQSPQSLHVQEGDSTNFTCSFPSSNFYALHWYRWETAKSPEALFVMTLNGDEKKKGRISATLNTKEGYSYLYIKGSQPEDSATYLC AFTTGNQFYFGTGTSLTVIPNIQNPEPAVYQLKDPKSDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRIILLKVAGFNL LMTLRLWSS	1610
CDR1 β	SGHDYL	2601
CDR2 β	FNNNVP	2602
CDR3 β	ASSSYGGYSNQPOH	2603
V β w/o signal peptide (SignalP)	GVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKIQPSEPRDSAVYFCASSSYGGYSNQPOHFGDGRLSIL	2604
V β w/o signal peptide (IMGT)	DAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKIQPSEPRDSAVYFCASSSYGGYSNQPOHFGDGRLSIL	2605
V β	MXSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKIQPSEPRDSAVYFCASSSYGGYSNQPOHFGDGRLSIL (X = any amino acid)	2606
		2607
β chain w/WT signal peptide, C β (substituted)	MGSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLFWYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFS AKMPNASFSTLKIQPSEPRDSAVYFCASSSYGGYSNQPOHFGDGRLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSAS YQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2608

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MASWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLF WYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFSKMPNASFSTLKIQPSEPR DSAVYFCASSSYGGYSNPQHFGDGTLSILEDLRNVTPPKVSLFEPKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2609
β chain w/alternative signal peptide, C β (substituted)	MHSWTLCCVSLCILVAKHTDAGVIQSPRHEVTEMGQEVTLRCKPISGHDYLF WYRQTMMRGLELLIYFNNNVPIDDSGMPEDRFSKMPNASFSTLKIQPSEPR DSAVYFCASSSYGGYSNPQHFGDGTLSILEDLRNVTPPKVSLFEPKAEI ANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLS SRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRA DCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2610

[00355] In some embodiments, TCR061 interacts with and/or is specific for tumor protein KRAS (KRAS). In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12C relative to the wild type KRAS sequence. In some embodiments, TCR061 interacts with the neoantigen in the context of HLA-DRB1*11 :01 as described in International Publication No. WO 2019/060349, incorporated herein by reference in its entirety.

Table 6BJ. Amino acid sequences of TCR062.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1611
CDR2 α	GYKTK	1612
CDR3 α	LVGDMDQAGTALI	1613
V α w/o signal peptide (SignalP)	KTQTPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTK VTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGKGT TSLVSS	1614
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYK TKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMDQAGTALIFGK GTTLSVSS	1615
V α	MXQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMDQAGTALIFGKGTTLSVSS	1616
	(X = any amino acid)	1617
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMDQAGTALIFGKGTTLSVSSNIQNPEPAVYQLKDPKSDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLLEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1618
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMDQAGTALIFGKGTTLSVSSNIQNPEPAVYQLKDPKSDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLLEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1619

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFPSQGRPFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDMQAGTALIFGKGTTLVSSNIQNPEPAVYQLKDP RSQDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1620
CDR1 β	SGHDT	2611
CDR2 β	YYEEEE	2612
CDR3 β	ASSLGEGRVDGYT	2613
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYYEEEE RQRGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGEGRVDGYTFG SGTRLTVV	2614
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYYEE EERQRGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGEGRVDGYT FGSGTRLTVV	2615
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSLGEGRVDGYTFGSGTRLTVV (X = any amino acid)	2616
		2617
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSLGEGRVDGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2618
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSLGEGRVDGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2619
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYYEEEEERQRGNFPDRFSGHQFPNYSSELNVNALLGD SALYLCASSLGEGRVDGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATI ILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2620

[00356] In some embodiments, TCR062 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR062 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BK. Amino acid sequences of TCR063.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1621

Description	Sequence	SEQ ID NO:
CDR2 α	GYKTK	1622
CDR3 α	LVGDMDQAGTALI	1623
V α w/o signal peptide (SignalP)	KTTPISMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSS	1624
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSS	1625
V α	MXQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSS	1626
	(X = any amino acid)	1627
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1628
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1629
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPSQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1630
CDR1 β	SGHDT	2621
CDR2 β	YEEEE	2622
CDR3 β	ASSLGRASNQPQH	2623
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQGRNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGRASNQPQHFGDGTLSIL	2624
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEERQGRNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGRASNQPQHFGDGTLSIL	2625
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQGRNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGRASNQPQHFGDGTLSIL	2626
	(X = any amino acid)	2627
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQGRNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGRASNQPQHFGDGTLSILEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2628

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYQQALGQGPFQFYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPHFGDGTLSILEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2629
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYQQALGQGPFQFYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGRASNQPHFGDGTLSILEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKKRNS	2630

[00357] In some embodiments, TCR063 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR063 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BL. Amino acid sequences of TCR064.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1631
CDR2 α	GYKTK	1632
CDR3 α	LVGDRDQAGTALI	1633
V α w/o signal peptide (SignalP)	KTTPQISMDSYEGQEVNITCSHNNIATNDYITWYQQFSPQGPRFIIQGYKTK VTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDRDQAGTALIFGKGT TLVSVS	1634
V α w/o signal peptide (IMGT)	LAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITWYQQFSPQGPRFIIQGYK TKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDRDQAGTALIFGK GTTLSVS	1635
V α	MXQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLSVS (X = any amino acid)	1636
		1637
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLSVSSNIQNPEPAVYQLKDPRSQDSTLCFLTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1638
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFSPQGPRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLSVSSNIQNPEPAVYQLKDPRSQDSTLCFLTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1639

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPI SMDSYEGQEVNITCSHNNIATNDYITW YQQFPSQGRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYY CLVGDRDQAGTALIFGKGTTLVSSNIQNPEPAVYQLKDPQSQDSTLCLFTD FDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKE TNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMT LRLWSS	1640
CDR1 β	SGHDT	2631
CDR2 β	YYEEEE	2632
CDR3 β	ASSFGQSSTYGYT	2633
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEE RQRGNFPDRFSGHQFPNYSELNVNALLGDSALYLCASSFGQSSTYGYTFG SGTRLTVV	2634
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEE EERQRGNFPDRFSGHQFPNYSELNVNALLGDSALYLCASSFGQSSTYGYT FGSGTRLTVV	2635
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSELNVNALLGD SALYLCASSFGQSSTYGYTFGSGTRLTVV (X = any amino acid)	2636
		2637
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSELNVNALLGD SALYLCASSFGQSSTYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATIILYEILLGKATLYAVLVSTLVVMAMVKRKN	2638
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSELNVNALLGD SALYLCASSFGQSSTYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATIILYEILLGKATLYAVLVSTLVVMAMVKRKN	2639
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTV WYQQALGQGPQFIFQYEEEEERQRGNFPDRFSGHQFPNYSELNVNALLGD SALYLCASSFGQSSTYGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYQQGVLSATIILYEILLGKATLYAVLVSTLVVMAMVKRKN	2640

[00358] In some embodiments, TCR064 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR064 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BM. Amino acid sequences of TCR065.

Description	Sequence	SEQ ID NO:
CDR1 α	NIATNDY	1641

Description	Sequence	SEQ ID NO:
CDR2 α	GYKTK	1642
CDR3 α	LVGDMDQAGTALI	1643
V α w/o signal peptide (SignalP)	KTTPISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPFRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSS	1644
V α w/o signal peptide (IMGT)	LAKTTQPIISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPFRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSS	1645
V α	MXQVARVIVFLTLSTLSLAKTTQPIISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPFRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSS	1646
	(X = any amino acid)	1647
α chain w/WT signal peptide, C α (substituted)	MRQVARVIVFLTLSTLSLAKTTQPIISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPFRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1648
α chain w/alternative signal peptide, C α (substituted)	MAQVARVIVFLTLSTLSLAKTTQPIISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPFRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1649
α chain w/alternative signal peptide, C α (substituted)	MHQVARVIVFLTLSTLSLAKTTQPIISMDSYEGQEVNITCSHNNIATNDYITWYQQFPSQGPFRFIIQGYKTKVTNEVASLFIPADRKSSTLSLPRVSLSDTAVYYCLVGDMQAGTALIFGKGTLSVSSNIQNPEPAVYQLKDPQSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1650
CDR1 β	SGHDT	2641
CDR2 β	YEEEE	2642
CDR3 β	ASSLGQTNNGYT	2643
V β w/o signal peptide (SignalP)	GVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGQTNNGYTFGSGTRLTVV	2644
V β w/o signal peptide (IMGT)	DAGVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEERQGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGQTNNGYTFGSGTRLTVV	2645
V β	MXPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGQTNNGYTFGSGTRLTVV	2646
	(X = any amino acid)	2647
β chain w/WT signal peptide, C β (substituted)	MGPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQVTLRCSPKSGHDTVSWYQQALGQGPQFIFQYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLGDSALYLCASSLGQTNNGYTFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2648

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MAPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYWYQQALGQGQPFIFQYYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGQTNYGTYFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2649
β chain w/alternative signal peptide, C β (substituted)	MHPGLLCWALLCLLGAGLVDAGVTQSPTHLIKTRGQQVTLRCSPKSGHDTVSYWYQQALGQGQPFIFQYYEEEEERQGNFPDRFSGHQFPNYSSELNVNALLLGD SALYLCASSLGQTNYGTYFGSGTRLTVVEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2650

[00359] In some embodiments, TCR065 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR065 interacts with the neoantigen in the context of HLA-Cw*08:02 as described in International Publication No. WO 2017/048593, incorporated herein by reference in its entirety.

Table 6BN. Amino acid sequences of TCR066.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1651
CDR2 α	IYSNGD	1652
CDR3 α	AAAMDSSYKLI	1653
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAAAMDSSYKLIFGSGTRLLVRP	1654
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAAAMDSSYKLIFGSGTRLLVRP	1655
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAAAMDSSYKLIFGSGTRLLVRP	1656
	(X = any amino acid)	1657
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAAAMDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPQRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1658
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAAAMDSSYKLIFGSGTRLLVRPNIQNPEPAVYQLKDPQRSQDSTLCLETFDSDQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1659

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQ SFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSD SATYLCAAAMDSSYKLIFGSGTRLLVRENIQNPEPAVYQLKDPQRSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNL LMTLRWSS	1660
CDR1 β	WSHSY	2651
CDR2 β	SAAADI	2652
CDR3 β	ASSDPGTEAF	2653
V β w/o signal peptide (SignalP)	GITQSPRYKITETGRQVTLMCHQTSWHSYMFWYRQDLGHGLRLIYSSAAADI TDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSDPGTEAFFGQGT RLTVV	2654
V β w/o signal peptide (IMGT)	DAGITQSPRYKITETGRQVTLMCHQTSWHSYMFWYRQDLGHGLRLIYSSAAA DITDKGEVPDGYVVSRSKTENFPLTLESATRSQTSVYFCASSDPGTEAFFGQ GTRLTVV	2655
V β	MXTRLFFYVALCLLWAGHRDAGITQSPRYKITETGRQVTLMCHQTSWHSYMF WYRQDLGHGLRLIYSSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVV (X = any amino acid)	2656
		2657
β chain w/WT signal peptide, C β (substituted)	MGTRLFFYVALCLLWAGHRDAGITQSPRYKITETGRQVTLMCHQTSWHSYMF WYRQDLGHGLRLIYSSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVVEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2658
β chain w/alternative signal peptide, C β (substituted)	MATRLFFYVALCLLWAGHRDAGITQSPRYKITETGRQVTLMCHQTSWHSYMF WYRQDLGHGLRLIYSSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVVEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2659
β chain w/alternative signal peptide, C β (substituted)	MHTRLFFYVALCLLWAGHRDAGITQSPRYKITETGRQVTLMCHQTSWHSYMF WYRQDLGHGLRLIYSSAAADITDKGEVPDGYVVSRSKTENFPLTLESATRSQ TSVYFCASSDPGTEAFFGQGTRLTVVEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2660

[00360] In some embodiments, TCR066 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12D relative to the wild type KRAS sequence. In some embodiments, TCR066 interacts with the neoantigen in the context of HLA-C*08:02 as described in International Publication No. WO 2018/026691, incorporated herein by reference in its entirety.

Table 6BO. Amino acid sequences of TCR067.

Description	Sequence	SEQ ID NO:
CDR1 α	TIYSNPF	1661

Description	Sequence	SEQ ID NO:
CDR2 α	SFTDNKR	1662
CDR3 α	ALRGNAGAKLT	1663
V α w/o signal peptide (SignalP)	DGDSVTQTEGLVTLTEGLPVMLNCTYQTIYSNPFLFWYVQHLNESPRLLLSKSF FTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALRGNAGAKLTF GGGTRLTVRPD	1664
V α w/o signal peptide (IMGT)	GDSVTQTEGLVTLTEGLPVMLNCTYQTIYSNPFLFWYVQHLNESPRLLLSKSF TDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALRGNAGAKLTFG GGTRLTVRPD	1665
V α	MXPVTCSVLVLLLMLRRSNGDGDSVTQTEGLVTLTEGLPVMLNCTYQTIYSN PFLFWYVQHLNESPRLLLSKSF TDNKRTEHQGFHATLHKSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPD (X = any amino acid)	1666
		1667
α chain w/WT signal peptide, C α (substituted)	MRPVTCSVLVLLLMLRRSNGDGDSVTQTEGLVTLTEGLPVMLNCTYQTIYSN PFLFWYVQHLNESPRLLLSKSF TDNKRTEHQGFHATLHKSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPDIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVSMGLRIILLKVAGF NLLMTLRLWSS	1668
α chain w/alternative signal peptide, C α (substituted)	MAPVTCSVLVLLLMLRRSNGDGDSVTQTEGLVTLTEGLPVMLNCTYQTIYSN PFLFWYVQHLNESPRLLLSKSF TDNKRTEHQGFHATLHKSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPDIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVSMGLRIILLKVAGF NLLMTLRLWSS	1669
α chain w/alternative signal peptide, C α (substituted)	MHPVTCSVLVLLLMLRRSNGDGDSVTQTEGLVTLTEGLPVMLNCTYQTIYSN PFLFWYVQHLNESPRLLLSKSF TDNKRTEHQGFHATLHKSSSSFHLQKSSAQL SDSALYYCALRGNAGAKLTFGGGTRLTVRPDIQNPEPAVYQLKDPQSQDSTL CLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQ DIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVSMGLRIILLKVAGF NLLMTLRLWSS	1670
CDR1 β	LGHDT	2661
CDR2 β	YNNKQL	2662
CDR3 β	ASSSRDWSAETLY	2663
V β w/o signal peptide (SignalP)	AVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNKQL IVNETVPRRFSPQSSDKAHLNLRIKSVEPEDSAVYLCASSSRDWSAETLYFG SGTRLTVL	2664
V β w/o signal peptide (IMGT)	ETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNK QLIVNETVPRRFSPQSSDKAHLNLRIKSVEPEDSAVYLCASSSRDWSAETLY FGSGTRLTVL	2665
V β	MXCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVL (X = any amino acid)	2666
		2667
β chain w/WT signal peptide, C β (substituted)	MGCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRIKSVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEPSKAEIAN KQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYCYLSSR LRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADC GITSASYHQVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2668

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MACRLLSVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRISVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2669
β chain w/alternative signal peptide, C β (substituted)	MHCRLLSVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFSPQSSDKAHLNLRISVEPED SAVYLCASSSRDWSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEPKAEIAN KQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKESNYSYCLSSR LRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADC GITSASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2670

[00361] In some embodiments, TCR067 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR067 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BP. Amino acid sequences of TCR068.

Description	Sequence	SEQ ID NO:
CDR1 α	DPNSYY	1671
CDR2 α	VFSSTEI	1672
CDR3 α	AVSGGTNSAGNKLT	1673
V α w/o signal peptide (SignalP)	EQVEQRPPHLSVREGDSAVITCTYTDPNSSYFFWYKQEPGASLQLLMKVFSS TEINEGQGFTVLLNKKDKRLSLNLTAHPGDSAAYFCAVSGGTNSAGNKLT FGIGTRVLVRP	1674
V α w/o signal peptide (IMGT)	GEQVEQRPPHLSVREGDSAVITCTYTDPNSSYFFWYKQEPGASLQLLMKVFS STEINEGQGFTVLLNKKDKRLSLNLTAHPGDSAAYFCAVSGGTNSAGNKLT FGIGTRVLVRP	1675
V α	MXTVTGPLFLCFWLQNLNCSVRGEQVEQRPPHLSVREGDSAVITCTYTDPNSSY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTAHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRP (X = any amino acid)	1676
		1677
α chain w/WT signal peptide, C α (substituted)	MXTVTGPLFLCFWLQNLNCSVRGEQVEQRPPHLSVREGDSAVITCTYTDPNSSY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTAHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRPDIQNPEPAVYQLKDPKSDS TLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPDATLTEKSFETDMNLNFQNLVSMGLRILLKVA GFNLLMTLRLWSS	1678

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MATVTGPLFLCFWLQNLNCSRGEQVEQRPPLSVREGDSAVITCTYTDPN SY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTAHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRPDIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRILLKVA GFNLLMTLRLWSS	1679
α chain w/alternative signal peptide, C α (substituted)	MHTVTGPLFLCFWLQNLNCSRGEQVEQRPPLSVREGDSAVITCTYTDPN SY YFFWYKQEPGASLQLLMKVFSSTEINEGQGFTVLLNKKDKRLSLNLTAHPG DSAAYFCAVSGGTNSAGNKLTFGIGTRVLVRPDIQNPEPAVYQLKDPRSQDS TLCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFT CQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRILLKVA GFNLLMTLRLWSS	1680
CDR1 β	LGHDT	2671
CDR2 β	YNNKQL	2672
CDR3 β	ASSRDWGP AEQF	2673
V β w/o signal peptide (SignalP)	AVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNKQL IVNETVPRRFPQSSDKAHLNLRKSV EPEDSAVYLCASSRDWGP AEQFFGP GTRLTVL	2674
V β w/o signal peptide (IMGT)	ETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMYWYKQDSKKLLKIMFSYNNK QLIVNETVPRRFPQSSDKAHLNLRKSV EPEDSAVYLCASSRDWGP AEQFF GPGTRLTVL	2675
V β	MXCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFPQSSDKAHLNLRKSV EPED SAVYLCASSRDWGP AEQFFGP GTRLTVL (X = any amino acid)	2676
		2677
β chain w/WT signal peptide, C β (substituted)	MGCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFPQSSDKAHLNLRKSV EPED SAVYLCASSRDWGP AEQFFGP GTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCG ITSASYHQVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKNS	2678
β chain w/alternative signal peptide, C β (substituted)	MACRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFPQSSDKAHLNLRKSV EPED SAVYLCASSRDWGP AEQFFGP GTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCG ITSASYHQVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKNS	2679
β chain w/alternative signal peptide, C β (substituted)	MHCRLLSCVAFCLLGIGPLETAVFQTPNYHVTQVGNEVSFNCKQTLGHDTMY WYKQDSKKLLKIMFSYNNKQLIVNETVPRRFPQSSDKAHLNLRKSV EPED SAVYLCASSRDWGP AEQFFGP GTRLTVLEDLRNVT PPKVSLFEP SKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPV TQNISAEAWGRADCG ITSASYHQVLSATILYEILLGKATLYAVLVSGVLVLMAMVKKNS	2680

[00362] In some embodiments, TCR068 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR068 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BQ. Amino acid sequences of TCR069.

Description	Sequence	SEQ ID NO:
CDR1 α	NDMFDY	1681
CDR2 α	VRSNVDK	1682
CDR3 α	AAGDSGGSNYKLT	1683
V α w/o signal peptide (SignalP)	QQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWKYPDNSPTLLISVRSNVDKREDGRFTVFLNKGKHFSLHITASQPEDTAVYLCAAGDSGGSNYKLTFGKGTLLTVTP	1684
V α w/o signal peptide (IMGT)	QQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWKYPDNSPTLLISVRSNVDKREDGRFTVFLNKGKHFSLHITASQPEDTAVYLCAAGDSGGSNYKLTFGKGTLLTVTP	1685
V α	MXGFLKALLVLCLRPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWKYPDNSPTLLISVRSNVDKREDGRFTVFLNKGKHFSLHITASQPEDTAVYLCAAGDSGGSNYKLTFGKGTLLTVTP (X = any amino acid)	1686
		1687
α chain w/WT signal peptide, C α (substituted)	MTGFLKALLVLCLRPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWKYPDNSPTLLISVRSNVDKREDGRFTVFLNKGKHFSLHITASQPEDTAVYLCAAGDSGGSNYKLTFGKGTLLTVTPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRILL LKVAGFNLLMTLRLWSS	1688
α chain w/alternative signal peptide, C α (substituted)	MAGFLKALLVLCLRPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWKYPDNSPTLLISVRSNVDKREDGRFTVFLNKGKHFSLHITASQPEDTAVYLCAAGDSGGSNYKLTFGKGTLLTVTPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRILL LKVAGFNLLMTLRLWSS	1689
α chain w/alternative signal peptide, C α (substituted)	MHGFLKALLVLCLRPEWIKSQQKTGGQQVKQSSPSLTVQEGGILILNCDYENDMFDYFAWKYPDNSPTLLISVRSNVDKREDGRFTVFLNKGKHFSLHITASQPEDTAVYLCAAGDSGGSNYKLTFGKGTLLTVTPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL SVMGLRILL LKVAGFNLLMTLRLWSS	1690
CDR1 β	NSHNY	2681
CDR2 β	SYGAGN	2682
CDR3 β	ASASWGGYAEQF	2683
V β w/o signal peptide (SignalP)	AVTQSPRNKVTVTGGNVTLSCRQTNSHNYMYWYRQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTSLYFCASASWGGYAEQFFGPGTRLTVL	2684
V β w/o signal peptide (IMGT)	EAAVTQSPRNKVTVTGGNVTLSCRQTNSHNYMYWYRQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTSLYFCASASWGGYAEQFFGPGTRLTVL	2685
V β	MXSRLFLVLSLLCTKHMEAAVTQSPRNKVTVTGGNVTLSCRQTNSHNYMYWYRQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTSLYFCASASWGGYAEQFFGPGTRLTVL (X = any amino acid)	2686
		2687

Description	Sequence	SEQ ID NO:
β chain w/WT signal peptide, C β (substituted)	MGSRLFLVLSLLCTKHMEAAVTQSPRNKVTVTGGNVTLSRQTNSHNYMYWY RQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTS LYFCASASWGGYAEQFFGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2688
β chain w/alternative signal peptide, C β (substituted)	MASRLFLVLSLLCTKHMEAAVTQSPRNKVTVTGGNVTLSRQTNSHNYMYWY RQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTS LYFCASASWGGYAEQFFGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2689
β chain w/alternative signal peptide, C β (substituted)	MHSRLFLVLSLLCTKHMEAAVTQSPRNKVTVTGGNVTLSRQTNSHNYMYWY RQDTGHGLRLIHYSYGAGNLQIGDVPDGYKATRTTQEDFFLLLELASPSQTS LYFCASASWGGYAEQFFGPGTRLTVLEDLRNVTTPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVSTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYHQGVLSATILYEILLGKATLYAVLVSGLVLMAMVKKKNS	2690

[00363] In some embodiments, TCR069 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR069 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BR. Amino acid sequences of TCR070.

Description	Sequence	SEQ ID NO:
CDR1 α	TTMRS	1691
CDR2 α	LASGT	1692
CDR3 α	AADSSNTGYQNFY	1693
V α w/o signal peptide (SignalP)	DQVEQSPSALSHEGTDALRCNFTTTMRSVQWFRQNSRGLISLFYLASGT KENGRLKSAFDSKERRYSTLHIRDAQLED SGTYFCAADSSNTGYQNFYFGKG TSLTVIP	1694
V α w/o signal peptide (IMGT)	GDQVEQSPSALSHEGTDALRCNFTTTMRSVQWFRQNSRGLISLFYLASG TKENGRLKSAFDSKERRYSTLHIRDAQLED SGTYFCAADSSNTGYQNFYFGK GTSLTVIP	1695
V α	MXRNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASG TKENGRLKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTGYQNFYFGKG TSLTVIP (X = any amino acid)	1696
		1697

Description	Sequence	SEQ ID NO:
α chain w/WT signal peptide, C α (substituted)	MQRNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGTEKNGRLKSAFDSKERRYSTLHIRDAQLEDSTG TYFCAADSSNTGYQNFYFGKGTSLTVIPNIQNPEPAVYQLKDPQSQDSTLCL FTDDFSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS	1698
α chain w/alternative signal peptide, C α (substituted)	MARNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGTEKNGRLKSAFDSKERRYSTLHIRDAQLEDSTG TYFCAADSSNTGYQNFYFGKGTSLTVIPNIQNPEPAVYQLKDPQSQDSTLCL FTDDFSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS	1699
α chain w/alternative signal peptide, C α (substituted)	MHRNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGTEKNGRLKSAFDSKERRYSTLHIRDAQLEDSTG TYFCAADSSNTGYQNFYFGKGTSLTVIPNIQNPEPAVYQLKDPQSQDSTLCL FTDDFSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS	1700
CDR1 β	SGHLS	2691
CDR2 β	HYDKME	2692
CDR3 β	ASSLTDPLDSDYT	2693
V β w/o signal peptide (SignalP)	NSGVVQSPRYIIKGKERSILKCIPISGHLSVAWYQQTQGQELKFFIQHYDK MERDKNLPSRFSVQQFDDYHSEMMSALELEDSAVYFCASSLTDPLDSDYT FSGSTRLLVI	2694
V β w/o signal peptide (IMGT)	SGVVQSPRYIIKGKERSILKCIPISGHLSVAWYQQTQGQELKFFIQHYDKM ERDKNLPSRFSVQQFDDYHSEMMSALELEDSAVYFCASSLTDPLDSDYTF GSGTRLLVI	2695
V β	MXNTAFDPDPAWNTTLLSWVALFLLGTSSANSQGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGQELKFFIQHYDKMERDKNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPLDSDYTFGSGTRLLVI (X = any amino acid)	2696
		2697
β chain w/WT signal peptide, C β (substituted)	MSNTAFDPDPAWNTTLLSWVALFLLGTSSANSQGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGQELKFFIQHYDKMERDKNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPLDSDYTFGSGTRLLVIEDLRNVTTPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVK RKNS	2698
β chain w/alternative signal peptide, C β (substituted)	MANTAFDPDPAWNTTLLSWVALFLLGTSSANSQGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGQELKFFIQHYDKMERDKNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPLDSDYTFGSGTRLLVIEDLRNVTTPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVK RKNS	2699
β chain w/alternative signal peptide, C β (substituted)	MHNTAFDPDPAWNTTLLSWVALFLLGTSSANSQGVVQSPRYIIKGKERSILKC IPISGHLSVAWYQQTQGQELKFFIQHYDKMERDKNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDPLDSDYTFGSGTRLLVIEDLRNVTTPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVK RKNS	2700

[00364] In some embodiments, TCR070 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some embodiments, TCR070 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BS. Amino acid sequences of TCR071.

Description	Sequence	SEQ ID NO:
CDR1 α	TTMRS	1701
CDR2 α	LASGT	1702
CDR3 α	AADSSNTZYQNFY (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1703
V α w/o signal peptide (SignalP)	DQVEQSPSALSHEGTDALRCNFTTTMRSVQWFRQNSRGLISLFYLASGT KENGRLKSAFDSKERRYSTLHIRDAQLEDSTYFCAADSSNTZYQNFYFGKG TSLTVIP (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1704
V α w/o signal peptide (IMGT)	GDQVEQSPSALSHEGTDALRCNFTTTMRSVQWFRQNSRGLISLFYLASG TKENGRLKSAFDSKERRYSTLHIRDAQLEDSTYFCAADSSNTZYQNFYFGK GTSLTVIP (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1705
V α	MXRNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGT KENGRLKSAFDSKERRYSTLHIRDAQLEDSTYFCAADSSNTZYQNFYFGKG TSLTVIP (X = any amino acid) (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1706
		1707
α chain w/WT signal peptide, C α (substituted)	MQRNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGT KENGRLKSAFDSKERRYSTLHIRDAQLEDSTYFCAADSSNTZYQNFYFGKG TSLTVIP NIQNPEPAVYQLKDP RSQDSTLCL FTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNL SVMGLRI LLKVGAFNL LMTLRLWSS (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1708

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MARNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGTEKENGRLKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTZYQNFYFGKGTSLTVIPNIQNPEPAVYQLKDP RSQDSTLCL FTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCD ATLTEKSFETDMNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1709
α chain w/alternative signal peptide, C α (substituted)	MHRNLGAVLGILWVQICWVRGDQVEQSPSALSHEGTDALRCNFTTTMRSV QWFRQNSRGLISLFYLASGTEKENGRLKSAFDSKERRYSTLHIRDAQLED SG TYFCAADSSNTZYQNFYFGKGTSLTVIPNIQNPEPAVYQLKDP RSQDSTLCL FTDFDSQINVPKTMESGTFITDKTVLDMKAMDSKNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCD ATLTEKSFETDMNLFQNL SVMGLRI LLLKVAGFNL LMTLRLWSS (Z = alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, tryptophan, tyrosine, or valine)	1710
CDR1 β	SGHLS	2701
CDR2 β	HYDKME	2702
CDR3 β	CASSLTDP L DSDYTF	2703
V β w/o signal peptide (SignalP)	NSGVVQSPRYIIKGK GERSILKCIPI SGHLSVAWYQQTQGQELKFFIQHYDK MERDKGNLPSRFSVQQFDDYHSEMNMSALELEDSAVYFCASSLTDP L DSDYT FGSGTRLLVI	2704
V β w/o signal peptide (IMGT)	SGVVQSPRYIIKGK GERSILKCIPI SGHLSVAWYQQTQGQELKFFIQHYDKM ERDKGNLPSRFSVQQFDDYHSEMNMSALELEDSAVYFCASSLTDP L DSDYTF GSGTRLLVI	2705
V β	MXNTAFDPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDP L DSDYTFGSGTRLLVI (X = any amino acid)	2706
		2707
β chain w/WT signal peptide, C β (substituted)	MSNTAFDPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDP L DSDYTFGSGTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVK RKNS	2708
β chain w/alternative signal peptide, C β (substituted)	MANTAFDPDPAWNTTLLSWVALFLLGTSSANS GVVQSPRYIIKGK GERSILKC IPI SGHLSVAWYQQTQGQELKFFIQHYDKMERDKGNLPSRFSVQQFDDYHSE MNMSALELEDSAVYFCASSLTDP L DSDYTFGSGTRLLVIEDLRNVT PPKVSL FEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVSTDPQAYKE SNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVK RKNS	2709
		2710

[00365] In some embodiments, TCR071 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid changes G12D and/or G12V relative to the wild type KRAS sequence. In some

embodiments, TCR071 interacts with the neoantigen in the context of HLA-A11, as described in International Publication No. WO 2016/085904, incorporated herein by reference in its entirety.

Table 6BT. Amino acid sequences of TCR072.

Description	Sequence	SEQ ID NO:
CDR1 α	DRGSQS	1711
CDR2 α	IYSNGD	1712
CDR3 α	AVEGAGSYQLT	1713
V α w/o signal peptide (SignalP)	QQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIP	1714
V α w/o signal peptide (IMGT)	QKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIP	1715
V α	MXSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIP	1716
	(X = any amino acid)	1717
α chain w/WT signal peptide, C α (substituted)	MKSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLMTLRLWSS	1718
α chain w/alternative signal peptide, C α (substituted)	MASLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLMTLRLWSS	1719
α chain w/alternative signal peptide, C α (substituted)	MHSLRVLLVILWLQLSWVWSQQKEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMFIYSNGDKEDGRFTAQLNKASQYVSLIRDSQPSDSATYLCAVEGAGSYQLTFGKGTKLSVIPNIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKVGAFNLMTLRLWSS	1720
CDR1 β	DFQATT	2711
CDR2 β	SNEGSKA	2712
CDR3 β	SASNRLAVNEQF	2713
V β w/o signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASASNRLAVNEQFFGPGTRLTVL	2714
V β w/o signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASASNRLAVNEQFFGPGTRLTVL	2715
V β	MXLLLLLLGPGISLLLPGLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSLTVTSAHPEDSSFYICASASNRLAVNEQFFGPGTRLTVL	2716
	(X = any amino acid)	2717

Description	Sequence	SEQ ID NO:
β chain w/WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICASNRLAVNEQFFGPGTRLTVLEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2718
β chain w/alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICASNRLAVNEQFFGPGTRLTVLEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2719
β chain w/alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSL TVTSAHPEDSSFYICASNRLAVNEQFFGPGTRLTVLEDLRNVTPPKVSLFE PSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESN YSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISA EAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NS	2720

[00366] In some embodiments, TCR072 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12R relative to the wild type KRAS sequence. In some embodiments, TCR072 interacts with the neoantigen in the context of HLA-DQA1*05:05:HLA-DQB1*03:01 heterodimer as described in International Publication No. WO 2020/154275, incorporated herein by reference in its entirety.

Table 6BU. Amino acid sequences of TCR073.

Description	Sequence	SEQ ID NO:
CDR1 α	NSMFDY	1721
CDR2 α	ISISSIKDK	1722
CDR3 α	AASGNTGTASKLT	1723
V α w/o signal peptide (SignalP)	QQKNDDQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFL ISISSIKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAASGNTGT ASKLTFTGTGTRLQVTL	1724
V α w/o signal peptide (IMGT)	DQQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISS IKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAASGNTGTASKLT FTGTGTRLQVTL	1725
V α	MXMLLGASVLILWLQPDWVNSQQKNDDQVKQNSPSLSVQEGRISILNCDYT NSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIV PSQPGDSAVYFCAASGNTGTASKLTFTGTGTRLQVTL (X = any amino acid)	1726
		1727

Description	Sequence	SEQ ID NO:
α chain w/WT signal peptide, C α (substituted)	MAMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAASGNTGTASKLTFGTGTRLQVTLNIQNPEPAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILL LKVAGFNLLMTLRLWSS	1728
α chain w/alternative signal peptide, C α (substituted)	MHMLLGASVLILWLQPDWVNSQQKNDDQQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISSIKDKNEDGRFTVFLNKS AKHLSLHIVPSQPGDSAVYFCAASGNTGTASKLTFGTGTRLQVTLNIQNPEPAVYQLKDP RSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILL LKVAGFNLLMTLRLWSS	1729 1730
CDR1 β	LNHDA	2721
CDR2 β	SQIVND	2722
CDR3 β	ASSNQLVTGGYGYT	2723
V β w/o signal peptide (SignalP)	GITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLVTGGYGYTFGSGTRLTVV	2724
V β w/o signal peptide (IMGT)	DGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLVTGGYGYTFGSGTRLTVV	2725
V β	MXNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLVTGGYGYTFGSGTRLTVV (X = any amino acid)	2726 2727
β chain w/WT signal peptide, C β (substituted)	MSNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLVTGGYGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2728
β chain w/alternative signal peptide, C β (substituted)	MANQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLVTGGYGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2729
β chain w/alternative signal peptide, C β (substituted)	MHNQVLCCVVL CFLGANTVDGGITQSPKYLFRKEGQNVTLSC EQNLNHDAMYWYRQDPGQGLRLIYYSQIVNDFQKGDIAEGYSVSREKKESFPLTVTSAQKNPTAFYLCASSNQLVTGGYGYTFGSGTRLTVVEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2730

[00367] In some embodiments, TCR073 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12R relative to the wild type KRAS sequence. In some embodiments, TCR073 interacts with the neoantigen in the context of HLA-DRB5*01:HLA-DRA*01:01 heterodimer as described in International Publication No. WO 2020/154275, incorporated herein

by reference in its entirety.

Table 6BV. Amino acid sequences of TCR074.

Description	Sequence	SEQ ID NO:
CDR1 α	TIYSNAF	1731
CDR2 α	SSTDNKR	1732
CDR3 α	ALSEGGNYKYV	1733
V α w/o signal peptide (SignalP)	DGDSVTQKEGLVTLTEGLPVMNLCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIA	1734
V α w/o signal peptide (IMGT)	GDSVTQKEGLVTLTEGLPVMNLCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIA	1735
V α	MXPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMNLCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIA (X = any amino acid)	1736
		1737
α chain w/WT signal peptide, C α (substituted)	MRPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMNLCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIANIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1738
α chain w/alternative signal peptide, C α (substituted)	MAPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMNLCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIANIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1739
α chain w/alternative signal peptide, C α (substituted)	MHPGTCSVLVLLMLRRSNGDGDSVTQKEGLVTLTEGLPVMNLCTYQTIYSNAFLFWYVHYLNESPRLLKSSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIANIQNPEPAVYQLKDPQSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNLFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1740
CDR1 β	NSQYPW	2731
CDR2 β	LRSPGD	2732
CDR3 β	TCSARHSAETLY	2733
V β w/o signal peptide (SignalP)	DPTVTLLLEQNPRWRLVPRGQAVNLRICILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRITLYCTCSARHSAETLYFGSGTRLTVL	2734
V β w/o signal peptide (IMGT)	VTLLLEQNPRWRLVPRGQAVNLRICILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRITLYCTCSARHSAETLYFGSGTRLTVL	2735
V β	MXQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRICILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRITLYCTCSARHSAETLYFGSGTRLTVL (X = any amino acid)	2736
		2737

Description	Sequence	SEQ ID NO:
β chain w/WT signal peptide, C β (substituted)	MWQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRICILKNSQYP WMSWYQQDLQKQLQWLFTLRSPGDKEVKS LPGA DYLA TRVTD TELRLQVANM SQGRTLYCTCSARHSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2738
β chain w/alternative signal peptide, C β (substituted)	MAQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRICILKNSQYP WMSWYQQDLQKQLQWLFTLRSPGDKEVKS LPGA DYLA TRVTD TELRLQVANM SQGRTLYCTCSARHSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2739
β chain w/alternative signal peptide, C β (substituted)	MHQFCILCLCVLMASVATDPTVTLLLEQNPRWRLVPRGQAVNLRICILKNSQYP WMSWYQQDLQKQLQWLFTLRSPGDKEVKS LPGA DYLA TRVTD TELRLQVANM SQGRTLYCTCSARHSAETLYFGSGTRLTVLEDLRNVTPPKVSLFEP SKAEIA NKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSS RLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2740

[00368] In some embodiments, TCR074 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR074 interacts with the neoantigen in the context of HLA-A3 heterodimer as described in International Publication No. WO 2020/086827, incorporated herein by reference in its entirety.

Table 6BW. Amino acid sequences of TCR075.

Description	Sequence	SEQ ID NO:
CDR1 α	TSDPSYG	1741
CDR2 α	QGSYDQQN	1742
CDR3 α	AMRGASQGGSEKLV	1743
V α w/o signal peptide (SignalP)	QKITQTQPGMFVQEKEAVTLDCTYDTS DPSYGLFWYKQPSSGEMIFLIYQGS YDQQNATEGRYSLNFQKARKSANLVISASQLGDSAMYFCAMRGASQGGSEKL VFGKGTKLTVNP	1744
V α w/o signal peptide (IMGT)	AQKITQTQPGMFVQEKEAVTLDCTYDTS DPSYGLFWYKQPSSGEMIFLIYQG SYDQQNATEGRYSLNFQKARKSANLVISASQLGDSAMYFCAMRGASQGGSEK LVFGKGTKLTVNP	1745
V α	MXLSSLLKVVTASLWLGPGIAQKITQTQPGMFVQEKEAVTLDCTYDTS DPSY GLFWYKQPSSGEMIFLIYQGSYDQQNATEGRYSLNFQKARKSANLVISASQL GDSAMYFCAMRGASQGGSEKLVFGKGTKLTVNP	1746
	(X = any amino acid)	1747
α chain w/WT signal peptide, C α (substituted)	MSLSSLLKVVTASLWLGPGIAQKITQTQPGMFVQEKEAVTLDCTYDTS DPSY GLFWYKQPSSGEMIFLIYQGSYDQQNATEGRYSLNFQKARKSANLVISASQL GDSAMYFCAMRGASQGGSEKLVFGKGTKLTVNPNIQNPEPAVYQLKDP RSQD STLCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSF TCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLIVLRI LLLKV AGFNLLMTLRLWSS	1748

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MALSSLLKVVVTASLWLGPGIAQKITQTQPGMFVQEKEAVTLDCTYDTSDFSYGLFWYKQPSSGEMIFLIYQGSYDQQNATEGRYSLNFQKARKSANLVISASQLGDSAMYFCAMRGASQGGSEKLVFGKGTCLTVNPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1749
α chain w/alternative signal peptide, C α (substituted)	MHLSSLLKVVVTASLWLGPGIAQKITQTQPGMFVQEKEAVTLDCTYDTSDFSYGLFWYKQPSSGEMIFLIYQGSYDQQNATEGRYSLNFQKARKSANLVISASQLGDSAMYFCAMRGASQGGSEKLVFGKGTCLTVNPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1750
CDR1 β	SGHRS	2741
CDR2 β	YFSETQ	2742
CDR3 β	ASSLTSGGFDEQF	2743
V β w/o signal peptide (SignalP)	GVTQTTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEYFSETQRNKGNFGRFSGRQFNSRSEMNVSTLELGDSALYLCASSLTSGGFDEQFFGPGTRLTVL	2744
V β w/o signal peptide (IMGT)	KAGVTQTTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEYFSETQRNKGNFGRFSGRQFNSRSEMNVSTLELGDSALYLCASSLTSGGFDEQFFGPGTRLTVL	2745
V β	MXSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEYFSETQRNKGNFGRFSGRQFNSRSEMNVSTLELGDSALYLCASSLTSGGFDEQFFGPGTRLTVL (X = any amino acid)	2746
		2747
β chain w/WT signal peptide, C β (substituted)	MGSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEYFSETQRNKGNFGRFSGRQFNSRSEMNVSTLELGDSALYLCASSLTSGGFDEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2748
β chain w/alternative signal peptide, C β (substituted)	MASRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEYFSETQRNKGNFGRFSGRQFNSRSEMNVSTLELGDSALYLCASSLTSGGFDEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2749
β chain w/alternative signal peptide, C β (substituted)	MHSRLLCWVLLCLLGAGPVKAGVTQTTPRYLIKTRGQQVTLSCSPI SGHRSVSWYQQTPGQGLQFLFEYFSETQRNKGNFGRFSGRQFNSRSEMNVSTLELGDSALYLCASSLTSGGFDEQFFGPGTRLTVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVVRKNS	2750

[00369] In some embodiments, TCR075 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR075 interacts with the neoantigen in the context of HLA-A*11:01, as described in International Publication No. WO 2019/112941, incorporated herein by reference in its entirety.

Table 6BX. Amino acid sequences of TCR076.

Description	Sequence	SEQ ID NO:
CDR1 α	DSASNY	1751
CDR2 α	IRSNVGE	1752
CDR3 α	AASTGGGNKLT	1753
V α w/o signal peptide (SignalP)	ENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFTGTQQLKVEL	1754
V α w/o signal peptide (IMGT)	GENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFTGTQQLKVEL	1755
V α	MXSIRAVFIFLWLQDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFTGTQQLKVEL	1756
	(X = any amino acid)	1757
α chain w/WT signal peptide, C α (substituted)	MTSIRAVFIFLWLQDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFTGTQQLKVELNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1758
α chain w/alternative signal peptide, C α (substituted)	MASIRAVFIFLWLQDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFTGTQQLKVELNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1759
α chain w/alternative signal peptide, C α (substituted)	MHSIRAVFIFLWLQDLVNGENVEQHPSTLSVQEGDSAVIKCTYSDSASNYFPWYKQELGKGPQLIIDIRSNVGEKKDQRIAVTLNKTAKHFSLHITETQPEDSAVYFCAASTGGGNKLTFTGTQQLKVELNIQNPEPAVYQLKDPRSQDSTLCCLFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLLMTLRLWSS	1760
CDR1 β	DFQATT	2751
CDR2 β	SNEGSKA	2752
CDR3 β	SAREGAGGMGTQY	2753
V β w/o signal peptide (SignalP)	AVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSAREGAGGMGTQYFGPGTRLLVL	2754
V β w/o signal peptide (IMGT)	GAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSAREGAGGMGTQYFGPGTRLLVL	2755
V β	MXLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSAREGAGGMGTQYFGPGTRLLVL	2756
	(X = any amino acid)	2757
β chain w/WT signal peptide, C β (substituted)	MLLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTLSTLTVTSAHPEDSSFYICSAREGAGGMGTQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVMMAMVKKRNS	2758

Description	Sequence	SEQ ID NO:
β chain w/alternative signal peptide, C β (substituted)	MALLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLVTSAPEDS SFYICSAREGAGGMGTQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2759
β chain w/alternative signal peptide, C β (substituted)	MHLLLLLLGPAGSGLGAVVSQHPSRVICKSGTSVKIECRSLDFQATTMFWYR QFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLVTSAPEDS SFYICSAREGAGGMGTQYFGPGTRLLVLEDLRNVTPPKVSLFEPKAEIANK QKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRL RVSATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPKPVTONISAEAWGRADCG ITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2760

[00370] In some embodiments, TCR076 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR076 interacts with the neoantigen in the context of HLA-DRB1*07:01, as described in International Publication No. WO 2019/060349, incorporated herein by reference in its entirety.

Table 6BY. Amino acid sequences of TCR077.

Description	Sequence	SEQ ID NO:
CDR1 α	SSVPPY	1761
CDR2 α	YTSATLV	1762
CDR3 α	AVSEDSNYQLI	1763
V α w/o signal peptide (SignalP)	QSVTQLGSHVSVSEGAIVLLRCNYSSSVPPYLFWYVQYPNQGLQLLLKYTSA ATLVKGINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCAVSEDSNYQLIWGA GTKLI IKP	1764
V α w/o signal peptide (IMGT)	AQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPYLFWYVQYPNQGLQLLLKYTS AATLVKGINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCAVSEDSNYQLIWG AGTKLI IKP	1765
V α	MXLLLVVPVLEVI FTLGGTQAQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPYL FWYVQYPNQGLQLLLKYTSAATLVKGINGFEAEFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKP (X = any amino acid)	1766
		1767
α chain w/WT signal peptide, C α (substituted)	MLLLLVVPVLEVI FTLGGTQAQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPYL FWYVQYPNQGLQLLLKYTSAATLVKGINGFEAEFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPQSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1768
α chain w/alternative signal peptide, C α (substituted)	MALLLVVPVLEVI FTLGGTQAQSVTQLGSHVSVSEGAIVLLRCNYSSSVPPYL FWYVQYPNQGLQLLLKYTSAATLVKGINGFEAEFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPQSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNL LMTLRLWSS	1769

Description	Sequence	SEQ ID NO:
α chain w/alternative signal peptide, C α (substituted)	MHLLLPVLEVI FTLLGGTRAQSVTQLGSHVSVSEGA LVLLRCNYSSSVPPYL FWYVQYPNQGLQLLLKYTSAATLVKGINGF EA EFKKSETSFHLTKPSAHMSD AAEYFCAVSEDSNYQLIWGAGTKLI IKPNIQNPEPAVYQLKDPRS QDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQT SFTCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLNFQNL LVIVLRILLK VAGFNL LMTLR LWSS	1770
CDR1 β	GTSNPN	2761
CDR2 β	SVGIG	2762
CDR3 β	AYSPGLASDTQY	2763
V β w/o signal peptide (SignalP)	QTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYWYRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAYSPGLASDTQYFG PGTRLTVL	2764
V β w/o signal peptide (IMGT)	SQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYWYRQAAGRGLQLLFYSVG IGQISSEVPQNLSASRPQDRQFILSSKKLLLSDSGFYLCAYSPGLASDTQYF GPGTRLTVL	2765
V β	MXCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLTVL (X = any amino acid)	2766
		2767
β chain w/WT signal peptide, C β (substituted)	MLCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPK PVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2768
β chain w/alternative signal peptide, C β (substituted)	MACSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPK PVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2769
β chain w/alternative signal peptide, C β (substituted)	MHCSLLALLLGTFFGVRSQTIHQWPATLVQPVGSPLSLECTVEGTSNP NLYW YRQAAGRGLQLLFYSVGI GQISSEVPQNLSASRPQDRQFILSSKKLLLSDSG FYLCAYSPGLASDTQYFGPGTRLTVLEDLRNVT PPKVSLFEP SKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVFHGLSEEDKWPEGSPK PVTQNISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMV KRKNS	2770

[00371] In some embodiments, TCR077 interacts with and/or is specific for the epidermal growth factor receptor (EGFR) tumor protein. In some embodiments, the peptide is from a neoantigen of EGFR. In some embodiments, the neoantigen has the amino acid changes E746-A750del relative to the wild type EGFR sequence. In some embodiments, TCR077 interacts with the neoantigen in the context of a heterodimer of HLA-DPA1*02:01 and HLA-DPB1*01:01, as described in International Publication No. WO 2019/213195, incorporated herein by reference in its entirety.

Table 6BZ. Amino acid sequences of TCR078.

Description	Sequence	SEQ ID NO:
CDR1 α	TSINN	1771
CDR2 α	IRSNERE	1772
CDR3 α	ATDGETSGSRLT	1773
V α without signal peptide (SignalP)	QQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIRSNE REKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGEG TQLTVNP	1774
V α without signal peptide (IMGT)	SQQGEEDPQALSIQEGENATMNC SYKTSINN LQWYRQNSGRGLVHLILIRSNE EREKHSGRRLRVTLDTSKKSSSLITASRAADTASYFCATDGETSGSRLTFGE GTQLTVNP	1775
V α	MXTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDGETSGSRLTFGEGTQLTVNP (X = any amino acid)	1776
		1777
α chain with WT signal peptide, C α (substituted)	METLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPQSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNL LMTLRLWSS	1778
α chain with alternative signal peptide, C α (substituted)	MATLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPQSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNL LMTLRLWSS	1779
α chain with alternative signal peptide, C α (substituted)	MHTLLGVSLVILWLQLARVNSQQGEEDPQALSIQEGENATMNC SYKTSINN L QWYRQNSGRGLVHLILIRSNEREKHSGRRLRVTLDTSKKSSSLITASRAADT ASYFCATDGETSGSRLTFGEGTQLTVNPNIQNPEPAVYQLKDPQSQDSTLCL FTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRI LLLKVAGFNL LMTLRLWSS	1780
CDR1 β	DFQATT	2771
CDR2 β	SNEGSKA	2772
CDR3 β	SASRGATGQPQH	2773
V β without signal peptide (SignalP)	AVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEG SKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYIC SASRGATGQPQ HFGDGTRLSIL	2774
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYIC SASRGATGQP QHFGDGTRLSIL	2775
V β	MXLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSS FYIC SASRGATGQPQHFGDGTRLSIL (X = any amino acid)	2776
		2777
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSS FYIC SASRGATGQPQHFGDGTRLSILEDLRNVT PPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPV TQNI SAEAWGRADCGIT SASYQQGVLSATILYEILGKATLYAVLVSTLVVMAMV KRKNS	2778

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSS FYICSASRGATGQPQHFGDGTLSILEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2779
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQ FPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSS FYICSASRGATGQPQHFGDGTLSILEDLRNVTTPKVSLFEPKAEIANKQK ATLVCLARGFFPDHVELSWVWNGKEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQCQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGIT SASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2789

[00372] In some embodiments, TCR078 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR078 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

Table 6CA. Amino acid sequences of TCR079.

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1781
CDR2 α	IRSNMDK	1782
CDR3 α	AERGRGGKLI	1783
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSN MDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQGT ELSVKP	1784
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPQFIIDIRSN NMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLIFGQG TELSVKP	1785
V α	MXGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGD SAVYFCAERGRGGKLIFGQGT (X = any amino acid)	1786
		1787
α chain with WT signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGD SAVYFCAERGRGGKLIFGQGT TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1788
α chain with alternative signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGD SAVYFCAERGRGGKLIFGQGT TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSTFCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1789

Description	Sequence	SEQ ID NO:
α chain with alternative peptide, (substituted) C α	MHGIRALFMYLWLQLDWVSRGESVGLHLP T LSVQEGDNSIINCAYSNSASDY FIWYKQESGKGPQFIIDIRSNMDKRQQRVTVLLNKT VKHLSLQIAATQPGD SAVYFCAERGRGGKLI FGQGT ELSVKPNIQNPEPAVYQLKDPRSQDSTLCCLF TDFDSQINVPKTMESGTFITDKCVLDMKAMDSKNGAIAWSNQTSFTCQDIF KETNATYPSSDVPCDATLTEKSFETDMNLNFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1790
CDR1 β	DFQATT	2781
CDR2 β	SNEGSKA	2782
CDR3 β	SAGRASTDQY	2783
V β without signal peptide (SignalP)	GSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMA TSNEGSKATYEQGVEKDKFLINHASLT LSTLT VTS AHPEDSSFYICSAGRAS TDTQYFGPGTRLTVL	2784
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNE GSKATYEQGVEKDKFLINHASLT LSTLT VTS AHPEDSSFYICSAGRASTDQY YFGPGTRLTVL	2785
V β	MXLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLT LSTLT TVTSAHPEDSSFYICSAGRASTDQYFGPGTRLTVL (X = any amino acid)	2786
		2787
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLT LSTLT TVTSAHPEDSSFYICSAGRASTDQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2788
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLT LSTLT TVTSAHPEDSSFYICSAGRASTDQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2789
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGISLLLLPGSLAGSGLGAVVSQHPSWVICKSGTSVKIECRSLD FQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLT LSTLT TVTSAHPEDSSFYICSAGRASTDQYFGPGTRLT VLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTDPQAYKESNY SYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVTONISAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN S	2790

[00373] In some embodiments, TCR079 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR079 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

Table 6CB. Amino acid sequences of TCR080

Description	Sequence	SEQ ID NO:
CDR1 α	NSASDY	1791
CDR2 α	IRSNMDK	1792
CDR3 α	AERGRGGKLI	1793
V α without signal peptide (SignalP)	ESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLI FGQGT ELSVKP	1794
V α without signal peptide (IMGT)	GESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLI FGQG TELSVKP	1795
V α	MXGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLI FGQGT ELSVKP (X = any amino acid)	1796
		1797
α chain with WT signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLI FGQGT ELSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1798
α chain with alternative signal peptide, C α (substituted)	MAGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLI FGQGT ELSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1799
α chain with alternative signal peptide, C α (substituted)	MHGIRALFMYLWLQLDWVSRGESVGLHLPTLSVQEGDNSIINCAYSNSASDYFIWYKQESGKGPPQFIIDIRSNMDKRQGGQRTVLLNKTVKHLSLQIAATQPGDSAVYFCAERGRGGKLI FGQGT ELSVKPNIQNPEPAVYQLKDP RSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLL MTLRLWSS	1800
CDR1 β	DFQATT	2791
CDR2 β	SNEGSKA	2792
CDR3 β	SAGRASTDQY	2793
V β without signal peptide (SignalP)	AVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYIC SAGRASTDQY FGPGRRLTVL	2794
V β without signal peptide (IMGT)	GAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYIC SAGRASTDQY FGPGRRLTVL	2795
V β	MXLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYIC SAGRASTDQY FGPGRRLTVL (X = any amino acid)	2796
		2797
β chain with WT signal peptide, C β (substituted)	MLLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFYRQFPKQSLMLMATSNEGSKATYEQGVEKDKFLINHASLTSLTLTVTSAHPEDSSFYIC SAGRASTDQY FGPGRRLTVLEDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	2798

Description	Sequence	SEQ ID NO:
β chain with alternative signal peptide, C β (substituted)	MALLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQ FPKQSLMLMATSNESKATYEQQVEKDKFLINHASLTSLTLTVTSAHPEDSS FYICSAGRASTDYFQFGPGRRLTVLEDLRNVTTPKVSLEFEPKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2799
β chain with alternative signal peptide, C β (substituted)	MHLLLLLLGPGSGLGAVVSQHPSWVICKSGTSVKIECRSLDFQATTMFWYRQ FPKQSLMLMATSNESKATYEQQVEKDKFLINHASLTSLTLTVTSAHPEDSS FYICSAGRASTDYFQFGPGRRLTVLEDLRNVTTPKVSLEFEPKAEIANKQKA TLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKESNYSYCLSSRLRVS ATFWHNPRNHFRQVQFHGLSEEDKWPEGSPKPVTONISAEAWGRADCGITS ASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	2800

[00374] In some embodiments, TCR080 interacts with and/or is specific for KRAS. In some embodiments, the peptide is from a neoantigen of KRAS. In some embodiments, the neoantigen has the amino acid change G12V relative to the wild type KRAS sequence. In some embodiments, TCR080 interacts with the neoantigen in the context of an HLA-DPA1* 01:03 chain and an HLA-DPB1*03:01 chain, as described in International Publication No. WO 2021/173902, incorporated herein by reference in its entirety.

[00375] The disclosure also provides for the use of other TCR V α and V β sequences, as well as any other alpha or beta chains, in the polycistronic vectors, engineered cells or pharmaceutical compositions described herein. These TCR V α and V β sequences and alpha or beta chains include those described in International Publication Nos. WO 2016/085904, WO 2017/048593, WO 2018/026691, WO 2019/060349, WO 2019/067243, WO 2019/070435, WO 2019/112941, WO 2019/213195, WO 2020/086827, WO 2020/154275, WO 2020/264269, WO 2021/163434, WO 2021/163477, and WO 2021/173902 incorporated by reference herein in their entireties.

[00376] The CDRs of a TCR disclosed herein can be defined using any art recognized numbering convention. Additionally or alternatively, the CDRs can be defined empirically, *e.g.*, based upon structural analysis of the interaction of the TCR with a cognate antigen (*e.g.*, a peptide or a peptide-MHC complex). In some embodiments, CDR3 of the TCR can further comprise an N-terminal cysteine and/or a C-terminal phenylalanine or tryptophan.

[00377] The TCRs disclosed herein can be used in any TCR structural format. For example, in certain embodiments, the TCR is a full-length TCR comprising a full-length α chain and a full-length β chain. The transmembrane regions (and optionally also the cytoplasmic regions) can be removed from a full-length TCR to produce a soluble TCR. Accordingly, in certain embodiments, the TCR is a soluble TCR lacking transmembrane and/or cytoplasmic region(s). The methods of

producing soluble TCRs are well-known in the art. In some embodiments, the soluble TCR comprises an engineered disulfide bond that facilitates dimerization, see, *e.g.*, U.S. Patent No. 7,329,731, which is incorporated by reference herein in its entirety. In some embodiments, the soluble TCR is generated by fusing the extracellular domain of a TCR described herein to other protein domains, *e.g.*, maltose binding protein, thioredoxin, human constant kappa domain, or leucine zippers, see, *e.g.*, Løset et al., *Front Oncol.* 2014; 4: 378, which is incorporated by reference herein in its entirety. A single-chain TCR (scTCR) comprising V α and V β linked by a peptide linker can also be generated. Such scTCRs can comprise V α and V β , each linked to a TCR constant region. Alternatively, the scTCRs can comprise V α and V β , where either the V α , the V β , or both the V α and V β are not linked to a TCR constant region. Exemplary scTCRs are described in PCT Publication Nos. WO 2003/020763, WO 2004/033685, and WO 2011/044186, each of which is incorporated by reference herein in its entirety. Furthermore, the TCRs disclosed herein can comprise two polypeptide chains (*e.g.*, an α chain and a β chain) in which the chains have been engineered to each have a cysteine residue that can form an interchain disulfide bond. Accordingly, in certain embodiments, the TCRs disclosed herein comprise two polypeptide chains linked by an engineered disulfide bond. Exemplary TCRs having an engineered disulfide bond are described in U.S. Patent Nos. 8,361,794 and 8,906,383, each of which is incorporated by reference herein in its entirety.

[00378] In certain embodiments, the TCRs disclosed herein comprise one or more chains (*e.g.*, an α chain and/or a β chain) having a transmembrane region. In certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) having a transmembrane region. The transmembrane region can be the endogenous transmembrane region of that TCR chain, a variant of the endogenous transmembrane region, or a heterologous transmembrane region. In certain embodiments, the TCRs disclosed herein comprise an α chain and a β chain having endogenous transmembrane regions.

[00379] In certain embodiments, the TCRs disclosed herein comprise one or more chains (*e.g.*, an α chain and/or a β chain) having a cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) each having a cytoplasmic region. The cytoplasmic region can be the endogenous cytoplasmic region of that TCR chain, variant of the endogenous cytoplasmic region, or a heterologous cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) where both chains have transmembrane regions, but one chain is lacking a cytoplasmic region. In

certain embodiments, the TCRs disclosed herein comprise two chains (*e.g.*, an α chain and a β chain) where both chains have endogenous transmembrane regions but lack an endogenous cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise an α chain and a β chain where both chains have endogenous transmembrane regions but lack an endogenous cytoplasmic region. In certain embodiments, the TCRs disclosed herein comprise a co-stimulatory signaling region from a co-stimulatory molecule; see, *e.g.*, PCT Publication Nos.: WO 1996/018105, WO 1999/057268, and WO 2000/031239, and U.S. Patent No. 7,052,906, all of which are incorporated herein by reference in their entireties.

[00380] In certain embodiments, the instant disclosure provides a polypeptide comprising an α chain variable region ($V\alpha$) and a β chain variable region ($V\beta$) of a TCR fused together. For example, such polypeptide may comprise, in order, the $V\alpha$ and $V\beta$, or the $V\beta$ and the $V\alpha$, optionally with a linker (*e.g.*, a peptide linker) between the two regions. For example, a Furin and/or a 2A cleavage site (*e.g.*, one of the sequences in Tables 2 or 3), or combinations thereof, may be used in the linker for the $V\alpha/V\beta$ fusion polypeptide. In certain embodiments, the instant disclosure provides a polypeptide comprising an α chain and a β chain of a TCR fused together. For example, such polypeptide may comprise, in order, an α chain and a β chain, or a β chain and an α chain, optionally with a linker (*e.g.*, a peptide linker) between the two chains. For example, a Furin and/or a 2A cleavage site (*e.g.*, one of the sequences in Tables 2 or 3), or combinations thereof, may be used in the linker for the α/β fusion polypeptide. For example, a fusion polypeptide may comprise, from the N-terminus to the C-terminus: the α chain of a TCR, a furin cleavage site, a 2A cleavage site, and the β chain of the TCR. In certain embodiments, the polypeptide comprises, from the N-terminus to the C-terminus: the β chain of a TCR, a furin cleavage site, a 2A element, and the α chain of the TCR.

5.3 Methods of Use

[00381] In another aspect, the instant disclosure provides a method of treating a subject using the polycistronic polynucleotides, recombinant vectors, engineered cells (*e.g.*, a cell comprising a heterologous and/or recombinant nucleic acid), or pharmaceutical compositions disclosed herein. Any disease or disorder in a subject that would benefit from treatment with a recombinant cell of the present disclosure, or a polynucleotide or vector of the present disclosure can be treated using the methods disclosed herein.

[00382] In certain embodiments, the method comprises administering to the subject an effective amount of a recombinant cell or population thereof as disclosed herein.

[00383] As disclosed *infra*, cells administered to the subject can be autologous or allogeneic to the subject. In certain embodiments, autologous cells are obtained from a cancer patient directly following a cancer treatment. In this regard, it has been observed that following certain cancer treatments, in particular treatments with drugs that damage the immune system, shortly after treatment during the period when patients would normally be recovering from the treatment, the quality of T cells obtained may be optimal or improved for their ability to expand *ex vivo*. Likewise, following *ex vivo* manipulation using the methods described herein, these cells may be in a preferred state for enhanced engraftment and *in vivo* expansion. Thus, in certain embodiments, cells are collected from blood, bone marrow, lymph node, thymus, or another tissue or bodily fluid, or an apheresis product, during this recovery phase. Further, in certain aspects, mobilization and conditioning regimens can be used to create a condition in a subject wherein repopulation, recirculation, regeneration, and/or expansion of particular cell types is favored, especially during a defined window of time following therapy.

[00384] The number of cells that are employed will depend upon a number of circumstances including, the lifetime of the cells, the protocol to be used (*e.g.*, the number of administrations), the ability of the cells to multiply, the stability of the recombinant construct, and the like. In certain embodiments, the cells are applied as a dispersion, generally being injected at or near the site of interest. The cells may be administered in any physiologically acceptable medium.

[00385] In certain embodiments, the cancer is cancer of the lung, bile duct cancer (*e.g.*, cholangiocarcinoma), pancreatic cancer, colorectal cancer, ovarian, or gynecologic cancer. In certain embodiments, the cancer is leukemia (*e.g.*, mixed lineage leukemia, acute lymphocytic leukemia, acute myeloid leukemia, chronic lymphocytic leukemia, or chronic myeloid leukemia), alveolar rhabdomyosarcoma, bone cancer, brain cancer (*e.g.*, glioma, *e.g.*, glioblastoma), breast cancer, cancer of the anus, anal canal, or anorectum, cancer of the eye, cancer of the intrahepatic bile duct (*e.g.*, intrahepatic cholangiocellular cancer), cancer of the joints, cancer of the neck, gallbladder, or pleura, cancer of the nose, nasal cavity, or middle ear, cancer of the oral cavity, cancer of the vulva, myeloma (*e.g.*, chronic myeloid cancer), colon cancer, esophageal cancer, cervical cancer, gastrointestinal cancer, gastrointestinal carcinoid tumor, Hodgkin's lymphoma, hypopharynx cancer, kidney cancer, larynx cancer, liver cancer (*e.g.*, hepatocellular carcinoma), lung cancer (*e.g.*, non-small cell lung cancer), malignant mesothelioma, melanoma, multiple myeloma, nasopharynx cancer, non-Hodgkin's lymphoma, ovarian cancer, pancreatic cancer, peritoneum, omentum, and mesentery cancer, pharynx cancer, prostate cancer, rectal cancer, renal

cancer (*e.g.*, renal cell carcinoma (RCC)), gastric cancer, small intestine cancer, soft tissue cancer, stomach cancer, carcinoma, sarcoma (*e.g.*, synovial sarcoma, rhabdomyosarcoma), skin cancer, testicular cancer, thyroid cancer, head and neck cancer, ureter cancer, and urinary bladder cancer. In certain embodiments, the cancer is melanoma, breast cancer, lung cancer, prostate cancer, thyroid cancer, ovarian cancer, or synovial sarcoma. In one embodiment, the cancer is synovial sarcoma or liposarcoma (*e.g.*, myxoid/round cell liposarcoma). In certain embodiments, the cancer is lung, cholangiocarcinoma, pancreatic, colorectal, gynecological or ovarian cancer.

[00386] A polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein may be delivered to a subject by a variety of routes. These include, but are not limited to, parenteral, intranasal, intratracheal, oral, intradermal, topical, intramuscular, intraperitoneal, transdermal, intravenous, intratumoral, conjunctival, intrathecal, and subcutaneous routes. Pulmonary administration can also be employed, *e.g.*, by use of an inhaler or nebulizer, and formulation with an aerosolizing agent for use as a spray. In certain embodiments, the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein is delivered intravenously. In certain embodiments, the polycistronic polynucleotide, vector, engineered cell, or pharmaceutical composition described herein is delivered subcutaneously. In certain embodiments, the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein is delivered intratumorally. In certain embodiments, the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition described herein is delivered into a tumor draining lymph node.

[00387] The amount of the polycistronic polynucleotide, recombinant vector, engineered cell, or pharmaceutical composition which will be effective in the treatment and/or prevention of a condition will depend on the nature of the disease, and can be determined by standard clinical techniques.

[00388] The precise dose to be employed in a composition will also depend on various factors, including but not limited to the route of administration, and the seriousness of the infection or disease caused by it, and should be decided according to the judgment of the practitioner and each subject's circumstances. For example, effective doses may also vary depending upon means of administration, target site, physiological state of the patient (including age, body weight, and health), whether the patient is a human or an animal, other medications administered, or whether treatment is prophylactic or therapeutic. Usually, the patient is a human but non-human mammals

including transgenic mammals can also be treated. Treatment dosages are optimally titrated to optimize safety and efficacy.

5.4 IL-15/IL-15R α Fusion Proteins

[00389] The disclosure also provides recombinant vectors that include cytokines. In some embodiments, the cytokine is an interleukin. In some embodiments, the cytokine is membrane bound. In some embodiments, the cytokine is a fusion protein comprising a soluble cytokine, or a functional fragment or functional variant thereof, operably linked to a cognate receptor of the cytokine, or a functional fragment or functional variant thereof, optionally a membrane-bound form thereof. In some embodiments, the fusion protein comprises human IL-15 (hIL-15) operably linked to human IL-15R α (hIL-15R α). In membrane-bound form, this fusion protein is referred to herein as membrane bound IL-15 (mbIL15). In some embodiments, hIL-15 is directly operably linked to hIL-15R α . In some embodiments, hIL-15 is indirectly operably linked to hIL-15R α . In some embodiments, hIL-15 is indirectly operably linked to hIL-15R α via a peptide linker.

[00390] In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 81, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 81. In some embodiments, the linker comprises the amino acid sequence of SEQ ID NO: 81. In some embodiments, the amino acid of the linker consists of the amino acid sequence of SEQ ID NO: 81, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 81. In some embodiments, the amino acid of the linker consists of the amino acid sequence of SEQ ID NO: 81.

[00391] In some embodiments, the linker is encoded by a polynucleotide sequence at least 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 82. In some embodiments, the linker is encoded by the polynucleotide sequence of SEQ ID NO: 82. In some embodiments, hIL-15 comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 76. In some embodiments, hIL-15 comprises the amino acid sequence of SEQ ID NO: 76. In some embodiments, the amino acid sequence of hIL-15 consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 76. In some embodiments, the amino acid sequence of hIL-15 consists of the amino acid sequence of SEQ ID NO: 76.

[00392] In some embodiments, hIL-15 is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence

of SEQ ID NO: 77. In some embodiments, hIL-15 is encoded by the polynucleotide sequence of SEQ ID NO: 77.

[00393] In some embodiments, hIL-15R α comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 78. In some embodiments, hIL-15R α comprises the amino acid sequence of SEQ ID NO: 78. In some embodiments, the amino acid sequence of hIL-15R α consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 78. In some embodiments, the amino acid sequence of hIL-15R α consists of the amino acid sequence of SEQ ID NO: 78.

[00394] In some embodiments, hIL-15R α is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 79. In some embodiments, hIL-15R α is encoded by the polynucleotide sequence of SEQ ID NO: 79.

[00395] In some embodiments, the fusion protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 70 or 73. In some embodiments, the fusion protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 70. In some embodiments, the fusion protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 73. In some embodiments, the fusion protein comprises the amino acid sequence of SEQ ID NO: 70 or 73. In some embodiments, the fusion protein comprises the amino acid sequence of SEQ ID NO: 70. In some embodiments, the fusion protein comprises the amino acid sequence of SEQ ID NO: 73.

[00396] In some embodiments, the amino acid sequence of the fusion protein consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 70 or 73. In some embodiments, the amino acid sequence of the fusion protein consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 70. In some embodiments, the amino acid sequence of the fusion protein consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 73. In some embodiments, the amino acid sequence of the fusion protein consists of the amino acid sequence of SEQ ID NO: 70 or 73. In some embodiments, the amino acid sequence of the fusion protein consists of the amino acid sequence of SEQ ID NO: 70. In some embodiments, the amino acid sequence of the fusion protein consists of the amino acid sequence of SEQ ID NO: 73.

[00397] In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polynucleotide sequence of SEQ ID NO: 71 or 74. In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polynucleotide sequence of SEQ ID NO: 71. In some embodiments, the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the polynucleotide sequence of SEQ ID NO: 74.

[00398] In some embodiments, the fusion protein is encoded by the polynucleotide sequence of SEQ ID NO: 71 or 74. In some embodiments, the fusion protein is encoded by the polynucleotide sequence of SEQ ID NO: 71. In some embodiments, the fusion protein is encoded by the polynucleotide sequence of SEQ ID NO: 74.

[00399] Exemplary cytokine fusion proteins and components thereof are disclosed in Table 7. Additional exemplary mbIL15 fusions are disclosed in Hurton *et al.*, “Tethered IL-15 augments antitumor activity and promotes a stem-cell memory subset in tumor-specific T cells,” PNAS, 113(48) E7788-E7797 (2016), the entire contents of which are incorporated by reference herein.

[00400] The amino acid sequence and polynucleotide sequence of exemplary cytokine fusion proteins and component polypeptides are provided in Table 7, herein.

Table 7. Amino acid and polynucleotide sequences of exemplary IL-15/IL-15R α fusion proteins and components thereof.

Description	Sequence	SEQ ID NO
mbIL15 (with N-terminal signal sequence) (exemplary amino acid sequence)	MDWTWILFLVAAATRVHSNWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCK VTAMKCFLLLELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEE LEEKNIKEFLQSFVHIVQMFIN TSSGGGSGGGGSGGGGSGGGGSGGGSLQITCP PPMSVEHADIWKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPALVHQRPA PPSVTVTAGVTPQPESLSPSGKEPAASSPSSNNTAAT TAAIVPGSQLMPKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQPPGV YPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAMEALPVT WGTSSRDEDLNCSHHL	70
mbIL15 (with N-terminal signal sequence) (exemplary nucleotide sequence)	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGC AACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGC ATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAA GTGACCGCCATGAAGTGT TTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGCCAACAAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTT CATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGA GGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCT CCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTACAGCCTGTAC AGCAGAGAGAGATACATCTGCAACAGCGGCTTAAAGAGAAAGGCCGGCACCTCT TCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACA CCTAGCCTGAAGTGCATTAGAGATCTGCCCTGGTCCACCAGAGGCCTGCCCT CCATCTACAGTGACAACAGCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCT	71

Description	Sequence	SEQ ID NO
	TCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACA ACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACA GGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTG TATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTG CTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAG ACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	
mbIL15 (without N-terminal signal sequence) (exemplary amino acid sequence)	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECELEEKNIKEFLQSFVHIVQ MFINTSSGGSGGGSGGGSGGGSGGGSLQITCPPPMSVEHADIWVKSYSLSY SRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTTPSLKCI RDPALVHQRPA PSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAIVPGSQLMPSKSPST GTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVL LCGLSAVSL LACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	73
mbIL15 (without N-terminal signal sequence) (exemplary nucleotide sequence)	AAC TGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGC ATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAA GTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGA GGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCT CCTCCAATGTCTGTGGAGCACGCCGATATTGGGTGAAGTCTACAGCCTGTAC AGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGGCACCTCT TCTCTGACAGAGTGCGTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACA CCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCCTGCCCT CCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCT TCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACA ACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACA GGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTG TATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTG CTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAG ACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	74
Soluble hIL-15 (exemplary amino acid sequence)	NWVNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECELEEKNIKEFLQSFVHIVQ MFINTS	76
Soluble hIL-15 (exemplary nucleotide sequence)	AAC TGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGC ATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAA GTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCATCAATACAAGC	77
hIL-15R α (exemplary amino acid sequence)	ITCPPPMSVEHADIWVKSYSLSYSRERYICNSGFKRKAGTSSLTECVLNKATNVA HWTTTPSLKCI RDPALVHQRPA P PSTVTTAGVTPQPESLSPSGKEPAASSPSSNN TAATTAIVPGSQLMPSKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAMEA LPVTWGTSSRDEDLNCSHHL	78
hIL-15R α (exemplary nucleotide sequence)	ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACAAATGTGGCC CACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAG AGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAA	79

Description	Sequence	SEQ ID NO
	TCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAAT ACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAG TCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCAGGGAACA CCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAG CCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACA TCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTG AAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCC CTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCT CACCACCTG	
Linker (exemplary amino acid sequence)	SGGGSGGGSGGGSGGGSGGGSLQ	81
Linker (exemplary nucleotide sequence)	TCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGA GGATCTGGCGGAGGATCTCTGCAG	82
IgE N-terminal signal sequence (exemplary amino acid sequence)	MDWTWILFLVAAATRVHS	83
IgE N-terminal signal sequence (exemplary nucleotide sequence)	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGC	84

5.5 Marker Proteins

[00401] The marker proteins described herein function to allow for the selective depletion of cells contacted with the recombinant vector disclosed herein (*e.g.*, “recombinant cells”) *in vivo*, through the administration of an agent, *e.g.*, an antibody, that specifically binds to the marker protein and may mediate or catalyze killing of a recombinant cell. In some embodiments, marker proteins are expressed on the surface of the recombinant cell.

[00402] In some embodiments, the marker protein comprises the extracellular domain of a cell surface protein, or a functional fragment or functional variant thereof. In some embodiments, the cell surface protein is human epidermal growth factor receptor 1 (hHER1). In some embodiments, the marker protein comprises a truncated HER1 protein that is able to be bound by an anti-hHER1 antibody. In some embodiments, the marker protein comprises a variant of a truncated hHER1 protein that is able to be bound by an anti-hHER1 antibody. In some embodiments, the hHER1 marker protein provides a safety mechanism by allowing for depletion of infused recombinant cells through administering an antibody that recognizes the hHER1 marker protein expressed on the surface of recombinant cells. An exemplary antibody that binds the hHER1 marker protein is cetuximab.

[00403] In some embodiments, the hHER1 marker protein comprises from N terminus to C terminus: domain III of hHER1, or a functional fragment or functional variant thereof; an N-terminal portion of domain IV of hHER1; and the transmembrane region of human CD28.

[00404] In some embodiments, domain III of hHER1 comprises the amino acid sequence of SEQ ID NO: 104; or the amino acid sequence of SEQ ID NO: 104, comprising 1, 2, or 3 amino acid modifications. In some embodiments, the amino acid sequence of domain III of hHER1 consists of the amino acid sequence of SEQ ID NO: 104; or the amino acid sequence of SEQ ID NO: 10, comprising 1, 2, or 3 amino acid modifications.

[00405] In some embodiments, the N-terminal portion of domain IV of hHER1 comprises amino acids 1-40, 1-39, 1-38, 1-37, 1-36, 1-35, 1-34, 1-33, 1-32, 1-31, 1-30, 1-29, 1-28, 1-27, 1-26, 1-25, 1-24, 1-23, 1-22, 1-21, 1-20, 1-19, 1-18, 1-17, 1-16, 1-15, 1-14, 1-13, 1-12, 1-11, or 1-10 of SEQ ID NO: 105. In some embodiments, the C terminus of domain III of hHER1 is directly fused to the N terminus of the N-terminal portion of domain IV of hHER1.

[00406] In some embodiments, the C terminus of the N-terminal portion of domain IV of hHER1 is indirectly fused to the N terminus of the CD28 transmembrane domain via a peptide linker. In some embodiments, the peptide linker comprises glycine and serine amino acid residues. In some embodiments, the peptide linker is from about 5-25, 5-20, 5-15, 5-10, 10-20, or 10-15 amino acids in length.

[00407] In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 108, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 108. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 108. In some embodiments, the amino acid sequence of the peptide linker consists of the amino acid sequence of SEQ ID NO: 108, or an amino acid sequence comprising 1, 2, 3, 4 or 5 amino acid modifications to the amino acid sequence of SEQ ID NO: 108. In some embodiments, the amino acid sequence of the peptide linker consists of the amino acid sequence of SEQ ID NO: 108.

[00408] In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, 112, or 113. In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 103. In some

embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 112. In some embodiments, the marker protein comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 113.

[00409] In some embodiments, the marker protein comprises the amino acid sequence of SEQ ID NO: 100 or 103. In some embodiments, the marker protein comprises the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein comprises the amino acid sequence of SEQ ID NO: 103.

[00410] In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, 112, or 113. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 103. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 112. In some embodiments, the marker protein consists of an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 113.

[00411] In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 100, 103, 112, or 113. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 100. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 103. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 112. In some embodiments, the marker protein consists of the amino acid sequence of SEQ ID NO: 113.

[00412] In some embodiments, the marker protein is derived from human CD20 (hCD20). In some embodiments, the marker protein comprises a truncated hCD20 protein that comprises the extracellular region (hCD20t), or a functional fragment or functional variant thereof. In some embodiments, the hCD20 marker protein provides a safety mechanism by allowing for depletion of infused recombinant cells through administering an antibody that recognizes the hCD20 marker

protein expressed on the surface of recombinant cells. An exemplary antibody that binds the hCD20 marker protein is rituximab.

[00413] The amino acid sequences of exemplary marker proteins are provided in Table 8, herein.

Table 8. Amino acid sequences of exemplary marker proteins.

Description	Amino Acid Sequence	SEQ ID NO
HER1t (with N-terminal signal sequence) (exemplary amino acid sequence)	MRLPAQLLGLLMLWVPGSSGRKVCNGIGIGEFKDSLSINATNI KHFKNCTSI SGDLHILPVAFRGDSFTHTPPLDPQELDI LKTVK EITGFLLIQAWPENRTDLHAFENLEIIRGR TKQHGGQFSLAVVS LNITSLGLRSLKEISDGDV IISGNKNLCYANTINWKKLFGTSG QKTKIISNRGENSKATGQVCHALCSPEGCGWPEPRDCVSGGG GSGGGGSGGGGSGGGGFWVLVVGVLACYSLLVTVAFIIFW VRSKRS	100
HER1t (without N-terminal signal sequence) (exemplary amino acid sequence)	RKVCNGIGIGEFKDSLSINATNIKHFKNCTSI SGDLHILPVAF RGDSFTHTPPLDPQELDI LKTVKEITGFLLIQAWPENRTDLHA FENLEIIRGR TKQHGGQFSLAVVSLNITSLGLRSLKEISDGDV I ISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSKATGQV CHALCSPEGCGWPEPRDCVSGGGGSGGGGSGGGGSGGGGFWV LVVVGVLACYSLLVTVAFIIFWVRSKRS	103
Domain III of hHER1 (exemplary amino acid sequence)	RKVCNGIGIGEFKDSLSINATNIKHFKNCTSI SGDLHILPVAF RGDSFTHTPPLDPQELDI LKTVKEITGFLLIQAWPENRTDLHA FENLEIIRGR TKQHGGQFSLAVVSLNITSLGLRSLKEISDGDV I ISGNKNLCYANTINWKKLFGTSGQKTKIISNRGENSKATGQ	104
Domain IV of hHER1 (exemplary amino acid sequence)	VCHALCSPEGCGWPEPRDCVSCRNVSRGRCVDKCNLLEGEPR EFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPH CVKTCFAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGL EGCPTNGPKIPS	105
Truncated domain IV of hHER1 (exemplary amino acid sequence)	VCHALCSPEGCGWPEPRDCVS	106
CD28 transmembrane domain (exemplary amino acid sequence)	FWVLVVGVLACYSLLVTVAFIIFWVRSKRS	107
Linker (exemplary amino acid sequence)	GGGGSGGGGSGGGGSGGGG	108
Igk N-terminal signal sequence (exemplary amino acid sequence)	MRLPAQLLGLLMLWVPGSSG	109
Igk Variant 1 N-terminal signal sequence (exemplary amino acid sequence)	MRMRLPAQLLGLLMLWVPGSSG	110
Igk Variant 2 N-terminal signal sequence (exemplary amino acid sequence)	PRMRLPAQLLGLLMLWVPGSSG	111
HER1t-2 (with N-terminal signal sequence) (exemplary amino acid sequence)	MRLPAQLLGLLMLWVPGSSGRKVCNGIGIGEFKDSLSINATNI KHFKNCTSI SGDLHILPVAFRGDSFTHTPPLDPQELDI LKTVK EITGFLLIQAWPENRTDLHAFENLEIIRGR TKQHGGQFSLAVVS LNITSLGLRSLKEISDGDV IISGNKNLCYANTINWKKLFGTSG QKTKIISNRGENSKATGQVCHALCSPEGCGWPEPRDCVSCRN VSRGRCVDKCNLLEGEPRFVENSECIQCHPECLPQAMNITC TGRGPDNCIQCAHYIDGPHCVKTCFAGVMGENNTLVWKYADAG HVCHLCHPNCTYGCTGPGLGECPTNGPKIPSIATGMVGALLL	112

Description	Amino Acid Sequence	SEQ ID NO
	LVVALGIGLFM	
HER1t-2 (without N-terminal signal sequence) (exemplary amino acid sequence)	RKVCNGIGIGEFKDSLSINATNIKHFKNCTSSISGDLHILPVAF RGDSFTHTPPLDPQELDILKTVEITGFLLIQAWPENRTDLHA FENLEIIRGRTKQHGFSLAVVSLNITSLGLRSLKEISDGDVI ISGNKNLCYANTINWKKLFGTSGQTKIISNRGENSCKATGQV CHALCSPEGCWGPEDRDCVSCRNVSRGECVDKCNLLEGEPRE FVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHC VKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGGCTGPGLE GCPTNGPKIPSIATGMVGALLLLLVVALGIGLFM	113
hCD20 (full length) (exemplary amino acid sequence)	MTTPRNSVNGTFPAEPMKGPIAMQSGPKPLFRMSSLVGPTQS FFMRESKTLGAVQIMNGLFHIALGGLLMIPAGIYAPICVTWVY PLWGGIMYIISGSLAATEKNSRKCLVKGMIMNSLSLFAAIS GMILSMDILNLIKISHFLKMESLNFIRAHTPYINIYNCEPANP SEKNSPSTQYCYSIQSLFLGILSVMLIFAFFQELVIAGIVENE WKRTCSRPKSNIVLLSAEEKKEQTIEIKEEVVGLTETSSQPKN EEDIEIPIQEEEEETETNFPEPPQDQESSPIENDSSP	114
hCD20t-1 (exemplary amino acid sequence)	MTTPRNSVNGTFPAEPMKGPIAMQSGPKPLFRMSSLVGPTQS FFMRESKTLGAVQIMNGLFHIALGGLLMIPAGIYAPICVTWVY PLWGGIMYIISGSLAATEKNSRKCLVKGMIMNSLSLFAAIS GMILSMDILNLIKISHFLKMESLNFIRAHTPYINIYNCEPANP SEKNSPSTQYCYSIQSLFLGILSVMLIFAFFQELVIAGIVENE WKRTCSRPKSNIVLLSAEEKKEQTIEIKEEVVGLTETSSQPKN EEDIE	115

5.6 Vectors

[00414] In one aspect, provided herein are recombinant vectors comprising a polycistronic expression cassette that comprises at least three cistrons. In some embodiments, the polycistronic expression cassette comprises at least 4, 5, or 6 cistrons. In some embodiments, the polycistronic expression cassette comprises 3 cistrons. In some embodiments, the polycistronic expression cassette comprises 4 cistrons. In some embodiments, the polycistronic expression cassette comprises 5 cistrons. In some embodiments, the polycistronic expression cassette comprises 6 cistrons.

[00415] In some embodiments, the vector is a non-viral vector. Exemplary non-viral vectors include, but are not limited to, plasmid DNA, transposons, episomal plasmids, minicircles, ministrings, and oligonucleotides (*e.g.*, mRNA, naked DNA). In some embodiments, the polycistronic vector is a DNA plasmid vector.

[00416] In some embodiments, the vector is a viral vector. Viral vectors can be replication competent or replication incompetent. Viral vectors can be integrating or non-integrating. A number of viral based systems have been developed for gene transfer into mammalian cells, and a suitable viral vector can be selected by a person of ordinary skill in the art. Exemplary viral vectors include, but are not limited to, adenovirus vectors (*e.g.*, adenovirus 5), adeno-associated virus

(AAV) vectors (*e.g.*, AAV2, 3, 5, 6, 8, 9), retrovirus vectors (MMSV, MSCV), lentivirus vectors (*e.g.*, HIV-1, HIV-2), gammaretrovirus vectors, herpes virus vectors (*e.g.*, HSV1, HSV2), alphavirus vectors (*e.g.*, SFV, SIN, VEE, M1), flavivirus (*e.g.*, Kunjin, West Nile, Dengue virus), rhabdovirus vectors (*e.g.*, rabies virus, VSV), measles virus vector (*e.g.*, MV-Edm), Newcastle disease virus vectors, poxvirus vectors (*e.g.*, VV), measles virus, and picornavirus vectors (*e.g.*, Cocksackievirus).

[00417] In some embodiments, the vector or polycistronic expression cassette comprises one or more additional elements. Additional elements include, but are not limited to, promoters, enhancers, polyadenylation (polyA) sequences, and selection genes.

[00418] In some embodiments, the vector comprises a polynucleotide sequence that encodes for a selectable marker that confers a specific trait on cells in which the selectable marker is expressed enabling artificial selection of those cells. Exemplary selectable markers include, but are not limited to, antibiotic resistance genes, *e.g.*, resistance to kanamycin, ampicillin, or triclosan.

[00419] In some embodiments, the polycistronic expression cassette comprises a transcriptional regulatory element. Exemplary transcriptional regulatory elements include, but are not limited to promoters and enhancers. In some embodiments, the polycistronic expression cassette comprises a promoter sequence 5' of the first 5' cistron. In some embodiments, the promoter comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 150. In some embodiments, the promoter comprises the polynucleotide sequence of SEQ ID NO: 150. In some embodiments, the polynucleotide sequence of the promoter consists of a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 150. In some embodiments, the polynucleotide sequence of the promoter consists of the polynucleotide sequence of SEQ ID NO: 150.

[00420] In some embodiments, the polycistronic expression cassette comprises a polyA sequence 3' of the 3' terminal cistron. In some embodiments, the polyA sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 151. In some embodiments, the polyA sequence comprises the nucleic acid sequence of SEQ ID NO: 151. In some embodiments, the polyA sequence consists of a sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 151. In some embodiments, the polyA sequence consists of the nucleic acid sequence of SEQ ID NO: 151.

[00421] The polynucleotide sequence of exemplary promoters and polyA sequences are provided in Table 9, herein.

Table 9. Polynucleotide sequences of exemplary promoters and polyA sequences.

Description	Nucleic Acid Sequence	SEQ ID NO
hEF-1 α Hybrid Promoter	GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATC GCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACC GGTGCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCG TGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATAT AAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCC GCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCAC GCGCCCGCCGCTTACCTGAGGCCGCCATCCACGCCGGTTGAGTCG CGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACGCGTCCGCC GTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGG CGTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTG CCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTT CTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGAT	150
BGH polyA sequence	GATCTGCTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC CCCCGTGCCTTCCTTGACCTTGGAAAGGTGCCACTCCCCTGTCTT TCCTAATAAAATGAGGAAATTGCATCGCATTTGTCTGAGTAGGTGTC ATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGA TTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATG G	151

[00422] In some embodiments, the polycistronic expression cassette comprises a polynucleotide sequence that encodes an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence recited in Tables 10A-10C.

Table 10A. Exemplary amino acid sequences encoded by polycistronic expression cassettes.

Description	Sequence	SEQ ID NO:
α (murine, degenerate)-fP2A	XIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	160
$\text{C}\beta$ (murine, degenerate)-fT2A-mbIL15	EDLRNVTTPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEIILGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGEGRGSLLTCGDVEENPGMDWTWILFL VAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECELEEKN I KEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSLQITCPPPM SVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCI RDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAA TTA AIVPGSQLMPSPSTGTTEISSHES SHGTPSQTTAKNWELTASASHQ PGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKS RQTPPLASVEMEAME ALPVTWGTSSRDEDELENC SHHL X at position 57 is Ser or Cys	161
α (murine, degenerate)-fT2A	XIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	162
$\text{C}\beta$ (murine, degenerate)-fP2A-mbIL15	EDLRNVTTPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEIILGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGATNFSLLKQAGDVEENPGMDWTWILFL LVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKC FLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECELEEKN NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSLQITCPPP MSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCI RDPALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTA AIVPGSQLMPSPSTGTTEISSHES SHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKS RQTPPLASVEMEAM EALPVTWGTSSRDEDELENC SHHL X at position 57 is Ser or Cys	163

Description	Sequence	SEQ ID NO:
α (murine, degenerate)-fP2A-mbIL15-fT2A	XIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLESGDASIHDTVENLIILANNSLSSNG NVTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGGSGGSLQITCPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHLRAKRSGSGEGRGS LLTCGDVEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	164
α (murine, degenerate)-fT2A-mbIL15-fP2A	XIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLESGDASIHDTVENLIILANNSLSSNG VTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLT ECVLNKAATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHLRAKRSGSGATNFSLL LKQAGDVEENPGP X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	165
$C\beta$ (murine, degenerate)-fP2A	EDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGATNFSLLKQAGDVEENPGP X at position 57 is Ser or Cys	166
α (murine, degenerate)-fT2A-mbIL15	XIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKXVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLESGDASIHDTVENLIILANNSLSSNGN VTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLT ECVLNKAATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	167

Description	Sequence	SEQ ID NO:
Cβ (murine, degenerate)-fT2A	EDLRNVTTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKKRNSRAKRSGSGEGRGSLLTCGDVEENPGP X at position 57 is Ser or Cys	168
Cα (murine, degenerate)-fP2A-mbIL15	XIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKXVLDM KAMDSKSNGAIAWSNQTSTFCQDI FKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLXVXXLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWNVNSDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLESGDASIHDVTENLII LANNSLSSNG NVTEGCKECEELEEKNIKEFLQSFVHIVQMFINTESSGGSGGGSGGGSGG GGSGGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMPSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL X at position 1 is Asn, Asp, His, or Tyr; X at position 48 is Thr or Cys; X at position 112 is Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; X at position 114 is Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; X at position 115 is Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	169
Cβ (murine, degenerate)-fP2A-mbIL15-fT2A	EDLRNVTTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKKRNSRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILFL LVAAATRVHSNWNVNSDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LELQVISLESGDASIHDVTENLII LANNSLSSNGNVTEGCKECEELEEK NIKEFLQSFVHIVQMFINTESSGGSGGGSGGGSGGGSGGGSLQITCPPP MSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAIVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDLNCSHHLRAKRSGSGEGRGSLLTCGDVEENPGP X at position 57 is Ser or Cys	170
Cβ (murine, degenerate)-fT2A-mbIL15-fP2A	EDLRNVTTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVXTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKKRNSRAKRSGSGEGRGSLLTCGDVEENPGPMDWTWILFL VAAATRVHSNWNVNSDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLESGDASIHDVTENLII LANNSLSSNGNVTEGCKECEELEEK I KEFLQSFVHIVQMFINTESSGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA TAAIVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDLNCSHHLRAKRSGSGATNFSLLKQAGDVEENPGP X at position 57 is Ser or Cys	171
mbIL15-fP2A	MDWTWILFLVAAATRVHSNWNVNSDLKKIEDLIQSMHIDATLYTESDVHPS CKVTAMKCFLELQVISLESGDASIHDVTENLII LANNSLSSNGNVTEGCK ECEELEEKNIKEFLQSFVHIVQMFINTESSGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRDPAHVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA TAAIVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDLNCSHHLRAKRSGSGATNFSLLKQAGDVEENPGP EENPGP	172

Description	Sequence	SEQ ID NO:
mbIL15-ft2A	MDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPS CKVTAMKCFLLLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSGGG LQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKA TNVAHWTTPSLKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAAS SPSSNNTAATTA AIVPGSQLMPSKSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPL ASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGEGRGSLLTCGDVE ENPGP	173

Table 10B. Exemplary amino acid sequences encoded by polycistronic expression cassettes

Description	Sequence	SEQ ID NO:
C α (murine, cysteine- and LIV-substituted)-fP2A	NIQNPEPAVYQLKDPRS QDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSN GAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNL LVIVLRILLK VAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGP	180
C β (murine, cysteine-substituted)-fT2A-mbIL15	EDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDK WPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEI LLGKATLYA VLVSTLVVMAMVKRKN SRAKRSGSGEGRGSLLTCGDVEENPGPMDWTWILFL VAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECEELEEK IKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT SLKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAA TTAAIIVPGSQLMPSKSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQ PGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDLENC SHHL	181
C α (murine, cysteine- and LIV-substituted)-fT2A	NIQNPEPAVYQLKDPRS QDSTLCLETFDSDQINVPKTMESGTFITDKCVLDM KAMDSKSN GAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNL LVIVLRILLK VAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGP	182
C β (murine, cysteine-substituted)-fP2A-mbIL15	EDLRNVT PPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFR CQVQFHGLSEEDK WPEGSPKPV TQNI SAEAWGRADCGITSASYQQGVLSATILYEI LLGKATLYA VLVSTLVVMAMVKRKN SRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILF LVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKC FLLLELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECEELEEK NIKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSLQITCPPPM MSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAIIVPGSQLMPSKSPSTGTTEISSHES SHGTPSQTTAKNWE LTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAM EALPVTWGTSSRDEDLENC SHHL	183

Description	Sequence	SEQ ID NO:
C α (murine, cysteine- and LIV-substituted)-fP2A-mbIL15-fT2A	NIQNPEPAVYQLKDPQRSQDSTLCFLTFDFSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNG NVTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSG GGGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGEGRS LLTCGDVEENPGP	184
C α (murine, cysteine- and LIV-substituted)-fT2A-mbIL15-fP2A	NIQNPEPAVYQLKDPQRSQDSTLCFLTFDFSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNGN VTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLT ECVLN KATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSP GKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAKRSGSGATNFS LKQAGDVEENPGP	185
C β (murine, cysteine-substituted)-fP2A	EDLRNVT PPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGATNFSLLKQAGDVEENPGP	186
C α (murine, cysteine- and LIV-substituted)-fT2A-mbIL15	NIQNPEPAVYQLKDPQRSQDSTLCFLTFDFSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLYT ESDVHPSCKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNGN VTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGG GGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLT ECVLN KATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSP GKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	187
C β (murine, cysteine-substituted)-fT2A	EDLRNVT PPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGEGRSLLTCGDVEENPGP	188
C α (murine, cysteine- and LIV-substituted)-fP2A-mbIL15	NIQNPEPAVYQLKDPQRSQDSTLCFLTFDFSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLVLVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWNVVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNG NVTESGCKECELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSG GGGSGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTPSLKCI RDPALVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHL	189

Description	Sequence	SEQ ID NO:
Cβ (murine, cysteine-substituted)-fP2A-mbIL15-fT2A	EDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGATNFSLLKQAGDVEENPGMDWTWILF LVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKC FLEELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECEEELEEK NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSLQITCPPP MSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA ATTAAIVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAM EALPVTWGTSSRDEDLNCSHHLRAKRSGSGEGRGSLLTCGDVEENPGP	190
Cβ (murine, cysteine-substituted)-fT2A-mbIL15-fP2A	EDLRNVTTPKVSLEFESKAEIANKQKATLVCLARGFFPDHVELSWVNGKEV HSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFHGLSEEDK WPEGSPKPVTONISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYA VLVSTLVVMAMVKRKNRAKRSGSGEGRGSLLTCGDVEENPGMDWTWILFL VAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCF LLEELQVISLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECEEELEEK NIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTT PSLKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTA TTAAIVPGSQLMPSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQ PPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYLKSRQTPPLASVEMEAME ALPVTWGTSSRDEDLNCSHHLRAKRSGSGATNFSLLKQAGDVEENPGP	191

Table 10C. Exemplary amino acid sequences encoded by polycistronic expression cassettes

Description	Sequence	SEQ ID NO:
Cα (murine, LIV substituted)-fP2A	NIQNPEPAVYQLKDPRSQDSTLCFLTFDFSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLIVLRIILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGP	210
Cα (murine, LIV substituted)-fT2A	NIQNPEPAVYQLKDPRSQDSTLCFLTFDFSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLIVLRIILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGP	212
Cα (murine, LIV substituted)-fP2A-mbIL15-fT2A	NIQNPEPAVYQLKDPRSQDSTLCFLTFDFSQINVPKTMESGTFITDKTVLDM KAMDSKSNGAIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLIVLRIILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLY TESDVHPSCKVTAMKCFLEELQVISLES GDASIHDTVENLII LANNSLSSNG NVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSG GGGSGGSLQITCPPPMMSVEHADIWVKSYSLSRERYICNSGFKRKAGTSSL TECVLNKATNVAHWTTPSLKCIRD PALVHQRPAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAAIVPGSQLMPSPSTGTTEISSHESHGTPS QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSL LACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHLRAKRSGSGEGRGS LLTCGDVEENPGP	214

Description	Sequence	SEQ ID NO:
α (murine, LIV substituted)-fT2A-mbIL15-fP2A	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKTVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYT ESDVHPSCVKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNGN VTESGCKECELEEKNIKEFLQSFVHIVQMFINTESSGGGSGGGGSGGGGSGG GGGSGGSLQITCPPPMSVEHADIWKSYSLSYRERYICNSGFKRKAGTSSLT ECVLNKATNVAHWTPSLKCIKIRDPALVHQRPAAPPSTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHLRAKRSGSGATNFSL LKQAGDVEENPGP	215
α (murine, LIV substituted)-fT2A-mbIL15	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKTVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLLTCGD VEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLYT ESDVHPSCVKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNGN VTESGCKECELEEKNIKEFLQSFVHIVQMFINTESSGGGSGGGGSGGGGSGG GGGSGGSLQITCPPPMSVEHADIWKSYSLSYRERYICNSGFKRKAGTSSLT ECVLNKATNVAHWTPSLKCIKIRDPALVHQRPAAPPSTVTTAGVTPQPESLSPS GKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ TTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLK SRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	217
α (murine, LIV substituted)-fP2A-mbIL15	NIQNPEPAVYQLKDPRSQDSTLCLETFDSDQINVPKTMESGTFITDKTVLDM KAMDSKSNAGIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDM NLNFQNLIVIVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAG DVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATLY TESDVHPSCVKVTAMKCFLELQVISLESGDASIHDVTENLIILANNSLSSNG NVTESGCKECELEEKNIKEFLQSFVHIVQMFINTESSGGGSGGGGSGGGGSGG GGGSGGSLQITCPPPMSVEHADIWKSYSLSYRERYICNSGFKRKAGTSSL TECVLNKAATNVAHWTPSLKCIKIRDPALVHQRPAAPPSTVTTAGVTPQPESLSP SGKEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQ QTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYL KSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	219

[00423] Tables 11A, B and C below provide exemplary polynucleotide sequences for use in constructing vectors of the present disclosure. As shown in Tables 11A, B and C, vectors of the present disclosure can include one or more of the following sequences: (1) an “AP” sequence which encodes (i) a α sequence disclosed herein and (ii) a P2A element sequence disclosed herein; (2) a “BT” sequence which encodes (i) a β sequence disclosed herein and (ii) a T2A element sequence disclosed herein; (3) a “BT15” sequence which encodes (i) a β sequence disclosed herein, (ii) a T2A element sequence disclosed herein, and (iii) a mbIL15 sequence disclosed herein; (4) an “AT” sequence which encodes (i) a α sequence disclosed herein and (ii) a T2A element sequence disclosed herein; (5) a “BP” sequence which encodes (i) a β sequence disclosed herein and (ii) a P2A element sequence disclosed herein; (6) a “BP15” sequence which encodes (i) a β sequence disclosed herein, (ii) a P2A element sequence disclosed herein, and (iii)

a mbIL15 sequence disclosed herein; (7) an “AP15” sequence which encodes (i) a C α sequence disclosed herein, (ii) a P2A element sequence disclosed herein, and (iii) a mbIL15 sequence disclosed herein; (8) a “15T” sequence which encodes (i) a mbIL15 sequence disclosed herein and (ii) a T2A element sequence disclosed herein; (9) an “AP15T” sequence which encodes (i) a C α sequence disclosed herein, (ii) a P2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a T2A element sequence disclosed herein (10) an “AT15” sequence which encodes (i) a C α sequence disclosed herein, (ii) a T2A element sequence disclosed herein, and (iii) a mbIL15 sequence disclosed herein; (11) a “15P” sequence which encodes (i) a mbIL15 sequence disclosed herein, and (ii) a P2A element sequence disclosed herein; (12) an “AT15P” sequence which encodes (i) a C α sequence disclosed herein, (ii) a T2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a P2A element sequence disclosed herein; (13) an “BP15T” sequence which encodes (i) a C β sequence disclosed herein, (ii) a P2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a T2A element sequence disclosed herein; (14) an “BT15P” sequence which encodes (i) a C β sequence disclosed herein, (ii) a T2A element sequence disclosed herein, (iii) a mbIL15 sequence disclosed herein, and (iv) a P2A element sequence disclosed herein.

[00424] The nucleotide sequences provided herein (and their corresponding amino acid sequences) may be used in any appropriate combination. An “appropriate combination” is a combination where desired molecular function(s) are provided by one or more of the sequences disclosed herein. For example, in general, any 2A element sequence provided herein can provide the function of ribosome skipping (via the 2A element) and, optionally, furin-mediated cleavage (via the furin recognition site). Thus, an “AT” sequence in a vector of the present disclosure could, in alternative embodiments, be replaced by an “AP” sequence of the present disclosure. Similarly, “AE” and “AF” sequences, comprising C α region sequences and E2A or F2A element sequences can also be used. “BT,” “BP,” “BE,” and “BF” sequences comprising C β region sequences and 2A element sequences are all also interchangeable. “15T,” “15P,” “15E,” and “15F” sequences comprising mbIL15 sequences and 2A element sequences are all also interchangeable. Additionally, any combination of TCR α , TCR β , and mbIL15 sequences may appear from 5’ to 3’ on a vector of the present disclosure in any order and may be separated by sequences which provide appropriate 2A element sequence function (e.g., ribosome skipping, furin cleavage).

[00425] Accordingly, sequences of the present disclosure provide ribosome skipping, furin recognition, TCR α function, TCR β function, and mbIL15 function in any appropriate combination

or 5' to 3' order.

Table 11A. Exemplary polynucleotide sequences for use in polycistronic expression cassettes.

Description	Sequence	SEQ ID NO:
AP nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCCGACTTTGATAGCCAGATCAACGTGCCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	230
BT nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCAGCTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAGATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCTATCAGCAGGGCGTGCTGCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT NNN at positions 169-171 make up a codon that encodes Ser or Cys	231
BT15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCAGCTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACCCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTTCACGGCCTGTCCGAGGAGATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCTATCAGCAGGGCGTGCTGCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCAGAGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGAAAAGCGGAGATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCCTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGCGAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG	232

Description	Sequence	SEQ ID NO:
	TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGATTAGAGATCCTGCC CTGGTCCACCAGAGGCCTGCCCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGAAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 169-171 make up a codon that encodes Ser or Cys	
AT nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGACACTGTGCTGTTCCACGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCT NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	233
BP nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 169-171 make up a codon that encodes Ser or Cys	234
BP15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 169-171 make up a codon that encodes Ser or Cys	235

Description	Sequence	SEQ ID NO:
	CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAGTG ACCGCCATGAAGTGTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCAGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGCAGATGTTTCATCAATAACAAGCTCTGGCGGAGGATCTGGAGGAGC GGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTG AAGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGCGCGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCAGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCCTGCTGTGT GGACTGTCTGCCGTGTCTGTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 169-171 make up a codon that encodes Ser or Cys	
AP15 nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATAACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAAGT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCCGCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT	236

Description	Sequence	SEQ ID NO:
	CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
15T nucleotide sequence	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCAC AGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATC CAGAGCATGCACATTGATGCCACCCGTACACAGAATCTGATGTGCACCCCT AGCTGTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATT TCTCTGGAAAGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATC ATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGC TGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAG AGCTTTGTGCACATCGTGCAGATGTTTCAATACAAGCTCTGGCGGAGGA TCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGC GGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCC GATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGC AACAGCGGCTTTAAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTG CTGAATAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGC ATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTG ACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAA GAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCC GCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGC ACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACC ACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGA GTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACA GTGCTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAG TCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCC CTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGT TCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGT CTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	237
AP15T nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCTGTTTACCAGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCACAAGNNNGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAAGATCTGNNNGTCNNNNNNCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA	238

Description	Sequence	SEQ ID NO:
	AAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
AT15 nucleotide sequence	NNNATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTGCCCTAAACAAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCGCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTGCTGGAGCTGCAGGTGATTTCTCTGAAAGCGGAGATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGAGGAGAAGAATCATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGCCTGCCCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr;	239

Description	Sequence	SEQ ID NO:
	NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
15P nucleotide sequence	ATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTCTCTGGAAAGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCAGCCGATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGC AACAGCGGCTTTAAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCTCCATCTACAGTACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAA GAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCAGAGGCAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGCCACTCTGATACACAGTGGCCATCAGCAGATCTACAGTGCTGTGTGGACTGTCTGCCGTGTCTGTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	240
AT15P nucleotide sequence	NNNATCCAGAATCCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCTGTTCACCGACTTTGATAGCCAGATCAACGTGCCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGNNNGTGCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGNNNGTCNNNNNNCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTACAGCCTGTACAGCAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT	241

Description	Sequence	SEQ ID NO:
	CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAA CGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGAT GTGGAGGAGAACCCTGGCCCA NNN at positions 1-3 make up a codon that encodes Asn, Asp, His, or Tyr; NNN at positions 142-144 make up a codon that encodes Thr or Cys; NNN at positions 334-336 make up a codon that encodes Ser, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp; NNN at positions 340-342 make up a codon that encodes Met, Ala, Val, Leu, Ile, Pro, Phe, or Trp; NNN at positions 343-345 make up a codon that encodes Gly, Ala, Val, Leu, Ile, Pro, Phe, Met, or Trp	
BP15T nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAGTG ACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCAGCACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGAGATGTTTCATCAATAACAAGCTCTGGCGGAGGATCTGGAGGAGGC GGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTG AAGTCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCAATTAGAGATCCT GCCCTGGTCCACCAGAGGCCCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGTGTGT GGACTGTCTGCCGTGTCTGTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG CGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGC GGTGACGTGGAGGAGAATCCCGGCCCT	242

Description	Sequence	SEQ ID NO:
	NNN at positions 169-171 make up a codon that encodes Ser or Cys	
BT15P nucleotide sequence	GAGGACCTGAGGAACGTGACCCCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGNNNACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGG ATTCTGTTTCTGGTGGCGCTGCCACAAGAGTGACAGCAACTGGGTGAAT GTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATT GATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACC GCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGAAAAGCGGA GATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAG GAGCTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAG ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTCTCACCACCTGCGG GCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCTGCTGAAGCAGGCG GGCGATGTGGAGGAGAACCCTGGCCCA NNN at positions 169-171 make up a codon that encodes Ser or Cys	243

Table 11B. Exemplary polynucleotide sequences for use in polycistronic expression cassette.

Description	Sequence	SEQ ID NO:
AP nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	250
BT nucleotide	GAGGACCTGAGGAACGTGACCCCCACCTAAAGTGAGCCTGTTTCGAGCCATCC	251

Description	Sequence	SEQ ID NO:
sequence	AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCAGCTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	
BT15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCAGCTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGG ATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAAT GTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATT GATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACC GCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGA GATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAG GAGCTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAG ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG TCCTACAGCCTGTACAGCAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCTGCCCCCTCATCTACAGTGACAACAGCCGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCAGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	252
AT nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCAGACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGTGCCTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAAGATCTGCTGGTCACTCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT	253

Description	Sequence	SEQ ID NO:
	TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCT	
BP nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	254
BP15 nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTG ACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCTTGCCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGC GGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAATGTCTGTGGAGCAGCCGATATTTGGGTG AAGTCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGGTGTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCCTGCCCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCAGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGT GGACTGTCTGCCGTGTCTGTCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	255
AP15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGCACACTGTGCCTGTTTACCAGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG	256

Description	Sequence	SEQ ID NO:
	CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	
AP15T nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCT CAGGATAGCACACTGTGCCTGTTCCCGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTG	258

Description	Sequence	SEQ ID NO:
	TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCT	
AT15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTGCCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCGTGCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCCCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGTGCGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGT TTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGACAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGGCACCTTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCACTGGACAACACCTAGCCTGAAGTGCAATTAGAGATCCTGCCCTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAG AATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	259
AT15P nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTGCCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCGTGCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCCCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGTGCGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGT TTTCTGGTGGCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGACAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA	261

Description	Sequence	SEQ ID NO:
	GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCCGGCGAAA CGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAGCAGGCGGGCGAT GTGGAGGAGAACCCTGGCCCA	
BP15T nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG GGCTTCTTTCCCGATCAGCTGGAGCTGTCTGGTGGGTGAACGGCAAAGAG GTGCACCTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCATCAGCAG GGCGTGTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCCGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCTG CTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACC TGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTG AATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCAC ATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTG ACCGCCATGAAGTGTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAAC AATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGT GAGGAGCTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCAC ATCGTGCAGATGTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGC GGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTG CAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTG AAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTT AAGAGAAAGCGCGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCC ACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCT GCCCTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGA GTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCC AGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATC AGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAAT TGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAG GGCCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGT GGACTGTCTGCCGTGTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACA CCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACA TGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG CGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGC GGTGACGTGGAGGAGAATCCCGGCCCT	262
BT15P nucleotide sequence	GAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCC AAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCTGGTGTGCCTGGCGAGG	263

Description	Sequence	SEQ ID NO:
	GGCTTCTTTCCCGATCACGTGGAGCTGTCCTGGTGGGTGAACGGCAAAGAG GTGCACTCTGGCGTGTGCACAGACCTCAGGCGTACAAGGAGAGCAATTAC TCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAC CCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAG GATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCG GAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCCTATCAGCAG GGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACA CTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGG AAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTT CTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGG ATTCTGTTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAAT GTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATT GATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACC GCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGA GATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCACAAT AGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAG GAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATC GTGCAGATGTTCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGA TCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAG ATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAG TCCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAG AGAAAGGCCGGCACCTCTTCTCTGACAGAGTGCGTGCTGAATAAGGCCACA AATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTG ACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAGAAGCCTGCCGCCAGC TCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCTTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGC AGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGG GAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGC CACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGA CTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCT CCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGG GGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGG GCGAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCG GGCGATGTGGAGGAGAACCCTGGCCCA	

Table 11C. Exemplary polynucleotide sequences for use in polycistronic expression cassette.

Description	Sequence	SEQ ID NO:
AP nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCA	270
AT nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAAACAATGGAGTCCGGCACCTTCATCACCAGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT	273

Description	Sequence	SEQ ID NO:
	TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCT	
AP15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCGAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGATCCTCAGGGCCAC TCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	276
AP15T nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTCCACCGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGCTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAG CAGGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATT CTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTG ATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGAT GCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCC ATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGAT GCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGC CTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAG CTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTG CAGATGTTTATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCT	278

Description	Sequence	SEQ ID NO:
	GGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATT ACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCC TACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAAT GTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTG GTCCACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACA CCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCT CCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCT CAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGC CACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAG CTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCAC TCTGATACACAGTGGCCATCAGCACATCTACAGTGTCTGTGTGGACTG TCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCT CTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGA ACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCCGGCG AAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGAC GTGGAGGAGAATCCCGGCCCT	
AT15 nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGACG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	279
AT15P nucleotide sequence	AACATCCAGAATCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCCGCTCT CAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGATCAACGTG CCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGACCGTGTGGAT ATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAG ACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACA GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGACG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	281

Description	Sequence	SEQ ID NO:
	GACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGCTGAGAATCCTG CTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGT TCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACA TGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTG TTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATC AGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCC ACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATG AAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCC TCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTG AGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTG GAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAG ATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGA GGAGGAGGCACTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACA TGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTGGGTGAAGTCTCTAC AGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTG GCCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTC CACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCT CAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCT AGCTCTAATAATACCGCGCCACAACAGCCGCCATTGTGCCTGGATCTCAG CTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCAC GAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTG ACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCT GATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCT GCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTG GCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACA AGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCCGGCGAAA CGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAGCAGGCGGGCGAT GTGGAGGAGAACCCTGGCCCA	

5.7 Transposon and Transposase Systems

[00426] In some embodiments, transgenes of the recombinant vector are introduced into an immune effector cell via synthetic DNA transposable elements, *e.g.*, a DNA transposon/transposase system, *e.g.*, *Sleeping Beauty* (SB). SB belongs to the Tc1/mariner superfamily of DNA transposons. DNA transposons translocate from one DNA site to another in a simple, cut-and-paste manner. Transposition is a precise process in which a defined DNA segment is excised from one DNA molecule and moved to another site in the same or different DNA molecule or genome.

[00427] Exemplary DNA transposon/transposase systems include, but are not limited to, *Sleeping Beauty* (see, *e.g.*, US6489458, US8227432, the contents of each of which are incorporated by reference in their entirety herein), piggyBac transposon system (see *e.g.*, US9228180, Wilson et al, “PiggyBac Transposon-mediated Gene Transfer in Human Cells,” *Molecular Therapy*, 15:139-145 (2007), the contents of each of which are incorporated by reference in their entirety herein), piggyBac transposon system (see *e.g.*, Mitra *et al.*, “Functional

characterization of piggyBac from the bat *Myotis lucifugus* unveils an active mammalian DNA transposon,” *Proc. Natl. Acad. Sci. USA* 110:234- 239 (2013), the contents of which are incorporated by reference in their entirety herein), TcBuster (*see e.g.*, Woodard *et al.* “Comparative Analysis of the Recently Discovered hAT Transposon TcBuster in Human Cells,” *PLOS ONE*, 7(11): e42666 (Nov. 2012), the contents of which are incorporated by reference in their entirety herein), and the Tol2 transposon system (*see e.g.*, Kawakami, “Tol2: a versatile gene transfer vector in vertebrates,” *Genome Biol.* 2007; 8(Suppl 1): S7, the contents of each of which are incorporated by reference in their entirety herein). Additional exemplary transposon/transposase systems are provided in US7148203; US8227432; US20110117072; Mates *et al.*, *Nat Genet.* 41(6):753- 61 (2009); and Ivies *et al.*, *Cell*, 91(4):501-10, (1997), the contents of each of which are incorporated by reference in their entirety herein).

[00428] In some embodiments, the transgenes described herein are introduced into an immune effector cell via the SB transposon/transposase system. The SB transposon system comprises a SB a transposase and SB transposon(s). The SB transposon system can comprise a naturally occurring SB transposase or a derivative, variant, and/or fragment that retains activity, and a naturally occurring SB transposon, or a derivative, variant, and/or fragment that retains activity. An exemplary SB system is described in, Hackett *et al.*, “A Transposon and Transposase System for Human Application,” *Mol Ther* 18:674-83, (2010), the entire contents of which are incorporated by reference herein.

[00429] In some embodiments, the vector comprises a Left inverted terminal repeat (ITR), *i.e.*, an ITR that is 5' to an expression cassette, and a Right ITR, *i.e.*, an ITR that is 3' to an expression cassette. The Left ITR and Right ITR flank the polycistronic expression cassette of the vector. In some embodiments, the Left ITR is in reverse orientation relative to the polycistronic expression cassette, and the Right ITR is in the same orientation relative to the polycistronic expression cassette. In some embodiments, the Right ITR is in reverse orientation relative to the polycistronic expression cassette, and the Left ITR is in the same orientation relative to the polycistronic expression cassette.

[00430] In some embodiments, the Left ITR and the Right ITR are ITRs of a DNA transposon selected from the group consisting of a *Sleeping Beauty* transposon, a piggyBac transposon, TcBuster transposon, and a Tol2 transposon. In some embodiments, the Left ITR and the Right ITR are ITRs of the *Sleeping Beauty* DNA transposon.

[00431] In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290 or 291. In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290. In some embodiments, the Left ITR comprises the polynucleotide sequence of SEQ ID NO: 290. In some embodiments, the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 291. In some embodiments, the Left ITR comprises the polynucleotide sequence of SEQ ID NO: 291. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292, 293, or 294. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 293. In some embodiments, the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 294. In some embodiments, the Right ITR comprises the polynucleotide sequence of SEQ ID NO: 292. In some embodiments, the Right ITR comprises the polynucleotide sequence of SEQ ID NO: 293. In some embodiments, the Right ITR comprises the polynucleotide sequence of SEQ ID NO: 294.

[00432] The polynucleotide sequences of exemplary SB ITRs are provided in Table 12, herein.

Table 12. Polynucleotide sequence of exemplary SB ITRs.

Description	Polynucleotide Sequence	SEQ ID NO
Left ITR – A	AGTTGAAGTCGGAAGTTTACATACACTTAAGTTGGAGTCATTA CTCGTTTTTCACTACTCCACAAATTTCTTGTTAACAACAATAGT TTTGGCAAGTCAGTTAGGACATCTACTTTGTGCATGACACAAGTCA TTTTTCCAACAATTGTTTACAGACAGATTATTTCACTTATAATTCA CTGTATCACAATTCAGTGGGTCAGAAGTTTACATACACTAA	290
Left ITR – A2	TACAGTTGAAGTCGGAAGTTTACATACACTTAAGTTGGAGTCATTA AACTCGTTTTTCACTACTCCACAAATTTCTTGTTAACAACAAT AGTTTTGGCAAGTCAGTTAGGACATCTACTTTGTGCATGACACAAG TCATTTTTCCAACAATTGTTTACAGACAGATTATTTCACTTATAAT TCACTGTATCACAATTCAGTGGGTCAGAAGTTTACATACACTAA	295
Left ITR – B	ATATCAATTGAGTTGAAGTCGGAAGTTTACATACACTTAAGTTGGA GTCATTAACACTCGTTTTTCACTACACCACAAATTTCTTGTTAAT AAACAATAGTTTTTGGCAAGTCAGTTAGGACATCTACTTTGTGCATG	291

Description	Polynucleotide Sequence	SEQ ID NO
	ACACAAGTCATTTTCCAACAATTGTTTACAGACAGATTATTTTCAC TTATAATTCACGTGATCACAATTCAGTGGGTGAGAAGTTTACATA CACTAACAAATTGATAT	
Right ITR – A	TTGAGTGTATGTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAATAAAGTGGTGATCCTAACTGACCTAAGACAGGG AATTTTACTAGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTTT AAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACTG	292
Right ITR – A2	TTGAGTGTATGTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAATAAAGTGGTGATCCTAACTGACCTAAGACAGGG AATTTTACTAGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTTT AAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACTGTA	296
Right ITR – B	TTGAGTGTATGTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAATAAAGTGGTGATCCTAACTGACCTAAGACAGG GAATCTTTACTCGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTT TAAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACT	293
Right ITR – B2	TTGAGTGTATGTAACTTCTGACCCACTGGGAATGTGATGAAAGAA ATAAAAGCTGAAATGAATCATTCTCTCTACTATTATTCTGATATTT CACATTCTTAAATAAAGTGGTGATCCTAACTGACCTAAGACAGG GAATCTTTACTCGGATTAAATGTCAGGAATTGTGAAAAAGTGAGTT TAAATGTATTTGGCTAAGGTGTATGTAACTTCCGACTTCAACTGT A	297
Right ITR – C	ATATCTCGAGTTGAGTGTATGTTAACTTCTGACCCACTGGGAATGT GATGAAAGAAATAAAAGCTGAAATGAATCATTCTCTCTACTATTAT TCTGATATTTACATTCTTAAATAAAGTGGTGATCCTAACTGACC TTAAGACAGGGAATCTTTACTCGGATTAAATGTCAGGAATTGTGAA AAAGTGAGTTTAAATGTATTTGGCTAAGGTGTATGTAACTTCCGA CTTCAACTCTCGAGATAT	294

[00433] In some embodiments, the DNA transposase is a SB transposase. In some embodiments, the SB transposase is selected from the group consisting of SB11, SB100X, hSB110, and hSB81. In some embodiments, the SB transposase is SB11. Exemplary SB transposases are described in US9840696, US20160264949, US9228180, WO2019038197, US10174309, and US10570382, the full contents of each of which is incorporated by reference herein.

[00434] In some embodiments, the DNA transposase comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300. In some embodiments, the DNA transposase comprises the amino acid sequence of SEQ ID NO: 300. In some embodiments, the amino acid sequence of the DNA transposase consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300. In some embodiments, the amino acid sequence of the DNA transposase consists of the amino acid sequence of SEQ ID NO: 300.

[00435] In some embodiments, the DNA transposase comprises an amino acid sequence that

lacks its N-terminal methionine. In some embodiments, the DNA transposase comprises an amino acid sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300. In some embodiments, the DNA transposase comprises the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300. In some embodiments, the amino acid sequence of the DNA transposase consists of a sequence at least 95%, 96%, 97%, 98%, 99% or 100% identical to the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300. In some embodiments, the amino acid sequence of the DNA transposase consists of the amino acid sequence of SEQ ID NO: 300 lacking its N-terminal methionine, *i.e.*, amino acids 2-340 of SEQ ID NO:300.

[00436] In some embodiments, the DNA transposase is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 301. In some embodiments, the DNA transposase is encoded by the polynucleotide sequence of SEQ ID NO: 301.

[00437] In some embodiments, the DNA transposase is encoded by a polynucleotide that is introduced into a cell. In some embodiments, the polynucleotide encoding the DNA transposase is a DNA vector. In some embodiments, the polynucleotide encoding the DNA transposase is an RNA vector. In some embodiments, the DNA transposase is encoded on a first vector and the transgenes are encoded on a second vector. In some embodiments, the DNA transposase is directly introduced to a population of cells as a polypeptide.

[00438] The amino acid and polynucleotide sequence of an exemplary SB transposase is provided in Table 13, herein.

Table 13. Amino acid and polynucleotide sequence of an exemplary SB transposase.

Description	Sequence	SEQ ID NO
SB11 (exemplary amino acid sequence)	MGKSKEISQDLRKKIVDLHKSGLGAIKRLKVPRSSVQTIVRKYKH HGTTQPSYRSGRRRVLSPRDERTLVRKVQINPRTAKDLVKMLEETGT KVSISTVKRVLYRHNKGRSARKKPLLQNRHKKARLRFARAHGDKDRT FWRNVLWSDETKIELFGHNDHRYVWRKKGEACKPKNTIPTVKHGGGSI MLWGCFAAGGTGALHKIDGIMRKENYVDILKQHLKTSVRKCLKGRKWV FQQDNDPKHTSKHVRKWLKDNKVKVLEWPSQSPDLNPIENLWAEKKR VRARRPTNLTQLHQLCQEEWAKIHPTYCGKLVEGYPKRLTQVKQFKGN ATKY	300
SB11 (exemplary nucleotide sequence)	ATGGGAAAATCAAAAGAAATCAGCCAAGACCTCAGAAAAAAATTGTA GACCTCCACAAGTCTGGTTCATCCTTGGGAGCAATTTCAAACGCCTG AAAGTACCACGTTCTGTGTACAAACAATAGTACGCAAGTATAAACAC CATGGGACCACGCAGCCGTCATACCGCTCAGGAAGGAGACGCGTTCTG	301

Description	Sequence	SEQ ID NO
	TCTCCTAGAGATGAACGTACTTTGGTGCGAAAAAGTGCAAATCAATCCC AGAACAACAGCAAAGGACCTTGTGAAGATGCTGGAGGAAACAGGTACA AAAGTATCTATATCCACAGTAAACGAGTCCTATATCGACATAACCTG AAAGGCCGCTCAGCAAGGAAGAAGCCACTGCTCCAAAACCGACATAAG AAAGCCAGACTACGGTTTGCAAGAGCACATGGGGACAAAGATCGTACT TTTTGGAGAAATGTCCTCTGGTCTGATGAAACAAAAATAGAACTGTTT GGCCATAATGACCATCGTTATGTTGGAGGAAGAAGGGGGAGGCTTGC AAGCCGAAGAACACCATCCCAACCGTGAAGCACGGGGGTGGCAGCATC ATGTTGTGGGGGTGCTTTGCTGCAGGAGGGACTGGTGCACCTTCACAAA ATAGATGGCATCATGAGGAAGGAAAATTATGTGGATATATTGAAGCAA CATCTCAAGACATCAGTCAGGAAGTTAAAGCTTGGTCGCAAATGGGTC TTCCAACAAGACAATGACCCCAAGCATACTTCCAAACACGTGAGAAAA TGGCTTAAGGACAACAAAGTCAAGGTATTGGAGTGGCCATCACAAAGC CCTGACCTCAATCCTATAGAAAATTTGTGGGCAGAACTGAAAAAGCGT GTGCGAGCAAGGAGGCCTACAAACCTGACTCAGTTACACCAGCTCTGT CAGGAGGAATGGGCCAAAATTCACCCAACCTTATGTGGGAAGCTTGTG GAAGGCTACCCGAAACGTTTGACCCAAGTTAAACAATTTAAAGGCAAT GCTACCAAATAC	

5.8 Immune Effector Cells and Methods of Engineering

[00439] In one aspect, provided herein are cells, *e.g.*, immune effector cells, comprising a recombinant vector comprising a polycistronic expression cassette (*e.g.*, a vector described herein). In some embodiments, the immune effector cell is a T cell. For example, in certain embodiments, the T cell is selected from the group consisting of a naïve T cell (CD4⁺ or CD8⁺); a killer CD8⁺ T cell; a cytotoxic CD4⁺ T cell; a CD4⁺ T cell corresponding to Th1, Th2, Th9, Th17, Th22, follicular helper (Tfh), regulatory (Treg) lineages; a CD8⁺ cytotoxic T cell, a CD4⁺ cytotoxic T cell; a CD4⁺ helper T cell (*e.g.*, a Th1 or a Th2 cell); a CD4/CD8 double positive T cell; a tumor infiltrating T cell (TIL); a thymocyte; a memory T cell, (*e.g.*, a central memory T cell, an effector memory T cell, a stem cell-like memory T cell, or a stem cell memory T cell), and a natural killer T cell, *e.g.*, an invariant natural killer T cell. In some embodiments, the T cell is a CD39^{neg}CD69^{neg} T cell or a CD8⁺CD39^{neg}CD69^{neg} cell, as described, *e.g.*, in Krishna *et al.*, “Stem-like CD8 T cells mediate response of adoptive cell immunotherapy against human cancer,” 2020 370(6522):1328-1334, which is incorporated by reference herein in its entirety. Precursor cells of the cellular immune system (*e.g.*, precursors of T lymphocytes) are also useful for presenting a TCR disclosed herein because these cells may differentiate, develop, or mature into effector cells. Accordingly, in certain embodiments, the mammalian cell is a pluripotent stem cell (*e.g.*, an embryonic stem cell, an induced pluripotent stem cell), a hematopoietic stem cell, or a lymphocyte progenitor cell. In certain embodiments, the hematopoietic stem cell or lymphocyte progenitor cell is isolated and/or enriched from, *e.g.*, bone marrow, umbilical cord blood, or peripheral blood. In some

embodiments, the immune effector cell is a CD4⁺ T cell. In some embodiments, the immune effector cell is a CD8⁺ T cell. In one aspect, provided herein is a population of immune effector cells comprising a polycistronic vector described herein. In some embodiments, the population of immune effector cells comprises CD4⁺ T cells and CD8⁺ T cells. In some embodiments, the population of immune effector cells are an *ex vivo* culture.

[00440] In one aspect, provided herein are methods of introducing a vector described herein into a plurality of cells, *e.g.*, immune effector cells, to produce a plurality of engineered cells, *e.g.*, immune effector cells. Methods of introducing vectors into a cell are well known in the art. In the context of an expression vector, the vector can be readily introduced into a host cell, *e.g.*, mammalian (*e.g.*, human) cell by any method in the art. For example, the expression vector can be transferred into a host cell by transfection or transduction. Exemplary methods for introducing a vector into a host cell, include, but are not limited to, electroporation (also referred to herein as electro-transfer), sonication, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, mechanical deformation by passage through a microfluidic device, and the like, *see, e.g.*, Sambrook *et al.* Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York (2001), the entire contents of which is incorporated by reference herein. In some embodiments, a polycistronic vector is introduced into an immune effector cell or population of immune effector cells via electroporation. Alternative delivery systems include, *e.g.*, colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. In some embodiments, the polycistronic vector is introduced into a population of cells, *e.g.*, immune effector cells, *ex vivo*, *in vitro*, or *in vivo*. In some embodiments, the polycistronic vector is introduced into a population of cells, *e.g.*, immune effector cells, *ex vivo*.

[00441] In some embodiments, co-expression of mbIL-15 with a transgenic TCR in T cells produces a final drug product that contains T stem cell memory cells (Tscm) which are capable of self-renewal and differentiation into other effector T cell subsets. The expression of mbIL-15 on T cells maintains a population of self-renewing T stem cell memory or T stem cell memory like (Tscm-like) cells that are defined by the surface marker phenotype CD45RA⁺CD45RO⁻CD62L⁺CD95⁺ or CD45RA⁺CD45RO⁺CD62L⁺CD95⁺, respectively. In some embodiments, expression of mbIL-15 on T cells is able to maintain Tscm or Tscm-like subsets as defined above in the absence of external growth and survival factors (*i.e.*, cytokines or antigen stimulation).

[00442] In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic

TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% Tscm cells. In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% Tscm-like cells. In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95+ cells. In some embodiments, populations of T cells co-expressing mbIL-15 with a transgenic TCR produced by the tricistronic vectors described herein comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95+ cells.

5.8.1 Sources of immune effector cells

[00443] Immune effector cells may be obtained from a subject by any suitable method known in the art. For example, T cells (*e.g.*, CD4+ T cells and CD8+ T cells) can be obtained from several sources, including peripheral blood mononuclear cells, bone marrow, lymph node tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen tissue, and tumors. In some embodiments, immune effector cells (*e.g.*, T cells) are obtained from blood collected from a subject using any number of techniques known to the skilled artisan. In some embodiments, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocytes, B cells, other nucleated white blood cells, red blood cells, and platelets. T cells are isolated from peripheral blood lymphocytes by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a Percoll gradient or by counter flow centrifugal elutriation.

[00444] The cells collected by apheresis can be washed to remove the plasma fraction and to place the cells in an appropriate buffer (*e.g.*, phosphate buffered saline (PBS)) or media for subsequent processing steps. The washing step may be accomplished by methods known to those in the art, such as by using a semi-automated “flow-through” centrifuge. After washing, the cells may be resuspended in a variety of biocompatible buffers, such as, for example, Ca-free, Mg-free PBS, PlasmaLyte A, or other saline solution with or without buffer. Alternatively, the undesirable components of the apheresis sample may be removed and the cells directly resuspended in culture media.

[00445] A specific subpopulation of cells can be further isolated by positive or negative

selection techniques (*e.g.*, antibody coated beads, flow cytometry, etc.). In some embodiments, a specific subpopulation of T cells, such as CD3⁺, CD28⁺, CD4⁺, CD8⁺, CD45RA⁺, and CD45RO⁺T cells, can be further isolated by positive or negative selection techniques (*e.g.*, antibody coated beads, flow cytometry, etc.).

[00446] In certain embodiments, the mammalian cell is a population of cells presenting a TCR disclosed herein on the cell surface. The population of cells can be heterogeneous or homogenous. In certain embodiments, at least 50% (*e.g.*, at least 60%, 70%, 80%, 90%, 95%, 99%, 99.5%, or 99.9%) of the population is a cell as described herein. In certain embodiments, the population is substantially pure, wherein at least 50% (*e.g.*, at least 60%, 70%, 80%, 90%, 95%, 99%, 99.5%, or 99.9%) of the population is homogeneous. In certain embodiments, the population is heterogeneous and comprises a mixed population of cells (*e.g.*, the cells have different cell types, developmental stages, origins, are isolated, purified, or enriched by different methods, are stimulated with different agents, and/or are engineered by different methods). In certain embodiments, the cells are a population of peripheral blood mononuclear cells (PBMC) (*e.g.*, human PBMCs).

[00447] Populations of cells can be enriched or purified, as needed. In certain embodiments, regulatory T cells (*e.g.*, CD25⁺ T cells) are depleted from the population, *e.g.*, by using an anti-CD25 antibody conjugated to a surface such as a bead, particle, or cell. In certain embodiments, an anti-CD25 antibody is conjugated to a fluorescent dye (*e.g.*, for use in fluorescence-activated cell sorting). In certain embodiments, cells expressing checkpoint receptors (*e.g.*, CTLA-4, PD-1, TIM-3, LAG-3, TIGIT, VISTA, BTLA, TIGIT, CD137, or CEACAM1) are depleted from the population, *e.g.*, by using an antibody that binds specifically to a checkpoint receptor conjugated to a surface such as a bead, particle, or cell. In certain embodiments, a T cell population can be selected so that it expresses one or more of IFN- γ , TNF α , IL-17A, IL-2, IL-3, IL-4, GM-CSF, IL-13, granzyme (*e.g.*, granzyme B), and perforin, or other appropriate molecules, *e.g.*, other cytokines. Methods for determining such expression are described, for example, in PCT Publication No.: WO 2013/126712, which is incorporated by reference herein in its entirety.

5.8.2 Methods of Manufacture

[00448] Engineered cells described herein can be manufactured by any method known in the art. Exemplary methods are shown in U.S. Patent Publication No. 2020/0347350 and International Publication No. WO 2019/067242, incorporated by reference in their entireties.

5.9 Pharmaceutical Compositions

[00449] Provided herein are pharmaceutical compositions comprising a population of engineered immune effector cells disclosed herein having the desired degree of purity in a physiologically acceptable carrier, excipient or stabilizer (see, *e.g.*, Remington's Pharmaceutical Sciences (1990) Mack Publishing Co., Easton, PA). Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (*e.g.*, Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[00450] Pharmaceutical compositions described herein can be useful in inducing an immune response in a subject and treating a condition, such as cancer. In one embodiment, the present disclosure provides a pharmaceutical composition comprising a population of engineered immune effector cells described herein for use as a medicament. In another embodiment, the disclosure provides a pharmaceutical composition for use in a method for the treatment of cancer. In some embodiments, pharmaceutical compositions comprise a population of engineered immune effector cells disclosed herein, and optionally one or more additional prophylactic or therapeutic agents, in a pharmaceutically acceptable carrier.

[00451] A pharmaceutical composition may be formulated for any route of administration to a subject. Specific examples of routes of administration include parenteral administration (*e.g.*, intravenous, subcutaneous, intramuscular). In some embodiments, the pharmaceutical composition is formulated for intravenous administration. Injectables can be prepared in conventional forms, either as liquid solutions or suspensions. The injectables can contain one or more excipients. Exemplary excipients include, for example, water, saline, dextrose, glycerol or ethanol. In addition, if desired, the pharmaceutical compositions to be administered can also contain minor

amounts of non-toxic auxiliary substances such as wetting or emulsifying agents, pH buffering agents, stabilizers, solubility enhancers, and other such agents, such as for example, sodium acetate, sorbitan monolaurate, triethanolamine oleate and cyclodextrins.

[00452] In some embodiments, the pharmaceutical composition is formulated for intravenous administration. Suitable carriers for intravenous administration include physiological saline or phosphate buffered saline (PBS), and solutions containing thickening and solubilizing agents, such as glucose, polyethylene glycol, and polypropylene glycol and mixtures thereof.

[00453] The compositions to be used for *in vivo* administration can be sterile. This is readily accomplished by filtration through, *e.g.*, sterile filtration membranes.

[00454] Pharmaceutically acceptable carriers used in parenteral preparations include for example, aqueous vehicles, nonaqueous vehicles, antimicrobial agents, isotonic agents, buffers, antioxidants, local anesthetics, suspending and dispersing agents, emulsifying agents, sequestering or chelating agents and other pharmaceutically acceptable substances. Examples of aqueous vehicles include sodium chloride injection, Ringer's injection, isotonic dextrose injection, sterile water injection, dextrose and lactated Ringer's injection. Nonaqueous parenteral vehicles include fixed oils of vegetable origin, cottonseed oil, corn oil, sesame oil and peanut oil. Antimicrobial agents in bacteriostatic or fungistatic concentrations can be added to parenteral preparations packaged in multiple-dose containers which include phenols or cresols, mercurials, benzyl alcohol, chlorobutanol, methyl and propyl p-hydroxybenzoic acid esters, thimerosal, benzalkonium chloride and benzethonium chloride. Isotonic agents include sodium chloride and dextrose. Buffers include phosphate and citrate. Antioxidants include sodium bisulfate. Local anesthetics include procaine hydrochloride. Suspending and dispersing agents include sodium carboxymethylcellulose, hydroxypropyl methylcellulose and polyvinylpyrrolidone. Emulsifying agents include Polysorbate 80 (TWEEN[®] 80). A sequestering or chelating agent of metal ions includes EDTA. Pharmaceutical carriers also include ethyl alcohol, polyethylene glycol and propylene glycol for water miscible vehicles; and sodium hydroxide, hydrochloric acid, citric acid or lactic acid for pH adjustment.

The precise dose to be employed in a pharmaceutical composition will also depend on the route of administration, and the seriousness of the condition caused by it, and should be decided according to the judgment of the practitioner and each subject's circumstances. For example, effective doses may also vary depending upon means of administration, target site, physiological state of the subject (including age, body weight, and health), other medications administered, or whether treatment is prophylactic or therapeutic. Treatment dosages are optimally titrated to optimize

safety and efficacy.

5.10 Kits

[00455] In one aspect, provided herein are kits comprising one or more pharmaceutical composition, population of engineered effector cells (*e.g.*, recombinant cells), polynucleotide, or vector described herein and instructions for use. Such kits may include, *e.g.*, a carrier, package, or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like. Suitable containers include, for example, bottles, vials, syringes, and test tubes. In one embodiment, the containers are formed from a variety of materials such as glass or plastic.

[00456] In a specific embodiment, provided herein is a pharmaceutical kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions described herein, population of engineered immune effector cells, polynucleotides, or vectors provided herein. In one embodiment, the kit comprises a pharmaceutical composition comprising a population of engineered immune effector cells described herein. In one embodiment, the kit comprises a pharmaceutical composition comprising a population of immune effector cells engineered according to a method described herein. In some embodiments, the kit contains a pharmaceutical composition described herein and a prophylactic or therapeutic agent. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

6. EXAMPLES

[00457] The examples of the present disclosure are offered by way of illustration and explanation, and are not intended to limit the scope of the present disclosure.

6.1 Example 1: Construction of Transposon Plasmids

[00458] To improve homogeneity of multigene co-expression and product manufacturability, recombinant nucleic acid SB transposon plasmids comprising polycistronic expression cassettes were constructed. The polycistronic expression cassettes each include a transcriptional regulatory element operably linked to a polycistronic polynucleotide that encodes the TCR α chain of TCR001 (referred to herein as “TCR α ” or “A”), the TCR β chain of TCR001 (referred to herein as “TCR β ” or “B”), and membrane-bound IL-15/IL-15R α fusion protein (referred to herein as “mbIL15” or “15”), each separated by a furin recognition site and either a P2A element or a T2A element that mediates ribosome skipping to enable expression of separate polypeptide chains.

[00459] The TCR used in this Example, TCR001, is a chimeric TCR with murine-derived constant regions and with human V α and V β regions specific for the R175H mutation of the p53 protein (in which position 175 of the p53 protein is mutated from Arg to His) in the context of HLA-A*02:01.

[00460] Briefly, TCR α was generated by fusing a human V α region, including its N-terminal signal sequence (SEQ ID NO: 1006) with a glutamic acid at position 2, to a murine C α region modified by substituting a cysteine at amino acid position 48, a leucine at amino acid position 112, an isoleucine at amino acid position 114, and a valine at amino acid position 115 (SEQ ID NO: 41). TCR β was generated by fusing a human V β region, including its N-terminal signal sequence (SEQ ID NO: 2006) with an alanine at position 2, to a murine C β modified by substituting a cysteine at amino acid position 57 (SEQ ID NO: 51). mbIL15 was constructed by joining human IL-15 (SEQ ID NO: 76) to human IL-15R α (SEQ ID NO: 78) via a Gly-Ser-rich linker peptide (SEQ ID NO: 81), with an IgE signal sequence (SEQ ID NO: 83) N-terminal to the human IL-15. Schematics of each of these three polypeptide constructs are shown in **FIG. 1**, from N terminus (left) to C terminus (right) for each construct.

[00461] To explore the effect of gene/element order on expression and function, eight tricistronic polynucleotide expression cassettes were generated with polynucleotides encoding each of TCR α , TCR β , and mbIL15. In each expression cassette, these three elements were fused pairwise with a) a polynucleotide encoding a furin recognition site joined to a P2A element (SEQ ID NO: 11) (referred to herein as “fP2A” or “P”) and b) a polynucleotide encoding a furin recognition site joined to a T2A element (SEQ ID NO: 13) (referred to herein as “fT2A” or “T”). The resulting tricistronic expression cassettes, including suitable transcriptional regulatory elements, were inserted between the ITRs of *Sleeping Beauty* (SB) transposon plasmids. The 5' to 3' order of elements in the open reading frame (ORF) of each expression cassette and SB Plasmid is shown in **Table E1**, and schematics of the ORFs of these eight expression cassettes are shown in **FIG. 2A**.

Table E1. Tricistronic SB transposon plasmids.

Plasmid Name	Cassette Name	Order of Elements (5' to 3')
Plasmid APBT15	Cassette APBT15	TCR α -fP2A-TCR β -fT2A-mbIL15
Plasmid ATBP15	Cassette ATBP15	TCR α -fT2A-TCR β -fP2A-mbIL15
Plasmid AP15TB	Cassette AP15TB	TCR α -fP2A- mbIL15-fT2A-TCR β
Plasmid AT15PB	Cassette AT15PB	TCR α -fT2A- mbIL15-fP2A-TCR β
Plasmid BPAT15	Cassette BPAT15	TCR β -fP2A-TCR α -fT2A-mbIL15
Plasmid BTAP15	Cassette BTAP15	TCR β -fT2A-TCR α -fP2A-mbIL15

Plasmid Name	Cassette Name	Order of Elements (5' to 3')
Plasmid BP15TA	Cassette BP15TA	TCR β -fP2A- mbIL15-fT2A-TCR α
Plasmid BT15PA	Cassette BT15PA	TCR β -fT2A- mbIL15-fP2A-TCR α

[00462] The polynucleotide sequences of the ORFs of these transposon plasmids is shown in Table E2.

Table E2. Polynucleotide sequences of SB plasmid ORFs.

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
Plasmid APBT15	ATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATCCCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGTGTTTCTGCTGCTGATTCGGGAGAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACACACTGAAGCAGTCTCTGTTTCACATCACAGCGTCTCAGCC AGCGGACAGCGGACCTACCTGTGCGCGCTGGACATCTACCTCAGCATATGAGATTGCGC GCGGGCACAAAGGCTGACCGTGAAACCAACATCCAGAATCCCGAGCCTGCGGTGTACCAAGC TGAAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGAT CAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATACCGACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCT GCCAGGATATCTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTAAATCTGCTGATGACACTGCGGC TGTGGAGTTCGCGGGCAAACGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCA GGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGCGACAAGACTGCTGTGCTGGGCGGCG CTGTGCCTGCTGGGAGCGGAACTGACTGAAGCGGGGGTTCGCGCAGAGCCCTCGATACAAAA TCATTGAGAAGCGGCAGTCTGTGGCGTTCTGGTGCAACCCAATCAGCGGACACGCGACCCCT GTACTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATTCAGTTCCAGAACAAT GGCGTGGTGGACGATAGCCAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCG TGGACTCTACACTGAAAATTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGC GAGCTCCCTGGACCCAGGCGATACCGGAGAGCTGTCTTTGGAGAGGGCAGCCGGCTGACA GTGCTGGAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGG CGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGGCTTTTCCCGA TCACGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGTGCACAGAC CCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCG CGACCTTTTGGCACAACCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTC CGAGGAGGATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAG GCGTGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAGGGCGTGTGTCCG CGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCAC CCTGGTGGTCATGGCGATGGTGAAGAGGAAAAACTCTCGGGCGAAACGCTCTGGAAGCGGA GAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATT GGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGT GATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTG TACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGG AGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCCCTATCCACGACACAGTGAGGAATCT GATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAG GAGTGTGAGGAGCTGGAGGAGAAGACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCG TGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGG AGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTGCAGATTACATGCCCTCCTCCAATG TCTGTGGAGCACGCCGATATTTGGGTGAAGTCCTACAGCCTGTACAGCAGAGAGAGATACA TCTGCAACAGCGGCTTTAAGAGAAAGCCGGCACCTCTTCTCTGACAGAGTGGTGTCTGAA TAAGGCCACAAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGC CTGAATCTCTGAGCCCTCTGGAAGAAGACCTGCCGCGAGCTCTCTAGCTCTAATAATAC	320

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
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Plasmid ATBP15	ATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT CCCAGAAGATCGAGCAGAATCTGAGCGCTGAATATTAGGAGGGCAAGACCAGCAGACT GACCTGCAACTACACAAATTATTCCCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGTGTTTCTGCTGCTGATTCTGGGAGAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACACACTGAAGCAGTCTCTGTTTTCACATCAGACCTCTCAGCC AGCGGACAGCGGACCTACCTGTGCGCGCTGGACATCTACCCTCAGCATATGAGATTCTGGC GCGGGCACAAGGCTGACCGTGAAACCAACATCCAGAATCCCGAGCCTGCGGTGTACCAAGC TGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTTACCAGCTTTGATAGCAGAT CAACGTGCCTAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCT GCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAAGATCTGCTGGTC ATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGC TGTGGAGTTCCTGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATG CGGTGACGTGGAGGAGAATCCCGGCCCTATGGCGACAAGACTGCTGTGCTGGGCGGCGCTG TGCCTGCTGGGAGCGGAACCTGACTGAAGCGGGGGTGCAGCAGAGCCCTCGATACAAAATCA TTGAGAAGCGGCAGTCTGTGGCGTTCTGGTGCAACCCAATCAGCGGACACGCGACCCCTGTA CTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATTCTCAGTTCAGAACAAATGGC GTGGTGGACGATAGCCAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGG ACTCTACACTGAAAATTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAG CTCCCTGGACCCAGGCGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTG CTGGAGGACCTGAGGAACGTGACCCCACTAAAGTGAGCCTGTTTCAGGCCATCCAAGGCGG AGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCA CGTGGAGCTGTCTGGTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGTGCACAGACCCCT GAGCGGTACAAGGAGAGCAATTACTCTATTGTCTGTCTAGCAGACTGAGGGTGTGCTGCGCA CCTTTTGGCACAACCCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGA GGAGGATAAATGGCCTGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCG TGGGGAAGAGCGGACTGTGGCATTACAAGCGCGTCTATCAGCAGGGCGTGTGTCTCCGCGA CCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGTGTTGCCACCCCT GGTGGTCTATGGCGATGGTGAAGAGGAAAACTCTCGGGCGAAACGCTCTGGAAGCGGAGCG ACCAATTTTCAAGCCTGTGAAGCAGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATT GGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGT GATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCCTG TACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTTTCTGCTGG AGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCT GATCATCCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAG GAGTGTGAGGAGCTGGAGGAGAAGAATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCG TGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGG AGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATG TCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTACAGCCTGTACAGCAGAGAGAGATACA TCTGCAACAGCGGCTTTAAGAGAAAGGCCCGCACCTCTTCTCTGACAGAGTGGTGTCTGAA TAAGGCCACAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCAATTAGAGATCCTGCC CTGGTCCACCAGAGGCCTGCCCCCTCATCTACAGTGACAACAGCCGGAGTGACACCTCAGC CTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATAC CGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGC ACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCG CCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGG CCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGTCTGTGTGGACTGTCTGCC	321

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	GTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGA TGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGA GAATTGTTCTCACCACCTG	
Plasmid AP15TB	ATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATTCCCCAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGTGTTTCTGCTGCTGATTCCGGGAGAAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTCACATCACAGCGTCTCAGCC AGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCTCAGCATATGAGATTGCGC GCGGGCACAAGGCTGACCGTGAAACCAAACATCCAGAATCCCGAGCCTGCGGTGTACCAGC TGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGAT CAACGTGCCTAAACAATGGAGTCCGGCACCTTCATCACCAGACAGTGCCTGCTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCT GCCAGTATCTTCAAGGAGACAAACGCGACCTATCCTTCTGACGTGCCATGTGATGC GCACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGC TGTGGAGTTCCTGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTCAGCCTGCTGAAGCA GGCGGGCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATTCTGTTTCTGGTG GCCGCTGCCACAAGAGTGACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCG AGGATCTGATCCAGAGCATGCACATTGATGCCACCTGTACACAGAATCTGATGTGCACCC TAGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAA AGCGGAGATGCCTCTATCCAGCACAGTGGAGAATCTGATCATCCTGGCCACAATAGCC TGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAAGGAGTGTGAGGAGCTGGAGGAGAA GAACATCAAGGAGTTTCTGCAGAGCTTGTGTCACATCGTGCAGATGTTTCATCAATACAAGC TCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTG GCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTG GGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGA AAGGCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCACT GGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCTGCCCC TCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGA AAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTG CAGCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGAG CCACGAATCTTCTACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCC TCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCA TCAGCACATCTACAGTGTGCTGTGTGGACTGTCTGCCGTGTCTGCTGGCCTGTTACCT GAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCT GTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGG CGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGA GAATCCCGGCCCTATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCG GAACTGACTGAAGCGGGGGTCTGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGT CTGTGGCGTCTGCTGCAACCCAATCAGCGGACACGCGACCTGTACTGGTATCAGCAGAT CCTGGGCCAGGGCCCTAAGCTGCTGATTGATTCCAGAACAATGGCGTGGTGGACGATAGC CAGCTGGCAAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAA TTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGG CGATACCGGAGAGCTGTTCTTGGAGAGGGCAGCCGGCTGACAGTGTGAGGACCTGAGG AACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCAATAAGC AGAAAGCGACCTGGTGTGCTGCGGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTCTG GTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAG AGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGTGAGCGCGACCTTTTGGCACAACC CCCGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAGGATAAATGGCC TGAGGGCTCTCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGAC TGTGGCATTACAAGCGCGTCTATCAGCAGGGCGTGTGTCCGCGACCATCCTGTACGAGA TTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCTGGTGGTTCATGGCGAT GGTGAAGAGGAAAACTCT	322
Plasmid	ATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTGGGTGAAAT	323

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
AT15PB	CCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACCGCGACACT GACCTGCAACTACACAAATTATTTCCCGAGCGTACCTGCAGTGGTATAGGCAGGACCCAGGC AGGGGACCCGTGTTTCTGCTGCTGATTCGGGAGAATGAGAAGGAGAAAAGAAAGGAGAGGC TGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTCACATCACAGCGTCTCAGCC AGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCTCAGCATATGAGATTCGGC GCGGGCACAGGCTGACCGTGAAACCAACATCCAGAATCCCGAGCCTGCGGTGTACCAGC TGAAGGACCCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCGACTTTGATAGCCAGAT CAACGTGCCTAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCGTGTGGATATG AAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTACCT GCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCATGTGATGC GACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTC ATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTAACTGCTGATGACACTGCGGC TGTGGAGTTCCCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATG CGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCC GCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGG ATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGACCCCTAG CTGTAAAGTGACCGCCATGAAGTGTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGC GGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGA GCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAA CATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCT GGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGCAGTGGAGGCGGAGGATCTGGCG GAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGT GAAGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAG GCCGGCACCTCTTCTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGA CAACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCCCTGCCCTCC ATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAA GAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGC CTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCA CGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCT GCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCA GCACATCTACAGTGTCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAA GTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTG ACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGA AACGCTCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGA GAACCTTGGCCCAATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCG GAACTGACTGAAGCGGGGGTTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGT CTGTGGCGTTCTGGTGCAACCAATCAGCGGACACGCGACCTGTACTGGTATCAGCAGAT CCTGGGCCAGGGCCCTAAGCTGCTGATTTCAGTTCAGAACAAATGGCGTGGTGGACGATAGC CAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAA TTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGG CGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGTCTGGAGGACCTGAGG AACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGGAATAAGC AGAAAGCGACCTGGTGTGCCTGGCGAGGGGCTTTTCCCGATCACGTGGAGCTGTCTCTG GTGGGTGAACGGCAAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAG AGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAACC CCCGGAATCACTTCCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAATGGCC TGAGGGCTCTCCAAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGAC TGTGGCATTACAAGCGCGTCTATCAGCAGGGCGTGTGTCCGCGACCATCCTGTACGAGA TTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTTCATGGCGAT GGTGAAGAGGAAAACTCT	
Plasmid BPAT15	ATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAAGTACTGAAG CGGGGGTTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTG GTGCAACCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGC CCTAAGCTGCTGATTCAAGTTCAGAACAAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAG ATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAATTCAGCCTGCGAA	324

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	GCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGGCGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGTGGAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCGTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGCAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCTATTGTCTGTCTAGCAGACTGAGGGGTGAGCGCGACCTTTTGGCACACCCCCGGGAATCACTTCCGCTGCCAGGTGCAGTTTACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCAAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAAAGCGCTCCTATCAGCAGGGCGTGTCTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAAGGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAAAGTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTTCAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACCCTGGCCCCAATGGAGTCCCTTCTGGGCGGCGTGTCTGTATCCTGTGGCTGCAGGTGGACTGGGTGAAATCCAGAGATCGAGCAGAACTCTGAGGCGCTGAATTTCAGGAGGGCAAGACCGGACACTGACCTGCAACTACACAAATATTCCCGACGTACCTGTCAGTGGTATAGGCAGGACCCAGGCGAGGGGACCCGTGTTTCTGCTGCTGATTCTGGGAGAAATGAGAAGGAGAAAAGAAAGGAGAGGGCTGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTTCATCACAGCGTCTCAGCCAGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCCTCACGATATGAGATTGCGGCGGGGCACAAGGCTGACCGTGAAACCAAACATCCAAGTCCCGAGCCTGCGGTGTACAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCTGTTTACCGACTTTTGATAGCCAGATCAACGTGCCTAAAACAATGGAGTCCGGCACCTTCAACCGACAAGTGCGTGTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATCTGCTGGTCATCGTGTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGACACTGCGGCTGTGGAGTTCGCGGCGGAAACGCTCTGGAAGCGGAGAGGCGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATCCCGGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAGCGGAGATGCCTCTATCCACGACACAGTGGAGAATCTGATCATCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGAGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCAGCCGATATTTGGGTGAAGTCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGGCACCTCTTCTCTGACAGAGTGGTGTCTGAAATAGGCCACAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCTGGCCCTGGTCCACCAGAGGCCCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTCTGGAAGAAACCTGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAAACAGTGGCCATCAGCACATCTACAGTGCTGTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTG	
Plasmid BTAP15	ATGGCGACAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAACTGACTGAAGCGGGGTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTGTGCAACCCCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGCCCTAAGCTGCTGATTCAAGTTCCAGAACAATGGCGTGGTGACGATAGCCAGCTGCCAAAAGATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGACTCTACACTGAAAATTCAGCCTGCGAAGCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGGCGATACCGGAGAGCTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGTGGAGGACCTGAGGAACGTGACCCACCTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCCCTGGTGTGCCGTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGC	325

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	AAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAACCCCGGAATCACTT CCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCA AAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAA GCGCGTCTTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAA GGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTTCATGGCGATGGTGAAGAGGAAA AACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTG ACGTGGAGGAGAATCCCGGCCCTATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTG GCTGCAGGTGGACTGGGTGAAATCCAGAAATCGAGCAGAACTCTGAGGCGTGAAATATT CAGGAGGGCAAGACCGGACACTGACCTGCAACTACACAAATTATTCCCCAGCGTACCTGC AGTGGTATAGGCAGGACCCAGGCAGGGGACCCGTGTTCTGTGCTGCTGATTGCGGAGAATGA GAAGGAGAAAAGAAAGGAGAGGGCTGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTG TTTCACATCACAGCGTCTCAGCCAGCGGACAGCGGACCTACCTGTGCGCGCTGGACATCT ACCCTCACGATATGAGATTGCGGCGCGGACACAAGGCTGACCGTGAAACCAACATCCAGAA TCCCGAGCCTGCGGTGTACCAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTG TTCACCGACTTTGATAGCCAGATCAACGTGCCTAAACAATGGAGTCCGGCACCTTCATCA CCGACAAGTGCCTGCTGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTG GTCCAATCAGACATCTTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCT TCCTCTGACGTGCCATGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACC TGAATTTTTCAGAATCTGCTGGTCATCGTGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTT TAATCTGCTGATGACACTGCGGCTGTGGAGTTCCTGGGCGAAACGCTCTGGAAGCGGAGCG ACCAATTTTACGCTGTGAAGCAGGCGGGCGATGTGGAGGAGAACCTGGCCCAATGGATT GGACCTGGATTCTGTTTCTGGTGGCCGCTGCCACAAGAGTGACACAGCAACTGGGTGAATGT GATCAGCGACCTGAAGAAGATCGAGGATCTGATCCAGAGCATGCACATTGATGCCACCCTG TACACAGAATCTGATGTGCACCCTAGCTGTAAAGTGACCGCCATGAAGTGTCTTCTGCTGG AGCTGCAGGTGATTTCTCTGGAAAGCGGAGATGCCCTCTATCCACGACACAGTGGAGAATCT GATCATCTGGCCAACAATAGCCTGAGCAGCAATGGCAATGTGACAGAGTCTGGCTGTAAG GAGTGTGAGGAGCTGGAGGAGAAGAACATCAAGGAGTTTCTGCAGAGCTTTGTGCACATCG TGCAGATGTTTCATCAATACAAGCTCTGGCGGAGGATCTGGAGGAGGCGGATCTGGAGGAGG AGGCAGTGGAGGCGGAGGATCTGGCGGAGGATCTCTGCAGATTACATGCCCTCCTCCAATG TCTGTGGAGCACGCCGATATTTGGGTGAAGTCTTACAGCCTGTACAGCAGAGAGAGATACA TCTGCAACAGCGGCTTTAAGAGAAAGCCGGCACCTCTTCTCTGACAGAGTGGCTGCTGAA TAAGGCCACAATGTGGCCCACTGGACAACACCTAGCCTGAAGTGCATTAGAGATCCTGCC CTGGTCCACCAGAGGCTGCCCTCCATCTACAGTGACAACAGCCGGAGTGACACCTCAGC CTGAATCTCTGAGCCCTTCTGGAAAAGAACCTGCCGCCAGCTCTCCTAGCTCTAATAATAC CGCCGCCACAACAGCCGCCATTGTGCCTGGATCTCAGCTGATGCCTAGCAAGTCTCCTAGC ACAGGCACAACAGAGATCAGCAGCCACGAATCTTCTACGGAACACCTTCTCAGACACCG CCAAGAATTGGGAGCTGACAGCCTCTGCCCTCTCACCAGCCTCCAGGAGTGTATCCTCAGGG CCACTCTGATACAACAGTGGCCATCAGCACATCTACAGTGCTGCTGTGTGGACTGTCTGCC GTGTCTCTGCTGGCCTGTACCTGAAGTCTAGACAGACACCTCCTCTGGCCTCTGTGGAGA TGGAGGCCATGGAAGCCCTGCCTGTGACATGGGGAACAAGCAGCAGAGATGAAGACCTGGA GAATTGTTCTCACCACCTG	
Plasmid BP15TA	ATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAAGTACTGAAG CGGGGGTCCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTG GTGCAACCCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGC CCTAAGCTGCTGATTTCAGTTCCAGAACAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAG ATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGACTCTACACTGAAAATTCAGCCTGCGAA GCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCCTGGACCCAGGCGATACCGGAGAG CTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGCTGGAGGACCTGAGGAACGTGACCCAC CTAAAGTGAGCCTGTTTCGAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAAGCGACCT GGTGTGCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGC AAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAACCCCGGAATCACTT CCGCTGCCAGGTGCAGTTTCACGGCCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCA AAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAA	326

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	GCGCGTCCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAA GGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAA AACTCTCGGGCGAAACGCTCTGGAAGCGGAGCGACCAATTTACGCCTGCTGAAGCAGGCGG GCGATGTGGAGGAGAACCCTGGCCCAATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGC TGCCACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGAT CTGATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCT GTAAAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGG AGATGCCCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGC AGCAATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACA TCAAGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCAATACAAGCTCTGG CGGAGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGA GGATCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGA AGTCTTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGC CGGACCCTTCTCTGACAGAGTGGCTGCTGAATAAGGCCACAATGTGGCCACTGGACA ACACCTAGCCTGAAGTGCATTAGAGATCCTGCCCTGGTCCACCAGAGGCTGCCCTCCAT CTACAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGA ACCTGCCGCGAGCTCTCCTAGCTCTAATAATACCGCGGCCACAACAGCCGCCATTTGTGCCT GGATCTCAGCTGATGCCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACG AATCTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGC CTCTCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGC ACATCTACAGTGCTGCTGTGTGGACTGTCTGCCGTGTCTGTGCTGGCCTGTTACCTGAAGT CTAGACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGAC ATGGGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAA CGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTGACGTGGAGGAGAATC CCGGCCCTATGGAGTCCTTTCTGGGCGGCGTGCTGCTGATCCTGTGGCTGCAGGTGGACTG GGTGAATCCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACC GCGACACTGACCTGCAACTACACAAATTATTCCCCAGCGTACCTGCAGTGGTATAGGCAGG ACCCAGGCAGGGGACCCGTGTTTCTGCTGCTGATTGCGGAGAATGAGAAGGAGAAAAGAAA GGAGAGGCTGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTCACATCACAGCG TCTCAGCCAGCGGACAGCGGACCTACCTGTGCGCGCTGGACATCTACCCTCACGATATGA GATTCTGGCGGGGCACAAGGCTGACCGTGAAACCAACATCCAGAATCCCGAGCCTGCGGT GTACCAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCGTGTTACCCGACTTGTAT AGCCAGATCAACGTGCCATAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCCTGC TGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATC TTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCTCTGACGTGCCA TGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATC TGCTGGTCATCGTGCTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGAC ACTGCGGCTGTGGAGTTCC	
Plasmid BT15PA	ATGGCGACAAGACTGCTGTGCTGGGCGGCGCTGTGCCTGCTGGGAGCGGAAGTGAAG CGGGGGTTCGCGCAGAGCCCTCGATACAAAATCATTGAGAAGCGGCAGTCTGTGGCGTTCTG GTGCAACCAATCAGCGGACACGCGACCCTGTACTGGTATCAGCAGATCCTGGGCCAGGGC CCTAAGCTGCTGATTCAAGTCCAGAACAAATGGCGTGGTGGACGATAGCCAGCTGCCAAAAG ATAGATTTTCCGCGGAGAGGCTGAAGGGCGTGGAATCTACACTGAAAATTCAGCCTGCGAA GCTGGAGGATAGCGCGGTGTACCTGTGCGCGAGCTCCTGGACCCAGGCGATACCCGGAGAG CTGTTCTTTGGAGAGGGCAGCCGGCTGACAGTGTGGAGGACCTGAGGAACGTGACCCAC CTAAAGTGAGCCTGTTTCAGCCATCCAAGGCGGAGATCGCGAATAAGCAGAAAGCGACCT GGTGTGCCCTGGCGAGGGGCTTCTTTCCCGATCACGTGGAGCTGTCTGGTGGGTGAACGGC AAAGAGGTGCACTCTGGCGTGTGCACAGACCCTCAGGCGTACAAGGAGAGCAATTACTCCT ATTGTCTGTCTAGCAGACTGAGGGTGAGCGCGACCTTTTGGCACAAACCCCGGAATCACTT CCGCTGCCAGGTGCAGTTTTCAGCGCTGTCCGAGGAGGATAAATGGCCTGAGGGCTCTCCA AAGCCCGTGACACAGAATATCAGCGCGGAGGCGTGGGGAAGAGCGGACTGTGGCATTACAA GCGCGTCTATCAGCAGGGCGTGCTGTCCGCGACCATCCTGTACGAGATTCTGCTGGGCAA GGCGACACTGTATGCGGTGCTGGTGTCCACCCTGGTGGTCATGGCGATGGTGAAGAGGAAA AACTCTCGGGCGAAACGCTCTGGAAGCGGAGAGGGCAGAGGAAGTCTTCTAACATGCGGTG ACGTGGAGGAGAATCCCGCCCTATGGATTGGACCTGGATTCTGTTTCTGGTGGCCGCTGC	327

Plasmid	Polynucleotide Sequence of ORF	SEQ ID NO:
	CACAAGAGTGCACAGCAACTGGGTGAATGTGATCAGCGACCTGAAGAAGATCGAGGATCTG ATCCAGAGCATGCACATTGATGCCACCCTGTACACAGAATCTGATGTGCACCCTAGCTGTA AAGTGACCGCCATGAAGTGTTTTCTGCTGGAGCTGCAGGTGATTTCTCTGGAAAGCGGAGA TGCCTCTATCCACGACACAGTGGAGAATCTGATCATCCTGGCCAACAATAGCCTGAGCAGC AATGGCAATGTGACAGAGTCTGGCTGTAAGGAGTGTGAGGAGCTGGAGGAGAAGAACATCA AGGAGTTTCTGCAGAGCTTTGTGCACATCGTGCAGATGTTTCATCAATACAAGCTCTGGCGG AGGATCTGGAGGAGGCGGATCTGGAGGAGGAGGAGTGGAGGCGGAGGATCTGGCGGAGGA TCTCTGCAGATTACATGCCCTCCTCCAATGTCTGTGGAGCACGCCGATATTTGGGTGAAGT CCTACAGCCTGTACAGCAGAGAGAGATACATCTGCAACAGCGGCTTTAAGAGAAAGGCCGG CACCTCTTCTGACAGAGTGCCTGCTGAATAAGGCCACAAATGTGGCCCACTGGACAACA CCTAGCCTGAAGTGCAATTAGAGATCCTGCCCTGGTCCACCAGAGGCCTGCCCTCCATCTA CAGTGACAACAGCCGGAGTGACACCTCAGCCTGAATCTCTGAGCCCTTCTGGAAAAGAACC TGCCGCCAGCTCTCCTAGCTCTAATAATACCGCCGCCACAACAGCCGCCATTGTGCCTGGA TCTCAGCTGATGCCTAGCAAGTCTCCTAGCACAGGCACAACAGAGATCAGCAGCCACGAAT CTTCTCACGGAACACCTTCTCAGACCACCGCCAAGAATTGGGAGCTGACAGCCTCTGCCTC TCACCAGCCTCCAGGAGTGTATCCTCAGGGCCACTCTGATACAACAGTGGCCATCAGCACA TCTACAGTGTGCTGTGTGGACTGTCTGCCGTGTCTCTGCTGGCCTGTTACCTGAAGTCTA GACAGACACCTCCTCTGGCCTCTGTGGAGATGGAGGCCATGGAAGCCCTGCCTGTGACATG GGGAACAAGCAGCAGAGATGAAGACCTGGAGAATTGTTCTCACCACCTGCGGGCGAAACGC TCTGGAAGCGGAGCGACCAATTTAGCCTGCTGAAGCAGGCGGGCGATGTGGAGGAGAACC CTGGCCCAATGGAGTCTTTCTGGGCGGCGTGTCTGCTGATCCTGTGGCTGCAGGTGGACTG GGTGAAATCCAGAAGATCGAGCAGAACTCTGAGGCGCTGAATATTCAGGAGGGCAAGACC GCGACACTGACCTGCAACTACACAAATTATTCCCCAGCGTACCTGCAGTGGTATAGGCAGG ACCCAGGCAGGGGACCCGTGTTTCTGCTGCTGATTCTGGGAGAATGAGAAGGAGAAAAGAAA GGAGAGGCTGAAAGTGACCTTCGATACCACACTGAAGCAGTCTCTGTTTCACATCACAGCG TCTCAGCCAGCGGACAGCGCGACCTACCTGTGCGCGCTGGACATCTACCTCAGCATATGA GATTCTGGCGCGGGCACAAAGGCTGACCGTGAAACCAAAACATCCAGAATCCCGAGCCTGCGGT GTACCAGCTGAAGGACCCCGCTCTCAGGATAGCACACTGTGCCTGTTACCGACTTTGAT AGCCAGATCAACGTGCCATAAAACAATGGAGTCCGGCACCTTCATCACCGACAAGTGCGTGC TGGATATGAAAGCGATGGACTCCAAGTCTAACGGCGCGATCGCGTGGTCCAATCAGACATC TTTCACCTGCCAGGATATCTTCAAGGAGACAAACGCGACCTATCCTTCCTCTGACGTGCCA TGTGATGCGACACTGACCGAGAAGAGCTTCGAGACAGACATGAACCTGAATTTTCAGAATC TGCTGGTTCATCGTGTGAGAATCCTGCTGCTGAAGGTGGCGGGCTTTAATCTGCTGATGAC ACTGCGGCTGTGGAGTTCC	

[00463] The corresponding theoretical polypeptide translation product resulting from each ORF, not accounting for N-terminal signal sequence cleavage or ribosomal skipping at each P2A and T2A site, is shown in **Table E3**.

Table E3. Polypeptide sequences encoded by SB plasmid ORFs.

Plasmid	Amino Acid Translation of ORF	SEQ ID NO:
Plasmid APBT15	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRERLKVTFDTTLKQSLFHITASQPADSATYLCALDIYPHDMRFG AGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAGDVEENPGPMATRLLCWAA LCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGELFFGEGSRILT VLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTD PQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAE AWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNRAKRSGSG EGRGSLTTCGDVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLELQVISLESQDASIHDTVENLIILANNSLSSNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCPPPM QAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAE LVHQRPAAPPSTVTTAGVTPQPELSLSPSGKEPAASSPSSNNTAATTAIVPGSQLMPKSPS TGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLLACYLKSQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	330
Plasmid ATBP15	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRERLKVTFDTTLKQSLFHITASQPADSATYLCALDIYPHDMRFG AGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGEGRGSLTTCGDVEENPGPMATRLLCWAA LCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNN GVVDSDQLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGELFFGEGSRILT VLEDLRNVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTD PQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAE WGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNRAKRSGSGA TNFSLKQAGDVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLELQVISLESQDASIHDTVENLIILANNSLSSNGNVTESGCK ECEELEEKNIKEFLQSFVHIVQMFINTSSGGGSGGGGSGGGGSGGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPELSLSPSGKEPAASSPSSNNTAATTAIVPGSQLMPKSPS TGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLLACYLKSQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	331
Plasmid AP15TB	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRERLKVTFDTTLKQSLFHITASQPADSATYLCALDIYPHDMRFG AGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLNFQNLIV IVLRILLKLVAGFNLLMTLRLWSSRAKRSGSGATNFSLLKQAGDVEENPGPMDWTWILFLV AAATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLE SSGDASIHDTVENLIILANNSLSSNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTS SGGGSGGGGSGGGGSGGGGSGGGSLQITCPPPMSVEHADIWVKSYSLSRERYICNSGFKR KAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPELSLSPSG KEPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLLACYLKSQTPPLASVEMEAMEALP VTWGTSSRDEDLNCSHHLRAKRSGSGEGRGSLTTCGDVEENPGPMATRLLCWAA LCLLGA ELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQILGQGPKLLIQFQNNGVVDSD QLPKDRFSAERLKGVDSTLKIQPAKLEDSAVYLCASSLDPGDTGELFFGEGSRILT VLEDLR NVTPPKVSLFEPKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVCTD PQAYKE NYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGS PKPVTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKN	332
Plasmid AT15PB	MESFLGGVLLILWLQVDWVKSQKIEQNSEALNIQEGKTATLTCNYTNYSPAYLQWYRQDPG RGPVFLLLIRENEKEKRERLKVTFDTTLKQSLFHITASQPADSATYLCALDIYPHDMRFG	333

Plasmid	Amino Acid Translation of ORF	SEQ ID NO:
	AGTRLTVKPNIQNPEPAVYQLKDPQRSQDSTLCLFTDFDSQINVPKTMESGTFITDKCVLDM KAMDSKSNAGIAWSNQTSTFCQDIFKETNATYPSSDVPCDATLTEKSFETDMNLFQNLV IVLRILLKLVAGFNLLMTLRLWSSRAKRSKSGEGRSLTTCGDVEENPGPMDWTWILFLVA AATRVHSNWNVISDLKKIEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVLSLES GDASIHDTVENLII LANNSLSSNGNVTESGCKECEEELEEKNIKEFLQSFVHIVQMFINTESS GGSGGGSGGGSGGGSGGGSGGGSLQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRK AGTSSLTECVLNKATNVAHWTTPSLKCIRDPAVHQRPAAPPSTVTTAGVTPQPESLSPSGK EPAASSPSSNNTAATTAIVPGSQLMPKSPSTGTTEISSHESHGTPSQTTAKNWELTAS ASHQPPGVYPQGHSDTTVAISTSTVLLCGLSAVSLACYLKSRQTPPLASVEMEAMEALPV TWGTSSRDEDLNCSHHLRAKRSKSGATNFSLLKQAGDVEENPGPMATRLLCWAALCLLGA ELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQIILGQGPKLLIQFQNGVVDSDS QLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGELFFGEGSRLTVLEDLR NVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNGKEVHSGVCTDPQAYKE SNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSPKPVQTQNI SAEAWGRAD CGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRKNS	
Plasmid BPAT15	MATRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQIILGQG PKLLIQFQNGVVDSDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRLTVLEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSP KPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NSRAKRSKSGATNFSLLKQAGDVEENPGPMESFLGGVLLILWLQVDWVKSQKIEQNSEALN IQEGKTATLTCNYTNYPAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSL LFHITASQPADSATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPQRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATY PSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSSRAKRSKSG EGRSLTTCGDVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLELQVLSLES GDASIHDTVENLII LANNSLSSNGNVTESGCK ECEEELEEKNIKEFLQSFVHIVQMFINTESSGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAIVPGSQLMPKSPS TGTTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	334
Plasmid BTAP15	MATRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQIILGQG PKLLIQFQNGVVDSDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRLTVLEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSP KPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NSRAKRSKSGEGRSLTTCGDVEENPGPMESFLGGVLLILWLQVDWVKSQKIEQNSEALN IQEGKTATLTCNYTNYPAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSL LFHITASQPADSATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPQRSQDSTLC LFTDFDSQINVPKTMESGTFITDKCVLDMKAMDSKSNAGIAWSNQTSTFCQDIFKETNATY PSSDVPCDATLTEKSFETDMNLFQNLVIVLRILLKLVAGFNLLMTLRLWSSRAKRSKSGA TNFSLLKQAGDVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIEDLIQSMHIDATL YTESDVHPSCKVTAMKCFLELQVLSLES GDASIHDTVENLII LANNSLSSNGNVTESGCK ECEEELEEKNIKEFLQSFVHIVQMFINTESSGGSGGGSGGGSGGGSGGGSLQITCPPPM SVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWTTPSLKCIRDPA LVHQRPAAPPSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTAIVPGSQLMPKSPS TGTTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAISTSTVLLCGLSA VSLACYLKSRQTPPLASVEMEAMEALPVTWGTSSRDEDLNCSHHL	335
Plasmid BP15TA	MATRLLCWAALCLLGAELTEAGVAQSPRYKII EKRSVAFWCNPI SGHATLYWYQQIILGQG PKLLIQFQNGVVDSDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRLTVLEDLRNVT PPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWVNG KEVHSGVCTDPQAYKESNYSYCLSSRLRVSATFWHNP RNHFRCQVQFHGLSEEDKWPEGSP KPVQTQNI SAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NSRAKRSKSGATNFSLLKQAGDVEENPGPMDWTWILFLVAAATRVHSNWNVISDLKKIED	336

Plasmid	Amino Acid Translation of ORF	SEQ ID NO:
	LIQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSGG GSLQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCI RDPALVHQRPA PPSSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTA AIVP GSQLMPSKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAIS TSTVLLCGLSAVSL LACYLKS RQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAK RSGSGEGRGSLLTCGDVEENPGPMESFLGGVLLI LWLQVDWVKSQKIEQNSEALNIQEGKT ATLTCNYTNYSPAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITA SQPADSATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLFQNL LVIVLRILL LKVAGFNLLMTLRLWSS	
Plasmid BT15PA	MATRLLCWAALCLLGAELTEAGVAQSPRYKII EKQSVAFWCNPI SGHATLYWYQQI LGQG PKLLIQFQNNGVVDDSQLPKDRFSAERLKGVDSTLKI QPAKLEDSAVYLCASSLDPGDTGE LFFGEGSRLTVLEDLRNVTPPKVSLFEP SKAEIANKQKATLVCLARGFFPDHVELSWVWNG KEVHSGVCTDPQAYKESNYSYCLSSRLRV SATFWHNPRNHFRQVQFHGLSEEDKWPEGSP KPVTQNISAEAWGRADCGITSASYQQGVLSATILYEILLGKATLYAVLVSTLVVMAMVKRK NSRAKRS GSGEGRGSLLTCGDVEENPGPMDWTWILFLVAAATRVHSNWNVNIIDLKKIEDL IQSMHIDATLYTESDVHPSCKVTAMKCFLELQVISLES GDASIHDTVENLII LANNSLS SNGNVTESGCKECEELEEKNIKEFLQSFVHIVQMFINTSSGGSGGGSGGGSGGGSGGGSGG SLQITCPPPMSVEHADIWVKSYSLSYRERYICNSGFKRKAGTSSLTECVLNKATNVAHWT TPSLKCI RDPALVHQRPA PPSSTVTTAGVTPQPESLSPSGKEPAASSPSSNNTAATTA AIVP GSQLMPSKSPSTGTTEISSHESHGTPSQTTAKNWELTASASHQPPGVYPQGHSDTTVAIS TSTVLLCGLSAVSL LACYLKS RQTPPLASVEMEAMEALPVTWGTSSRDEDLENC SHHLRAK RSGSGATNFSLLKQAGDVEENPGPMESFLGGVLLI LWLQVDWVKSQKIEQNSEALNIQEGKT ATLTCNYTNYSPAYLQWYRQDPGRGPVFLLLIRENEKEKRKERLKVTFDTTLKQSLFHITA SQPADSATYLCALDIYPHDMRFGAGTRLTVKPNIQNPEPAVYQLKDPRSQDSTLCCLFTDFD SQINVPKTMESGTFITDKCVLDMKAMDSKSNGAIAWSNQTSTFTCQDIFKETNATYPSSDVP CDATLTEKSFETDMNLFQNL LVIVLRILL LKVAGFNLLMTLRLWSS	337

[00464] For control purposes, three additional SB transposon plasmids were prepared. Plasmid 15 contains a monocistronic expression cassette, Cassette 15, encoding mbIL15. Plasmid APB contains a bicistronic expression cassette, Cassette APB, encoding TCR α (5') and TCR β (3') with an intervening fP2A element. Plasmid BPA contains a bicistronic expression cassette, Cassette BPA, encoding TCR β (5') and TCR α (3') with an intervening fP2A element. These expression cassettes, including suitable transcriptional regulatory elements, were inserted between the ITRs of SB transposon plasmids. The 5' to 3' order of elements in the ORF of each control expression cassette and SB Plasmid is shown in **Table E4**, and schematics of the ORFs of these three expression cassettes are shown in **FIG. 2B**.

Table E4. Control SB transposon plasmids.

Plasmid Name	Cassette Name	Order of Elements (5' to 3')
Plasmid 15	Cassette 15	mbIL15
Plasmid APB	Cassette APB	TCR α -fP2A-TCR β
Plasmid BPA	Cassette BPA	TCR β -fP2A-TCR α

[00465] A plasmid encoding SB11 transposase, Plasmid TA, was also constructed.

6.2 Example 2: Generation and Evaluation of T Cells

[00466] This Example describes the generation and evaluation of T cells co-expressing TCR α , TCR β , and mbIL15 from the plasmids described in Example 1. A schematic of the gene transfer process for both double transposition (using separate plasmids encoding TCR α /TCR β and mbIL15) and single transposition (using a tricistronic plasmid encoding TCR α /TCR β and mbIL15 together) is shown in **FIG. 3**.

[00467] Briefly, peripheral blood mononuclear cells (PBMCs) were enriched from leukapheresis product obtained from a normal donor (Discovery Life Sciences, Austin, TX). The resulting PBMCs were collected, cryopreserved, and stored in the vapor phase of a liquid nitrogen tank.

[00468] To generate the TCR-T cells described in this Example 2, the plasmids described in Example 1 were electroporated into the enriched PBMCs. Briefly, cryopreserved PBMCs were thawed, resuspended in supplemented media, and incubated in a 37°C/5% CO₂ incubator for one hour. The PBMC test articles listed in **Table E5** were then prepared.

Table E5. PBMC test articles.

Group	Name	Description
1	NT cells	Non-transposed PBMCs
2	mbIL15 cells	PBMCs transposed with Plasmid 15 and Plasmid TA
3	APB cells	PBMCs transposed with Plasmid APB and Plasmid TA
4	BPA cells	PBMCs transposed with Plasmid BPA and Plasmid TA
5	APB+15 cells	PBMCs transposed with Plasmid APB, Plasmid 15, and Plasmid TA
6	BPA+15 cells	PBMCs transposed with Plasmid BPA, Plasmid 15, and Plasmid TA
7	APBT15 cells	PBMCs transposed with Plasmid APBT15 and Plasmid TA
8	ATBP15 cells	PBMCs transposed with Plasmid ATBP15 and Plasmid TA
9	AP15TB cells	PBMCs transposed with Plasmid AP15TB and Plasmid TA
10	AT15PB cells	PBMCs transposed with Plasmid AT15PB and Plasmid TA
11	BPAT15 cells	PBMCs transposed with Plasmid BPAT15 and Plasmid TA
12	BTAP15 cells	PBMCs transposed with Plasmid BTAP15 and Plasmid TA
13	BP15TA cells	PBMCs transposed with Plasmid BP15TA and Plasmid TA
14	BT15PA cells	PBMCs transposed with Plasmid BT15PA and Plasmid TA

[00469] Test articles were prepared as follows:

[00470] Group 1: Rested cells were harvested, spun down, resuspended in supplemented media, and incubated in a 37°C/5% CO₂ incubator overnight.

[00471] Groups 2-14: Rested cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E5**, and electroporated. Following

electroporation, cell suspensions were collected, transferred to supplemented media, and incubated in a 37°C/5% CO₂ incubator overnight.

[00472] Within 24 hours post-electroporation (Day 1), the cells were harvested from culture, counted, and sampled by flow cytometry to determine mbIL15 and TCR transgene expression. Briefly, up to 1×10^6 cells of each test article were stained with human Fc Block (BD Biosciences 564220) first to reduce background staining for 10 minutes at room temperature. Cell suspensions were further stained with fluorochrome conjugated antibodies (listed in **Table 1**) diluted in Brilliant Stain Buffer (BD Biosciences 566349) for 30 minutes at 4°C. TCR expression was detected using PerCP-Cy5.5 conjugated anti-mouse TCR β antibody specific for the murine constant region of TCR β . Other fluorescently conjugated antibodies used included: CD3 (Clone OKT-3), IL-15 (34559), CD8 (Clone RPA-T8), and Invitrogen violet live/Dead dye (**Table E6**).

Table E6. Fluorescently Conjugated Antibodies.

Antibody Target	Clone	Fluorophore	Company & Cat #
Live/Dead		Pacific Blue	Invitrogen L34955A
Human CD3	OKT3	BV510	Biolegend 317332
Human CD8	RPA-T8	PE-Cy7	BD Biosciences 557746
Human IL-15	34559	PE	R&D Systems IC2471P
Mouse TCR	H57-597	PerCP-Cy5.5	BD Biosciences 560657

[00473] Cells were washed with FACS buffer (PBS, 2% FBS, 0.1% sodium azide). Data were acquired using an NovoCyte Quanteon flow cytometer system (Agilent) and analyzed with FlowJo software (version 10.7.1; TreeStar, Ashland, OR) to determine the percentage of each transgenic subpopulation (mbIL15⁺mTCR⁺, mbIL15^{neg}mTCR⁺, mbIL15⁺mTCR^{neg}, mbIL15^{neg}mTCR^{neg}) present in each test article. Unless described otherwise, transgene expression was assessed on gated cell events, singlets, viable events, and CD3⁺ cells.

[00474] Results of flow cytometry are shown in **FIG. 4** and **Table E7**.

Table E7. Day 1 post-electroporation specifications and transgene expression of genetically modified T cells.

Group	Name	Viability (%)	mbIL15 ⁺ (% CD3 ⁺)	mTCR ⁺ (% CD3 ⁺)	mbIL15 ⁺ mTCR ⁺ (% CD3 ⁺)
1	NT cells	97.5	N/A	N/A	N/A
2	mbIL15 cells	83.9	33.4	N/A	N/A
3	APB cells	68.3	N/A	18.6	N/A
4	BPA cells	75.4	N/A	26.1	N/A
5	APB+15 cells	65.7	11.5	9.99	5.07
6	BPA+15 cells	78.5	20.7	23.0	15.2
7	APBT15 cells	78.0	9.91	21.9	7.60

Group	Name	Viability (%)	mbIL15 ⁺ (% CD3 ⁺)	mTCR ⁺ (% CD3 ⁺)	mbIL15 ⁺ mTCR ⁺ (% CD3 ⁺)
8	ATBP15 cells	82.7	13.9	29.1	11.1
9	AP15TB cells	84.1	9.45	20.6	6.05
10	AT15PB cells	81.6	12.6	23.2	8.58
11	BPAT15 cells	64.3	3.41	8.88	2.11
12	BTAP15 cells	73.8	8.66	20.9	5.47
13	BP15TA cells	83.7	13.3	29.9	9.52
14	BT15PA cells	74.5	6.68	12.9	3.12

6.3 Example 3: Generation and Evaluation of Expanded T Cells

[00475] This Example describes the generation and evaluation of T cells co-expressing TCR α , TCR β , and mbIL15 from the plasmids described in Example 1. TCR-T cells described in this Example 3 were generated similarly to those described in Example 2 except as indicated below.

[00476] Briefly, cryopreserved PBMCs were thawed, resuspended in supplemented media (IL-7 + IL-15), and incubated in a 37°C/5% CO₂ incubator for one hour.

[00477] Test articles as listed above in **Table E5** were then prepared as follows:

[00478] Group 1: Rested cells were harvested, spun down, resuspended in recovery media (50:50 media containing IL-7 + IL-15 + n-acetylcysteine (NAC)), and incubated in a 37°C/5% CO₂ incubator overnight.

[00479] Groups 2-14: Rested cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E5**, and electroporated. Following electroporation, cell suspensions were collected, transferred to recovery media (50:50 media containing IL-7 + IL-15 + NAC), and incubated in a 37°C/5% CO₂ incubator overnight.

[00480] Groups 3-14: Within 24 hours post-electroporation (Day 1), mTCR positive (mTCR⁺) cells were isolated using mTCR antibody and MACS® Cell Separation system (Miltenyi Biotec). Live cells from groups 1 & 2 and live TCR⁺ enriched cells from groups 3-14 were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a first expansion media (50:50 media containing IL-21 + IL-7) with irradiated allogeneic feeder cells and OKT3 antibody. Cells were fed regularly with cytokines. After 13 days of first phase expansion, cells were harvested, and expression of mTCR and mbIL15 was detected on CD3⁺ gated population with mouse TCR beta antibody and IL-15 antibody as described in Example 2. Cell count and viability was accessed with a NC3000 cell counter. Unless described otherwise, transgene expression was assessed on gated cell events, singlets, viable events, and CD3⁺ cells.

[00481] Expression of mTCR and mbIL15 and cell viability was assessed for each test article at two separate time points: 1) after electroporation (Day 1), and 2) after first expansion phase (Day 13).

[00482] TCR expression after electroporation (Day 1) is shown in **FIG. 5A-5B**. **FIG. 5A** provides representative TCR expression data from each test article. **FIG. 5B** provides TCR expression data from three donors presented as % mTCR+ cells out of CD3+ cells.

[00483] TCR and mbIL15 expression after first phase expansion (Day 13) is shown in **FIG. 6A-6C**. **FIG. 6A** provides representative TCR and mbIL15 expression data from each test article. **FIG. 6B** provides TCR expression data from three donors presented as % mTCR+ cells out of CD3+ cells and **FIG. 6C** provides % TCR+mbIL15+ cells out of CD3+ cells.

[00484] TCR+ and TCR+mbIL15+ cell number was also assessed after first phase expansion (Day 13) as shown in **FIG. 7A-7B**. **FIG. 7A** provides TCR expression data from three donors presented as total number of mTCR+ T cells and **FIG. 7B** provides total number of TCR+mbIL15+ T cells.

[00485] Cell viability after electroporation (Day 1) and after first phase expansion (Day 13) is shown in **FIG. 8A & 8B**, respectively.

[00486] The transgene expression data and cell count data demonstrate that BP15TA and AP15TB are the most potent candidates to have mbIL15+TCR+ T cells with the highest level of TCR and mbIL15 expression. Viability data demonstrated that despite of the size of the tricistronic mbIL15+TCR vectors (Groups 7-14), the viability is similar to the two-vector co-transfection system (Groups 5 & 6).

[00487] Functionality of the TCR-T cells was also measured following first phase expansion (Day 13) as described below.

[00488] Activation of TCR-T cells generated by electroporation with different polycistronic plasmids was assessed. After 13 days of first phase expansion, cells were co-cultured with wild-type or mutant neoantigen peptide pulsed T2 cells which have endogenous expression of HLA-A*02:01. After overnight incubation, cells were harvested and induction of 4-1BB molecule on CD3+CD8+ cells was detected with 4-1BB antibody. Results are shown in **FIG. 9A-9B** demonstrating that mbIL15/TCR-T cells were highly avid and specific to the target neoantigen as measured by upregulation of 4-1BB co-stimulatory receptor with negligible recognition of wild type sequence. There was no significant difference in function between the mbIL15/TCR-T cells generated using different polycistronic plasmids.

[00489] The level of phosphorylated STAT5 was also assessed for TCR-T cells electroporated with different polycistronic plasmids. After 13 days of first phase expansion, cells were washed and incubated in cytokine-free 50:50 media overnight to stabilize the phosphorylation of STAT5. Phosphorylation of STAT5 was detected the following day on CD3⁺ cells using pSTAT5 (pY694). Results are shown in **FIG. 10** demonstrating that the expressed mbIL15 is functional. IL15 signaling was activated, inducing phosphorylation of STAT5 (downstream of IL15 receptor). Phosphorylation of STAT5 in mbIL15 TCR-T cells generated with different polycistronic plasmids was not significantly different between plasmids but was increased in all mbIL15 containing plasmids relative to TCR only conditions that lacked mbIL15.

[00490] The level of apoptosis after 9 days of activation was assessed for TCR-T cells electroporated with different polycistronic plasmids. After 13 days of first phase expansion, cells were washed and activated with CD3/CD28 Dynabeads® (ThermoFisher) for 9 days. After activation, apoptosis of CD3⁺TCR⁺ cells was monitored with AnnexinV/7ADD kit (Biolegend). Results are shown in **FIG. 11** demonstrating that expression of mbIL15 on CD3⁺TCR⁺ cells inhibited AICD (activation-induced cell death) as measured by fewer cells stained for AnnexinV and/or PI. This inhibition of AICD was not significantly different between the different polycistronic plasmids tested, nor was it different from two-vector systems (APB+mbIL15 and BPA+mbIL15).

[00491] A second expansion phase was performed as described below and vector copy number (VCN) following the second expansion phase was assessed. Briefly, T cells from Groups 3-14 were isolated by MACS using mTCR antibodies. T cells from Groups 2-14 were then incubated with a second expansion media (50:50 media containing IL-21) and irradiated feeder cells and OKT3 antibody. Cells were fed regularly with cytokines. After 15 days second phase expansion, cells were harvested and VCN was detected using qPCR as average number of *Sleeping Beauty* transgene DNA copy per cell in a sample. Results are shown in **Table E8** demonstrating that low levels of vector were detected in TCR-T cells and mbIL15/TCR-T cells after two rounds of expansion.

Table E8. Vector Copy Number (VCN) after second expansion phase.

Group	Name	VCN
2	mbIL15 cells	0.3
3	APB cells	0.4
4	BPA cells	1.4
5	APB+15 cells	2.6

Group	Name	VCN
6	BPA+15 cells	2.1
7	APBT15 cells	4.7
8	ATBP15 cells	4.5
9	AP15TB cells	5.3
10	AT15PB cells	3.9
11	BPAT15 cells	1.5
12	BTAP15 cells	2.1
13	BP15TA cells	2.3
14	BT15PA cells	2.9

[00492] **Conclusion:** The series of data described in this example illustrate that BP15TA and AP15TB are the most potent candidates to generate mbIL15 TCR-T cell with the highest level of TCR and mbIL15 expression. All plasmids evaluated expressing mbIL15 increased phosphorylation of STAT5 indicating the mbIL15 expressed at sufficient levels in T cells to elicit downstream signaling. Moreover, co-expression of mbIL15 with a transgenic TCR, reduces AICD following T cell activation. Furthermore, all tricistronic mbIL15/TCR plasmids tested resulted in acceptable VCN values.

6.4 Example 4: Evaluation of polycistronic TCR constructs with different murine constant regions.

[00493] This Example evaluates the effect of different murine constant regions on the TCR constructs described above in Examples 1-3.

[00494] Briefly, the amino acid sequences of the TCR α chain and TCR β chain examined here are identical to the TCR α chain and TCR β chain described in Examples 1-3 except that the constant region of each chain is not cysteine-substituted. Specifically, the TCR α chain was generated by fusing a human V α region, including its N-terminal signal sequence (SEQ ID NO: 1006) with a glutamic acid at position 2, to a murine C α region modified by substituting a leucine at amino acid position 112, an isoleucine at amino acid position 114, and a valine at amino acid position 115 (SEQ ID NO: 42). The TCR β chain was generated by fusing a human V β region, including its N-terminal signal sequence (SEQ ID NO: 2006) with an alanine at position 2, to a murine wild-type C β (SEQ ID NO: 52). The constructs containing the cysteine-substituted constant domains, as described in Examples 1-3, are referred to below as the “S version” and the newly-generated constructs containing the non-cysteine-substituted constant domains are referred to below as the “N version”. A schematic of these constructs is provided in **FIG. 12**.

[00495] The unified plasmids, “NU version” referred to below, vary in the nucleotide sequence of the TCR constant regions compared to the “N version”. All “NU versions” contain the same nucleotide sequences encoding the TCR constant regions (C α and C β); however, the amino acid sequences of the TCR constant regions encoded by the “NU version” are identical to those of the “N version.” No other differences exist between the “N version” and “NU version.”

[00496] To generate the TCR-T cells described in this Example 4, the plasmids described above were electroporated into the enriched PBMCs. Briefly, cryopreserved PBMCs were thawed, exchanged into 50:50 media and electroporated. The PBMC test articles listed in **Table E9** were then prepared. Where it is indicated that cells were transposed, cells were co-electroporated with the indicated plasmid and plasmid TA.

Table E9. PBMC test articles.

Group	Name	Description
2.1	NT cells	Non-transposed PBMCs
2.2	BPA cells	PBMCs transposed with Plasmid BPA
2.3	BPA-N cells	PBMCs transposed with N version of Plasmid BPA
2.4	AP15TB cells	PBMCs transposed with Plasmid AP15TB
2.5	BP15TA cells	PBMCs transposed with Plasmid BP15TA
2.6	AP15TB-N cells	PBMCs transposed with N version of Plasmid AP15TB
2.7	BP15TA-N cells	PBMCs transposed with N version of Plasmid BP15TA
2.8	AP15TB-NU cells	PBMCs transposed with unified N version of Plasmid AP15TB
2.9	BP15TA-NU cells	PBMCs transposed with unified N version of Plasmid BP15TB

[00497] Test articles were prepared as follows:

[00498] Group 2.1: Cells were harvested, spun down, resuspended in recovery media (50:50 media containing IL-7 + IL-15 + n-acetylcysteine (NAC)), and incubated in a 37°C/5% CO₂ incubator overnight.

[00499] Groups 2.2-2.9: Cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E9**, and electroporated. Following electroporation, cell suspensions were collected, transferred to recovery media (50:50 media containing IL-7 + IL-15 + NAC), and incubated in a 37°C/5% CO₂ incubator overnight.

[00500] Within 24 hours post-electroporation (Day 1), live cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a first expansion media (50:50 media containing IL-21 + IL-7 + IL-12 + T Cell TransAct™). Cells were fed regularly with cytokines. After 11 days of first phase expansion, TCR+ cells were isolated with mTCR antibody.

The isolated TCR⁺ T cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a second expansion media (50:50 media containing 3000 IU/ml of IL-2 + T Cell TransAct™). Cells were fed regularly with cytokines. After 11 or 16 days of second phase expansion, cells were harvested, and the various assays described below were performed.

[00501] Transgene expression was assessed for T cells electroporated with different polycistronic plasmids. On Day 1 (post-electroporation), Day 11 pre-enrichment (post-1st phase expansion), Day 11 post-enrichment, and Day 22 (post-2nd phase expansion), cells were harvested and the expression of mTCR and mbIL15 was detected on CD3⁺ gated population with mouse TCR beta antibody and IL-15R α antibody. On Day 1 after electroporation the level of TCR expression was similar between the different versions of polycistronic plasmids (**FIG. 13A**). Prior to enrichment on Day 11, TCR expression trended lower in mbIL15/TCR T cells compared to TCR only; however, TCR expression was comparable post-enrichment on Day 11 (**FIG. 13B**). On Day 22, when the cells were harvested, TCR expression was comparable with no notable difference between “S” and “N” versions of the polycistronic plasmids. Co-expression of TCR and mbIL15 was found to be similar between the different versions of polycistronic plasmids throughout the process (**FIGS. 14-15**).

[00502] Fold expansion of total cell count (**FIG. 16A-16B**) and mTCR⁺ cell count (**FIG. 17A-17B**) was assessed for T cells electroporated with different polycistronic plasmids. Fold expansion value was calculated as: Cell number on Day 11/ Cell number on Day 1 (**FIG. 16A**) and Cell number on Day 22/ Cell number on Day 11 (**FIG. 16B**). Cells transposed with mbIL15/TCR tricistronic plasmids tended to expand less than cells transposed with TCR only bicistronic plasmids during both first and second phase expansion. However, significant degrees of expansion were achieved in all groups and no difference was seen between the different versions of the polycistronic plasmids. mTCR⁺ cell number was calculated as: Total cell number X CD3 population (%) X mTCR population (%).

[00503] The above transgene expression and cell growth data demonstrate that cells generated using N version and NU versions of the polycistronic plasmids were not phenotypically different from cells generated using the S version of the polycistronic plasmids.

[00504] To carry out the pSTAT5 assay, the 4-1BB induction assay, and IFN- γ assay described below, the second expansion phase was extended to 16 days (due to the logistic load). Phosphorylation of STAT5 in T cells at Day 27 was detected on CD3⁺ cells with pSTAT5

(pY694). The pSTAT5 data shown in **FIG. 18** demonstrated that the expressed mbIL15 is functional. IL15 signaling was activated, inducing phosphorylation of STAT5 (downstream of IL15 receptor). Phosphorylation of STAT5 in mbIL15 TCR-T cells generated with the different versions of polycistronic plasmids was not significantly different. The levels of phosphorylated STAT5 trended higher in cells co-expressing mbIL15 and TCR compared to those expressing TCR alone.

[00505] To assess antigen-specific activation of the generated TCR-T cells, overnight co-culture of the generated TCR-T cells with wild-type or mutant neoantigen pulsed DCs (HLA matched) was performed after 16 days of second phase expansion and 4-1BB induction and IFN- γ secretion were measured. Induction of 4-1BB on CD3+CD8+ cells was detected with 4-1BB antibody. Secretion of IFN- γ measured by ELISA (Clone 2G1 and B133.5, Thermo Fisher). The 4-1BB induction results shown in **FIG. 19A**, and IFN- γ secretion results shown in **FIG. 19B** demonstrate that the function of mbIL15 TCR-T cells generated with different versions of the polycistronic plasmids was not significantly different.

[00506] The long-term withdrawal (LTWD) assay was performed to examine the transgene expression, survival and activation of T cells cultured under cytokine-free conditions. The LTWD assay was performed as follows. The engineered T cells at Day 22 (post-first and second phase expansion) were transferred to T25 flask and cultured for 4 weeks in cytokine-free media (50:50). 50% of media was exchanged every week. For the control groups (groups 2.2 & 2.3, **Table E9**), cells were treated with 300U/ml IL-2 twice a week while exchanging the 50% of media. Flow data were acquired using an NovoCytte Quanteon flow cytometer system (Agilent) and analyzed with FlowJo software (version 10.7.1; TreeStar, Ashland, OR). (Data n = 4, pooled from 2 independent experiments)

[00507] After 4 weeks LTWD incubation, the expression of mTCR was detected on CD3+ gated population with mouse TCR beta antibody (**FIG. 20A**) and cell count and viability were accessed (**FIG. 20B**). This mTCR expression and cell count data demonstrated no significant difference between mbIL15 TCR-T cells generated with different versions of the polycistronic plasmids. The number of viable cells decreased after long-term cytokine withdrawal in all groups, but cells from the groups co-expressing mbIL15 and TCR survived 5~6 fold more compared to cells from the TCR only groups.

[00508] The activation of TCR-T cells after LTWD culture was assessed by 4-1BB induction and IFN- γ secretion after overnight co-culture with wild-type or mutant neoantigen (10 μ g/mL)

pulsed DCs (HLA matched). As described above, induction of 4-1BB on CD8⁺ T cells was detected with 4-1BB antibody (**FIG. 21A-21B**) and IFN- γ secretion was measured by ELISA (**FIG. 22A-22B**). These data demonstrate that mbIL15 TCR-T cells which survived LTWD culture retained their specific function and demonstrated more potent activation than T cells from control TCR only groups (IL-2 treated); however, the function of mbIL15 TCR-T cells generated with different versions of the polycistronic plasmids was not significantly different.

[00509] Memory phenotype of TCR-T cells electroporated with different polycistronic vectors was also assessed. T cell memory subsets are defined as: CD45RA⁺CD45RO⁺CD62L⁺CD95⁺ = stem cell memory-like (Tscm-like); CD45RA⁺CD45RO⁻CD62L⁺CD95⁺ = stem cell memory (Tscm); CD45RA⁻CD45RO⁺CD62L⁺CD95⁺ = central memory (Tcm); CD45RA⁻CD45RO⁺CD62L⁻CD95⁺ = effector memory (Tem). T cell effector (Teff) are defined as CD45RA⁻CD45RO⁻CD62L⁻CD95⁺. The pie charts in **FIG. 23A-23C** show the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-first phase expansion (**FIG. 23A**), day 22 post-second phase expansion (**FIG. 23B**), and after 4 weeks of LTWD culture (**FIG. 23C**) in cells transposed with the tested plasmids.

[00510] Memory phenotype data shows the kinetics of TCR-T memory and effector differentiation. At days 11 and 22 post-expansion, there is no difference between the different polycistronic TCR plasmids (**FIG. 23A-23B**). There were more Tscm and Teff cells and fewer Tcm cells in the TCR-T cells expressing mbIL15 relative to TCR-T cells without mbIL15. After 4 weeks of culture in absence or presence of IL-2, TCR-T cells predominantly differentiated into Teff cells (over 85%). TCR-T cells expressing mbIL15 cultured for 4 weeks in the absence of cytokines differentiated into 3 main subsets: Teff, Tscm-like and Tscm cells (**FIG. 23C**). These results suggest that mbIL15 is sufficient to support the Tscm phenotype.

[00511] **Conclusions:** The mbIL15 TCR-T cells generated from different versions of the polycistronic plasmids showed comparable features including TCR expression, memory phenotype, specificity, and IFN- γ secretion. This data supports that removal of cysteine-substitutions in the mouse constant domains used in the first-generation vectors and use of unified mouse constant regions will not produce any significant changes in the mbIL15 TCR-T cell product.

6.5 Example 5: Generation and Evaluation of T cells generated using various tricistronic TCR/mbIL15 vectors

[00512] This Example describes the evaluation of T cells expressing mbIL15 in combination with different TCR α /TCR β chains generated using tricistronic vectors as described below. Similar to the vectors described in Example 4, the tricistronic expression cassettes used in this Example each include a transcriptional regulatory element operably linked to a polycistronic polynucleotide that encodes a TCR α chain (referred to herein as “TCR α ” or “A”), a TCR β chain (referred to herein as “TCR β ” or “B”), and membrane-bound IL-15/IL-15R α fusion protein (referred to herein as “mbIL15” or “15”), each separated by a furin recognition site and either a P2A element or a T2A element that mediates ribosome skipping to enable expression of separate polypeptide chains.

[00513] The nine TCRs used in this Example are each directed against a different target as shown in **Table E10**. The V α amino acid sequences and V β amino acid sequences for each of the nine TCRs listed correspond to the sequences provided in **Table 6**. Each TCR α chain was generated by fusing the V α sequence to a murine C α region modified by substituting a leucine at amino acid position 112, an isoleucine at amino acid position 114, and a valine at amino acid position 115 (SEQ ID NO: 42). Each TCR β chain was generated by fusing the V β sequence to a murine wild-type C β (SEQ ID NO: 52).

Table E10. TCR Targets.

Target Protein	Mutation	HLA Type	TCR
TP53	R175H	A*02:01	TCR001
		DRB1*13:01	TCR009
	R248W	A*68:01	TCR057
	Y220C	DRB3*02:02	TCR016
KRAS	G12D	A*11:01	TCR022
		C*08:02	TCR064
	G12V	A*11:01	TCR075
		C*01:02	TCR055
EGFR	E746-A750del	DPA1*02:01/DPB1*01:01	TCR077

[00514] For each of the TCRs above, three vectors were constructed and evaluated: 1) TCR only (BA); 2) A15B; and 3) B15A. The TCR only (BA) vectors contain a bicistronic expression cassette encoding TCR β chain and TCR α chain separated by a furin recognition site and a P2A element in the following orientation from 5' to 3': TCR β -TCR α . The AP15TB vectors contain a tricistronic expression cassette encoding TCR α chain, TCR β chain, and mbIL15 in the following orientation from 5' to 3': TCR α -mbIL15-TCR β . The BP15TA vectors contain a tricistronic

expression cassette encoding TCR α chain, TCR β chain, and mbIL15 in the following orientation from 5' to 3': TCR β -mbIL15-TCR α .

[00515] TCR-T cells described in this Example were generated similarly to those described in Examples 2-4 except as indicated below. Where it is indicated that cells were transposed, cells were co-electroporated with the indicated plasmid as well as plasmid TA or similar Transposase expression plasmid unless otherwise stated.

[00516] Briefly, cryopreserved PBMCs were thawed, resuspended in 50:50 media and placed in a 37°C/5% CO₂ incubator before electroporation.

[00517] Test articles as listed in **Table E11** were then prepared.

Table E11. PBMC test articles.

Group	TCR	Name	Description
3.1	None	NT	Non-transposed PBMCs
3.2	TCR001	BPA-N ¹	PBMCs transposed with TCR001 BPA-N
3.3	TCR001	AP15TB-NU ²	PBMCs transposed with TCR001 AP15TB-NU
3.4	TCR001	BP15TA-NU ³	PBMCs transposed with TCR001 BP15TA-NU
3.5	TCR057	BPA-N	PBMCs transposed with TCR057 BPA-N
3.6	TCR057	AP15TB-NU	PBMCs transposed with TCR057 AP15TB-NU
3.7	TCR057	BP15TA-NU	PBMCs transposed with TCR057 BP15TA-NU
3.8	TCR009	BPA-N	PBMCs transposed with TCR009 BPA-N
3.9	TCR009	AP15TB-NU	PBMCs transposed with TCR009 AP15TB-NU
3.10	TCR009	BP15TA-NU	PBMCs transposed with TCR009 BP15TA-NU
3.11	TCR016	BPA-N	PBMCs transposed with TCR016 BPA-N
3.12	TCR016	AP15TB-NU	PBMCs transposed with TCR016 AP15TB-NU
3.13	TCR016	BP15TA-NU	PBMCs transposed with TCR016 BP15TA-NU
3.14	None	NT	Non-transposed PBMCs
3.15	TCR022	BPA-N	PBMCs transposed with TCR022 BPA-N
3.16	TCR022	AP15TB-NU	PBMCs transposed with TCR022 AP15TB-NU
3.17	TCR022	BP15TA-NU	PBMCs transposed with TCR022 BP15TA-NU
3.18	TCR075	BPA-N	PBMCs transposed with TCR075 BPA-N
3.19	TCR075	AP15TB-NU	PBMCs transposed with TCR075 AP15TB-NU
3.20	TCR075	BP15TA-NU	PBMCs transposed with TCR075 BP15TA-NU
3.21	TCR055	BPA-N	PBMCs transposed with TCR055 BPA-N
3.22	TCR055	AP15TB-NU	PBMCs transposed with TCR055 AP15TB-NU
3.23	TCR055	BP15TA-NU	PBMCs transposed with TCR055 BP15TA-NU
3.24	TCR064	BPA-N	PBMCs transposed with TCR064 BPA-N
3.25	TCR064	AP15TB-NU	PBMCs transposed with TCR064 AP15TB-NU
3.26	TCR064	BP15TA-NU	PBMCs transposed with TCR064 BP15TA-NU
3.27	None	NT	Non-transposed PBMCs
3.28	TCR077	BPA-N	PBMCs transposed with TCR077 BPA-N
3.29	TCR077	AP15TB-NU	PBMCs transposed with TCR077 AP15TB-NU
3.30	TCR077	BP15TA-NU	PBMCs transposed with TCR077 BP15TA-NU

¹ Generated using the same plasmid as BPA-N group in Example 4.

² Generated using the same plasmid as AP15TB-NU group in Example 4.

³ Generated using the same plasmid as BP15TA-NU group in Example 4.

[00518] Test articles were prepared in three batches (Batch 1 = Groups 3.1-3.13; Batch 2 = Groups 3.14-3.26; Batch 3 = Groups 3.27-3.30) as follows:

[00519] Groups 3.1, 3.14, & 3.27: Cells were harvested, spun down, resuspended in recovery media (50:50 media containing IL-7 + IL-15 + n-acetylcysteine (NAC)), and incubated in a 37°C/5% CO₂ incubator overnight.

[00520] Groups 3.2-3.13, 3.15-3.26, & 3.28-3.30: Cells were harvested, spun down, resuspended in electroporation buffer together with the plasmids listed in **Table E10**, and electroporated. Following electroporation, cell suspensions were collected, transferred to recovery media (50:50 media containing IL-7 + IL-15 + NAC), and incubated in a 37°C/5% CO₂ incubator overnight.

[00521] Within 24 hours post-electroporation (Day 1), live cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a first expansion media (50:50 media containing IL-21 + IL-7 + IL-12 + T Cell TransAct™). Cells were fed regularly with cytokines. After 11 days of first phase expansion, TCR+ cells were isolated with mTCR antibody. The isolated TCR+ T cells were transferred to G-REX® culture plates (Wilson Wolf Manufacturing) and incubated with a second expansion media (50:50 media containing 3000U/ml of IL-2 + T Cell TransAct™). During this second expansion phase, cells were fed regularly with cytokines. After 11 or 16 days of second phase expansion, cells were harvested, and the various assays described below were performed.

[00522] Transgene expression was assessed for T cells electroporated with different polycistronic plasmids. On Day 1 (post-electroporation), Day 11 (post-1st phase expansion) and Day 22 (post-2nd phase expansion), cells were harvested and the expression of mTCR and mbIL15 was detected on CD3+ gated population with mouse TCR beta antibody and IL-15Rα antibody. The results are shown in **FIGS. 24-28**.

[00523] Fold expansion of total cell count and mTCR+ cell count was assessed for T cells electroporated with different polycistronic plasmids. Fold expansion value was calculated as: Cell number on Day 11/ Cell number on Day 1 and Cell number on Day 22/ Cell number on Day 11. mTCR+ cell number was calculated as: Total cell number X CD3 population (%) X mTCR population (%). The results are shown in **Table E12**.

Table E12. Fold expansion of total cells and mTCR+ cell count during first and second expansion phases.

Group		Fold Expansion (FE)							
		Total Cell				mTCR+ Cell			
		First expansion		Second expansion		First expansion		Second expansion	
		Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
1	TCR001-BPA-N	83.86	19.60	121.97	11.81	6.11	2.09	171.56	9.57
	TCR001-AP15TB-NU	66.89	13.09	107.01	20.38	18.38	9.60	101.00	17.14
	TCR001-BP15TA-NU	62.93	17.70	108.50	20.15	19.04	7.72	104.08	16.79
2	TCR057-BPA-N	98.21	36.03	110.40	7.05	8.16	4.73	146.17	13.45
	TCR057-AP15TB-NU	58.90	16.21	107.38	16.76	17.34	9.77	104.42	16.05
	TCR057-BP15TA-NU	58.78	16.21	108.69	3.91	14.19	6.44	104.04	3.64
3	TCR009-BPA-N	104.97	30.03	142.34	25.63	11.62	4.92	154.58	28.38
	TCR009-AP15TB-NU	51.68	13.48	95.38	13.31	24.76	12.75	83.83	16.19
	TCR009-BP15TA-NU	49.99	4.70	75.43	10.92	7.03	3.49	77.03	17.45
4	TCR016-BPA-N	87.13	9.63	127.79	25.67	17.38	5.29	142.91	26.78
	TCR016-AP15TB-NU	61.46	12.58	95.42	16.34	26.02	18.67	82.78	10.34
	TCR016-BP15TA-NU	66.33	15.42	93.38	14.09	23.39	15.51	83.30	14.44
5	TCR022-BPA-N	85.99	6.51	169.56	16.12	8.39	1.15	202.20	37.63
	TCR022-AP15TB-NU	59.11	5.90	95.36	12.47	12.21	1.59	102.12	22.10
	TCR022-BP15TA-NU	63.98	5.28	120.10	17.30	11.70	1.79	161.60	69.66
6	TCR075-BPA-N	89.45	6.14	182.86	15.27	9.12	0.75	207.74	21.54
	TCR075-AP15TB-NU	63.30	7.06	106.07	14.15	12.71	2.11	102.37	32.40
	TCR075-BP15TA-NU	59.06	5.91	107.40	20.65	10.57	2.47	114.25	43.15
7	TCR055-BPA-N	78.21	3.52	165.43	25.40	6.05	1.34	198.11	98.27
	TCR055-AP15TB-NU	58.84	1.25	95.98	18.09	10.28	1.79	67.59	20.05
	TCR055-BP15TA-NU	59.15	6.69	87.57	13.96	8.76	2.03	78.66	25.73
8	TCR064-BPA-N	86.10	10.54	177.48	15.01	8.47	1.48	212.18	55.16
	TCR064-AP15TB-NU	55.46	5.95	120.98	12.99	12.61	1.78	162.44	67.74
	TCR064-BP15TA-NU	59.66	4.38	110.54	16.75	9.78	1.98	137.63	59.08
9	TCR077-BPA-N	91.68	6.43	217.14	17.84	12.72	5.26	332.66	29.27
	TCR077-AP15TB-NU	57.10	5.54	97.22	13.45	16.66	7.28	75.79	4.98
	TCR077-BP15TA-NU	63.14	3.27	94.38	19.73	13.41	3.60	75.86	14.16

[00524] Cells generated using the polycistronic plasmids containing different TCR sequences were not phenotypically different from each other as demonstrated by transgene expression and cell growth data.

[00525] To assess activation of the generated TCR-T cells, overnight co-culture of the generated TCR-T cells with wild-type or mutant neoantigen pulsed DCs (HLA matched) was performed after 16 days second phase expansion and 4-1BB induction and IFN- γ secretion were measured. Induction of 4-1BB on CD3+CD8+ cells was detected with 4-1BB antibody. Secretion of IFN- γ measured with the ELISA antibody pair. The 4-1BB induction results are shown in **FIG. 29A-29I**

and IFN- γ secretion results are shown in **FIG. 30A-30I**. The results demonstrate that when challenged with their cognate neoantigen, mbIL-15 TCR-T cells were highly avid and specific to the target neoantigens as measured by upregulation of 4-1BB co-stimulatory receptor and secretion of IFN- γ with negligible recognition of wild type sequences.

[00526] All data from electroporation to the second expansion phase of TCR vetting demonstrated that tricistronic system, expressing TCR α , TCR β and mbIL15 with one plasmid successfully generated mbIL15 TCR-T cells and the features of the generated mbIL15 TCR-T cells are comparable to TCR-T cells in terms of transgene expression, cell growth, and functional specificity (4-1BB induction and IFN- γ secretion).

[00527] Cytolytic activity of TCR-T cells was assessed for T cells electroporated with polycistronic plasmids encoding TCR001 +/- mbIL15 generated as described above (overnight recovery + 11 days first phase expansion + 11 days second phase expansion) and then harvested and frozen on Day 22. On experimental day, frozen Day 22 TCR-T cells were thawed and recovered for 3 days in media containing 3000U/ml of IL-2. Then, the recovered TCR-T cells were incubated with AU565 (Mut+HLA^{neg}) or Tyk-nu (Mut+HLA⁺) cells. After overnight incubation, the remaining T cells were extensively washed, and the extent of viable cells left in the culture after TCR-specific cytotoxicity was measured using the CellTiter Glo luminescence-based assay. The results are shown in **FIG. 31**.

[00528] Specific lysis was calculated from background subtracted values as:

$$= \left[\frac{("Tumor \& TCR-T" value - ("TCR-T" Value + Mean "Tumor" Value))}{"TCR-T" Value - ("TCR-T" Value + Mean "Tumor" Value)} \right] \times 100$$

[00529] Cytolytic activity of TCR-T cells was also assessed for T cells electroporated with polycistronic plasmids encoding TCR022 +/-mbIL15 or TCR075 +/- mbIL15 generated as described above (overnight recovery + 11 days first phase expansion + 11 days expansion) and then harvested and frozen on Day 22. On experimental day, frozen Day 22 TCR-T cells were thawed and recovered for 3 days in media containing 3000U/ml of IL-2. Meantime, Saos-2 cells were plated in 96 well plate. After overnight incubation, HLA*11:01 plasmid was transfected into the Saos-2 cells and on the following day, WT or MUT neoantigenic peptides (1 μ g/ml) were loaded on the transfected Saos-2 cells for 2 hours. Then, the recovered TCR-T cells were incubated with the resulting Saos-2 cells overnight. After the overnight incubation, the remaining T cells were extensively washed, and the extent of viable cells left in the culture after TCR-specific cytotoxicity was measured using the CellTiter Glo luminescence-based assay. The results are shown in **FIG.**

32A-32B.

[00530] Specific lysis was calculated from background subtracted values as:

$$= \left[\frac{("Peptide loaded tumor \& TCR-T" value - ("TCR-T" Value + Mean "Peptide loaded Tumor" Value))}{"TCR-T" Value - ("TCR-T" Value - Mean "Peptide loaded tumor" Value)} \right] \times 100$$

The cytolytic activity data demonstrated that mbIL15 TCR-T cells generated using the tricistronic system exhibited specific lytic activity against target tumor cells.

[00531] The long-term withdrawal (LTWD) assay was performed to examine the transgene expression, survival and activation of T cells cultured under cytokine-free conditions. The LTWD assay was performed as follows. The engineered T cells at Day 22 (post first phase and second phase expansion) were transferred to T25 flask and cultured for 4 weeks in cytokine-free media (50:50). 50% of media was exchanged every week. For the control TCR only (BA) groups, cells were treated with 300U/ml IL-2 twice a week while exchanging the 50% of media. Flow data were acquired using an NovoCyte Quanteon flow cytometer system (Agilent) and analyzed with FlowJo software (version 10.7.1; TreeStar, Ashland, OR). (Data n = 4, pooled from 2 independent experiments)

[00532] After 4 weeks LTWD incubation, the expression of mTCR was detected on CD3+ gated population with mouse TCR beta antibody (**FIG. 33**) and cell count and viability were accessed (**FIG. 34A-34C**). This mTCR expression and cell count data demonstrated no significant difference between mbIL15 TCR-T cells generated with the different polycistronic plasmids. The number of viable cells decreased after long-term cytokine withdrawal in all groups, but cells from the groups co-expressing mbIL15 and TCR survived 5-6 fold more compared to cells from the TCR only groups.

[00533] The activation of TCR-T cells after LTWD culture was assessed by 4-1BB induction and IFN- γ secretion after overnight co-culture with wild-type or mutant neoantigen pulsed DCs (HLA matched). As described above, induction of 4-1BB on CD3+CD8+ cells was detected with 4-1BB antibody (**FIG. 35A-35I**) and IFN- γ secretion was measured with the ELISA antibody pair (**FIG. 36A-36C**). A comparison of 4-1BB induction assessed for T cells harvested at Day 27 and after LTWD is shown in **FIG. 37A-37I**. These data demonstrate that mbIL15 TCR-T cells which survived LTWD culture are still functional and were more strongly activated than cells from TCR only groups. The data also demonstrate that after 4 week of cytokine withdrawal (LTWD), mbIL15 TCR-T cells showed even more potent induction of 4-1BB compared to those cells after the second expansion phase.

[00534] Memory phenotype of TCR-T cells electroporated with different polycistronic vectors was also assessed. T cell memory subsets are defined as: CD45RA+CD45RO+CD62L+CD95+ = stem cell memory-like (Tscm-like); CD45RA+CD45RO-CD62L+CD95+ = stem cell memory (Tscm); CD45RA-CD45RO+CD62L+CD95+ = central memory (Tcm); CD45RA-CD45RO+CD62L-CD95+ = effector memory (Tem). T cell effector (Teff) are defined as CD45RA+CD45RO+CD62L-CD95+. The data in **Tables E13** and **E14** and representative pie charts in **FIGS. 38-40** show the mean frequency of live CD3⁺ T cell memory and effector subsets at day 11 post-expansion (**Table E13** & **FIG. 38**), day 22 post-expansion (**Table E14** & **FIG. 39**), and after 4 weeks of LTWD culture (**FIGS. 40A-40E**) in cells transposed with the tested plasmids.

Table E13. Memory phenotype of engineered T cells at D11.

Plasmid		%Tscm-like	% Tscm	%Teff	% Tcm	% Tem
1	TCR001-BPA-N	35.8	0.5	10.3	36.5	16.9
	TCR001-AP15TB-NU	34.1	0.2	7.3	43.3	15.1
	TCR001-BP15TA-NU	29.0	nd	6.7	46.9	17.2
2	TCR057-BPA-N	37.1	0.4	12.3	31.6	18.6
	TCR057-AP15TB-NU	33.7	0.1	7.7	43.5	15.0
	TCR057-BP15TA-NU	31.4	0.2	6.8	45.5	16.1
3	TCR009-BPA-N	38.3	0.6	11.8	29.9	19.4
	TCR009-AP15TB-NU	34.8	0.1	7.1	44.0	14.0
	TCR009-BP15TA-NU	28.5	0.2	6.3	47.7	17.3
4	TCR016-BPA-N	40.2	0.6	12.6	30.0	16.6
	TCR016-AP15TB-NU	32.8	0.4	6.8	44.8	15.2
	TCR016-BP15TA-NU	32.1	0.3	7.0	45.1	15.5
5	TCR022-BPA-N	58.1	2.9	7.5	25.6	5.9
	TCR022-AP15TB-NU	55.1	0.8	2.4	38.7	3.0
	TCR022-BP15TA-NU	56.9	0.7	2.3	37.4	2.7
6	TCR075-BPA-N	59.7	2.8	8.5	23.9	5.1
	TCR075-AP15TB-NU	53.5	0.7	2.1	40.6	3.1
	TCR075-BP15TA-NU	56.8	0.8	2.5	37.2	2.7
7	TCR055-BPA-N	55.6	2.5	8.2	27.8	5.9
	TCR055-AP15TB-NU	56.0	0.9	2.5	38.1	2.5
	TCR055-BP15TA-NU	56.6	0.8	2.5	37.3	2.8
8	TCR064-BPA-N	57.3	3.3	8.2	25.5	5.7
	TCR064-AP15TB-NU	53.3	0.8	2.5	40.1	3.3
	TCR064-BP15TA-NU	54.0	0.6	2.4	39.6	3.4
9	TCR077-BPA-N	63.8	3.0	5.3	22.0	5.8
	TCR077-AP15TB-NU	50.7	0.2	3.7	41.2	4.2
	TCR077-BP15TA-NU	50.7	0.2	4.3	40.4	4.4

Table E14. Memory phenotype of engineered T cells at D22.

	Plasmid	%Tscm-like	% Tscm	%Teff	% Tcm	% Tem
1	TCR001-BPA-N	28.8	0.2	23.0	22.8	25.2
	TCR001-AP15TB-NU	33.6	0.9	29.8	15.3	20.4
	TCR001-BP15TA-NU	31.2	0.7	28.4	16.9	22.8
2	TCR057-BPA-N	31.2	0.2	22.7	23.1	22.8
	TCR057-AP15TB-NU	33.5	0.4	28.1	18.0	20.0
	TCR057-BP15TA-NU	34.4	0.7	28.5	16.5	19.9
3	TCR009-BPA-N	26.3	0.1	19.0	27.7	26.9
	TCR009-AP15TB-NU	34.7	0.2	29.4	15.3	19.4
	TCR009-BP15TA-NU	27.5	0.8	32.9	12.7	26.1
4	TCR016-BPA-N	30.7	0.1	22.1	23.3	23.8
	TCR016-AP15TB-NU	35.3	0.8	29.6	14.1	20.2
	TCR016-BP15TA-NU	33.4	0.8	28.9	14.7	22.2
5	TCR022-BPA-N	28.7	0.1	15.3	31.8	24.1
	TCR022-AP15TB-NU	32.3	0.7	22.1	25.1	19.8
	TCR022-BP15TA-NU	30.4	0.5	22.8	24.1	22.2
6	TCR075-BPA-N	26.9	0.2	15.6	33.4	23.9
	TCR075-AP15TB-NU	31.7	0.7	22.6	22.3	22.7
	TCR075-BP15TA-NU	31.4	0.5	23.9	22.2	22.0
7	TCR055-BPA-N	22.9	0.2	14.9	35.1	26.9
	TCR055-AP15TB-NU	28.8	0.5	27.5	19.7	23.5
	TCR055-BP15TA-NU	28.8	0.4	25.7	20.2	24.9
8	TCR064-BPA-N	24.1	0.1	13.9	34.3	27.6
	TCR064-AP15TB-NU	28.7	0.3	21.1	25.8	24.1
	TCR064-BP15TA-NU	28.8	0.6	22.5	23.6	24.5
9	TCR077-BPA-N	34.3	0.3	27.8	19.2	18.4
	TCR077-AP15TB-NU	37.8	2.2	34.8	10.7	14.6
	TCR077-BP15TA-NU	37.8	1.9	36.4	10.1	13.8

[00535] Memory phenotype data shows the kinetics of TCR-T memory and effector differentiation. The addition of mbIL15 to TCR-T cells resulted in changes to the memory phenotype in the expanded product to contain fewer central memory cells (Tcm) and more effector (Teff) and stem cell memory (Tscm) populations relative to conventional TCR-T cells. After 4 weeks of culture in presence of IL-2, TCR-T cells predominantly differentiated into Teff cells. TCR-T cells expressing mbIL15 cultured for 4 weeks in the absence of cytokines differentiated into 3 main subsets: Teff, Tscm-like and Tscm cells. These results suggest that mbIL15 is sufficient to guide T cell differentiation to the Tscm phenotype.

[00536] **Conclusions:** mbIL15 TCR-T cells were successfully generated using 18 different constructs (2 different orientations; AP15TB and BP15TA X 9 TCRs). The addition of mbIL15 to TCR-T cells resulted in changes to the memory phenotype in the expanded product to contain fewer central memory cells (Tcm) and more effector (Teff) and stem cell memory (Tscm) populations relative to conventional TCR-T cells. Furthermore, long-term withdrawal of cytokine support (LTWD) demonstrated survival of a fraction of mbIL15 TCR-T cells which was significantly higher than survival of TCR-T cells lacking mbIL15. Functional and phenotypic evaluation of the persistent mbIL15 TCR-T cells revealed that they retained their functional neoantigen specificity and potency while displaying a preponderance of Tscm TCR-T cells capable of regenerating TCR-T cell effector pools. This suggested that mbIL15 TCR-T cells could likely establish long-lived tumor-specific TCR-T cells that potentially overcome suppression by the tumor microenvironment or other negative regulators. This non-clinical data supports clinical application of mbIL15 TCR-T cell platform and provides evidence that this strategy could result in improved efficacy for cancer treatment.

* * *

[00537] The invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[00538] All references (*e.g.*, publications or patents or patent applications) cited herein are incorporated herein by reference in their entireties and for all purposes to the same extent as if each individual reference (*e.g.*, publication or patent or patent application) was specifically and individually indicated to be incorporated by reference in its entirety for all purposes.

Other embodiments are within the following claims.

WHAT IS CLAIMED:

1. A recombinant vector comprising a polycistronic expression cassette, wherein the polycistronic expression cassette comprises a transcriptional regulatory element operably linked to a polycistronic polynucleotide that comprises:
 - a. a first polynucleotide sequence that encodes a T cell receptor (TCR) alpha chain comprising an alpha chain variable ($V\alpha$) region and an alpha chain constant ($C\alpha$) region;
 - b. a second polynucleotide sequence that comprises a first 2A element;
 - c. a third polynucleotide sequence that encodes a TCR beta chain comprising a beta chain variable ($V\beta$) region and a beta chain constant ($C\beta$) region;
 - d. a fourth polynucleotide sequence that comprises a second 2A element; and
 - e. a fifth polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof.
2. The recombinant vector of claim 1, wherein either or both of the first 2A element and the second 2A element, independently, is a P2A element, a T2A element, an F2A element, or an E2A element.
3. The recombinant vector of claim 1, wherein the first 2A element is a P2A element.
4. The recombinant vector of claim 2 or 3, wherein the P2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 18 or 20, or the amino acid sequence of SEQ ID NO: 18 or 20 comprising 1, 2, or 3 amino acid modifications.
5. The recombinant vector of claim 2 or 3, wherein the P2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 19 or 21.
6. The recombinant vector of any one of claims 1 or 3-5, wherein the second 2A element is a T2A element.
7. The recombinant vector of claim 2 or 6, wherein the T2A element comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 22 or 24, or the amino acid sequence of SEQ ID NO: 22 or 24 comprising 1, 2, or 3 amino acid modifications.

8. The recombinant vector of claim 2 or 6, wherein the T2A element comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 23 or 25.
9. The recombinant vector of any one of claims 1-8, wherein either or both of the second polynucleotide sequence and the fourth polynucleotide sequence, independently, encode a furin recognition site.
10. The recombinant vector of claim 9, wherein the furin recognition site comprises the amino acid sequence of SEQ ID NO: 2 or 4, or the amino acid sequence of SEQ ID NO: 2 or 4 comprising 1, 2, or 3 amino acid modifications.
11. The recombinant vector of claim 9, wherein the furin recognition site is encoded by the polynucleotide sequence of SEQ ID NO: 3 or 5 or the polynucleotide sequence of SEQ ID NO: 3 or 5 comprising 1, 2, or 3 nucleotide modifications.
12. The recombinant vector of any one of claims 1-11, wherein the second polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 10, or the amino acid sequence of SEQ ID NO: 10 comprising 1, 2, or 3 amino acid modifications.
13. The recombinant vector of any one of claims 1-11, wherein the second polynucleotide sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 11.
14. The recombinant vector of any one of claims 1-13, wherein the fourth polynucleotide sequence comprises a polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 12, or the amino acid sequence of SEQ ID NO: 12 comprising 1, 2, or 3 amino acid modifications.
15. The recombinant vector of any one of claims 1-13, wherein the fourth polynucleotide sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 13.
16. The recombinant vector of any one of claims 1-15, wherein the IL-15, or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 76.
17. The recombinant vector of any one of claims 1-15, wherein the IL-15, or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least

- 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 77.
18. The recombinant vector of any one of claims 1-15, wherein the IL-15R α , or functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 78.
 19. The recombinant vector of any one of claims 1-15, wherein the IL-15R α , or functional fragment or functional variant thereof, is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 79.
 20. The recombinant vector of any one of claims 1-19, wherein the IL-15, or functional fragment or functional variant thereof, is operably linked to the IL-15R α , or functional fragment or functional variant thereof, via a peptide linker.
 21. The recombinant vector of claim 20, wherein the peptide linker comprises the amino acid sequence of SEQ ID NO: 81, or the amino acid sequence of SEQ ID NO: 81 comprising 1, 2, or 3 amino acid modifications.
 22. The recombinant vector of claim 20, wherein the peptide linker is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 82.
 23. The recombinant vector of any one of claims 1-22, wherein the fusion protein is membrane bound.
 24. The recombinant vector of any one of claims 1-23, wherein the fusion protein comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 70 or 73.
 25. The recombinant vector of any one of claims 1-22, wherein the fusion protein is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 71 or 74.
 26. The recombinant vector of any one of claims 1-24, wherein the C α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 40-49.

27. The recombinant vector of any one of claims 1-24, wherein the C α region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 55, 57, or 58.
28. The recombinant vector of any one of claims 1-26, wherein the C β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 50-54 or 60.
29. The recombinant vector of any one of claims 1-26, wherein the C β region is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 56 or 59.
30. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.
31. The recombinant vector of claim 30, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.
32. The recombinant vector of claim 31, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.
33. The recombinant vector of claim 30, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161.

34. The recombinant vector of claim 30, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; and the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 181.
35. The recombinant vector of claim 33, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232.
36. The recombinant vector of claim 35, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; and the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 252.
37. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.
38. The recombinant vector of claim 37, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.
39. The recombinant vector of claim 38, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.

40. The recombinant vector of claim 37, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; and the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163.
41. The recombinant vector of claim 37, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; and the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 183.
42. The recombinant vector of claim 40, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235.
43. The recombinant vector of claim 41, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; and the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 255.
44. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.
45. The recombinant vector of claim 44, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of

- SEQ ID NO: 173; or the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164.
46. The recombinant vector of claim 45, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; or the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238.
47. The recombinant vector of claim 44, wherein the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 164; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
48. The recombinant vector of claim 44, wherein the first polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a ninth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 184 or 214; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
49. The recombinant vector of claim 47, wherein the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 238; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
50. The recombinant vector of claim 48, wherein the ninth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 258 or 278; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.
51. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.
52. The recombinant vector of claim 51, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide

sequence that encodes the amino acid sequence of SEQ ID NO: 162; the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165.

53. The recombinant vector of claim 52, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241.
54. The recombinant vector of claim 51, wherein the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 165; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
55. The recombinant vector of claim 51, wherein the first polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a twelfth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 185 or 215; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
56. The recombinant vector of claim 54, wherein the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 241; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
57. The recombinant vector of claim 55, wherein the twelfth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 261 or 281; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

58. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence.
59. The recombinant vector of claim 58, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.
60. The recombinant vector of claim 59, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.
61. The recombinant vector of claim 58, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 167.
62. The recombinant vector of claim 58, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; and the first polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a tenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 187 or 217.
63. The recombinant vector of claim 61, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; and the tenth

- combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 239.
64. The recombinant vector of claim 62, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; and the tenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 259 or 279.
65. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence.
66. The recombinant vector of claim 65, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.
67. The recombinant vector of claim 66, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.
68. The recombinant vector of claim 65, wherein the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; and the first polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 169.
69. The recombinant vector of claim 65, wherein the third polynucleotide sequence, and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; and the first

- polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a seventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 189 or 219.
70. The recombinant vector of claim 68, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 236.
71. The recombinant vector of claim 69, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; and the seventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 256 or 276.
72. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.
73. The recombinant vector of claim 72, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the third polynucleotide sequence, the second polynucleotide sequence, and the fifth polynucleotide sequence together comprise a sixth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 163; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; or the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170.
74. The recombinant vector of claim 73, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the sixth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 235; the eighth combination polynucleotide sequence comprises the polynucleotide

- sequence of SEQ ID NO: 237; or the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242.
75. The recombinant vector of claim 72, wherein the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 170; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
76. The recombinant vector of claim 72, wherein the third polynucleotide sequence, the second polynucleotide sequence, the fifth polynucleotide sequence, and the fourth polynucleotide sequence together comprise a thirteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 190; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.
77. The recombinant vector of claim 75, wherein the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 242; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
78. The recombinant vector of claim 76, wherein the thirteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 262; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
79. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.
80. The recombinant vector of claim 79, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the third polynucleotide sequence, the fourth polynucleotide sequence, and the fifth polynucleotide sequence together comprise a third combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 161; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; or the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth

polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171.

81. The recombinant vector of claim 80, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the third combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 232; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; or the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243.
82. The recombinant vector of claim 79, wherein the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 171; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
83. The recombinant vector of claim 79, wherein the third polynucleotide sequence, the fourth polynucleotide sequence, the fifth polynucleotide sequence, and the second polynucleotide sequence together comprise a fourteenth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 191; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.
84. The recombinant vector of claim 82, wherein the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 243; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
85. The recombinant vector of claim 83, wherein the fourteenth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 263; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
86. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the first polynucleotide sequence, the fourth polynucleotide sequence, and the third polynucleotide sequence.
87. The recombinant vector of claim 86, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide

- sequence that encodes the amino acid sequence of SEQ ID NO: 162; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.
88. The recombinant vector of claim 87, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.
89. The recombinant vector of claim 86, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 162; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
90. The recombinant vector of claim 86, wherein the first polynucleotide sequence and the fourth polynucleotide sequence together comprise a fourth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 182 or 212; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
91. The recombinant vector of claim 89, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 233; and the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
92. The recombinant vector of claim 90, wherein the fourth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 253 or 273; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.

93. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the first polynucleotide sequence, the second polynucleotide sequence, and the third polynucleotide sequence.
94. The recombinant vector of claim 93, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.
95. The recombinant vector of claim 94, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; or the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237.
96. The recombinant vector of claim 93, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 160; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 50.
97. The recombinant vector of claim 93, wherein the first polynucleotide sequence and the second polynucleotide sequence together comprise a first combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 180 or 210; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the third polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 51.
98. The recombinant vector of claim 96, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 230; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID

- NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 59.
99. The recombinant vector of claim 97, wherein the first combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 250 or 270; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the third polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 56.
100. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the second polynucleotide sequence, the third polynucleotide sequence, the fourth polynucleotide sequence, and the first polynucleotide sequence.
101. The recombinant vector of claim 100, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; or the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172.
102. The recombinant vector of claim 101, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; or the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240.
103. The recombinant vector of claim 100, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 168; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
104. The recombinant vector of claim 100, wherein the third polynucleotide sequence and the fourth polynucleotide sequence together comprise a second combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 188; the fifth polynucleotide sequence and the second polynucleotide sequence together comprise an

eleventh combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 172; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.

105. The recombinant vector of claim 103, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 231; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
106. The recombinant vector of claim 104, wherein the second combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 251; the eleventh combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 240; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
107. The recombinant vector of any one of claims 1-29, wherein the polycistronic polynucleotide comprises, in order from 5' to 3': the fifth polynucleotide sequence, the fourth polynucleotide sequence, the third polynucleotide sequence, the second polynucleotide sequence, and the first polynucleotide sequence.
108. The recombinant vector of claim 107, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; or the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173.
109. The recombinant vector of claim 108, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; or the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237.
110. The recombinant vector of claim 107, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 166; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of

- SEQ ID NO: 173; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 40.
111. The recombinant vector of claim 107, wherein the third polynucleotide sequence and the second polynucleotide sequence together comprise a fifth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 186; the fifth polynucleotide sequence and the fourth polynucleotide sequence together comprise an eighth combination polynucleotide sequence that encodes the amino acid sequence of SEQ ID NO: 173; and the first polynucleotide sequence encodes the amino acid sequence of SEQ ID NO: 41 or 42.
112. The recombinant vector of claim 110, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 234; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 57.
113. The recombinant vector of claim 111, wherein the fifth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 254; the eighth combination polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 237; and the first polynucleotide sequence comprises the polynucleotide sequence of SEQ ID NO: 55 or 58.
114. The recombinant vector of any one of claims 1-113, wherein the polycistronic polynucleotide further comprises
- f. a sixth polynucleotide sequence that comprises a third 2A element; and
 - g. a seventh polynucleotide sequence that comprises a marker protein.
115. The recombinant vector of claim 114, wherein the third 2A element is a P2A element, a T2A element, an F2A element, or an E2A element.
116. The recombinant vector of any one of claims 114 or 115, wherein the marker protein comprises: domain III of HER1, or a functional fragment or functional variant thereof; an N-terminal portion of domain IV of HER1; and a transmembrane domain of CD28, or a functional fragment or functional variant thereof.
117. The recombinant vector of claim 116, wherein the domain III of HER1, or a functional fragment or functional variant thereof, comprises an amino acid sequence at least 90%,

- 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 104.
118. The recombinant vector of claim 116, wherein the N-terminal portion of domain IV of HER1 comprises amino acids 1-40, 1-39, 1-38, 1-37, 1-36, 1-35, 1-34, 1-33, 1-32, 1-31, 1-30, 1-29, 1-28, 1-27, 1-26, 1-25, 1-24, 1-23, 1-22, 1-21, 1-20, 1-19, 1-18, 1-17, 1-16, 1-15, 1-14, 1-13, 1-12, 1-11, or 1-10 of SEQ ID NO: 105.
119. The recombinant vector of claim 116, wherein the N-terminal portion of domain IV of HER1 comprises amino acids 1-21 of SEQ ID NO: 105.
120. The recombinant vector of claim 116, wherein the N-terminal portion of domain IV of HER1 comprises the amino acid sequence of SEQ ID NO: 106, or the amino acid sequence of SEQ ID NO: 106, comprising 1, 2, or 3 amino acid modifications.
121. The recombinant vector of any one of claims 114-120, wherein the transmembrane region of CD28 comprises the amino acid sequence of SEQ ID NO: 107, or the amino acid sequence of SEQ ID NO: 107, comprising 1, 2, or 3 amino acid modifications.
122. The recombinant vector of any one of claims 114-121, wherein the marker protein comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 100, 103, or 112.
123. The recombinant vector of any one of claims 1-122, wherein the V α region comprises complementarity determining region 1 α (CDR1 α), CDR2 α , and CDR3 α , comprising the amino acid sequences of SEQ ID NO: 1001 + 10n, 1002 + 10n, and 1003 + 10n, respectively, wherein n is an integer from 0 to 79.
124. The recombinant vector of any one of claims 1-123, wherein the V β region comprises CDR1 β , CDR2 β , and CDR3 β , comprising the amino acid sequences of SEQ ID NO: 2001 + 10n, 2002 + 10n, and 2003 + 10n, respectively, wherein n is an integer from 0 to 79.
125. The recombinant vector of any one of claims 1-124, wherein the V α region comprises the CDR1 α , CDR2 α , and CDR3 α from a V α region comprising the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79.
126. The recombinant vector of any one of claims 1-125, wherein the V β region comprises the CDR1 β , CDR2 β , and CDR3 β from a V β region comprising the amino acid sequence of

- SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79.
127. The recombinant vector of any one of claims 1-126, wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, 1005 + 10n, 1006 + 10n, or 1007 + 10n, wherein n is an integer from 0 to 79.
128. The recombinant vector of any one of claims 1-127, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2004 + 10n, 2005 + 10n, 2006 + 10n, or 2007 + 10n, wherein n is an integer from 0 to 79.
129. The recombinant vector of any one of claims 1-128, wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1004 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2004 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1005 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2005 + 10n, and wherein n is an integer from 0 to 79; wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1006 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2006 + 10n, and wherein n is an integer from 0 to 79; or wherein the V α region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1007 + 10n, wherein the V β region comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2007 + 10n, and wherein n is an integer from 0 to 79.
130. The recombinant vector of any one of claims 1-129, wherein the TCR alpha chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100%

- identical to the amino acid sequence of SEQ ID NO: 1008 + 10n, wherein n is an integer from 0 to 79.
131. The recombinant vector of any one of claims 1-129, wherein the TCR alpha chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1009 + 10n, wherein n is an integer from 0 to 79.
132. The recombinant vector of any one of claims 1-129, wherein the TCR alpha chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 1010 + 10n, wherein n is an integer from 0 to 79.
133. The recombinant vector of any one of claims 1-132, wherein the TCR beta chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2008 + 10n, wherein n is an integer from 0 to 79.
134. The recombinant vector of any one of claims 1-132, wherein the TCR beta chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2009 + 10n, wherein n is an integer from 0 to 79.
135. The recombinant vector of any one of claims 1-132, wherein the TCR beta chain comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 2010 + 10n, wherein n is an integer from 0 to 79.
136. The recombinant vector of any one of claims 1-135, wherein the transcriptional regulatory element comprises a promoter.
137. The recombinant vector of claim 136, wherein the promoter is a human elongation factor 1-alpha (hEF-1 α) hybrid promoter.
138. The recombinant vector of claim 136 or 137, wherein the promoter comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:150.
139. The recombinant vector of any one of claims 1-138, further comprising a polyA sequence at the 3' end of the polycistronic expression cassette.

140. The recombinant vector of claim 139, wherein the polyA sequence comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO:151.
141. The recombinant vector of any one of claims 1-140, further comprising a Left inverted terminal repeat (ITR) and a Right ITR, wherein the Left ITR and the Right ITR flank the polycistronic expression cassette.
142. The recombinant vector of claim 141, which comprises, in order from 5' to 3':
 - i. the Left ITR;
 - ii. the transcriptional regulatory element;
 - iii. the first polynucleotide sequence;
 - iv. the second polynucleotide sequence;
 - v. the third polynucleotide sequence;
 - vi. the fourth polynucleotide sequence;
 - vii. the fifth polynucleotide sequence; and
 - viii. the Right ITR.
143. The recombinant vector of any one of claims 1-142, wherein the recombinant vector is a non-viral vector.
144. The recombinant vector of claim 143, wherein the non-viral vector is a plasmid.
145. The recombinant vector of any one of claims 1-142, wherein the recombinant vector is a viral vector.
146. The recombinant vector of any one of claims 1-145, wherein the recombinant vector is a polynucleotide.
147. A polynucleotide encoding an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 161, 163, 164, 165, 167, 169, 170, and 171.
148. A polynucleotide comprising a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NOs: 232, 235, 236, 238, 239, 241, 242, and 243.
149. A population of cells that comprise the recombinant vector of any one of claims 1-146 or the polynucleotide of claim 147 or 148.
150. The population of cells of claim 149, wherein the recombinant vector or the polynucleotide is integrated into the genome of the population of cells.

151. The population of cells of claims 149 or 150, wherein the cells are immune effector cells.
152. The population of cells of claim 151, wherein the immune effector cells are selected from the group consisting of T cells, natural killer (NK) cells, B cells, mast cells, and myeloid-derived phagocytes.
153. The population of cells of claim 152, wherein the immune effector cells are one or more T cells selected from the group consisting of naïve T cells (CD4⁺ or CD8⁺); killer CD8⁺ T cells; cytotoxic CD4⁺ T cells; helper CD4⁺ T cells; CD4⁺ T cells corresponding to Th1, Th2, Th9, Th17, Th22, follicular helper (Tfh), regulatory (Treg) lineages; tumor infiltrating lymphocytes (TILs); and memory T cells (central memory, effector memory, stem cell memory, stem cell-like memory).
154. The population of cells of claim 152, comprising alpha/beta T cells, gamma/delta T cells, or natural killer T (NKT) cells.
155. The population of cells of claim 152, comprising CD4⁺ T cells, CD8⁺ T cells, or both CD4⁺ T cells and CD8⁺ T cells.
156. The population of cells of any one of claims 149-155, wherein the cells are *ex vivo*.
157. The population of cells of any one of claims 149-156, wherein the cells are human.
158. The population of cells of any one of claims 149-157, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95⁺ cells.
159. The population of cells of any one of claims 149-157, wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95⁺ cells.
160. A population of cells comprising a polycistronic expression cassette comprising
 - a. a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof;
 - b. a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and
 - c. a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region,wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO-CD62L+CD95⁺ cells.

161. A population of cells comprising a polycistronic expression cassette comprising
- a first cistron comprising a polynucleotide sequence that encodes a fusion protein that comprises IL-15, or a functional fragment or functional variant thereof, and IL-15R α , or a functional fragment or functional variant thereof;
 - a second cistron comprising a polynucleotide sequence that encodes a TCR beta chain comprising a V β region and a C β region; and
 - a third cistron comprising a polynucleotide sequence that encodes a TCR alpha chain comprising a V α region and a C α region,
- wherein the population of cells are T cells that comprise more than 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45% or 50% CD45RA+CD45RO+CD62L+CD95+ cells.
162. A method of producing a population of engineered cells, comprising:
introducing into a population of cells the recombinant vector of claim 141 or 142, and a DNA transposase or a polynucleotide encoding a DNA transposase; and
culturing the population of cells under conditions wherein the transposase integrates the polycistronic expression cassette into the genome of the population of cells, thereby producing the population of engineered cells.
163. The method of claim 162, wherein the Left ITR and the Right ITR are ITRs of a DNA transposon selected from the group consisting of a *Sleeping Beauty* transposon, a piggyBac transposon, a TcBuster transposon, and a Tol2 transposon.
164. The method of claim 163, wherein the DNA transposon is the *Sleeping Beauty* transposon.
165. The method of any one of claims 162-164, wherein the transposase is a *Sleeping Beauty* transposase.
166. The method of claim 165, wherein the *Sleeping Beauty* transposase is selected from the group consisting of SB11, SB10, SB100X, hSB110, and hSB81.
167. The method of claim 166, wherein the *Sleeping Beauty* transposase is SB11.
168. The method of claim 167, wherein the SB11 comprises an amino acid sequence at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of SEQ ID NO: 300.
169. The method of claim 167, wherein the SB11 is encoded by a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 301.

170. The method of any one of claims 162-169, wherein the polynucleotide encoding the DNA transposase is a DNA vector or an RNA vector.
171. The method of any one of claims 162-170, wherein the Left ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 290 or 291; and the Right ITR comprises a polynucleotide sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the polynucleotide sequence of SEQ ID NO: 292, 293 or 294.
172. The method of any one of claims 162-171, wherein the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation, sonication, calcium phosphate precipitation, lipofection, particle bombardment, microinjection, mechanical deformation by passage through a microfluidic device, or a colloidal dispersion system.
173. The method of claim 172, wherein the recombinant vector, and the DNA transposase or polynucleotide encoding the DNA transposase, are introduced to the population of cells using electroporation.
174. The method of any one of claims 162-173, wherein the method is completed within 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.
175. The method of any one of claims 162-173, wherein the method is completed in less than 30 days, 25 days, 20 days, 15 days, 14 days, 10 days, 7 days, 6 days, 5 days, 4 days, 3 days, 2 days, or 1 day.
176. The method of any one of claims 162-175, wherein the population of cells is cryopreserved and thawed before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.
177. The method of any one of claims 162-176, wherein the population of cells is rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.
178. The method of any one of claims 162-177, wherein the population of cells is not rested before introduction of the recombinant vector and the DNA transposase or polynucleotide encoding the DNA transposase.

179. The method of any one of claims 162-178, wherein the population of cells comprises expanded human *ex vivo* cells.
180. The method of any one of claims 162-179, wherein the population of cells is not activated *ex vivo*.
181. The method of any one of claims 162-180, wherein the population of cells comprises T cells.
182. A method of treating cancer in a subject in need thereof comprising administering to the subject a therapeutically effective amount of the population of cells of any one of claims 149-161, thereby treating the cancer.
183. The method of claim 182, wherein the cancer is selected from lung, cholangiocarcinoma, pancreatic, colorectal, gynecological and ovarian cancer.
184. A method of treating an autoimmune disease or disorder in a subject in need thereof comprising administering to the subject a therapeutically effective amount of the population of cells of any one of claims 149-161, thereby treating the autoimmune disease or disorder.