Figure 1A

CD38 (Full Sequence)

MANCEFSPVSGDKPCCRLSRRAQLCLGVSILVLILVVVLAVVVPRWRQQWSGPGTTKRFPETVLARCVKYTEIHPEMRH
VDCQSVWDAFKGAFISKHPCNITEEDYQPLMKLGTQTVPCNKILLWSRIKDLAHQFTQVQRDMFTLEDTLLGYLADDL
TWCGEFNTSKINYQSCPDWRKDCSNNPVSVFWKTVSRRFAEAACDVVHVMLNGSRSKIFDKNSTFGSVEVHNLQPEK
VQTLEAWVIHGGREDSRDLCQDPTIKELESIISKRNIQFSCKNIYRPDKFLQCVKNPEDSSCTSEI

Figure 1B

CD38 (Extracellular domain only)

VPRWRQQWSGPGTTKRFPETVLARCVKYTEIHPEMRHVDCQSVWDAFKGAFISKHPCNITEEDYQPLMKLGTQTVPC
NKILLWSRIKDLAHQFTQVQRDMFTLEDTLLGYLADDLTWCGEFNTSKINYQSCPDWRKDCSNNPVSVFWKTVSRRFA
EAACDVVHVMLNGSRSKIFDKNSTFGSVEVHNLQPEKVQTLEAWVIHGGREDSRDLCQDPTIKELESIISKRNIQFSCKN
IYRPDKFLQCVKNPEDSSCTSEI

Figure 2

HUMAN T-cell surface glycoprotein CD3 epsilon chain

MQSGTHWRVLGLCLLSVGVWGQDGNEEMGGITQTPYKVSISGTTVILTCPQYPG
SEILWQHNDKNIGGDEDDKNIGSDEDHLSLKEFSELEQSGYYVCYPRGSK
PEDANFYLYLRARVCENCMEMDVMSVATIVIVDICITGGLLLLVYYWSK
NRKAKAKPVTRGAGAGGRQRGQNKERPPPVPNPDYEPIRKGQRDLYSGL
NQRRI

Figure 3A

Humanized anti-CD3 heavy chain variable region

SEQ ID NO. 1.

EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

Humanized anti-CD3 light chain variable region

SEQ ID NO. 2.

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11502 H1_L1.4

SEQ ID NO. 3.

EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 4.

EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 5.

EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 6.

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11794 H1.3_L1.4

SEQ ID NO. 7.

EVQLVESGGGDVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 8.

EVQLVESGGGDVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3B

SEQ ID NO. 9.
EVQLVESGGGDVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 10.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11795 H1.4_L1.4

SEQ ID NO. 11.
EVQLVESGGGKVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 12.
EVQLVESGGGKVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 13.
EVQLVESGGGKVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 14.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11796 H1.5_L1.4
SEQ ID NO. 15.
EVQLVESGGGNVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

XENP11796 H1.5_L1.4, cont.
SEQ ID NO. 16.
EVQLVESGGGNVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 17.
EVQLVESGGGNVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

Figure 3C

SEQ ID NO. 18.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11801 H1.6_L1.4

SEQ ID NO. 19.
EVQLVESGGGSVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 20.
EVQLVESGGGSVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 21.
EVQLVESGGGSVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 22.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11802 H1.7_L1.4

SEQ ID NO. 23.
EVQLVESGGGLVQPGGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 24.
EVQLVESGGGLVQPGGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 25.
EVQLVESGGGLVQPGGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 26.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3D

XENP11803 H1.8_L1.4

SEQ ID NO. 27.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 28.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 29.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 30.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11804 H1.9_L1.4

SEQ ID NO. 31.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMHWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 32.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMHWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 33.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMHWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 34.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3E

XENP11805 H1.10_L1.4

SEQ ID NO. 35.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 36.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 37.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 38.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11806 H1.11_L1.4

SEQ ID NO. 39.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQASGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 40.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQASGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 41.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQASGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 42.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3F

XENP11807 H1.12_L1.4

SEQ ID NO. 43.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 44.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 45.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 46.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11808 H1.13_L1.4

SEQ ID NO. 47.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKANSYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 48.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKANSYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 49.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKANSYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 50.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3G

XENP11809 H1.14_L1.4

SEQ ID NO. 51.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATAYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 52.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATAYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 53.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATAYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 54.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11810 H1.15_L1.4

SEQ ID NO. 55.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYAASVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 56.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYAASVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 57.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYAASVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 58.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3H

XENP11811 H1.16_L1.4

SEQ ID NO. 59.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 60.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 61.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDNSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 62.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11812 H1.17_L1.4

SEQ ID NO. 63.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDTSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 64.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDTSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 65.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDTSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTV

SEQ ID NO. 66.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3I

XENP11813 H1.18_L1.4

SEQ ID NO. 67.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTAYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 68.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTAYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 69.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTAYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 70.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

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SEQ ID NO. 71.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRDEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 72.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRDEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 73.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRDEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 74.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3J

XENP11815 H1.20_L1.4

SEQ ID NO. 75.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRKEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 76.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRKEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 77.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRKEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 78.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11816 H1.21_L1.4

SEQ ID NO. 79.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRSEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 80.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRSEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 81.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRSEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 82.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3K

XENP11817 H1.22_L1.4

SEQ ID NO. 83.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCARHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 84.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCARHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 85.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCARHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 86.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11818 H1.23_L1.4

SEQ ID NO. 87.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCTRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 88.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCTRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 89.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCTRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 90.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3L

XENP11819 H1.24_L1.4

SEQ ID NO. 91.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 92.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 93.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 94.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11820 H1.25_L1.4

SEQ ID NO. 95.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGQSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 96.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGQSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 97.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGQSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 98.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3M

XENP11821 H1.26_L1.4

SEQ ID NO. 99.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNTYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 100.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNTYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 101.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNTYVSWFAYWGQGTLVTVSS

SEQ ID NO. 102.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11822 H1.27_L1.4

SEQ ID NO. 103.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFDYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 104.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFDYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 105.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFDYWGQGTLVTVSS

SEQ ID NO. 106.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3N

XENP11823 H1.28_L1.4

SEQ ID NO. 107.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTTVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 108.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTTVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 109.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTTVTVSS

SEQ ID NO. 110.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11824 H1.29_L1.30

SEQ ID NO. 111.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKSLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 112.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKSLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 113.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKSLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 114.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3O

XENP11825 H1_L1.10

SEQ ID NO. 115.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQPPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 116.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQPPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 117.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 118.
QAVVTQPPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11826 H1_L1.11

SEQ ID NO. 119.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 120.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 121.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 122.
QAVVTQEPSLSVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3P

XENP11827 H1_L1.12

SEQ ID NO. 123.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGATVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 124.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGATVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 125.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 126.
QAVVTQEPSLTVSPGATVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11828 H1_L1.13

SEQ ID NO. 127.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGQTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 128.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGQTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 129.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 130.
QAVVTQEPSLTVSPGQTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3Q

XENP11829 H1_L1.14

SEQ ID NO. 131.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 132.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 133.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 134.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11830 H1_L1.15

SEQ ID NO. 135.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 136.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 137.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 138.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3R

XENP11831 H1_L1.16

SEQ ID NO. 139.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIYDTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 140.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIYDTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 141.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 142.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIYDTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11832 H1_L1.17

SEQ ID NO. 143.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNNRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 144.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNNRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 145.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 146.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNNRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3S

XENP11833 H1_L1.18

SEQ ID NO. 147.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRASGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 148.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRASGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 149.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 150.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRASGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11834 H1_L1.19

SEQ ID NO. 151.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTSNKHSWTPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 152.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTSNKHSWTPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 153.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 154.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTSNKHSWTPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3T

XENP11835 H1_L1.20

SEQ ID NO. 155.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPDRFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 156.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPDRFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 157.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 158.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPDRFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11836 H1_L1.21

SEQ ID NO. 159.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSKSG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 160.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSKSG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 161.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 162.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSKSG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3U

XENP11837 H1_L1.22

SEQ ID NO. 163.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSSSG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 164.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSSSG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 165.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 166.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSSSG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11838 H1_L1.23

SEQ ID NO. 167.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 168.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 169.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 170.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3V

XENP11839 H1_L1.24

SEQ ID NO. 171.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQAEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 172.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQAEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 173.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 174.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQAEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP11840 H1_L1.25

SEQ ID NO. 175.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQSEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 176.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQSEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 177.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 178.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQSEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3W

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SEQ ID NO. 179.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEADYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 180.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEADYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 181.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 182.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEADYYCALWYSNLWVFGGGTKLTVL

XENP11842 H1_L1.27

SEQ ID NO. 183.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCLLWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 184.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCLLWYSNLWVFGGGTKLTVL

SEQ ID NO. 185.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 186.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCLLWYSNLWVFGGGTKLTVL

Figure 3X

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SEQ ID NO. 187.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 188.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 189.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 190.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

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SEQ ID NO. 191.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLEIKGSHHHHHH

SEQ ID NO. 192.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLEIKGS

SEQ ID NO. 193.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 194.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLEIKGS

Figure 3Y

XENP11920 H1_L3.1

SEQ ID NO. 195.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
EIVMTQSPATLSLSPGERATLSCRSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSGS
GTDFTLTISSLQPEDFAVYYCALWYSNLWVFGGGTKVEIKGSHHHHHH

SEQ ID NO. 196.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
EIVMTQSPATLSLSPGERATLSCRSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSGS
GTDFTLTISSLQPEDFAVYYCALWYSNLWVFGGGTKVEIKGS

SEQ ID NO. 197.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 198.
EIVMTQSPATLSLSPGERATLSCRSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSGS
GTDFTLTISSLQPEDFAVYYCALWYSNLWVFGGGTKVEIKGS

XENP11921 H1_L5.1

SEQ ID NO. 199.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
DIVMTQSPDSLAVSLGERATINCKSSTGAVTTSNYANWVQQKPGQPPKGLIGGTNKRAPGVPDRFSGSGS
GTDFTLTISSLQAEDVAVYYCALWYSNLWVFGGGTKVEIKGSHHHHHH

SEQ ID NO. 200.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
DIVMTQSPDSLAVSLGERATINCKSSTGAVTTSNYANWVQQKPGQPPKGLIGGTNKRAPGVPDRFSGSGS
GTDFTLTISSLQAEDVAVYYCALWYSNLWVFGGGTKVEIKGS

SEQ ID NO. 201.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 202.
DIVMTQSPDSLAVSLGERATINCKSSTGAVTTSNYANWVQQKPGQPPKGLIGGTNKRAPGVPDRFSGSGS
GTDFTLTISSLQAEDVAVYYCALWYSNLWVFGGGTKVEIKGS

Figure 3Z

XENP11922 H1_L1.31

SEQ ID NO. 203.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTDSGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 204.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTDSGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 205.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 206.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTDSGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP11923 H1_L1.32

SEQ ID NO. 207.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQEKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 208.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQEKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 209.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 210.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQEKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3AA

XENP12107 H1.38_L1.4

SEQ ID NO. 211.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTATYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 212.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTATYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 213.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTATYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 214.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12108 H1_L1.33

SEQ ID NO. 215.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 216.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 217.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 218.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLT

Figure 3BB

XENP12109 H1_L1.34

SEQ ID NO. 219.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGTAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 220.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGTAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 221.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 222.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGTAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12110 H1_L1.35

SEQ ID NO. 223.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGSPPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 224.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGSPPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 225.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 226.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGSPPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3CC

XENP12111 H1_L1.36

SEQ ID NO. 227.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQPPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 228.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQPPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 229.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 230.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQPPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12112 H1_L1.37

SEQ ID NO. 231.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQGPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 232.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQGPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 233.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 234.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQGPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3DD

XENP12113 H1_L1.38

SEQ ID NO. 235.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 236.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 237.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 238.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12114 H1_L1.39

SEQ ID NO. 239.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQDPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 240.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQDPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 241.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 242.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQDPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3EE

XENP12131 H1.30_L1.4

SEQ ID NO. 243.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 244.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 245.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 246.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12132 H1.31_L1.4

SEQ ID NO. 247.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 248.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 249.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 250.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3FF

XENP12133 H1.32_L1.4

SEQ ID NO. 251.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 252.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 253.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 254.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

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SEQ ID NO. 255.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 256.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 257.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS

SEQ ID NO. 258.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3GG

XENP12135 H1.34_L1.4

SEQ ID NO. 259.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 260.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 261.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS

SEQ ID NO. 262.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12136 H1.35_L1.4

SEQ ID NO. 263.
EVQLVESGGEVKKPGESLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 264.
EVQLVESGGEVKKPGESLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 265.
EVQLVESGGEVKKPGESLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 266.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3HH

XENP12137 H1.36_L1.4

SEQ ID NO. 267.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSNGGSTYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGSQA
VVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 268.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSNGGSTYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGSQA
VVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLGGK
AALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 269.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSNGGSTYYADSVKGRFTI
SRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 270.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12138 H1.37_L1.4

SEQ ID NO. 271.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 272.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 273.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 274.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

Figure 3II

XENP12139 H1.37_L1.32

SEQ ID NO. 275.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQEKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 276.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQEKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

SEQ ID NO. 277.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 278.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQEKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTLSGAQPEDEAEYYCALWYSNLWVFGGGTKLTVL

XENP12149 H1_L1.40

SEQ ID NO. 279.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 280.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 281.
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 282.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3JJ

XENP12213 H1.30_L1.40

SEQ ID NO. 283.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 284.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 285.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 286.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP12214 H1.8_L1.40

SEQ ID NO. 287.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 288.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 289.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 290.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3KK

XENP12215 H1.39_L1.40

SEQ ID NO. 291.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 292.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 293.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 294.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP12216 H1.40_L1.40

SEQ ID NO. 295.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 296.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 297.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 298.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3LL

XENP12217 H1.30_L1.41

SEQ ID NO. 299.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 300.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 301.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 302.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12218 H1.8_L1.41

SEQ ID NO. 303.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 304.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 305.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 306.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3MM

XENP12219 H1.39_L1.41

SEQ ID NO. 307.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 308.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 309.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 310.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12220 H1.40_L1.41

SEQ ID NO. 311.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 312.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 313.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 314.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3NN

XENP12221 H1.30_L1.42

SEQ ID NO. 315.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 316.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 317.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 318.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12222 H1.8_L1.42

SEQ ID NO. 319.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 320.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 321.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 322.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3OO

XENP12223 H1.39_L1.42

SEQ ID NO. 323.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 324.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 325.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 326.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12224 H1.40_L1.42

SEQ ID NO. 327.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 328.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 329.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 330.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3PP

XENP12225 H1.30_L1.43

SEQ ID NO. 331.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 332.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 333.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 334.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12226 H1.8_L1.43

SEQ ID NO. 335.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 336.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 337.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 338.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3QQ

XENP12227 H1.39_L1.43

SEQ ID NO. 339.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 340.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 341.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 342.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12228 H1.40_L1.43

SEQ ID NO. 343.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 344.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 345.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 346.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3RR

XENP12229 H1.30_L1.44

SEQ ID NO. 347.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 348.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 349.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 350.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12230 H1.8_L1.44

SEQ ID NO. 351.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 352.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 353.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 354.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3SS

XENP12231 H1.39_L1.44

SEQ ID NO. 355.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 356.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 357.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 358.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

XENP12232 H1.40_L1.44

SEQ ID NO. 359.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 360.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 361.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 362.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEAEYYCALWYSNHWVFGGGTKLTVL

Figure 3TT

XENP12233 H1.30_L1.45

SEQ ID NO. 363.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 364.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 365.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 366.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP12234 H1.8_L1.45

SEQ ID NO. 367.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 368.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 369.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 370.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3UU

XENP12235 H1.39_L1.45

SEQ ID NO. 371.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 372.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 373.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 374.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

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SEQ ID NO. 375.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 376.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 377.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 378.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKAPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3VV

XENP12237 H1.30_L1.46

SEQ ID NO. 379.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 380.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 381.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 382.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

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SEQ ID NO. 383.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 384.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 385.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 386.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3WW

XENP12239 H1.39_L1.46

SEQ ID NO. 387.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 388.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 389.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 390.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP12240 H1.40_L1.46

SEQ ID NO. 391.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 392.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 393.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 394.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGQSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3XX

XENP12241 H1.30_L1.47

SEQ ID NO. 395.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 396.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 397.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 398.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP12242 H1.8_L1.47

SEQ ID NO. 399.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 400.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 401.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 402.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 3YY

XENP12243 H1.39_L1.47

SEQ ID NO. 403.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 404.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 405.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGNSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 406.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

XENP12244 H1.40_L1.47

SEQ ID NO. 407.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVLGSHHHHHH

SEQ ID NO. 408.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGGGGSGGGGSGGGGS
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

SEQ ID NO. 409.
EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRKAPGKGLEWVGRIRSKYNNYATYYADSVKGRF
TISRDDSKNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

SEQ ID NO. 410.
QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLG
GKAALTISGAQPEDEADYYCALWYSNHWVFGGGTKLTVL

Figure 4A

Optimized scFv CD3 variable regions

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP11502 H1_L1.4 SEQ ID NO: 4	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11794 H1.3_L1.4 SEQ ID NO: 8	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11795 H1.4_L1.4 SEQ ID NO: 12	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11796 H1.5_L1.4 SEQ ID NO: 16	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11801 H1.6_L1.4 SEQ ID NO: 20	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11802 H1.7_L1.4 SEQ ID NO: 24	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11803 H1.8_L1.4 SEQ ID NO: 28	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11804 H1.9_L1.4 SEQ ID NO: 32	TYAMH SEQ ID NO: 432	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11805 H1.10_L1.4 SEQ ID NO: 36	TYAMS SEQ ID NO: 412	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11806 H1.11_L1.4 SEQ ID NO: 40	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11807 H1.12_L1.4 SEQ ID NO: 44	TYAMN SEQ ID NO: 411	RIRSKANNYATYYADSVKG SEQ ID NO: 414	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430

Figure 4B

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP11808 H1.13_L1.4 SEQ ID NO: 48	TYAMN SEQ ID NO: 411	RIRSKANSYATYYADSVKG SEQ ID NO: 434	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11809 H1.14_L1.4 SEQ ID NO: 52	TYAMN SEQ ID NO: 411	RIRSKYNNYATAYADSVKG SEQ ID NO: 478	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11810 H1.15_L1.4 SEQ ID NO: 56	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYAASVKG SEQ ID NO: 479	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11811 H1.16_L1.4 SEQ ID NO: 60	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11812 H1.17_L1.4 SEQ ID NO: 64	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11813 H1.18_L1.4 SEQ ID NO: 68	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11814 H1.19_L1.4 SEQ ID NO: 72	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11815 H1.20_L1.4 SEQ ID NO: 76	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11816 H1.21_L1.4 SEQ ID NO: 80	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11817 H1.22_L1.4 SEQ ID NO: 84	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11818 H1.23_L1.4 SEQ ID NO: 88	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11819 H1.24_L1.4 SEQ ID NO: 92	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430

SUBSTITUTE SHEET (RULE 26)

Figure 4C

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP11820 H1.25_L1.4 SEQ ID NO: 96	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGQSYVSWFAY SEQ ID NO: 418	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11821 H1.26_L1.4 SEQ ID NO: 100	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNTYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11822 H1.27_L1.4 SEQ ID NO: 104	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFDY SEQ ID NO: 480	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11823 H1.28_L1.4 SEQ ID NO: 108	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11824 H1.29_L1.30 SEQ ID NO: 112	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11825 H1_L1.10 SEQ ID NO: 116	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11826 H1_L1.11 SEQ ID NO: 120	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11827 H1_L1.12 SEQ ID NO: 124	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11828 H1_L1.13 SEQ ID NO: 128	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11829 H1_L1.14 SEQ ID NO: 132	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTSSNYAN SEQ ID NO: 421	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11830 H1_L1.15 SEQ ID NO: 136	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTSGHYAN SEQ ID NO: 422	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11831 H1_L1.16 SEQ ID NO: 140	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	DTNKRAP SEQ ID NO: 426	ALWYSNLWV SEQ ID NO: 430

SUBSTITUTE SHEET (RULE 26)

Figure 4D

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP11832 H1_L1.17 SEQ ID NO: 144	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNNRAP SEQ ID NO: 427	ALWYSNLWV SEQ ID NO: 430
XENP11833 H1_L1.18 SEQ ID NO: 148	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAS SEQ ID NO: 428	ALWYSNLWV SEQ ID NO: 430
XENP11834 H1_L1.19 SEQ ID NO: 152	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTSNKHS SEQ ID NO: 482	ALWYSNLWV SEQ ID NO: 430
XENP11835 H1_L1.20 SEQ ID NO: 156	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11836 H1_L1.21 SEQ ID NO: 160	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11837 H1_L1.22 SEQ ID NO: 164	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11838 H1_L1.23 SEQ ID NO: 168	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11839 H1_L1.24 SEQ ID NO: 172	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11840 H1_L1.25 SEQ ID NO: 176	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11841 H1_L1.26 SEQ ID NO: 180	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11842 H1_L1.27 SEQ ID NO: 184	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	LLWYSNLWV SEQ ID NO: 417
XENP11843 H1_L1.28 SEQ ID NO: 188	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433

SUBSTITUTE SHEET (RULE 26)

Figure 4E

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP11844 H1_L1.29 SEQ ID NO: 192	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11920 H1_L3.1 SEQ ID NO: 196	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	RSSTGAVTTSNYAN SEQ ID NO: 423	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11921 H1_L5.1 SEQ ID NO: 200	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	KSSTGAVTTSNYAN SEQ ID NO: 424	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP11922 H1_L1.31 SEQ ID NO: 204	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP11923 H1_L1.32 SEQ ID NO: 208	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12107 H1.38_L1.4 SEQ ID NO: 212	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12108 H1_L1.33 SEQ ID NO: 216	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12109 H1_L1.34 SEQ ID NO: 220	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12110 H1_L1.35 SEQ ID NO: 224	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12111 H1_L1.36 SEQ ID NO: 228	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12112 H1_L1.37 SEQ ID NO: 232	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12113 H1_L1.38 SEQ ID NO: 236	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430

SUBSTITUTE SHEET (RULE 26)

Figure 4F

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP12114 H1_L1.39 SEQ ID NO: 240	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12131 H1.30_L1.4 SEQ ID NO: 244	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12132 H1.31_L1.4 SEQ ID NO: 248	TYAMS SEQ ID NO: 412	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12133 H1.32_L1.4 SEQ ID NO: 252	TYAMN SEQ ID NO: 411	RIRSKANNYATYYADSVKG SEQ ID NO: 414	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12134 H1.33_L1.4 SEQ ID NO: 256	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFDY SEQ ID NO: 419	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12135 H1.34_L1.4 SEQ ID NO: 260	TYAMS SEQ ID NO: 412	RIRSKANNYATYYADSVKG SEQ ID NO: 414	HGNFGDSYVSWFDY SEQ ID NO: 419	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12136 H1.35_L1.4 SEQ ID NO: 264	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12137 H1.36_L1.4 SEQ ID NO: 268	TYAMN SEQ ID NO: 411	RIRSNGGSTYYADSVKG SEQ ID NO: 415	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12138 H1.37_L1.4 SEQ ID NO: 272	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12139 H1.37_L1.32 SEQ ID NO: 276	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNLWV SEQ ID NO: 430
XENP12149 H1_L1.40 SEQ ID NO: 280	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12213 H1.30_L1.40 SEQ ID NO: 284	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433

Figure 4G

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP12214 H1.8_L1.40 SEQ ID NO: 288	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12215 H1.39_L1.40 SEQ ID NO: 292	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12216 H1.40_L1.40 SEQ ID NO: 296	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12217 H1.30_L1.41 SEQ ID NO: 300	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12218 H1.8_L1.41 SEQ ID NO: 304	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12219 H1.39_L1.41 SEQ ID NO: 308	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12220 H1.40_L1.41 SEQ ID NO: 312	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12221 H1.30_L1.42 SEQ ID NO: 316	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12222 H1.8_L1.42 SEQ ID NO: 320	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12223 H1.39_L1.42 SEQ ID NO: 324	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12224 H1.40_L1.42 SEQ ID NO: 328	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12225 H1.30_L1.43 SEQ ID NO: 332	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433

Figure 4H

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP12226 H1.8_L1.43 SEQ ID NO: 336	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12227 H1.39_L1.43 SEQ ID NO: 340	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12228 H1.40_L1.43 SEQ ID NO: 344	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12229 H1.30_L1.44 SEQ ID NO: 348	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12230 H1.8_L1.44 SEQ ID NO: 352	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12231 H1.39_L1.44 SEQ ID NO: 356	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12232 H1.40_L1.44 SEQ ID NO: 360	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12233 H1.30_L1.45 SEQ ID NO: 364	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12234 H1.8_L1.45 SEQ ID NO: 368	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12235 H1.39_L1.45 SEQ ID NO: 372	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12236 H1.40_L1.45 SEQ ID NO: 376	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12237 H1.30_L1.46 SEQ ID NO: 380	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433

Figure 4I

Xen #	vhCDR1	vhCDR2	vhCDR3	vlCDR1	vlCDR2	vlCDR3
XENP12238 H1.8_L1.46 SEQ ID NO: 384	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12239 H1.39_L1.46 SEQ ID NO: 388	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12240 H1.40_L1.46 SEQ ID NO: 392	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12241 H1.30_L1.47 SEQ ID NO: 396	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12242 H1.8_L1.47 SEQ ID NO: 400	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12243 H1.39_L1.47 SEQ ID NO: 404	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGNSYVSWFAY SEQ ID NO: 416	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP12244 H1.40_L1.47 SEQ ID NO: 408	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
XENP ?? SEQ ID NO: 1 and 2	TYAMN SEQ ID NO: 411	RIRSKYNNYATYYADSVKG SEQ ID NO: 413	HGNFGDSYVSWFAY SEQ ID NO: 417	GSSTGAVTTSNYAN SEQ ID NO: 420	GTNKRAP SEQ ID NO: 425	ALWYSNHWV SEQ ID NO: 433
Consensus sequences	TYAMXaa1, wherein Xaa1 is N, S or H (SEQ ID NO:435)	R-I-R-S-K-Xaa1-N-Xaa2-Y-A-T-Xaa3-Y-Y-A-Xaa4-S-V-K-G, wherein Xaa1 is Y or A, Xaa2 is N or S, Xaa3 is Y or A and Xaa4 is D or A(SEQ ID NO:436)	H-G-N-F-G-Xaa1-S-Y-V-S-W-F-Xaa2-Y, wherein Xaa1 is N, D or Q and Xaa2 is A or D (SEQ ID NO:437)	Xaa1-S-S-T-G-A-V-T-Xaa2-Xaa3-Xaa4-Y-A-N, wherein Xaa1 is G, R or K, Xaa2 is T or S, Xaa3 is S or G and Xaa4 is N or H, (SEQ ID NO:438)	Xaa1-T-N-Xaa2-R-A-Xaa3, wherein Xaa1 is G or D, Xaa2 is K or N, and Xaa3 is P or S (SEQ ID NO:439)	Xaa1-L-W-Y-S-N-Xaa2-W-V, wherein Xaa1 is A or L and Xaa2 is L or H (SEQ ID NO:440)

Figure 5

Positive charged scFv linkers

Name	Sequence	Length	Charge	SEQ ID NO:
Gly-Ser 15	GGGGSGGGGSGGGGS	15	0	441
Whitlow linker	GSTSGSGKPGSGEGSTKG	18	+1	442
6paxA_1 (+A)	IRPRAIGGSKPRVA	14	+4	443
+B	GKGGSGKGGSGKGGS	15	+3	444
+C	GGKGSGGKGSGGKGS	15	+3	445
+D	GGGKSGGGKSGGGKS	15	+3	446
+E	GKGKSGKGKSGKGKS	15	+6	447
+F	GGGKSGGKGSGKGGS	15	+3	448
+G	GKPGSGKPGSGKPGS	15	+3	449
+H	GKPGSGKPGSGKPGSGKPGS	20	+4	450
+I	GKGKSGKGKSGKGKSGKGKS	20	+8	451

Negative charged scFv linkers

Name	Sequence	Length	Charge	
Gly-Ser 15	GGGGSGGGGSGGGGSGGGGS	20	0	452
3hsc_2 (-A)	STAGDTHLGGEDFD	14	-4	453
-B	GEGGSGEGGSGEGGS	15	-3	454
-C	GGEGSGGEGSGGEGS	15	-3	455
-D	GGGESGGGESGGGES	15	-3	456
-E	GEGESGEGESGEGES	15	-6	457
-F	GGGESGGEGSGEGGS	15	-3	458
-G	GEGESGEGESGEGESGEGES	20	-8	459

Figure 6A

Preferred steric variants that favor Fc heterodimerization.

Monomer 1	Monomer 2
F405A	T394F
S364D	Y349K
S364E	L368K
S364E	Y349K
S364F	K370G
S364H	Y349K
S364H	Y349T
S364Y	K370G
T411K	K370E
V397S/F405A	T394F
K370R/T411K	K370E/T411E
L351E/S364D	Y349K/L351K
L351E/S364E	Y349K/L351K
L351E/T366D	L351K/T366K
P395T/V397S/F405A	T394F
S364D/K370G	S364Y/K370R
S364D/T394F	Y349K/F405A
S364E/F405A	Y349K/T394F
S364E/F405S	Y349K/T394Y
S364E/T411E	Y349K/D401K
S364H/D401K	Y349T/T411E
S364H/F405A	Y349T/T394F
S364H/T394F	Y349T/F405A
Y349C/S364E	Y349K/S354C
L351E/S364D/F405A	Y349K/L351K/T394F
L351K/S364H/D401K	Y349T/L351E/T411E
S364E/T411E/F405A	Y349K/T394F/D401K
S364H/D401K/F405A	Y349T/T394F/T411E
S364H/F405A/T411E	Y349T/T394F/D401K
Y349T	S364H
T394F	F405A
Y349T/T394F	S364H/F405A
K370E	T411K
K370E/T411D	T411K
K370E/T411E	K370R/T411K
L368E/K409E	L368K
Y349T/T411E	S364H/D401K
Y349T/T394F/S354C	S364H/F405A/Y349C
T411E	D401K
T411E	D401R/T411R
Q347E/K360E	Q347R
L368E	S364K
L368E/K370S	S364K
L368E/K370T	S364K
L368E/D401R	S364K
L368E/D401N	S364K
L368E	E357S/S364K
L368E	S364K/K409E
L368E	S364K/K409V
L368D	S364K

Figure 6B

Monomer 1	Monomer 2
L368D/K370S	S364K
L368D/K370S	S364K/E357L
L368D/K370S	S364K/E357Q
T411E/K360E/Q362E	D401K
L368E/K370S	S364K
K370S	S364K
L368E/K370S	S364K/E357Q
K370S	S364K/E357Q
L368E/K370S	S364K
K370S	S364K
L368E/K370S	S364K/E357Q
K370S	S364K/E357Q

Figure 6C

Monomer 1	Monomer 2
ISO(-) side	ISO(+) or ISO(++RR)) side
T411E	D401K
T411E K360D	D401K
T411E K360E	D401K
T411E Q362E	D401K
T411E N390D	D401K
T411E	D401K Q347K
T411E	D401K Q347R
T411E K360D Q362E	D401K
T411E K360E Q362E	D401K
T411E K360E N390D	D401K
T411E Q362E N390D	D401K
T411E Q347R	D401K K360D
T411E Q347R	D401K K360E
T411E K360	D401K Q347K
T411E K360D	D401K Q347R
T411E K360E	D401K Q347K
T411E K360E	D401K Q347R
T411E S364K	D401K K370S
T411E K370S	D401K S364K
Q347E	E357Q
Q347E	E357Q Q362K
K360D Q362E	Q347R
K360D Q362E	D401K
K360D Q362E	Q347R D401K
K360E Q362E	Q347R
K360E Q362E	D401K
K360E Q362E	Q347R D401K
Q362E N390D	D401K
Q347E K360D	D401N
K360D	Q347R N390K
K360D	N390KD401N
K360E	Y349H
K370S Q347E	S364K
K370S E357L	S364K
K370S E357Q	S364K
K370S Q347E E357L	S364K
K370S Q347E E357Q	S364K
L368D K370S Q347E	S364K
L368D K370S E357L	S364K
L368D K370S E357Q	S364K
L368D K370S Q347E E357L	S364K
L368D K370S Q347E E357Q	S364K
L368E K370S Q347E	S364K
L368E K370S E357L	S364K
L368E K370S E357Q	S364K
L368E K370S Q347E E357L	S364K
L368E K370S Q347E E357Q	S364K
L368D K370T Q347E	S364K
L368D K370T E357L	S364K
L368D K370T E357Q	S364K

Figure 6D

Monomer 1	Monomer 2
L368D K370T Q347E E357L	S364K
L368D K370T Q347E E357Q	S364K
L368E K370T Q347E	S364K
L368E K370T E357L	S364K
L368E K370T E357Q	S364K
L368E K370T Q347E E357L	S364K
L368E K370T Q347E E357Q	S364K
T411E Q362E	D401K T411K
T411E N390D	D401K T411K
T411E Q362E	D401R T411R
T411E N390D	D401R T411R

Figure 7

XENP	Heterodimer-skewing variant, Chain 1	Heterodimer-skewing variant, Chain 2	Heterodimer Yield (%)	CH3 Tm (°C)
12757	none	none	52.7	83.1
12758	L368D/K370S	S364K	94.4	76.6
12759	L368D/K370S	S364K/E357L	90.2	77.2
12760	L368D/K370S	S364K/E357Q	95.2	77.5
12761	T411E/K360E/Q362E	D401K	85.6	80.6
12496	L368E/K370S	S364K	91.5	n.d.
12511	K370S	S364K	59.9	n.d.
12840	L368E/K370S	S364K/E357Q	59.5	n.d.
12841	K370S	S364K/E357Q	90.4	n.d.
12894	L368E/K370S	S364K	41.0	n.d.
12895	K370S	S364K	49.3	n.d.
12896	L368E/K370S	S364K/E357Q	73.9	n.d.
12901	K370S	S364K/E357Q	87.9	n.d.

Figure 8

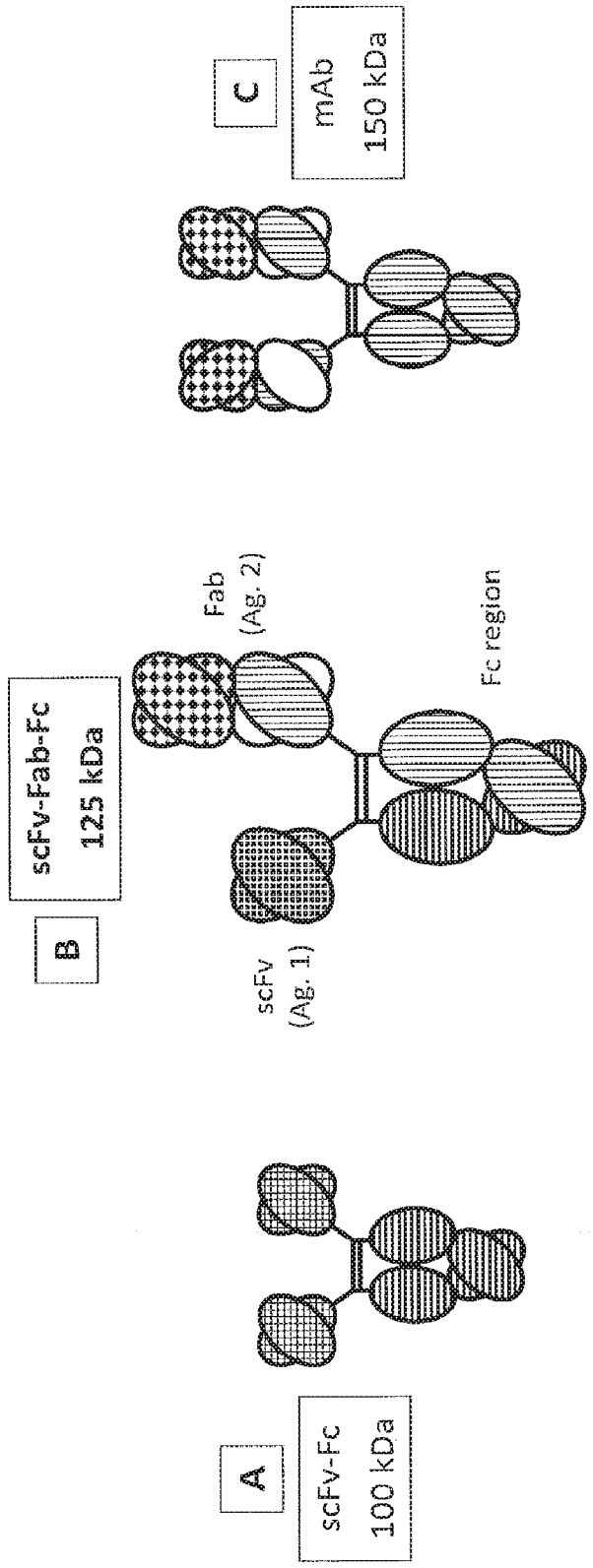

A
scFv-Fc
100 kDa
B
scFv-Fab-Fc
125 kDa
scFv
(Ag. 1)
Fab
(Ag. 2)
Fc region
C
mAb
150 kDa

Figure 9

Ablation Variants

Variant	Variant(s), cont.
G236R	P329K
S239G	A330L
S239K	A330S/P331S
S239Q	I332K
S239R	I332R
V266D	V266D/A327Q
S267K	V266D/P329K
S267R	S267R/A327Q
H268K	S267R/P329K
E269R	G236R/L328R
299R	E233P/L234V/L235A/G236del/S239K
299K	E233P/L234V/L235A/G236del/S267K
K322A	E233P/L234V/L235A/G236del/S239K/A327G
A327G	E233P/L234V/L235A/G236del/S267K/A327G
A327L	E233P/L234V/L235A/G236del
A327N	S239K/S267K
A327Q	
L328E	
L328R	
P329A	
P329H	

Figure 10

XENP	Heterodimer-skewing variant, Chain 1	Heterodimer-skewing variant, Chain 2	Heterodimer Yield (%)	CH3 Tm (°C)
12757	none	none	52.7	83.1
12758	L368D/K370S	S364K	94.4	76.6
12759	L368D/K370S	S364K/E357L	90.2	77.2
12760	L368D/K370S	S364K/E357Q	95.2	77.5
12761	T411E/K360E/Q362E	D401K	85.6	80.6
12496	L368E/K370S	S364K	91.5	n.d.
12511	K370S	S364K	59.9	n.d.
12840	L368E/K370S	S364K/E357Q	59.5	n.d.
12841	K370S	S364K/E357Q	90.4	n.d.
12894	L368E/K370S	S364K	41.0	n.d.
12895	K370S	S364K	49.3	n.d.
12896	L368E/K370S	S364K/E357Q	73.9	n.d.
12901	K370S	S364K/E357Q	87.9	n.d.

Figure 11

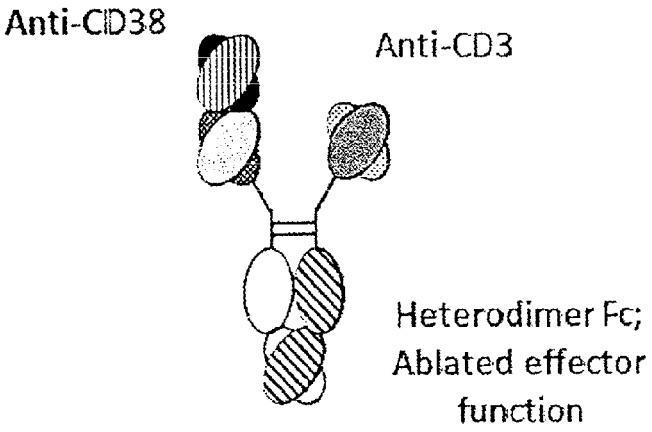

Anti-CD38
Anti-CD3
Heterodimer Fc;
Ablated effector
function

Figure 12

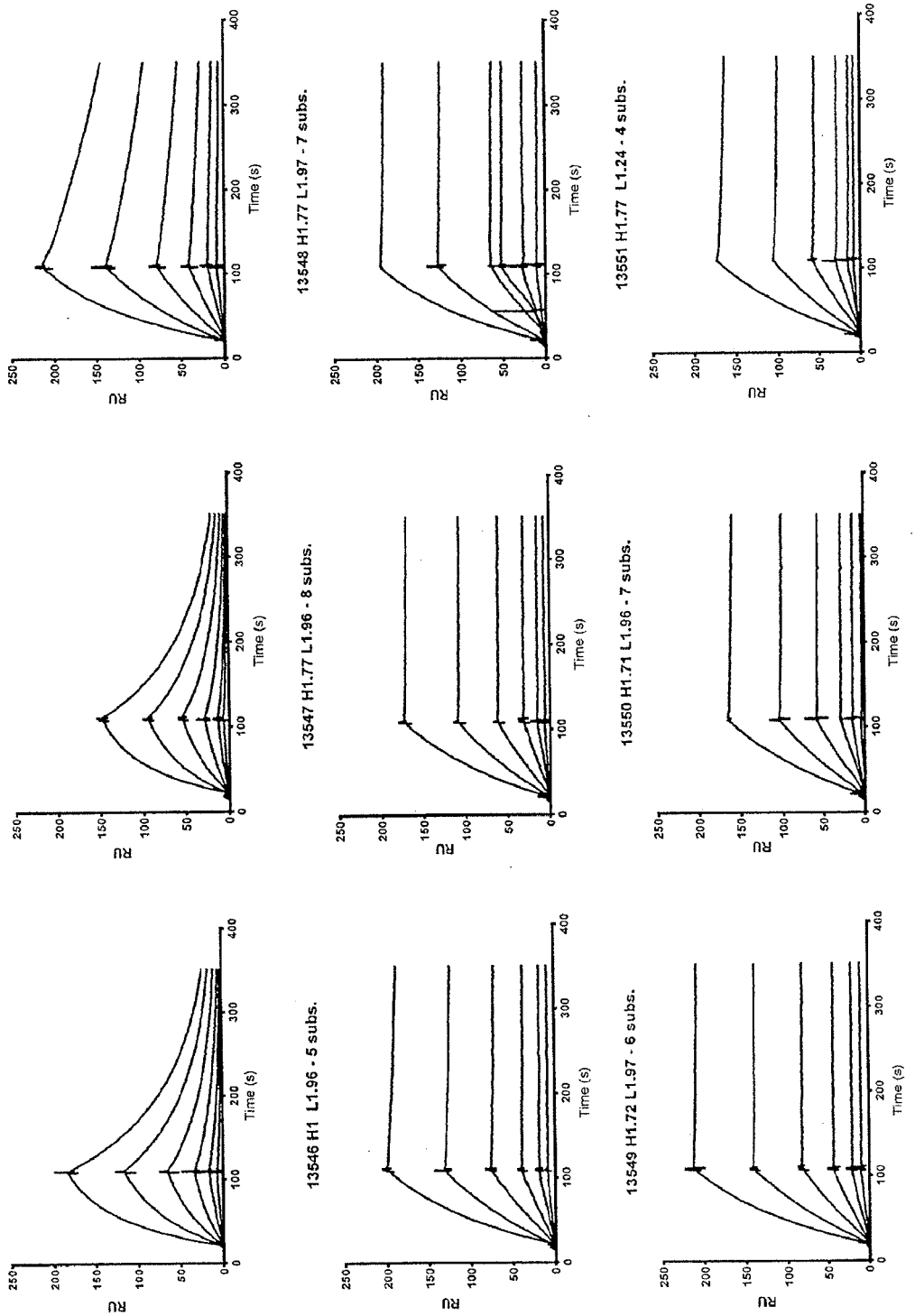

13243 H1 L1
13544 H1 L1
13545 H1 L1.24 - 1 sub.
13546 H1 L1.96 - 5 subs.
13547 H1.77 L1.96 - 8 subs.
13548 H1.77 L1.97 - 7 subs.
13549 H1.72 L1.97 - 6 subs.
13550 H1.71 L1.96 - 7 subs.
13551 H1.77 L1.24 - 4 subs.
RU
Time (s)

Figure 13

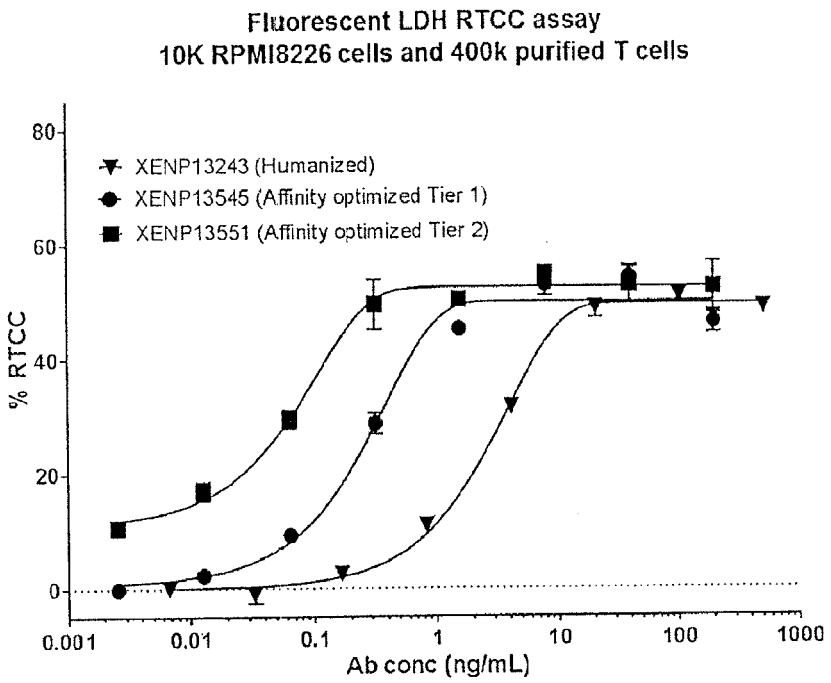

Fluorescent LDH RTCC assay
10K RPMI8226 cells and 400k purified T cells
XENP13243 (Humanized)
XENP13545 (Affinity optimized Tier 1)
XENP13551 (Affinity optimized Tier 2)
% RTCC
80
60
40
20
0
0.001
0.01
0.1
1
10
100
1000
Ab conc (ng/mL)

Figure 14

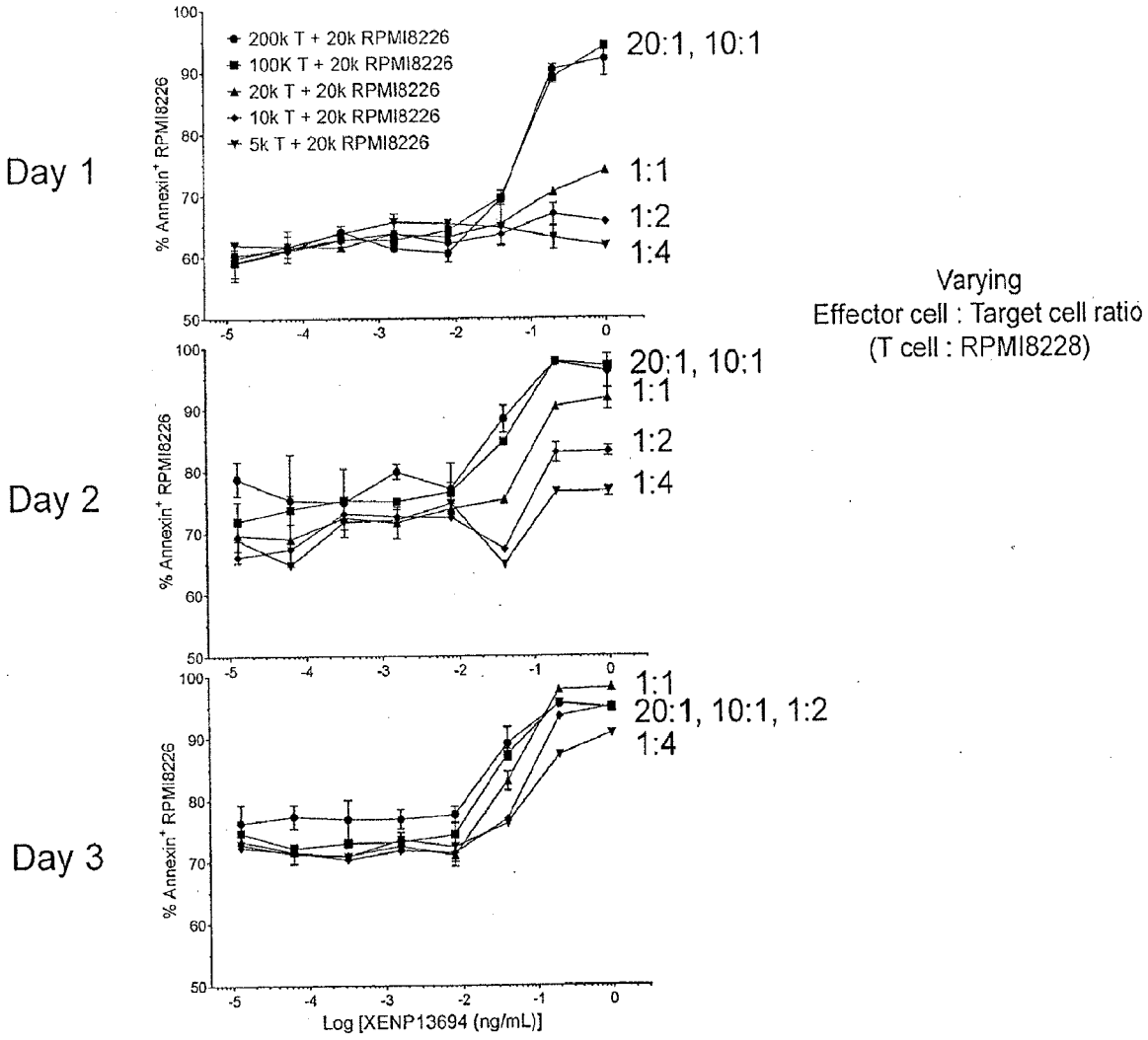

Day 1
Day 2
Day 3
200k T + 20k RPMI8226
100K T + 20k RPMI8226
20k T + 20k RPMI8226
10k T + 20k RPMI8226
5k T + 20k RPMI8226
% Annexin+ RPMI8226
Log [XENP13694 (ng/mL)]
20:1, 10:1
1:1
1:2
1:4
20:1, 10:1
1:1
1:2
1:4
1:1
20:1, 10:1, 1:2
1:4
Varying
Effector cell : Target cell ratio
(T cell : RPMI8228)

Figure 15

Anti-CD38 VH	Anti-CD38 VL	Anti-CD38 VH subs.	Anti-CD38 VL subs.	Bispecific XENP		K_D (CD38 binding)	Fold Improved K_D (CD38 binding)	RTCC EC50 (RPMI8226)	Fold improved EC50	Expression Yield (mg/L)	Half-life (d)
				Paired with Anti-CD3 H1.30_L1.47	Paired with Anti-CD3 H1.79_L1.48						
H1	L1	H1	L1	13243		57 nM	--	20 pM		83.31	7.60 ± 0.87
H1	L1	H1	L1		13544	52 nM	--	60 pM		75.12	7.27 ± 0.84
H1	L1.24	H1	N32W	13545	13752	12 nM	4.9	2 pM	10.0	73.06	7.11 ± 0.47
H1	L1.96	H1	T31Y N32W S50A Y53W S93V	13546	13753	1.6 nM	35	2 pM	10.0	80.22	6.81 ± 0.62
H1.77	L1.96	D28T R31Y D53Q	T31Y N32W S50A Y53W S93V	13547	13754	0.7 nM	84	1 pM	20.0	67.89	6.89 ± 0.77
H1.77	L1.97	D28T R31Y D53Q	T31Y N32W Y53W S93V	13548	13755	1.0 nM	57.6	0.9 pM	22.2	52.35	7.13 ± 0.62
H1.72	L1.97	R31Y D53Q	T31Y N32W Y53W S93V	13549	13756	0.5 nM	115	0.8 pM	25.0	37.30	3.67 ± 0.34
H1.71	L1.96	D28T D53Q	T31Y N32W S50A Y53W S93V	13550	13757	1.2 nM	45.7	0.8 pM	25.0	55.29	7.90 ± 0.76
H1.77	L1.24	D28T R31Y D53Q	N32W	13551	13694	2.0 nM	28.3	0.6 pM	33.3	71.14	8.29 ± 0.77

Figure 16

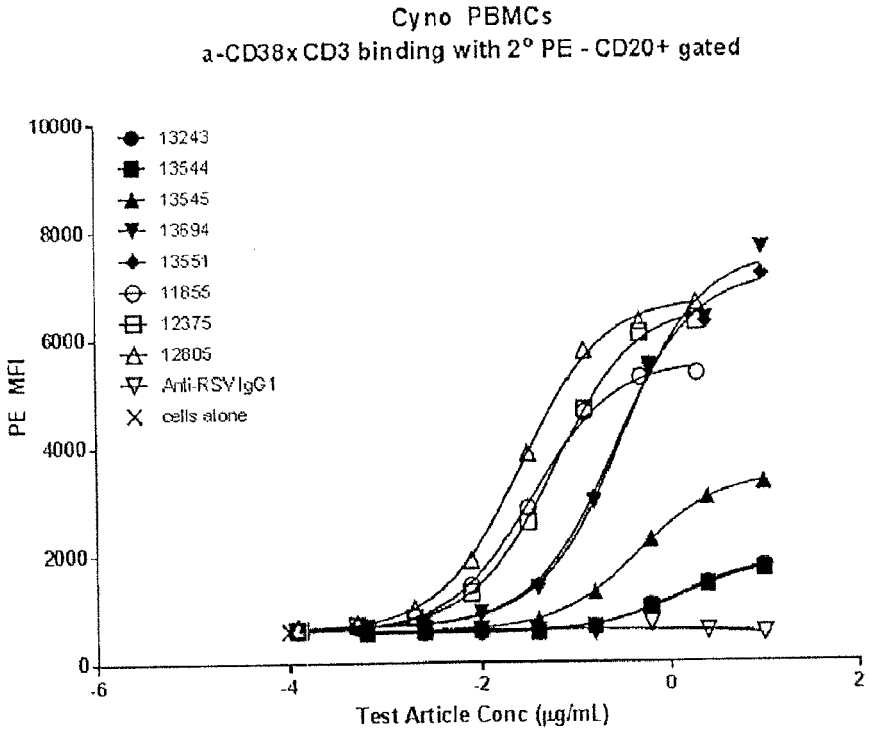

Cyno PBMCs
a-CD38x CD3 binding with 2° PE - CD20+ gated
PE MFI
10000
8000
6000
4000
2000
0
-6
-4
-2
0
2
Test Article Conc (µg/mL)
13243
13544
13545
13694
13551
11855
12375
12805
Anti-RSV IgG1
cells alone

Figure 17

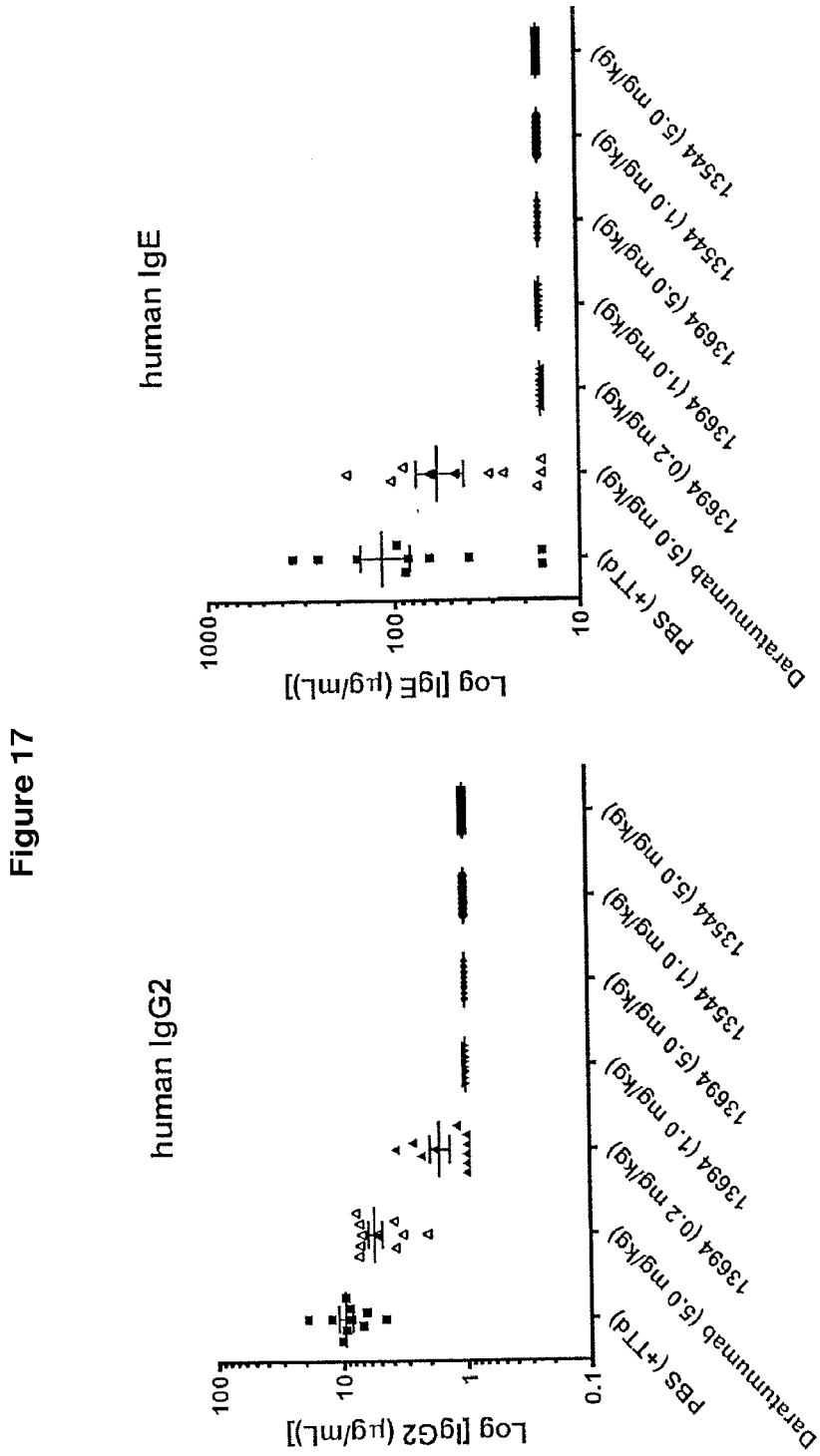

human IgE
Log [IgE (μg/mL)]
1000
100
10
PBS (+TTd)
Daratumumab (5.0 mg/kg)
13694 (0.2 mg/kg)
13694 (1.0 mg/kg)
13694 (5.0 mg/kg)
13544 (1.0 mg/kg)
13544 (5.0 mg/kg)
human IgG2
Log [IgG2 (μg/mL)]
100
10
1
0.1
PBS (+TTd)
Daratumumab (5.0 mg/kg)
13694 (0.2 mg/kg)
13694 (1.0 mg/kg)
13694 (5.0 mg/kg)
13544 (1.0 mg/kg)
13544 (5.0 mg/kg)

Figure 18

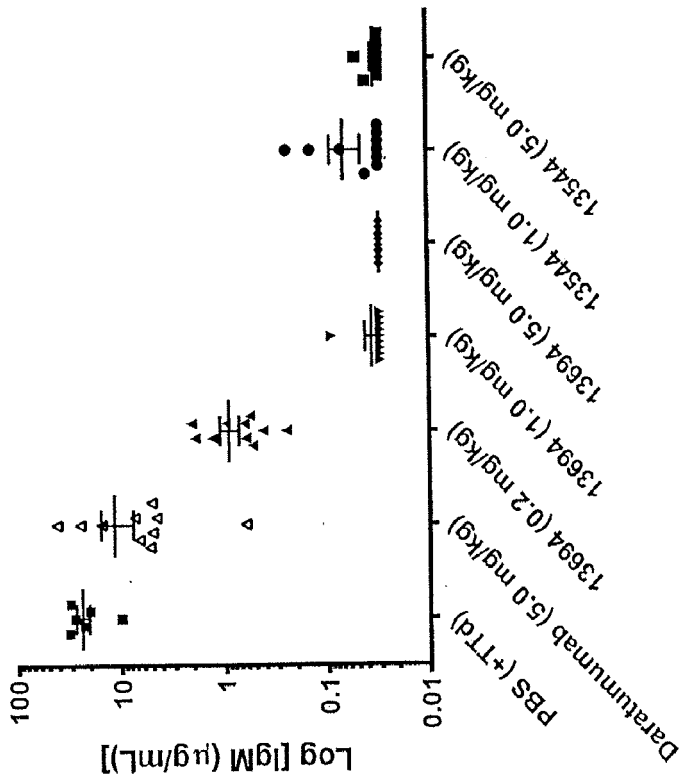

human IgM
Log [IgM (μg/mL)]
100
10
1
0.1
0.01
PBS (+TTd)
Daratumumab (5.0 mg/kg)
13694 (0.2 mg/kg)
13694 (1.0 mg/kg)
13694 (5.0 mg/kg)
13544 (1.0 mg/kg)
13544 (5.0 mg/kg)

Figure 19

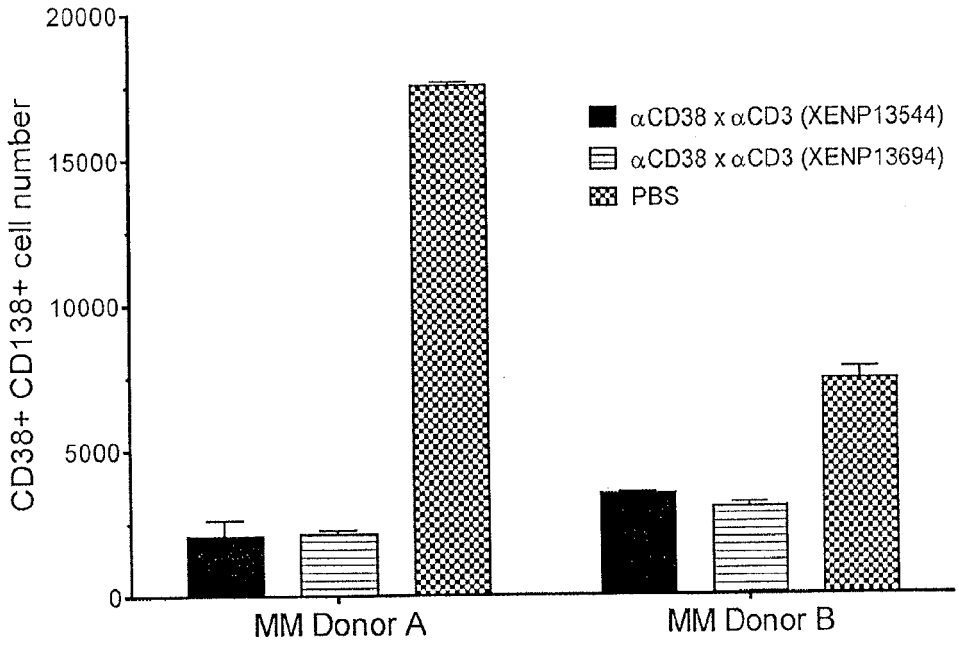

20000
15000
10000
5000
0
CD38+ CD138+ cell number
αCD38 x αCD3 (XENP13544)
αCD38 x αCD3 (XENP13694)
PBS
MM Donor A
MM Donor B

Figure 20A

OKT10

VH

EVKLQESGGGLVQPGGSLKLSCAASGFDFSRSWMNWVRQAPGKGLEWIGEINPDSSTINYTTSLKDKFIISRDNAKNTL
YLQMTKVRSEDTALYYCARYGNWFPYWGQGTLVTVSA

VL

DIVMTQSPKIMPTSVGDRVSVTCKASQNVDTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTITNV
QSEDLAEYFCQQYDSYPLTFGAGTKLDLK

XENP11855 (Anti-CD38 H1L1 IgG1)

Heavy chain

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Light chain

DIVMTQSPSSLSASVGDRVTITCRASQNVDTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQP
EDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20B

XENP13243 (Anti-CD38_H1_L1 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1)

DIVMTQSPSSLSASVGDRVTITCRASQNVDTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQP
EDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20C

XENP13544 (Anti-CD38_H1_L1 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1)

DIVMTQSPSSLSASVGDRVTITCRASQNVDTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQP
EDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20D

XENP13545 (Anti-CD38_H1_L1.24 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.24)

DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQ
PEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20E

XENP13546 (Anti-CD38_H1_L1.96 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.96)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20F

XENP13547 (Anti-CD38_H1.77_L1.96 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1.77)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.96)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20G

XENP13548 (Anti-CD38_H1.77_L1.97 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1.77)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.97)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYSASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20H

XENP13549 (Anti-CD38_H1.72_L1.97 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1.72)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.97)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYSASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20I

XENP13550 (Anti-CD38_H1.71_L1.96 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1.71)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.96)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20J

XENP13551 (Anti-CD38_H1.77_L1.24 x Anti-CD3_H1.30_L1.47)

Heavy chain 1 (Anti-CD38 H1.77)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.30 L1.47)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.24)

DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQ
PEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20K

XENP13694 (Anti-CD38_H1.77_L1.24 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1.77)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.24)

DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQ
PEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20L

XENP13752 (Anti-CD38_H1_L1.24 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.24)

DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQ
PEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20M

XENP13753 (Anti-CD38_H1_L1.96 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.96)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20N

XENP13754 (Anti-CD38_H1.77_L1.96 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1.77)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.96)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20O

XENP13755 (Anti-CD38_H1.77_L1.97 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1.77)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.97)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYSASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20P

XENP13756 (Anti-CD38_H1.72_L1.97 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1.72)

EVQLVESGGGLVQPGGSLRLSCAASGFDFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.97)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYSASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 20Q

XENP13757 (Anti-CD38_H1.71_L1.96 x Anti-CD3_H1.79_L1.48)

Heavy chain 1 (Anti-CD38 H1.71)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSRSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

Heavy chain 2 (Anti-CD3 H1.79 L1.48)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKCLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGCGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

Light chain (Anti-CD38 L1.96)

DIVMTQSPSSLSASVGDRVTITCRASQNVDYWVAWYQQKPGQSPKALIYAASWRYSGVPDRFTGSGSGTDFTLTISSL
QPEDFATYFCQQYDVYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 21

scFv monomer (+)	Fab monomer (-)
Heterodimer pI variants S364K/E357Q	Heterodimerization pI variants L368D/K370S
scFv charged linker (GKPGS)4	Isosteric pI substitutions N208D/Q295E/N384D/Q418E/N421D
FcKO E233P/L234V/L235A/G236del/S267K	FcKO E233P/L234V/L235A/G236del/S267K
± 428L/434S for FcRn (optional)	± 428L/434S for FcRn (optional)
CD3 scFv is H.1.30_L1.47 (no disulfide) or H1.79_L1.48 (with disulfide) ±charged linkers (optional)	Fv sequences for anti-CD38 as shown herein

scFv monomer	Fab monomer
Heterodimer pI variants S364K/E357Q	Heterodimerization pI variants L368D/K370S
scFv charged linker (GKPGS)4	pI substitutions I199T N203D K274Q R355Q Q419E K447del
FcKO E233P/L234V/L235A/G236del/S267K	FcKO E233P/L234V/L235A/G236del/S267K
± 428L/434S for FcRn (optional)	± 428L/434S for FcRn (optional)
CD3 scFv is H.1.30_L1.47 (no disulfide) or H1.79_L1.48 (with disulfide) ±charged linkers (optional)	Fv sequences for anti-CD38 as shown herein

Figure 22A

XENP13243 HC-Fab

EVQLVESGGGLVQPGGSLRLSCAASGFDFSRSWMNWVRQAPGKGLEWVSEINPDSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

XENP13243 HC-scFv

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

XENP13243 LC

DIVMTQSPSSLSASVGDRVTITCRASQNVDTNVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQP
EDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

scFv of XENP13242 including charged linker

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVL

Figure 22B

XENP13551 HC-Fab

EVQLVESGGGLVQPGGSLRLSCAASGFTFSYSWMNWVRQAPGKGLEWVSEINPQSSTINYATSVKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARYGNWFPYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSDTKVDKKVEPKSCDKTHTCPPCPAPPVAG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEVKFNWYVDGVEVHNAKTKPREEEYNSTYRVVSVLTVLHQDWLN
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCDVSGFYPSDIAVEWESDGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWEQGDVFSCSVMHEALHNHYTQKSLSLSPGK

XENP13551 HC-scFv

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVLEPKSSDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVKHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
PPSREQMTKNQVKLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
HEALHNHYTQKSLSLSPGK

XENP13551 LC

DIVMTQSPSSLSASVGDRVTITCRASQNVDTWVAWYQQKPGQSPKALIYSASYRYSGVPDRFTGSGSGTDFTLTISSLQ
PEDFATYFCQQYDSYPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

scFv of XENP13551 including charged linker

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSSGKPGSGKPGSGKPGSGKPGSQAVVTQEPS
LTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTISGAQPEDEAD
YYCALWYSNHWVFGGGTKLTVL

Figure 23A

XENP13243 HC-Fab (XenD08502)

GAAGTCCAGCTCGTGGAGTCGGGTGGCGGCCTCGTCCAGCCCGGCGGCTCGCTCCGGCTGTCATGCGCCGCGAG
CGGGTTCGATTTCAGTCGTTCGTGGATGAACTGGGTACGCCAGGCCCCGGGCAAGGGCCTCGAATGGGTCTCCGA
GATCAACCCGGACAGCAGCACGATCAACTACGCCACCTCGGTGAAGGGCCGGTTCACGATCAGCCGCGACAACTC
CAAGAACACCCTCTACCTGCAGATGAACTCCCTGCGCGCCGAGGACACGGCCGTCTACTACTGCGCGCGCTACGG
AAACTGGTTCCCGTACTGGGGCCAGGGCACACTGGTCACTGTCTCCAGCGCGTCCACGAAGGGCCCGTCGGTCTT
CCCCCTGGCGCCAAGCTCGAAAAGTACGTCCGGCGGGACCGCAGCGCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAGCCCGTGACCGTGAGCTGGAACTCGGGCGCGCTGACCTCCGGCGTCCACACCTTCCCGGCAGTCCTCCAGTC
GTCGGGCCTGTACTCGCTGTCCAGCGTCGTCACGGTGCCGTCGTCCTCCCTGGGCACGCAGACGTACATCTGCAAC
GTGAACCACAAGCCGAGCGACACCAAGGTCGACAAGAAGGTCGAGCCCAAGTCGTGCGACAAGACCCACACGTG
CCCGCCGTGCCCGGCCCCCCCTGTCGCCGGCCCCAGTGTCTTCCTCTTCCCGCCGAAGCCGAAGGACACCCTCATG
ATCTCGCGCACCCCCGAGGTCACCTGCGTGGTCGTGGACGTGAAGCACGAGGACCCTGAGGTTAAGTTCAACTGG
TATGTCGACGGGGTGGAGGTCCACAACGCGAAGACCAAGCCGCGCGAGGAGGAGTACAACAGTACGTACCGCGT
GGTCTCGGTGCTCACCGTCCTCCACCAGGACTGGCTGAACGGCAAGGAATACAAGTGTAAGGTCAGCAACAAGGC
CTTGCCCGCCCCCATCGAGAAGACCATAAGCAAGGCCAAGGGTCAGCCAAGGGAACCGCAGGTGTACACCCTCCC
GCCCTCCCGCGAGGAGATGACCAAGAACCAGGTATCACTGACCTGCGACGTGTCCGGGTTCTACCCGTCCGACAT
CGCGGTGGAGTGGGAGTCCGACGGCCAGCCGGAGAACAACTACAAGACCACCCCCCCGGTACTCGACTCCGACG
GTTCGTTCTTCCTCTACTCCAAGCTGACGGTGGACAAGTCCCGGTGGGAGCAAGGCGACGTGTTCAGCTGTTCCGT
CATGCACGAGGCCCTGCACAACCACTACACCCAGAAGAGTCTGTCCCTCTCCCCTGGCAAATGA

Figure 23B

XENP13243 HC-scFv (XenD08438)

GAAGTCCAGCTCGTGGAGTCGGGCGGCGGCCTCGTGCAACCGGGTGGCTCGCTGCGGCTCTCCTGCGCCGCGTCC
GGCTTCACGTTCTCCACCTACGCCATGAACTGGGTCCGCCAGGCGCCGGGCAAGGGGCTCGAGTGGGTGGGGCG
TATCCGCTCCAAGTACAACAACTACGCGACGTACTACGCCGATAGCGTAAAGGGACGCTTCACAATCTCGCGGGA
CGACAGCAAGAACACCCTTTACCTCCAGATGAACAGCCTGCGCGCCGAAGACACCGCCGTGTACTACTGTGTCCG
GCACGGGAACTTCGGCGACTCCTACGTCTCGTGGTTCGCCTACTGGGGCCAGGGCACCCTCGTCACCGTGTCCTCG
GGAAAGCCGGGGAGCGGAAAGCCGGGTTCGGGCAAGCCAGGCTCCGGTAAGCCGGGCTCGCAGGCGGTGGTG
ACCCAGGAGCCATCCCTGACCGTGTCCCCGGGGGGCACCGTCACGCTGACTTGCGGCTCCTCGACCGGTGCCGTC
ACCACCTCCAACTACGCCAACTGGGTGCAGCAGAAGCCCGGCAAGAGCCCCCGCGGCCTGATCGGCGGCACGAA
CAAGCGCGCGCCCGGCGTCCCGGCCCGCTTCTCCGGCTCCCTGCTGGGCGGGAAGGCCGCGCTCACCATCAGCGG
CGCGCAGCCCGAGGACGAGGCCGACTACTACTGCGCGCTCTGGTACTCGAACCACTGGGTCTTCGGCGGCGGGA
CCAAGCTCACCGTGCTCGAGCCGAAGTCCTCGGACAAGACCCACACATGCCCCCCCTGCCCGGCCCCCCCCGTGGC
GGGCCCCTCTGTCTTCCTGTTTCCCCCGAAGCCGAAGGACACCCTGATGATCTCGCGCACGCCGGAAGTGACCTGC
GTCGTCGTCGACGTGAAGCACGAGGACCCAGAGGTCAAGTTCAACTGGTACGTCGACGGCGTCGAGGTGCACAA
CGCGAAGACGAAGCCCCGTGAGGAGCAGTACAACTCCACCTACCGGGTGGTGTCGGTGCTGACGGTGCTCCACC
AGGACTGGCTGAACGGCAAGGAGTACAAGTGTAAGGTCTCCAACAAGGCCCTCCCGGCCCCCATCGAGAAGACC
ATCTCGAAGGCCAAGGGCCAGCCGCGCGAGCCGCAGGTGTACACGCTCCCGCCCTCGCGGGAGCAGATGACCAA
GAACCAGGTGAAGCTGACCTGCCTCGTGAAGGGCTTCTACCCGAGCGACATCGCGGTGGAGTGGGAGTCCAACG
GCCAACCGGAGAACAACTACAAGACCACTCCGCCGGTGCTGGACTCGGATGGGTCGTTCTTCCTCTACTCGAAGCT
CACGGTAGACAAGTCCCGCTGGCAGCAGGGCAACGTCTTCTCCTGCTCCGTCATGCACGAGGCCCTCCACAACCAC
TATACCCAGAAGTCGCTCTCGCTCTCCCCGGGAAAGTGA

Figure 23C

XENP13243 LC (XenD07263)

GACATCGTCATGACGCAGTCGCCGAGCAGCCTCTCCGCATCGGTGGGTGACCGCGTCACCATCACCTGCCGGGCG
AGCCAGAACGTCGACACCAACGTGGCCTGGTATCAGCAGAAGCCGGGCCAGAGTCCGAAGGCCCTGATCTACAG
CGCCTCGTACCGCTACTCGGGCGTGCCCGACCGGTTCACGGGCAGCGGCTCGGGGACGGACTTCACGCTGACCAT
CTCCTCGCTGCAGCCGGAGGACTTCGCCACCTACTTCTGCCAGCAGTACGACTCCTATCCCCTGACGTTCGGGGGA
GGGACCAAGCTCGAGATCAAGCGCACCGTCGCCGCCCCCTCCGTGTTCATCTTCCCGCCGAGCGACGAGCAGCTG
AAGAGCGGGACCGCCAGCGTGGTGTGCCTCCTCAACAACTTCTACCCGCGCGAGGCCAAGGTGCAGTGGAAGGT
GGACAACGCGCTGCAGAGCGGCAACTCCCAAGAGTCCGTGACCGAGCAGGACAGCAAGGATTCCACCTATTCGCT
GTCCTCCACCCTGACCCTCTCGAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTCACGCACCAGGG
TCTCAGCAGCCCCGTCACCAAGTCCTTCAATCGGGGCGAGTGCTGA

XENP13551 HC-Fab (XenD08503)

GAAGTCCAGCTCGTGGAGTCGGGTGGCGGCCTCGTCCAGCCCGGCGGCTCGCTCCGGCTGTCATGCGCCGCGAG
CGGGTTCACTTTCAGTTACTCGTGGATGAACTGGGTACGCCAGGCCCCGGGCAAGGGCCTCGAATGGGTCTCCGA
GATCAACCCGCAGAGCAGCACGATCAACTACGCCACCTCGGTGAAGGGCCGGTTCACGATCAGCCGCGACAACTC
CAAGAACACCCTCTACCTGCAGATGAACTCCCTGCGCGCCGAGGACACGGCCGTCTACTACTGCGCGCGCTACGG
AAACTGGTTCCCGTACTGGGGCCAGGGCACACTGGTCACTGTCTCCAGCGCGTCCACGAAGGGCCCGTCGGTCTT
CCCCCTGGCGCCAAGCTCGAAAAGTACGTCCGGCGGGACCGCAGCGCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAGCCCGTGACCGTGAGCTGGAACTCGGGCGCGCTGACCTCCGGCGTCCACACCTTCCCGGCAGTCCTCCAGTC
GTCGGGCCTGTACTCGCTGTCCAGCGTCGTCACGGTGCCGTCGTCCTCCCTGGGCACGCAGACGTACATCTGCAAC
GTGAACCACAAGCCGAGCGACACCAAGGTCGACAAGAAGGTCGAGCCCAAGTCGTGCGACAAGACCCACACGTG
CCCGCCGTGCCCGGCCCCCCCTGTCGCCGGCCCCAGTGTCTTCCTCTTCCCGCCGAAGCCGAAGGACACCCTCATG
ATCTCGCGCACCCCCGAGGTCACCTGCGTGGTCGTGGACGTGAAGCACGAGGACCCTGAGGTTAAGTTCAACTGG
TATGTCGACGGGGTGGAGGTCCACAACGCGAAGACCAAGCCGCGCGAGGAGGAGTACAACAGTACGTACCGCGT
GGTCTCGGTGCTCACCGTCCTCCACCAGGACTGGCTGAACGGCAAGGAATACAAGTGTAAGGTCAGCAACAAGGC
CTTGCCCGCCCCCATCGAGAAGACCATAAGCAAGGCCAAGGGTCAGCCAAGGGAACCGCAGGTGTACACCCTCCC
GCCCTCCCGCGAGGAGATGACCAAGAACCAGGTATCACTGACCTGCGACGTGTCCGGGTTCTACCCGTCCGACAT
CGCGGTGGAGTGGGAGTCCGACGGCCAGCCGGAGAACAACTACAAGACCACCCCCCCGGTACTCGACTCCGACG
GTTCGTTCTTCCTCTACTCCAAGCTGACGGTGGACAAGTCCCGGTGGGAGCAAGGCGACGTGTTCAGCTGTTCCGT
CATGCACGAGGCCCTGCACAACCACTACACCCAGAAGAGTCTGTCCCTCTCCCCTGGCAAATGA

Figure 23D

XENP13551 HC-scFv (XenD08438)

GAAGTCCAGCTCGTGGAGTCGGGCGGCGGCCTCGTGCAACCGGGTGGCTCGCTGCGGCTCTCCTGCGCCGCGTCC
GGCTTCACGTTCTCCACCTACGCCATGAACTGGGTCCGCCAGGCGCCGGGCAAGGGGCTCGAGTGGGTGGGGCG
TATCCGCTCCAAGTACAACAACTACGCGACGTACTACGCCGATAGCGTAAAGGGACGCTTCACAATCTCGCGGGA
CGACAGCAAGAACACCCTTTACCTCCAGATGAACAGCCTGCGCGCCGAAGACACCGCCGTGTACTACTGTGTCCG
GCACGGGAACTTCGGCGACTCCTACGTCTCGTGGTTCGCCTACTGGGGCCAGGGCACCCTCGTCACCGTGTCCTCG
GGAAAGCCGGGGAGCGGAAAGCCGGGTTCGGGCAAGCCAGGCTCCGGTAAGCCGGGCTCGCAGGCGGTGGTG
ACCCAGGAGCCATCCCTGACCGTGTCCCCGGGGGGCACCGTCACGCTGACTTGCGGCTCCTCGACCGGTGCCGTC
ACCACCTCCAACTACGCCAACTGGGTGCAGCAGAAGCCCGGCAAGAGCCCCCGCGGCCTGATCGGCGGCACGAA
CAAGCGCGCGCCCGGCGTCCCGGCCCGCTTCTCCGGCTCCCTGCTGGGCGGGAAGGCCGCGCTCACCATCAGCGG
CGCGCAGCCCGAGGACGAGGCCGACTACTACTGCGCGCTCTGGTACTCGAACCACTGGGTCTTCGGCGGCGGGA
CCAAGCTCACCGTGCTCGAGCCGAAGTCCTCGGACAAGACCCACACATGCCCCCCCTGCCCGGCCCCCCCCGTGGC
GGGCCCCTCTGTCTTCCTGTTTCCCCCGAAGCCGAAGGACACCCTGATGATCTCGCGCACGCCGGAAGTGACCTGC
GTCGTCGTCGACGTGAAGCACGAGGACCCAGAGGTCAAGTTCAACTGGTACGTCGACGGCGTCGAGGTGCACAA
CGCGAAGACGAAGCCCCGTGAGGAGCAGTACAACTCCACCTACCGGGTGGTGTCGGTGCTGACGGTGCTCCACC
AGGACTGGCTGAACGGCAAGGAGTACAAGTGTAAGGTCTCCAACAAGGCCCTCCCGGCCCCCATCGAGAAGACC
ATCTCGAAGGCCAAGGGCCAGCCGCGCGAGCCGCAGGTGTACACGCTCCCGCCCTCGCGGGAGCAGATGACCAA
GAACCAGGTGAAGCTGACCTGCCTCGTGAAGGGCTTCTACCCGAGCGACATCGCGGTGGAGTGGGAGTCCAACG
GCCAACCGGAGAACAACTACAAGACCACTCCGCCGGTGCTGGACTCGGATGGGTCGTTCTTCCTCTACTCGAAGCT
CACGGTAGACAAGTCCCGCTGGCAGCAGGGCAACGTCTTCTCCTGCTCCGTCATGCACGAGGCCCTCCACAACCAC
TATACCCAGAAGTCGCTCTCGCTCTCCCCGGGAAAGTGA

XENP13551 LC (XenD07821)

GACATCGTCATGACGCAGTCGCCGAGCAGCCTCTCCGCATCGGTGGGTGACCGCGTCACCATCACCTGCCGGGCG
AGCCAGAACGTCGACACCTGGGTGGCCTGGTATCAGCAGAAGCCGGGCCAGAGTCCGAAGGCCCTGATCTACAG
CGCCTCGTACCGCTACTCGGGCGTGCCCGACCGGTTCACGGGCAGCGGCTCGGGGACGGACTTCACGCTGACCAT
CTCCTCGCTGCAGCCGGAGGACTTCGCCACCTACTTCTGCCAGCAGTACGACTCCTATCCCCTGACGTTCGGGGGA
GGGACCAAGCTCGAGATCAAGCGCACCGTCGCCGCCCCCTCCGTGTTCATCTTCCCGCCGAGCGACGAGCAGCTG
AAGAGCGGGACCGCCAGCGTGGTGTGCCTCCTCAACAACTTCTACCCGCGCGAGGCCAAGGTGCAGTGGAAGGT
GGACAACGCGCTGCAGAGCGGCAACTCCCAAGAGTCCGTGACCGAGCAGGACAGCAAGGATTCCACCTATTCGCT
GTCCTCCACCCTGACCCTCTCGAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAGGTCACGCACCAGGG
TCTCAGCAGCCCCGTCACCAAGTCCTTCAATCGGGGCGAGTGCTGA

Figure 24

XENP	Pool ID#	HC-Fab	HC-scFv	LC	HC-Fab : HC-scFv : LC Ratio
13243	43A	1	0.667	1.5	1 : 0.667 : 1.5
	43B	1	1	1.5	1 : 1 : 1.5
	43C	1	1.5	1.5	1 : 1.5 : 1.5
	43D	1	2	1.5	1 : 2 : 1.5
	43E	1	0.667	2	1 : 0.667 : 2
	43F	1	1	2	1 : 1 : 2
	43G	1	1.5	2	1 : 1.5 : 2
	43H	1	2	2	1 : 2 : 2

XENP	Pool ID#	HC-Fab	HC-scFv	LC	HC-Fab : HC-scFv : LC Ratio
13551	51A	1	0.667	1.5	1 : 0.667 : 1.5
	51B	1	1	1.5	1 : 1 : 1.5
	51C	1	1.5	1.5	1 : 1.5 : 1.5
	51D	1	2	1.5	1 : 2 : 1.5
	51E	1	0.667	2	1 : 0.667 : 2
	51F	1	1	2	1 : 1 : 2
	51G	1	1.5	2	1 : 1.5 : 2
	51H	1	2	2	1 : 2 : 2

Figure 25A

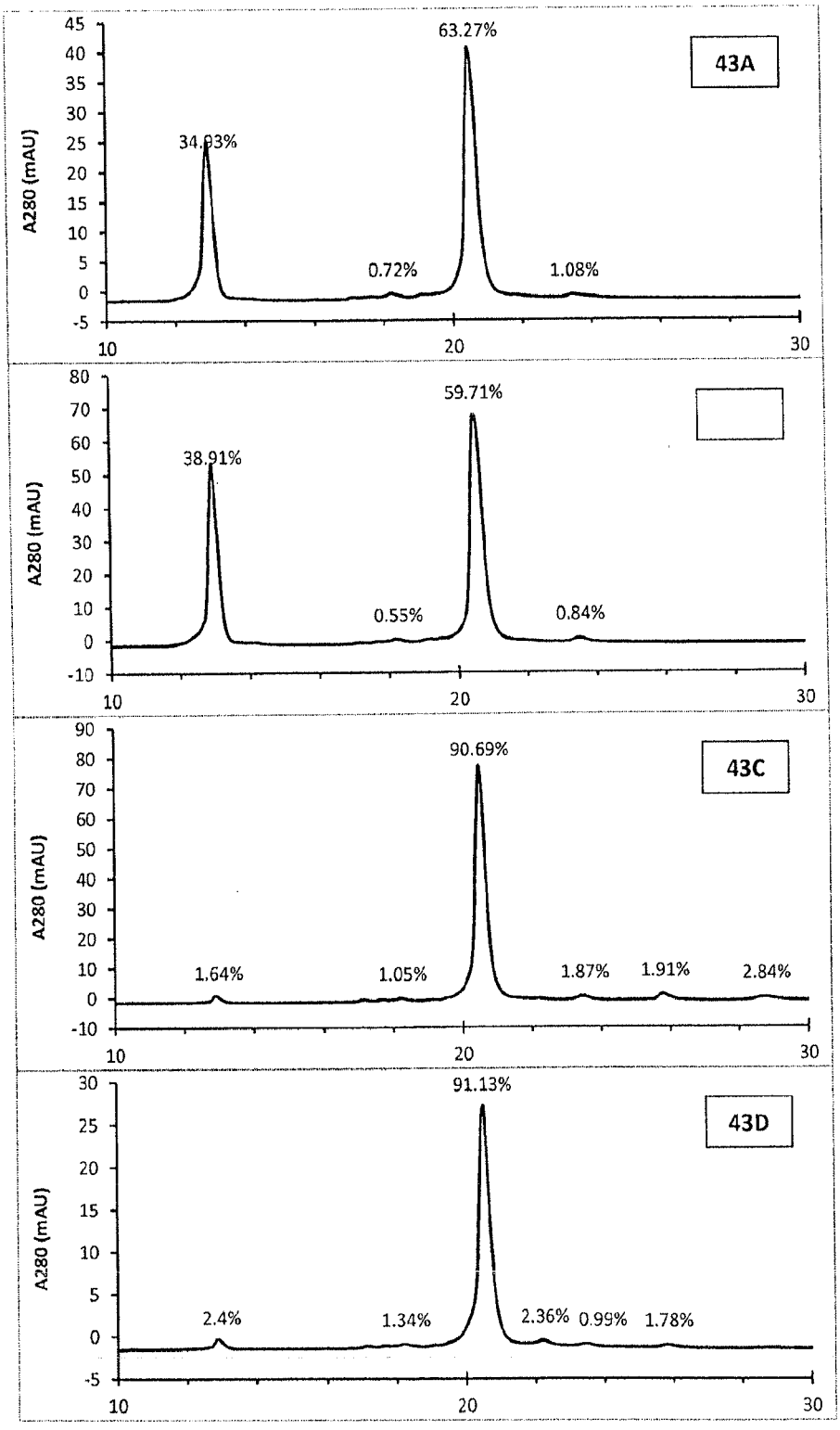

43A
A280 (mAU)
63.27%
34.93%
0.72%
1.08%
59.71%
38.91%
0.55%
0.84%
43C
90.69%
1.64%
1.05%
1.87%
1.91%
2.84%
43D
91.13%
2.4%
1.34%
2.36%
0.99%
1.78%

Figure 25B

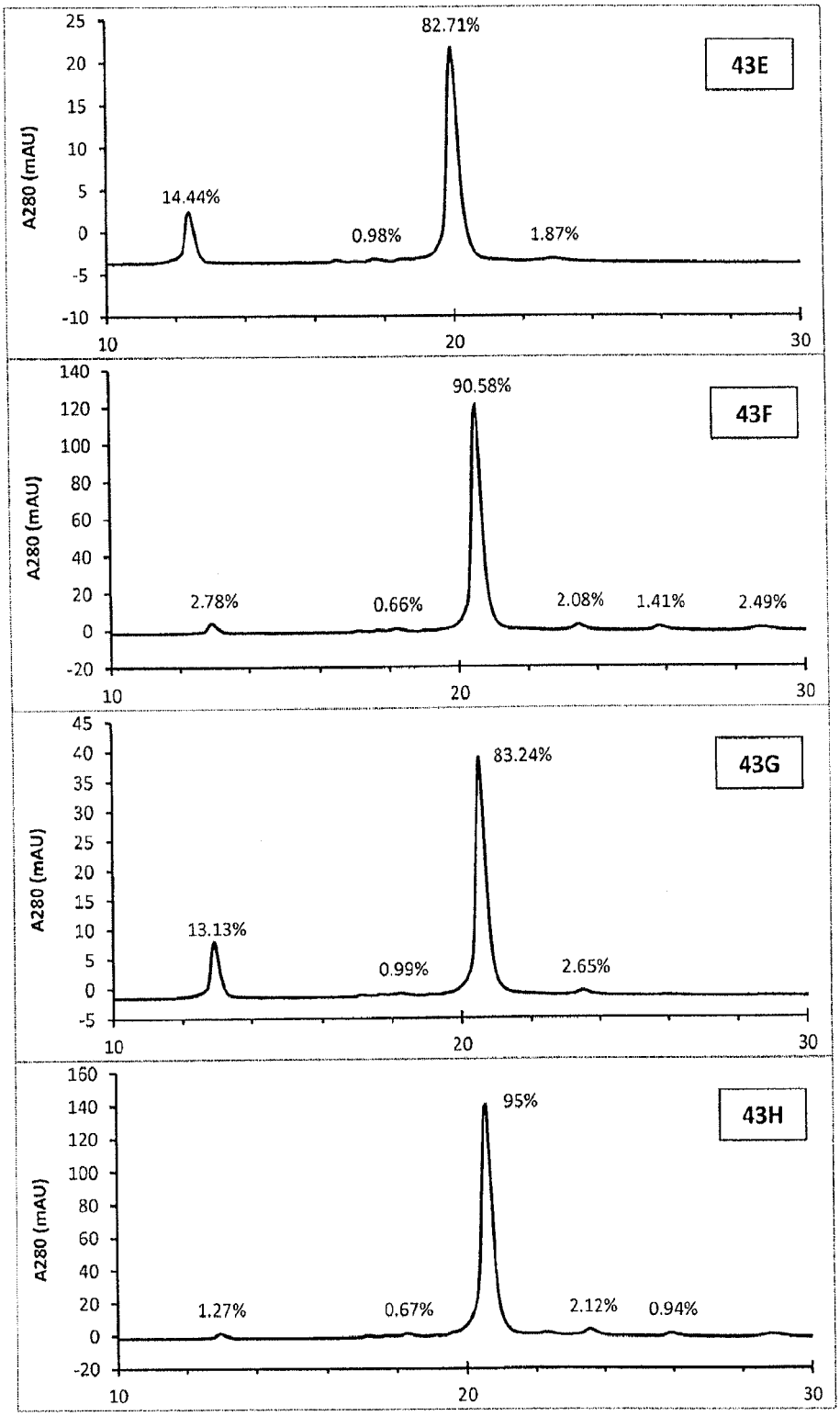

43E
A280 (mAU)
82.71%
14.44%
0.98%
1.87%
43F
90.58%
2.78%
0.66%
2.08%
1.41%
2.49%
43G
83.24%
13.13%
0.99%
2.65%
43H
95%
1.27%
0.67%
2.12%
0.94%

Figure 25C

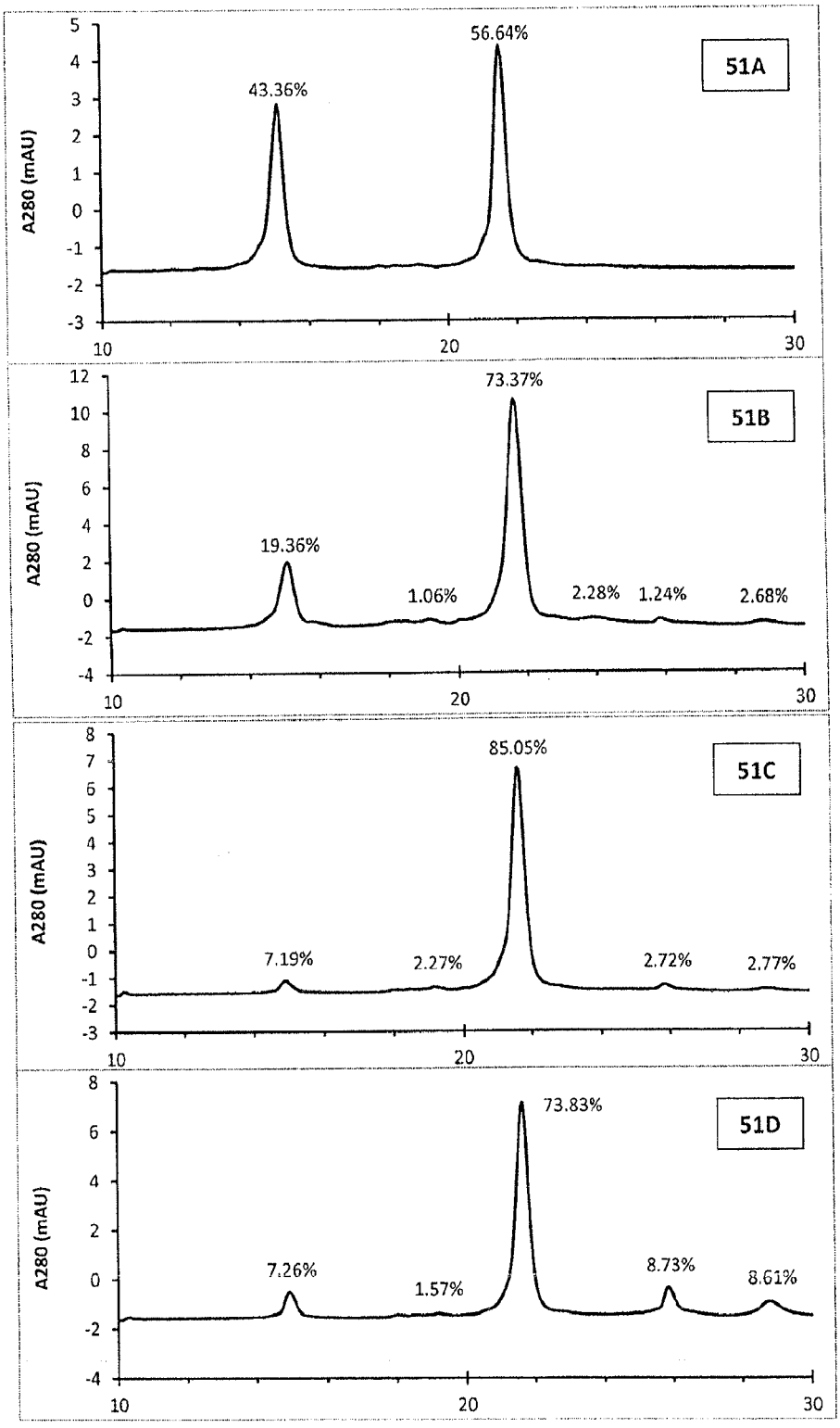

51A
A280 (mAU)
43.36%
56.64%
51B
A280 (mAU)
19.36%
1.06%
73.37%
2.28%
1.24%
2.68%
51C
A280 (mAU)
7.19%
2.27%
85.05%
2.72%
2.77%
51D
A280 (mAU)
7.26%
1.57%
73.83%
8.73%
8.61%

Figure 25D

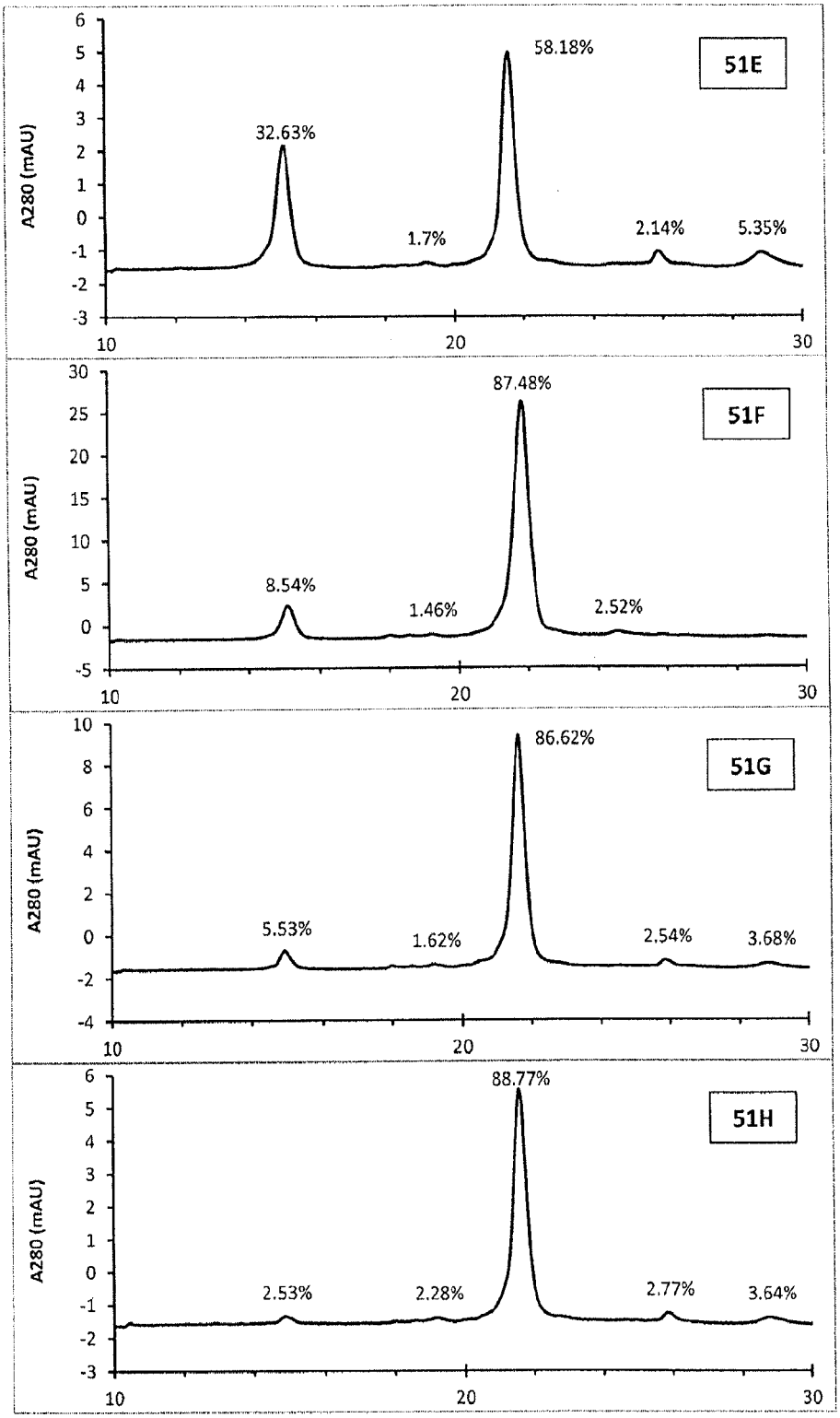

51E
A280 (mAU)
32.63%
1.7%
58.18%
2.14%
5.35%
51F
A280 (mAU)
8.54%
1.46%
87.48%
2.52%
51G
A280 (mAU)
5.53%
1.62%
86.62%
2.54%
3.68%
51H
A280 (mAU)
2.53%
2.28%
88.77%
2.77%
3.64%
10
20
30

Figure 26

XENP	Pool ID#	HC-Fab : HC-scFv : LC Ratio	% HC-Fab Homodimer plus Monomer	% Heterodimer	% HC-scFv Homodimer plus Monomer
13243	43A	1 : 0.667 : 1.5	34.93	65.07	-
	43B	1 : 1 : 1.5	38.91	61.09	-
	43C	1 : 1.5 : 1.5	1.64	93.61	4.75
	43D	1 : 2 : 1.5	2.40	94.83	2.77
	43E	1 : 0.667 : 2	14.44	85.56	-
	43F	1 : 1 : 2	2.78	93.32	3.90
	43G	1 : 1.5 : 2	13.13	86.67	-
	43H	1 : 2 : 2	1.27	95.00	3.06

XENP	Pool ID#	HC-Fab : HC-scFv : LC Ratio	% HC-Fab Homodimer plus Monomer	% Heterodimer	% HC-scFv Homodimer plus Monomer
13551	51A	1 : 0.667 : 1.5	43.36	56.64	-
	51B	1 : 1 : 1.5	19.36	76.72	3.92
	51C	1 : 1.5 : 1.5	7.19	87.32	5.49
	51D	1 : 2 : 1.5	7.26	75.40	17.33
	51E	1 : 0.667 : 2	32.63	59.88	7.49
	51F	1 : 1 : 2	8.54	91.46	-
	51G	1 : 1.5 : 2	5.53	88.24	6.23
	51H	1 : 2 : 2	2.53	91.06	6.41

Figure 27

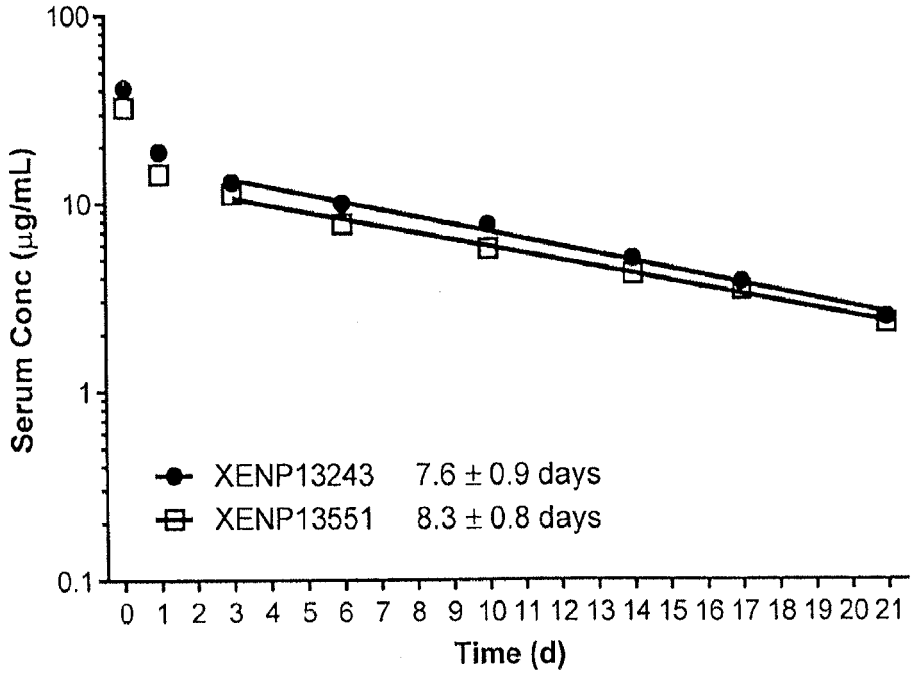

100
10
1
0.1
Serum Conc (μg/mL)
XENP13243 7.6 ± 0.9 days
XENP13551 8.3 ± 0.8 days
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
Time (d)

Figure 28

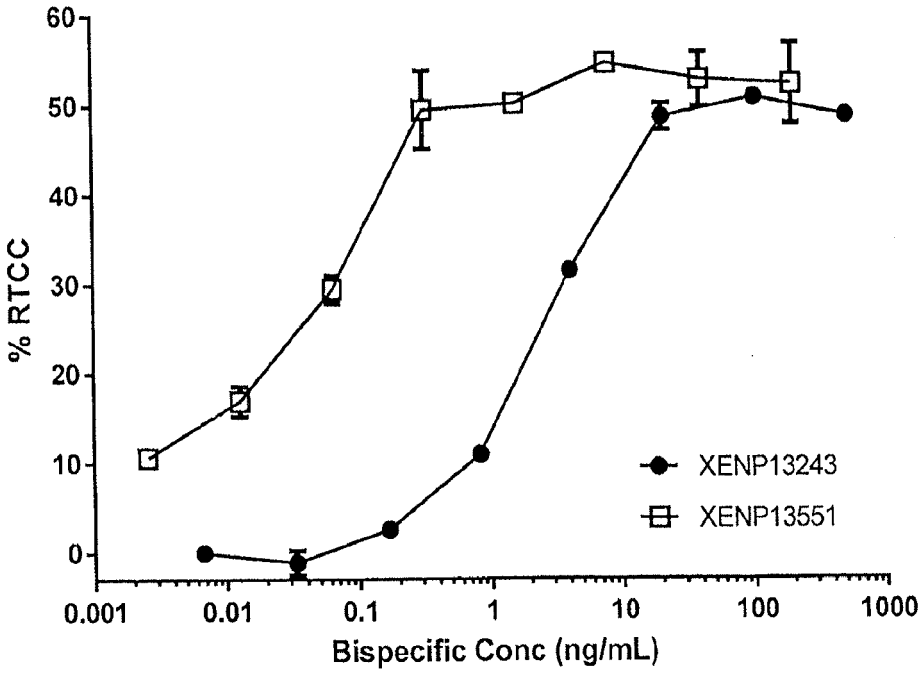

60
50
40
30
20
10
0
% RTCC
0.001
0.01
0.1
1
10
100
1000
Bispecific Conc (ng/mL)
XENP13243
XENP13551

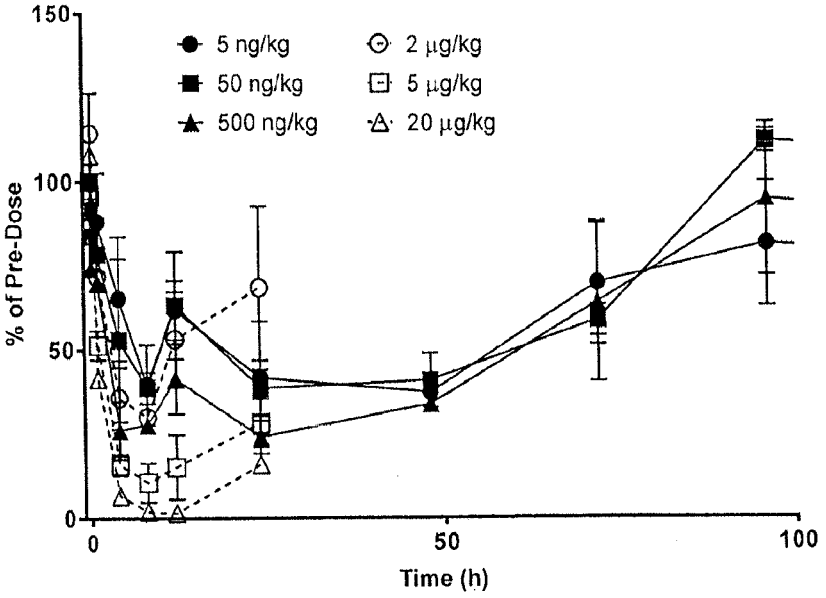
Figure 29

Variant	Antigen	ka (1/M*s)	kd (1/s)	KA (1/M)	KD (M)	Format
XENP13243	human CD38	1.57E+05	8.88E-03	1.77E+07	5.66E-08	Protein A capture[1]
XENP13243	human CD38	5.41E+05	9.07E-03	5.97E+07	1.68E-08	Antigen directly coupled[2]
XENP13243	human CD3	6.25E+05	5.07E-03	1.23E+08	8.10E-09	Protein A capture[1]
XENP13243	cyno CD38	6.23E+05	1.01E-02	6.17E+07	1.62E-08	Antigen directly coupled[2]
XENP13243	cyno CD3	7.58E+05	4.29E-03	1.77E+08	5.65E-09	Protein A capture[1]
XENP13551	human CD38	1.03E+05	2.06E-04	5.00E+08	2.00E-09	Protein A capture[1]
XENP13551	human CD38	1.01E+06	1.98E-04	5.12E+09	1.95E-10	Antigen directly coupled[2]
XENP13551	cyno CD38	1.50E+06	4.17E-04	3.61E+09	2.77E-10	Antigen directly coupled[2]

[1]Protein A capture: Bispecific protein is captured by a protein A chip, followed by soluble antigen.

[2]Antigen directly coupled: Antigen is covalently coupled to the chip surface, bispecific protein follows.

Figure 30


150
100
50
0
% of Pre-Dose
5 ng/kg
50 ng/kg
500 ng/kg
2 µg/kg
5 µg/kg
20 µg/kg
0
50
100
Time (h)

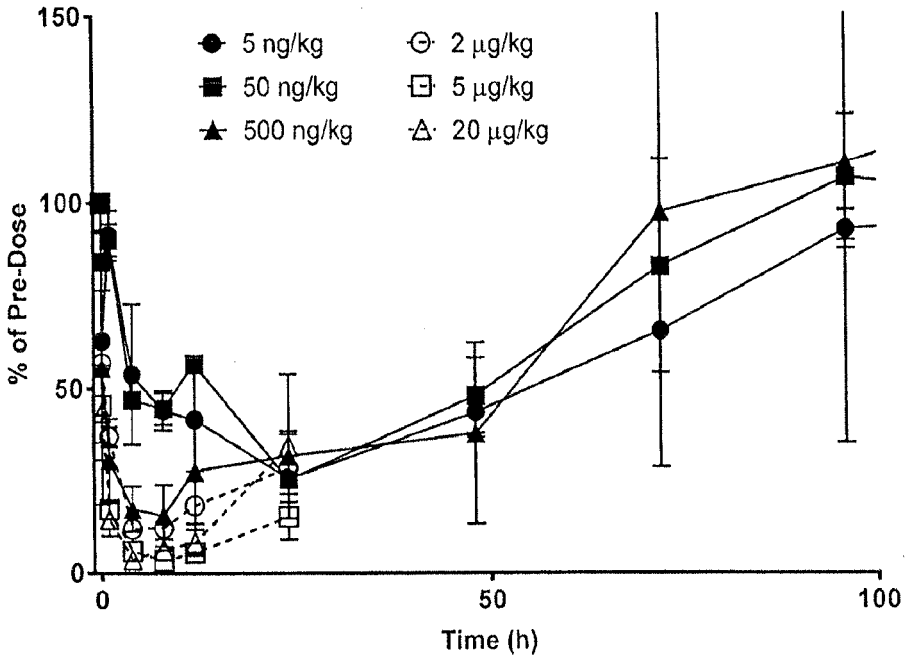

150
100
50
0
% of Pre-Dose
5 ng/kg
50 ng/kg
500 ng/kg
2 µg/kg
5 µg/kg
20 µg/kg
0
50
100
Time (h)

Figure 31

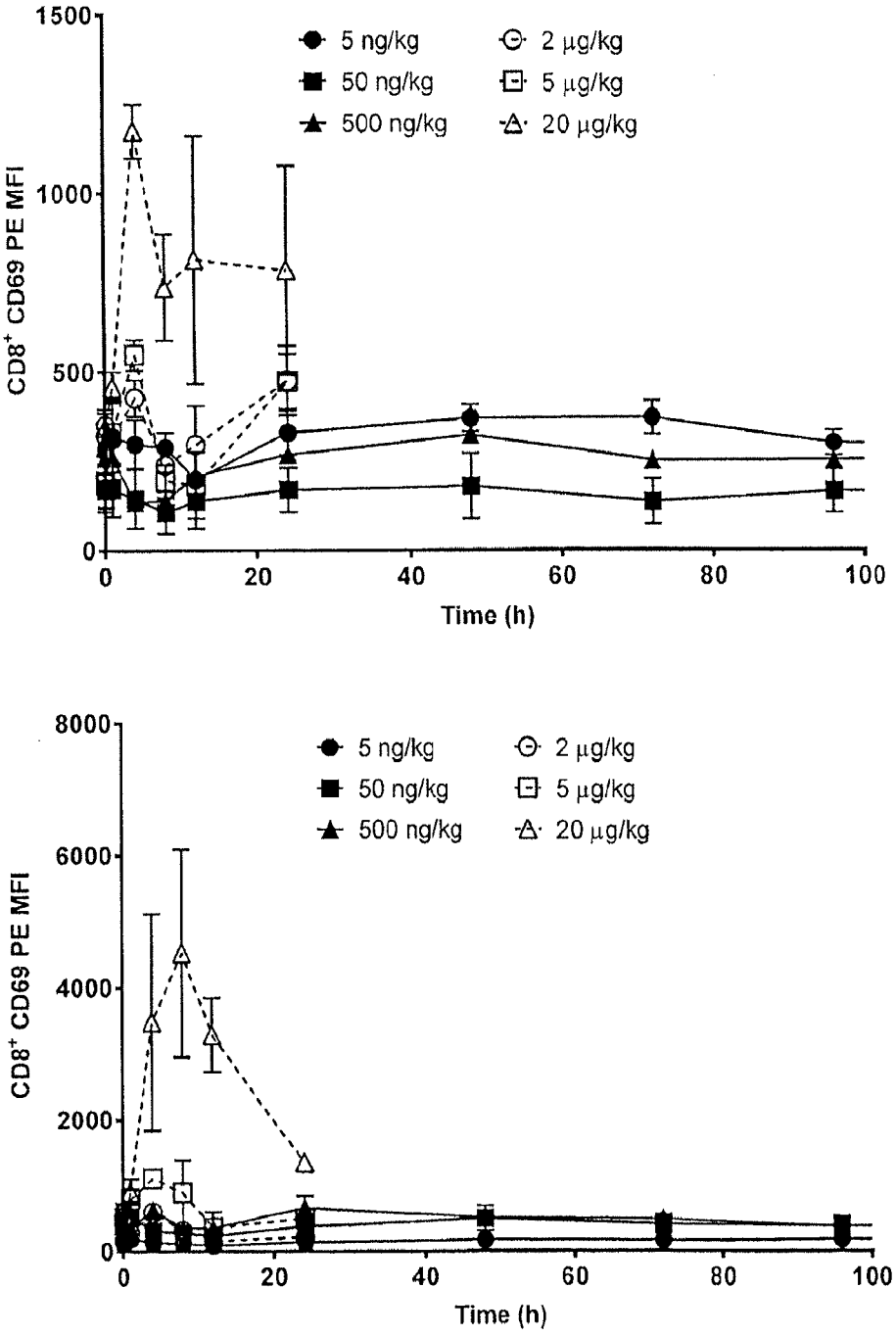

1500
1000
500
0
CD8+ CD69 PE MFI
5 ng/kg
50 ng/kg
500 ng/kg
2 µg/kg
5 µg/kg
20 µg/kg
0
20
40
60
80
100
Time (h)
8000
6000
4000
2000
0
CD8+ CD69 PE MFI
5 ng/kg
50 ng/kg
500 ng/kg
2 µg/kg
5 µg/kg
20 µg/kg
0
20
40
60
80
100
Time (h)

Figure 32

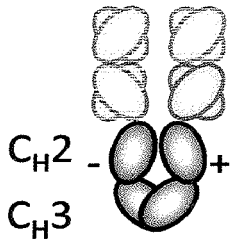
Variant constant region	Substitutions
pI_ISO(-)	I199T N203D K274Q R355Q N384S K392N V397M Q419E DEL447
pI_(-)_isosteric_A	N208D Q295E N384D Q418E N421D
pI_(-)_isosteric_B	N208D Q295E Q418E N421D
pI_ISO(+RR)	Q196K I199T P217R P228R N276K
pI_ISO(+)	Q196K I199T N276K
pI_(+)_isosteric_A	E269Q E272Q E283Q E357Q
pI_(+)_isosteric_B	E269Q E272Q E283Q
pI_(+)_isosteric_E269Q/E272Q	E269Q E272Q
pI_(+)_isosteric_E269Q/E283Q	E269Q E283Q
pI_(+)_isosteric_E272Q/E283Q	E272Q E283Q
pI_(+)_isosteric_E269Q	E269Q

Figure 33

XENP	Variant	Linker Sequence	SEQ ID NO	Length	Charge	Tm1 (°C)
12241	CD3_H1.30_L1.47_scFv_His	GGGGSGGGGSGGGGS	441	15	0	68.0
12782	CD3_H1.30_L1.47_scFv_His_scFvLinker(+A)	IRPRAIGGSKPRVA	443	14	+4	66.0
12783	CD3_H1.30_L1.47_scFv_His_scFvLinker(+B)	GKGGSGKGGSGKGGS	444	15	+3	68.0
12784	CD3_H1.30_L1.47_scFv_His_scFvLinker(+C)	GGKGSGGKGSGGKGS	445	15	+3	68.0
12785	CD3_H1.30_L1.47_scFv_His_scFvLinker(+D)	GGGKSGGGKSGGGKS	446	15	+3	68.5
12786	CD3_H1.30_L1.47_scFv_His_scFvLinker(+E)	GKGKSGKGKSGKGKS	447	15	+6	68.5
12787	CD3_H1.30_L1.47_scFv_His_scFvLinker(+F)	GGGKSGGKGSGKGGS	448	15	+3	68.0
12788	CD3_H1.30_L1.47_scFv_His_scFvLinker(+G)	GKPGSGKPGSGKPGS	449	15	+3	68.0
12789	CD3_H1.30_L1.47_scFv_His_scFvLinker(+H)	GKPGSGKPGSGKPGSGKPGS	450	20	+4	69.0
12790	CD3_H1.30_L1.47_scFv_His_scFvLinker(+I)	GKGKSGKGKSGKGKSGKGKS	451	20	+8	69.5

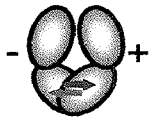
Figure 34

1) Engineered Fc for bispecific separation



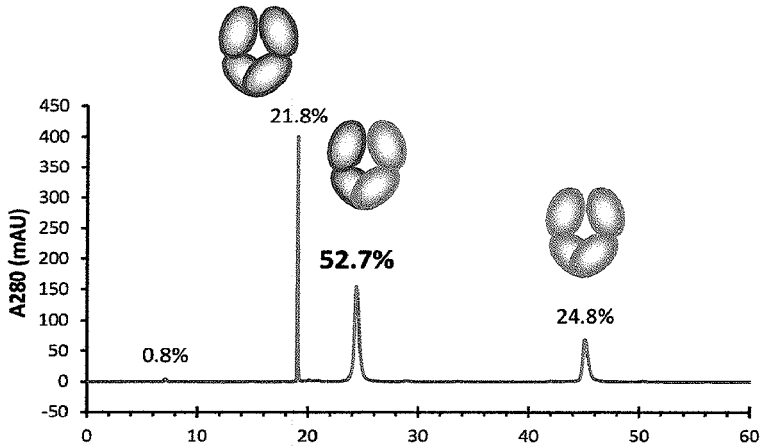
IgG1
(ΔpI engineered)

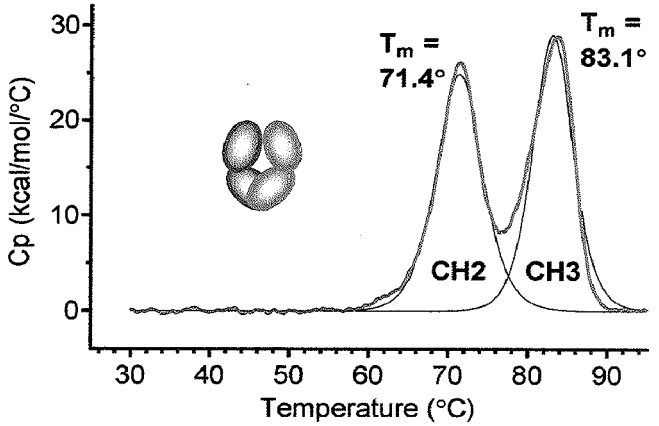
2) Engineered Fc for bispecific assembly



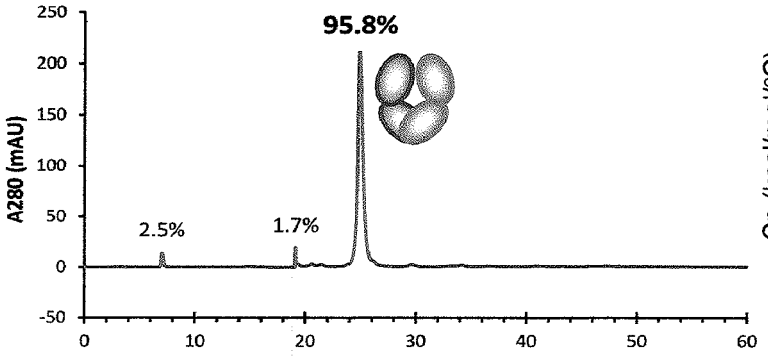
2 + 2
substitutions

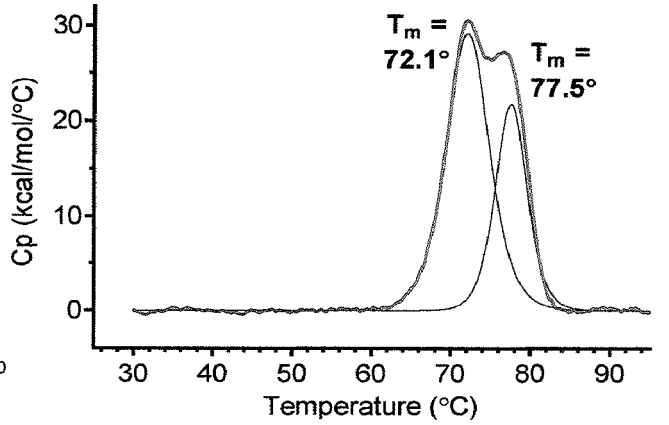
Step 1: ΔpI Fc domains simplify bispecific purification by IEX





Step 2: CH3 substitutions drive efficient bispecific assembly





After Protein A column

Figure 35

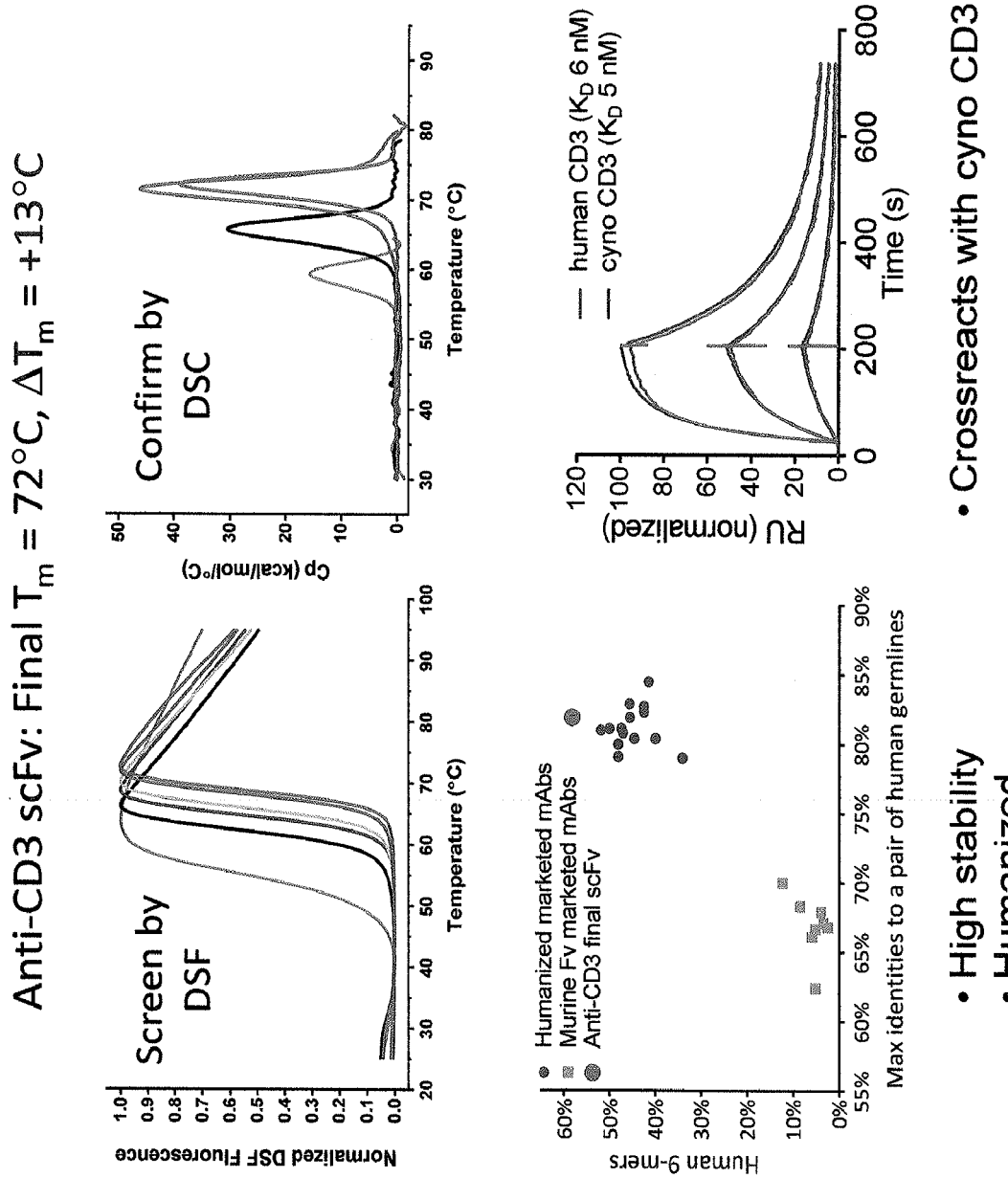

Anti-CD3 scFv: Final T_m = 72°C, ΔT_m = +13°C
Screen by DSF
Normalized DSF Fluorescence
Temperature (°C)
Confirm by DSC
Cp (kcal/mol/°C)
Temperature (°C)
Humanized marketed mAbs
Murine Fv marketed mAbs
Anti-CD3 final scFv
Human 9-mers
Max identities to a pair of human germlines
human CD3 (K_D 6 nM)
cyno CD3 (K_D 5 nM)
RU (normalized)
Time (s)
• High stability
• Humanized
• Crossreacts with cyno CD3

Figure 36

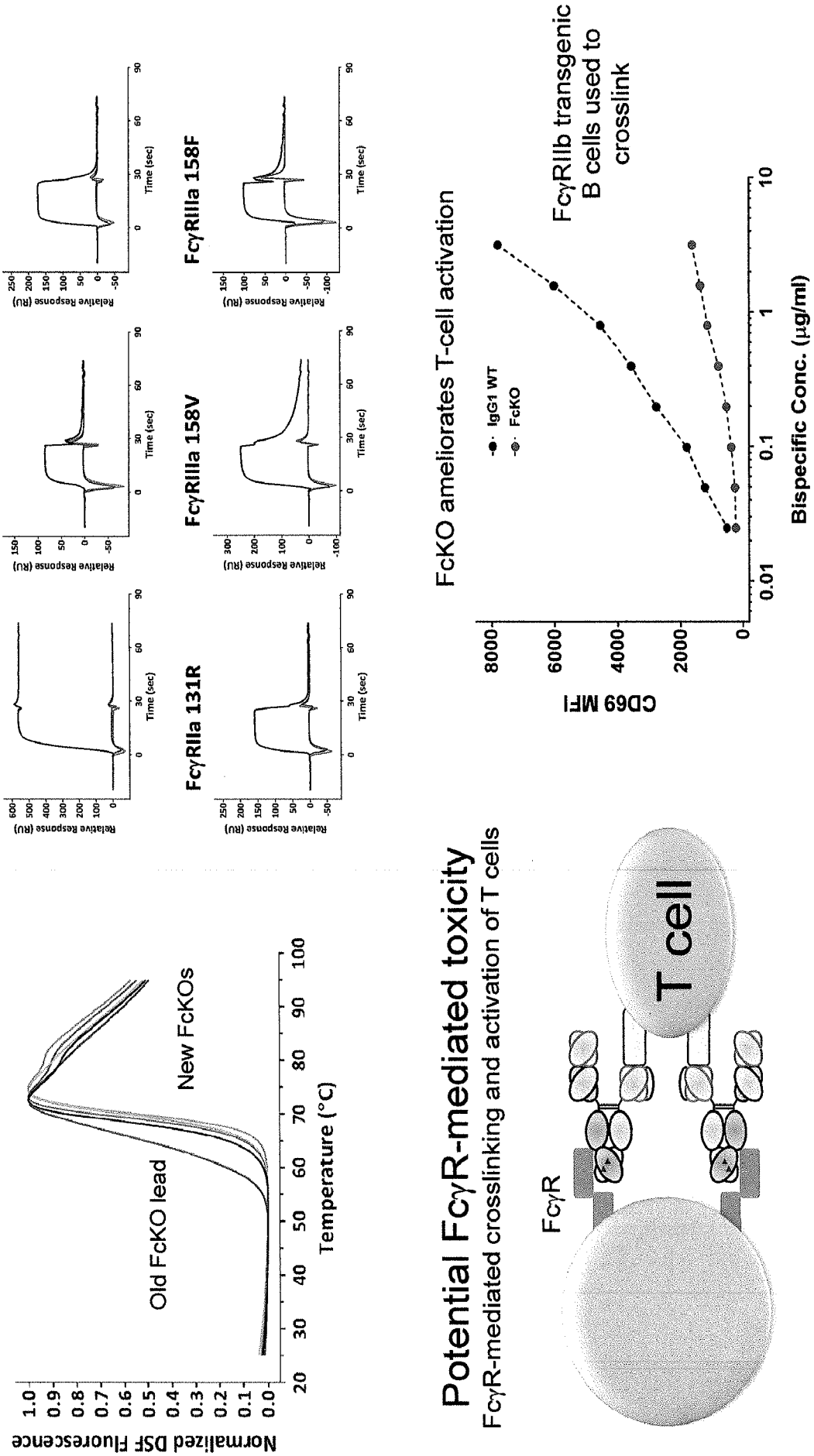

FcγRIIa 131H
FcγRIIb
FcγRIIIa 158F
FcγRI
FcγRIIIa 158V
FcγRIIa 131R
Relative Response (RU)
Time (sec)
Normalized DSF Fluorescence
Temperature (°C)
Old FcKO lead
New FcKOs
FcKO ameliorates T-cell activation
IgG1 WT
FcKO
CD69 MFI
Bispecific Conc. (μg/ml)
FcγRIIb transgenic B cells used to crosslink
Potential FcγR-mediated toxicity
FcγR-mediated crosslinking and activation of T cells
FcγR
T cell

Figure 37

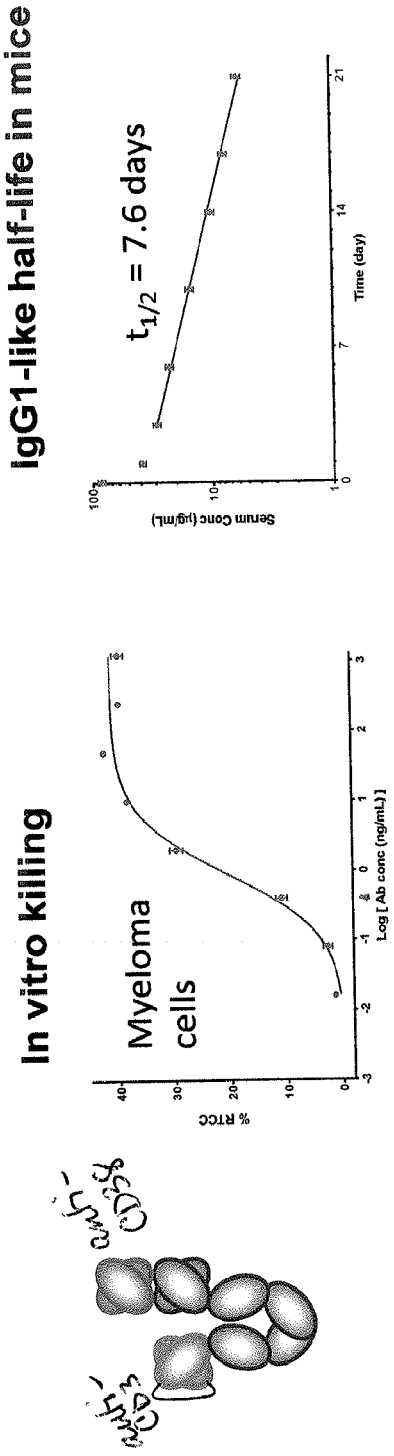
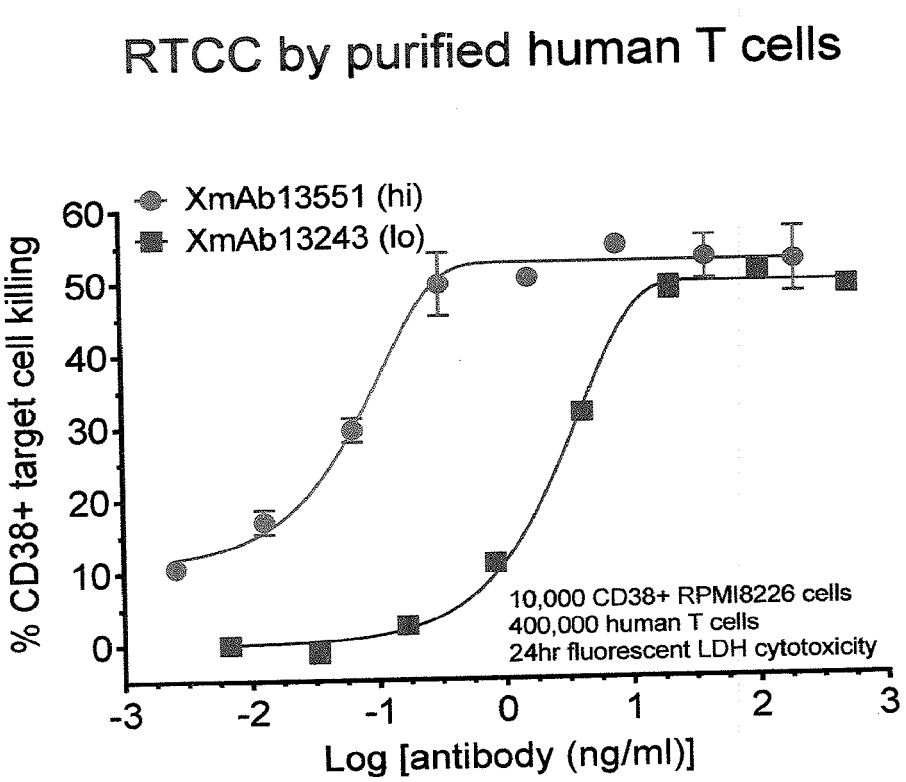
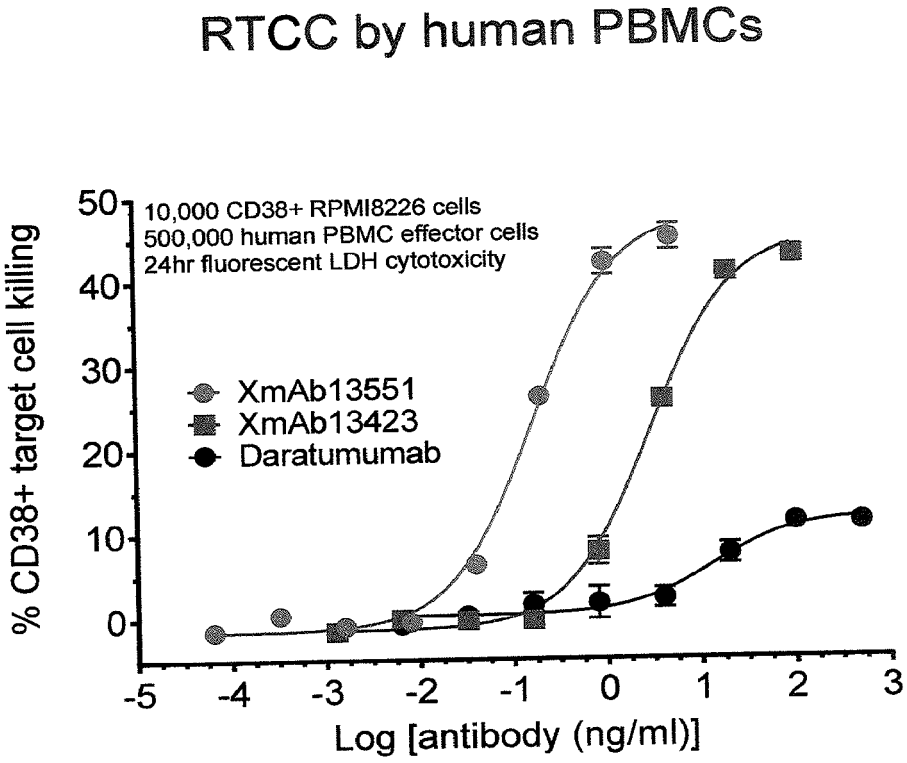

IgG1-like half-life in mice
$t_{1/2}$ = 7.6 days
Serum Conc (µg/mL)
Time (day)
In vitro killing
Myeloma cells
% RTCC
Log [Ab conc (ng/mL)]

Figure 38





K_D	Human CD38	Cyno CD38	Human CD3	Cyno CD3
XmAb13243	16.8 nM	16.2 nM	5 nM	5 nM
XmAb13551	0.20 nM	0.28 nM	4 nM	2 nM

Biacore, Ag coupled

Figure 39

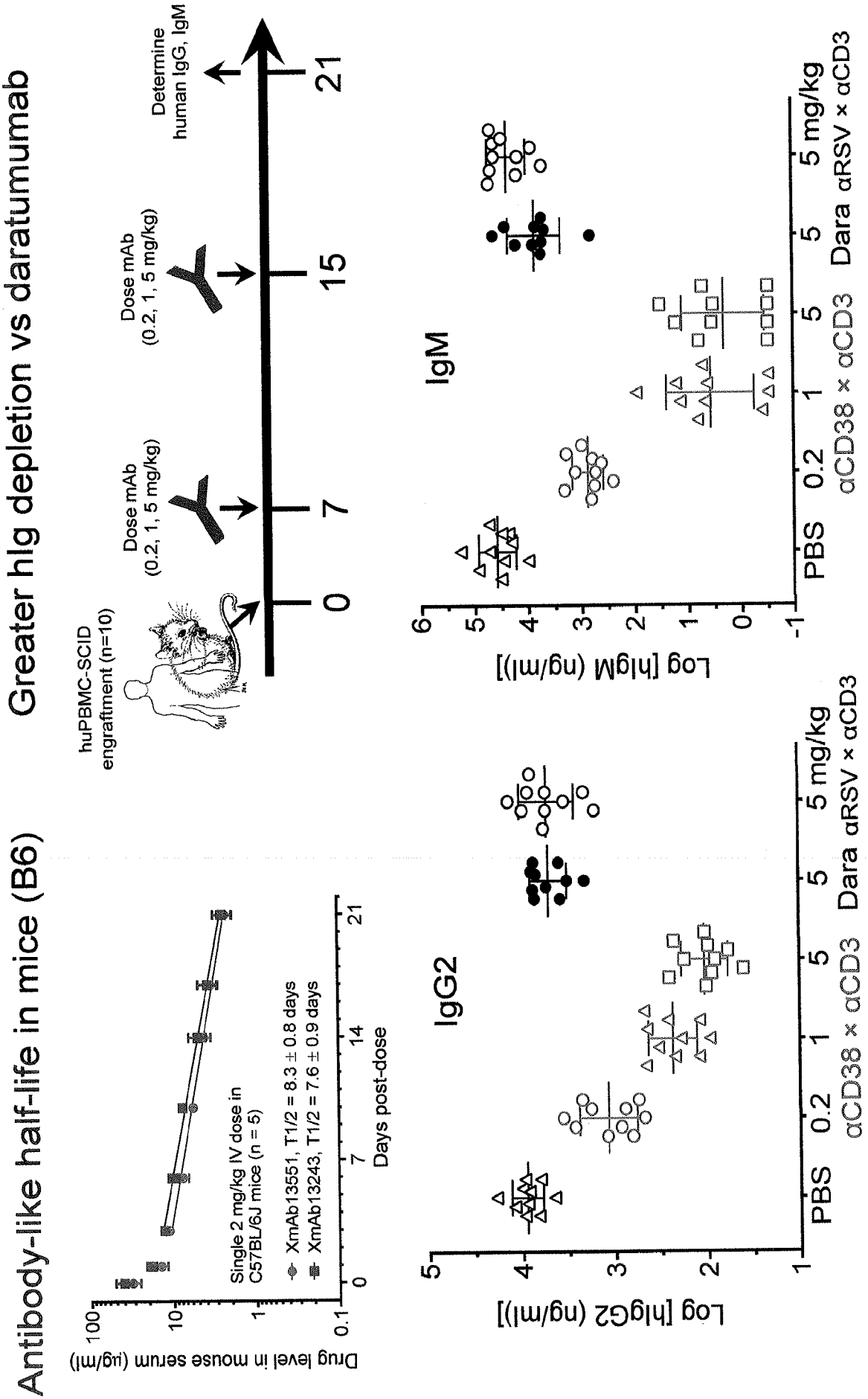

Antibody-like half-life in mice (B6)
Drug level in mouse serum (µg/ml)
100
10
1
0.1
0
7
14
21
Days post-dose
Single 2 mg/kg IV dose in C57BL/6J mice (n = 5)
XmAb13551, T1/2 = 8.3 ± 0.8 days
XmAb13243, T1/2 = 7.6 ± 0.9 days
Greater hIg depletion vs daratumumab
huPBMC-SCID engraftment (n=10)
Dose mAb (0.2, 1, 5 mg/kg)
Dose mAb (0.2, 1, 5 mg/kg)
Determine human IgG, IgM
0
7
15
21
IgG2
Log [hIgG2 (ng/ml)]
PBS
0.2
1
5
5 mg/kg
αCD38 × αCD3
Dara αRSV × αCD3
IgM
Log [hIgM (ng/ml)]

Figure 40

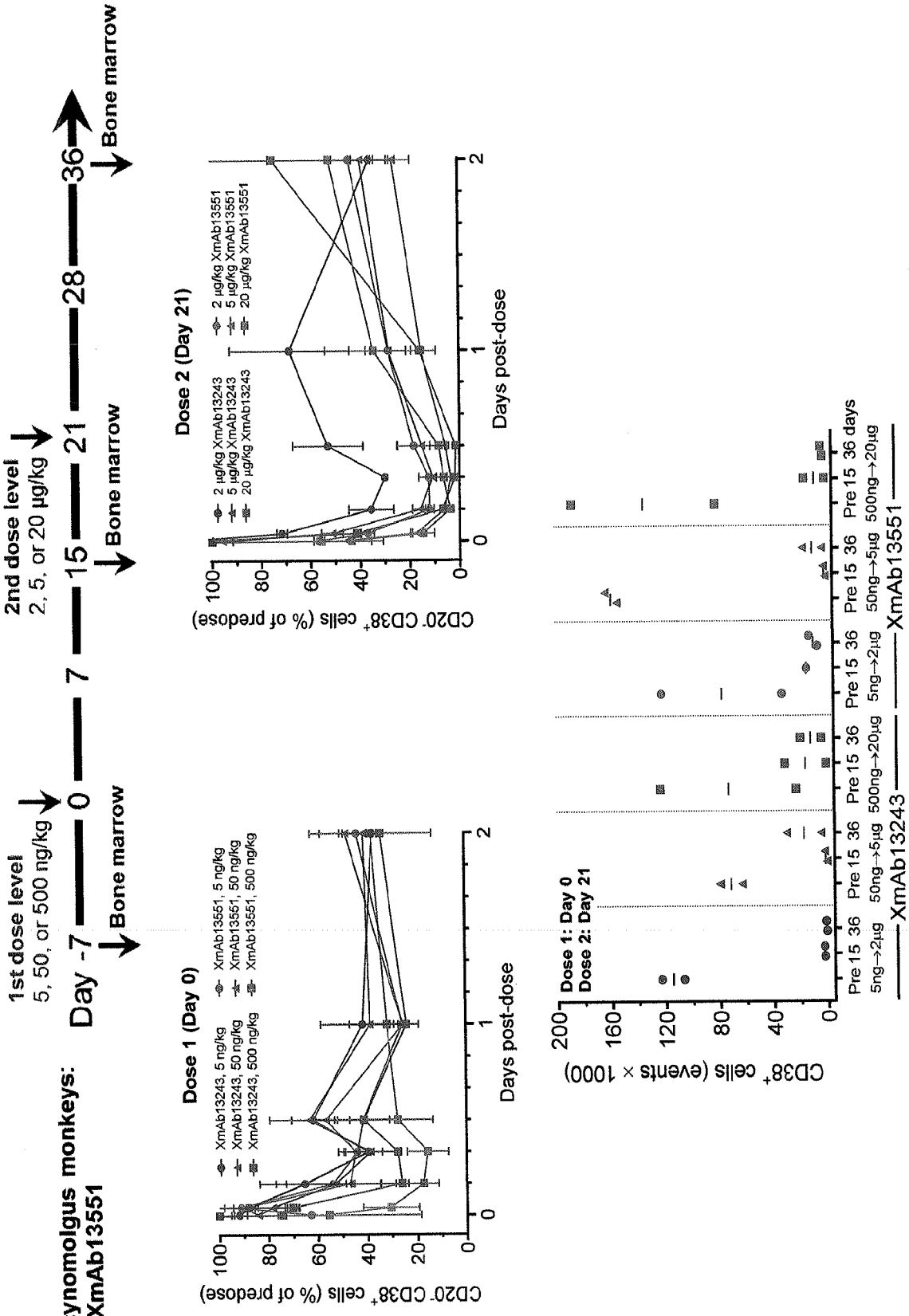

3 groups of 3 cynomolgus monkeys:
XmAb13243 & XmAb13551
Day -7
0
7
15
21
28
36
1st dose level
5, 50, or 500 ng/kg
2nd dose level
2, 5, or 20 µg/kg
Bone marrow
Bone marrow
Bone marrow
Dose 1 (Day 0)
XmAb13243, 5 ng/kg
XmAb13243, 50 ng/kg
XmAb13243, 500 ng/kg
XmAb13551, 5 ng/kg
XmAb13551, 50 ng/kg
XmAb13551, 500 ng/kg
CD20- CD38+ cells (% of predose)
Days post-dose
Dose 2 (Day 21)
2 µg/kg XmAb13243
5 µg/kg XmAb13243
20 µg/kg XmAb13243
2 µg/kg XmAb13551
5 µg/kg XmAb13551
20 µg/kg XmAb13551
CD20- CD38+ cells (% of predose)
Days post-dose
Dose 1: Day 0
Dose 2: Day 21
CD38+ cells (events × 1000)
Pre 15 36 Pre 15 36 Pre 15 36 Pre 15 36 Pre 15 36 Pre 15 36 days
5ng→2µg 50ng→5µg 500ng→20µg 5ng→2µg 50ng→5µg 500ng→20µg
XmAb13243
XmAb13551

Figure 41

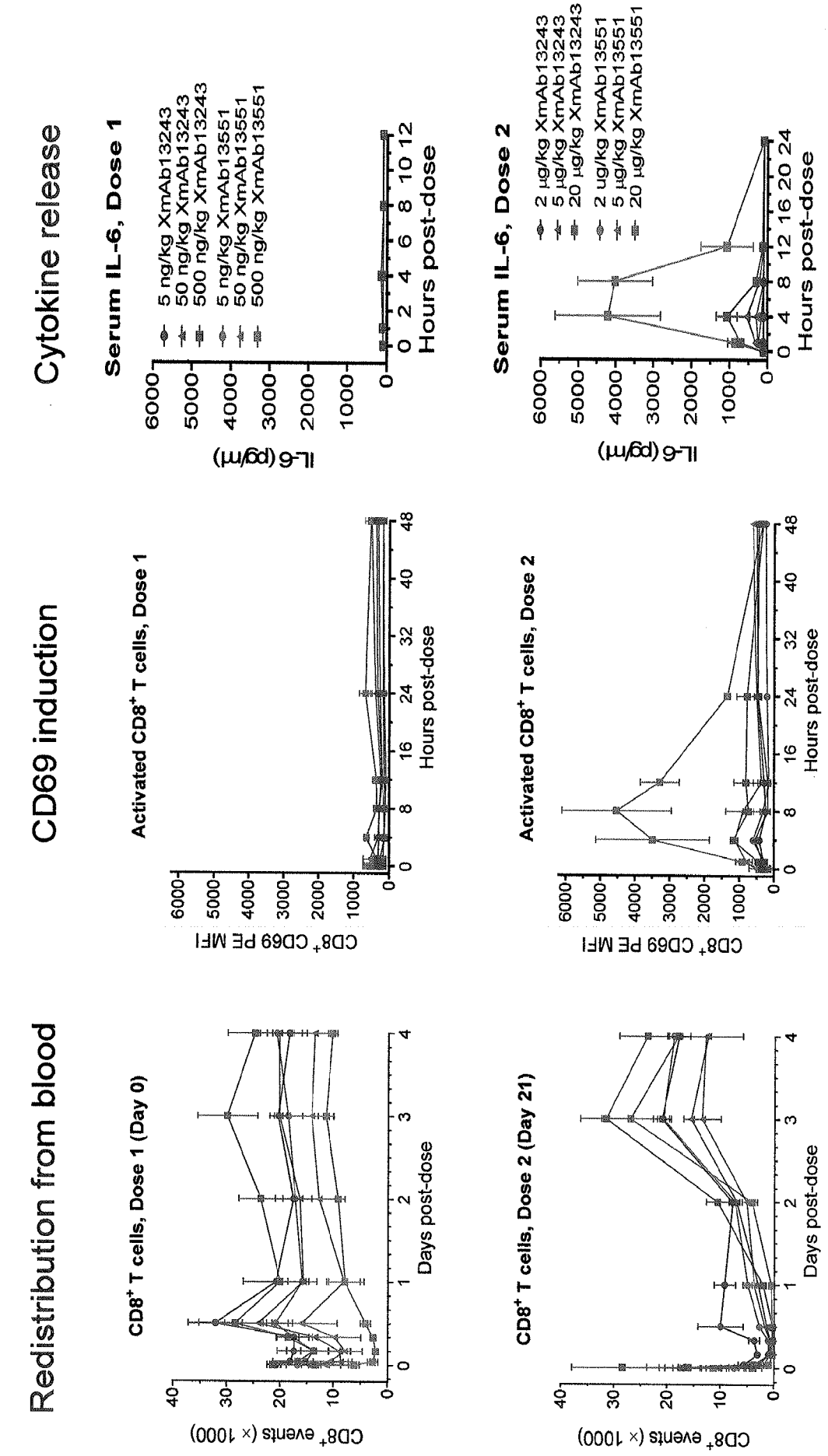
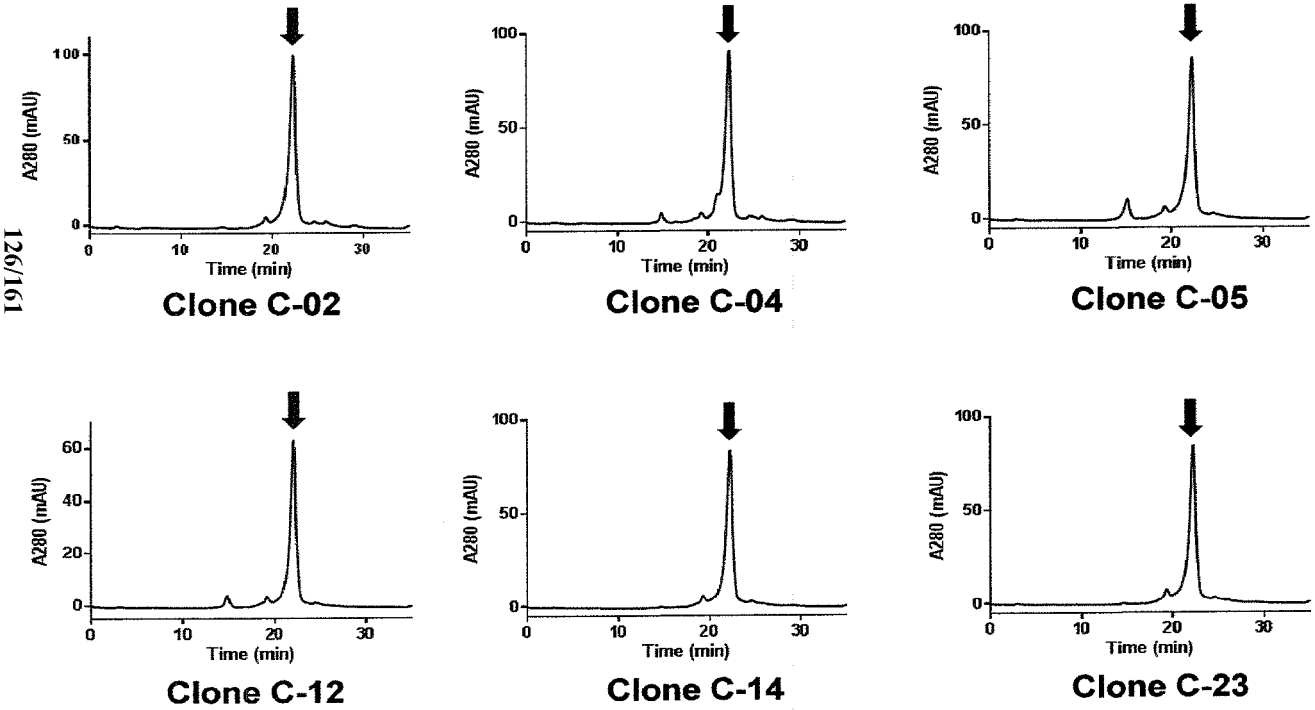

Redistribution from blood
CD69 induction
Cytokine release
1st Dose Level
2nd Dose Level
CD8+ T cells, Dose 1 (Day 0)
CD8+ T cells, Dose 2 (Day 21)
CD8+ events (× 1000)
Days post-dose
Activated CD8+ T cells, Dose 1
Activated CD8+ T cells, Dose 2
CD8+ CD69 PE MFI
Hours post-dose
Serum IL-6, Dose 1
Serum IL-6, Dose 2
IL-6 (pg/ml)
5 ng/kg XmAb13243
50 ng/kg XmAb13243
500 ng/kg XmAb13243
5 ng/kg XmAb13551
50 ng/kg XmAb13551
500 ng/kg XmAb13551
2 µg/kg XmAb13243
5 µg/kg XmAb13243
20 µg/kg XmAb13243
2 ug/kg XmAb13551
5 µg/kg XmAb13551
20 µg/kg XmAb13551

Figure 42

Stable Cell Clones (Stage 1) – Top Individual clones from Pool C

Analytical IEX profiles of protein A purified product (⬇ - Heterodimer)



Clone	Heterodimer (%)	Yield (mg/L)
C-02	94.7	1498
C-04	95.3	1381
C-05	90.1	1508
C-12	93.8	1061
C-14	97.9	1459
C-23	97.4	1241

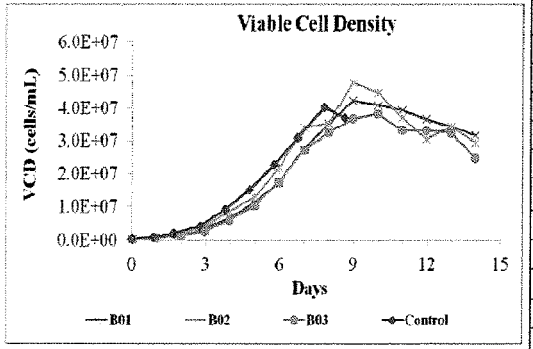
Clones 02, 12, 14 and 23 are in final stages (SCC2) of cell line development

Figure 43

3L Bioreactor Optimization (3 conditions)

BalanCD medium with ActiCHO Feed A & B (varying schedule and percentage), Glucose supplementation, pH set point, Temp shift

Yield & Product Profile (Heterodimer content)



Sample Name	% Fab-Fc Homodimer	% Heterodimer	% scFV-Fc Homodimer	Titer (g/L)
Bioreactor B01				
B01 Day 08	5.6	92.9	1.5	0.63
B01 Day 10	7.4	92.0	0.6	1.19
B01 Day 12	9.2	90.1	0.7	1.79
B01 Day 13	10.5	89.4	0.2	2.31
B01 Day 14	11.1	88.8	0.1	2.54
Bioreactor B02				
B02 Day 08	6.7	92.3	1.0	0.76
B02 Day 10	7.1	91.8	1.1	1.74
B02 Day 12	9.4	90.1	0.5	2.11
B02 Day 13	10.2	89.3	0.5	2.68
B02 Day 14	11.0	88.7	0.3	3.14
Bioreactor B03				
B03 Day 08	6.9	91.7	1.5	0.51
B03 Day 10	8.7	90.6	0.8	1.06
B03 Day 12	10.3	89.1	0.6	1.58
B03 Day 13	11.4	88.5	0.2	1.65
B03 Day 14	11.7	88.3	LOQ	1.83

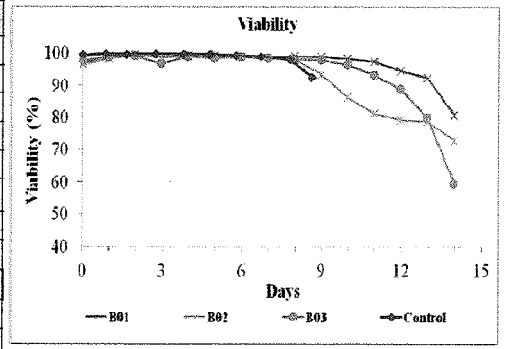


Figure 44

Material Supply Run	Product-related Tests			Impurity Tests		
ID	Product Yield (%)	Protein Conc. (g/L)	HMW/Main/LMW (%)	HCP (ppm)	Fab-Fc Homodimer /Heterodimer/scFv-Fc Homodimer (%)
Assay Method	A280	A280/Protein A Titer	SEC-HPLC	ELISA	CEX-HPLC
Clarified Harvest	n/a	0.95	n/a	n/a	n/a
MabSelect SuRe Eluate	92	13.8	7.3/92.2/0.5	307	9.6/90.2/0.3
Capto S ImpAct Load	93	6.08	7.2/92.2/0.6	<83	9.5/90.0/0.6
Capto S ImpAct Eluate	76	12.4	2.6/97.4/0.0	21	ND/100/ND
Capto adhere Load	n/a	3.04	3.3/96.7/0.0	23	ND/100/ND
Capto adhere Eluate	87	12.0	1.6/98.4/0.0	3.1	ND/100/ND

Figure 45A

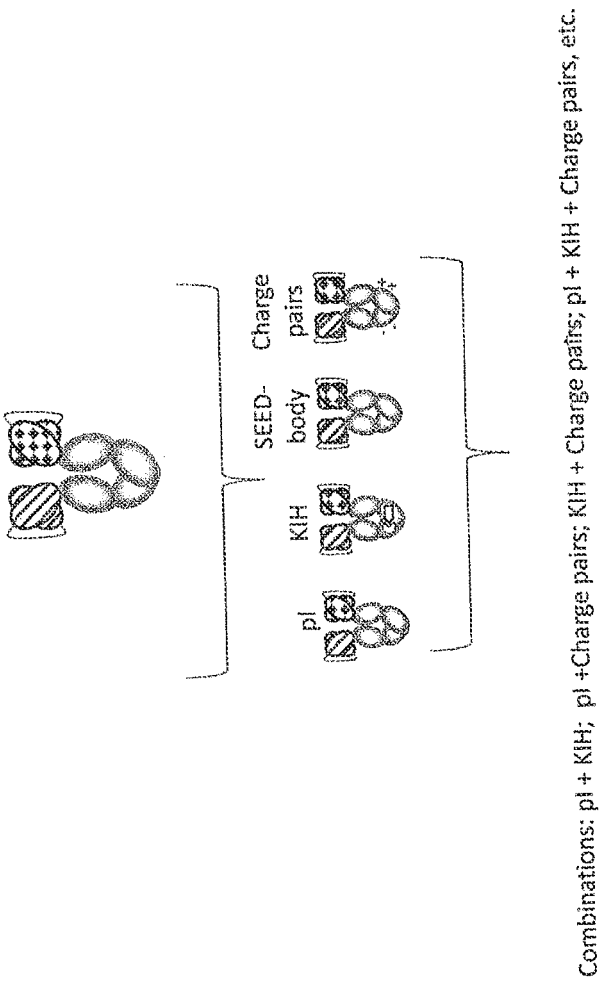

Dual scFv-Fc
pI
KIH
SEED-body
Charge pairs
Combinations: pI + KIH; pI +Charge pairs; KIH + Charge pairs; pI + KIH + Charge pairs, etc.

Figure 45B

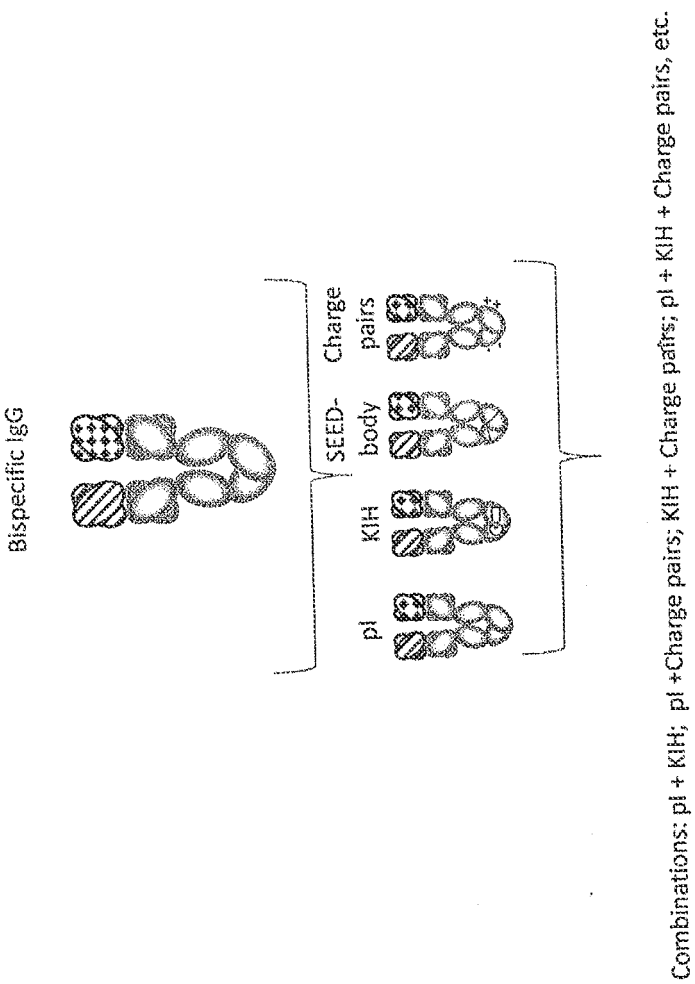

Bispecific IgG
pI
KIH
SEED-body
Charge pairs
Combinations: pI + KIH; pI +Charge pairs; KIH + Charge pairs; pI + KIH + Charge pairs, etc.

Figure 45C-45F

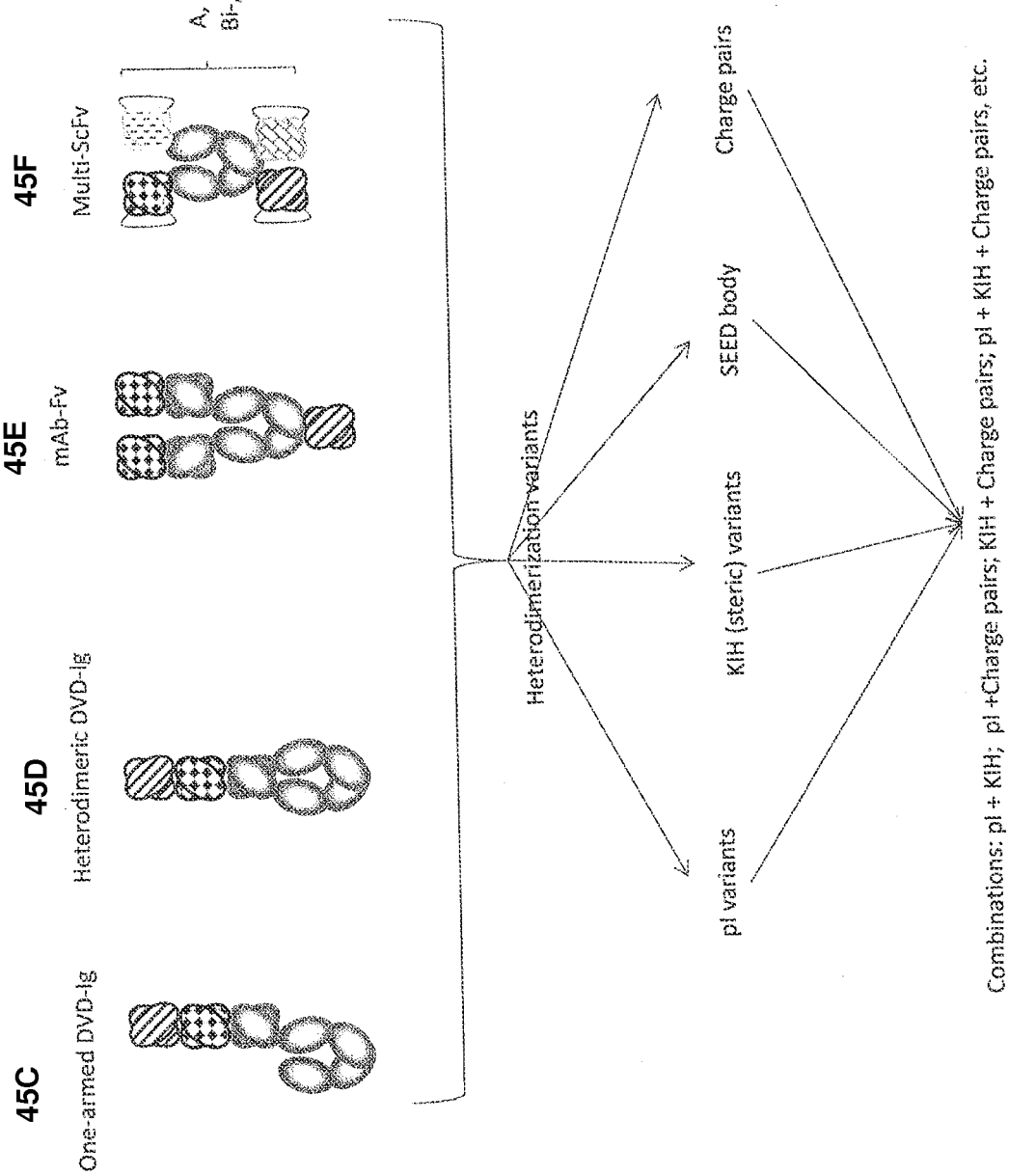


Figure 45G-45J

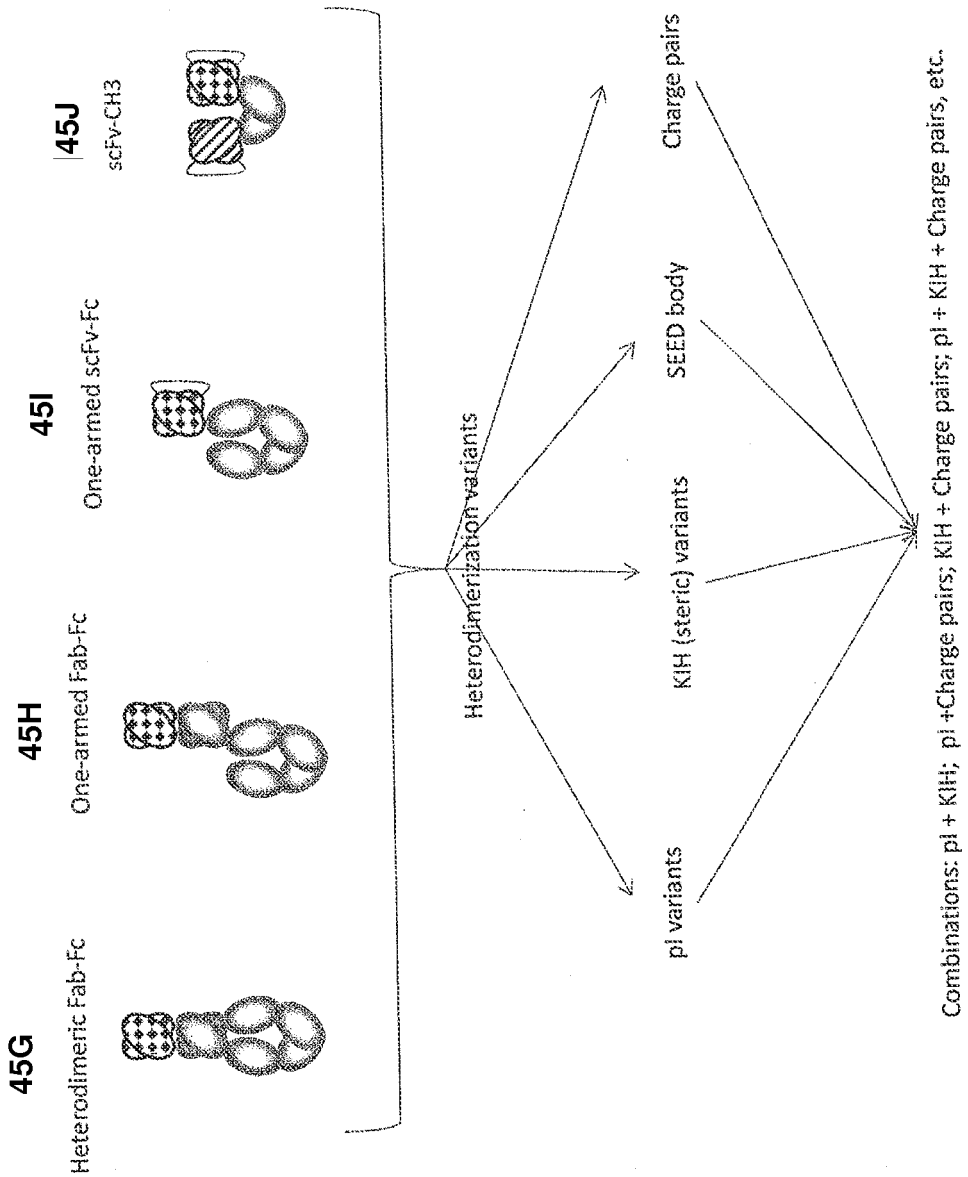


Figure 45K-45L

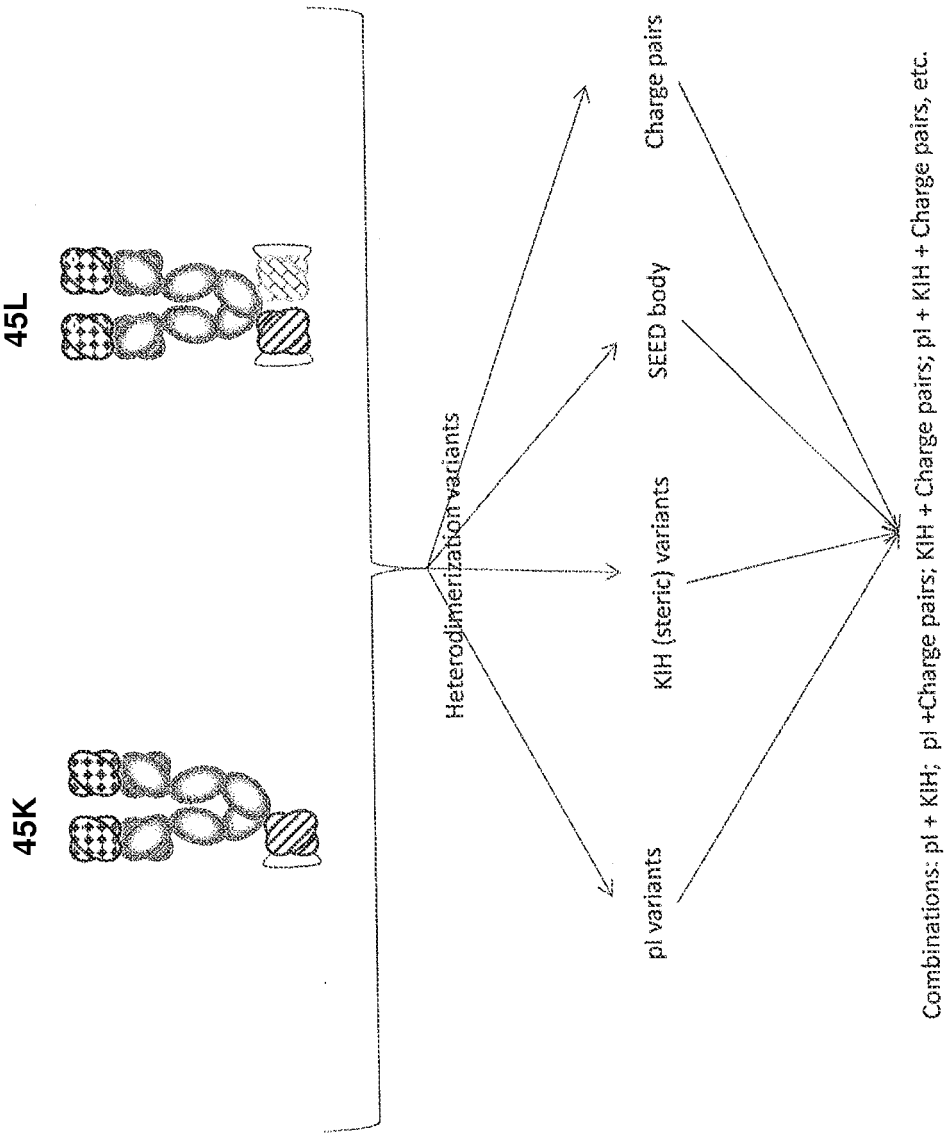


Figure 45M

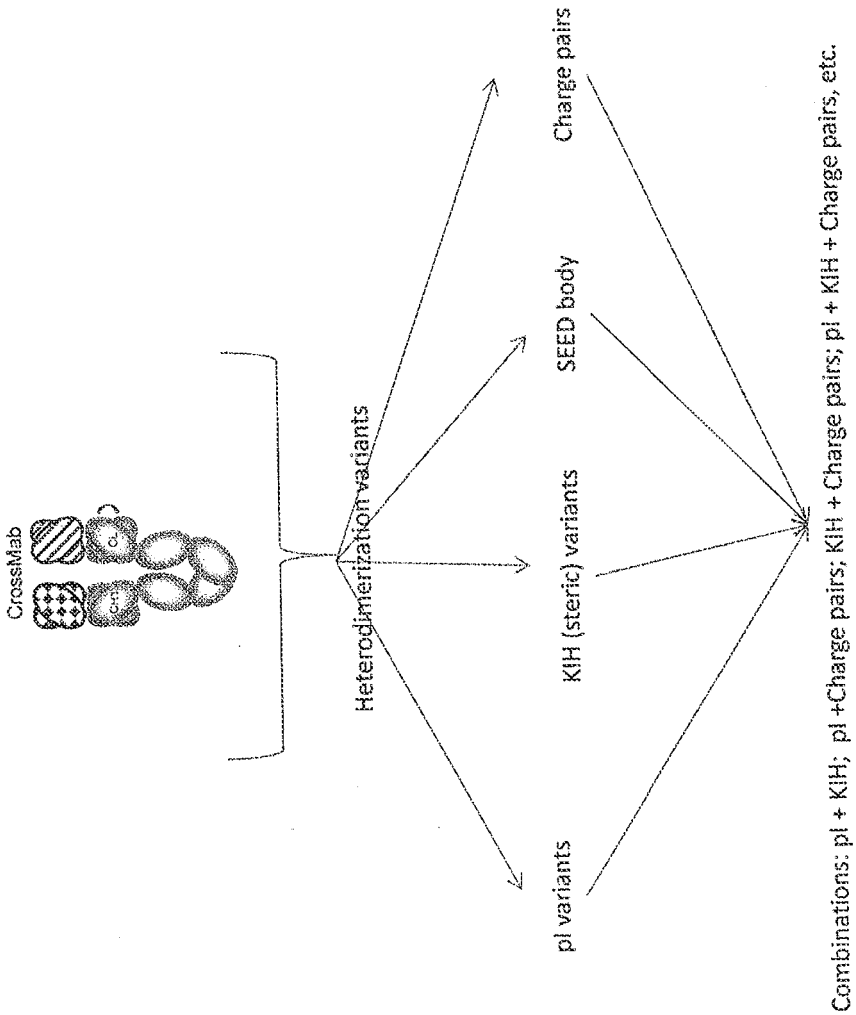

CrossMab
Heterodimerization variants
pI variants
KIH (steric) variants
SEED body
Charge pairs
Combinations: pI + KIH; pI +Charge pairs; KIH + Charge pairs; pI + KIH + Charge pairs, etc.

Figure 45N-49R

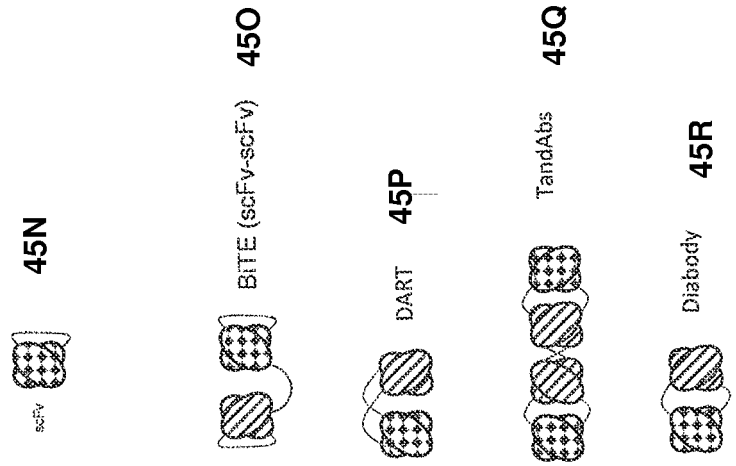


Figure 45S-45U

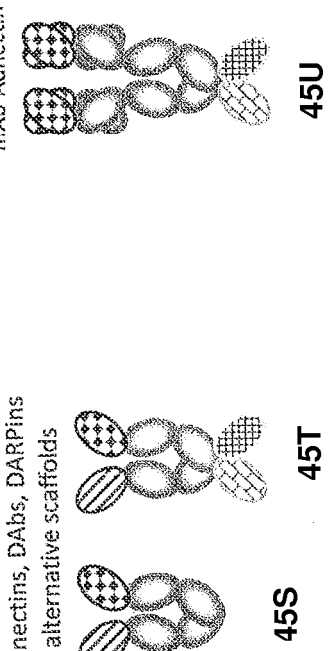


Figure 46A

XENP	VH ID	VL ID	VH Substitutions	VL Substitutions
11502	H1	L1.4		
11794	H1.3	L1.4	L11D	
11795	H1.4	L1.4	L11K	
11796	H1.5	L1.4	L11N	
11801	H1.6	L1.4	L11S	
11802	H1.7	L1.4	R19K	
11803	H1.8	L1.4	N30S	
11804	H1.9	L1.4	N35H	
11805	H1.10	L1.4	N35S	
11806	H1.11	L1.4	P41S	
11807	H1.12	L1.4	Y52CA	
11808	H1.13	L1.4	Y52CA/N54S	
11809	H1.14	L1.4	Y58A	
11810	H1.15	L1.4	D61A	
11811	H1.16	L1.4	D73N	
11812	H1.17	L1.4	D73T	
11813	H1.18	L1.4	L78A	
11814	H1.19	L1.4	A84D	
11815	H1.20	L1.4	A84K	
11816	H1.21	L1.4	A84S	
11817	H1.22	L1.4	V93A	
11818	H1.23	L1.4	V93T	
11819	H1.24	L1.4	N100D	
11820	H1.25	L1.4	N100Q	
11821	H1.26	L1.4	S100AT	
11822	H1.27	L1.4	A101D	
11823	H1.28	L1.4	L108T	
11824	H1.29	L1.30	G44S	G100S
11825	H1	L1.10		E7P
11826	H1	L1.11		T12S
11827	H1	L1.12		G17A
11828	H1	L1.13		G17Q
11829	H1	L1.14		T29S
11830	H1	L1.15		T29S/S30G/N31H
11831	H1	L1.16		G49Y/G50D
11832	H1	L1.17		K53N
11833	H1	L1.18		P56S
11834	H1	L1.19		N52S/K53N/R54K/A55H/P56S/G57W/V58T
11835	H1	L1.20		A60D
11836	H1	L1.21		L66K/L67S
11837	H1	L1.22		L66S/L67S

Figure 46B

XENP	VH ID	VL ID	VH Substitutions	VL Substitutions
11838	H1	L1.23		L75I
11839	H1	L1.24		P80A
11840	H1	L1.25		P80S
11841	H1	L1.26		E85D
11842	H1	L1.27		A89L
11843	H1	L1.28		L95H
11844	H1	L1.29		T105E/V106I/L106AK
11920	H1	L3.1		
11921	H1	L5.1		
11922	H1	L1.31		L75D/E85D/L95H
11923	H1	L1.32		Q38E
12107	H1.38	L1.4	V89T	
12108	H1	L1.33		Q42K
12109	H1	L1.34		Q42T
12110	H1	L1.35		Q42S/A43P
12111	H1	L1.36		A43P
12112	H1	L1.37		A43G
12113	H1	L1.38		A43S
12114	H1	L1.39		A43D
12131	H1.30	L1.4	N30S/N100D	
12132	H1.31	L1.4	N30S/N35S/N100D	
12133	H1.32	L1.4	N30S/Y52CA/N100D	
12134	H1.33	L1.4	N30S/N100D/A101D	
12135	H1.34	L1.4	N30S/N35S/Y52CA/N100D/A101D	
12136	H1.35	L1.4	G10E/L11V/V12K/Q13K/G16E	
12137	H1.36	L1.4	K52BN/Y52C_/N53_/N54G/Y55G/A56S	
12138	H1.37	L1.4	Q39K	
12139	H1.37	L1.32	Q39K	Q38E
12149	H1	L1.40		L75I/E85D/L95H
12213	H1.30	L1.40	N30S/N100D	L75I/E85D/L95H
12214	H1.8	L1.40	N30S	L75I/E85D/L95H
12215	H1.39	L1.40	N30S/Q39K	L75I/E85D/L95H
12216	H1.40	L1.40	N30S/Q39K/N100D	L75I/E85D/L95H
12217	H1.30	L1.41	N30S/N100D	L75I/L95H
12218	H1.8	L1.41	N30S	L75I/L95H
12219	H1.39	L1.41	N30S/Q39K	L75I/L95H
12220	H1.40	L1.41	N30S/Q39K/N100D	L75I/L95H
12221	H1.30	L1.42	N30S/N100D	L75I/Q42K/L95H

Figure 46C

XENP	VH ID	VL ID	VH Substitutions	VL Substitutions
12222	H1.8	L1.42	N30S	L75I/Q42K/L95H
12223	H1.39	L1.42	N30S/Q39K	L75I/Q42K/L95H
12224	H1.40	L1.42	N30S/Q39K/N100D	L75I/Q42K/L95H
12225	H1.30	L1.43	N30S/N100D	L75I/A43S/L95H
12226	H1.8	L1.43	N30S	L75I/A43S/L95H
12227	H1.39	L1.43	N30S/Q39K	L75I/A43S/L95H
12228	H1.40	L1.43	N30S/Q39K/N100D	L75I/A43S/L95H
12229	H1.30	L1.44	N30S/N100D	L75I/Q42K/A43S/L95H
12230	H1.8	L1.44	N30S	L75I/Q42K/A43S/L95H
12231	H1.39	L1.44	N30S/Q39K	L75I/Q42K/A43S/L95H
12232	H1.40	L1.44	N30S/Q39K/N100D	L75I/Q42K/A43S/L95H
12233	H1.30	L1.45	N30S/N100D	L75I/Q42K/E85D/L95H
12234	H1.8	L1.45	N30S	L75I/Q42K/E85D/L95H
12235	H1.39	L1.45	N30S/Q39K	L75I/Q42K/E85D/L95H
12236	H1.40	L1.45	N30S/Q39K/N100D	L75I/Q42K/E85D/L95H
12237	H1.30	L1.46	N30S/N100D	L75I/A43S/E85D/L95H
12238	H1.8	L1.46	N30S	L75I/A43S/E85D/L95H
12239	H1.39	L1.46	N30S/Q39K	L75I/A43S/E85D/L95H
12240	H1.40	L1.46	N30S/Q39K/N100D	L75I/A43S/E85D/L95H
12241	H1.30	L1.47	N30S/N100D	L75I/Q42K/A43S/E85D/L95H
12242	H1.8	L1.47	N30S	L75I/Q42K/A43S/E85D/L95H
12243	H1.39	L1.47	N30S/Q39K	L75I/Q42K/A43S/E85D/L95H
12244	H1.40	L1.47	N30S/Q39K/N100D	L75I/Q42K/A43S/E85D/L95H

Figure 47A

αCD3_H1.31_L1.47 VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

αCD3_H1.31_L1.47 VL

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTIS
GAQPEDEADYYCALWYSNHWVFGGGTKLTVL

αCD3_H1.32_L1.47 VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKANNYATYYADSVKGRFTISRDDS
KNTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFAYWGQGTLVTVSS

αCD3_H1.32_L1.47 VL

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTIS
GAQPEDEADYYCALWYSNHWVFGGGTKLTVL

αCD3_H1.33_L1.47 VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDSYVSWFDYWGQGTLVTVSS

αCD3_H1.33_L1.47 VL

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTIS
GAQPEDEADYYCALWYSNHWVFGGGTKLTVL

αCD3_H1.89_L1.47 VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDEYVSWFAYWGQGTLVTVSS

αCD3_H1.89_L1.47 VL

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTIS
GAQPEDEADYYCALWYSNHWVFGGGTKLTVL

αCD3_H1.90_L1.47 VH

EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYAMNWVRQAPGKGLEWVGRIRSKYNNYATYYADSVKGRFTISRDDSK
NTLYLQMNSLRAEDTAVYYCVRHGNFGDPYVSWFAYWGQGTLVTVSS

Figure 47B

αCD3_H1.90_L1.47 VL

QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTTSNYANWVQQKPGKSPRGLIGGTNKRAPGVPARFSGSLLGGKAALTIS
GAQPEDEADYYCALWYSNHWVFGGGTKLTVL

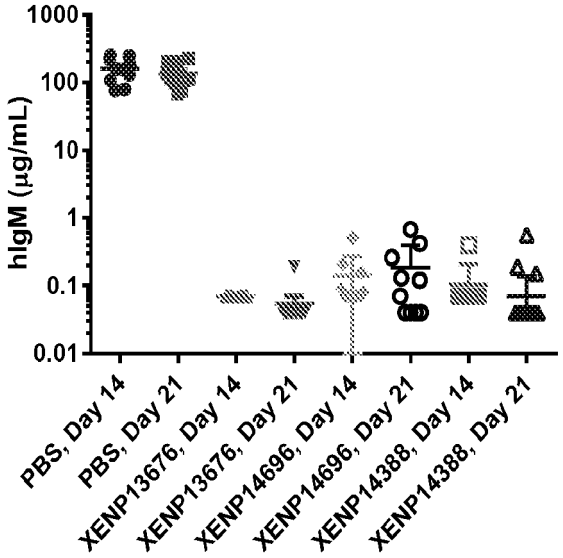
Figure 48

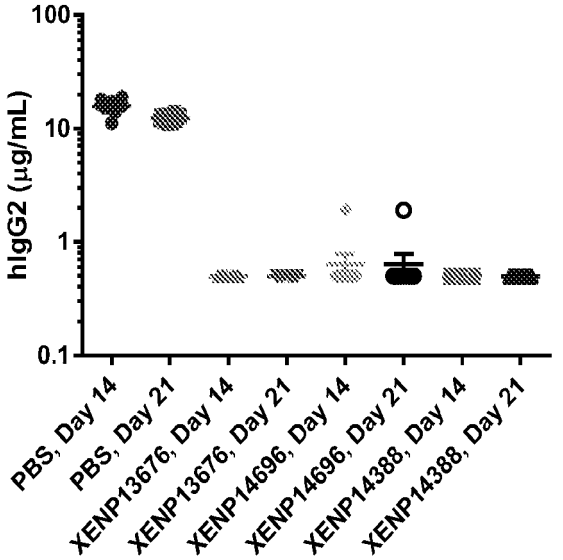
XENP	CD38 affinity	αCD3 scFv-Fc	K_D (nM)*	Fold Decrease in CD3 binding from H1.30_L1.47
13243	low	H1.30_L1.47	4.91	1
14701	low	H1.31_L1.47	1640	330
14702	high	H1.31_L1.47	1640	330
14703	v. low	H1.31_L1.47	1640	330

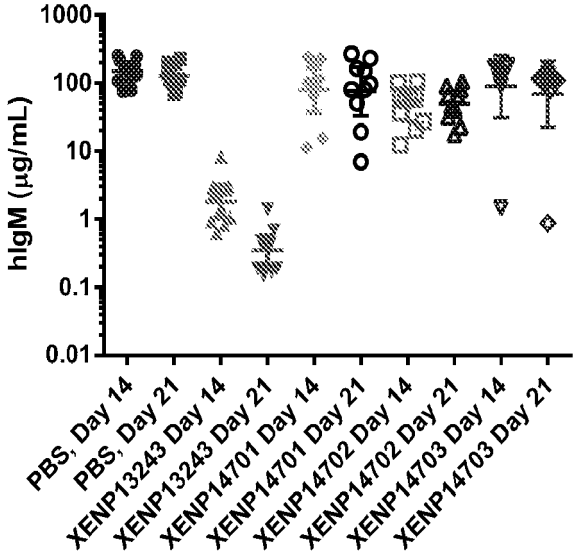
Figure 49

	DNA amount (%)				
Pool	Light chain	HC1 (Fab-Fc)	HC2 (scFv-Fc)	XENP13243 Heterodimer (%)	XENP13551 Heterodimer (%)
A	47.4	31.6	21.1	65.6	57.6
B	42.9	28.6	28.6	61.2	83.5
C	37.5	25.0	37.5	96.2	90.5
D	33.3	22.2	44.4	92.8	84.4
E	54.5	27.3	18.2	--	65.7
F	50.0	25.0	25.0	93.0	91.1
G	44.4	22.2	33.3	85.7	89.6
H	40.0	20.0	40.0	95.0	100.0

Figure 50


hIgM (µg/mL)
1000
100
10
1
0.1
0.01
PBS, Day 14
PBS, Day 21
XENP13676, Day 14
XENP13676, Day 21
XENP14696, Day 14
XENP14696, Day 21
XENP14388, Day 14
XENP14388, Day 21


hIgG2 (µg/mL)
100
10
1
0.1
PBS, Day 14
PBS, Day 21
XENP13676, Day 14
XENP13676, Day 21
XENP14696, Day 14
XENP14696, Day 21
XENP14388, Day 14
XENP14388, Day 21


hIgM (µg/mL)
1000
100
10
1
0.1
0.01
PBS, Day 14
PBS, Day 21
XENP13243 Day 14
XENP13243 Day 21
XENP14701 Day 14
XENP14701 Day 21
XENP14702 Day 14
XENP14702 Day 21
XENP14703 Day 14
XENP14703 Day 21

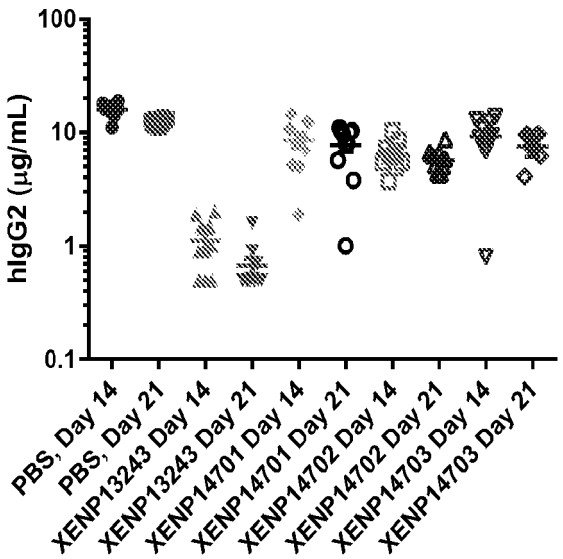

hIgG2 (µg/mL)
100
10
1
0.1
PBS, Day 14
PBS, Day 21
XENP13243 Day 14
XENP13243 Day 21
XENP14701 Day 14
XENP14701 Day 21
XENP14702 Day 14
XENP14702 Day 21
XENP14703 Day 14
XENP14703 Day 21

Figure 51A

SEC after Protein A column

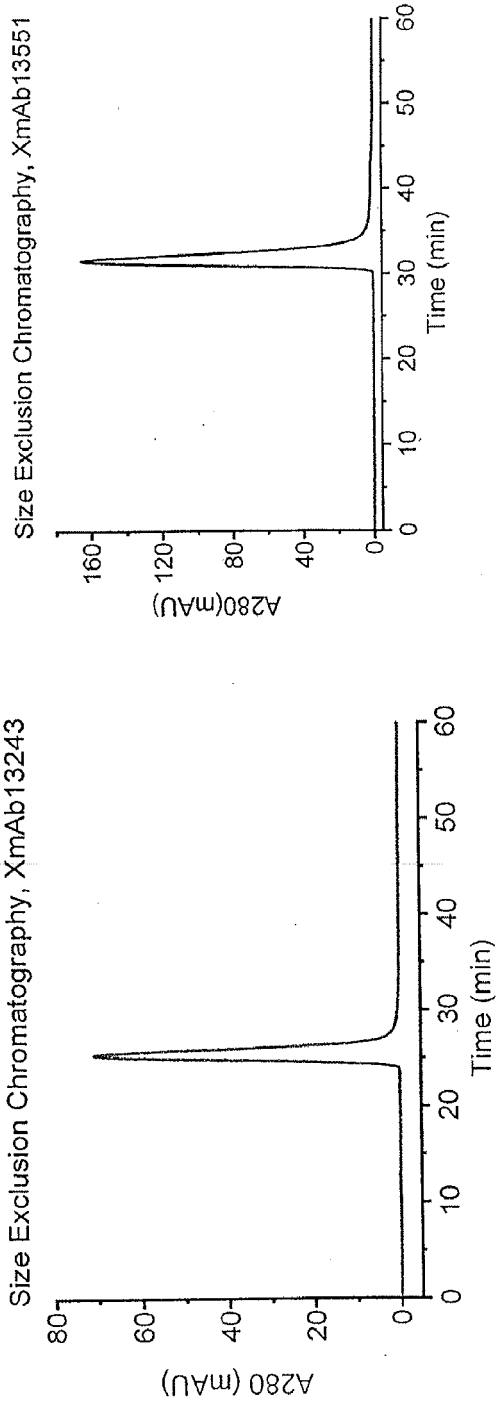


Figure 51B

IEX after Protein A column

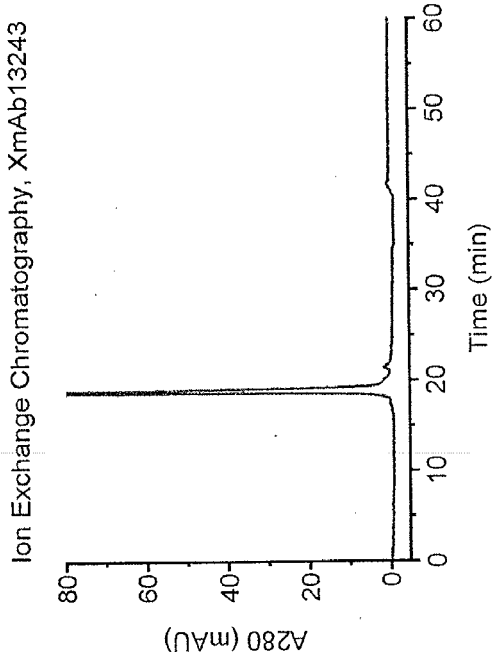


Figure 52A

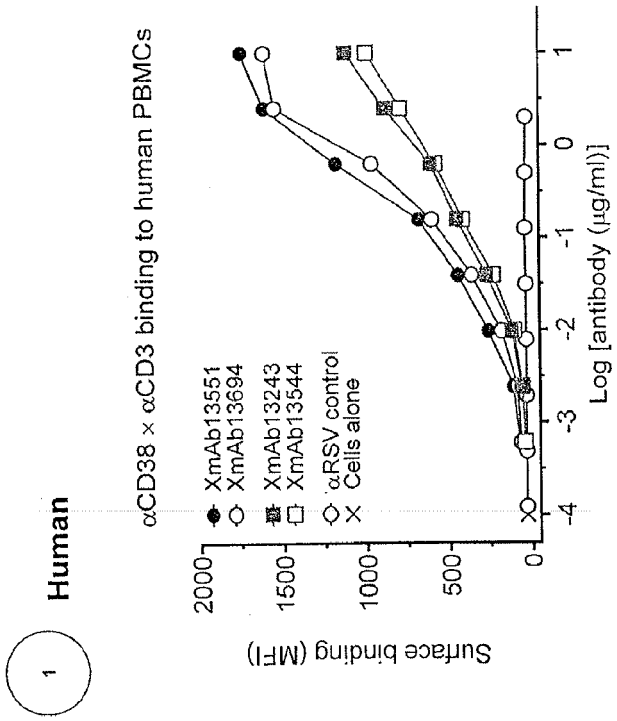

1
Human
αCD38 × αCD3 binding to human PBMCs
XmAb13551
XmAb13694
XmAb13243
XmAb13544
αRSV control
Cells alone
Surface binding (MFI)
2000
1500
1000
500
0
-4
-3
-2
-1
0
1
Log [antibody (μg/ml)]

Figure 52B

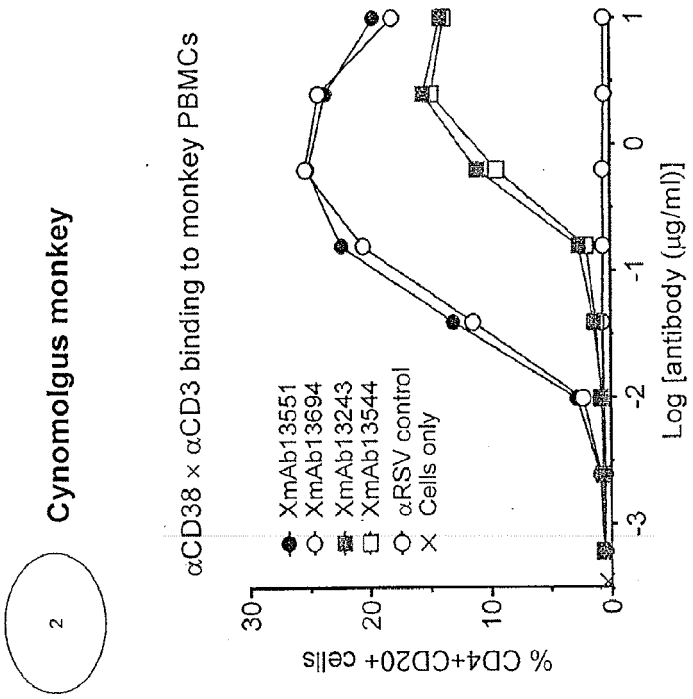

2
Cynomolgus monkey
αCD38 × αCD3 binding to monkey PBMCs
% CD4+CD20+ cells
Log [antibody (µg/ml)]
XmAb13551
XmAb13694
XmAb13243
XmAb13544
αRSV control
Cells only
30
20
10
0
-3
-2
-1
0
1

Figure 52C

K_D	Human CD38	Cyno CD38	Human CD3	Cyno CD3
XmAb13243	16.8 nM	16.2 nM	8.1 nM	5.7 nM
XmAb13551	0.20 nM	0.28 nM	As above	As above
Biacore, Ag coupled				

Figure 53

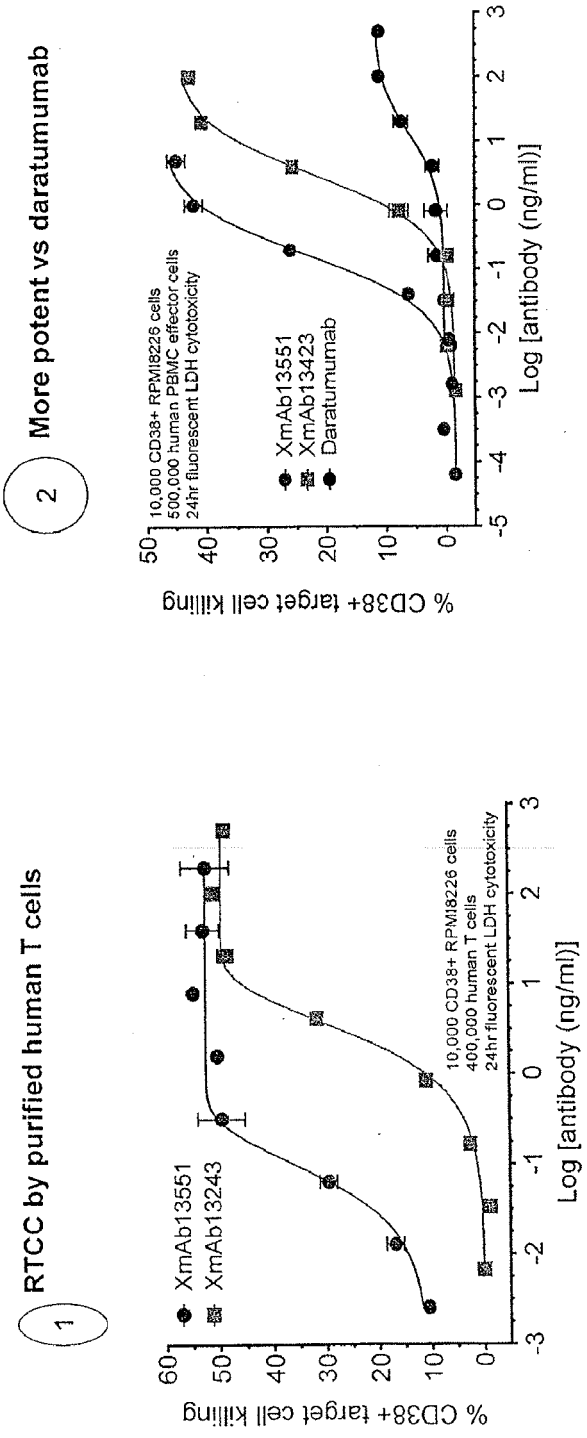

Bispecifics kill myeloma cells
1
RTCC by purified human T cells
XmAb13551
XmAb13243
10,000 CD38+ RPMI8226 cells
400,000 human T cells
24hr fluorescent LDH cytotoxicity
% CD38+ target cell killing
Log [antibody (ng/ml)]
2
More potent vs daratumumab
XmAb13551
XmAb13423
Daratumumab
10,000 CD38+ RPMI8226 cells
500,000 human PBMC effector cells
24hr fluorescent LDH cytotoxicity
% CD38+ target cell killing
Log [antibody (ng/ml)]

Figure 54

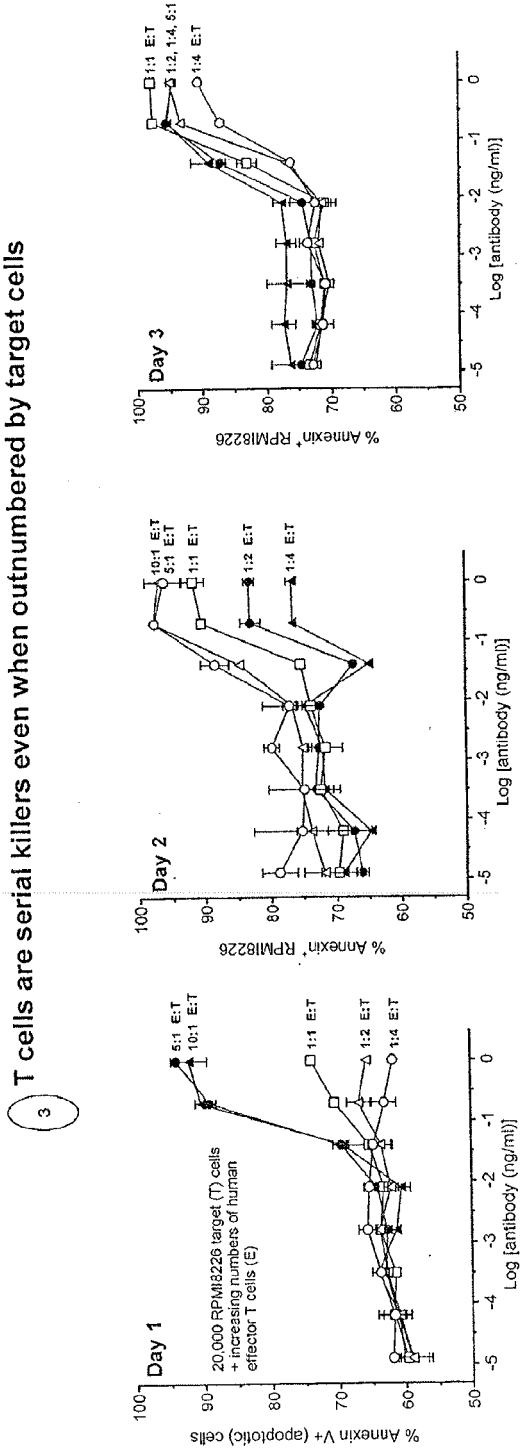

T cells are serial killers even when outnumbered by target cells
3
Day 1
Day 2
Day 3
20,000 RPMI8226 target (T) cells
+ increasing numbers of human
effector T cells (E)
% Annexin V+ (apoptotic) cells
% Annexin+ RPMI8226
Log [antibody (ng/ml)]
10:1 E:T
5:1 E:T
1:1 E:T
1:2 E:T
1:4 E:T
1:2, 1:4, 5:1

Figure 55

Fc domain prolongs half-life

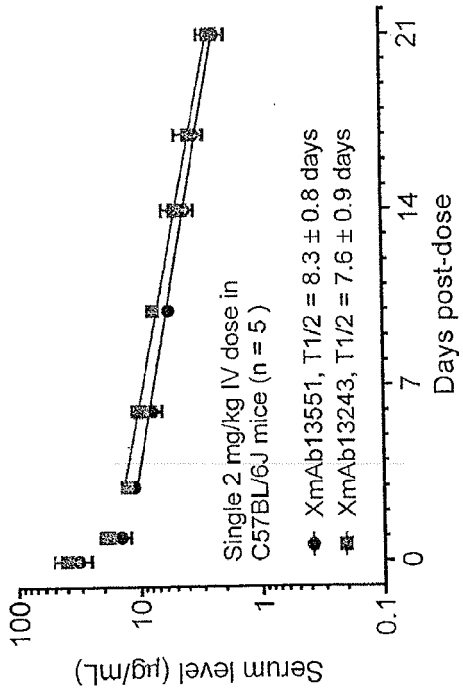


Figure 56

Greater hIg depletion vs daratumumab

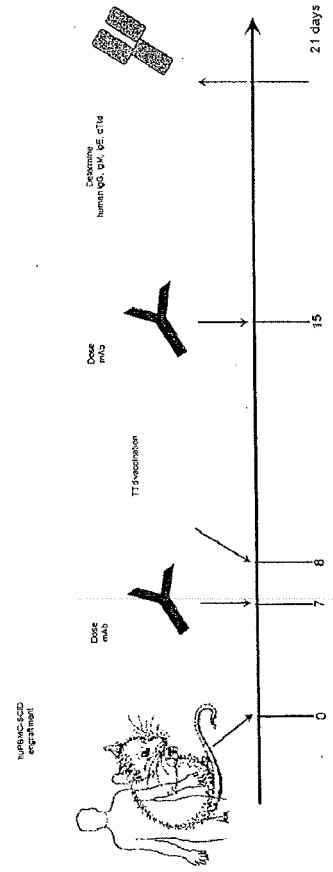


Figure 57

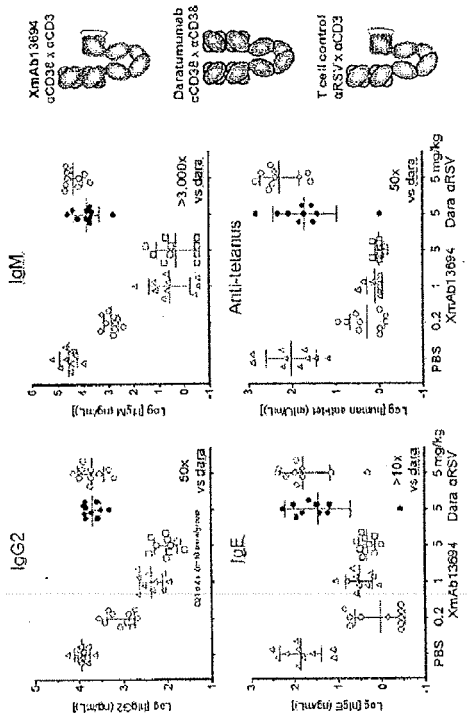

XmAb13694
αCD38 x αCD3
Daratumumab
αCD38 x αCD38
T cell control
αRSV x αCD3
IgM
IgG2
IgE
Anti-tetanus
>3,000x
vs data
50x
vs data
>10x
vs data
50x
vs data
PBS
0.2
1
3
5
5 mg/kg
XmAb13694
Dara αRSV

Figure 58

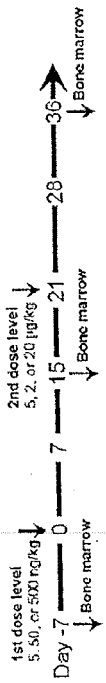

1st dose level
5, 50, or 500 ng/kg
Day -7
0
Bone marrow
7
2nd dose level
5, 2, or 20 µg/kg
15
Bone marrow
21
28
36
Bone marrow

Figure 59A

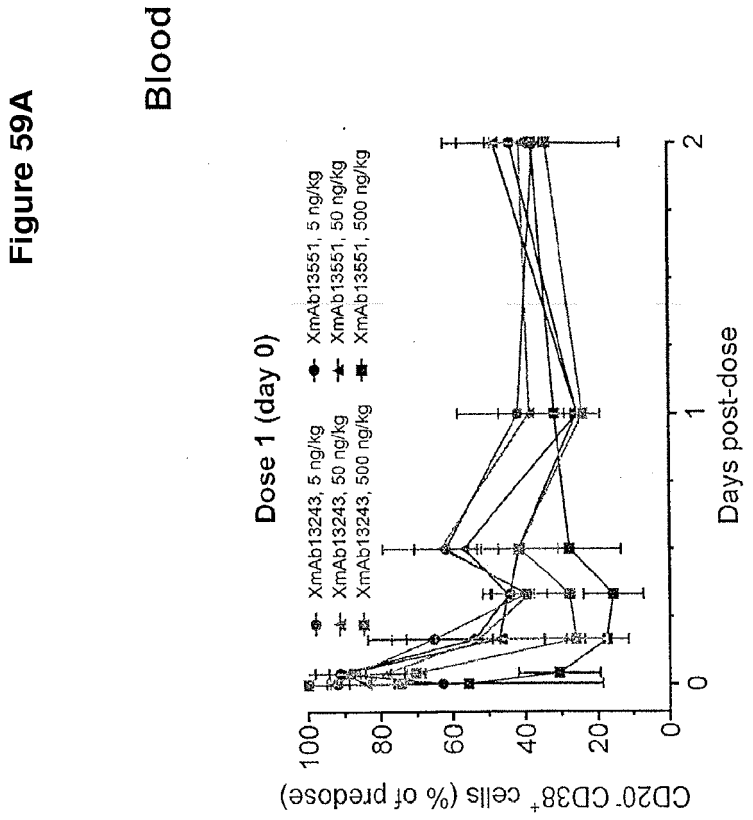

Blood
Dose 1 (day 0)
XmAb13243, 5 ng/kg
XmAb13243, 50 ng/kg
XmAb13243, 500 ng/kg
XmAb13551, 5 ng/kg
XmAb13551, 50 ng/kg
XmAb13551, 500 ng/kg
CD20- CD38+ cells (% of predose)
Days post-dose
Dose 2 (day 21)
2 µg/kg XmAb13243
5 µg/kg XmAb13243
20 µg/kg XmAb13243
2 µg/kg XmAb13551
5 µg/kg XmAb13551
20 µg/kg XmAb13551
CD20- CD38+ cells (% of predose)
Days post-dose

Figure 59B

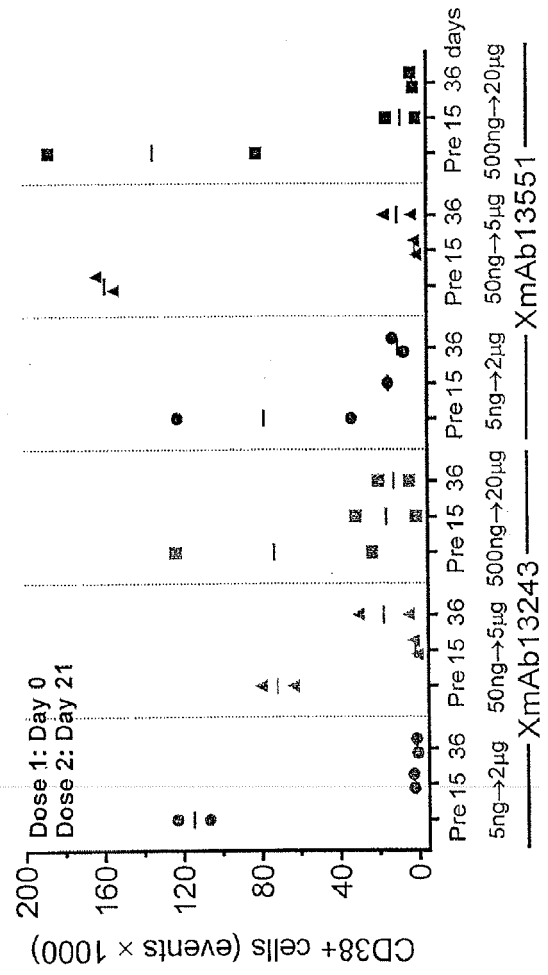

Bone marrow
CD38+ cells (events × 1000)
200
160
120
80
40
0
Dose 1: Day 0
Dose 2: Day 21
Pre 15 36 Pre 15 36 Pre 15 36 Pre 15 36 Pre 15 36 days
5ng→2μg 50ng→5μg 500ng→20μg 5ng→2μg 50ng→5μg 500ng→20μg
XmAb13243
XmAb13551

Figure 60A

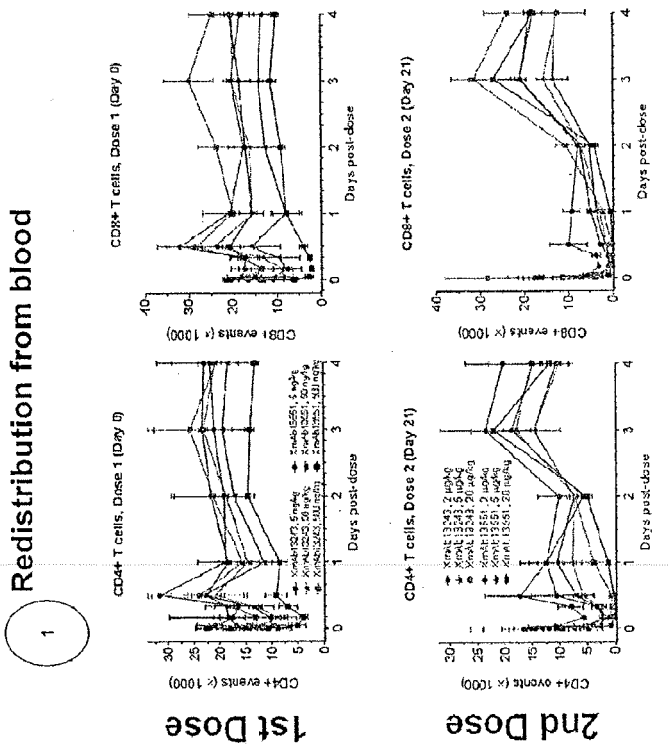

1
Redistribution from blood
1st Dose
2nd Dose
CD4+ T cells, Dose 1 (Day 0)
CD8+ T cells, Dose 1 (Day 0)
CD4+ T cells, Dose 2 (Day 21)
CD8+ T cells, Dose 2 (Day 21)
CD4+ events (x 1000)
CD8+ events (x 1000)
Days post-dose

Figure 60B

② CD69 induction

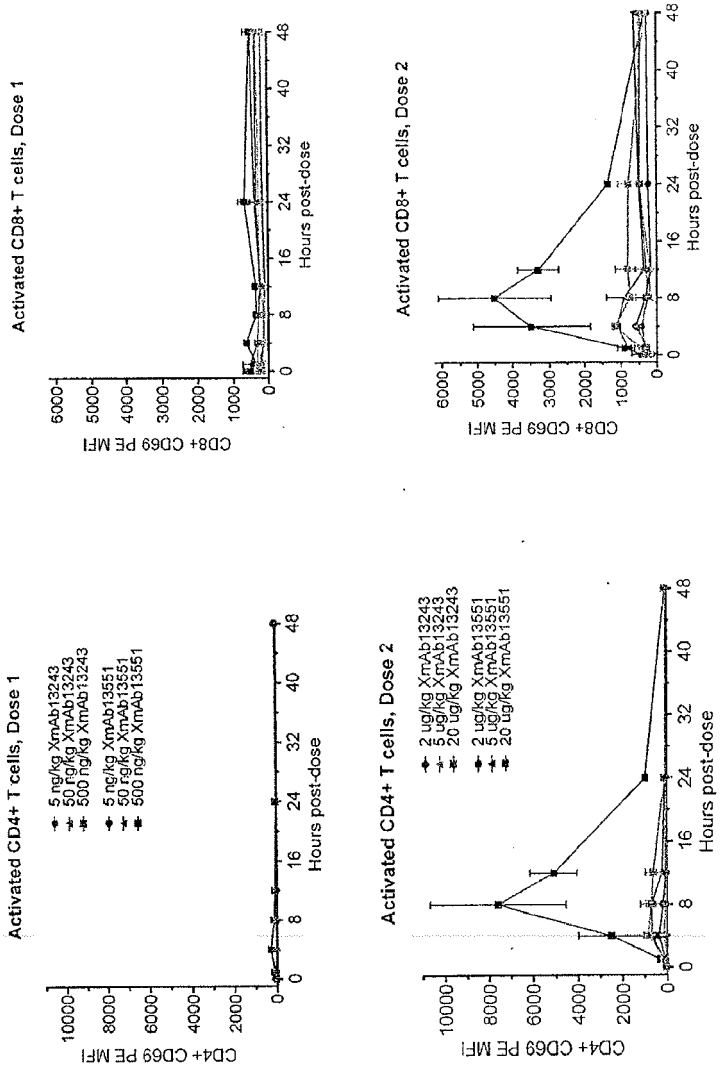


Figure 60C

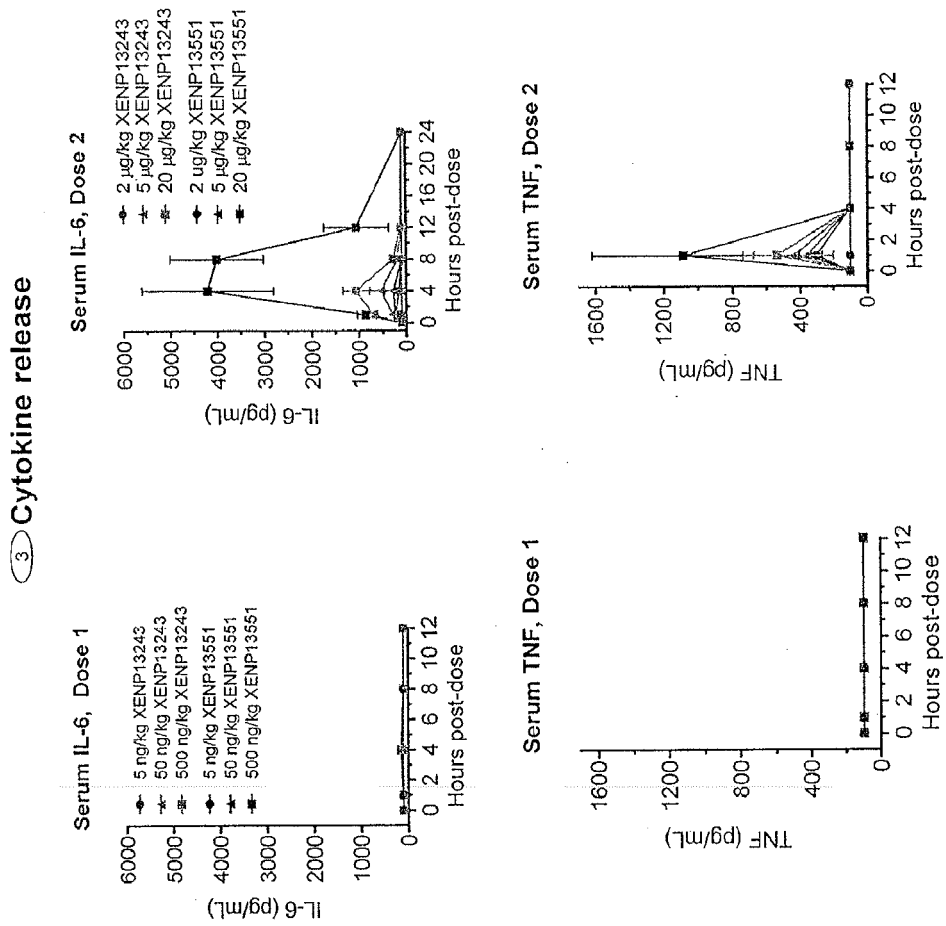

3 Cytokine release
Serum IL-6, Dose 1
5 ng/kg XENP13243
50 ng/kg XENP13243
500 ng/kg XENP13243
5 ng/kg XENP13551
50 ng/kg XENP13551
500 ng/kg XENP13551
IL-6 (pg/mL)
Hours post-dose
Serum IL-6, Dose 2
2 µg/kg XENP13243
5 µg/kg XENP13243
20 µg/kg XENP13243
2 ug/kg XENP13551
5 µg/kg XENP13551
20 µg/kg XENP13551
IL-6 (pg/mL)
Hours post-dose
Serum TNF, Dose 1
TNF (pg/mL)
Hours post-dose
Serum TNF, Dose 2
TNF (pg/mL)
Hours post-dose

Figure 61

scFv monomer (+)	Fab monomer (-)
Heterodimer pI variants S364K/E357Q	Heterodimerization pI variants L368D/K370S
scFv charged linker (GKPGS)4	Isosteric pI substitutions N208D/Q295E/N384D/Q418E/N421D
FcKO E233P/L234V/L235A/G236del/S267K	FcKO E233P/L234V/L235A/G236del/S267K
± 428L/434S for FcRn	± 428L/434S for FcRn
CD3 scFv	Fv sequences for anti-CD38

scFv monomer	Fab monomer
Heterodimer pI variants S364K/E357Q	Heterodimerization pI variants L368D/K370S
scFv charged linker (GKPGS)4	pI substitutions I199T N203D K274Q R355Q Q419E K447del
FcKO E233P/L234V/L235A/G236del/S267K	FcKO E233P/L234V/L235A/G236del/S267K
± 428L/434S for FcRn (optional)	± 428L/434S for FcRn (optional)
CD3 scFv	Fv sequences for anti-CD38