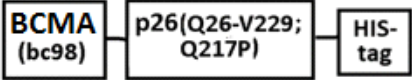
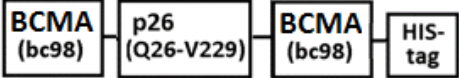
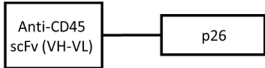
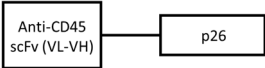
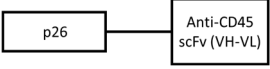
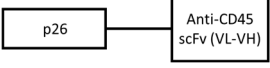
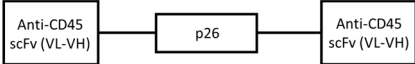
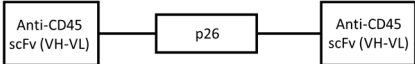
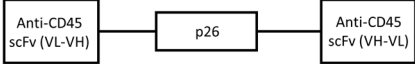
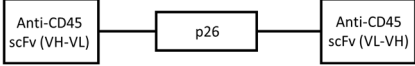
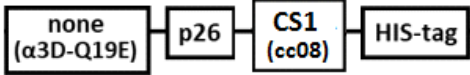
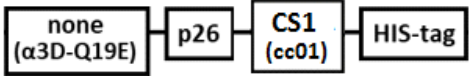
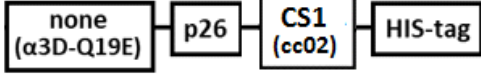
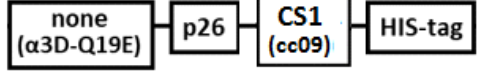


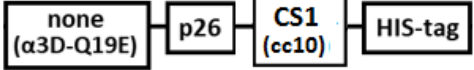
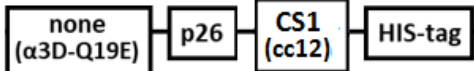
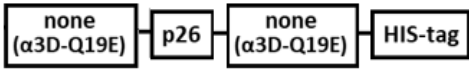
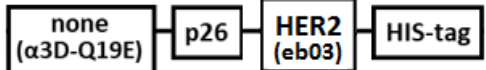
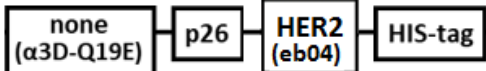
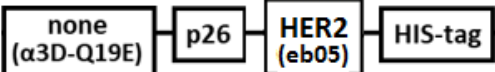
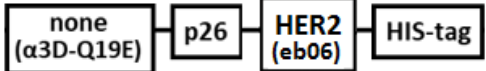
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1105	cynomolgus CD45RABC	MTMCLWLKLLAFVFAFLDTEVFTVGQGSTLSPTGRRTTKMPVPLSSDPLPHTHTTAFSPASISERENDF SETTPSLSSDNTSTQVSPDSLNDASAFNTTGVSALTPLHPTHADSQTPTSTGTDQTTPSGSAANTTLSP TPRSNDISDVPGERSTASTFTDPI SPLATTLIPARNSSAALPARTSNTTITANTSVSYLNASETTTPS PSGSTVISTPTIATTTSKPTCAEKYATIPVDYLYNNKTKLFTAKLNVNENVECTNNNHTHNICTNNEVL NLPECKEMNVFVSHNSCTDRHKEKLDVPPVEVEKFQLDCTPDVEANTTICLKWKI IETFACDKSKITY RFQCGNKTYNKEGIYLENLEPEYEYKCDSEILYNNHKYINITKLIKTDGFIGPQGPQNVVCRHEDAHQGV ITWNPPQRSFHNFTLCYVKNPAKKCLILDKHLTTYHLQNLKPYTNYSLSLHAYIIAKVQRNGTAATCNF TTESAPPSQVQNMIVSTSDNSMHVKCEVPRDVNGPTGLYHLEVEAGNTLVRNLSQSKCDFSVNNLQYST YYNLKAYYHNGKYSGEFVILRESTSYNSKALIAFLAFLIIVTSIALLVLYKIYDLHKKRSCNLDEQQE LVERDDEKQLMNVPIHADILLETYKRKIADEGRFLAEFQSIPRVFSKFPIKEARKPFNQKNRYVDI LPYDYNRVELSEINGDAGSNYINASYIDGFEPRKYIAAQGPRDETVDDFWRMIWEQKATVIVMVRCE EGNRNKA EYWP SMEEGTAFGDIVVKINQHKRCPDYIIQKLNIVNKEKATGREVTHIQFTSWPDHGV PEDPHLLKLRRRVNAF SNFFSGPIVHCSAGVGRGTIYIGIDAMLEGLEAENKVDVYGYVVKLRQRC LMVQVEAQYILIHQALVEYNQFGETEVLNSELHPYLHNMKKRDPPSEFSPLEAEFQRLPSYRSWRTQHI GNQEENKNKNRNSNVIPYDYNRVPLKHELEMSKESDHDSDDESSDDSDSEEPSKYINASFIMSYWKPEV MIAAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWEGEKQTYGDIIEVDMKDTNKSSTYT LRVFE LRHRSKRKDSRTVYQYQYTNWSVEQLPAEPKELVSLIQVLKEKLPQKNFSEGNKHHKSTPLLIHC RDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARPGMVSTFEQYQFLYDIIASTYPAQNGQVKK NNHQEDKIEFDNEVDKVKQDANCVNPLGATEKLPEAKEQATGSEPTSGTEGPEHSVNGPASPALNQGS
1106	Human CD45RABC ECD	QSPTPSPTGLTTAKMPVPLSSDPLPHTHTTAFSPASTFERENDFSETTTLSPDNTSTQVSPDSLNDAS AFNTTGVS SVQTPHLP THADSQTPSAGTDTQTFSGSAANAKLNPTPGSNAISDVPGERSTASTFTDPI SPLTTTSLAHSSAALPARTSNTTITANTS DAYLNASETTTLSPSGSAVISTTTIATTPSKPTCDEKY ANITVDYLYNKETKLTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPP GVEKFQLHDCTQVEKADTTICLKWKNIETFTCDTQNIITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSE ILYNNHKFTNASKI IKTDGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHNFTLCYIKETEKDCLNLDK NLIKYDLQNLKPYTKYVLSLHAYIIAKVQRNGSAAMCHFTTKSAPPSQVWNMTVSMSTSDNSMHVKCRPP RDRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFKAYFHNGDYPGEPFILHHSTSYNSK
1107	Human CD45RO ECD	QSPTPSPTDAYLNASETTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETKLTAKLNVN ENVECGNNTCTNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLK WKNIETFTCDTQNIITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNNHKFTNASKI IKTDGSPG EPQIIFCRSEAAHQGVITWNPPQRSFHNFTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAY IIAKVQRNGSAAMCHFTTKSAPPSQVWNMTVSMSTSDNSMHVKCRPPRDRNGPHERYHLEVEAGNTLVRN ESHKNCDFRVKDLQYSTDYTFKAYFHNGDYPGEPFILHHSTSYNSK
1108	Human CD45RA ECD	QSPTPSPTGLTTAKMPVPLSSDPLPHTHTTAFSPASTFERENDFSETTTLSPDNTSTQVSPDSLNDAS AFNTT DAYLNASETTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETKLTAKLNVNEN VECGNNTCTNNEVHNLTECKNASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKWK NIETFTCDTQNIITYRFQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNNHKFTNASKI IKTDGSPGEP QIIFCRSEAAHQGVITWNPPQRSFHNFTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA KVQRNGSAAMCHFTTKSAPPSQVWNMTVSMSTSDNSMHVKCRPPRDRNGPHERYHLEVEAGNTLVRNESH KNCDFRVKDLQYSTDYTFKAYFHNGDYPGEPFILHHSTSYNSK
1109	Human CD45RB	QSPTPSPTGVSSVQTPHLP THADSQTPSAGTDTQTFSGSAANAKLNPTPGSNAISDAYLNASETTTLSP SGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETKLTAKLNVNENVECGNNTCTNNEVHNLTECK NASVSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKWKNIETFTCDTQNIITYRFQCGN MIFDNKEIKLENLEPEHEYKCDSEILYNNHKFTNASKI IKTDGSPGEPQIIFCRSEAAHQGVITWNPP QRSFHNFTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIAKVQRNGSAAMCHFTTKSAP PSQVWNMTVSMSTSDNSMHVKCRPPRDRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK AYFHNGDYPGEPFILHHSTSYNSK
1110	Human CD45RAB ECD	QSPTPSPTGLTTAKMPVPLSSDPLPHTHTTAFSPASTFERENDFSETTTLSPDNTSTQVSPDSLNDAS AFNTTGVS SVQTPHLP THADSQTPSAGTDTQTFSGSAANAKLNPTPGSNAISDAYLNASETTTLSPSGS AVISTTTIATTPSKPTCDEKYANITVDYLYNKETKLTAKLNVNENVECGNNTCTNNEVHNLTECKNAS VSISHNSCTAPDKTLILDVPPGVEKFQLHDCTQVEKADTTICLKWKNIETFTCDTQNIITYRFQCGNMIF

		DNKEIKLENLEPEHEYKCDSEILYNNHKFTNASKIIKTDGSPGEPQIIFCRSEAAHQGVITWNPPQRS FHNFTLCYIKETEKDCLNLDKNLIKDYDLQNLKPYTKYVLSLHAYIIIAKVQRNGSAAMCHFTTKSAPPSQ VWNMTVSMTSDNSMHVKCRPPDRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFKAYF HNGDYPGEPFILHHSTSNSK
1111	Human CD45RAC ECD	QSPTPSPTGLTTAKMPSVPLSSDPLTHHTAFSPASTFERENDFSETTSLSPDNTSTQVSPDSDLDNAS AFNTTDVPGERSTASTFPTDPVSPLTTTSLAHSSAALPARTSNTTITANTSDAYLNASETTTLSPSG SAVISTTTIATTPSKPTCDEKYANITVDYLYNKETKLF TAKLNVNENVECGNNTCTNNEVHNLTECKNA SVSISHNSCTAPDKTLILDVPPGVEKFLHDCTQVEKADTTICLKWKNIETFTCDTQNIYRFQCGNMI FDNKEIKLENLEPEHEYKCDSEILYNNHKFTNASKIIKTDGSPGEPQIIFCRSEAAHQGVITWNPPQR SFHNFTLCYIKETEKDCLNLDKNLIKDYDLQNLKPYTKYVLSLHAYIIIAKVQRNGSAAMCHFTTKSAPPS QVWNMTVSMTSDNSMHVKCRPPDRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFKAY FHNGDYPGEPFILHHSTSNSK
1112	Human CD45RBC ECD	QSPTPSPTGVSSVQTPHLP THADSQTPTSAGTDTQTFSGSAANAKLNPTPGSNAISDVPGERSTASTFPT DPVSPLTTTSLAHSSAALPARTSNTTITANTSDAYLNASETTTLSPSGSAVISTTTIATTPSKPTCD EKYANITVDYLYNKETKLF TAKLNVNENVECGNNTCTNNEVHNLTECKNASVISHSCTAPDKTLILD VPPGVEKFLHDCTQVEKADTTICLKWKNIETFTCDTQNIYRFQCGNMI FDNKEIKLENLEPEHEYK DSEILYNNHKFTNASKIIKTDGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHNFTLCYIKETEKDCLN LDKNLIKDYDLQNLKPYTKYVLSLHAYIIIAKVQRNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSMHVK RPPDRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKDLQYSTDYTFKAYFHNGDYPGEPFILHHSTS NSK
1113	Human CD26	MKTPWKVLLGLLGAAALVTIITVPVLLNKGTD DATADSRKTYTLTDYLNKTYRLKLYSLRWISDHEYL YKQENNILVFNAEYGNSSVFLENSTFDEFGHSINDYSISP DGQFILLEYNVYKQWRHSYASYDIYDLN KRQLITEERIPNNTQWVTWSPVGHKLAYVWNNDIYVKIEPNLPSYRITWTGKEDIYNGITDWVYEEV FSAYSALWWSPNGTFLAYAQFNDTEVPLIEYSFYSDSLQYPKTVRVPYPKAGAVNPTVKFFVVNTDSL SSVTNATSITITAPASMLIGDHLYCDVTWATQERISLQWLRRIQNYSVMDICDYDESSGRWNCLVARQH IEMSTTGWVGRFRPSEPHTLDGNSFYKIIISNEEGYRHICYFQIDKKDCTFITKGTEWIEVIGIEALTSY LYYISNEYKGMPPGGRNLYKIQLSDYTKVTCLSCELNPERCQYYSVSFSKEAKYYQLRCSGPGPLPLYTLH SSVNDKGLRVLEDNSALDKMLQNVQMP SKKLDFIILNETKFWYQMLP PHFDKSKKYP LLLLDVYAGPCS QKADTVFRLNWATYLASTENIIVASFDRGSGYQGDKIMHAINRRLGTFEVEDQIEARQFSKMGFVDN KRIAIWGSYGGYVTSMVLGSGSVFKCGIAVAPVSRWEYDVSVYTERYMGLPTPEDNLDHYRNSTVMS RAENFKQVEYLLIHGTADDNVHFQQSAQISKALVDVGVDQAMWYTDDEHGIASSTAQHIIYTHMSHFI KQCFSLP
1114	Human CD30	MRVLLAALGLLFLGALRAFPQDRPFEDTCHGNPSHYIDKAVRRCCYRCPMGLFPTQQCPQRPTDCRKQC EPDYLLDEADRCTACVTC SRDDLVEKTPCAWNSSRVCECRPGMFCSTSAVNSCARCFHSHVCPAGMIVK FPGTAQKNTVCEPASPGVSPACASPENCKEPPSGTIPQAKPTPVSPATSSASTMPVRGGTRLAQEAAASK LTRAPDSPSSVGRPSSDPGLSPTQPCPEGSGDCRQCEPDYLLDEAGRCTACVCSRRDDLVEKTPCAWN SSRTCECRPGMICATSATNSCARCVYPICAAETVTKPQDMAEKDTTFEAPPLGTQPCDNPTPENGEAP ASTSPTQSLLVDSQASKTLP IPTSAPVALSSTGKPVLDAGPVLFWVILVLV VVGSSAFLLCRRACRK RIRQKLHLCYPVQTSQPKLELVDSRPRRSSTQLRSGASVTEPVAEERGLMSQPLMETCHSVGAAYLES LPLQDASPAGGPSSPRDLPEPRVSTEHTNNKIEKIYIMKADTVIVGTVAELPEGRGLAGPAEPELEEL EADHTPHYPEQETEPPLGSCSDVMLSVEEEGKEDPLTAASGK
1115	Human CD33	MPLLLLPLLLWAGALAMPNFWLQVQESVTVQEGLCVLPCTFFHPIPYDKNSPVHGYWFREGAII SR DSPVATNKLDQEVQETQGRFRLGDP SRNNCSLSIVDARRRDNGSYFFRMERGSTKYSYKSPQLSVHV TDLTHRPKILIPGTLEPGHSKNLTCVSWACEQGTPIFSWLSAAPTSLGPRTHSSVLIITPRPDHG TNLTCQVKFAGAGVTERTIQLNVTYVPQNPTTGIFFGDGSQKQETRAGVVHGAIGGAGVTALLALCLC LIFFIVKTHRRKAARTAVGRNDTHPTTGSASPKHQKSKLHGPTETSSCSGAAPTVMEMDEELHYASLNF HGMNPSKDTSTEYSEVRTQ
1116	Human CD38	MANCEFSPVSGDKPCCRLSRRAQLCLGV SILVLILVVVLAVVVPWRQQWSGPGTTKRFPETVLARCVK YTEIHPEMRHVDCQSVWDAFKGAFISKHPCNITEEDYQPLMKLGTQTVPCNKILLWSRIKDLAQHTQV QRDMFTLEDTLGLYLADDLTWCGEFNTSKINYQSCPDWRKDCSNNPVSVFWKTVSRRFAEAACDVVHVM LNGSRSKIFDKNSTFGSVEVHNLQPEKVQTL EAWVIHGGREDSRDLCQDPTIKELESII SKRNIQFSCK NIYRPDKFLQCVKNPEDSSCTSEI
1138	CS1 mature ECD	SGPVKELVGSVGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTII VQTQNRNRERVDFPDGGYSLK LSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLTCCMEHGEEDV IYTWKALGQAANESHNGSILPISWRGESDMTFICVARNPVSRNFSPI LARKLCEGAADDPDSSM
1139	CS1	MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGT IIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQ SNKNGTCVTNLTCCMEHGEEDVIYTWKALGQAANESHNGSILPISWRGESDMTFICVARNPVSRNFS PILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICP HSGENT EYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

		GSMGSWSEFWARLGAIRERLDALGGSEAEAAFEKEIAAFESEL QAYKGKGNPEVEKLRYTAGTIKRFLQAYRHNGGGSGGGSGGG GSHHHHHHHHHH
1131		DEMGSWSEFWARLGAIRERLDALGGSEAEAAFEKEIAAFESEL QAYKGKGNPEVEKLRYTAGTIKRFLQAYRHNGGGSGGGSGGG GSGQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSE LMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEM TPVNPVGVCCTSSYANRRPCFSSLVDETYVPPAFSDDKFIH KDLCCQAQGVVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGL LEKCCQGGQEQEVCFAEEGPKLISKTRALGVGGGGSGGGSGGG GSHHHHHHHHHH
1132		DEMGSWSEFWARLGAIRERLDALGGSEAEAAFEKEIAAFESEL QAYKGKGNPEVEKLRYTAGTIKRFLQAYRHNGGGSGGGSGGG GSGQESQALAKRSCGLFQKLGEYYLQNAFLVAYTKKAPQLTSSE LMAITRKMAATAATCCQLSEDKLLACGEGAADIIIGHLCIRHEM TPVNPVGVCCTSSYANRRPCFSSLVDETYVPPAFSDDKFIH KDLCCQAQGVVALQTMKQEFLINLVKQKPQITEEQLEAVIADFSGL LEKCCQGGQEQEVCFAEEGQKLISKTRALGVGGGGSGGGSGGG GSMGSWSEFWARLGAIRERLDALGGSEAEAAFEKEIAAFESEL QAYKGKGNPEVEKLRYTAGTIKRFLQAYRHNGGGSGGGSGGG GSHHHHHHHHHH
1141		QVQLVESGGGLVQPGGSLKLSCAASGFDfsRYWMSWVRQAPGKG LEWIGEINPTSSSTINFTPSLKDQVFI SRDNAKNTLYLQMSKVR EDTALYYCARGNYRYGDAMDYWGQTSVTVSGGGSGGGGSAG GGSDIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYLHWYQ QKPGQPPELLIYLASNLESGVPARFSGSGSGTDFTLNHPVEEE DAATYYCQHSRELPTFTGSGTKLEIKGGGGSGGGSGGGSGGLE KCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYY LQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSEDKLL ACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIH KDLCCQAQGVVALQTMKQEFLINLVK QKPQITEEQLEAVIADFSGLLEKCCQGGQEQEVCFAEEGQKLISK TRALGV
1142		DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYLHWYQQKP GQPPKLLIYLASNLESGVPARFSGSGSGTDFTLNHPVEEEDAA TYYCQHSRELPTFTGSGTKLEIKGGGGSGGGSGAGGSQVQLVE SGGGLVQPGGSLKLSCAASGFDfsRYWMSWVRQAPGKGLEWIGE INPTSSSTINFTPSLKDQVFI SRDNAKNTLYLQMSKVRSED TAL YCARGNYRYGDAMDYWGQTSVTVSGGGSGGGSGGGSGGLE KCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYY LQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSEDKLL ACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIH KDLCCQAQGVVALQTMKQEFLINLVK QKPQITEEQLEAVIADFSGLLEKCCQGGQEQEVCFAEEGQKLISK TRALGV
1143		LEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGE YYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSEDK LLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCF SSLVDETYVPPAFSDDKFIH KDLCCQAQGVVALQTMKQEFLINL VKQKPQITEEQLEAVIADFSGLLEKCCQGGQEQEVCFAEEGQKLISK TRALGVGGGGSGGGSGGGSGGGSGGVQLVESGGGLVQPGGSLK LSCAASGFDfsRYWMSWVRQAPGKGLEWIGEINPTSSSTINFTPS LKDKVFI SRDNAKNTLYLQMSKVRSED TALYYCARGNYRYGDA MDYWGQTSVTVSGGGSGGGSGAGGSDIVLTQSPASLAVSLG QRATISCRASKSVSTSGYSYLHWYQQKPGQPPKLLIYLASNLES GVPARFSGSGSGTDFTLNHPVEEEDATYYCQHSRELPTFTGS GTKLEIK
1144		LEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGE YYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSEDK LLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCF SSLVDETYVPPAFSDDKFIH KDLCCQAQGVVALQTMKQEFLINL

		VKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLI SKTRALGVGGGSGGGGSGGGSGDIVLTQSPASLAVSLGQRA TISCRASKSVSTSGYSYLHWYQQKPGQPPKLLIYLASNLESGVP ARFSGSGSGTDFTLNHPVEEEDAATYYCQHSRELPTFTGSGTK LEIKGGGSGGGGSAGGGSQVQLVESGGGLVQPGGSLKLSAAS GFDFSRYSWMSWVRQAPGKGLEWIGEINPTSTINFTPSLKDKVF ISRDNAKNTLYLQMSKVRSEDTALYYCARGNYRYRGDAMDYWGQ GTSVTVS
1145		DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYLHWYQQK GQPPKLLIYLASNLESGVPAARFSGSGSGTDFTLNHPVEEEDA TYYCQHSRELPTFTGSGTKLEIKGGGSGGGGSAGGGSQVQLVE SGGGLVQPGGSLKLSAASGFDFSRYSWMSWVRQAPGKLEWIGE INPTSTINFTPSLKDKVFISRDNAKNTLYLQMSKVRSEDTALY YCARGNYRYRGDAMDYWGQGTSTVTVSGGGGSGGGGSGGGSGLE KCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYY LQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSEDKLL ACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIHKLCLCAQGVVALQTMKQEFLLNLVK QKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLI SKTRALGVGGGSGGGGSGGGSGDIVLTQSPASLAVSLGQRATIS CRASKSVSTSGYSYLHWYQQKPGQPPKLLIYLASNLESGVPA ARFSGSGSGTDFTLNHPVEEEDAATYYCQHSRELPTFTGSGTKLE IKGGGSGGGGSAGGGSQVQLVESGGGLVQPGGSLKLSAASGF DFSRYSWMSWVRQAPGKLEWIGEINPTSTINFTPSLKDKVFIS RDNAKNTLYLQMSKVRSEDTALYYCARGNYRYRGDAMDYWGQGT SVTVS
1146		QVQLVESGGGLVQPGGSLKLSAASGFDFSRYSWMSWVRQAPGK LEWIGEINPTSTINFTPSLKDKVFISRDNAKNTLYLQMSKVR SEDTALYYCARGNYRYRGDAMDYWGQGTSTVTVSGGGGSGGGGSAG GGSDIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYLHWYQ QKPGQPPKLLIYLASNLESGVPAARFSGSGSGTDFTLNHPVEE DAATYYCQHSRELPTFTGSGTKLEIKGGGSGGGGSAGGSGGLE KCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYY LQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSEDKLL ACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIHKLCLCAQGVVALQTMKQEFLLNLVK QKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLI SKTRALGVGGGSGGGGSGGGSGQVQLVESGGGLVQPGGSLKLS CAASGFDFSRYSWMSWVRQAPGKLEWIGEINPTSTINFTPSLK DKVFISRDNAKNTLYLQMSKVRSEDTALYYCARGNYRYRGDAMD YWQGTSTVTVSGGGGSGGGGSAGGSDIVLTQSPASLAVSLGQR ATISCRASKSVSTSGYSYLHWYQQKPGQPPKLLIYLASNLESGV PARFSGSGSGTDFTLNHPVEEEDAATYYCQHSRELPTFTGSGT KLEIK
1147		DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYLHWYQQK GQPPKLLIYLASNLESGVPAARFSGSGSGTDFTLNHPVEEEDA TYYCQHSRELPTFTGSGTKLEIKGGGSGGGGSAGGGSQVQLVE SGGGLVQPGGSLKLSAASGFDFSRYSWMSWVRQAPGKLEWIGE INPTSTINFTPSLKDKVFISRDNAKNTLYLQMSKVRSEDTALY YCARGNYRYRGDAMDYWGQGTSTVTVSGGGGSGGGGSGGGSGLE KCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYY LQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSEDKLL ACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIHKLCLCAQGVVALQTMKQEFLLNLVK QKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFAEEGQKLI SKTRALGVGGGSGGGGSGGGSGQVQLVESGGGLVQPGGSLKLS CAASGFDFSRYSWMSWVRQAPGKLEWIGEINPTSTINFTPSLK DKVFISRDNAKNTLYLQMSKVRSEDTALYYCARGNYRYRGDAMD YWQGTSTVTVSGGGGSGGGGSAGGSDIVLTQSPASLAVSLGQR ATISCRASKSVSTSGYSYLHWYQQKPGQPPKLLIYLASNLESGV PARFSGSGSGTDFTLNHPVEEEDAATYYCQHSRELPTFTGSGT KLEIK

1148		<p>QVQLVESGGGLVQPGGSLKLSCAASGFDPSRYWMSWVRQAPGKG LEWIGEINPTSTINFTPSLKDQVFI SRD NAKNTLYLQMSKVRSE EDTALYYCARGNYRYGDAMDYWGQGTSTVTVSGGGSGGGGSAG GGSDIVLTQSPASLAVSLGQRATISCRASKSVSTSGYSYLHWYQ QKPGQPPKLLIYLASNLESGVPARFSGSGGTDFTLNIHPVEEE DAATYYCQHSRELPTFTFGSGTKLEIKGGGSGGGSGGGSGGLE KCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLGEYY LQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSEDKLL ACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPCFSS LVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFNLINLVK QKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCF AEEGQKLISK TRAALGVGGGSGGGSGGGSGGDI VLTQSPASLAVSLGQRATI SCRASKSVSTSGYSYLHWYQKPGQPPKLLIYLASNLESGVPAR FSGSGGTDFTLNIHPVEEEDAATYYCQHSRELPTFTFGSGTKLE IKGGGSGGGSGAGGSQVQLVESGGGLVQPGGSLKLSCAASGF DFSRYWMSWVRQAPGKLEWIGEINPTSTINFTPSLKDQVFI S RDNAKNTLYLQMSKVRSEDTALYYCARGNYRYGDAMDYWGQGT SVTVS</p>
1150	<p>α3D Q19E-p26-cc08.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAE LA AFEKEIA AFESELQA YKKGKNPEVEALRKEAAAIRDELQAYRHNGGGSGGGSGGGGS GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKL EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSE KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFNLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCF AEEGQKL ISKTRAALGVGGGSGGGSGGGSGMGSWVEFNERLHAIYLRRL DALGGSEAE LA AFEKEIA AFESELQAYKKGKNPEVETLRRHAAG IRWQLQAYRHNGGGSGGGSGGGSGGGSHHHHHHHHHH</p>
1151	<p>α3D Q19E-p26-cc01.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAE LA AFEKEIA AFESELQA YKKGKNPEVEALRKEAAAIRDELQAYRHNGGGSGGGSGGGGS GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKL EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSE KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFNLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCF AEEGQKL ISKTRAALGVGGGSGGGSGGGSGMGSWVEFEARLSAIYERL EALGGSEAE LA AFEKEIA AFESELQAYKKGKNPEVEKLRRHAAG IRSNLQAYRHNGGGSGGGSGGGSGGGSHHHHHHHHHH</p>
1152	<p>α3D Q19E-p26-cc02.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAE LA AFEKEIA AFESELQA YKKGKNPEVEALRKEAAAIRDELQAYRHNGGGSGGGSGGGGS GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKL EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSE KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFNLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCF AEEGQKL ISKTRAALGVGGGSGGGSGGGSGMGSWVEFFVRLDAIWERL EALGGSEAE LA AFEKEIA AFESELQAYKKGKNPEVETLRFHAAG IRQKLQAYRHNGGGSGGGSGGGSGGGSHHHHHHHHHH</p>
1153	<p>α3D Q19E-p26-cc09.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAE LA AFEKEIA AFESELQA YKKGKNPEVEALRKEAAAIRDELQAYRHNGGGSGGGSGGGGS GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKL EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSE KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFNLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCF AEEGQKL ISKTRAALGVGGGSGGGSGGGSGMGSWNEFKLELAFIKDWL EALGGSEAE LANFEEAIAEF EAGLQGYKKGKNPEVEALRKEAAA IRDELQAYRHNGGGSGGGSGGGSGGGSHHHHHHHHHH</p>
1154	<p>α3D Q19E-p26-cc10.HIS</p>	<p>MGSWAEFKQRLAAIKTRLEALGGSEAE LA AFEKEIA AFESELQA YKKGKNPEVEALRKEAAAIRDELQAYRHNGGGSGGGSGGGGS GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKL EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSE KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC</p>

		<p>FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWMEFEARLEAIWDRLEALGGSEAEALAAFEKEIAAFESELQAYKGKGNPEVESLRFAAG IRQHLQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH</p>
1155	<p>α3D Q19E-p26-cc12.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAEALAAFEKEIAAFESELQA YKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGSGGGGSG GLEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWHFFKMHLAGIKLQLEALGGSEAEALAAFEWIAADFEGALQDYKGKGNPEVEALRKEAAA IRDELQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH</p>
1156	<p>α3D(Q19E).3xGS.p26.3xGS.α3D(Q19E).HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAEALAAFEKEIAAFESELQA YKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGSGGGGSG GLEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWAEFKQRLAAIKTRL EALGGSEAEALAAFEKEIAAFESELQAYKGKGNPEVEALRKEAAA IRDELQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH</p>
1157	<p>α3D(Q19E).3xGS.p26.3xGS.eb03.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAEALAAFEKEIAAFESELQA YKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGSGGGGSG GLEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWAEFRWRRLHAIWLQLEALGGSEAEALAAFEKEIAAFESELQAYKGKGNPEVEWLRQDAAQ IKYILQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH</p>
1158	<p>α3D(Q19E).3xGS.p26.3xGS.eb04.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAEALAAFEKEIAAFESELQA YKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGSGGGGSG GLEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWKTFKIELAGIKLELEALGGSEAEALAGFENAIQFESSLYYKGKGNPEVEALRKEAAA IRDELQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH</p>
1159	<p>α3D(Q19E).3xGS.p26.3xGS.eb05.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAEALAAFEKEIAAFESELQA YKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGSGGGGSG GLEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWHEFLRRLLAEMRLYALGGSEAEALAAFEKEIAAFESELQAYKGKGNPEVEHLRVRAAS IRQMLQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH</p>
1160	<p>α3D(Q19E).3xGS.p26.3xGS.eb06.HIS</p> 	<p>MGSWAEFKQRLAAIKTRLEALGGSEAEALAAFEKEIAAFESELQA YKGKGNPEVEALRKEAAAIRDELQAYRHNGGGGSGGGGSGGGGSG GLEKCFQTNPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLIN LVKQKPQITEEQLEAVIADFSGLLEKCCQGQEQEVCFEAEQGKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWWEFRVRLEAIDYRL</p>

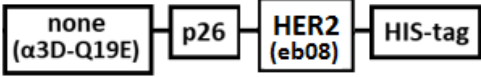
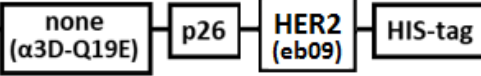
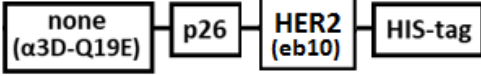
		KALGGSEAEIAAFEKEIAAFESEIQAYKGKGNPEVEYLRMKAAT IRAILQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH
1161	α 3D(Q19E).3xGS.p26.3xGS.eb08.HIS 	MGSWAEFKQRLAAIKTRLEALGGSEAEIAAFEKEIAAFESEIQAY YKGKGNPEVEALRKEAAAIIRDELQAYRHNGGGGSGGGGSGGGG GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLN LVKQKPQITEEQLEAVIADFSGLLEKCCQGEQEVCFAEEGQKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWYEFWRWLHAIWLRL GALGGSEAEIAAFEKEIAAFESEIQAYKGKGNPEVEWLQDAAQ IRYILQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH
1162	α 3D(Q19E).3xGS.p26.3xGS.eb09.HIS 	MGSWAEFKQRLAAIKTRLEALGGSEAEIAAFEKEIAAFESEIQAY YKGKGNPEVEALRKEAAAIIRDELQAYRHNGGGGSGGGGSGGGG GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLN LVKQKPQITEEQLEAVIADFSGLLEKCCQGEQEVCFAEEGQKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWWFEFNIRLHAIDYRL KALGGSEAEIAAFEKEIAAFESEIQAYKGKGNPEVELLREKAAQ IRAQLQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH
1163	α 3D(Q19E).3xGS.p26.3xGS.eb10.HIS 	MGSWAEFKQRLAAIKTRLEALGGSEAEIAAFEKEIAAFESEIQAY YKGKGNPEVEALRKEAAAIIRDELQAYRHNGGGGSGGGGSGGGG GLEKCFQTENPLECQDKGEEELQKYIQESQALAKRSCGLFQKLG EYYLQNAFLVAYTKKAPQLTSSSELMAITRKMAATAATCCQLSED KLLACGEGAADIIIGHLCIRHEMTPVNPVGVCCTSSYANRRPC FSSLVDETYVPPAFSDDKFIHFKDLCQAQGVALQTMKQEFLLN LVKQKPQITEEQLEAVIADFSGLLEKCCQGEQEVCFAEEGQKL ISKTRAAALGVGGGSGGGGSGGGGSGMGSWWFEFNMLSAIKYRL YALGGSEAEIAAFEKEIAAFESEIQAYKGKGNPEVEILRLAAD IRERLQAYRHNGGGGSGGGGSGGGGSHHHHHHHHHH

TABLE: 6 Exemplary ADBD CAR Sequences

SEQ ID NO:	CAR Design	CAR Sequence
1089	CTsp-Flag-GSlinker- α 3D(Q19E)-GSlinker-CD8H-TM-41BB-CD3 ζ	MAFLWLLSCWALLGTTTFGDYKDDDDKGGGSGGGGSMGSWAEFKQRLAAIKTRLEALGGSE AELAAFEKEIAAFESEIQAYKGKGNPEVEALRKEAAAIIRDELQAYRHNGGAGSGTTTPAPR PPTPAPTPTASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSLVITLY CKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQN QLYNELNLGRREEYDVLDRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGDGLYQGLSTATKDTYDALHMQALPPR
1090	CTsp-Flag-GSlinker-cg06-GSlinker-CD8H-TM-41BB-CD3 ζ	MAFLWLLSCWALLGTTTFGDYKDDDDKGGGSGGGGSMGSWDEFGRRLYAIEWRLYALGGSE AELAAFEKEIAAFESEIQAYKGKGNPEVEKLREIAAVIRSNLQAYRHNGGGGSGGGGSGTT TPAPRPPTPAPTPTASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSL VITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAY KQGQNQLYNELNLGRREEYDVLDRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
1091	CTsp-Flag-GSlinker-bc40-GSlinker-CD8H-TM-41BB-CD3 ζ	MAFLWLLSCWALLGTTTFGDYKDDDDKGGGSGGGGSMGSWSEFVRLGAIIRERLDALGGSE AELAAFEKEIAAFESEIQAYKGKGNPEVEKLRYTAATIRRFQAYRHNGGGGSGGGGSGTT TPAPRPPTPAPTPTASQPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAPLAGTCGVLLLSL VITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAY KQGQNQLYNELNLGRREEYDVLDRGRDPPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGDGLYQGLSTATKDTYDALHMQALPPR
1092	CTsp-Flag-GSlinker-af03-GSlinker-CD8H-TM-41BB-CD3 ζ	MAFLWLLSCWALLGTTTFGDYKDDDDKGGGSGGGGSMGSWFEFYDRNLDAIDARLWALGGSE AELAAFEKEIAAFESEIQAYKGKGNPEVENLRVHAAAIREWQAYRHNGGGGSGGGGSGTT TPAPRPPTPAPTPTASMGSWAEFKQRLAAIKTRLEALGGSEAEIAAFEKEIAAFESEIQAYK GKGNPEVEALRKEAAAIIRDELQAYRHNPPLSLRPEACRPAAGGAVHTRGLDFACDIYIWAP LAGTCGVLLLSLVITLYCKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGCELR

WHAT IS CLAIMED IS:

1. A protein comprising a D domain that specifically binds an AFP P26 polypeptide, wherein the AFP P26 polypeptide consists of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123.
2. The protein of claim 1, wherein the D domain comprises the amino acid sequence of SEQ ID NO: 841-984.
3. The protein of claim 1, wherein the D domain comprises the amino acid sequence of SEQ ID NO: 842-850, 859-875, 878, 881 or 888.
4. The protein of any one of claims 1 to 3 wherein the D domain is fused to a heterologous polypeptide.
5. A chimeric antigen receptor (CAR) which comprises a target binding domain comprising the protein according to any one of claims 1 to 4.
6. The CAR of claim 5, which comprises, a target binding domain, a transmembrane domain, and an intracellular signaling domain.
7. The CAR of claim 5 or 6, wherein transmembrane domain comprises a CD8, 41BB or CD28 transmembrane domain.
8. The CAR of any one of claims 5 to 7, wherein the intracellular signaling domain is selected from the group consisting of a domain of a human T cell receptor alpha, beta, or zeta chain; a human 41BB domain; a human CD28 domain; and any combination thereof.
9. An isolated nucleic acid encoding the protein according to any one of claims 1 to 4.
10. An isolated nucleic acid encoding the CAR according to any one of claims 5 to 8.
11. A host cell comprising the nucleic acid according to claim 9.
12. A host cell comprising the nucleic acid according to claim 10.
13. The cell according to claim 12, wherein the cell is an immune effector cell.
14. A fusion protein comprising an AFP P26 polypeptide, wherein the AFP P26 polypeptide consists of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123.
15. The fusion protein of claim 14, further comprising an Antigenic Determinant Binding Domain (ADBD).
16. The fusion protein of claim 15, wherein the ADBD is an antigen-binding antibody fragment.

17. The fusion protein of claim 15, wherein the ADBD is an scFv.
18. The fusion protein of claim 15, wherein the Antigenic Determinant Binding Domain (ADBD) is a D domain.
19. The fusion protein of any one of claim 15-18, wherein the ADBD binds to a tumor antigen.
20. The fusion protein of claim 19, wherein the tumor antigen is selected from the group consisting of BCMA, CD123, CD19, CD22, CS1, HER2, TACI, BAFFR, and PDL1.
21. The fusion protein of claim 20, wherein the ADBD is a D domain that binds BCMA, wherein the D domain comprises the amino acid sequence of SEQ ID NO: 193, 197 or 201.
22. Use of (a) an immune effector cell expressing a chimeric antigen receptor (CAR) and (b) an Adapter in the manufacture of a medicament comprising the immune cell and a medicament comprising the Adapter, respectively, for treating a proliferative disorder, cancer, autoimmune disease, infection, or allograft rejection, wherein the treatment comprises the administration of the medicament comprising the immune cell and the medicament comprising the Adapter to a patient in need thereof, wherein
 - the CAR comprises a D domain that binds to a AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123,
 - the Adapter comprises (i) said AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic determinant binding domain (ADBD) that binds to an antigenic determinant (AD) on a target cell,
 - the immune effector cell used in combination with the Adapter is capable of directing an immune response to a cell expressing the AD in an in vitro assay, and
 - the medicament comprising the immune effector cell and the medicament comprising the Adapter is to be administered to a patient simultaneously or consecutively in any order.
23. The use of claim 22, wherein
 - the D domain that binds to the AFP P26 polypeptide comprises the amino acid sequence of SEQ ID NO: 841-984,
24. The use of claim 26, wherein the D that binds to the AFP P26 polypeptide domain comprises the amino acid sequence of SEQ ID NO: 842-850, 859-875, 878, 881 or 888.
25. The use of any one of claims 22 to 24, wherein the ADBD that binds to an AD on the target cell is an antigen-binding antibody fragment.

26. The use of any one of claims 22 to 24, wherein the ADBD that binds to an AD on the target cell is an scFv.
27. The use of any one of claims 22 to 24, wherein the ADBD that binds to an AD on the target cell is a D domain.
28. The use of any one of claims 22 to 27, wherein the target cell is a tumor cell.
29. The use of any one of claims 22 to 28, wherein the ADBD binds to a tumor antigen.
30. The use of claim 29, wherein the tumor antigen is selected from the group consisting of BCMA, CD123, CD19, CD22, CS1, HER2, TACI, BAFFR, and PDL1.
31. The use of claim 29, wherein the ADBD is a D domain that binds BCMA, wherein the D domain comprises the amino acid sequence of SEQ ID NO: 193, 197 or 201.
32. Use of (a) an immune effector cell expressing a chimeric antigen receptor (CAR) comprising a D domain that binds to a AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (b) an Adapter comprising (i) said AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic determinant binding domain (ADBD) that binds to tumor antigen on a target cell in the manufacture of a medicament comprising the immune effector cell and a medicament comprising the Adapter, respectively, for
 - treating cancerin a patient, wherein the treatment comprises the administration of the medicament comprising the immune cell and the medicament comprising the Adapter to the patient, wherein the immune effector cell used in combination with the Adapter is capable of directing an immune response to a cell expressing the tumor antigen in an in vitro assay, and wherein the medicament comprising the immune effector cell and the medicament comprising the Adapter is to be administered to the patient simultaneously or consecutively in any order.
33. The use of claim 32, wherein
 - the cancer is selected from: acute leukemia, chronic leukemia, polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma, multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia, myelodysplasia, breast cancer, prostate cancer, ovarian cancer, pancreatic cancer, colon cancer, and lung cancer.
34. The use of claim 32, wherein the cancer is a hematological cancer.

35. The use of any one of claims 32 to 34, wherein the D domain that binds to the AFP P26 polypeptide comprises the amino acid sequence of SEQ ID NO: 842-850, 859-875, 878, 881 or 888.
36. The use of any one of claims 32 to 35, wherein the ADBD that binds to the tumor antigen on the target cell is a D domain.
37. The use of any one of claims 32 to 36, wherein the tumor antigen is selected from the group consisting of BCMA, CD123, CD19, CD22, CS1, HER2, TACI, BAFFR, and PDL1.
38. The use of any one of claims 32 to 36, wherein the ADBD is a D domain that binds BCMA, wherein the D domain comprises the amino acid sequence of SEQ ID NO: 193, 197 or 201.
39. Use of an Adapter in the manufacture of a medicament for
- treating a proliferative disorder, cancer, autoimmune disease, infection, or allograft rejection in a patient, wherein
 - the patient has been administered an immune effector cell expressing a chimeric antigen receptor (CAR) comprising a D domain that binds to a AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123,
 - the Adapter comprises (i) said AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic determinant binding domain (ADBD) that binds to an antigenic determinant (AD) on a target cell, and
 - the immune effector cell used in combination with the Adapter is capable of directing an immune response to a cell expressing the AD in an in vitro assay.
40. The use of claim 39, wherein
- the AD is CS1, BCMA, CD19, CD22, CD45, CD123, HER2, TACI, BAFFR, or PDL1,
 - the D domain that binds to the AFP P26 polypeptide comprises the amino acid sequence of SEQ ID NO: 842-850, 859-875, 878, 881 or 888,
 - the ADBD is a D domain, and/or
 - the proliferative disorder, cancer, or hematological cancer is selected from: acute leukemia, chronic leukemia, polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma, multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease,

myelodysplastic syndrome, hairy cell leukemia, myelodysplasia, breast cancer, prostate cancer, ovarian cancer, pancreatic cancer, colon cancer, and lung cancer.

41. Use of an immune effector cell expressing a chimeric antigen receptor (CAR) comprising a D domain that binds to a AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 in the manufacture of a medicament for making a patient receptive to Adapter mediated
- treatment of a proliferative disorder, cancer, autoimmune disease, infection, or allograft rejection,
- wherein the Adapter comprises (i) said AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic determinant binding domain (ADBD) that binds to an antigenic determinant (AD) on a target cell, and
- wherein the immune effector cell used in combination with the Adapter is capable of directing an immune response to a cell expressing the AD in an in vitro assay.
42. The use of claim 41, wherein
- the AD is CS1, BCMA, CD19, CD22, CD45, CD123, HER2, TACI, BAFFR, or PDL1,
 - the D domain that binds to the AFP P26 polypeptide comprises the amino acid sequence of SEQ ID NO: 842-850, 859-875, 878, 881 or 888,
 - the ADBD is a D domain, and/or
 - the proliferative disorder, cancer, or hematological cancer is selected from: acute leukemia, chronic leukemia, polycythemia vera, lymphoma, Hodgkin's disease, non-Hodgkin's lymphoma, multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, myelodysplastic syndrome, hairy cell leukemia, myelodysplasia, breast cancer, prostate cancer, ovarian cancer, pancreatic cancer, colon cancer, and lung cancer.
43. An immune effector cell expressing a chimeric antigen receptor (CAR) and an Adapter for use in therapy, wherein
- the CAR comprises a D domain that binds to a AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123,
 - the Adapter comprises (i) said AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic

determinant binding domain (ADBD) that binds to an antigenic determinant (AD) on a target cell, and

- the immune effector cell used in combination with the Adapter is capable of directing an immune response to a cell expressing the AD in an in vitro assay
44. An immune effector cell expressing a chimeric antigen receptor (CAR) for use in therapy, wherein
- the CAR comprises a D domain that binds to a AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123, and
 - the immune effector cell used in combination with an Adapter is capable of directing an immune response to a target cell expressing an antigenic determinant (AD) in an in vitro assay, wherein the Adapter comprises (i) said AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic determinant binding domain (ADBD) that binds to the AD expressed on the target cell.
45. An Adapter for use in therapy, wherein
- the Adapter comprises (i) an AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123 and (ii) an antigenic determinant binding domain (ADBD) that binds to an antigenic determinant (AD) on a target cell, and
 - the Adapter used in combination with an immune effector cell is capable of directing an immune response to a target cell expressing the AD in an in vitro assay, wherein the immune effector cell expresses a chimeric antigen receptor (CAR) comprising a D domain that binds to the AFP P26 polypeptide consisting of the amino acid sequence of SEQ ID NO: 16, 1117, 1118, 1119, 1120, 1121, 1122, or 1123.