

SEQUENCE LISTING

<110> BIOVERATIV THERAPEUTICS INC.
Seregin, Alexey
Liu, Tongyao
Patarroyo-White, Susannah
Drager, Douglas
Peters, Robert T.
Liu, Jiayun

<120> Nucleic Acid Molecules and Uses Thereof

<130> 4159.493PC01/C-K/BMD

<150> US 62/543,297

<151> 2017-08-09

<160> 184

<170> PatentIn version 3.5

<210> 1

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> coFVIII-5

<400> 1

atgcaaatcg aactgagcac ctgtttcttc ctctgcctgc tgagattctg tttctccgcg	60
acccgccgat actacctggg agcagtggag ctctcctggg attacatgca gagcgacctt	120
ggggagctgc ccgtggatgc caggttccct ccccggggtgc caaagtcgtt tccgttcaac	180
acctccgtgg tgtacaagaa aactctgttc gtggagttca ccgaccacct gttcaatata	240
gccaagccca gacctccctg gatggggctg ttgggacctt ccatccaagc ggaggtgtac	300
gacactgtgg tcatcactct gaagaacatg gcctcgcata ccgtgtccct gcacgccgtg	360
ggagtgtctt actggaaagc gtccgagggg gccgaatacg acgaccagac ctcgagaga	420
gaaaaggaag atgacaaggt gttcccagga ggatcgaca cctacgtgtg gcaagtgttg	480
aaggagaacg gcccaatggc ctccgacctg ctgtgcctga cctactcgta cctgtccac	540
gtggacctcg tgaaggacct caactcggga ctgattggag ccctgctggt ctgcagggaa	600
ggctcactgg cgaaagaaaa gactcagacc ttgcacaagt tcattctgct gttcgctgtg	660
ttcgacgagg ggaagtcgtg gcacagcgag actaagaact ccctgatgca agatagagat	720
gccgcctccg cccgggcctg gcctaagatg cacaccgtga acggttacgt gaaccgctcc	780
ctccctggcc tgattggatg ccaccggaag tccgtgtact ggcacgtgat cgggatgggg	840
accacccccg aggtgcacag catcttcctg gaaggtcaca catttctcgt gcgcaaccac	900
cggcaggcct ccctggaaat cagccccatt accttcctca ctgccagac tctgctgatg	960
gacctgggac agttcctgct gttctgcat atctcctccc accaacaatga cggaatggag	1020

gcatacgtga	aggtcgattc	ctgccctgag	gaaccccagc	tccgcatgaa	gaacaatgag	1080
gaagccgagg	actacgacga	cgacctgacg	gatagcgaga	tggatgtggt	ccggttcgat	1140
gacgataaca	gcccttcctt	catccaaatt	cgctcgggtg	caaagaagca	ccccaaagacc	1200
tgggtgcatt	acattgcggc	ggaagaagag	gactgggatt	atgccccgct	tgtcctcgct	1260
cctgacgacc	ggagctacaa	gagccagtac	ctgaacaacg	gtccacagag	gatcggtaga	1320
aagtacaaga	aggtccgctt	catggcctat	accgacgaaa	ccttcaaaac	tagagaggcc	1380
atccaacacg	aatccggcat	cctgggcccg	ctcttgtacg	gagaagtcgg	cgacaccctt	1440
ctcattatct	tcaagaacca	ggcttcccgg	ccgtacaaca	tctatccgca	tgggatcact	1500
gacgtgcgcc	cactgtactc	gcggcgccctg	cccaaggggtg	tcaaacacct	gaaggatttt	1560
ccgatccttc	cgggagaaat	cttcaagtac	aagtggaccg	tgaccgtgga	agatggccca	1620
actaagtctg	accctagatg	cctcaccgcg	tactactcat	ccttcgtcaa	catggagcgc	1680
gacctggcca	gcggactgat	cggcccgcctg	ctgatttgct	acaaggaatc	agtggaccaa	1740
cggggaaacc	agatcatgtc	ggataagagg	aacgtcatcc	tcttctccgt	gtttgacgaa	1800
aaccggtcgt	ggtacctgac	tgaaaacatc	cagcggttcc	tccccaaccc	cgcgggcgctg	1860
cagctggaag	atcctgagtt	tcaggcatca	aacatcatgc	actccattaa	cggctacgtg	1920
ttcgattcgc	tgcagctgag	cgtgtgtctg	cacgaagtgg	cctactggta	catcctgtcc	1980
attggtgccc	agactgactt	cctgtccgtg	tttttctccg	gctacacgtt	caagcacaag	2040
atggtgtacg	aggacaccct	gaccctcttc	cctttttccg	gcgaaactgt	gtttatgagc	2100
atggagaatc	ccggcctgtg	gatcttgggc	tgccacaaca	gcgacttccg	taacagagga	2160
atgactgcgc	tgctcaaggt	gtccagctgc	gacaagaaca	ccggagacta	ttatgaggac	2220
tcatacgagg	acatctccgc	ctacctcctg	tccaagaata	acgccattga	acctcggagc	2280
ttcagccaga	accacccgt	gcttaagaga	catcaacggg	agatcactag	gaccaccctg	2340
cagtcagacc	aggaggaaat	cgactacgat	gacaccatct	cggtcgagat	gaagaaggag	2400
gactttgaca	tctacgacga	agatgaaaac	cagagcccga	ggtcgttcca	aaagaaaacc	2460
cgccactact	ttattgctgc	tgtcgagcgg	ctgtgggact	acggaatgtc	gtcctcgccg	2520
cacgtgctcc	gcaaccgagc	ccagagcggc	tcggtgccgc	aattcaagaa	ggtcgtgttc	2580
caggagttca	ctgacgggag	cttcactcag	cctttgtacc	ggggagaact	caatgaacat	2640
ctcggcctcc	tcggacctta	catcagagca	gaagtggaag	ataacatcat	ggtcactttc	2700
cgtaaccaag	ccagccgccc	gtactcgttc	tactcctccc	tcattttcta	cgaagaggac	2760
cagcggcagg	gcgcagaacc	gcgcaagaac	ttcgtgaagc	ccaacgaaac	caagacctac	2820
ttctggaaaag	tgcagcatca	tatggccccg	actaaggacg	agtttgactg	caaagcctgg	2880
gcctacttct	ccgatgtgga	cttgggagaag	gacgtccact	ccggcctcat	cggtcccctg	2940

ctcgtgtgcc	ataccaatac	cctgaacccc	gcacacggtc	gccaggtcac	cgtgcaggag	3000
ttcgtctgt	tcttcactat	cttcgacgaa	actaagtcct	ggtacttcac	cgagaacatg	3060
gagaggaact	gcagagcccc	ctgtaacatc	cagatggagg	acccgacgtt	caaggaaaac	3120
taccggttcc	acgccattaa	cggatacatc	atggatacgc	tgccgggtct	tgtgatggcc	3180
caggatcaac	ggatcagatg	gtacttattg	tcgatgggca	gcaacgagaa	catccactct	3240
attcacttct	ccggtcattg	gttcactgtg	cggaagaagg	aagagtacaa	gatggccctg	3300
tacaaccttt	atcccggagt	gttcgaaact	gtggaaatgc	tgccgtcgaa	ggccggcatt	3360
tggcgcgtgg	agtgtttgat	tggagaacat	ctccatgcgg	ggatgtcaac	cctgttcctg	3420
gtgtatagca	acaagtgcc	gactccgctt	gggatggcgt	caggacacat	tagggatttc	3480
cagatcactg	cgtccggcca	gtacggccaa	tggggcccta	agctggcccc	cctgcattac	3540
tccggatcca	ttaacgcctg	gtcaaccaag	gagccattct	cctggatcaa	ggtggacctt	3600
ctggccccca	tgattatcca	cggaattaag	accagggggg	cccggcagaa	gttctcctca	3660
ctgtacatca	gccagttcat	aatcatgtac	tccctggacg	gaaagaagtg	gcaaacctac	3720
agggggaaca	gcaccggcac	actgatggtc	tttttcggaa	atgtggactc	ctccgggatt	3780
aagcataaca	tcttcaacct	tccgattatc	gctcggtaga	ttagacttca	ccctaccac	3840
tacagcattc	gctccacctt	gcggatggaa	ctgatgggct	gcgatctgaa	ctcgtgcagc	3900
atgccgttgg	gaatggagtc	caaagcaatt	tccgacgcgc	agatcacccg	ctcgtcctac	3960
tttaccaaca	tgttcgccac	gtggtcaccg	tccaaggccc	ggctgcacct	ccagggaaga	4020
tccaacgcat	ggcggccaca	ggtcaacaac	cctaaggagt	ggctccaggt	ggacttccag	4080
aaaaccatga	aggtcacccg	agtcacaacc	caggagtgga	agtcgctgct	gacttctatg	4140
tacgtcaagg	agttcctgat	ctccagcagc	caggacgggc	accagtggac	cctgttcttc	4200
caaatggaa	aggtcaagg	gtttcagggc	aatcaggatt	cattcacccc	ggtggtgaac	4260
tcccttgatc	cacctctcct	gacctgctac	cttcgcatcc	accacagtc	ctgggtgcac	4320
cagatcgcg	tgaggatgga	ggtcctggga	tgcgaagccc	aggacctgta	ctga	4374

<210> 2

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> coFVIII-4

<400> 2

atgcagatcg	agctgagcac	gtgcttcttc	ctgtgcctgc	tgaggttctg	cttcagcgcc	60
------------	------------	------------	------------	------------	------------	----

accaggaggt	actacctggg	cgccgtggag	ctgagctggg	actacatgca	gagcgacctg	120
------------	------------	------------	------------	------------	------------	-----

ggcgagctgc	ccgtggacgc	caggttcccc	cccagggtgc	ccaagagctt	ccccttcaac	180
------------	------------	------------	------------	------------	------------	-----

acgagcgtgg	tgtacaagaa	gaccctgttc	gtggagttca	ccgaccatct	gttcaatata	240
gccaagccca	ggccccctg	gatggggctg	ctggggccca	cgatccaggc	cgaggtgtac	300
gacaccgtgg	tcatcaccct	gaagaacatg	gccagccacc	ccgtgagcct	gcacgccgtg	360
ggcgtgagct	actggaaggc	cagcgagggc	gccgagtacg	acgaccagac	cagccagagg	420
gagaaggagg	acgacaaggt	gttccccggc	ggcagccaca	cctacgtgtg	gcaggtgctg	480
aaggagaatg	ggcccatggc	cagcgacccc	ctgtgcctga	cctactctta	cctgagccac	540
gtggatctgg	tgaaggacct	gaacagcggc	ctgatcggcg	ccctgctggg	gtgcagggag	600
ggcagcctgg	ccaaggagaa	gacccagacc	ctgcacaagt	tcatcctgct	gttcgccgtg	660
ttcgacgagg	gcaagagctg	gcacagcgag	accaagaaca	gcctgatgca	ggatagggac	720
gccgccagcg	ccagggcctg	gcccagaatg	cacaccgtga	acggctacgt	gaacaggtct	780
ctgcccggcc	tgatcggctg	ccacaggaag	agcgtgtact	ggcacgtgat	cggcatgggg	840
accacccccg	aggtgcacag	catcttcctg	gagggccaca	cgttcctggg	gaggaatcac	900
aggcaggcca	gcctggagat	cagcccgatc	accttcctga	ccgcccagac	cctgctgatg	960
gacctggggc	agttcctgct	gttctgccat	atcagctctc	accagcacga	cggcatggag	1020
gcctacgtga	aggtggatag	ctgccccgag	gagccccagc	tgaggatgaa	gaacaacgag	1080
gaggccgagg	actacgacga	cgacctgacc	gacagcgaga	tggacgtggg	gaggttcgac	1140
gacgacaata	gcccagagctt	catccagatc	aggagcgtgg	ccaagaagca	ccccaaagacc	1200
tgggtgcatt	acatcgccgc	cgaggaggag	gattgggact	acgccccctt	ggtgctggcc	1260
cccgacgaca	ggtcttataa	gagccagtac	ctgaacaacg	ggccccagag	gatcggcagg	1320
aagtacaaga	aggtgagggt	catggcctac	accgacgaga	ccttcaagac	cagggaggcg	1380
atccagcacg	agagcgggat	cctggggccc	ctgctgtacg	gcgaggtggg	cgacacgctg	1440
ctgatcatct	tcaagaacca	ggccagcagg	ccgtacaata	tctaccccca	cgggatcacc	1500
gacgtgaggc	ccctgtactc	taggaggctg	ccaagggcg	tgaagcacct	gaaggacttc	1560
cccatcctgc	ccggcgagat	cttcaagtac	aagtggaccg	tgaccgtgga	ggacggggccc	1620
acgaagagcg	accccaggtg	cctgaccagg	tactacagct	ctttcgtgaa	catggagagg	1680
gacctggcca	gcggcctgat	cggggcccctg	ctgatctgct	acaaggagag	cgtggatcag	1740
aggggcaacc	agatcatgag	cgacaagagg	aacgtgatcc	tgttcagcgt	gttcgacgag	1800
aataggtctt	ggtacctgac	cgagaatatc	cagaggttcc	tgcccaaccc	cgccggcgtg	1860
cagctggagg	atcccagatt	ccaggccagc	aacatcatgc	acagcatcaa	cggctacgtg	1920
ttcgacagcc	tgacagctgag	cgtgtgcctg	cacgaggtgg	cctactggta	catcctgagc	1980
atcggcgccc	agaccgactt	cctgagcgtg	ttcttcagcg	gctacacctt	caagcacaag	2040
atggtgtacg	aggataccct	gaccctgttc	cccttcagcg	gcgagaccgt	gttcatgagc	2100

atggagaacc	ccggcctgtg	gatcctgggc	tgccataact	ccgacttcag	gaataggggc	2160
atgaccgccc	tgctgaaggt	gagctcttgc	gacaagaaca	ccggcgacta	ctacgaggat	2220
agctacgagg	atatcagcgc	ctacctgctg	agcaagaaca	acgccatcga	gcccgaggtct	2280
ttcagccaga	acccccccgt	gctgaagagg	caccagaggg	agatcaccag	gacgaccctg	2340
cagagcgacc	aggaggagat	cgactacgac	gacacgatca	gcgtggagat	gaagaaggag	2400
gatttcgaca	tctacgacga	ggacgagaat	cagagcccca	ggctctttcca	gaagaagacc	2460
aggcattact	tcatcgccgc	cgtggagagg	ctgtgggact	acggcatgag	cagctctccc	2520
cacgtgctga	ggaatagggc	ccagagcggc	agcgtgcccc	agttcaagaa	ggtggtgttc	2580
caggagttca	ccgacggcag	cttcacccag	cccctgtaca	ggggcgagct	gaacgagcac	2640
ctgggcctgc	tggggcccta	catcagggcc	gaggtggagg	ataacatcat	ggtgaccttc	2700
aggaatcagg	ccagcaggcc	ctatagcttc	tatagctctc	tgatcagcta	cgaggaggat	2760
cagaggcagg	gcgccgagcc	caggaagaac	ttcgtgaagc	ccaacgagac	caagacctac	2820
ttctggaagg	tgcagcacca	catggccccc	acgaaggacg	agttcgactg	caaggcctgg	2880
gcctacttca	gcgacgtgga	tctggagaag	gacgtgcaca	gcggcctgat	cggggccctg	2940
ctggtgtgcc	acaccaacac	cctgaacccc	gcccacggca	ggcaggtgac	cgtgcaggag	3000
ttcgccctgt	tcttcaccat	cttcgacgag	accaagagct	ggtacttcac	cgagaatatg	3060
gagaggaatt	gcagggcccc	ctgcaatatc	cagatggagg	acccgacctt	caaggagaat	3120
tacaggttcc	acgccatcaa	cggctacatc	atggacacgc	tgcccggcct	ggtcatggcc	3180
caggatcaga	ggatcaggtg	gtatctgctg	agcatgggga	gcaacgagaa	tatccacagc	3240
atccacttca	gcggccacgt	gttcaccgtg	aggaagaagg	aggagtacaa	gatggccctg	3300
tacaatctgt	accccggcgt	gttcgagacc	gtggagatgc	tgcccagcaa	ggccgggatac	3360
tggaggggtg	agtgcctgat	cggcgagcac	ctgcacgccg	gcatgagcac	gctgttcctg	3420
gtgtactcta	acaagtgcca	gacccccctg	gggatggcca	gcggccacat	cagggacttc	3480
cagatcaccg	ccagcggcca	gtacggccag	tgggccccca	agctggccag	gctgcactat	3540
tccggaagca	tcaacgcctg	gagcacgaag	gagcccttca	gctggatcaa	ggtggatctg	3600
ctggccccca	tgatcatcca	cgggatcaag	accagggcg	ccaggcagaa	gttcagctct	3660
ctgtatatca	gccagttcat	catcatgtac	tctctggacg	gcaagaagtg	gcagacctac	3720
aggggcaaca	gcaccggcac	gctgatggtg	ttcttcggca	acgtggactc	tagcgggatac	3780
aagcacaata	tcttcaaccc	ccccatcatc	gccaggtaca	tcaggctgca	ccccacccat	3840
tactctatca	ggtctaccct	gaggatggag	ctgatgggct	gcgacctgaa	cagctgcagc	3900
atgcccttgg	ggatggagag	caaggccatc	agcgacgccc	agatcaccgc	cagctcttac	3960
ttcaccaaca	tgttcgccac	ctggagcccc	agcaaggcca	ggctgcacct	gcagggcagg	4020

tctaacgcct	ggaggcccca	ggtgaacaac	cccaaggagt	ggctgcaggt	ggatttccag	4080
aagaccatga	aggtgaccgg	cgtgaccacg	cagggcgtga	agagcctgct	gaccagcatg	4140
tacgtgaagg	agttcctgat	cagctctagc	caggacggcc	accagtggac	cctgtttcttc	4200
cagaacggca	aggtgaaggt	gttccagggc	aaccaggata	gcttcacccc	cgtggtgaac	4260
agcctggacc	ccccctgct	gaccaggtat	ctgaggatcc	accccagag	ctgggtgcac	4320
cagatcgccc	tgaggatgga	ggtgctgggc	tgcgaggccc	aggatctgta	ttga	4374

<210> 3
 <211> 4374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-52

<400> 3						
atgcaaatacg	aactgagcac	ctgtttcttc	ctctgcctgc	tgagattctg	tttctccgcg	60
acccgccgat	actacctggg	agcagtggag	ctctcctggg	attacatgca	gagcgacctt	120
ggggagctgc	ccgtggatgc	caggttccct	ccccgggtgc	caaagtcgtt	tccgttcaac	180
acctccgtgg	tgtacaagaa	aactctgttc	gtggagttca	ccgaccacct	gttcaatata	240
gccaagccca	gacctccctg	gatggggctg	ttgggacctt	ccatccaagc	ggaggtgtac	300
gacactgtgg	tcatcactct	gaagaacatg	gcctcgcatc	ccgtgtccct	gcacgccgtg	360
ggagtgtctt	actggaaagc	gtccgagggg	gccgaatacg	acgaccagac	ctcgcagaga	420
gaaaaggaag	atgacaaggt	gttcccagga	ggatcgacac	cctacgtgtg	gcaagtgttg	480
aaggagaacg	gccaatggc	ctccgacccg	ctgtgcctga	cctactcgta	cctgtcccac	540
gtggacctcg	tgaaggacct	caactcggga	ctgattggag	ccctgctggg	ctgcagggaa	600
ggctcactgg	cgaaagaaaa	gactcagacc	ttgcacaagt	tcattctgct	gttcgctgtg	660
ttcgacgagg	ggaagtcgtg	gcacagcgag	actaagaact	ccctgatgca	agatagagat	720
gccgcctccg	cccgggcctg	gcctaagatg	cacaccgtga	acggttacgt	gaaccgctcc	780
ctccctggcc	tgattggatg	ccaccggaag	tccgtgtact	ggcacgtgat	cgggatgggg	840
accacccccg	aggtgcacag	catcttcctg	gaaggtcaca	catttctcgt	gcgcaaccac	900
cggcaggcct	ccctggaaat	cagccccatt	accttcctca	ctgccagac	tctgctgatg	960
gacctgggac	agttcctgct	gttctgccat	atctcctccc	accaacatga	cggaatggag	1020
gcatacgtga	aggtcgattc	ctgccctgag	gaacccagc	tccgcatgaa	gaacaatgag	1080
gaagccgagg	actacgacga	cgacctgacg	gatagcgaga	tggatgtggg	ccggttcgat	1140
gacgataaca	gcccttcctt	catccaaatt	cgctcgggtg	caaagaagca	ccccaagacc	1200
tgggtgcatt	acattgcggc	ggaagaagag	gactgggatt	atgccccgct	tgtcctcgtc	1260

cctgacgacc	ggagctacaa	gagccagtac	ctgaacaacg	gtccacagag	gatcggtaga	1320
aagtacaaga	aggtccgctt	catggcctat	accgacgaaa	ccttcaaaac	tagagaggcc	1380
atccaacacg	aatccggcat	cctgggcccg	ctcttgtagc	gagaagtcgg	cgacaccctt	1440
ctcattatct	tcaagaacca	ggcttcccgg	ccgtacaaca	tctatccgca	tgggatcact	1500
gacgtgcgcc	cactgtactc	gcggcgccctg	cccaaggggtg	tcaaacacct	gaaggatttt	1560
ccgatccttc	cgggagaaat	cttcaagtac	aagtggaccg	tgaccgtgga	agatggccca	1620
actaagtctg	accctagatg	cctcaccgcg	tactactcat	ccttcgtcaa	catggagcgc	1680
gacctggcca	gcggactgat	cggcccgcctg	ctgatttgct	acaaggaatc	agtggaccaa	1740
cggggaaaacc	agatcatgtc	ggataagagg	aacgtcatcc	tcttctccgt	gtttgacgaa	1800
aaccggctcg	ggtacctgac	cgagaacatc	cagaggttcc	tgcccaaccc	tgctgggggtg	1860
cagctggagg	accccagatt	ccaggccagc	aacatcatgc	acagcatcaa	tggctacgtg	1920
ttcgacagcc	tgcagctgag	cgtgtgcctg	cacgaggtgg	cctactggta	catcctgagc	1980
atcggcgccc	agaccgactt	cctgagcgtg	ttcttctctg	gtacacactt	caagcacaag	2040
atggtgtatg	aggacaccct	gaccctgttc	cccttcagcg	gggagactgt	cttcatgagc	2100
atggagaacc	ctggcctgtg	gatcctgggc	tgccacaaca	gcgacttcag	gaacaggggc	2160
atgactgccc	tgctgaaagt	ctccagctgt	gacaagaaca	ccggggacta	ctacgaggac	2220
agctacgagg	acatcagcgc	ctacctgctg	agcaagaaca	atgccatcga	gcccaggagc	2280
ttctctcaga	acccccagt	gctgaagagg	caccagaggg	agatcaccag	gaccaccctg	2340
cagtctgacc	aggaggagat	cgactatgat	gacaccatca	gcgtggagat	gaagaaggag	2400
gacttcgaca	tctacgacga	ggacgagaac	cagagcccca	ggagcttcca	gaagaagacc	2460
aggcactact	tcattgctgc	tgtggagagg	ctgtgggact	atggcatgtc	cagcagcccc	2520
catgtgctga	ggaacagggc	ccagtctggc	agcgtgcccc	agttcaagaa	agtcgtgttc	2580
caggagttca	ccgacggcag	cttcaccag	cccctgtaca	gaggggagct	gaacgagcac	2640
ctgggcctgc	tgggccccta	catcagggcc	gaggtggagg	acaacatcat	ggtgaccttc	2700
aggaaccagg	ccagcaggcc	ctacagcttc	tacagcagcc	tgatcagcta	cgaggaggac	2760
cagaggcagg	gggctgagcc	caggaagaac	tttgtgaagc	ccaatgaaac	caagacctac	2820
ttctggaagg	tgcagcacca	catggccccc	accaaggacg	agttcgactg	caaggcctgg	2880
gcctacttct	ctgacgtgga	cctggagaag	gacgtgcact	ctggcctgat	tggccccctg	2940
ctggtgtgcc	acaccaacac	cctgaaccct	gcccattggca	ggcaggtgac	tgtgcaggag	3000
ttcgccctgt	tcttcaccat	cttcgatgaa	accaagagct	ggtacttcac	tgagaacatg	3060
gagaggaaact	gcagggcccc	ctgcaacatc	cagatggagg	accccacctt	caaggagaac	3120
tacaggttcc	atgccatcaa	tggctacatc	atggacaccc	tgcttggcct	ggtcatggcc	3180

caggaccaga	ggatcaggtg	gtatctgctg	agcatgggca	gcaacgagaa	catccacagc	3240
atccacttct	ctggccacgt	gttcaactgtg	aggaagaagg	aggagtacaa	gatggccctg	3300
tacaacctgt	accctgggggt	gttcgaaacc	gtggagatgc	tgccagcaa	ggccggcatc	3360
tggaggggtg	agtgcctgat	tggggagcac	ctgcacgccg	gcatgagcac	cctgttcctg	3420
gtgtacagca	acaagtgcc	gacccccctg	ggcatggcct	ctggccacat	cagggacttc	3480
cagatcactg	cctctggcca	gtacggccag	tgggccccca	agctggccag	gctgcactac	3540
tccggaagca	tcaatgcctg	gagcaccaag	gagcccttca	gctggatcaa	agtggacctg	3600
ctggccccca	tgatcatcca	cggcataaag	accagggggg	ccaggcagaa	gttctccagc	3660
ctgtacatca	gccagttcat	catcatgtac	agcctggacg	gcaagaagtg	gcagacctac	3720
aggggcaaca	gcaccggcac	cctgatgggtg	ttcttcggca	acgtggacag	cagcggcatc	3780
aagcacaaca	tcttcaacct	ccccatcatc	gccagataca	tcaggctgca	ccccacctac	3840
tacagcatca	ggagcacctt	gaggatggag	ctgatgggct	gtgacctgaa	cagctgcagc	3900
atgcccctgg	gcatggagag	caaggccatc	tctgacgcc	agatcactgc	ctccagctac	3960
ttcaccaaca	tgtttgccac	ctggagcccc	agcaaggcca	ggctgcacct	gcagggcagg	4020
agcaatgcct	ggaggcccc	ggtcaacaac	ccaaggagt	ggctgcagg	ggacttccag	4080
aagaccatga	aggtgactgg	ggtgaccacc	caggggggtga	agagcctgct	gaccagcatg	4140
tacgtgaagg	agttcctgat	ctccagcagc	caggacggcc	accagtggac	cctgtttcttc	4200
cagaatggca	aggtgaaggt	gttccagggc	aaccaggaca	gcttcacccc	tgtggtcaac	4260
agcctggacc	ccccctgct	gaccagatac	ctgaggatcc	accccagag	ctgggtgcac	4320
cagatcgccc	tgaggatgga	ggtgctgggc	tgtgaggccc	aggacctgta	ctga	4374

<210> 4

<211> 4374

<212> DNA

<213> Artificial Sequence

<220>

<223> coFVIII-62

<400> 4

atgcagattg	agctgtccac	ttgtttcttc	ctgtgcctcc	tgcgcttctg	tttctccgcc	60
actcgccggt	actaccttgg	agccgtggag	ctttcatggg	actacatgca	gagcgacctg	120
ggcgaactcc	ccgtggatgc	cagattcccc	ccccgcgtgc	caaagtcctt	cccctttaac	180
acctccgtgg	tgtacaagaa	aaccctcttt	gtcgagttca	ctgaccacct	gttcaacatc	240
gccaagccgc	gccaccttgg	gatgggcctc	ctgggaccga	ccattcaagc	tgaagtgtac	300
gacaccgtgg	tgatcacctt	gaagaacatg	gcgtcccacc	ccgtgtccct	gcatgcggtc	360
ggagtgtcct	actggaaggc	ctccgaagga	gctgagtacg	acgaccagac	tagccagcgg	420

gaaaaggagg	acgataaagt	gttcccgggc	ggctcgcata	cttacgtgtg	gcaagtcctg	480
aaggaaaacg	gacctatggc	atccgatcct	ctgtgcctga	cttactccta	cctttcccat	540
gtggacctcg	tgaaggacct	gaacagcggg	ctgattgggtg	cacttctcgt	gtgccgcgaa	600
ggttcgctcg	ctaaggaaaa	gacccagacc	ctccataagt	tcatcctttt	gttcgctgtg	660
ttcgatgaag	gaaagtcatg	gcattccgaa	actaagaact	cgctgatgca	ggaccgggat	720
gccgcctcag	cccgcgcctg	gcctaaaatg	catacagtca	acggatacgt	gaatcgggtca	780
ctgcccgggc	tcatcggttg	tcacagaaa	tccgtgtact	ggcacgtcat	cggcatgggc	840
actacgcctg	aagtgcactc	catcttcctg	gaagggcaca	ccttcctcgt	gcgcaaccac	900
cgccaggcct	ctctggaaat	ctccccgatt	acctttctga	ccgccagac	tctgctcatg	960
gacctggggc	agttccttct	cttctgccac	atctccagcc	atcagcacga	cggaatggag	1020
gcctacgtga	aggtggactc	atgcccggaa	gaacctcagt	tgcggatgaa	gaacaacgag	1080
gaggccgagg	actatgacga	cgatttgact	gactccgaga	tggacgtcgt	gcggttcgat	1140
gacgacaaca	gccccagctt	catccagatt	cgcagcgtgg	ccaagaagca	ccccaaaacc	1200
tgggtgcact	acatcgcggc	cgaggaagaa	gattgggact	acgccccgtt	ggtgctggca	1260
cccgatgacc	ggtcgtacaa	gtcccagtat	ctgaacaatg	gtccgcagcg	gattggcaga	1320
aagtacaaga	aagtgcgggt	catggcgtac	actgacgaaa	cgtttaagac	ccgggaggcc	1380
attcaacatg	agagcggcat	tctgggacca	ctgctgtacg	gagaggtcgg	cgataccctg	1440
ctcatcatct	tcaaaaacca	ggcctcccgg	ccttacaaca	tctaccctca	cggaatcacc	1500
gacgtgcggc	cactctactc	gcggcgcctg	ccgaagggcg	tcaagcacct	gaaagacttc	1560
cctatcctgc	cgggcgaaat	cttcaagtat	aagtggaccg	tcaccgtgga	ggacgggccc	1620
accaagagcg	atcctaggtg	tctgactcgg	tactactcca	gcttcgtgaa	catggaacgg	1680
gacctggcat	cgggactcat	tggaccgctg	ctgatctgct	acaaagagtc	ggtggatcaa	1740
cgcggcaacc	agatcatgtc	cgacaagcgc	aacgtgatcc	tgttctccgt	gtttgatgaa	1800
aacagatcct	ggtacctgac	cgagaacatc	cagaggttcc	tgcccaaccc	tgctgggggtg	1860
cagctggagg	accccagatt	ccaggccagc	aacatcatgc	acagcatcaa	tggctacgtg	1920
ttcgacagcc	tgcagctgag	cgtgtgcctg	cacgagggtg	cctactggta	catcctgagc	1980
atcggcgccc	agaccgactt	cctgagcgtg	ttcttctctg	gctacacctt	caagcacaag	2040
atggtgtatg	aggacaccct	gaccctgttc	cccttcagcg	gggagactgt	cttcatgagc	2100
atggagaacc	ctggcctgtg	gatcctgggc	tgccacaaca	gcgacttcag	gaacaggggc	2160
atgactgccc	tgctgaaagt	ctccagctgt	gacaagaaca	ccggggacta	ctacgaggac	2220
agctacgagg	acatcagcgc	ctacctgctg	agcaagaaca	atgccatcga	gcccaggagc	2280
ttctctcaga	accccccagt	gctgaagagg	caccagaggg	agatcaccag	gaccaccctg	2340

cagtctgacc	aggaggagat	cgactatgat	gacaccatca	gcgtggagat	gaagaaggag	2400
gacttcgaca	tctacgacga	ggacgagaac	cagagcccca	ggagcttcca	gaagaagacc	2460
aggcactact	tcattgctgc	tgtggagagg	ctgtgggact	atggcatgtc	cagcagcccc	2520
catgtgctga	ggaacagggc	ccagtctggc	agcgtgcccc	agttcaagaa	agtcgtgttc	2580
caggagttca	ccgacggcag	cttcacccag	cccctgtaca	gaggggagct	gaacgagcac	2640
ctgggcctgc	tgggccccta	catcagggcc	gaggtggagg	acaacatcat	ggtgaccttc	2700
aggaaccagg	ccagcaggcc	ctacagcttc	tacagcagcc	tgatcagcta	cgaggaggac	2760
cagaggcagg	gggctgagcc	caggaagaac	tttgtgaagc	ccaatgaaac	caagacctac	2820
ttctggaagg	tgcagcacca	catggccccc	accaaggacg	agttcgactg	caaggcctgg	2880
gcctacttct	ctgacgtgga	cctggagaag	gacgtgcact	ctggcctgat	tggccccctg	2940
ctggtgtgcc	acaccaacac	cctgaaccct	gcccatggca	ggcaggtgac	tgtgcaggag	3000
ttcgccctgt	tcttcaccat	cttcgatgaa	accaagagct	ggtacttcac	tgagaacatg	3060
gagaggaact	gcagggcccc	ctgcaacatc	cagatggagg	accccacctt	caaggagAAC	3120
tacaggttcc	atgccatcaa	tggctacatc	atggacaccc	tgcctggcct	ggtcatggcc	3180
caggaccaga	ggatcaggtg	gtatctgctg	agcatgggca	gcaacgagaa	catccacagc	3240
atccacttct	ctggccacgt	gttcaactgt	aggaagaagg	aggagtacaa	gatggccctg	3300
tacaacctgt	accctggggg	gttcgaaacc	gtggagatgc	tgccagcaa	ggccggcatc	3360
tggaggggtg	agtgcctgat	tggggagcac	ctgcacgccg	gcatgagcac	cctgttctctg	3420
gtgtacagca	acaagtgccA	gacccccctg	ggcatggcct	ctggccacat	cagggacttc	3480
cagatcactg	cctctggcca	gtacggccag	tgggccccca	agctggccag	gctgcactac	3540
tccggaagca	tcaatgcctg	gagcaccaag	gagcccttca	gctggatcaa	agtggacctg	3600
ctggccccca	tgatcatcca	cggcatcaag	accagggggg	ccaggcagaa	gttctccagc	3660
ctgtacatca	gccagttcat	catcatgtac	agcctggacg	gcaagaagtg	gcagacctac	3720
aggggcaaca	gcaccggcac	cctgatgggt	ttcttcggca	acgtggacag	cagcggcatc	3780
aagcacaaca	tcttcaaccc	ccccatcatc	gccagataca	tcaggctgca	ccccaccac	3840
tacagcatca	ggagcaccct	gaggatggag	ctgatgggct	gtgacctgaa	cagctgcagc	3900
atgcccctgg	gcatggagag	caaggccatc	tctgacgccc	agatcactgc	ctccagctac	3960
ttcaccaaca	tgtttgccac	ctggagcccc	agcaaggcca	ggctgcacct	gcagggcagg	4020
agcaatgcct	ggaggcccca	ggtcaacaac	cccaaggagt	ggctgcaggt	ggacttccag	4080
aagaccatga	aggtgactgg	ggtgaccacc	caggggggtga	agagcctgct	gaccagcatg	4140
tacgtgaagg	agttcctgat	ctccagcagc	caggacggcc	accagtggac	cctgtttcttc	4200
cagaatggca	aggtgaaggt	gttccagggc	aaccaggaca	gcttcacccc	tgtggtcaac	4260

agcctggacc	ccccctgct	gaccagatac	ctgaggatcc	accccagag	ctgggtgcac	4320
cagatcgccc	tgaggatgga	ggtgctgggc	tgtgaggccc	aggacctgta	ctga	4374
<210>	5					
<211>	4374					
<212>	DNA					
<213>	Artificial Sequence					
<220>						
<223>	coFVIII-25					
<400>	5					
atgcagattg	agctgagcac	ctgcttcttc	ctgtgcctgc	tgaggttctg	cttctctgcc	60
accaggagat	actacctggg	cgccgtggag	ctgagctggg	actacatgca	gtctgacctg	120
ggcgagctgc	cagtggacgc	caggttcccc	cccagagtgc	ccaagagctt	ccccttcaac	180
accagcgtgg	tgtacaagaa	gaccctgttc	gtggagttca	ctgaccacct	gttcaacatc	240
gccaagccca	ggccccctg	gatgggcctg	ctgggccccca	ccatccaggc	cgaggtgtac	300
gacaccgtgg	tcatcacctt	gaagaacatg	gccagccacc	ccgtctccct	gcacgccgtg	360
ggggtgagct	actggaaggc	ctctgagggc	gccgagtacg	acgaccagac	cagccagagg	420
gagaaggagg	acgacaaggt	gttccctggg	ggcagccaca	cctacgtgtg	gcaggtcctg	480
aaggagaacg	gccccatggc	ctctgacccc	ctgtgcctga	cctacagcta	cctgagccac	540
gtggacctgg	tgaaggacct	gaactctggc	ctgattgggg	ccctgctggg	gtgcagggag	600
ggcagcctgg	ccaaggagaa	gaccagacc	ctgcacaagt	tcatcctgct	gttcgccgtg	660
ttcgacgagg	gcaagagctg	gcactctgaa	accaagaaca	gcctgatgca	ggacagggac	720
gccgcctctg	ccagggcctg	gcccagatg	cacaccgtca	acggctacgt	caacaggagc	780
ctgcctggcc	tgattggctg	ccacaggaag	agcgtgtact	ggcatgtgat	cggcatgggc	840
accacccttg	aggtgcacag	catcttcctg	gagggccaca	ccttcctggg	caggaaccac	900
aggcaggcca	gcctggagat	cagccccatc	accttcctga	ccgcccagac	cctgctgatg	960
gacctgggcc	agttcctgct	gttctgccac	atctccagcc	accagcacga	cggcatggag	1020
gcctacgtga	aagtggacag	ctgccctgag	gagccccagc	tgaggatgaa	gaacaacgag	1080
gaggccgagg	actatgatga	cgacctgacc	gacagcgaga	tggacgtggg	caggttcgac	1140
gacgacaaca	gccccagctt	catccagatc	aggagcgtgg	ccaagaagca	ccccaagacc	1200
tgggtgcact	acatcgctgc	tgaggaggag	gactgggact	atgccccctt	ggtgctggcc	1260
cctgatgaca	ggagctacaa	gagccagtac	ctgaacaatg	gccccagag	gattggcagg	1320
aagtacaaga	aagtcagggt	catggcctac	actgatgaaa	ccttcaagac	cagggaggcc	1380
atccagcatg	agtctggcat	cctgggcccc	ctgctgtacg	gggaggtggg	ggacaccctg	1440
ctgatcatct	tcaagaacca	ggccagcagg	ccctacaaca	tctaccccca	tggcatcacc	1500

gacgtgaggc	ccctgtacag	caggaggctg	cctaaggggg	tgaagcacct	gaaagacttc	1560
cccatcctgc	ctggggagat	cttcaagtac	aagtggactg	tgactgtgga	ggacggcccc	1620
accaagagcg	accccaggtg	cctgaccaga	tactacagca	gcttcgtcaa	catggagagg	1680
gacctggcct	ctggcctgat	tggccccctg	ctgatctgct	acaaggagtc	tgtggaccag	1740
aggggcaacc	agatcatgag	cgacaagagg	aacgtgatcc	tgttctctgt	cttcgacgag	1800
aacaggagct	ggtacctgac	tgaaaacatc	cagcggttcc	tccccaaccc	cgcgggcggtg	1860
cagctggaag	atcctgagtt	tcaggcatca	aacatcatgc	actccattaa	cggtctacgtg	1920
ttcgattcgc	tgacagctgag	cgtgtgtctg	cacgaagtgg	cctactggta	catcctgtcc	1980
attggtgccc	agactgactt	cctgtccgtg	tttttctccg	gctacacgtt	caagcacaag	2040
atggtgtacg	aggacaccct	gaccctcttc	cctttttccg	gcgaaactgt	gtttatgagc	2100
atggagaatc	ccggcctgtg	gatcttgggc	tgccacaaca	gcgacttccg	taacagagga	2160
atgactgcmc	tgctcaaggt	gtccagctgc	gacaagaaca	ccggagacta	ttatgaggac	2220
tcatacgagg	acatctccgc	ctacctcctg	tccaagaata	acgccattga	acctcggagc	2280
ttcagccaga	acccaccctg	gcttaagaga	catcaacggg	agatcactag	gaccaccctg	2340
cagtcagacc	aggaggaaat	cgactacgat	gacaccatct	cggtcgagat	gaagaaggag	2400
gactttgaca	tctacgacga	agatgaaaac	cagagcccga	ggtcgttcca	aaagaaaacc	2460
cgccactact	ttattgctgc	tgtcgagcgg	ctgtgggact	acggaatgtc	gtcctcgccg	2520
cacgtgctcc	gcaaccgagc	ccagagcggc	tcggtgccgc	aattcaagaa	ggtcgtgttc	2580
caggagttca	ctgacgggag	cttcactcag	cctttgtacc	ggggagaact	caatgaacat	2640
ctcggcctcc	tcggacctta	catcagagca	gaagtggaag	ataacatcat	ggtcactttc	2700
cgtaaccaag	ccagccgccc	gtactcgttc	tactcctccc	tcattttctta	cgaagaggac	2760
cagcggcagg	gcgcagaacc	gcgcaagaac	ttcgtgaagc	ccaacgaaac	caagacctac	2820
ttctggaaaag	tgacagcatca	tatggccccg	actaaggacg	agtttgactg	caaagcctgg	2880
gcctacttct	ccgatgtgga	cttgggagaag	gacgtccact	ccggcctcat	cgggtcccctg	2940
ctcgtgtgcc	ataccaatac	cctgaacccc	gcacacggtc	gccaggtcac	cgtgcaggag	3000
ttcgctctgt	tcttcactat	cttcgacgaa	actaagtcct	ggtacttcac	cgagaacatg	3060
gagaggaaact	gcagagcccc	ctgtaacatc	cagatggagg	acccgacgtt	caaggaaaac	3120
taccggttcc	acgccattaa	cggatacatc	atggatacgc	tgccgggtct	tgtgatggcc	3180
caggatcaac	ggatcagatg	gtacttattg	tcgatgggca	gcaacgagaa	catccactct	3240
attcacttct	ccggtcatgt	gttcactgtg	cggaagaagg	aagagtacaa	gatggccctg	3300
tacaaccttt	atcccggagt	gttcgaaaact	gtggaaatgc	tgccgtcgaa	ggccggcatt	3360
tggcgcgtgg	agtgtttgat	tggagaacat	ctccatgcgg	ggatgtcaac	cctgttcctg	3420

gtgtatagca	acaagtgcc	gactccgctt	gggatggcgt	caggacacat	tagggatttc	3480
cagatcactg	cgtccggcca	gtacggccaa	tgggccccta	agctggcccc	cctgcattac	3540
tccggatcca	ttaacgcctg	gtcaaccaag	gagccattct	cctggatcaa	ggtggacctt	3600
ctggccccca	tgattatcca	cggaattaag	accagggggg	cccggcagaa	gttctcctca	3660
ctgtacatca	gccagttcat	aatcatgtac	tccctggacg	gaaagaagtg	gcaaacctac	3720
agggggaaca	gcaccggcac	actgatggtc	tttttcggaa	atgtggactc	ctccgggatt	3780
aagcataaca	tcttcaacct	tccgattatc	gctcgggtaca	ttagacttca	ccctacctac	3840
tacagcattc	gctccaccct	gcggatggaa	ctgatgggct	gcgatctgaa	ctcgtgcagc	3900
atgccgttgg	gaatggagtc	caaagcaatt	tccgacgcgc	agatcaccgc	ctcgtcctac	3960
tttaccaaca	tgttcgccac	gtggtcaccg	tccaaggccc	ggctgcacct	ccagggaaga	4020
tccaacgcat	ggcggccaca	ggtcaacaac	cctaaggagt	ggctccaggt	ggacttccag	4080
aaaaccatga	aggtcaccgg	agtcacaacc	caggagtgga	agtcgctgct	gacttctatg	4140
tacgtcaagg	agttcctgat	ctccagcagc	caggacgggc	accagtggac	cctgtttctt	4200
caaatggaa	aggtcaaggt	gtttcagggc	aatcaggatt	cattcacccc	ggtggtgaac	4260
tcccttgatc	cacctctcct	gacctgctac	cttcgcatcc	acctacagtc	ctgggtgcac	4320
cagatcgcg	tgaggatgga	ggtcctggga	tgcaagccc	aggacctgta	ctga	4374

<210> 6
 <211> 4374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-26

<400>	6					
atgcagattg	agctgagcac	ctgcttcttc	ctgtgcctgc	tgaggttctg	cttctctgcc	60
accaggagat	actacctggg	cgccgtggag	ctgagctggg	actacatgca	gtctgacctg	120
ggcgagctgc	cagtggacgc	caggttcccc	cccagagtgc	ccaagagctt	ccccttcaac	180
accagcgtgg	tgtacaagaa	gacctgttc	gtggagttca	ctgaccacct	gttcaacatc	240
gccaagccca	ggccccctg	gatgggcctg	ctgggcccc	ccatccaggc	cgaggtgtac	300
gacaccgtgg	tcataccct	gaagaacatg	gccagccacc	ccgtctccct	gcacgccgtg	360
ggggtgagct	actggaaggc	ctctgagggc	gccgagtacg	acgaccagac	cagccagagg	420
gagaaggagg	acgacaaggt	gttccctggg	ggcagccaca	cctacgtgtg	gcaggtcctg	480
aaggagaacg	gccccatggc	ctctgacccc	ctgtgcctga	cctacagcta	cctgagccac	540
gtggacctgg	tgaaggacct	gaactctggc	ctgattgggg	ccctgctggg	gtgcaggagg	600
ggcagcctgg	ccaaggagaa	gacctagacc	ctgcacaagt	tcatacctgt	gttcgccgtg	660

ttcgacgagg	gcaagagctg	gcactctgaa	accaagaaca	gcctgatgca	ggacagggac	720
gccgcctctg	ccagggcctg	gcccagatg	cacaccgtca	acggctacgt	caacaggagc	780
ctgcctggcc	tgattggctg	ccacaggaag	agcgtgtact	ggcatgtgat	cggcatgggc	840
accacccctg	aggtgcacag	catcttcctg	gagggccaca	ccttcctggt	caggaaccac	900
aggcaggcca	gcctggagat	cagccccatc	accttcctga	ccgcccagac	cctgctgatg	960
gacctgggcc	agttcctgct	gttctgccac	atctccagcc	accagcacga	cggcatggag	1020
gcctacgtga	aagtggacag	ctgccctgag	gagccccagc	tgaggatgaa	gaacaacgag	1080
gagggccgagg	actatgatga	cgacctgacc	gacagcgaga	tggacgtggt	caggttcgac	1140
gacgacaaca	gccccagctt	catccagatc	aggagcgtgg	ccaagaagca	ccccaagacc	1200
tgggtgcact	acatcgctgc	tgaggaggag	gactgggact	atgccccctt	ggtgctggcc	1260
cctgatgaca	ggagctacaa	gagccagtac	ctgaacaatg	gccccagag	gattggcagg	1320
aagtacaaga	aagtcaggtt	catggcctac	actgatgaaa	ccttcaagac	cagggaggcc	1380
atccagcatg	agtctggcat	cctgggcccc	ctgctgtacg	gggaggtggg	ggacaccctg	1440
ctgatcatct	tcaagaacca	ggccagcagg	ccctacaaca	tctaccccca	tggcatcacc	1500
gacgtgaggc	ccctgtacag	caggaggctg	cctaaggggg	tgaagcacct	gaaagacttc	1560
cccatcctgc	ctggggagat	cttcaagtac	aagtggactg	tgactgtgga	ggacggcccc	1620
accaagagcg	accccaggtg	cctgaccaga	tactacagca	gcttcgtcaa	catggagagg	1680
gacctggcct	ctggcctgat	tggccccctg	ctgatctgct	acaaggagtc	tgtggaccag	1740
aggggcaacc	agatcatgag	cgacaagagg	aacgtgatcc	tgttctctgt	cttcgacgag	1800
aacaggagct	ggtacctcac	tgaaaacatc	cagaggttcc	tcccaaacc	cgcaggagtg	1860
caactggagg	accctgagtt	tcaggcctcg	aatatcatgc	actcgattaa	cggttacgtg	1920
ttcgactcgc	tgacagctgag	cgtgtgcctc	catgaagtcg	cttactggta	cattctgtcc	1980
atcggcgccc	agactgactt	cctgagcgtg	ttcttttccg	gttacacctt	taagcacaag	2040
atggtgtacg	aagataccct	gaccctgttc	cctttctccg	gcgaaacggg	gttcatgtcg	2100
atggagaacc	cgggtctgtg	gattctggga	tgccacaaca	gcgactttcg	gaaccgcgga	2160
atgactgccc	tgctgaaggt	gtcctcatgc	gacaagaaca	ccggagacta	ctacgaggac	2220
tcctacgagg	atatctcagc	ctacctcctg	tccaagaaca	acgcgatcga	gccgcgcagc	2280
ttcagccaga	acccgcctgt	gctgaagagg	caccagcgag	aaattacccg	gaccaccctc	2340
caatcggatc	aggaggaaat	cgactacgac	gacaccatct	cggtggaat	gaagaaggaa	2400
gatttcgata	tctacgacga	ggacgaaaat	cagtcccctc	gctcattcca	aaagaaaact	2460
agacactact	ttatcgccgc	ggtggaaaga	ctgtgggact	atggaatgtc	atccagccct	2520
cacgtccttc	ggaaccgggc	ccagagcgga	tcggtgcctc	agttcaagaa	agtgggtgttc	2580

caggagttca	ccgacggcag	cttcacccag	ccgctgtacc	ggggagaact	gaacgaacac	2640
ctgggcctgc	tcggtcacct	catccgcgcg	gaagtggagg	ataacatcat	ggtgaccttc	2700
cgtaaccaag	catccagacc	ttactccttc	tattcctccc	tgatctcata	cgaggaggac	2760
cagcgccaag	gcgccgagcc	ccgcaagaac	ttcgtcaagc	ccaacgagac	taagacctac	2820
ttctggaagg	tccaacacca	tatggccccg	accaaggatg	agtttgactg	caaggcctgg	2880
gcctacttct	ccgacgtgga	ccttgagaag	gatgtccatt	ccggcctgat	cgggccgctg	2940
ctcgtgtgtc	acaccaacac	cctgaacca	gcgcatggac	gccaggtcac	cgtccaggag	3000
tttgcctctgt	tcttcacat	ttttgacgaa	actaagtcct	ggtacttcac	cgagaatatg	3060
gagcgaaaact	gtagagcgcc	ctgcaatatc	cagatggaag	atccgacttt	caaggagaac	3120
tatagattcc	acgccatcaa	cgggtacatc	atggatactc	tgccggggct	ggtcatggcc	3180
caggatcaga	ggattcggtg	gtacttgctg	tcaatgggat	cgaacgaaaa	cattcactcc	3240
attcacttct	ccggtcacgt	gttcaactgtg	cgcaagaagg	aggagtacaa	gatggcgctg	3300
tacaatctgt	accccggggg	gttcgaaaact	gtggagatgc	tgccgtccaa	ggccggcatc	3360
tggagagtgg	agtgcctgat	cggagagcac	ctccacgcgg	ggatgtccac	cctcttcctg	3420
gtgtactcga	ataagtgcc	gaccccgctg	ggcatggcct	cgggccacat	cagagacttc	3480
cagatcacag	caagcggaca	atacggccaa	tgggcgccga	agctggcccc	cttgcaactac	3540
tccgatcga	tcaacgcgatg	gtccaccaag	gaaccgttct	cgtggattaa	ggtggacctc	3600
ctggccccta	tgattatcca	cggaattaag	acccagggcg	ccaggcagaa	gttctcctcc	3660
ctgtacatct	cgcaattcat	catcatgtac	agcctggacg	ggaagaagtg	gcagacttac	3720
aggggaaaact	ccaccggcac	cctgatggtc	tttttcggca	acgtggattc	ctccggcatt	3780
aagcacaaca	tcttcaaccc	accgatcata	gccagatata	ttaggctcca	ccccactcac	3840
tactcaatcc	gctcaactct	tcggatggaa	ctcatggggg	gcgacctgaa	ctcctgctcc	3900
atgccgttgg	ggatggaatc	aaaggctatt	agcgacgccc	agatcaccgc	gagctcctac	3960
ttcactaaca	tgttcgccac	ctggagcccc	tccaaggcca	ggctgcactt	gcagggacgg	4020
tcaaatgcct	ggcgggccgca	agtgaacaat	ccgaagggaat	ggcttcaagt	ggatttccaa	4080
aagaccatga	aagtgaccgg	agtcaccacc	caggagagtga	agtcccttct	gacctcgatg	4140
tatgtgaagg	agttcctgat	tagcagcagc	caggacgggc	accagtggac	cctgttcttc	4200
caaaacggaa	aggtcaaggt	gttccagggg	aaccaggact	cgttcacacc	cgtggtgaac	4260
tccctggacc	ccccactgct	gacgcggtac	ttgaggattc	atcctcagtc	ctgggtccat	4320
cagattgcat	tgccaatgga	agtcctgggc	tgcgaggccc	aggacctgta	ctga	4374

<210> 7
<211> 1734

<212> DNA
<213> Artificial Sequence

<220>
<223> coFVIII-52-NT58

<400> 7
gcgacccgcc gatactacct gggagcagtg gagctctcct gggattacat gcagagcgac 60
cttgggggagc tgcccgtgga tgccagggttc cctccccggg tgccaaagtc gtttccgttc 120
aacacctccg tgggtgtacaa gaaaactctg ttcgtggagt tcaccgacca cctgttcaat 180
atcgccaagc ccagacctcc ctggatgggg ctggtgggac ctaccatcca agcggagggtg 240
tacgacactg tggatcatcac tctgaagaac atggcctcgc atcccgtgtc cctgcacgcc 300
gtgggagtggt cttactggaa agcgtccgag ggggccgaat acgacgacca gacctcgag 360
agagaaaagg aagatgacaa ggtgttccca ggaggatcgc acacctacgt gtggcaagtg 420
ttgaaggaga acggcccaat ggcctccgac ccgctgtgce tgacctactc gtacctgtcc 480
cacgtggacc tcgtgaagga cctcaactcg ggactgattg gagccctgct ggtctgcagg 540
gaaggctcac tggcgaaaga aaagactcag accttgaca agttcattct gctgttcgct 600
gtgttcgacg aggggaagtc gtggcacagc gagactaaga actccctgat gcaagataga 660
gatgccgcct ccgcccgggc ctggcctaag atgcacaccg tgaacgggta cgtgaaccgc 720
tcctccctg gcctgattgg atgccaccgg aagtccgtgt actggcacgt gatcgggatg 780
gggaccaccc ccgaggtgca cagcatcttc ctggaaggtc acacatttct cgtgcgcaac 840
caccggcagg cctccctgga aatcagcccc attaccttcc tcaactgcca gactctgctg 900
atggacctgg gacagttcct gctgttctgc catatctcct cccaccaaca tgacggaatg 960
gaggcatacg tgaaggtcga ttccctgccct gaggaacccc agctccgcat gaagaacaat 1020
gaggaagccg aggactacga cgacgacctg acggatagcg agatggatgt ggtccgggtc 1080
gatgacgata acagcccttc cttcatccaa attcgctcgg tggcaaagaa gcaccccaag 1140
acctgggtgc attacattgc ggcggaagaa gaggactggg attatgcccc gcttgtcctc 1200
gctcctgacg accggagcta caagagccag tacctgaaca acggtccaca gaggatcggt 1260
agaaagtaca agaagggtccg cttcatggcc tataccgacg aaaccttcaa aactagagag 1320
gccatccaac acgaatccgg catcctgggc ccgctcttgt acggagaagt cggcgacacc 1380
cttctcatta tcttcaagaa ccaggcttcc cggccgtaca acatctatcc gcatgggatc 1440
actgacgtgc gccactgta ctgcggcgc ctgcccgaag gtgtcaaaca cctgaaggat 1500
tttccgatcc ttccgggaga aatcttcaag tacaagtgga ccgtgaccgt ggaagatggc 1560
ccaactaagt ctgaccctag atgcctcacc cgctactact catccttcgt caacatggag 1620
cgcgacctgg ccagcggact gatcggcccc ctgctgattt gctacaagga atcagtggac 1680
caacggggaa accagatcat gtcggataag aggaacgtca tcctcttctc cgtg 1734

<210> 8
<211> 2583
<212> DNA
<213> Artificial Sequence

<220>
<223> coFVIII-52-CT

<400> 8

tttgacgaaa accggtcgtg gtacctgacc gagaacatcc agaggttcct gccaaccct	60
gctgggggtgc agctggagga ccccgagttc caggccagca acatcatgca cagcatcaat	120
ggctacgtgt tcgacagcct gcagctgagc gtgtgcctgc acgagggtggc ctactggtac	180
atcctgagca tcggcgccca gaccgacttc ctgagcgtgt tcttctctgg ctacaccttc	240
aagcacaaga tgggtgatga ggacaccctg accctgttcc ccttcagcgg ggagactgtc	300
ttcatgagca tggagaacct tggcctgtgg atcctgggct gccacaacag cgacttcagg	360
aacaggggca tgactgccct gctgaaagtc tccagctgtg acaagaacac cggggactac	420
tacgaggaca gctacgagga catcagcgcc tacctgctga gcaagaacaa tgccatcgag	480
cccaggagct tctctcagaa ccccccagtg ctgaagaggc accagagga gatcaccagg	540
accaccctgc agtctgacca ggaggagatc gactatgatg acaccatcag cgtggagatg	600
aagaaggagg acttcgacat ctacgacgag gacgagaacc agagccccag gagcttccag	660
aagaagacca ggcactactt cattgctgct gtggagaggc tgtgggacta tggcatgtcc	720
agcagcccc atgtgctgag gaacagggcc cagtctggca gcgtgcccc gttcaagaaa	780
gtcgtgttcc aggagtccac cgacggcagc ttcaccacag ccctgtacag aggggagctg	840
aacgagcacc tgggcctgct gggcccctac atcagggccg aggtggagga caacatcatg	900
gtgaccttca ggaaccaggc cagcaggccc tacagcttct acagcagcct gatcagctac	960
gaggaggacc agaggcaggg ggctgagccc aggaagaact ttgtgaagcc caatgaaacc	1020
aagacctact tctggaaggt gcagcaccac atggccccca ccaaggacga gttcgactgc	1080
aaggcctggg cctacttctc tgacgtggac ctggagaagg acgtgcactc tggcctgatt	1140
ggccccctgc tgggtgtgcca caccaacacc ctgaaccctg cccatggcag gcaggtgact	1200
gtgcaggagt tcgccctggt cttcaccatc ttcgatgaaa ccaagagctg gtacttcaact	1260
gagaacatgg agaggaactg caggggcccc tgcaacatcc agatggagga cccaccttc	1320
aaggagaact acaggttcca tgccatcaat ggctacatca tggacaccct gcctggcctg	1380
gtcatggccc aggaccagag gatcagggtg tatctgctga gcatgggcag caacgagaac	1440
atccacagca tccacttctc tggccacgtg ttcactgtga ggaagaagga ggagtacaag	1500
atggccctgt acaacctgta ccctgggggtg ttcgaaaccg tggagatgct gccagcaag	1560
gccggcatct ggagggtgga gtgcctgatt ggggagcacc tgcacgccgg catgagcacc	1620

ctgttcctgg	tgtacagcaa	caagtgccag	acccccctgg	gcatggcctc	tggccacatc	1680
agggacttcc	agatcactgc	ctctggccag	tacggccagt	gggcccccaa	gctggccagg	1740
ctgcactact	ccggaagcat	caatgcctgg	agcaccaagg	agcccttcag	ctggatcaaa	1800
gtggacctgc	tggcccccat	gatcatccac	ggcatcaaga	cccagggggc	caggcagaag	1860
ttctccagcc	tgtacatcag	ccagttcatc	atcatgtaca	gcctggacgg	caagaagtgg	1920
cagacctaca	ggggcaacag	caccggcacc	ctgatggtgt	tcttcggcaa	cgtggacagc	1980
agcggcatca	agcacaacat	cttcaacccc	cccatcatcg	ccagatacat	caggctgcac	2040
cccacccact	acagcatcag	gagcaccctg	aggatggagc	tgatgggctg	tgacctgaac	2100
agctgcagca	tgcccctggg	catggagagc	aaggccatct	ctgacgcca	gatcactgcc	2160
tccagctact	tcaccaacat	gtttgccacc	tggagcccca	gcaaggccag	gctgcacctg	2220
cagggcagga	gcaatgcctg	gaggccccag	gtcaacaacc	ccaaggagtg	gctgcagggtg	2280
gacttccaga	agaccatgaa	ggtgactggg	gtgaccaccc	agggggtgaa	gagcctgctg	2340
accagcatgt	acgtgaagga	gttcctgatc	tccagcagcc	aggacggcca	ccagtggacc	2400
ctgttcttcc	agaatggcaa	ggtgaagggtg	ttccagggca	accaggacag	cttcacccct	2460
gtggtcaaca	gcctggaccc	ccccctgctg	accagatacc	tgaggatcca	ccccagagc	2520
tgggtgcacc	agatcgccct	gaggatggag	gtgctgggct	gtgaggccca	ggacctgtac	2580
tga						2583

<210> 9
 <211> 1734
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-62-NT58

<400> 9	
gccactcgcc	ggtactacct
tggagccgtg	gagctttcat
gggactacat	gcagagcgac
	60
ctgggcgaac	tccccgtgga
tgccagattc	cccccccgcg
tgccaaagtc	cttccccctt
	120
aacacctccg	tggtgtacaa
gaaaaccctc	tttgtcgagt
tactgacca	cctgtttcaac
	180
atcgccaagc	cgcgcccacc
ttggatgggc	ctcctgggac
cgaccattca	agctgaagtg
	240
tacgacaccg	tggtgatcac
cctgaagaac	atggcgctcc
accccggtgc	cctgcatgcg
	300
gtcggagtgt	cctactggaa
ggcctccgaa	ggagctgagt
acgacgacca	gactagccag
	360
cgggaaaagg	aggacgataa
agtgttcccg	ggcggctcgc
atacttacgt	gtggcaagtc
	420
ctgaaggaaa	acggacctat
ggcatccgat	cctctgtgcc
tgacttactc	ctacctttcc
	480
catgtggacc	tcgtgaagga
cctgaacagc	gggctgattg
gtgcacttct	cgtgtgcgcg
	540
gaaggttcgc	tcgctaagga
aaagaccag	accctccata
agttcatcct	tttgttcgct
	600

gtgttcgatg aaggaaagtc atggcattcc gaaactaaga actcgctgat gcaggaccgg	660
gatgccgcct cagcccgcgc ctggcctaaa atgcatacag tcaacggata cgtgaatcgg	720
tcactgcccg ggctcatcgg ttgtcacaga aagtccgtgt actggcacgt catcggcatg	780
ggcactacgc ctgaagtgca ctccatcttc ctggaagggc acaccttcct cgtgcgcaac	840
caccgccagg cctctctgga aatctccccg attacctttc tgaccgcca gactctgctc	900
atggacctgg ggcagttcct tctcttctgc cacatctcca gccatcagca cgacggaatg	960
gaggcctacg tgaaggtgga ctcatgcccg gaagaacctc agttgcggat gaagaacaac	1020
gaggaggccg aggactatga cgacgatttg actgactccg agatggacgt cgtgcggttc	1080
gatgacgaca acagccccag cttcatccag attcgcagcg tggccaagaa gcaccccaaa	1140
acctgggtgc actacatcgc ggccgaggaa gaagattggg actacgcccc gttggtgctg	1200
gcacccgatg accggtcgta caagtcccag tatctgaaca atgggtccgca gcggattggc	1260
agaaagtaca agaaagtgcg gttcatggcg tacactgacg aaacgtttaa gacccgggag	1320
gccattcaac atgagagcgg cattctggga ccactgctgt acggagaggt cggcgatacc	1380
ctgctcatca tcttcaaaaa ccaggcctcc cggccttaca acatctaccc tcacggaatc	1440
accgacgtgc ggccactcta ctgcgggcgc ctgccgaagg gcgtcaagca cctgaaagac	1500
ttccctatcc tgccgggcga aatcttcaag tataagtgga ccgtcaccgt ggaggacggg	1560
cccaccaaga gcgacctag gtgtctgact cgggtactact ccagcttcgt gaacatggaa	1620
cgggacctgg catcgggact cattggaccg ctgctgatct gctacaaaga gtcggtggat	1680
caacgcggca accagatcat gtccgacaag cgcaacgtga tcctgttctc cgtg	1734

<210> 10
 <211> 2583
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-62-CT

<400> 10	
tttgatgaaa acagatcctg gtacctgacc gagaacatcc agaggttcct gccaaccct	60
gctgggggtgc agctggagga ccccgagtgc caggccagca acatcatgca cagcatcaat	120
ggctacgtgt tcgacagcct gcagctgagc gtgtgcctgc acgaggtggc ctactggtac	180
atcctgagca tcggcgccca gaccgacttc ctgagcgtgt tcttctctgg ctacaccttc	240
aagcacaaga tgggtgatga ggacaccctg accctgttcc ccttcagcgg ggagactgtc	300
ttcatgagca tggagaacct tggcctgtgg atcctgggct gccacaacag cgacttcagg	360
aacaggggca tgactgccct gctgaaagtc tccagctgtg acaagaacac cggggactac	420
tacgaggaca gctacgagga catcagcgcc tacctgctga gcaagaacaa tgccatcgag	480

cccaggagct	tctctcagaa	ccccccagt	ctgaagaggc	accagaggga	gatcaccagg	540
accacctg	agtcctgacca	ggaggagatc	gactatgatg	acaccatcag	cgtggagatg	600
aagaaggagg	acttcgacat	ctacgacgag	gacgagaacc	agagccccag	gagcttccag	660
aagaagacca	ggcactactt	cattgctgct	gtggagaggc	tgtgggacta	tggcatgtcc	720
agcagcccc	atgtgctgag	gaacagggcc	cagtctggca	gcgtgcccc	gttcaagaaa	780
gtcgtgttcc	aggagtccac	cgacggcagc	ttcaccacgc	ccctgtacag	aggggagctg	840
aacgagcacc	tgggcctgct	gggcccctac	atcagggccg	aggtggagga	caacatcatg	900
gtgaccttca	ggaaccaggc	cagcaggccc	tacagcttct	acagcagcct	gatcagctac	960
gaggaggacc	agaggcagg	ggctgagccc	aggaagaact	ttgtgaagcc	caatgaaacc	1020
aagacctact	tctggaaggt	gcagcaccac	atggccccca	ccaaggacga	gttcgactgc	1080
aaggcctggg	cctactttct	tgacgtggac	ctggagaagg	acgtgcactc	tggcctgatt	1140
ggccccctgc	tgggtgtgcca	caccaacacc	ctgaaccctg	cccatggcag	gcaggtgact	1200
gtgcaggagt	tcgccctgtt	cttcaccatc	ttcgatgaaa	ccaagagctg	gtacttcaact	1260
gagaacatgg	agaggaactg	cagggcccc	tgcaacatcc	agatggagga	ccccaccttc	1320
aaggagaact	acaggttcca	tgccatcaat	ggctacatca	tggacaccct	gcctggcctg	1380
gtcatggccc	aggaccagag	gatcagggtg	tatctgctga	gcatgggcag	caacgagaac	1440
atccacagca	tccactttct	tggccacgtg	ttcactgtga	ggaagaagga	ggagtacaag	1500
atggccctgt	acaacctgta	ccctgggggtg	ttcgaaaccg	tggagatgct	gccagcaag	1560
gccggcatct	ggaggggtga	gtgcctgatt	ggggagcacc	tgcacgccgg	catgagcacc	1620
ctgttcctgg	tgtacagcaa	caagtgccag	acccccctgg	gcatggcctc	tggccacatc	1680
agggacttcc	agatcactgc	ctctggccag	tacggccagt	gggcccccaa	gctggccagg	1740
ctgcactact	ccggaagcat	caatgcctgg	agcaccaagg	agcccttcag	ctggatcaaa	1800
gtggacctgc	tggcccccat	gatcatccac	ggcatcaaga	cccagggggc	caggcagaag	1860
ttctccagcc	tgtacatcag	ccagttcatc	atcatgtaca	gcctggacgg	caagaagtgg	1920
cagacctaca	ggggcaacag	caccggcacc	ctgatggtgt	tcttcggcaa	cgtggacagc	1980
agcggcatca	agcacaacat	cttcaacccc	cccatcatcg	ccagatacat	caggctgcac	2040
cccacccact	acagcatcag	gagcaccctg	aggatggagc	tgatgggctg	tgacctgaac	2100
agctgcagca	tgcccctggg	catggagagc	aaggccatct	ctgacgcca	gatcactgcc	2160
tccagctact	tcaccaacat	gtttgccacc	tggagcccc	gcaaggccag	gctgcacctg	2220
cagggcagga	gcaatgcctg	gaggccccag	gtcaacaacc	ccaaggagtg	gctgcagggtg	2280
gacttccaga	agaccatgaa	ggtgactggg	gtgaccaccc	agggggtgaa	gagcctgctg	2340
accagcatgt	acgtgaagga	gttcctgatc	tccagcagcc	aggacggcca	ccagtggacc	2400

ctgtttcttcc agaatggcaa ggtgaaggtg ttccagggca accaggacag cttcaccct	2460
gtggtcaaca gcctggaccc cccctgctg accagatacc tgaggatcca ccccagagc	2520
tgggtgcacc agatcgccct gaggatggag gtgctgggct gtgaggcca ggacctgtac	2580
tga	2583

<210> 11
 <211> 1734
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-25-NT58

<400> 11	
gccaccagga gatactacct gggcgccgtg gagctgagct gggactacat gcagtctgac	60
ctgggcgagc tgccagtga cgccaggctc cccccagag tgccaagag cttccccttc	120
aacaccagcg tgggtgtacaa gaagaccctg ttcgtggagt tcactgacca cctgttcaac	180
atcgccaagc ccaggccccc ctggatgggc ctgctgggcc ccaccatcca ggccgaggtg	240
tacgacaccg tggatcatcac cctgaagaac atggccagcc acccgtctc cctgcacgcc	300
gtgggggtga gctactggaa ggcctctgag ggcgccgagt acgacgacca gaccagccag	360
agggagaagg aggacgacaa ggtgttccct gggggcagcc acacctacgt gtggcaggtc	420
ctgaaggaga acggccccc at ggcctctgac cccctgtgcc tgacctacag ctacctgagc	480
cacgtggacc tgggtgaagga cctgaactct ggcctgattg gggccctgct ggtgtgcagg	540
gagggcagcc tggccaagga gaagaccag accctgcaca agttcatcct gctgttcgcc	600
gtgttcgacg agggcaagag ctggcactct gaaaccaaga acagcctgat gcaggacagg	660
gacgccgcct ctgccagggc ctggcccaag atgcacaccg tcaacggcta cgtcaacagg	720
agcctgcctg gcctgattgg ctgccacagg aagagcgtgt actggcatgt gatcggcattg	780
ggcaccaccc ctgagggtgca cagcatcttc ctggaggggc acaccttcct ggtcaggaac	840
cacaggcagg ccagcctgga gatcagcccc atcaccttcc tgaccgcca gacctgctg	900
atggacctgg gccagttcct gctgttctgc cacatctcca gccaccagca cgacggcatg	960
gaggcctacg tgaaagtgga cagctgccct gaggagcccc agctgaggat gaagaacaac	1020
gaggaggccg aggactatga tgacgacctg accgacagcg agatggacgt ggtcaggttc	1080
gacgacgaca acagccccag cttcatccag atcaggagcg tggccaagaa gcacccaag	1140
acctgggtgc actacatcgc tgctgaggag gaggactggg actatgcccc cctggtgctg	1200
gcccctgatg acaggagcta caagagccag tacctgaaca atggcccca gaggattggc	1260
aggaagtaca agaaagtcag gttcatggcc tacactgatg aaaccttcaa gaccaggag	1320
gcatccagc atgagtctgg catcctgggc cccctgctgt acggggagggt gggggacacc	1380

ctgctgatca tcttcaagaa ccaggccagc aggcctaca acatctaccc ccatggcatc	1440
accgacgtga ggcccctgta cagcaggagg ctgcctaagg gggatgaagca cctgaaagac	1500
ttccccatcc tgcctgggga gatcttcaag tacaagtgga ctgtgactgt ggaggacggc	1560
cccaccaaga gcgacccag gtgcctgacc agatactaca gcagcttcgt caacatggag	1620
agggacctgg cctctggcct gattggcccc ctgctgatct gctacaagga gtctgtggac	1680
cagaggggca accagatcat gagcgacaag aggaacgtga tctgtttctc tgtc	1734

<210> 12
 <211> 2583
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-25-CT

<400> 12	
ttcgacgaga acaggagctg gtacctgact gaaaacatcc agcggttcct cccaacccc	60
gcgggcgtgc agctggaaga tcttgagttt caggcatcaa acatcatgca ctccattaac	120
ggctacgtgt tcgattcgct gcagctgagc gtgtgtctgc acgaagtggc ctactggtac	180
atcctgtcca ttgggtgcca gactgacttc ctgtccgtgt ttttctccgg ctacacgttc	240
aagcacaaga tgggtgtacga ggacaccctg accctcttcc ctttttccgg cgaaactgtg	300
tttatgagca tggagaatcc cggcctgtgg atcttgggct gccacaacag cgacttccgt	360
aacagaggaa tgactgcgct gctcaagggtg tccagctgcg acaagaacac cggagactat	420
tatgaggact catacgagga catctccgcc tacctcctgt ccaagaataa cgccattgaa	480
cctcggagct tcagccagaa cccacccgtg ctttaagagac atcaacggga gatcactagg	540
accaccctgc agtcagacca ggaggaaatc gactacgatg acaccatctc ggtcgagatg	600
aagaaggagg actttgacat ctacgacgaa gatgaaaacc agagcccgag gtcgttccaa	660
aagaaaaccc gccactactt tattgctgct gtcgagcggc tgtgggacta cggaatgtcg	720
tctcgcgcgc acgtgctccg caaccgagcc cagagcggct cggtgccgca attcaagaag	780
gtcgtgttcc aggagttcac tgacgggagc ttactcagc ctttgtaccg gggagaactc	840
aatgaacatc tcggcctcct cggaccttac atcagagcag aagtggaaga taacatcatg	900
gtcactttcc gtaaccaagc cagccgcccg tactcgttct actcctccct catttcttac	960
gaagaggacc agcggcaggg cgcagaaccg cgcaagaact tcgtgaagcc caacgaaacc	1020
aagacctact tctggaaagt gcagcatcat atggccccga ctaaggacga gtttgactgc	1080
aaagcctggg cctacttctc cgatgtggac ttggagaagg acgtccactc cggcctcatc	1140
gggtcccctgc tcgtgtgcca taccaatacc ctgaaccccg cacacggtcg ccaggtcacc	1200
gtgcaggagt tcgctctgtt cttcactatc ttcgacgaaa ctaagtcctg gtacttcacc	1260

gagaacatgg agaggaactg cagagccccc tgtaacatcc agatggagga cccgacgttc	1320
aaggaaaaact accggttcca cgccattaac ggatacatca tggatacgct gccgggtctt	1380
gtgatggccc aggatcaacg gatcagatgg tacttattgt cgatgggcag caacgagaac	1440
atccactcta ttcacttctc cgggtcatgtg ttcactgtgc ggaagaagga agagtacaag	1500
atggccctgt acaaccttta tcccggagtg ttcgaaactg tggaaatgct gccgtcgaag	1560
gccggcattt ggcgcgtgga gtgtttgatt ggagaacatc tccatgcggg gatgtcaacc	1620
ctgttcctgg tgtatagcaa caagtgccag actccgcttg ggatggcgtc aggacacatt	1680
agggatttcc agatcactgc gtccggccag tacggccaat gggcccctaa gctggcccgc	1740
ctgcattact ccggatccat taacgcctgg tcaaccaagg agccattctc ctggatcaag	1800
gtggaccttc tggcccccat gattatccac ggaattaaga cccagggggc ccggcagaag	1860
ttctcctcac tgtacatcag ccagttcata atcatgtact ccctggacgg aaagaagtgg	1920
caaacctaca gggggaacag caccggcaca ctgatggtct ttttcggaaa tgtggactcc	1980
tccgggatta agcataacat cttcaaccct ccgattatcg ctcggtacat tagacttcac	2040
cctaccact acagcattcg ctccaccctg cggatggaac tgatgggctg cgatctgaac	2100
tcgtgcagca tgccgttggg aatggagtcc aaagcaattt ccgacgcgca gatcaccgcc	2160
tcgtcctact ttaccaacat gttcgccacg tggtcaccgt ccaaggcccg gctgcacctc	2220
caggaagat ccaacgcag ggcggccacag gtcaacaacc ctaaggagtg gctccaggtg	2280
gacttccaga aaaccatgaa ggtcaccgga gtcacaaccc agggagtga gtcgctgctg	2340
acttctatgt acgtcaagga gttcctgatc tccagcagcc aggacgggca ccagtggacc	2400
ctgttcttcc aaaatggaaa ggtcaagggtg tttcagggca atcaggattc attcaccocg	2460
gtggtgaact cccttgatcc acccctcctg acccgctacc ttcgcatcca cccacagtcc	2520
tgggtgcacc agatcgcgct gaggatggag gtcctgggat gcgaagccca ggacctgtac	2580
tga	2583

<210> 13
 <211> 1734
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-26-NT58

<400> 13	
gccaccagga gatactacct gggcgccgtg gagctgagct gggactacat gcagtctgac	60
ctgggcgagc tgccagtgga cgccagggtc cccccagag tgcccaagag cttccccttc	120
aacaccagcg tgggtgtacaa gaagaccctg ttcgtggagt tcactgacca cctgttcaac	180
atcgccaagc ccaggccccc ctggatgggc ctgctgggcc ccaccatcca ggccgaggtg	240

tacgacaccg	tggatcatcac	cctgaagaac	atggccagcc	accccgctctc	cctgcacgcc	300
gtgggggtga	gctactggaa	ggcctctgag	ggcgccgagt	acgacgacca	gaccagccag	360
agggagaagg	aggacgacaa	ggtgttccct	gggggcagcc	acacctacgt	gtggcaggtc	420
ctgaaggaga	acggcccat	ggcctctgac	cccctgtgcc	tgacctacag	ctacctgagc	480
cacgtggacc	tggatgaagga	cctgaactct	ggcctgattg	gggccctgct	ggtgtgcagg	540
gagggcagcc	tggccaagga	gaagacccag	accctgcaca	agttcatcct	gctgttcgcc	600
gtgttcgacg	agggaagag	ctggcactct	gaaaccaaga	acagcctgat	gcaggacagg	660
gacgccgcct	ctgccagggc	ctggcccaag	atgcacaccg	tcaacggcta	cgtcaacagg	720
agcctgcctg	gcctgattgg	ctgccacagg	aagagcgtgt	actggcatgt	gatcggcattg	780
ggcaccaccc	ctgaggtgca	cagcatcttc	ctggagggcc	acaccttcct	ggtcaggaac	840
cacaggcagg	ccagcctgga	gatcagcccc	atcaccttcc	tgaccgcca	gacctgctg	900
atggacctgg	gccagttcct	gctgttctgc	cacatctcca	gccaccagca	cgacggcatg	960
gaggcctacg	tgaagtga	cagctgccct	gaggagcccc	agctgaggat	gaagaacaac	1020
gaggaggccg	aggactatga	tgacgacctg	accgacagcg	agatggacgt	ggtcaggttc	1080
gacgacgaca	acagccccag	cttcatccag	atcaggagcg	tggccaagaa	gcacccaag	1140
acctgggtgc	actacatcgc	tgctgaggag	gaggactggg	actatgcccc	cctgggtgctg	1200
gcccctgatg	acaggagcta	caagagccag	tacctgaaca	atggcccca	gaggattggc	1260
aggaagtaca	agaaagtcag	gttcatggcc	tacactgatg	aaaccttcaa	gaccagggag	1320
gccatccagc	atgagtctgg	catcctgggc	cccctgctgt	acggggagggt	gggggacacc	1380
ctgctgatca	tcttcaagaa	ccaggccagc	aggccctaca	acatctaccc	ccatggcatc	1440
accgacgtga	ggcccctgta	cagcaggagg	ctgcctaagg	gggtgaagca	cctgaaagac	1500
ttccccatcc	tgcttgggga	gatcttcaag	tacaagtga	ctgtgactgt	ggaggacggc	1560
cccaccaaga	gcgaccccag	gtgcctgacc	agatactaca	gcagcttcgt	caacatggag	1620
agggacctgg	cctctggcct	gattggcccc	ctgctgatct	gctacaagga	gtctgtggac	1680
cagaggggca	accagatcat	gagcgacaag	aggaacgtga	tcctgttctc	tgtc	1734

<210> 14
 <211> 2583
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-26-CT

<400> 14	
ttcgacgaga	acaggagctg gtacctcact gaaaacatcc agaggttcct cccaaacccc 60
gcaggagtgc	aactggagga ccctgagttt caggcctcga atatcatgca ctcgattaac 120

ggttacgtgt	tcgactcgct	gcagctgagc	gtgtgcctcc	atgaagtcgc	ttactggtac	180
attctgtcca	tcggcgccca	gactgacttc	ctgagcgtgt	tcttttccgg	ttacaccttt	240
aagcacaaga	tgggtgtacga	agataccctg	accctgttcc	ctttctccgg	cgaaacggtg	300
ttcatgtcga	tggagaaccc	gggtctgtgg	attctgggat	gccacaacag	cgactttcgg	360
aaccgcggaa	tgactgccct	gctgaagggt	tcctcatgcg	acaagaacac	cggagactac	420
tacgaggact	cctacgagga	tatctcagcc	tacctcctgt	ccaagaacaa	cgcgatcgag	480
ccgcgcagct	tcagccagaa	cccgccctgt	ctgaagaggc	accagcgaga	aattaccctg	540
accacctctc	aatcggatca	ggaggaaaatc	gactacgacg	acaccatctc	ggtggaaatg	600
aagaagggaag	atttcgatata	ctacgacgag	gacgaaaatc	agtcccctcg	ctcattccaa	660
aagaaaacta	gacactactt	tatcgccgcg	gtggaaagac	tgtgggacta	tggaatgtca	720
tccagccctc	acgtccttcg	gaaccggggc	cagagcggat	cggtgcctca	gttcaagaaa	780
gtggtgttcc	aggagtccac	cgacggcagc	ttcaccagc	cgctgtaccg	gggagaactg	840
aacgaacacc	tgggcctgct	cggtccctac	atccgcgcgg	aagtggagga	taacatcatg	900
gtgaccttcc	gtaaccaagc	atccagacct	tactccttct	attcctccct	gatctcatac	960
gaggaggacc	agcgccaagg	cgccgagccc	cgcaagaact	tcgtcaagcc	caacgagact	1020
aagacctact	tctggaagg	ccaacacccat	atggccccga	ccaaggatga	gtttgactgc	1080
aaggcctggg	cctactttctc	cgacgtggac	cttgagaagg	atgtccattc	cggcctgac	1140
gggccgctgc	tcgtgtgtca	caccaacacc	ctgaaccag	cgcatggacg	ccaggtcacc	1200
gtccaggagt	ttgctctgtt	cttcaccatt	tttgacgaaa	ctaagtcctg	gtacttcacc	1260
gagaatatgg	agcgaaactg	tagagcgccc	tgcaatatcc	agatggaaga	tccgactttc	1320
aaggagaact	atagattcca	cgccatcaac	gggtacatca	tggatactct	gccggggctg	1380
gtcatggccc	aggatcagag	gattcgggtg	tacttgctgt	caatgggatc	gaacgaaaac	1440
attcactcca	ttcactttctc	cggtcacgtg	ttcactgtgc	gcaagaagga	ggagtacaag	1500
atggcgctgt	acaatctgta	ccccgggggtg	ttcgaaactg	tggagatgct	gccgtccaag	1560
gccggcatct	ggagagtggga	gtgcctgac	ggagagcacc	tccacgcggg	gatgtccacc	1620
ctcttcctgg	tgtactcgaa	taagtgccag	accccgctgg	gcatggcctc	gggccacatc	1680
agagacttcc	agatcacagc	aagcggacaa	tacggccaat	gggcgccgaa	gctggcccg	1740
ttgcactact	ccggatcgat	caacgcgatg	tccaccaagg	aaccgttctc	gtggattaag	1800
gtggacctcc	tggcccctat	gattatccac	ggaattaaga	cccagggcgc	caggcagaag	1860
ttctcctccc	tgtacatctc	gcaattcatc	atcatgtaca	gcctggacgg	gaagaagtgg	1920
cagacttaca	ggggaaactc	caccggcacc	ctgatgggtct	ttttcggcaa	cgtggattcc	1980
tccggcatta	agcacaacat	cttcaaccca	ccgatcatag	ccagatatat	taggctccac	2040

```

cccactcact actcaatccg ctcaactctt cggatggaac tcatggggtg cgacctgaac      2100
tcctgctcca tgccgttggg gatggaatca aaggctatta gcgacgcca gatcacgcg      2160
agctcctact tcactaacat gttcgccacc tggagcccct ccaaggccag gctgcacttg      2220
cagggacggt caaatgcctg gcggccgcaa gtgaacaatc cgaaggaatg gcttcaagtg      2280
gatttcctaaa agaccatgaa agtgaccgga gtcaccaccc agggagtga gtccttctg      2340
acctcgatgt atgtgaagga gttcctgatt agcagcagcc aggacgggca ccagtggacc      2400
ctgttcttcc aaaacggaaa ggtcaagggtg ttccagggga accaggactc gttcacaccc      2460
gtgggtgaact ccctggaccc cccactgctg acgcggtact tgaggattca tcctcagtcc      2520
tggggtccatc agattgcatt gcgaatggaa gtcctgggct gcgaggccca ggacctgtac      2580
tga                                                                           2583

```

```

<210> 15
<211> 2332
<212> PRT
<213> Homo sapiens

```

```

<400> 15

```

```

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1          5          10          15

```

```

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
          20          25          30

```

```

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
          35          40          45

```

```

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
          50          55          60

```

```

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
          65          70          75          80

```

```

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
          85          90          95

```

```

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
          100          105          110

```

```

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
          115          120          125

```

```

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
          130          135          140

```

Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	Tyr	Leu	Ser	145	150	155	160
His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	Gly	Ala	Leu	165	170	175	
Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	Gln	Thr	Leu	180	185	190	
His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	Lys	Ser	Trp	195	200	205	
His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	Ala	Ala	Ser	210	215	220	
Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	Val	Asn	Arg	225	230	235	240
Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	Tyr	Trp	His	245	250	255	
Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	Phe	Leu	Glu	260	265	270	
Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	Leu	Glu	Ile	275	280	285	
Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	Asp	Leu	Gly	290	295	300	
Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	Asp	Gly	Met	305	310	315	320
Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg	325	330	335	
Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp	Leu	Thr	Asp	340	345	350	
Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser	Pro	Ser	Phe	355	360	365	
Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr	Trp	Val	His	370	375	380	
Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro	Leu	Val	Leu	385	390	395	400

Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn	Asn	Gly	Pro		
				405					410					415			
Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met	Ala	Tyr	Thr		
			420					425						430			
Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu	Ser	Gly	Ile		
		435					440					445					
Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu	Leu	Ile	Ile		
	450					455					460						
Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro	His	Gly	Ile		
465					470					475					480		
Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys	Gly	Val	Lys		
				485					490					495			
His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe	Lys	Tyr	Lys		
			500					505					510				
Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	Pro	Arg	Cys		
		515					520					525					
Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	Asp	Leu	Ala		
	530					535					540						
Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	Ser	Val	Asp		
545					550					555					560		
Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	Ile	Leu	Phe		
				565					570					575			
Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	Asn	Ile	Gln		
			580					585					590				
Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	Pro	Glu	Phe		
		595					600					605					
Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	Phe	Asp	Ser		
	610					615					620						
Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	Tyr	Ile	Leu		
625					630					635					640		
Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	Ser	Gly	Tyr		
				645					650					655			

Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	Leu	Phe	Pro	660	665	670	
Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp	675	680	685	
Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	Met	Thr	Ala	690	695	700	
Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	Tyr	Tyr	Glu	705	710	715	720
Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala	725	730	735	
Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	Ser	Thr	Arg	740	745	750	
Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys	755	760	765	
Thr	Asp	Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn	770	775	780	
Val	Ser	Ser	Ser	Asp	Leu	Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro	785	790	795	800
His	Gly	Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe	805	810	815	
Ser	Asp	Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Leu	Ser	820	825	830	
Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val	835	840	845	
Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly	850	855	860	
Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser	865	870	875	880
Thr	Ser	Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn	Leu	Ala	Ala	885	890	895	
Gly	Thr	Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met	Pro	Val	His	900	905	910	

Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys Ser Ser Pro
 915 920 925

Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn Asn Asp
 930 935 940

Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp
 945 950 955 960

Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys
 965 970 975

Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys
 980 985 990

Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala
 995 1000 1005

Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu Ile Glu
 1010 1015 1020

Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr Glu
 1025 1030 1035

Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
 1040 1045 1050

Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr
 1055 1060 1065

Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly
 1070 1075 1080

Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met Ser Phe Phe Lys
 1085 1090 1095

Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile Gln Arg Thr His
 1100 1105 1110

Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro Lys Gln
 1115 1120 1125

Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe
 1130 1135 1140

Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr
 1145 1150 1155

Lys	Asp	Val	Gly	Leu	Lys	Glu	Met	Val	Phe	Pro	Ser	Ser	Arg	Asn
1160						1165					1170			
Leu	Phe	Leu	Thr	Asn	Leu	Asp	Asn	Leu	His	Glu	Asn	Asn	Thr	His
1175						1180					1185			
Asn	Gln	Glu	Lys	Lys	Ile	Gln	Glu	Glu	Ile	Glu	Lys	Lys	Glu	Thr
1190						1195					1200			
Leu	Ile	Gln	Glu	Asn	Val	Val	Leu	Pro	Gln	Ile	His	Thr	Val	Thr
1205						1210					1215			
Gly	Thr	Lys	Asn	Phe	Met	Lys	Asn	Leu	Phe	Leu	Leu	Ser	Thr	Arg
1220						1225					1230			
Gln	Asn	Val	Glu	Gly	Ser	Tyr	Asp	Gly	Ala	Tyr	Ala	Pro	Val	Leu
1235						1240					1245			
Gln	Asp	Phe	Arg	Ser	Leu	Asn	Asp	Ser	Thr	Asn	Arg	Thr	Lys	Lys
1250						1255					1260			
His	Thr	Ala	His	Phe	Ser	Lys	Lys	Gly	Glu	Glu	Glu	Asn	Leu	Glu
1265						1270					1275			
Gly	Leu	Gly	Asn	Gln	Thr	Lys	Gln	Ile	Val	Glu	Lys	Tyr	Ala	Cys
1280						1285					1290			
Thr	Thr	Arg	Ile	Ser	Pro	Asn	Thr	Ser	Gln	Gln	Asn	Phe	Val	Thr
1295						1300					1305			
Gln	Arg	Ser	Lys	Arg	Ala	Leu	Lys	Gln	Phe	Arg	Leu	Pro	Leu	Glu
1310						1315					1320			
Glu	Thr	Glu	Leu	Glu	Lys	Arg	Ile	Ile	Val	Asp	Asp	Thr	Ser	Thr
1325						1330					1335			
Gln	Trp	Ser	Lys	Asn	Met	Lys	His	Leu	Thr	Pro	Ser	Thr	Leu	Thr
1340						1345					1350			
Gln	Ile	Asp	Tyr	Asn	Glu	Lys	Glu	Lys	Gly	Ala	Ile	Thr	Gln	Ser
1355						1360					1365			
Pro	Leu	Ser	Asp	Cys	Leu	Thr	Arg	Ser	His	Ser	Ile	Pro	Gln	Ala
1370						1375					1380			
Asn	Arg	Ser	Pro	Leu	Pro	Ile	Ala	Lys	Val	Ser	Ser	Phe	Pro	Ser
1385						1390					1395			

Ile	Arg	Pro	Ile	Tyr	Leu	Thr	Arg	Val	Leu	Phe	Gln	Asp	Asn	Ser
1400						1405					1410			
Ser	His	Leu	Pro	Ala	Ala	Ser	Tyr	Arg	Lys	Lys	Asp	Ser	Gly	Val
1415						1420					1425			
Gln	Glu	Ser	Ser	His	Phe	Leu	Gln	Gly	Ala	Lys	Lys	Asn	Asn	Leu
1430						1435					1440			
Ser	Leu	Ala	Ile	Leu	Thr	Leu	Glu	Met	Thr	Gly	Asp	Gln	Arg	Glu
1445						1450					1455			
Val	Gly	Ser	Leu	Gly	Thr	Ser	Ala	Thr	Asn	Ser	Val	Thr	Tyr	Lys
1460						1465					1470			
Lys	Val	Glu	Asn	Thr	Val	Leu	Pro	Lys	Pro	Asp	Leu	Pro	Lys	Thr
1475						1480					1485			
Ser	Gly	Lys	Val	Glu	Leu	Leu	Pro	Lys	Val	His	Ile	Tyr	Gln	Lys
1490						1495					1500			
Asp	Leu	Phe	Pro	Thr	Glu	Thr	Ser	Asn	Gly	Ser	Pro	Gly	His	Leu
1505						1510					1515			
Asp	Leu	Val	Glu	Gly	Ser	Leu	Leu	Gln	Gly	Thr	Glu	Gly	Ala	Ile
1520						1525					1530			
Lys	Trp	Asn	Glu	Ala	Asn	Arg	Pro	Gly	Lys	Val	Pro	Phe	Leu	Arg
1535						1540					1545			
Val	Ala	Thr	Glu	Ser	Ser	Ala	Lys	Thr	Pro	Ser	Lys	Leu	Leu	Asp
1550						1555					1560			
Pro	Leu	Ala	Trp	Asp	Asn	His	Tyr	Gly	Thr	Gln	Ile	Pro	Lys	Glu
1565						1570					1575			
Glu	Trp	Lys	Ser	Gln	Glu	Lys	Ser	Pro	Glu	Lys	Thr	Ala	Phe	Lys
1580						1585					1590			
Lys	Lys	Asp	Thr	Ile	Leu	Ser	Leu	Asn	Ala	Cys	Glu	Ser	Asn	His
1595						1600					1605			
Ala	Ile	Ala	Ala	Ile	Asn	Glu	Gly	Gln	Asn	Lys	Pro	Glu	Ile	Glu
1610						1615					1620			
Val	Thr	Trp	Ala	Lys	Gln	Gly	Arg	Thr	Glu	Arg	Leu	Cys	Ser	Gln
1625						1630					1635			

Asn	Pro	Pro	Val	Leu	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr
1640						1645					1650			
Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile
1655						1660					1665			
Ser	Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp
1670						1675					1680			
Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr
1685						1690					1695			
Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser
1700						1705					1710			
Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro
1715						1720					1725			
Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe
1730						1735					1740			
Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu
1745						1750					1755			
Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val
1760						1765					1770			
Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser
1775						1780					1785			
Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg
1790						1795					1800			
Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys
1805						1810					1815			
Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys
1820						1825					1830			
Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His
1835						1840					1845			
Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu
1850						1855					1860			
Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu
1865						1870					1875			

Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu
1880						1885					1890			
Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu
1895						1900					1905			
Asp	Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly
1910						1915					1920			
Tyr	Ile	Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln
1925						1930					1935			
Arg	Ile	Arg	Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile
1940						1945					1950			
His	Ser	Ile	His	Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys
1955						1960					1965			
Glu	Glu	Tyr	Lys	Met	Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe
1970						1975					1980			
Glu	Thr	Val	Glu	Met	Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val
1985						1990					1995			
Glu	Cys	Leu	Ile	Gly	Glu	His	Leu	His	Ala	Gly	Met	Ser	Thr	Leu
2000						2005					2010			
Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	Ala
2015						2020					2025			
Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr
2030						2035					2040			
Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser
2045						2050					2055			
Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val
2060						2065					2070			
Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	Gly
2075						2080					2085			
Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile
2090						2095					2100			
Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn
2105						2110					2115			

Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser
2120						2125					2130			
Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr
2135						2140					2145			
Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg
2150						2155					2160			
Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu
2165						2170					2175			
Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser
2180						2185					2190			
Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala
2195						2200					2205			
Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val
2210						2215					2220			
Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met
2225						2230					2235			
Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr
2240						2245					2250			
Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly
2255						2260					2265			
His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe
2270						2275					2280			
Gln	Gly	Asn	Gln	Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp
2285						2290					2295			
Pro	Pro	Leu	Leu	Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp
2300						2305					2310			
Val	His	Gln	Ile	Ala	Leu	Arg	Met	Glu	Val	Leu	Gly	Cys	Glu	Ala
2315						2320					2325			
Gln	Asp	Leu	Tyr											
2330														

<210> 16
 <211> 4371
 <212> DNA

<213> Artificial Sequence

<220>

<223> BDD-FVIII (non-optimized; "parental"), Nucleotide Sequence

<400> 16

atgcaaatag agctctccac ctgcttcttt ctgtgccttt tgcgattctg ctttagtgcc	60
accagaagat actacctggg tgcagtggaa ctgtcatggg actatatgca aagtgatctc	120
ggtgagctgc ctgtggacgc aagatttcct cctagagtgc caaaatcttt tccattcaac	180
acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct tttcaacatc	240
gctaagccaa ggccaccctg gatgggtctg ctaggtccta ccatccaggc tgaggtttat	300
gatacagtgg tcattacact taagaacatg gcttcccatc ctgtcagtct tcatgctggt	360
ggtgtatcct actggaaagc ttctgagggg gctgaatatg atgatcagac cagtcaaagg	420
gagaaagaag atgataaagt cttccctggg ggaagccata catatgtctg gcaggtcctg	480
aaagagaatg gtccaatggc ctctgaccca ctgtgcctta cctactcata tctttctcat	540
gtggacctgg taaaagactt gaattcaggc ctcattggag ccctactagt atgtagagaa	600
gggagtctgg ccaaggaaaa gacacagacc ttgcacaaat ttatactact ttttgctgta	660
tttgatgaag ggaaaagttg gcactcagaa acaaagaact ccttgatgca ggatagggat	720
gctgcatctg ctcgggcctg gcctaaaatg cacacagtca atggttatgt aaacaggctct	780
ctgccaggtc tgattggatg ccacaggaaa tcagtctatt ggcattgtgat tggaatgggc	840
accactcctg aagtgcactc aatattcctc gaaggtcaca catttcttgt gaggaaccat	900
cgccaggcgt ccttggaat ctcgccaata actttcctta ctgctcaaac actccttgatg	960
gaccttggac agtttctact gttttgtcat atctcttccc accaacaatga tggcatggaa	1020
gcttatgtca aagtagacag ctgtccagag gaacccaac tacgaatgaa aaataatgaa	1080
gaagcggaa actatgatga tgatcttact gattctgaaa tggatgtggg caggtttgat	1140
gatgacaact ctcttcctt tatccaaatt cgctcagttg ccaagaagca tcctaaaact	1200
tgggtacatt acattgctgc tgaagaggag gactgggact atgctccctt agtcctcgcc	1260
cccgatgaca gaagttataa aagtcaatat ttgaacaatg gccctcagcg gattggtagg	1320
aagtacaaaa aagtccgatt tatggcatac acagatgaaa cctttaagac tcgtgaagct	1380
attcagcatg aatcaggaat cttgggacct ttactttatg gggaaagttg agacacactg	1440
ttgattatat ttaagaatca agcaagcaga ccatataaca tctaccctca cggaatcact	1500
gatgtccgtc ctttgtattc aaggagatta ccaaaggtg taaaacattt gaaggatttt	1560
ccaattctgc caggagaaat attcaaatat aaatggacag tgactgtaga agatgggcca	1620
actaaatcag atcctcgggtg cctgaccgcg tattactcta gtttcgttaa tatggagaga	1680
gatctagctt caggactcat tggccctctc ctcatctgct acaaagaatc tgtagatcaa	1740

agaggaaacc	agataatgtc	agacaagagg	aatgtcatcc	tgttttctgt	atttgatgag	1800
aaccgaagct	ggtacctcac	agagaatata	caacgctttc	tccccaatcc	agctggagtg	1860
cagcttgagg	atccagagtt	ccaagcctcc	aacatcatgc	acagcatcaa	tggctatggt	1920
tttgatagtt	tgcagttgtc	agtttgtttg	catgaggtgg	catactggta	cattctaagc	1980
attggagcac	agactgactt	cctttctgtc	ttcttctctg	gatatacctt	caaacacaaa	2040
atggtctatg	aagacacact	caccctattc	ccattctcag	gagaaactgt	cttcatgtcg	2100
atggaaaacc	caggtctatg	gattctgggg	tgccacaact	cagactttcg	gaacagaggc	2160
atgaccgcct	tactgaaggt	ttctagttgt	gacaagaaca	ctggtgatta	ttacgaggac	2220
agttatgaag	atatttcagc	atacttgctg	agtaaaaaca	atgccattga	accaagaagc	2280
ttctctcaaa	accaccagt	cttgaaacgc	catcaacggg	aaataactcg	tactactctt	2340
cagtcagatc	aagaggaaat	tgactatgat	gataccatat	cagttgaaat	gaagaaggaa	2400
gattttgaca	tttatgatga	ggatgaaaat	cagagccccc	gcagctttca	aaagaaaaca	2460
cgacactatt	ttattgctgc	agtggagagg	ctctgggatt	atgggatgag	tagctcccca	2520
catgttctaa	gaaacagggc	tcagagtggc	agtgtccctc	agttcaagaa	agttgttttc	2580
caggaattta	ctgatggctc	ctttactcag	cccttatacc	gtggagaact	aatgaacat	2640
ttgggactcc	tggggccata	tataagagca	gaagttgaag	ataatatcat	ggtaactttc	2700
agaaatcagg	cctctcgtcc	ctattccttc	tattctagcc	ttattttcta	tgaggaagat	2760
cagaggcaag	gagcagaacc	tagaaaaaac	tttgtcaagc	ctaataaaac	caaaacttac	2820
ttttggaaaag	tgcaacatca	tatggcaccc	actaaagatg	agtttgactg	caaagcctgg	2880
gcttattttct	ctgatgttga	cctggaaaaa	gatgtgcact	caggcctgat	tggacccctt	2940
ctggtctgcc	acactaacac	actgaaccct	gctcatggga	gacaagtgac	agtacaggaa	3000
tttgctctgt	ttttcaccat	ctttgatgag	accaaagct	ggtacttcac	tgaaaatatg	3060
gaaagaaact	gcagggtcc	ctgcaatatc	cagatggaag	atcccacttt	taaagagaat	3120
tatcgcttcc	atgcaatcaa	tggctacata	atggatacac	tacctggctt	agtaatggct	3180
caggatcaaa	ggattcgatg	gtatctgctc	agcatgggca	gcaatgaaaa	catccattct	3240
attcattttca	gtggacatgt	gttcaactgta	cgaaaaaaaag	aggagtataa	aatggcactg	3300
tacaatctct	atccaggtgt	ttttgagaca	gtggaaatgt	taccatccaa	agctggaatt	3360
tggcggttg	aatgccttat	tggcgagcat	ctacatgctg	ggatgagcac	actttttctg	3420
gtgtacagca	ataagtgtca	gactcccctg	ggaatggctt	ctggacacat	tagagatttt	3480
cagattacag	cttcaggaca	atatggacag	tgggccccaa	agctggccag	acttcattat	3540
tccggatcaa	tcaatgcctg	gagcaccaag	gagccctttt	cttggatcaa	ggtggatctg	3600
ttggcaccaa	tgattattca	cggcatcaag	accaggggtg	cccgtcagaa	gttctccagc	3660

ctctacatct ctcagtttat catcatgtat agtcttgatg ggaagaagtg gcagacttat 3720
 cgaggaaatt ccactggaac cttaatggtc ttctttggca atgtggattc atctgggata 3780
 aaacacaata tttttaaccc tccaattatt gctcgatata tccgtttgca cccaactcat 3840
 tatagcattc gcagcactct tcgcatggag ttgatgggct gtgatttaaa tagttgcagc 3900
 atgccattgg gaatggagag taaagcaata tcagatgcac agattactgc ttcacacctac 3960
 tttaccaata tgtttgccac ctggtctcct tcaaaagctc gacttcacct ccaagggagg 4020
 agtaatgcct ggagacctca ggtgaataat ccaaagagt ggctgcaagt ggacttccag 4080
 aagacaatga aagtcacagg agtaactact cagggagtaa aatctctgct taccagcatg 4140
 tatgtgaagg agttcctcat ctccagcagt caagatggcc atcagtggac tctctttttt 4200
 cagaatggca aagtaaaggt ttttcagga aatcaagact ccttcacacc tgtggtgaac 4260
 tctctagacc caccgttact gactcgctac cttcgaattc acccccagag ttgggtgcac 4320
 cagattgccc tgaggatgga ggttctgggc tgcgaggcac aggacctta c 4371

<210> 17
 <211> 1438
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BDD-FVIII (non-optimized; "parental"), Amino Acid Sequence

<400> 17

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
 1 5 10 15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
 20 25 30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
 35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
 50 55 60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
 65 70 75 80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
 85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
 100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val

115

120

125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
 130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
 145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
 165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
 180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
 195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
 210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
 225 230 235 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
 245 250 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
 260 265 270

Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
 275 280 285

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
 290 295 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
 305 310 315 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
 325 330 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
 340 345 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
 355 360 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His

370

375

380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
 385 390 395 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
 405 410 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
 420 425 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
 435 440 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
 450 455 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
 465 470 475 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
 485 490 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
 500 505 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
 515 520 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
 530 535 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
 545 550 555 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
 565 570 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
 580 585 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
 595 600 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
 610 615 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu

625		630		635		640
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr	645	650	655			
Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro	660	665	670			
Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp	675	680	685			
Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala	690	695	700			
Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu	705	710	715			720
Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala	725	730	735			
Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg His	740	745	750			
Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile	755	760	765			
Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp	770	775	780			
Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys	785	790	795			800
Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly	805	810	815			
Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser	820	825	830			
Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser	835	840	845			
Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu	850	855	860			
Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr	865	870	875			880
Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile						

885

890

895

Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe
 900 905 910

Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His
 915 920 925

Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
 930 935 940

Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro
 945 950 955 960

Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln
 965 970 975

Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr
 980 985 990

Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro
 995 1000 1005

Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg
 1010 1015 1020

Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu
 1025 1030 1035

Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met
 1040 1045 1050

Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val
 1055 1060 1065

Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn
 1070 1075 1080

Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys
 1085 1090 1095

Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His
 1100 1105 1110

Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln
 1115 1120 1125

Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile

1130						1135						1140			
Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	
1145						1150					1155				
Leu	His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	
1160						1165					1170				
Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	
1175						1180					1185				
Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	
1190						1195					1200				
Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	
1205						1210					1215				
Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	
1220						1225					1230				
Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	
1235						1240					1245				
Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	
1250						1255					1260				
Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	
1265						1270					1275				
Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	
1280						1285					1290				
Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	
1295						1300					1305				
Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	
1310						1315					1320				
Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	
1325						1330					1335				
Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	
1340						1345					1350				
Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	
1355						1360					1365				
Ser	Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	

1370

1375

1380

Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro
1385 1390 1395

Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg
1400 1405 1410

Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu
1415 1420 1425

Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
1430 1435

<210> 18

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> XTEN nucleotide sequence

<400> 18

ggcgcgccaa catcagagag cgccaccct gaaagtggc cgggagcga gccagccaca 60
tctgggtcgg aaacgccagg cacaagtgg tctgcaactc ccgagtccgg acctggctcc 120
gagcctgcca ctagcggctc cgagactccg ggaacttccg agagcgctac accagaaagc 180
ggacccggaa ccagtaccga acctagcgag ggctctgctc cgggcagccc agccggctct 240
cctacatcca cggaggaggg cacttccgaa tccgccaccc cggagtcagg gccaggatct 300
gaacccgcta cctcaggcag tgagacgcc ggaacgagcg agtccgctac accggagagt 360
gggccaggga gccctgctgg atctcctacg tccactgagg aagggtcacc agcgggctcg 420
cccaccagca ctgaagaagg tgcctcgagc 450

<210> 19

<211> 4824

<212> DNA

<213> Artificial Sequence

<220>

<223> coFVIII-52-XTEN

<400> 19

atgcaaatcg aactgagcac ctgtttcttc ctctgcctgc tgagattctg tttctccgcg 60
acccgccgat actacctggg agcagtggag ctctcctggg attacatgca gagcgacctt 120
ggggagctgc ccgtggatgc caggttccct ccccggggtgc caaagtcgtt tccgttcaac 180
acctccgtgg tgtacaagaa aactctgttc gtggagttca ccgaccacct gttcaatata 240
gccaaagcca gacctccctg gatgggggctg ttgggacctt ccatccaagc ggaggtgtac 300

gacactgtgg	tcatactct	gaagaacatg	gcctcgcata	ccgtgtccct	gcacgccgtg	360
ggagtgtctt	actggaaagc	gtccgagggg	gccgaatacg	acgaccagac	ctcgcagaga	420
gaaaagggaag	atgacaaggt	gttcccagga	ggatcgcaca	cctacgtgtg	gcaagtgttg	480
aaggagaacg	gccaatggc	ctccgacccg	ctgtgcctga	cctactcgta	cctgtcccac	540
gtggacctcg	tgaaggacct	caactcggga	ctgattggag	ccctgctggg	ctgcagggaa	600
ggctcactgg	cgaagaaaa	gactcagacc	ttgcacaagt	tcattctgct	gttcgctgtg	660
ttcgacgagg	ggaagtcgtg	gcacagcgag	actaagaact	ccctgatgca	agatagagat	720
gccgcctccg	cccgggcctg	gcctaagatg	cacaccgtga	acggttacgt	gaaccgctcc	780
ctccctggcc	tgattggatg	ccaccggaag	tccgtgtact	ggcacgtgat	cgggatgggg	840
accacccccg	aggtgcacag	catcttcctg	gaaggtcaca	catttctcgt	gcgcaaccac	900
cggcaggcct	ccctggaaat	cagccccatt	accttcctca	ctgcccagac	tctgctgatg	960
gacctgggac	agttcctgct	gttctgccat	atctcctccc	accaacatga	cggaatggag	1020
gcatactga	aggtcgattc	ctgccctgag	gaaccccagc	tccgcatgaa	gaacaatgag	1080
gaagccgagg	actacgacga	cgacctgacg	gatagcgaga	tggatgtggg	ccggttcgat	1140
gacgataaca	gcccttcctt	catccaaatt	cgctcgggtg	caaagaagca	ccccagacc	1200
tgggtgcatt	acattgcggc	ggaagaagag	gactgggatt	atgccccgct	tgtcctcgct	1260
cctgacgacc	ggagctacaa	gagccagtac	ctgaacaacg	gtccacagag	gatcggtaga	1320
aagtacaaga	aggtccgctt	catggcctat	accgacgaaa	ccttcaaaac	tagagaggcc	1380
atccaacacg	aatccggcat	cctgggcccg	ctcttgtagc	gagaagtcgg	cgacaccctt	1440
ctcattatct	tcaagaacca	ggcttcccgg	ccgtacaaca	tctatccgca	tgggatcact	1500
gacgtgcgcc	cactgtactc	gcggcgcctg	cccaaggggtg	tcaaacacct	gaaggatttt	1560
ccgatccttc	cgggagaaat	cttcaagtac	aagtggaccg	tgaccgtgga	agatggccca	1620
actaagtctg	accctagatg	cctcaccgcg	tactactcat	ccttcgtcaa	catggagcgc	1680
gacctggcca	gcggactgat	cggcccgcgtg	ctgatttgct	acaaggaatc	agtggaccaa	1740
cggggaaacc	agatcatgtc	ggataagagg	aacgtcatcc	tcttctccgt	gtttgacgaa	1800
aaccggtcgt	ggtacctgac	cgagaacatc	cagaggttcc	tgcccaaccc	tgctgggggtg	1860
cagctggagg	accccagatt	ccaggccagc	aacatcatgc	acagcatcaa	tggctacgtg	1920
ttcgacagcc	tgcagctgag	cgtgtgcctg	cacgaggtgg	cctactggta	catcctgagc	1980
atcggcgccc	agaccgactt	cctgagcgtg	ttcttctctg	gctacacctt	caagcacaag	2040
atgggtgtatg	aggacaccct	gaccctgttc	cccttcagcg	gggagactgt	cttcatgagc	2100
atggagaacc	ctggcctgtg	gatcctgggc	tgccacaaca	gcgacttcag	gaacaggggc	2160
atgactgccc	tgctgaaagt	ctccagctgt	gacaagaaca	ccgggggacta	ctacgaggac	2220

agctacgagg	acatcagcgc	ctacctgctg	agcaagaaca	atgccatcga	gcccaggagc	2280
ttctctcaga	acggcgcgcc	aacatcagag	agcgccaccc	ctgaaagtgg	tcccgggagc	2340
gagccagcca	catctgggtc	ggaaacgcca	ggcacaagtg	agtctgcaac	tcccgagtcc	2400
ggacctggct	ccgagcctgc	cactagcggc	tccgagactc	cgggaacttc	cgagagcgct	2460
acaccagaaa	gcggacccgg	aaccagtacc	gaacctagcg	agggctctgc	tccgggcagc	2520
ccagccggct	ctcctacatc	cacggaggag	ggcacttccg	aatccgccac	cccggagtca	2580
gggccaggat	ctgaaccgcg	tacctcaggc	agtgagacgc	caggaacgag	cgagtccgct	2640
acaccggaga	gtggggccagg	gagccctgct	ggatctccta	cgtccactga	ggaagggta	2700
ccagcgggct	cggccaccag	cactgaagaa	ggtgcctcga	gccccccagt	gctgaagagg	2760
caccagaggg	agatcaccag	gaccaccctg	cagtctgacc	aggaggagat	cgactatgat	2820
gacaccatca	gcgtggagat	gaagaaggag	gacttcgaca	tctacgacga	ggacgagaac	2880
cagagcccca	ggagcttcca	gaagaagacc	aggcactact	tcattgctgc	tgtggagagg	2940
ctgtgggact	atggcatgtc	cagcagcccc	catgtgctga	ggaacagggc	ccagtctggc	3000
agcgtgcccc	agttcaagaa	agtcgtgttc	caggagtcca	ccgacggcag	cttcacccag	3060
cccctgtaca	gaggggagct	gaacgagcac	ctgggcctgc	tggggccccta	catcagggcc	3120
gaggtggagg	acaacatcat	ggtgaccttc	aggaaccagg	ccagcaggcc	ctacagcttc	3180
tacagcagcc	tgatcagcta	cgaggaggac	cagaggcagg	gggctgagcc	caggaagaac	3240
tttgtgaagc	ccaatgaaac	caagacctac	ttctggaagg	tgcagcacca	catggccccc	3300
accaaggacg	agttcgactg	caaggcctgg	gcctacttct	ctgacgtgga	cctggagaag	3360
gacgtgcact	ctggcctgat	tggccccctg	ctggtgtgcc	acaccaacac	cctgaaccct	3420
gcccattggca	ggcaggtgac	tgtgcaggag	ttcgccctgt	tcttcaccat	cttcgatgaa	3480
accaagagct	ggtacttcac	tgagaacatg	gagaggaact	gcagggcccc	ctgcaacatc	3540
cagatggagg	acccacctt	caaggagaac	tacaggttcc	atgccatcaa	tggctacatc	3600
atggacaccc	tgcttggcct	ggtcatggcc	caggaccaga	ggatcagggtg	gtatctgctg	3660
agcatgggca	gcaacgagaa	catccacagc	atccacttct	ctggccacgt	gttcactgtg	3720
aggaagaagg	aggagtacaa	gatggccctg	tacaacctgt	accctggggg	gttcgaaacc	3780
gtggagatgc	tgcccagcaa	ggccggcatc	tggaggggtg	agtgcctgat	tggggagcac	3840
ctgcacgccg	gcatgagcac	cctgttcctg	gtgtacagca	acaagtgcc	gacccccctg	3900
ggcatggcct	ctggccacat	cagggacttc	cagatcactg	cctctggcca	gtacggccag	3960
tggggcccca	agctggccag	gctgcactac	tccggaagca	tcaatgcctg	gagcaccaag	4020
gagcccttca	gctggatcaa	agtggacctg	ctggcccca	tgatcatcca	cggcatcaag	4080
accagggggg	ccaggcagaa	gttctccagc	ctgtacatca	gccagttcat	catcatgtac	4140

agcctggacg gcaagaagtg gcagacctac aggggcaaca gcaccggcac cctgatggtg	4200
tttttcggca acgtggacag cagcggcatc aagcacaaca ttttcaaccc ccccatcatc	4260
gccagataca tcaggctgca ccccacccac tacagcatca ggagcaccct gaggatggag	4320
ctgatgggct gtgacctgaa cagctgcagc atgcccctgg gcatggagag caaggccatc	4380
tctgacgccc agatcactgc ctccagctac ttcaccaaca tgtttgccac ctggagcccc	4440
agcaaggcca ggctgcacct gcagggcagg agcaatgcct ggaggcccca ggtcaacaac	4500
cccaaggagt ggctgcaggt ggacttccag aagaccatga aggtgactgg ggtgaccacc	4560
caggggggtga agagcctgct gaccagcatg tacgtgaagg agttcctgat ctccagcagc	4620
caggacggcc accagtggac cctgttcttc cagaatggca aggtgaagggt gttccagggc	4680
aaccaggaca gcttcacccc tgtgggtcaac agcctggacc cccccctgct gaccagatac	4740
ctgaggatcc acccccagag ctgggtgcac cagatcgccc tgaggatgga ggtgctgggc	4800
tgtgaggccc aggacctgta ctga	4824

<210> 20
 <211> 4824
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-1-XTEN

<400> 20	
atgcagattg agctgtctac ttgctttttc ctgtgcctgc tgaggttttg cttttccgct	60
acacgaagggt attatctggg ggctgtggaa ctgtcttggg attacatgca gagtgcctg	120
ggagagctgc cagtggacgc aaggtttccc cctagagtcc ctaagtcatt ccccttcaac	180
actagcgtgg tctacaagaa aacactgttc gtggagttta ctgatcacct gttcaacatc	240
gcaaagccta ggccaccctg gatgggactg ctggggccaa caatccaggc cgagggtgtac	300
gacaccgtgg tcattacact taagaacatg gcctcacacc ccgtgagcct gcatgctgtg	360
ggcgctcagct actggaaggc ttccgaagga gcagagtatg acgatcagac ttcccagaga	420
gaaaaagagg acgataagggt gtttcctggc ggatctcata cctacgtgtg gcaggtcctg	480
aaagagaatg gccctatggc ctccgaccct ctgtgcctga cctactctta tctgagtcac	540
gtggacctgg tcaaggatct gaacagcggc ctgatcggag ccctgctggt gtgcagggaa	600
ggaagcctgg ctaaggagaa aaccagaca ctgcataagt tcattctgct gttcgccgtg	660
tttgacgaag ggaaatcatg gcacagcgag acaaagaata gtctgatgca ggacagggat	720
gccgcttcag ccagagcttg gcccaaaatg cacactgtga acggctacgt caatcgctca	780
ctgcctgggc tgatcggctg ccaccgaaag agcgtgtatt ggcatgtcat cgggatgggc	840
accacacctg aagtgcactc cattttcctg gagggacata cctttctggt ccgcaaccac	900

cgacaggctt	ccctggagat	ctctccaatt	accttcctga	cagcacagac	tctgctgatg	960
gacctggggc	agttcctgct	gttttgccac	atcagctccc	accagcatga	tgccatggag	1020
gcttacgtga	aagtggactc	ttgtcccag	gaacctcagc	tgcggatgaa	gaacaatgag	1080
gaagcagaag	actatgacga	tgacctgacc	gactccgaga	tggatgtggt	ccgattcgat	1140
gacgataaca	gcccctcctt	tatccagatt	agatctgtgg	ccaagaaaca	ccctaagaca	1200
tgggtccatt	acatcgcagc	cgaggaagag	gactgggatt	atgcaccact	ggtgctggca	1260
ccagacgatc	gctcctacaa	atctcagtat	ctgaacaatg	ggccacagag	gattggcaga	1320
aagtacaaga	aagtgcggtt	catggcatat	accgatgaga	ccttcaagac	tcgcgaagcc	1380
atccagcacg	agagcggcat	cctgggacca	ctgctgtacg	gagaagtggg	agacaccctg	1440
ctgatcattt	tcaagaacca	ggccagccgg	ccttacaata	tctatccaca	tggtattaca	1500
gatgtgcgcc	ctctgtacag	caggagactg	ccaaagggcg	tcaaacacct	gaaggacttc	1560
ccaatcctgc	ccggagaaat	cttcaagtac	aagtggactg	tcaccgtcga	ggatggcccc	1620
actaagagcg	accctcgggtg	cctgaccgcg	tactattcta	gtttcgtgaa	tatggaaaga	1680
gatctggcaa	gcggactgat	cggaccactg	ctgatttggt	acaaagagag	cgtggatcag	1740
agaggcaacc	agatcatgtc	cgacaagcgg	aatgtgattc	tgttcagtgt	ctttgacgaa	1800
aacagggtcat	ggtacctgac	cgagaacatc	cagagattcc	tgccataatcc	agctgggggtg	1860
cagctggaag	atcctgagtt	tcaggcatct	aacatcatgc	atagtattaa	tggtctacgtg	1920
ttcgacagtt	tgcagctgag	cgtgtgcctg	cacgaggtcg	cttactggta	tatcctgagc	1980
attggggcac	agacagattt	cctgagcgtg	ttcttttccg	gctacacttt	taagcataaa	2040
atggtctatg	aggacacact	gactctgttc	cccttcagcg	gcgaaaccgt	gtttatgagc	2100
atggagaatc	ccggactgtg	gattctgggg	tgccacaaca	gcgatttcag	aaatcgcgga	2160
atgactgccc	tgctgaaagt	gtcaagctgt	gacaagaaca	ccggggacta	ctatgaagat	2220
tcatacgagg	acatcagcgc	atatctgctg	tccaaaaaca	atgccattga	accccggtct	2280
tttagtcaga	atggcgcgcc	aacatcagag	agcgccaccc	ctgaaagtgg	tcccgggagc	2340
gagccagcca	catctgggtc	ggaaacgcca	ggcacaagtg	agtctgcaac	tcccgagtcc	2400
ggacctggct	ccgagcctgc	cactagcggc	tccgagactc	cgggaaacttc	cgagagcgct	2460
acaccagaaa	gcggacccgg	aaccagtacc	gaacctagcg	agggctctgc	tccgggcagc	2520
ccagccggct	ctcctacatc	cacggaggag	ggcacttccg	aatccgccac	cccggagtca	2580
gggccaggat	ctgaaccgcg	tacctcaggc	agtgagacgc	caggaacgag	cgagtccgct	2640
acaccggaga	gtgggcccagg	gagccctgct	ggatctccta	cgtccactga	ggaagggcca	2700
ccagcgggct	cgcccaccag	cactgaagaa	ggtgcctcga	gccctccagt	gctgaagcgg	2760
caccagcgcg	agatcaccgc	cactaccctg	cagagtgatc	aggaagagat	cgactacgac	2820

gatacaat	ctgtggaa	at	gaagaa	agag	gacttc	gata	tctatg	acga	agatgaga	ac	2880	
cagagtc	cctc	gatcatt	cca	gaagaaa	aacc	aggcatt	act	ttattg	ccgc	agtggag	cgg	2940
ctgtggg	att	atggcat	gtc	ctctag	tcct	cacgtg	ctgc	gaaatag	ggc	ccagtc	agga	3000
agcgtccc	ac	agttca	agaa	agtgg	tcttc	caggag	ttta	cagacg	gggtc	ctttact	cag	3060
ccactgt	taca	ggggc	gaact	gaacg	agcac	ctggg	actgc	tgggg	cccta	tatcag	agca	3120
gaagtgg	agg	ataac	attat	ggtcac	ccttc	agaaat	cagg	cctctc	ggcc	ttacag	tttt	3180
tattca	agcc	tgatct	ctta	cgaag	aggac	cagcg	acagg	gagctg	aacc	acgaaaa	aac	3240
ttcgtg	aagc	ctaatg	agac	caaaac	atac	ttttg	gaag	tgcag	cacca	tatgg	cccca	3300
acaaaag	acg	agttc	gattg	caagg	catgg	gcctat	tttt	ctgac	gtga	tctgg	agaag	3360
gacgtgc	caca	gtggc	ctgat	tggccc	actg	ctgg	tgtgc	atact	aacac	cctga	atcca	3420
gcccac	ggcc	ggcag	gtcac	tgtcc	aggag	ttcg	ctctgt	tcttt	accat	ctttg	atgag	3480
acaaag	agct	ggtact	tcac	cgaaa	acatg	gagcg	aaatt	gcagg	gctcc	atgta	acatt	3540
cagatgg	aag	acccc	acatt	caagg	agaac	taccg	ctttc	atgct	atcaa	tggata	catc	3600
atggata	ctc	tgccc	gggct	ggtc	atggca	cagg	accaga	gaatc	cggtg	gtatc	tgtctg	3660
agcatgg	gca	acgaga	aa	tatcc	actca	attcat	tttca	gcggg	cacgt	gtttact	gtc	3720
aggaaga	aaag	aagagt	tacaa	gatgg	ccctg	taca	acctgt	atccc	ggcgt	gttcg	aaacc	3780
gtcgaga	tgc	cctag	caa	ggccg	gaatc	tggag	agtgg	aatgc	ctgat	tggag	agcac	3840
ctgcat	gctg	ggatg	tctac	cctgt	tttctg	gtgt	acagta	ataag	tgtca	gacac	ccctg	3900
ggaatg	gcat	ccggg	catat	cagg	gatttc	cagatt	accg	catct	ggaca	gtacg	gacag	3960
tgggca	cccta	agctg	gctag	actgc	actat	tccg	gatcta	tcaac	gcttg	gtccac	aaaa	4020
gagcct	tttct	cttgg	attaa	ggtgg	acctg	ctgg	cccca	tgatc	attca	tggcat	caaa	4080
actcag	ggag	ctcgg	cagaa	gttct	cctct	ctgt	acatct	cacag	tttat	catcat	gtac	4140
agcctg	gatg	ggaag	aaatg	gcag	acatac	cg	cggaata	gcac	aggaac	tctgat	gggtg	4200
ttcttt	ggca	acgtg	gacag	cagc	ggaatc	aagca	caaca	tttt	caatcc	cc	tatcatt	4260
gctaga	taca	tccg	gctgca	ccca	acccat	tatt	ctattc	gaag	tacact	gaggat	ggaa	4320
ctgatg	gggat	gcgat	ctgaa	cag	ttgttca	atg	ccccctgg	ggat	ggagtc	caagg	caatc	4380
tctgac	gccc	agatt	accgc	cag	ctcctac	ttc	actaata	tgttt	gctac	ctgg	agccct	4440
tccaa	agcaa	gactg	cacct	gca	aggccgc	agca	acgcat	ggc	gaccaca	ggtga	acaat	4500
cccaag	gagt	ggtt	gcaggt	cgat	ttttcag	aaa	actatga	aggt	gaccgg	ggtc	acaact	4560
cagggc	gtga	aaagt	ctgct	gacct	caatg	tacgt	caagg	agtt	cctgat	ctct	agtcca	4620
caggac	ggac	atcag	tggac	actg	ttcttt	caga	acggga	aggt	gaaagt	cttcc	agggc	4680
aatcag	gatt	ccttt	acacc	tgtg	gtcaac	agt	ctagacc	ctcc	actgct	gacc	agatac	4740

ctgagaatcc accctcagtc ctgggtgcac cagattgccc tgagaatgga agtgctggga	4800
tgcgaggccc aggatctgta ctga	4824
<210> 21	
<211> 6	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> MAR/ARS	
<400> 21	
atattt	6
<210> 22	
<211> 6	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> MAR/ARS	
<400> 22	
aaatat	6
<210> 23	
<211> 5	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> destabilizing element	
<400> 23	
attta	5
<210> 24	
<211> 5	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> destabilizing element	
<400> 24	
taa	5
<210> 25	
<211> 6	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> poly-T site	
<400> 25	
tttttt	6

<210> 26
<211> 7
<212> DNA
<213> Artificial Sequence

<220>
<223> poly-A site

<400> 26
aaaaaaa

7

<210> 27
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> splice site

<400> 27
ggtgat

6

<210> 28
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<223> TATA box

<400> 28
tataa

5

<210> 29
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<223> TATA box

<400> 29
ttata

5

<210> 30
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<223> AU rich sequence element

<400> 30
atattatt

8

<210> 31
<211> 8
<212> DNA

<213> Artificial Sequence

<220>

<223> AU rich sequence element

<400> 31

attttttaa

8

<210> 32

<211> 13

<212> DNA

<213> Artificial Sequence

<220>

<223> kozak consensus sequence

<400> 32

gccgccacca tgc

13

<210> 33

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> CTP peptide

<400> 33

Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser
1 5 10 15

Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu
20 25 30

<210> 34

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> CTP peptide

<400> 34

Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
1 5 10 15

Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
20 25

<210> 35

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> albumin-binding peptide core sequence

<400> 35

Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10

<210> 36

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 36

Ala Ser Pro Ala Ala Pro Ala Pro Ala Ser Pro Ala Ala Pro Ala Pro
1 5 10 15

Ser Ala Pro Ala
20

<210> 37

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 37

Ala Ala Pro Ala Ser Pro Ala Pro Ala Ala Pro Ser Ala Pro Ala Pro
1 5 10 15

Ala Ala Pro Ser
20

<210> 38

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 38

Ala Pro Ser Ser Pro Ser Pro Ser Ala Pro Ser Ser Pro Ser Pro Ala
1 5 10 15

Ser Pro Ser Ser
20

<210> 39

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 39

Ala Pro Ser Ser Pro Ser Pro Ser Ala Pro Ser Ser Pro Ser Pro Ala
1 5 10 15

Ser Pro Ser

<210> 40

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 40

Ser Ser Pro Ser Ala Pro Ser Pro Ser Ser Pro Ala Ser Pro Ser Pro
1 5 10 15

Ser Ser Pro Ala
20

<210> 41

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 41

Ala Ala Ser Pro Ala Ala Pro Ser Ala Pro Pro Ala Ala Ala Ser Pro
1 5 10 15

Ala Ala Pro Ser Ala Pro Pro Ala
20

<210> 42

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> PAS sequence

<400> 42

Ala Ser Ala Ala Ala Pro Ala Ala Ala Ser Ala Ala Ala Ser Ala Pro
1 5 10 15

Ser Ala Ala Ala
20

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> miR142 target

<400> 43
tccataaagt aggaaacact aca

23

<210> 44
<211> 2332
<212> PRT
<213> Homo sapiens

<400> 44

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1 5 10 15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
20 25 30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65 70 75 80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
 165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
 180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
 195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
 210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
 225 230 235 240

Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
 245 250 255

Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
 260 265 270

Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
 275 280 285

Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
 290 295 300

Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
 305 310 315 320

Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
 325 330 335

Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
 340 345 350

Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
 355 360 365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
 370 375 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
 385 390 395 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
 405 410 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
 420 425 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
 435 440 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
 450 455 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
 465 470 475 480

Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
 485 490 495

His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
 500 505 510

Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
 515 520 525

Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
 530 535 540

Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
 545 550 555 560

Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
 565 570 575

Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
 580 585 590

Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
 595 600 605

Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
 610 615 620

Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
 625 630 635 640

Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
 645 650 655

Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
 660 665 670

Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp
		675					680					685			
Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	Met	Thr	Ala
	690					695					700				
Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	Tyr	Tyr	Glu
705					710					715					720
Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	Asn	Asn	Ala
				725					730					735	
Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Ser	Arg	His	Pro	Ser	Thr	Arg
			740					745					750		
Gln	Lys	Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys
		755					760					765			
Thr	Asp	Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn
	770					775					780				
Val	Ser	Ser	Ser	Asp	Leu	Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro
785					790					795					800
His	Gly	Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe
				805					810					815	
Ser	Asp	Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Leu	Ser
			820					825						830	
Glu	Met	Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val
		835					840					845			
Phe	Thr	Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly
	850					855					860				
Thr	Thr	Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser
865					870					875					880
Thr	Ser	Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn	Leu	Ala	Ala
				885					890					895	
Gly	Thr	Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met	Pro	Val	His
			900					905					910		
Tyr	Asp	Ser	Gln	Leu	Asp	Thr	Thr	Leu	Phe	Gly	Lys	Lys	Ser	Ser	Pro
		915					920					925			

Leu	Thr	Glu	Ser	Gly	Gly	Pro	Leu	Ser	Leu	Ser	Glu	Glu	Asn	Asn	Asp
930						935					940				
Ser	Lys	Leu	Leu	Glu	Ser	Gly	Leu	Met	Asn	Ser	Gln	Glu	Ser	Ser	Trp
945					950					955					960
Gly	Lys	Asn	Val	Ser	Ser	Thr	Glu	Ser	Gly	Arg	Leu	Phe	Lys	Gly	Lys
				965					970					975	
Arg	Ala	His	Gly	Pro	Ala	Leu	Leu	Thr	Lys	Asp	Asn	Ala	Leu	Phe	Lys
			980					985					990		
Val	Ser	Ile	Ser	Leu	Leu	Lys	Thr	Asn	Lys	Thr	Ser	Asn	Asn	Ser	Ala
		995					1000					1005			
Thr	Asn	Arg	Lys	Thr	His	Ile	Asp	Gly	Pro	Ser	Leu	Leu	Ile	Glu	
	1010					1015					1020				
Asn	Ser	Pro	Ser	Val	Trp	Gln	Asn	Ile	Leu	Glu	Ser	Asp	Thr	Glu	
	1025					1030					1035				
Phe	Lys	Lys	Val	Thr	Pro	Leu	Ile	His	Asp	Arg	Met	Leu	Met	Asp	
	1040					1045					1050				
Lys	Asn	Ala	Thr	Ala	Leu	Arg	Leu	Asn	His	Met	Ser	Asn	Lys	Thr	
	1055					1060					1065				
Thr	Ser	Ser	Lys	Asn	Met	Glu	Met	Val	Gln	Gln	Lys	Lys	Glu	Gly	
	1070					1075					1080				
Pro	Ile	Pro	Pro	Asp	Ala	Gln	Asn	Pro	Asp	Met	Ser	Phe	Phe	Lys	
	1085					1090					1095				
Met	Leu	Phe	Leu	Pro	Glu	Ser	Ala	Arg	Trp	Ile	Gln	Arg	Thr	His	
	1100					1105					1110				
Gly	Lys	Asn	Ser	Leu	Asn	Ser	Gly	Gln	Gly	Pro	Ser	Pro	Lys	Gln	
	1115					1120					1125				
Leu	Val	Ser	Leu	Gly	Pro	Glu	Lys	Ser	Val	Glu	Gly	Gln	Asn	Phe	
	1130					1135					1140				
Leu	Ser	Glu	Lys	Asn	Lys	Val	Val	Val	Gly	Lys	Gly	Glu	Phe	Thr	
	1145					1150					1155				
Lys	Asp	Val	Gly	Leu	Lys	Glu	Met	Val	Phe	Pro	Ser	Ser	Arg	Asn	
	1160					1165					1170				

Leu	Phe	Leu	Thr	Asn	Leu	Asp	Asn	Leu	His	Glu	Asn	Asn	Thr	His
1175						1180					1185			
Asn	Gln	Glu	Lys	Lys	Ile	Gln	Glu	Glu	Ile	Glu	Lys	Lys	Glu	Thr
1190						1195					1200			
Leu	Ile	Gln	Glu	Asn	Val	Val	Leu	Pro	Gln	Ile	His	Thr	Val	Thr
1205						1210					1215			
Gly	Thr	Lys	Asn	Phe	Met	Lys	Asn	Leu	Phe	Leu	Leu	Ser	Thr	Arg
1220						1225					1230			
Gln	Asn	Val	Glu	Gly	Ser	Tyr	Asp	Gly	Ala	Tyr	Ala	Pro	Val	Leu
1235						1240					1245			
Gln	Asp	Phe	Arg	Ser	Leu	Asn	Asp	Ser	Thr	Asn	Arg	Thr	Lys	Lys
1250						1255					1260			
His	Thr	Ala	His	Phe	Ser	Lys	Lys	Gly	Glu	Glu	Glu	Asn	Leu	Glu
1265						1270					1275			
Gly	Leu	Gly	Asn	Gln	Thr	Lys	Gln	Ile	Val	Glu	Lys	Tyr	Ala	Cys
1280						1285					1290			
Thr	Thr	Arg	Ile	Ser	Pro	Asn	Thr	Ser	Gln	Gln	Asn	Phe	Val	Thr
1295						1300					1305			
Gln	Arg	Ser	Lys	Arg	Ala	Leu	Lys	Gln	Phe	Arg	Leu	Pro	Leu	Glu
1310						1315					1320			
Glu	Thr	Glu	Leu	Glu	Lys	Arg	Ile	Ile	Val	Asp	Asp	Thr	Ser	Thr
1325						1330					1335			
Gln	Trp	Ser	Lys	Asn	Met	Lys	His	Leu	Thr	Pro	Ser	Thr	Leu	Thr
1340						1345					1350			
Gln	Ile	Asp	Tyr	Asn	Glu	Lys	Glu	Lys	Gly	Ala	Ile	Thr	Gln	Ser
1355						1360					1365			
Pro	Leu	Ser	Asp	Cys	Leu	Thr	Arg	Ser	His	Ser	Ile	Pro	Gln	Ala
1370						1375					1380			
Asn	Arg	Ser	Pro	Leu	Pro	Ile	Ala	Lys	Val	Ser	Ser	Phe	Pro	Ser
1385						1390					1395			
Ile	Arg	Pro	Ile	Tyr	Leu	Thr	Arg	Val	Leu	Phe	Gln	Asp	Asn	Ser
1400						1405					1410			

Ser	His	Leu	Pro	Ala	Ala	Ser	Tyr	Arg	Lys	Lys	Asp	Ser	Gly	Val
1415						1420					1425			
Gln	Glu	Ser	Ser	His	Phe	Leu	Gln	Gly	Ala	Lys	Lys	Asn	Asn	Leu
1430						1435					1440			
Ser	Leu	Ala	Ile	Leu	Thr	Leu	Glu	Met	Thr	Gly	Asp	Gln	Arg	Glu
1445						1450					1455			
Val	Gly	Ser	Leu	Gly	Thr	Ser	Ala	Thr	Asn	Ser	Val	Thr	Tyr	Lys
1460						1465					1470			
Lys	Val	Glu	Asn	Thr	Val	Leu	Pro	Lys	Pro	Asp	Leu	Pro	Lys	Thr
1475						1480					1485			
Ser	Gly	Lys	Val	Glu	Leu	Leu	Pro	Lys	Val	His	Ile	Tyr	Gln	Lys
1490						1495					1500			
Asp	Leu	Phe	Pro	Thr	Glu	Thr	Ser	Asn	Gly	Ser	Pro	Gly	His	Leu
1505						1510					1515			
Asp	Leu	Val	Glu	Gly	Ser	Leu	Leu	Gln	Gly	Thr	Glu	Gly	Ala	Ile
1520						1525					1530			
Lys	Trp	Asn	Glu	Ala	Asn	Arg	Pro	Gly	Lys	Val	Pro	Phe	Leu	Arg
1535						1540					1545			
Val	Ala	Thr	Glu	Ser	Ser	Ala	Lys	Thr	Pro	Ser	Lys	Leu	Leu	Asp
1550						1555					1560			
Pro	Leu	Ala	Trp	Asp	Asn	His	Tyr	Gly	Thr	Gln	Ile	Pro	Lys	Glu
1565						1570					1575			
Glu	Trp	Lys	Ser	Gln	Glu	Lys	Ser	Pro	Glu	Lys	Thr	Ala	Phe	Lys
1580						1585					1590			
Lys	Lys	Asp	Thr	Ile	Leu	Ser	Leu	Asn	Ala	Cys	Glu	Ser	Asn	His
1595						1600					1605			
Ala	Ile	Ala	Ala	Ile	Asn	Glu	Gly	Gln	Asn	Lys	Pro	Glu	Ile	Glu
1610						1615					1620			
Val	Thr	Trp	Ala	Lys	Gln	Gly	Arg	Thr	Glu	Arg	Leu	Cys	Ser	Gln
1625						1630					1635			
Asn	Pro	Pro	Val	Leu	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr
1640						1645					1650			

Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile
1655						1660					1665			
Ser	Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp
1670						1675					1680			
Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr
1685						1690					1695			
Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser
1700						1705					1710			
Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro
1715						1720					1725			
Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe
1730						1735					1740			
Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu
1745						1750					1755			
Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val
1760						1765					1770			
Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser
1775						1780					1785			
Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg
1790						1795					1800			
Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys
1805						1810					1815			
Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys
1820						1825					1830			
Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His
1835						1840					1845			
Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu
1850						1855					1860			
Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu
1865						1870					1875			
Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu
1880						1885					1890			

Asn Met 1895	Glu Arg Asn Cys Arg 1900	Ala Pro Cys Asn Ile 1905	Gln Met Glu
Asp Pro 1910	Thr Phe Lys Glu Asn 1915	Tyr Arg Phe His Ala 1920	Ile Asn Gly
Tyr Ile 1925	Met Asp Thr Leu Pro 1930	Gly Leu Val Met Ala 1935	Gln Asp Gln
Arg Ile 1940	Arg Trp Tyr Leu Leu 1945	Ser Met Gly Ser Asn 1950	Glu Asn Ile
His Ser 1955	Ile His Phe Ser Gly 1960	His Val Phe Thr Val 1965	Arg Lys Lys
Glu Glu 1970	Tyr Lys Met Ala Leu 1975	Tyr Asn Leu Tyr Pro 1980	Gly Val Phe
Glu Thr 1985	Val Glu Met Leu Pro 1990	Ser Lys Ala Gly Ile 1995	Trp Arg Val
Glu Cys 2000	Leu Ile Gly Glu His 2005	Leu His Ala Gly Met 2010	Ser Thr Leu
Phe Leu 2015	Val Tyr Ser Asn Lys 2020	Cys Gln Thr Pro Leu 2025	Gly Met Ala
Ser Gly 2030	His Ile Arg Asp Phe 2035	Gln Ile Thr Ala Ser 2040	Gly Gln Tyr
Gly Gln 2045	Trp Ala Pro Lys Leu 2050	Ala Arg Leu His Tyr 2055	Ser Gly Ser
Ile Asn 2060	Ala Trp Ser Thr Lys 2065	Glu Pro Phe Ser Trp 2070	Ile Lys Val
Asp Leu 2075	Leu Ala Pro Met Ile 2080	Ile His Gly Ile Lys 2085	Thr Gln Gly
Ala Arg 2090	Gln Lys Phe Ser Ser 2095	Leu Tyr Ile Ser Gln 2100	Phe Ile Ile
Met Tyr 2105	Ser Leu Asp Gly Lys 2110	Lys Trp Gln Thr Tyr 2115	Arg Gly Asn
Ser Thr 2120	Gly Thr Leu Met Val 2125	Phe Phe Gly Asn Val 2130	Asp Ser Ser

Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr
2135						2140					2145			
Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg
2150						2155					2160			
Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu
2165						2170					2175			
Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser
2180						2185					2190			
Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala
2195						2200					2205			
Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val
2210						2215					2220			
Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met
2225						2230					2235			
Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr
2240						2245					2250			
Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly
2255						2260					2265			
His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe
2270						2275					2280			
Gln	Gly	Asn	Gln	Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp
2285						2290					2295			
Pro	Pro	Leu	Leu	Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp
2300						2305					2310			
Val	His	Gln	Ile	Ala	Leu	Arg	Met	Glu	Val	Leu	Gly	Cys	Glu	Ala
2315						2320					2325			
Gln	Asp	Leu	Tyr											
2330														

<210> 45

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> amino acids 233-236 of human IgG1

<400> 45

Glu Leu Leu Gly

1

<210> 46

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN AE42-4, protein sequence

<400> 46

Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser
35 40

<210> 47

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> XTEN AE42-4, DNA sequence

<400> 47

ggcgcgccag gttctcctgc tggctcccc acctcaacag aagaggggac aagcgaaagc 60

gctacgcctg agagtggccc tggctctgag ccagccacct ccggctctga aaccctgcc 120

tcgagc 126

<210> 48

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN AE144-2A, protein sequence

<400> 48

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
1 5 10 15

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65 70 75 80

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
100 105 110

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
130 135 140

<210> 49
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AE144-2A, DNA sequence

<400> 49
ggcgcgccaa ccagtacgga gccgtccgag gggagcgcac caggaagccc ggctgggagc 60
ccgacttcta ccgaagaggg tacatctacc gaaccaagtg aagggttcagc accaggcacc 120
tcaacagaac cctctgaggg ctcggcgcct ggtacaagtg agtccgccac ccagaatcc 180
gggcctggga caagcacaga accttcggaa gggagtgtccc ctggaacatc cgaatcggca 240
accccagaat cagggccagg atctgagccc gcgacttcgg gctccgagac gcctgggaca 300
tccaccgagc cctccgaagg atcagcccca ggcaccagca cggagccctc tgagggaagc 360
gcacctggta ccagcgaaag cgcaactccc gaatcaggtc ccggtacgag cgagtcggcg 420
accccgagga gcgggcccagg tgcctcgagc 450

<210> 50
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AE144-3B, protein sequence

<400> 50

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
65 70 75 80

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
100 105 110

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
115 120 125

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 51
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AE144-3B, DNA sequence

<400> 51
ggcgcgcgcaa gtcccgcctgg aagcccaact agcaccgaag aggggacctc agagtccgcc 60
acccccgagt ccggccctgg ctctgagcct gccactagcg gctccgagac tcctggcaca 120
tccgaaagcg ctacaccgga gaggggaccc ggcacctcta ccgagcccag tgagggctcc 180
gcccctggaa caagcaccga gccagcgaa ggcagcgccc cagggacctc cacagagccc 240
agtgaaggca gtgctcctgg caccagcacc gaaccaagcg agggctctgc acccgggacc 300
tccaccgagc caagcgaagg ctctgcccct ggcacttcca ccgagcccag cgaaggcagc 360
gcccctggga gcccgcctgg ctctcccacc agcactgagg agggcacatc taccgaacca 420
agtgaaggct ctgcaccagg tgcctcgagc 450

<210> 52
<211> 144
<212> PRT
<213> Artificial Sequence

<220>

<223> XTEN AE144-4A, protein sequence

<400> 52

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65 70 75 80

Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
85 90 95

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
100 105 110

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 53

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> XTEN AE144-4A, DNA sequence

<400> 53

ggcgcgccaa cgtccgaaag tgctaccctt gagtcaggcc ctggtagtga gcctgccaca 60

agcgggaagcg aaactccggg gacctcagag tctgccactc ccgaatcggg gccaggctct 120

gaaccggcca cttcagggag cgaaacacca ggaacatcgg agagcgctac cccggagagc 180

gggccaggaa ctagtactga gcctagcgag ggaagtgcac ctggtacaag cgagtccgcc 240

acacccgagt ctggccctgg ctctccagcg ggctcaccca cgagcactga agagggctct 300

cccgtggca gcccaacgtc gacagaagaa ggatcaccag caggctcccc cacatcaaca 360

gaggagggta catcagaatc tgctactccc gagagtggac ccggtacctc cactgagccc 420

agcgagggga gtgcaccagg tgcctcgagc

450

<210> 54

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN AE144-5A, protein sequence

<400> 54

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
65 70 75 80

Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
85 90 95

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
100 105 110

Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
115 120 125

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
130 135 140

<210> 55

<211> 450

<212> DNA

<213> Artificial Sequence

<220>

<223> XTEN AE144-5A, DNA sequence

<400> 55

ggcgcgccaa catcagagag cgccaccct gaaagtggtc ccgggagcga gccagccaca 60

tctgggtcgg aaacgccagg cacaagtgag tctgcaactc ccgagtccgg acctggctcc 120

gagcctgcca ctagcggctc cgagactccg ggaacttccg agagcgctac accagaaagc 180

ggacccggaa ccagtaccga acctagcgag ggctctgctc cgggcagccc agccggctct	240
cctacatcca cggaggaggg cacttccgaa tccgccaccc cggagtcagg gccaggatct	300
gaacccgcta cctcaggcag tgagacgcca ggaacgagcg agtccgctac accggagagt	360
gggccaggga gccctgctgg atctcctacg tccactgagg aagggtcacc agcgggctcg	420
cccaccagca ctgaagaagg tgcctcgagc	450

<210> 56
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> XTEN AE144-6B, protein sequence

<400> 56

Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Glu	Ser
1				5					10					15	

Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu
			20					25					30		

Ser	Gly	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly
		35					40					45			

Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Ser	Glu	Pro	Ala
	50					55					60				

Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser
65					70					75					80

Thr	Glu	Glu	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly
				85					90					95	

Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ser	Glu	Pro	Ala
			100					105					110		

Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu
		115					120					125			

Ser	Gly	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly
	130					135					140				

<210> 57
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>

<223> XTEN AE144-6B, DNA sequence

<400> 57

```
ggcgcgccaa catctaccga gccttccgaa ggctctgccc ctgggacctc agaatctgca      60
acccttgaaa gcggccctgg aacctccgaa agtgccactc ccgagagcgg ccaggggaca      120
agcgagtcag caaccctga gtctggaccc ggcagcgagc ctgcaacctc tggctcagag      180
actcccggtc cagaaccgc tacctcaggc tccgagacac ccggctctcc tgctgggagt      240
cccacttcca ccgaggaagg aacatccact gagcctagtg agggctctgc ccctggaacc      300
agcacagagc caagtgaggg cagtgcacca ggatccgagc cagcaaccag cgggtccgag      360
actcccgga cctctgagtc tgccacccca gagagcggac ccggcacttc aaccgagccc      420
tccgaaggat cagcaccagg tgctctgagc                                     450
```

<210> 58

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN AG144-1, protein sequence

<400> 58

```
Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser
1          5          10          15
```

```
Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
20          25          30
```

```
Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
35          40          45
```

```
Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser
50          55          60
```

```
Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
65          70          75          80
```

```
Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
85          90          95
```

```
Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser
100         105         110
```

```
Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
115         120         125
```

```
Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser
130         135         140
```

<210> 59
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-1, DNA sequence

<400> 59
ggcgcgccac ccgggtcgtc cccgtcggcg tccaccggaa cagggccagg gtcatccccg 60
tcagcgtcga ctgggacggg acccgggaca cccggttcgg ggactgcatc ctctctgcct 120
ggttcgtcca ccccgtcagg agccacgggt tcgccgggaa gcagcccaag cgcattccact 180
ggtacagggc ctggggcttc accgggtact tcattccagg ggtcaccggg aacgcccga 240
tcggggacgg cttctctatc accaggatcg tcaacaccct cgggcgcaac gggcagcccc 300
ggaacccttg gttcgggtac ggcgtcgtcg agccccggtg cgagcccggg aacaagctcg 360
acaggatcgc ctggggcgtc acccggcacg tcgagcacag gcagccccgg aaccctgga 420
tcgggaaccg cgtcgtcaag cgctctgagc 450

<210> 60
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AG144-A, protein sequence

<400> 60

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1 5 10 15
Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
20 25 30
Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45
Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60
Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65 70 75 80
Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
85 90 95
Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
100 105 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 61
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-A, DNA sequence

<400> 61
ggcgcgccag gtgcctcgcc gggaacatca tcaactgggt caccggggtc atccccctcg 60
gcctcaaccg ggacgggtcc cggctcatcc cccagcgcca gcaactggaac aggtcctggc 120
actcctgggt ccggtacggc atcgatcatcc ccgggaagct caacaccgtc cggagcgaca 180
ggatcacctg gctcgtcacc ttcggcgatca actggaacgg ggccaggggc ctcaccggga 240
acgtcctcga ctgggtcgcc tggtagccg ggatcaggaa cggcctcatc ctcgcctggg 300
tcctcaacgc cctcgggtgc gactggttcg ccgggaactc ctgggtcggg gacggcctcg 360
tcgtcgcttg gggcatcacc ggggacgagc tccacggggg cccctggagc gtcaccgggg 420
acctcctcga caggtagccc ggctcgcgagc 450

<210> 62
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AG144-B, protein sequence

<400> 62
Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
1 5 10 15
Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
20 25 30
Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45
Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60
Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
65 70 75 80

Gly Thr Gly Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
85 90 95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro
100 105 110

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 63
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-B, DNA sequence

<400> 63
ggcgcgcag gtacaccggg cagcggcacg gcttcgtcgt caccgggctc gtccacaccg 60
tcgggagcta cgggaagccc aggagcgtca ccgggaacgt cgtcaacggg gtcaccgggt 120
acgccaggta gcggcacggc cagcagctcg ccaggttcat cgaccccgtc gggagcgact 180
gggtcgcccg gatcaagccc gtcagcttcc actggaacag gaccggggtc gtcgcccgtca 240
gcctcaacgg ggacaggacc tggttcatcg acgccgtcag gggcgacagg ctgccccgga 300
tcgtcaacac cctcgggggc aacggggagc cctgggtgcgt cgccctggaac ctcatccacc 360
ggaagcccgg gggcctcgcc ggggtacgagc tccacgggat cgcccggagc gtcccccgga 420
acttcaagca caggagccc tgcctcgagc 450

<210> 64
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN AG144-C, protein sequence

<400> 64

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro
1 5 10 15

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
20 25 30

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
35 40 45

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
 50 55 60

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
 65 70 75 80

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 85 90 95

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
 100 105 110

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
 115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 130 135 140

<210> 65
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> XTEN AG144-C, DNA sequence

<400> 65
 ggcgcgccag gtacacccgg atcgggtaca gcgtcatcga gccccggtgc gtcacctggt 60
 acgtcgagca cggggtcgcc aggggctcc cctgggacgt cctcaacagg ctgccccggt 120
 gcgtcaccgc gcacgtcgtc cacgggttca cctggtagct ccccttccgc gtccactggc 180
 accgggcctg gaactccggg gagcggcaca gcgagctcgt cgccgggagc atcgccctggg 240
 acatcgagca ccgggtcgcc aggagcatcg cccggaacat ccagcacagg aagccccggc 300
 gcgtcgcccg ggacatcaag cacagggtcc ccgggatcga gcacgccgtc cggagccact 360
 ggatcaccag ggagctcgac accttccggc gcaacgggat cgcccggagc cagcccgggt 420
 acgtcaagca ctggctcccc tgcctcgagc 450

<210> 66
 <211> 144
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> XTEN AG144-F, protein sequence

<400> 66

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
 1 5 10 15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
20 25 30

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65 70 75 80

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
85 90 95

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
100 105 110

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 67
<211> 450
<212> DNA
<213> Artificial Sequence

<220>
<223> XTEN AG144-F, DNA sequence

<400> 67
ggcgcgccag gctccagccc ctccgcgagc acgggaaccg gaccagggtc gtcaccctca 60
gcatcaacgg ggacgggacc gggggcggtca ccaggaacgt cctccaccgg ctcgccgggt 120
gcatcacccg gaacgtcatc gaccggatcg ccagggagct cgacgccatc aggcgcaaca 180
ggatcacctg gctcaagccc tagcgcgtca accggcacgg gtccgggtgc ctcccctggc 240
acgtccagca ccggatcacc cggatcgagc ccatccgcct caaccggaac cggaccgggt 300
acaccagggg cggaacagc ctctcgtca ccaggctcct caaccccctc gggagccacg 360
ggttcgcccc gttcgtcaac gccttccgga gcaactggta gcccgggagc atcgccagga 420
acttcgagca cggggtcgcc cgcctcgagc 450

<210> 68
<211> 4374
<212> DNA
<213> Artificial Sequence

<220>

<223> coFVIII-1 DNA Sequence

<400> 68

atgcagattg agctgtctac ttgctttttc ctgtgcctgc tgaggttttg cttttccgct	60
acacgaaggt attatctggg ggctgtggaa ctgtcttggg attacatgca gagtgacctg	120
ggagagctgc cagtggacgc aaggtttccc cctagagtcc ctaagtcatt ccccttcaac	180
actagcgtgg tctacaagaa aacactgttc gtggagttta ctgatcacct gttcaacatc	240
gcaaagccta ggccaccctg gatgggactg ctggggccaa caatccaggc cgaggtgtac	300
gacaccgtgg tcattacact taagaacatg gcctcacacc ccgtgagcct gcatgctgtg	360
ggcgctcagct actggaaggc ttccgaagga gcagagtatg acgatcagac ttcccagaga	420
gaaaaagagg acgataaggt gtttctctggc ggatctcata cctacgtgtg gcaggtcctg	480
aaagagaatg gccctatggc ctccgaccct ctgtgcctga cctactctta tctgagtcac	540
gtggacctgg tcaaggatct gaacagcggc ctgatcggag ccctgctggg gtgcagggaa	600
ggaagcctgg ctaaggagaa aaccagaca ctgcataagt tcattctgct gttcgccgtg	660
tttgacgaag ggaaatcatg gcacagcgag acaaagaata gtctgatgca ggacagggat	720
gccgcttcag ccagagcttg gcccaaaatg cacactgtga acggctacgt caatcgctca	780
ctgcctgggc tgatcggctg ccaccgaaag agcgtgtatt ggcatgtcat cgggatgggc	840
accacacctg aagtgcactc cattttctctg gagggacata ctttcttggt ccgcaaccac	900
cgacaggctt ccctggagat ctctccaatt accttctctga cagcacagac tctgctgatg	960
gacctggggc agttcctgct gttttgccac atcagctccc accagcatga tggcatggag	1020
gcttacgtga aagtggactc ttgtcccagag gaacctcagc tgcggatgaa gaacaatgag	1080
gaagcagaag actatgacga tgacctgacc gactccgaga tggatgtggg ccgattcgat	1140
gacgataaca gccctcctt tatccagatt agatctgtgg ccaagaaaca ccctaagaca	1200
tgggtccatt acatcgcagc cgaggaagag gactgggatt atgcaccact ggtgctggca	1260
ccagacgatc gtccttacia atctcagtat ctgaacaatg ggccacagag gattggcaga	1320
aagtacaaga aagtgcggtt catggcatat accgatgaga ctttcaagac tcgcgaagcc	1380
atccagcacg agagcggcat cctgggacca ctgctgtacg gagaagtggg agacaccctg	1440
ctgatcattt tcaagaacca ggccagccgg ctttacaata tctatccaca tgggattaca	1500
gatgtgcgcc ctctgtacag caggagactg ccaaagggcg tcaaacacct gaaggacttc	1560
ccaatcctgc ccggagaaat cttcaagtac aagtggactg tcaccgtcga ggatggcccc	1620
actaagagcg accctcgggtg cctgaccgcg tactattcta gtttcgtgaa tatggaaaga	1680
gatctggcaa gcggactgat cggaccactg ctgatttggt acaaagagag cgtggatcag	1740
agaggcaacc agatcatgtc cgacaagcgg aatgtgattc tgttcagtgt ctttgacgaa	1800

aacagggtcat	ggtacctgac	cgagaacatc	cagagattcc	tgcctaatacc	agctggggtg	1860
cagctggaag	atcctgagtt	tcaggcatct	aacatcatgc	atagtattaa	tggtctacgtg	1920
ttcgacagtt	tgcagctgag	cgtgtgcctg	cacgaggtcg	cttactggta	tatcctgagc	1980
attggggcac	agacagatth	cctgagcgtg	ttcttttccg	gctacactth	taagcataaa	2040
atggtctatg	aggacacact	gactctgttc	cccttcagcg	gcgaaaccgt	gtttatgagc	2100
atggagaatc	ccggactgtg	gattctgggg	tgccacaaca	gcgatttcag	aaatcgcgga	2160
atgactgccc	tgctgaaagt	gtcaagctgt	gacaagaaca	ccggggacta	ctatgaagat	2220
tcatacgagg	acatcagcgc	atatctgctg	tccaaaaaca	atgccattga	accccggtct	2280
tttagtcaga	atcctccagt	gctgaagagg	caccagaggg	agatcacccg	cactaccctg	2340
cagagtgatc	aggaagagat	cgactacgac	gatacaatth	ctgtggaaat	gaagaaagag	2400
gacttcgata	tctatgacga	agatgagaac	cagagtcctc	gatcattcca	gaagaaaacc	2460
aggcattact	ttattgccgc	agtggagcgg	ctgtgggatt	atggcatgtc	ctctagtctt	2520
cacgtgctgc	gaaatagggc	ccagtcagga	agcgtcccac	agttcaagaa	agtggctctc	2580
caggagttta	cagacgggtc	ctttactcag	ccactgtaca	ggggcgaact	gaacgagcac	2640
ctgggactgc	tggggcccta	tatcagagca	gaagtggagg	ataacattat	ggtcaccttc	2700
agaaatcagg	cctctcgggc	ttacagttth	tattcaagcc	tgatctctta	cgaagaggac	2760
cagcgacagg	gagctgaacc	acgaaaaaac	ttcgtgaagc	ctaagtagac	caaaacatac	2820
ttttggaagg	tgcagcacca	tatggcccca	acaaaagacg	agttcgattg	caaggcatgg	2880
gcctatthth	ctgacgtgga	tctggagaag	gacgtgcaca	gtggcctgat	tggccactg	2940
ctggtgtgcc	atactaacac	cctgaatcca	gccacgggc	ggcaggtcac	tgtccaggag	3000
ttcgctctgt	tctttaccat	ctttgatgag	acaaagagct	ggtacttcac	cgaaaacatg	3060
gagcgaaatt	gcagggtctc	atgtaacatt	cagatggaag	acccacatt	caaggagaac	3120
taccgctthc	atgctatcaa	tggatacatc	atggatactc	tgcccgggct	ggcatggca	3180
caggaccaga	gaatccggtg	gtatctgctg	agcatgggca	gcaacgagaa	tatccactca	3240
attcattthc	gcgggcacgt	gtttactgtc	aggaagaaag	aagagtacaa	gatggccctg	3300
tacaacctgt	atcccggcgt	gttcgaaacc	gtcgagatgc	tgcctagcaa	ggccggaatc	3360
tggagagtgg	aatgcctgat	tggagagcac	ctgcatgctg	ggatgtctac	cctgtthctg	3420
gtgtacagta	ataagtgtca	gacaccctg	ggaatggcat	ccgggcatat	cagggattth	3480
cagattaccg	catctggaca	gtacggacag	tgggcaccta	agctggctag	actgcactat	3540
tccggatcta	tcaacgcttg	gtccacaaaa	gagcctthct	cttggattaa	ggtggacctg	3600
ctggccccaa	tgatcattca	tggcatcaaa	actcaggag	ctcggcagaa	gttctctctt	3660
ctgtacatct	cacagthtat	catcatgtac	agcctggatg	ggaagaaatg	gcagacatac	3720

cgcggaata	gcacaggaac	tctgatggtg	ttctttggca	acgtggacag	cagcggaatc	3780
aagcacaaca	ttttcaatcc	ccctatcatt	gctagataca	tccggctgca	cccaacccat	3840
tattctattc	gaagtacact	gaggatggaa	ctgatgggat	gcgatctgaa	cagttgttca	3900
atgcccctgg	ggatggagtc	caaggcaatc	tctgacgccc	agattaccgc	cagctcctac	3960
ttcactaata	tgtttgctac	ctggagccct	tccaaagcaa	gactgcacct	gcaaggccgc	4020
agcaacgcat	ggcgaccaca	ggtgaacaat	cccaaggagt	ggttgacagg	cgattttcag	4080
aaaactatga	aggtgaccgg	ggtcacaact	cagggcgtga	aaagtctgct	gacctcaatg	4140
tacgtcaagg	agttcctgat	ctctagttca	caggacggac	atcagtggac	actgttcttt	4200
cagaacggga	aggtgaaagt	cttcacgggc	aatcaggatt	cctttacacc	tgtggtcaac	4260
agtctagacc	ctccactgct	gaccagatac	ctgagaatcc	accctcagtc	ctgggtgcac	4320
cagattgccc	tgagaatgga	agtgctggga	tgcgaggccc	aggatctgta	ctga	4374

<210> 69
 <211> 577
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> ET Promoter, DNA sequence

<400> 69	
ctcgagggtca	attcacgcga
gttaataatt	accagcgcgg
gccaataaaa	taatccgcga
60	
ggggcagggtg	acgtttgccc
agcgcgcgct	ggtaattatt
aacctcgcga	atattgattc
120	
gaggccgcga	ttgccgcaat
cgcgaggggc	aggtgacctt
tgcccagcgc	gcgttcgccc
180	
cgccccggac	ggtatcgata
agcttaggag	cttgggctgc
aggtcgaggg	cactgggagg
240	
atgttgagta	agatggaaaa
ctactgatga	cccttgacga
gacagagtat	taggacatgt
300	
ttgaacaggg	gccgggagat
cagcaggtag	ctctagagga
tccccgtctg	tctgcacatt
360	
tcgtagagcg	agtgttccga
tactctaata	tccctaggca
aggttcatat	ttgtgtaggt
420	
tacttattct	ccttttggtg
actaagtcaa	taatcagaat
cagcagggtt	ggagtcagct
480	
tggcagggat	cagcagcctg
ggttggaagg	aggggggtata
aaagcccctt	caccaggaga
540	
agccgtcaca	cagatccaca
agctcctgcc	accatgg
577	

<210> 70
 <211> 4374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-5

<400> 70	
atgcaaatcg	aactgagcac
ctgtttcttc	ctctgcctgc
tgagattctg	tttctccgcg
60	

acccgccgat	actacctggg	agcagtggag	ctctcctggg	attacatgca	gagcgacctt	120
ggggagctgc	ccgtggatgc	caggttccct	ccccgggtgc	caaagtcgtt	tccgttcaac	180
acctccgtgg	tgtacaagaa	aactctgttc	gtggagttca	ccgaccacct	gttcaatatc	240
gccaagccca	gacctccctg	gatggggctg	ttgggacctt	ccatccaagc	ggaggtgtac	300
gacactgtgg	tcatactctt	gaagaacatg	gcctcgcata	ccgtgtccct	gcacgccgtg	360
ggagtgtctt	actggaaagc	gtccgagggg	gccgaatacg	acgaccagac	ctcgcagaga	420
gaaaaggaag	atgacaaggt	gttcccagga	ggatcgcaca	cctacgtgtg	gcaagtgttg	480
aaggagaacg	gccaatggc	ctccgacccg	ctgtgcctga	cctactcgta	cctgtcccac	540
gtggacctcg	tgaaggacct	caactcggga	ctgattggag	ccctgctggg	ctgcagggaa	600
ggctcactgg	cgaagaaaa	gactcagacc	ttgcacaagt	tcattctgct	gttcgctgtg	660
ttcgacgagg	ggaagtcgtg	gcacagcgag	actaagaact	ccctgatgca	agatagagat	720
gccgcctccg	cccgggcctg	gcctaagatg	cacaccgtga	acggttacgt	gaaccgctcc	780
ctccctggcc	tgattggatg	ccaccggaag	tccgtgtact	ggcacgtgat	cgggatgggg	840
accacccccg	aggtgcacag	catcttcctg	gaaggtcaca	catttctcgt	gcgcaaccac	900
cggcaggcct	ccctggaaat	cagccccatt	accttcctca	ctgcccagac	tctgctgatg	960
gacctgggac	agttcctgct	gttctgccat	atctcctccc	accaacatga	cggaatggag	1020
gcatactgta	aggtcgattc	ctgccctgag	gaacccagc	tccgcatgaa	gaacaatgag	1080
gaagccgagg	actacgacga	cgacctgacg	gatagcgaga	tggatgtggg	ccggttcgat	1140
gacgataaca	gcccttcctt	catccaaatt	cgctcgggtg	caaagaagca	ccccaagacc	1200
tgggtgcatt	acattgcggc	ggaagaagag	gactgggatt	atgccccgct	tgtcctcgtt	1260
cctgacgacc	ggagctacaa	gagccagtac	ctgaacaacg	gtccacagag	gatcggtaga	1320
aagtacaaga	aggtccgctt	catggcctat	accgacgaaa	ccttcaaaac	tagagaggcc	1380
atccaacacg	aatccggcat	cctgggcccg	ctcttgtacg	gagaagtcgg	cgacaccctt	1440
ctcattatct	tcaagaacca	ggcttcccgg	ccgtacaaca	tctatccgca	tgggatcact	1500
gacgtgcgcc	cactgtactc	gcggcgctg	cccaagggtg	tcaaacacct	gaaggatttt	1560
ccgatccttc	cgggagaaat	cttcaagtac	aagtggaccg	tgaccgtgga	agatggccca	1620
actaagtctg	accctagatg	cctcaccgcg	tactactcat	ccttcgtcaa	catggagcgc	1680
gacctggcca	gcggactgat	cggcccgtg	ctgatttgct	acaaggaatc	agtggaccaa	1740
cggggaaacc	agatcatgtc	ggataagagg	aacgtcatcc	tcttctccgt	gtttgacgaa	1800
aaccggctcg	ggtacctgac	tgaaaacatc	cagcggttcc	tccccaaccc	cgcgggcgtg	1860
cagctggaag	atcctgagtt	tcaggcatca	aacatcatgc	actccattaa	cggctacgtg	1920
ttcgattcgc	tgcagctgag	cgtgtgtctg	cacgaagtgg	cctactggta	catcctgtcc	1980

attggtgccc	agactgactt	cctgtccgtg	tttttctccg	gctacacgtt	caagcacaag	2040
atggtgtacg	aggacaccct	gaccctcttc	cctttttccg	gcgaaactgt	gtttatgagc	2100
atggagaatc	ccggcctgtg	gatcttgggc	tgccacaaca	gcgacttccg	taacagagga	2160
atgactgcg	tgctcaaggt	gtccagctgc	gacaagaaca	ccggagacta	ttatgaggac	2220
tcatacgagg	acatctccgc	ctacctcctg	tccaagaata	acgccattga	acctcggagc	2280
ttcagccaga	acccaccctg	gcttaagaga	catcaacggg	agatcactag	gaccaccctg	2340
cagtcagacc	aggaggaaat	cgactacgat	gacaccatct	cggtcgagat	gaagaaggag	2400
gactttgaca	tctacgacga	agatgaaaac	cagagcccga	ggtcgttcca	aaagaaaacc	2460
cgccactact	ttattgctgc	tgtcgagcgg	ctgtgggact	acggaatgtc	gtcctcgccg	2520
cacgtgctcc	gcaaccgagc	ccagagcggc	tcggtgccgc	aattcaagaa	ggtcgtgttc	2580
caggagttca	ctgacgggag	cttcactcag	cctttgtacc	ggggagaact	caatgaacat	2640
ctcggcctcc	tcggacctta	catcagagca	gaagtggaag	ataacatcat	ggtcactttc	2700
cgtaaccaag	ccagccgccc	gtactcgttc	tactcctccc	tcattttcta	cgaagaggac	2760
cagcggcagg	gcgcagaacc	gcgcaagaac	ttcgtgaagc	ccaacgaaac	caagacctac	2820
ttctggaaaag	tgcagcatca	tatggccccg	actaaggacg	agtttgactg	caaagcctgg	2880
gcctacttct	ccgatgtgga	cttgagagaag	gacgtccact	ccggcctcat	cgggtcccctg	2940
ctcgtgtgcc	ataccaatac	cctgaacccc	gcacacggtc	gccaggtcac	cgtgcaggag	3000
ttcgctctgt	tcttcactat	cttcgacgaa	actaagtcct	ggtacttcac	cgagaacatg	3060
gagaggaact	gcagagcccc	ctgtaacatc	cagatggagg	acccgacgtt	caaggaaaac	3120
taccggttcc	acgccattaa	cggatacatc	atggatacgc	tgccgggtct	tgtgatggcc	3180
caggatcaac	ggatcagatg	gtacttattg	tcgatgggca	gcaacgagaa	catccactct	3240
attcacttct	ccggtcatgt	gttcactgtg	cggaagaagg	aagagtacaa	gatggccctg	3300
tacaaccctt	atcccggagt	gttcgaaaact	gtggaaatgc	tgccgtcgaa	ggccggcatt	3360
tggcgcgtgg	agtgtttgat	tggagaacat	ctccatgcgg	ggatgtcaac	cctgttcctg	3420
gtgtatagca	acaagtgcc	gactccgctt	gggatggcgt	caggacacat	tagggatttc	3480
cagatcactg	cgtccggcca	gtacggccaa	tggggcccta	agctggcccc	cctgcattac	3540
tccggatcca	ttaacgcctg	gtcaaccaag	gagccattct	cctggatcaa	ggtggacctt	3600
ctggccccca	tgattatcca	cggaattaag	acccaggggg	cccggcagaa	gttctcctca	3660
ctgtacatca	gccagttcat	aatcatgtac	tccctggacg	gaaagaagtg	gcaaacctac	3720
aggggggaaca	gcaccggcac	actgatggtc	tttttcggaa	atgtggactc	ctccgggatt	3780
aagcataaca	tcttcaacct	tccgattatc	gctcgggtaca	ttagacttca	ccctaccac	3840
tacagcattc	gctccaccct	gcggatggaa	ctgatgggct	gcgatctgaa	ctcgtgcagc	3900

atgccgttgg	gaatggagtc	caaagcaatt	tccgacgcgc	agatcaccgc	ctcgtcctac	3960
tttaccaaca	tgttcgccac	gtggtcaccg	tccaaggccc	ggctgcacct	ccagggaaga	4020
tccaacgcat	ggcggccaca	ggtcaacaac	cctaaggagt	ggctccaggt	ggacttccag	4080
aaaaccatga	aggtcaccgg	agtcacaacc	caggagtgta	agtcgctgct	gacttctatg	4140
tacgtcaagg	agttcctgat	ctccagcagc	caggacgggc	accagtggac	cctgtttctt	4200
caaaatggaa	aggtcaaggt	gtttcagggc	aatcaggatt	cattcacccc	ggtggtgaac	4260
tcccttgatc	caccctcct	gacccgctac	cttcgcatcc	acccacagtc	ctgggtgcac	4320
cagatcgcg	tgaggatgga	ggtcctggga	tgcaagccc	aggacctgta	ctga	4374

<210> 71
 <211> 4374
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-6

<400> 71	
atgcagattg	agctgtccac ttgtttcttc ctgtgcctcc tgcgcttctg tttctccgcc 60
actcgccggt	actaccttgg agccgtggag ctttcatggg actacatgca gagcgacctg 120
ggcgaactcc	ccgtggatgc cagattcccc ccccgcgctgc caaagtcctt cccctttaac 180
acctccgtgg	tgtacaagaa aaccctcttt gtcgagttca ctgaccacct gttcaacatc 240
gccaagccgc	gccaccttg gatgggcctc ctgggaccga ccattcaagc tgaagtgtac 300
gacaccgtgg	tgatcacctt gaagaacatg gcgtcccacc ccgtgtccct gcatgcggtc 360
ggagtgtcct	actggaaggc ctccgaagga gctgagtacg acgaccagac tagccagcgg 420
gaaaaggagg	acgataaagt gttcccgggc ggctcgcata cttacgtgtg gcaagtcctg 480
aaggaaaacg	gacctatggc atccgatcct ctgtgcctga cttactccta cttttcccat 540
gtggacctcg	tgaaggacct gaacagcggg ctgattggtg cacttctcgt gtgccgcgaa 600
ggttcgctcg	ctaaggaaaa gaccagacc ctccataagt tcatcctttt gttcgctgtg 660
ttcgatgaag	gaaagtcatg gcattccgaa actaagaact cgctgatgca ggaccgggat 720
gccgcctcag	cccgcgcctg gcctaaaatg catacagtca acggatacgt gaatcgggtca 780
ctgcccgggc	tcatcggttg tcacagaaag tccgtgtact ggcacgtcat cggcatgggc 840
actacgcctg	aagtgcactc catcttcctg gaagggcaca ccttcctcgt gcgcaaccac 900
cgccaggcct	ctctggaaat ctccccgatt acctttctga ccgccagac tctgctcatg 960
gacctggggc	agttccttct cttctgccac atctccagcc atcagcacga cggaatggag 1020
gcctacgtga	aggtggactc atgcccggaa gaacctcagt tgcggatgaa gaacaacgag 1080
gaggccgagg	actatgacga cgatttgact gactccgaga tggacgtcgt gcggttcgat 1140

gacgacaaca	gccccagctt	catccagatt	cgcagcgtgg	ccaagaagca	ccccaaaacc	1200
tgggtgcact	acatcgcggc	cgaggaagaa	gattgggact	acgccccgtt	ggtgctggca	1260
cccgatgacc	ggtcgtacaa	gtcccagtat	ctgaacaatg	gtccgcagcg	gattggcaga	1320
aagtacaaga	aagtgcggtt	catggcgtac	actgacgaaa	cgtttaagac	ccgggaggcc	1380
attcaacatg	agagcggcat	tctgggacca	ctgctgtacg	gagaggtcgg	cgataccctg	1440
ctcatcatct	tcaaaaacca	ggcctcccgg	ccttacaaca	tctaccctca	cggaatcacc	1500
gacgtgcggc	cactctactc	gcggcgcttg	ccgaagggcg	tcaagcacct	gaaagacttc	1560
cctatcctgc	cgggcgaaat	cttcaagtat	aagtggaccg	tcaccgtgga	ggacggggccc	1620
accaagagcg	atcctaggtg	tctgactcgg	tactactcca	gcttcgtgaa	catggaacgg	1680
gacctggcat	cgggactcat	tggaccgctg	ctgatctgct	acaagagtc	ggtggatcaa	1740
cgcggcaacc	agatcatgtc	cgacaagcgc	aacgtgatcc	tgttctccgt	gtttgatgaa	1800
aacagatcct	ggtacctcac	tgaaaacatc	cagaggttcc	tcccaaacc	cgcaggagtg	1860
caactggagg	accctgagtt	tcaggcctcg	aatatcatgc	actcgattaa	cggttacgtg	1920
ttcgactcgc	tgcagctgag	cgtgtgcctc	catgaagtcg	cttactggtg	cattctgtcc	1980
atcggcgccc	agactgactt	cctgagcgtg	ttcttttccg	gttacacctt	taagcacaag	2040
atgggtgtacg	aagataccct	gaccctgttc	cctttctccg	gcgaaacggg	gttcatgtcg	2100
atggagaacc	cgggtctgtg	gattctggga	tgccacaaca	gcgactttcg	gaaccgcgga	2160
atgactgccc	tgctgaaggt	gtcctcatgc	gacaagaaca	ccggagacta	ctacgaggac	2220
tcctacgagg	atatctcagc	ctacctcctg	tccaagaaca	acgcgatcga	gccgcgcagc	2280
ttcagccaga	acccgcctgt	gctgaagagg	caccagcgag	aaattacccg	gaccaccctc	2340
caatcggatc	aggaggaaat	cgactacgac	gacaccatct	cggtggaat	gaagaaggaa	2400
gatttcgata	tctacgacga	ggacgaaaat	cagtcccctc	gctcattcca	aaagaaaact	2460
agacactact	ttatcgccgc	ggtggaaaaga	ctgtgggact	atggaatgtc	atccagccct	2520
cacgtccttc	ggaaccgggc	ccagagcgga	tcggtgcctc	agttcaagaa	agtgggtgttc	2580
caggagttca	ccgacggcag	cttcaccag	ccgctgtacc	ggggagaact	gaacgaacac	2640
ctgggcctgc	tcggtcctta	catccgcgcg	gaagtggagg	ataacatcat	ggtgaccttc	2700
cgtaaccaag	catccagacc	ttactccttc	tattcctccc	tgatctcata	cgaggaggac	2760
cagcgccaag	gcgccgagcc	ccgcaagaac	ttcgtcaagc	ccaacgagac	taagacctac	2820
ttctggaagg	tccaacacca	tatggccccg	accaaggatg	agtttgactg	caaggcctgg	2880
gcctacttct	ccgacgtgga	ccttgagaag	gatgtccatt	ccggcctgat	cgggccgctg	2940
ctcgtgtgtc	acaccaacac	cctgaaccca	gcgcatggac	gccaggtcac	cgtccaggag	3000
tttgctctgt	tcttcaccat	ttttgacgaa	actaagtcct	ggtacttcac	cgagaatatg	3060

gagcgaaaact gtagagcgcc ctgcaatatc cagatggaag atccgacttt caaggagaac	3120
tatagattcc acgccatcaa cgggtacatc atggatactc tgccgggggct ggtcatggcc	3180
caggatcaga ggattcgggtg gtacttgctg tcaatgggat cgaacgaaaa cattcactcc	3240
attcacttct ccggtcacgt gttcactgtg cgcaagaagg aggagtacaa gatggcgctg	3300
tacaatctgt accccgggggt gttcgaaaact gtggagatgc tgccgtccaa ggccggcatc	3360
tggagagtgg agtgcctgat cggagagcac ctccacgcgg ggatgtccac cctcttctg	3420
gtgtactcga ataagtgcc aaccccgctg ggcatggcct cgggccacat cagagacttc	3480
cagatcacag caagcggaca atacggccaa tgggcgccga agctggcccg cttgcactac	3540
tccggatcga tcaacgcatg gtccaccaag gaaccgttct cgtggattaa ggtggacctc	3600
ctggccccta tgattatcca cggaattaag acccagggcg ccaggcagaa gttctcctcc	3660
ctgtacatct cgcaattcat catcatgtac agcctggacg ggaagaagtg gcagacttac	3720
aggggaaaact ccaccggcac cctgatggtc tttttcggca acgtggattc ctccggcatt	3780
aagcacaaca tcttcaacct accgatcata gccagatata ttaggctcca cccactcac	3840
tactcaatcc gctcaactct tcggatggaa ctcatggggg gcgacctgaa ctctgctcc	3900
atgccgttgg ggatggaatc aaaggctatt agcgacgcc agatcaccgc gagctcctac	3960
ttactaaca tgttcgccac ctggagcccc tccaaggcca ggctgcactt gcagggacgg	4020
tcaaatgcct ggcggccgca agtgaacaat ccgaaggaat ggcttcaagt ggatttccaa	4080
aagaccatga aagtgaccgg agtcaccacc caggagtgta agtcccttct gacctcgatg	4140
tatgtgaagg agttcctgat tagcagcagc caggacgggc accagtggac cctgttcttc	4200
caaaacggaa aggtcaagggt gttccagggg aaccaggact cgttcacacc cgtggtgaac	4260
tccttgacc cccactgct gacgcggtac ttgaggattc atcctcagtc ctgggtccat	4320
cagattgcat tgcgaatgga agtcctgggc tgcgaggccc aggacctgta ctga	4374

<210> 72
 <211> 4824
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> coFVIII-6-XTEN

<400> 72	
atgcagattg agctgtccac ttgtttcttc ctgtgcctcc tgcgcttctg tttctccgcc	60
actcgccggt actaccttgg agccgtggag ctttcatggg actacatgca gagcgacctg	120
ggcgaactcc ccgtggatgc cagattcccc ccccgcgctgc caaagtcctt cccctttaac	180
acctccgtgg tgtacaagaa aaccctcttt gtcgagttca ctgaccacct gttcaacatc	240
gccaaaggcg gccaccttg gatgggcctc ctgggaccga ccattcaagc tgaagtgtac	300

gacaccgtgg	tgatcacctt	gaagaacatg	gcgtcccacc	ccgtgtccct	gcatgcggtc	360
ggagtgtcct	actggaaggc	ctccgaagga	gctgagtaag	acgaccagac	tagccagcgg	420
gaaaaggagg	acgataaagt	gttcccgggc	ggctcgcata	cttacgtgtg	gcaagtccctg	480
aaggaaaacg	gacctatggc	atccgatcct	ctgtgcctga	cttactccta	cctttcccat	540
gtggacctcg	tgaaggacct	gaacagcggg	ctgattgggtg	cacttctcgt	gtgccgcgaa	600
ggttcgctcg	ctaaggaaaa	gaccagagcc	ctccataagt	tcatcctttt	gttcgctgtg	660
ttcgatgaag	gaaagtcatg	gcattccgaa	actaagaact	cgctgatgca	ggaccgggat	720
gccgcctcag	cccgcgcctg	gcctaaaatg	catacagtca	acggatacgt	gaatcgggtca	780
ctgcccgggc	tcatcggttg	tcacagaaa	tccgtgtact	ggcacgtcat	cggcatgggc	840
actacgcctg	aagtgcactc	catcttcctg	gaagggcaca	ccttcctcgt	gcgcaaccac	900
cgccaggcct	ctctggaaat	ctccccgatt	acctttctga	ccgccagac	tctgctcatg	960
gacctggggc	agttccttct	cttctgccac	atctccagcc	atcagcacga	cggaatggag	1020
gcctacgtga	aggtggactc	atgcccggaa	gaacctcagt	tgcggatgaa	gaacaacgag	1080
gaggccgagg	actatgacga	cgatttgact	gactccgaga	tggacgtcgt	gcggttcgat	1140
gacgacaaca	gccccagctt	catccagatt	cgcagcgtgg	ccaagaagca	ccccaaaacc	1200
tgggtgcact	acatcgcggc	cgaggaagaa	gattgggact	acgccccgtt	ggtgctggca	1260
cccgatgacc	ggtcgtacaa	gtcccagtat	ctgaacaatg	gtccgcagcg	gattggcaga	1320
aagtacaaga	aagtgcgggt	catggcgtac	actgacgaaa	cgtttaagac	ccgggaggcc	1380
attcaacatg	agagcggcat	tctgggacca	ctgctgtacg	gagaggctcg	cgataccctg	1440
ctcatcatct	tcaaaaacca	ggcctcccgg	ccttacaaca	tctaccctca	cggaatcacc	1500
gacgtgcggc	cactctactc	gcggcgcctg	ccgaagggcg	tcaagcacct	gaaagacttc	1560
cctatcctgc	cgggcgaaat	cttcaagtat	aagtggaccg	tcaccgtgga	ggacgggccc	1620
accaagagcg	atcctaggtg	tctgactcgg	tactactcca	gcttcgtgaa	catggaacgg	1680
gacctggcat	cgggactcat	tggaccgctg	ctgatctgct	acaaagagtc	ggtggatcaa	1740
cgcggcaacc	agatcatgtc	cgacaagcgc	aacgtgatcc	tgttctccgt	gtttgatgaa	1800
aacagatcct	ggtacctcac	tgaaaacatc	cagaggttcc	tcccaaacc	cgcaggagtg	1860
caactggagg	accctgagtt	tcaggcctcg	aatatcatgc	actcgattaa	cggttacgtg	1920
ttcgactcgc	tgcagctgag	cgtgtgcctc	catgaagtcg	cttactggta	cattctgtcc	1980
atcggcgccc	agactgactt	cctgagcgtg	ttcttttccg	gttacacctt	taagcacaag	2040
atgggtgtacg	aagataccct	gaccctgttc	cctttctccg	gcgaaacgg	gttcatgtcg	2100
atggagaacc	cgggtctgtg	gattctggga	tgccacaaca	gcgactttcg	gaaccgcgga	2160
atgactgccc	tgctgaaggt	gtcctcatgc	gacaagaaca	ccggagacta	ctacgaggac	2220

tcctacgagg	atatctcagc	ctacctcctg	tccaagaaca	acgcgatcga	gccgcgcagc	2280
ttcagccaga	acggcgcgcc	aacatcagag	agcgccaccc	ctgaaagtgg	ttccgggagc	2340
gagccagcca	catctgggtc	ggaaacgcca	ggcacaagtg	agtctgcaac	ttccgagttc	2400
ggacctggct	ccgagcctgc	cactagcggc	tccgagactc	cgggaaacttc	cgagagcgct	2460
acaccagaaa	gcggacccgg	aaccagtacc	gaacctagcg	agggctctgc	ttcgggcagc	2520
ccagccggct	ctcctacatc	cacggaggag	ggcacttccg	aatccgccac	cccggagtca	2580
gggccaggat	ctgaaccgcg	tacctcaggc	agtgagacgc	caggaacgag	cgagtccgct	2640
acaccggaga	gtggggccagg	gagccctgct	ggatctccta	cgtccactga	ggaaggggtca	2700
ccagcgggct	cgcccaccag	cactgaagaa	ggtgcctcga	gcccgcctgt	gctgaagagg	2760
caccagcgag	aaattacccg	gaccaccctc	caatcggatc	aggaggaaat	cgactacgac	2820
gacaccatct	cggtggaaat	gaagaaggaa	gatttcgata	tctacgacga	ggacgaaaat	2880
cagtcccctc	gctcattcca	aaagaaaact	agacactact	ttatcgccgc	ggtggaaaga	2940
ctgtgggact	atggaatgtc	atccagccct	cacgtccttc	ggaaccgggc	ccagagcgga	3000
tcggtgcctc	agttcaagaa	agtgggtgtc	caggagttca	ccgacggcag	cttcacccag	3060
ccgctgtacc	ggggagaact	gaacgaacac	ctgggcctgc	tcggtcccta	catccgcgcg	3120
gaagtggagg	ataacatcat	ggtgaccttc	cgtaaccaag	catccagacc	ttactccttc	3180
tattcctccc	tgatctcata	cgaggaggac	cagcgccaag	gcgccgagcc	ccgcaagaac	3240
ttcgtcaagc	ccaacgagac	taagacctac	ttctggaagg	tccaacacca	tatggccccg	3300
accaaggatg	agtttgactg	caaggcctgg	gcctacttct	ccgacgtgga	ccttgagaag	3360
gatgtccatt	ccggcctgat	cgggccgctg	ctcgtgtgtc	acaccaacac	cctgaaccca	3420
gcgcatggac	gccaggtcac	cgtccaggag	tttgctctgt	tcttcaccat	ttttgacgaa	3480
actaagtcct	ggtacttcac	cgagaatatg	gagcgaaact	gtagagcgcc	ctgcaatatc	3540
cagatggaag	atccgacttt	caaggagaac	tatagattcc	acgccatcaa	cggggtacatc	3600
atggatactc	tgccggggct	ggtcatggcc	caggatcaga	ggattcggtg	gtacttgctg	3660
tcaatgggat	cgaacgaaaa	cattcactcc	attcacttct	ccggtcacgt	gttcactgtg	3720
cgcaagaagg	aggagtacaa	gatggcgctg	tacaatctgt	accccggggg	gttcgaaact	3780
gtggagatgc	tgccgtccaa	ggccggcatc	tggagagtgg	agtgcctgat	cggagagcac	3840
ctccacgcgg	ggatgtccac	cctcttcctg	gtgtactcga	ataagtgcca	gaccccgctg	3900
ggcatggcct	cgggccacat	cagagacttc	cagatcacag	caagcggaca	atacggccaa	3960
tgggcgccga	agctggcccc	cttgcactac	tccggatcga	tcaacgcatg	gtccaccaag	4020
gaaccgttct	cgtggattaa	ggtggacctc	ctggccccta	tgattatcca	cggaattaag	4080
accagggcg	ccaggcagaa	gttctcctcc	ctgtacatct	cgcaattcat	catcatgtac	4140

```

agcctggacg ggaagaagtg gcagacttac aggggaaact ccaccggcac cctgatggtc 4200
tttttcggca acgtggattc ctccggcatt aagcacaaca tcttcaaccc accgatcata 4260
gccagatata ttaggctcca cccactcac tactcaatcc gctcaactct tcggatggaa 4320
ctcatggggt gcgacctgaa ctctgctcc atgccgttgg ggatggaatc aaaggctatt 4380
agcgacgccc agatcacgcg gagctcctac ttcactaaca tgttcgccac ctggagcccc 4440
tccaaggcca ggctgcactt gcagggacgg tcaaatgcct ggcggccgca agtgaacaat 4500
ccgaaggaat ggcttcaagt ggatttccaa aagaccatga aagtgaccgg agtcaccacc 4560
cagggagtga agtcccttct gacctcgatg tatgtgaagg agttcctgat tagcagcagc 4620
caggacgggc accagtggac cctgttcttc caaaacggaa aggtcaaggt gttccagggg 4680
aaccaggact cgttcacacc cgtggtgaac tccctggacc cccactgct gacgcggtac 4740
ttgaggattc atcctcagtc ctgggtccat cagattgcat tgcgaatgga agtcctgggc 4800
tgcgaggccc aggacctgta ctga 4824

```

```

<210> 73
<211> 12
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> AD motif

```

```

<400> 73

```

```

Gly Glu Ser Pro Gly Gly Ser Ser Gly Ser Glu Ser
1          5          10

```

```

<210> 74
<211> 12
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> AD motif

```

```

<400> 74

```

```

Gly Ser Glu Gly Ser Ser Gly Pro Gly Glu Ser Ser
1          5          10

```

```

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> AD motif

```

```

<400> 75

```

Gly Ser Ser Glu Ser Gly Ser Ser Glu Gly Gly Pro
1 5 10

<210> 76
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AD motif

<400> 76

Gly Ser Gly Gly Glu Pro Ser Glu Ser Gly Ser Ser
1 5 10

<210> 77
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AE, AM motif

<400> 77

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
1 5 10

<210> 78
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AE, AM, AQ motif

<400> 78

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
1 5 10

<210> 79
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AE, AM, AQ motif

<400> 79

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
1 5 10

<210> 80
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AE, AM, AQ motif

<400> 80

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
1 5 10

<210> 81
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 81

Gly Ser Thr Ser Glu Ser Pro Ser Gly Thr Ala Pro
1 5 10

<210> 82
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 82

Gly Thr Ser Thr Pro Glu Ser Gly Ser Ala Ser Pro
1 5 10

<210> 83
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 83

Gly Thr Ser Pro Ser Gly Glu Ser Ser Thr Ala Pro
1 5 10

<210> 84
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AF, AM motif

<400> 84

Gly Ser Thr Ser Ser Thr Ala Glu Ser Pro Gly Pro
1 5 10

<210> 85
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AG, AM motif

<400> 85

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
1 5 10

<210> 86
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AG, AM motif

<400> 86

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
1 5 10

<210> 87
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AG, AM motif

<400> 87

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
1 5 10

<210> 88
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AG, AM motif

<400> 88

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
1 5 10

<210> 89
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> AQ motif

<400> 89

Gly Glu Pro Ala Gly Ser Pro Thr Ser Thr Ser Glu
1 5 10

<210> 90

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AQ motif

<400> 90

Gly Thr Gly Glu Pro Ser Ser Thr Pro Ala Ser Glu
1 5 10

<210> 91

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AQ motif

<400> 91

Gly Ser Gly Pro Ser Thr Glu Ser Ala Pro Thr Glu
1 5 10

<210> 92

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AQ motif

<400> 92

Gly Ser Glu Thr Pro Ser Gly Pro Ser Glu Thr Ala
1 5 10

<210> 93

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> AQ motif

<400> 93

Gly Pro Ser Glu Thr Ser Thr Ser Glu Pro Gly Ala
1 5 10

<210> 94
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> AQ motif

<400> 94

Gly Ser Pro Ser Glu Pro Thr Glu Gly Thr Ser Ala
1 5 10

<210> 95
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BC motif

<400> 95

Gly Ser Gly Ala Ser Glu Pro Thr Ser Thr Glu Pro
1 5 10

<210> 96
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BC motif

<400> 96

Gly Ser Glu Pro Ala Thr Ser Gly Thr Glu Pro Ser
1 5 10

<210> 97
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BC motif

<400> 97

Gly Thr Ser Glu Pro Ser Thr Ser Glu Pro Gly Ala
1 5 10

<210> 98
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BC motif

<400> 98

Gly Thr Ser Thr Glu Pro Ser Glu Pro Gly Ser Ala
1 5 10

<210> 99

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BD motif

<400> 99

Gly Ser Thr Ala Gly Ser Glu Thr Ser Thr Glu Ala
1 5 10

<210> 100

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BD motif

<400> 100

Gly Ser Glu Thr Ala Thr Ser Gly Ser Glu Thr Ala
1 5 10

<210> 101

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BD motif

<400> 101

Gly Thr Ser Glu Ser Ala Thr Ser Glu Ser Gly Ala
1 5 10

<210> 102

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BD motif

<400> 102

Gly Thr Ser Thr Glu Ala Ser Glu Gly Ser Ala Ser
1 5 10

<210> 103

<211> 1607

<212> PRT

<213> Artificial Sequence

<220>

<223> coFVIII-6-XTEN Protein Sequence

<400> 103

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe
1 5 10 15

Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
20 25 30

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35 40 45

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50 55 60

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65 70 75 80

Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85 90 95

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
210 215 220

Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	225	230	235	240
Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr		245	250	255
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val		260	265	270
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile		275	280	285
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser		290	295	300
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	305	310	315	320
Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His		325	330	335
Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro		340	345	350
Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp		355	360	365
Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser	370	375	380	
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr	385	390	395	400
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro		405	410	415
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn		420	425	430
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met		435	440	445
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu	450	455	460	
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu	465	470	475	480

Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro	485	490	495
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys	500	505	510
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe	515	520	525
Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	530	535	540
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	545	550	555
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu	565	570	575
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	580	585	590
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	595	600	605
Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp	610	615	620
Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	625	630	635
Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	645	650	655
Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	660	665	670
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	675	680	685
Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	690	695	700
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	705	710	715
Met	Thr	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	725	730	735

Tyr	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys	740	745	750
Asn	Asn	Ala	Ile	Glu	Pro	Arg	Ser	Phe	Ser	Gln	Asn	Gly	Ala	Pro	Thr	755	760	765
Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	770	775	780
Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	785	790	795
Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	805	810	815
Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	Glu	Pro	820	825	830
Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	835	840	845
Glu	Glu	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	850	855	860
Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	865	870	875
Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	885	890	895
Glu	Glu	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	Gly	Ala	900	905	910
Ser	Ser	Pro	Pro	Val	Leu	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr	915	920	925
Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	930	935	940
Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	945	950	955
Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	965	970	975
Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	980	985	990

Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val
		995					1000					1005			
Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	
	1010					1015					1020				
Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	
	1025					1030					1035				
Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	
	1040					1045					1050				
Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	
	1055					1060					1065				
Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	
	1070					1075					1080				
Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	
	1085					1090					1095				
Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	
	1100					1105					1110				
Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly	
	1115					1120					1125				
Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly	
	1130					1135					1140				
Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	
	1145					1150					1155				
Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	
	1160					1165					1170				
Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe	Lys	
	1175					1180					1185				
Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp	Thr	
	1190					1195					1200				
Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp	Tyr	
	1205					1210					1215				
Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	Phe	
	1220					1225					1230				

Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met
1235						1240					1245			
Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met
1250						1255					1260			
Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly
1265						1270					1275			
Glu	His	Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser
1280						1285					1290			
Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg
1295						1300					1305			
Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro
1310						1315					1320			
Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser
1325						1330					1335			
Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro
1340						1345					1350			
Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe
1355						1360					1365			
Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp
1370						1375					1380			
Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu
1385						1390					1395			
Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn
1400						1405					1410			
Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro
1415						1420					1425			
Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly
1430						1435					1440			
Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys
1445						1450					1455			
Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn
1460						1465					1470			

Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln
1475						1480					1485			
Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu
1490						1495					1500			
Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val
1505						1510					1515			
Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys
1520						1525					1530			
Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu
1535						1540					1545			
Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val	Phe	Gln	Gly	Asn	Gln	Asp
1550						1555					1560			
Ser	Phe	Thr	Pro	Val	Val	Asn	Ser	Leu	Asp	Pro	Pro	Leu	Leu	Thr
1565						1570					1575			
Arg	Tyr	Leu	Arg	Ile	His	Pro	Gln	Ser	Trp	Val	His	Gln	Ile	Ala
1580						1585					1590			
Leu	Arg	Met	Glu	Val	Leu	Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr	
1595						1600					1605			

<210> 104
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Rep-binding site (RBS) for AAV2

<400> 104
 gcgcgctcgc tcgctc

16

<210> 105
 <211> 6
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> terminal resolution site (TRS) for AAV2

<400> 105
 agttgg

6

<210> 106
 <211> 2328
 <212> PRT
 <213> Artificial Sequence

<220>

<223> mature full length FVIII

<400> 106

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1 5 10 15

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
20 25 30

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
35 40 45

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
50 55 60

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
65 70 75 80

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
85 90 95

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala
100 105 110

Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val
115 120 125

Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn
130 135 140

Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser
145 150 155 160

His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu
165 170 175

Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu
180 185 190

His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp
195 200 205

His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
210 215 220

Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
225 230 235 240

Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	Tyr	Trp	His	245	250	255
Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	Phe	Leu	Glu	260	265	270
Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	Leu	Glu	Ile	275	280	285
Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	Asp	Leu	Gly	290	295	300
Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	Asp	Gly	Met	305	310	315
Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg	325	330	335
Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp	Leu	Thr	Asp	340	345	350
Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser	Pro	Ser	Phe	355	360	365
Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr	Trp	Val	His	370	375	380
Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro	Leu	Val	Leu	385	390	395
Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn	Asn	Gly	Pro	405	410	415
Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met	Ala	Tyr	Thr	420	425	430
Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu	Ser	Gly	Ile	435	440	445
Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu	Leu	Ile	Ile	450	455	460
Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro	His	Gly	Ile	465	470	475
Thr	Asp	Val	Arg	Pro	Lys	Arg	Arg	Leu	Pro	Lys	Gly	Val	Lys	His	Leu	485	490	495

Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr
 500 505 510

Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr
 515 520 525

Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly
 530 535 540

Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg
 545 550 555 560

Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val
 565 570 575

Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe
 580 585 590

Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala
 595 600 605

Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln
 610 615 620

Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile
 625 630 635 640

Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe
 645 650 655

Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser
 660 665 670

Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu
 675 680 685

Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu
 690 695 700

Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser
 705 710 715 720

Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu
 725 730 735

Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro Ser Thr Arg Gln Lys
 740 745 750

Gln	Phe	Asn	Ala	Thr	Thr	Ile	Pro	Glu	Asn	Asp	Ile	Glu	Lys	Thr	Asp	755	760	765
Pro	Trp	Phe	Ala	His	Arg	Thr	Pro	Met	Pro	Lys	Ile	Gln	Asn	Val	Ser	770	775	780
Ser	Ser	Asp	Leu	Leu	Met	Leu	Leu	Arg	Gln	Ser	Pro	Thr	Pro	His	Gly	785	790	795
Leu	Ser	Leu	Ser	Asp	Leu	Gln	Glu	Ala	Lys	Tyr	Glu	Thr	Phe	Ser	Asp	805	810	815
Asp	Pro	Ser	Pro	Gly	Ala	Ile	Asp	Ser	Asn	Asn	Ser	Leu	Ser	Glu	Met	820	825	830
Thr	His	Phe	Arg	Pro	Gln	Leu	His	His	Ser	Gly	Asp	Met	Val	Phe	Thr	835	840	845
Pro	Glu	Ser	Gly	Leu	Gln	Leu	Arg	Leu	Asn	Glu	Lys	Leu	Gly	Thr	Thr	850	855	860
Ala	Ala	Thr	Glu	Leu	Lys	Lys	Leu	Asp	Phe	Lys	Val	Ser	Ser	Thr	Ser	865	870	875
Asn	Asn	Leu	Ile	Ser	Thr	Ile	Pro	Ser	Asp	Asn	Leu	Ala	Ala	Gly	Thr	885	890	895
Asp	Asn	Thr	Ser	Ser	Leu	Gly	Pro	Pro	Ser	Met	Pro	Val	His	Tyr	Asp	900	905	910
Ser	Gln	Leu	Asp	Thr	Thr	Leu	Phe	Gly	Lys	Lys	Ser	Ser	Pro	Leu	Thr	915	920	925
Glu	Ser	Gly	Gly	Pro	Leu	Ser	Leu	Ser	Glu	Glu	Asn	Asn	Asp	Ser	Lys	930	935	940
Leu	Leu	Glu	Ser	Gly	Leu	Met	Asn	Ser	Gln	Glu	Ser	Ser	Trp	Gly	Lys	945	950	955
Asn	Val	Ser	Ser	Thr	Glu	Ser	Gly	Arg	Leu	Phe	Lys	Gly	Lys	Arg	Ala	965	970	975
His	Gly	Pro	Ala	Leu	Leu	Thr	Lys	Asp	Asn	Ala	Leu	Phe	Lys	Val	Ser	980	985	990
Ile	Ser	Leu	Leu	Lys	Thr	Asn	Lys	Thr	Ser	Asn	Asn	Ser	Ala	Thr	Asn	995	1000	1005

Arg	Lys	Thr	His	Ile	Asp	Gly	Pro	Ser	Leu	Leu	Ile	Glu	Asn	Ser
1010						1015					1020			
Pro	Ser	Val	Trp	Gln	Asn	Ile	Ser	Asp	Thr	Glu	Phe	Lys	Lys	Val
1025						1030					1035			
Thr	Pro	Leu	Ile	His	Asp	Arg	Met	Leu	Met	Asp	Lys	Asn	Ala	Thr
1040						1045					1050			
Ala	Leu	Arg	Leu	Asn	His	Met	Ser	Asn	Lys	Thr	Thr	Ser	Ser	Lys
1055						1060					1065			
Asn	Met	Glu	Met	Val	Gln	Gln	Lys	Lys	Glu	Gly	Pro	Ile	Pro	Pro
1070						1075					1080			
Asp	Ala	Gln	Asn	Pro	Asp	Met	Ser	Phe	Phe	Lys	Met	Leu	Phe	Leu
1085						1090					1095			
Pro	Glu	Ser	Ala	Arg	Trp	Ile	Gln	Arg	Thr	His	Gly	Lys	Asn	Ser
1100						1105					1110			
Leu	Asn	Ser	Gly	Gln	Gly	Pro	Ser	Pro	Lys	Gln	Leu	Val	Ser	Leu
1115						1120					1125			
Gly	Pro	Glu	Lys	Ser	Val	Glu	Gly	Gln	Asn	Phe	Leu	Ser	Glu	Lys
1130						1135					1140			
Asn	Lys	Val	Val	Val	Gly	Lys	Gly	Glu	Phe	Thr	Lys	Asp	Val	Gly
1145						1150					1155			
Leu	Lys	Glu	Met	Val	Phe	Pro	Ser	Ser	Arg	Asn	Leu	Phe	Leu	Thr
1160						1165					1170			
Asn	Leu	Asp	Asn	Leu	His	Glu	Asn	Asn	Thr	His	Asn	Gln	Glu	Lys
1175						1180					1185			
Lys	Ile	Gln	Glu	Glu	Ile	Glu	Lys	Lys	Glu	Thr	Leu	Ile	Gln	Glu
1190						1195					1200			
Asn	Val	Val	Leu	Pro	Gln	Ile	His	Thr	Val	Thr	Gly	Thr	Lys	Asn
1205						1210					1215			
Phe	Met	Lys	Asn	Leu	Phe	Leu	Leu	Ser	Thr	Arg	Gln	Asn	Val	Glu
1220						1225					1230			
Gly	Ser	Tyr	Asp	Gly	Ala	Tyr	Ala	Pro	Val	Leu	Gln	Asp	Phe	Arg
1235						1240					1245			

Ser	Leu	Asn	Asp	Ser	Thr	Asn	Arg	Thr	Lys	Lys	His	Thr	Ala	His
1250						1255					1260			
Phe	Ser	Lys	Lys	Gly	Glu	Glu	Glu	Asn	Leu	Glu	Gly	Leu	Gly	Asn
1265						1270					1275			
Gln	Thr	Lys	Gln	Ile	Val	Glu	Lys	Tyr	Ala	Cys	Thr	Thr	Arg	Ile
1280						1285					1290			
Ser	Pro	Asn	Thr	Ser	Gln	Gln	Asn	Phe	Val	Thr	Gln	Arg	Ser	Lys
1295						1300					1305			
Arg	Ala	Leu	Lys	Gln	Phe	Arg	Leu	Pro	Leu	Glu	Glu	Thr	Glu	Leu
1310						1315					1320			
Glu	Lys	Arg	Ile	Ile	Val	Asp	Asp	Thr	Ser	Thr	Gln	Trp	Ser	Lys
1325						1330					1335			
Asn	Met	Lys	His	Leu	Thr	Pro	Ser	Thr	Leu	Thr	Gln	Ile	Asp	Tyr
1340						1345					1350			
Asn	Glu	Lys	Glu	Lys	Gly	Ala	Ile	Thr	Gln	Ser	Pro	Leu	Ser	Asp
1355						1360					1365			
Cys	Leu	Thr	Arg	Ser	His	Ser	Ile	Pro	Gln	Ala	Asn	Arg	Ser	Pro
1370						1375					1380			
Leu	Pro	Ile	Ala	Lys	Val	Ser	Ser	Phe	Pro	Ser	Ile	Arg	Pro	Ile
1385						1390					1395			
Tyr	Leu	Thr	Arg	Val	Leu	Phe	Gln	Asp	Asn	Ser	Ser	His	Leu	Pro
1400						1405					1410			
Ala	Ala	Ser	Tyr	Arg	Lys	Lys	Asp	Ser	Gly	Val	Gln	Glu	Ser	Ser
1415						1420					1425			
His	Phe	Leu	Gln	Gly	Ala	Lys	Lys	Asn	Asn	Leu	Ser	Leu	Ala	Ile
1430						1435					1440			
Leu	Thr	Leu	Glu	Met	Thr	Gly	Asp	Gln	Arg	Glu	Val	Gly	Ser	Leu
1445						1450					1455			
Gly	Thr	Ser	Ala	Thr	Asn	Ser	Val	Thr	Tyr	Lys	Lys	Val	Glu	Asn
1460						1465					1470			
Thr	Val	Leu	Pro	Lys	Pro	Asp	Leu	Pro	Lys	Thr	Ser	Gly	Lys	Val
1475						1480					1485			

Glu	Leu	Leu	Pro	Lys	Val	His	Ile	Tyr	Gln	Lys	Asp	Leu	Phe	Pro
1490						1495					1500			
Thr	Glu	Thr	Ser	Asn	Gly	Ser	Pro	Gly	His	Leu	Asp	Leu	Val	Glu
1505						1510					1515			
Gly	Ser	Leu	Leu	Gln	Gly	Thr	Glu	Gly	Ala	Ile	Lys	Trp	Asn	Glu
1520						1525					1530			
Ala	Asn	Arg	Pro	Gly	Lys	Val	Pro	Phe	Leu	Arg	Val	Ala	Thr	Glu
1535						1540					1545			
Ser	Ser	Ala	Lys	Thr	Pro	Ser	Lys	Leu	Leu	Asp	Pro	Leu	Ala	Trp
1550						1555					1560			
Asp	Asn	His	Tyr	Gly	Thr	Gln	Ile	Pro	Lys	Glu	Glu	Trp	Lys	Ser
1565						1570					1575			
Gln	Glu	Lys	Ser	Pro	Glu	Lys	Thr	Ala	Phe	Lys	Lys	Lys	Asp	Thr
1580						1585					1590			
Ile	Leu	Ser	Leu	Asn	Ala	Cys	Glu	Ser	Asn	His	Ala	Ile	Ala	Ala
1595						1600					1605			
Ile	Asn	Glu	Gly	Gln	Asn	Lys	Pro	Glu	Ile	Glu	Val	Thr	Trp	Ala
1610						1615					1620			
Lys	Gln	Gly	Arg	Thr	Glu	Arg	Leu	Cys	Ser	Gln	Asn	Pro	Pro	Val
1625						1630					1635			
Leu	Lys	Arg	His	Gln	Arg	Glu	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser
1640						1645					1650			
Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met
1655						1660					1665			
Lys	Lys	Glu	Asp	Phe	Asp	Ile	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser
1670						1675					1680			
Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala
1685						1690					1695			
Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val
1700						1705					1710			
Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys
1715						1720					1725			

Val	Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu
1730						1735					1740			
Tyr	Arg	Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr
1745						1750					1755			
Ile	Arg	Ala	Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn
1760						1765					1770			
Gln	Ala	Ser	Arg	Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr
1775						1780					1785			
Glu	Glu	Asp	Gln	Arg	Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val
1790						1795					1800			
Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His
1805						1810					1815			
Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr
1820						1825					1830			
Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	His	Ser	Gly	Leu	Ile
1835						1840					1845			
Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His
1850						1855					1860			
Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile
1865						1870					1875			
Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg
1880						1885					1890			
Asn	Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	Pro	Thr	Phe
1895						1900					1905			
Lys	Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	Met	Asp
1910						1915					1920			
Thr	Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	Trp
1925						1930					1935			
Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His
1940						1945					1950			
Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys
1955						1960					1965			

Met	Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu
1970						1975					1980			
Met	Leu	Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile
1985						1990					1995			
Gly	Glu	His	Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr
2000						2005					2010			
Ser	Asn	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile
2015						2020					2025			
Arg	Asp	Phe	Gln	Ile	Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala
2030						2035					2040			
Pro	Lys	Leu	Ala	Arg	Leu	His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp
2045						2050					2055			
Ser	Thr	Lys	Glu	Pro	Phe	Ser	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala
2060						2065					2070			
Pro	Met	Ile	Ile	His	Gly	Ile	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys
2075						2080					2085			
Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu
2090						2095					2100			
Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr
2105						2110					2115			
Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His
2120						2125					2130			
Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His
2135						2140					2145			
Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met
2150						2155					2160			
Gly	Cys	Asp	Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser
2165						2170					2175			
Lys	Ala	Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr
2180						2185					2190			
Asn	Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
2195						2200					2205			

Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys
2210 2215 2220

Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly
2225 2230 2235

Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val
2240 2245 2250

Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr
2255 2260 2265

Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln
2270 2275 2280

Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu
2285 2290 2295

Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile
2300 2305 2310

Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
2315 2320 2325

<210> 107
<211> 7053
<212> DNA
<213> Artificial Sequence

<220>
<223> mature full length FVIII

<400> 107
atgcaaatag agctctccac ctgcttcttt ctgtgccttt tgcgattctg ctttagtgcc 60
accagaagat actacctggg tgcagtggaa ctgtcatggg actatatgca aagtgatctc 120
ggtagagctgc ctgtggacgc aagatttcct cctagagtgc caaaatcttt tccattcaac 180
acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct tttcaacatc 240
gctaagccaa ggccaccctg gatgggtctg ctaggctcta ccatccaggc tgaggtttat 300
gatacagtgg tcattacact taagaacatg gcttcccatc ctgtcagtct tcatgctgtt 360
gggtgtatcct actggaaagc ttctgaggga gctgaatatg atgatcagac cagtcaaagg 420
gagaaagaag atgataaagt cttccctggg ggaagccata catatgtctg gcaggctcctg 480
aaagagaatg gtccaatggc ctctgaccca ctgtgcctta cctactcata tcttttctcat 540
gtggacctgg taaaagactt gaattcaggc ctcatggag ccctactagt atgtagagaa 600
gggagtctgg ccaaggaaaa gacacagacc ttgcacaaat ttatactact ttttgctgta 660

tttgatgaag	ggaaaagttg	gcactcagaa	acaaagaact	ccttgatgca	ggatagggat	720
gctgcatctg	ctcgggcctg	gcctaaaatg	cacacagtca	atggttatgt	aaacaggtct	780
ctgccaggtc	tgattggatg	ccacaggaaa	tcagtctatt	ggcatgtgat	tggaatgggc	840
accactcctg	aagtgcactc	aatattcctc	gaaggtcaca	catttcttgt	gaggaaccat	900
cgccaggcgt	ccttggaat	ctcgccaata	actttcctta	ctgctcaaac	actccttgatg	960
gaccttggac	agtttctact	gttttgtcat	atctcttccc	accaacatga	tggcatggaa	1020
gcttatgtca	aagtagacag	ctgtccagag	gaaccccaac	tacgaatgaa	aaataatgaa	1080
gaagcggaa	actatgatga	tgatcttact	gattctgaaa	tggatgtggt	caggtttgat	1140
gatgacaact	ctccttcctt	tatccaaatt	cgctcagttg	ccaagaagca	tcctaaaact	1200
tgggtacatt	acattgctgc	tgaagaggag	gactgggact	atgctccctt	agtcctcgcc	1260
cccgatgaca	gaagttataa	aagtcaatat	ttgaacaatg	gccctcagcg	gattggtagg	1320
aagtacaaaa	aagtccgatt	tatggcatac	acagatgaaa	cctttaagac	tcgtgaagct	1380
attcagcatg	aatcaggaat	cttgggacct	ttactttatg	gggaagttgg	agacacactg	1440
ttgattatat	ttaagaatca	agcaagcaga	ccatataaca	tctaccctca	cggaatcact	1500
gatgtccgtc	ctttgtattc	aaggagatta	ccaaaagggtg	taaaacattt	gaaggatttt	1560
ccaattctgc	caggagaaat	attcaaatat	aatggacag	tgactgtaga	agatgggcca	1620
actaaatcag	atcctcggtg	cctgaccgcg	tattactcta	gtttcgtaa	tatggagaga	1680
gatctagctt	caggactcat	tggccctctc	ctcatctgct	acaaagaatc	tgtagatcaa	1740
agaggaaacc	agataatgtc	agacaagagg	aatgtcatcc	tgttttctgt	atttgatgag	1800
aaccgaagct	ggtacctcac	agagaatata	caacgctttc	tccccaatcc	agctggagtg	1860
cagcttgagg	atccagagtt	ccaagcctcc	aacatcatgc	acagcatcaa	tggctatggt	1920
tttgatagtt	tgcaagtgtc	agtttgtttg	catgagggtg	catactggta	cattctaagc	1980
attggagcac	agactgactt	cctttctgtc	ttcttctctg	gatatacctt	caaacacaaa	2040
atggtctatg	aagacacact	caccctattc	ccattctcag	gagaaactgt	cttcatgtcg	2100
atggaaaacc	caggtctatg	gattctgggg	tgccacaact	cagactttcg	gaacagaggc	2160
atgaccgcct	tactgaaggt	ttctagttgt	gacaagaaca	ctggtgatta	ttacgaggac	2220
agttatgaag	atatttcagc	atacttgctg	agtaaaaaca	atgccattga	accaagaagc	2280
ttctcccaga	attcaagaca	ccctagcact	aggcaaaagc	aatttaatgc	caccacaatt	2340
ccagaaaatg	acatagagaa	gactgaccct	tggtttgcac	acagaacacc	tatgcctaaa	2400
atacaaaatg	tctcctctag	tgatttggtg	atgctcttgc	gacagagtcc	tactccacat	2460
gggctatcct	tatctgatct	ccaagaagcc	aaatatgaga	ctttttctga	tgatccatca	2520
cctggagcaa	tagacagtaa	taacagcctg	tctgaaatga	cacacttcag	gccacagctc	2580

catcacagtg	gggacatggt	atttaccct	gagtcaggcc	tccaattaag	attaaatgag	2640
aaactgggga	caactgcagc	aacagagttg	aagaaacttg	atttcaaagt	ttctagtaca	2700
tcaaataatc	tgatttcaac	aattccatca	gacaatttgg	cagcaggtac	tgataataca	2760
agttccttag	gacccccaag	tatgccagtt	cattatgata	gtcaattaga	taccactcta	2820
tttggcaaaa	agtcattctc	ccttactgag	tctggtggac	ctctgagctt	gagtgaagaa	2880
aataatgatt	caaagttggt	agaatcaggt	ttaatgaata	gccaaagaaag	ttcatgggga	2940
aaaaatgtat	cgtcaacaga	gagtggtagg	ttattttaaag	ggaaaagagc	tcatggacct	3000
gctttgttga	ctaaagataa	tgcccttattc	aaagtttagca	tctctttgtt	aaagacaaac	3060
aaaacttcca	ataattcagc	aactaataga	aagactcaca	ttgatggccc	atcattatta	3120
attgagaata	gtccatcagt	ctggcaaaat	atattagaaa	gtgacactga	gtttaaaaaa	3180
gtgacacctt	tgattcatga	cagaatgctt	atggacaaaa	atgctacagc	tttgaggcta	3240
aatcatatgt	caaataaaac	tacttcatca	aaaaacatgg	aatgggtcca	acagaaaaaa	3300
gagggcccca	ttccaccaga	tgacaaaaat	ccagatatgt	cgttctttaa	gatgctattc	3360
ttgccagaat	cagcaaggtg	gatacaaagg	actcatggaa	agaactctct	gaactctggg	3420
caaggcccca	gtccaaagca	attagtatcc	ttaggaccag	aaaaatctgt	ggaaggtcag	3480
aatttcttgt	ctgagaaaaa	caaagtggta	gtaggaaagg	gtgaatttac	aaaggacgta	3540
ggactcaaag	agatggtttt	tccaagcagc	agaaacctat	ttcttactaa	cttggataat	3600
ttacatgaaa	ataatacaca	caatcaagaa	aaaaaaattc	aggaagaaat	agaaaagaag	3660
gaaacattaa	tccaagagaa	tgtagttttg	cctcagatac	atacagtgac	tggcactaag	3720
aatttcatga	agaacctttt	cttactgagc	actaggcaaa	atgtagaagg	ttcatatgac	3780
ggggcatatg	ctccagtact	tcaagatttt	aggtcattaa	atgattcaac	aaatagaaca	3840
aagaaacaca	cagctcattt	ctcaaaaaaa	ggggaggaag	aaaacttgga	aggcttggga	3900
aatcaaacca	agcaaattgt	agagaaatat	gcatgcacca	caaggatatc	tcctaataca	3960
agccagcaga	attttgtcac	gcaacgtagt	aagagagctt	tgaaacaatt	cagactccca	4020
ctagaagaaa	cagaacttga	aaaaaggata	attgtggatg	acacctcaac	ccagtgggtcc	4080
aaaaacatga	aacatttgac	cccgagcacc	ctcacacaga	tagactacaa	tgagaaggag	4140
aaaggggcca	ttactcagtc	tcccttatca	gattgcctta	cgaggagtca	tagcatccct	4200
caagcaaata	gatctccatt	acctattgca	aaggtatcat	catttccatc	tattagacct	4260
atatatctga	ccagggtcct	attccaagac	aactcttctc	atcttccagc	agcatcttat	4320
agaaagaaaag	attctggggg	ccaagaaaagc	agtcatttct	tacaaggagc	caaaaaaaat	4380
aacctttctt	tagccattct	aaccttggag	atgactgggtg	atcaaagaga	ggttggctcc	4440
ctgggggacaa	gtgccacaaa	ttcagtcaca	tacaagaaag	ttgagaacac	tgttctcccg	4500

aaaccagact	tgcccaaaac	atctggcaaa	gttgaattgc	ttccaaaagt	tcacatttat	4560
cagaaggacc	tattccctac	ggaaactagc	aatgggtctc	ctggccatct	ggatctcgtg	4620
gaagggagcc	ttcttcaggg	aacagaggga	gcgattaagt	ggaatgaagc	aaacagacct	4680
ggaaaagttc	cctttctgag	agtagcaaca	gaaagctctg	caaagactcc	ctccaagcta	4740
ttggatcctc	ttgcttggga	taaccactat	ggtactcaga	tacccaaaaga	agagtggaaa	4800
tccaagaga	agtcaccaga	aaaaacagct	tttaagaaaa	aggataccat	tttgtccctg	4860
aacgcttggtg	aaagcaatca	tgcaatagca	gcaataaatg	agggacaaaa	taagcccga	4920
atagaagtca	cctgggcaaa	gcaaggtagg	actgaaaggc	tgtgctctca	aaaccaccca	4980
gtcttgaaac	gccatcaacg	ggaaataact	cgtactactc	ttcagtcaga	tcaagaggaa	5040
attgactatg	atgataccat	atcagttgaa	atgaagaagg	aagattttga	catttatgat	5100
gaggatgaaa	atcagagccc	ccgcagcttt	caaaagaaaa	cacgacacta	ttttattgct	5160
gcagtggaga	ggctctggga	ttatgggatg	agtagctccc	cacatgttct	aagaaacagg	5220
gctcagagtg	gcagtgtccc	tcagttcaag	aaagttgttt	tccaggaatt	tactgatggc	5280
tcctttactc	agcccttata	ccgtggagaa	ctaaatgaac	atttgggact	cctggggcca	5340
tatataagag	cagaagttga	agataatatc	atggtaactt	tcagaaatca	ggcctctcgt	5400
ccctattcct	tctattctag	ccttatttct	tatgaggaag	atcagaggca	aggagcagaa	5460
cctagaaaaa	actttgtcaa	gcctaataga	acccaaaactt	acttttgga	agtgaacat	5520
catatggcac	ccactaaaga	tgagtttgac	tgcaaagcct	gggcttattt	ctctgatgtt	5580
gacctggaaa	aagatgtgca	ctcaggcctg	attggacccc	ttctggtctg	ccacactaac	5640
acactgaacc	ctgctcatgg	gagacaagtg	acagtacagg	aatttgctct	gtttttcacc	5700
atctttgatg	agacccaaaag	ctggtacttc	actgaaaata	tggaaagaaa	ctgcagggct	5760
ccctgcaata	tccagatgga	agatcccact	tttaagaga	attatcgctt	ccatgcaatc	5820
aatggctaca	taatggatac	actacctggc	ttagtaatgg	ctcaggatca	aaggattcga	5880
tggtatctgc	tcagcatggg	cagcaatgaa	aacatccatt	ctattcattt	cagtggacat	5940
gtgttcactg	tacgaaaaaa	agaggagtat	aaaatggcac	tgtacaatct	ctatccaggt	6000
gtttttgaga	cagtggaaat	gttaccatcc	aaagctggaa	tttggcgggt	ggaatgcctt	6060
attggcgagc	atctacatgc	tgggatgagc	acactttttc	tgggtgtacag	caataagtgt	6120
cagactcccc	tgggaatggc	ttctggacac	attagagatt	ttcagattac	agcttcagga	6180
caatatggac	agtgggcccc	aaagctggcc	agacttcatt	attccggatc	aatcaatgcc	6240
tggagcacca	aggagccctt	ttcttggatc	aaggtggatc	tgttggcacc	aatgattatt	6300
cacggcatca	agaccagggg	tgcccgtcag	aagttctcca	gcctctacat	ctctcagttt	6360
atcatcatgt	atagtcttga	tgggaagaag	tggcagactt	atcgaggaaa	ttccactgga	6420

```

accttaatgg tcttctttgg caatgtggat tcatctggga taaaacacaa tatttttaac      6480
cctccaatta ttgctcgata catccgtttg cacccaactc attatagcat tcgcagcact      6540
cttcgcgatgg agttgatggg ctgtgattta aatagttgca gcatgccatt gggaatggag      6600
agtaaagcaa tatcagatgc acagattact gcttcacacct actttaccaa tatgtttgcc      6660
acctgggtctc cttcaaaagc tcgacttcac ctccaaggga ggagtaatgc ctggagacct      6720
caggtgaata atccaaaaga gtggctgcaa gtggacttcc agaagacaat gaaagtcaca      6780
ggagtaacta ctcagggagt aaaatctctg cttaccagca tgtatgtgaa ggagttcctc      6840
atctccagca gtcaagatgg ccatcagtgg actctctttt ttcagaatgg caaagtaaag      6900
gtttttcagg gaaatcaaga ctcccttcaca cctgtggtga actctctaga cccaccgtta      6960
ctgactcgct accttcgaat tcacccccag agttgggtgc accagattgc cctgaggatg      7020
gaggttctgg gctgcgaggc acaggacctc tac                                  7053

```

<210> 108

<400> 108
000

<210> 109

<211> 1718

<212> PRT

<213> Artificial Sequence

<220>

<223> BIVV001 BDD-FVIII(XTEN) Sequence (no Fc)

<400> 109

```

Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr
1           5           10           15

```

```

Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro
          20           25           30

```

```

Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys
          35           40           45

```

```

Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile Ala Lys Pro
          50           55           60

```

```

Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val
          65           70           75           80

```

```

Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val
          85           90           95

```

```

Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala

```

100					105					110					
Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp	Asp	Lys	Val
		115					120					125			
Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu	Lys	Glu	Asn
	130					135					140				
Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	Tyr	Leu	Ser
145					150					155					160
His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	Gly	Ala	Leu
			165						170					175	
Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	Gln	Thr	Leu
			180					185					190		
His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	Lys	Ser	Trp
		195					200					205			
His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	Ala	Ala	Ser
	210					215					220				
Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	Val	Asn	Arg
225					230					235					240
Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	Tyr	Trp	His
				245					250					255	
Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	Phe	Leu	Glu
			260					265					270		
Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	Leu	Glu	Ile
		275					280					285			
Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	Asp	Leu	Gly
	290					295					300				
Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	Asp	Gly	Met
305					310					315					320
Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg
				325					330					335	
Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp	Leu	Thr	Asp
			340					345					350		
Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser	Pro	Ser	Phe

355

360

365

Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
 370 375 380

Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
 385 390 395 400

Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
 405 410 415

Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
 420 425 430

Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
 435 440 445

Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
 450 455 460

Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
 465 470 475 480

Thr Asp Val Arg Pro Lys Arg Arg Leu Pro Lys Gly Val Lys His Leu
 485 490 495

Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr
 500 505 510

Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr
 515 520 525

Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser Gly
 530 535 540

Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg
 545 550 555 560

Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val
 565 570 575

Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe
 580 585 590

Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe Gln Ala
 595 600 605

Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln

610

615

620

Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile
 625 630 635 640

Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe
 645 650 655

Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser
 660 665 670

Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu
 675 680 685

Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala Leu Leu
 690 695 700

Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser
 705 710 715 720

Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu
 725 730 735

Pro Arg Ser Phe Ser Gln Asn Gly Thr Ser Glu Ser Ala Thr Pro Glu
 740 745 750

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
 755 760 765

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
 770 775 780

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
 785 790 795 800

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
 805 810 815

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
 820 825 830

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
 835 840 845

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
 850 855 860

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly

865		870		875		880
Ser Pro Thr Ser	Thr Glu Glu Gly Thr	Ser Thr Glu Pro Ser	Glu Gly			
	885	890	895			
Ser Ala Pro Gly	Thr Ser Glu Ser Ala Thr	Pro Glu Ser Gly	Pro Gly			
	900	905	910			
Thr Ser Glu Ser	Ala Thr Pro Glu Ser	Gly Pro Gly Thr	Ser Glu Ser			
	915	920	925			
Ala Thr Pro Glu	Ser Gly Pro Gly Ser Glu	Pro Ala Thr Ser	Gly Ser			
	930	935	940			
Glu Thr Pro Gly	Ser Glu Pro Ala Thr Ser	Gly Ser Glu Thr	Pro Gly			
	945	950	955	960		
Ser Pro Ala Gly	Ser Pro Thr Ser Thr	Glu Glu Gly Thr	Ser Thr Glu			
	965	970	975			
Pro Ser Glu Gly	Ser Ala Pro Gly Thr Ser	Thr Glu Pro Ser	Glu Gly			
	980	985	990			
Ser Ala Pro Gly	Ser Glu Pro Ala Thr Ser	Gly Ser Glu Thr	Pro Gly			
	995	1000	1005			
Thr Ser Glu Ser	Ala Thr Pro Glu Ser	Gly Pro Gly Thr	Ser Thr			
	1010	1015	1020			
Glu Pro Ser Glu	Gly Ser Ala Pro Ala Ser	Ser Glu Ile Thr	Arg			
	1025	1030	1035			
Thr Thr Leu Gln	Ser Asp Gln Glu Glu Ile	Asp Tyr Asp Asp	Thr			
	1040	1045	1050			
Ile Ser Val Glu	Met Lys Lys Glu Asp Phe	Asp Ile Tyr Asp	Glu			
	1055	1060	1065			
Asp Glu Asn Gln	Ser Pro Arg Ser Phe	Gln Lys Lys Thr	Arg His			
	1070	1075	1080			
Tyr Phe Ile Ala	Ala Val Glu Arg Leu Trp	Asp Tyr Gly Met	Ser			
	1085	1090	1095			
Ser Ser Pro His	Val Leu Arg Asn Arg	Ala Gln Ser Gly	Ser Val			
	1100	1105	1110			
Pro Gln Phe Lys	Lys Val Val Phe Gln	Glu Phe Thr Asp	Gly Ser			

1115		1120		1125
Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly 1130 1135 1140				
Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met 1145 1150 1155				
Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser 1160 1165 1170				
Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro 1175 1180 1185				
Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp 1190 1195 1200				
Lys Val Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys 1205 1210 1215				
Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val 1220 1225 1230				
His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr 1235 1240 1245				
Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln Glu Phe Ala 1250 1255 1260				
Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr 1265 1270 1275				
Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met 1280 1285 1290				
Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn 1295 1300 1305				
Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln Asp 1310 1315 1320				
Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn 1325 1330 1335				
Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys 1340 1345 1350				
Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val				

1355		1360		1365
Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg 1370 1375 1380				
Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr 1385 1390 1395				
Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met 1400 1405 1410				
Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln 1415 1420 1425				
Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly 1430 1435 1440				
Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys 1445 1450 1455				
Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln 1460 1465 1470				
Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile 1475 1480 1485				
Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly 1490 1495 1500				
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser 1505 1510 1515				
Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg 1520 1525 1530				
Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu 1535 1540 1545				
Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro 1550 1555 1560				
Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala 1565 1570 1575				
Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys 1580 1585 1590				
Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln				

1595		1600		1605
Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr				
1610		1615		1620
Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu				
1625		1630		1635
Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp				
1640		1645		1650
Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val				
1655		1660		1665
Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu				
1670		1675		1680
Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser				
1685		1690		1695
Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu				
1700		1705		1710
Ala Gln Asp Leu Tyr				
1715				

<210> 110
 <211> 6526
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> NB15.1v32 construct (AAV-FVIIIco6XTEN-ssDNA)

<400> 110	
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgtcg ggcgaccttt	60
ggtcgccccg cctcagtgag cgagcgagcg cgcagagagg gaggggccaa ctccatcact	120
aggggttcct gcggcaattc agtcgataac tataacggtc ctaaggtagc gatttaaata	180
cgcgctctct taaggtagcc ccgggacgcg tcaattgaga tctggatccg gtaccgaatt	240
cgcggccgcc tcgacgacta gcgtttaatt aaacgcgtgt ctgtctgcac atttcgtaga	300
gcgagtggtc cgatactcta atctccctag gcaaggttca tatttggtga ggttacttat	360
tctccttttg ttgactaagt caataatcag aatcagcagg tttggagtca gcttggcagg	420
gatcagcagc ctgggttgga aggagggggt ataaaagccc cttcaccagg agaagccgtc	480
acacagatcc acaagctcct gaggtaagtg ccgtgtgtgg ttcccgcggg cctggcctct	540
ttacgggtta tggcccttgc gtgccttgaa ttactgacac tgacatccac tttttctttt	600

tctccacagc	tagcgccacc	atgcagattg	agctgtccac	ttgtttcttc	ctgtgcctcc	660
tgcgcttctg	tttctccgcc	actcgccggt	actaccttgg	agccgtggag	ctttcatggg	720
actacatgca	gagcgacctg	ggcgaactcc	ccgtggatgc	cagattcccc	ccccgcgtgc	780
caaagtcctt	cccctttaac	acctccgtgg	tgtacaagaa	aaccctcttt	gtcgagttca	840
ctgaccacct	gttcaacatc	gccaaagccgc	gcccaccttg	gatgggcctc	ctgggaccga	900
ccattcaagc	tgaagtgtac	gacaccgtgg	tgatcaccct	gaagaacatg	gcgtcccacc	960
ccgtgtccct	gcatgcggtc	ggagtgtcct	actggaaggc	ctccgaagga	gctgagtacg	1020
acgaccagac	tagccagcgg	gaaaaggagg	acgataaagt	gttcccgggc	ggctcgcata	1080
cttacgtgtg	gcaagtcctg	aaggaaaacg	gacctatggc	atccgatcct	ctgtgcctga	1140
cttactccta	cctttcccat	gtggacctcg	tgaaggacct	gaacagcggg	ctgattggtg	1200
cacttctcgt	gtgccgcgaa	ggttcgctcg	ctaaggaaaa	gaccagacc	ctccataagt	1260
tcatcctttt	gttcgctgtg	ttcgatgaag	gaaagtcatg	gcattccgaa	actaagaact	1320
cgctgatgca	ggaccgggat	gccgcctcag	cccgcgccctg	gcctaaaatg	catacagtca	1380
acggatacgt	gaatcgggtca	ctgcccgggc	tcatcggttg	tcacagaaag	tccgtgtact	1440
ggcacgtcat	cggcatgggc	actacgcctg	aagtgcactc	catcttcctg	gaagggcaca	1500
ccttcctcgt	gcgcaaccac	cgccaggcct	ctctggaaat	ctccccgatt	acctttctga	1560
ccgcccagac	tctgctcatg	gacctggggc	agttccttct	cttctgccac	atctccagcc	1620
atcagcacga	cggaatggag	gcctacgtga	aggtggactc	atgcccgga	gaacctcagt	1680
tgcggatgaa	gaacaacgag	gaggccgagg	actatgacga	cgatttgact	gactccgaga	1740
tggacgtcgt	gcggttcgat	gacgacaaca	gccccagctt	catccagatt	cgcagcgtgg	1800
ccaagaagca	ccccaaaacc	tgggtgcact	acatcgcggc	cgaggaagaa	gattgggact	1860
acgccccgtt	ggtgctggca	cccgatgacc	ggtcgtacaa	gtcccagtat	ctgaacaatg	1920
gtccgcagcg	gattggcaga	aagtacaaga	aagtgcggtt	catggcgtac	actgacgaaa	1980
cgtttaagac	ccgggaggcc	attcaacatg	agagcggcat	tctgggacca	ctgctgtacg	2040
gagaggtcgg	cgataccctg	ctcatcatct	tcaaaaacca	ggcctcccgg	ccttacaaca	2100
tctaccctca	cggaatcacc	gacgtgcggc	cactctactc	gcggcgcctg	ccgaagggcg	2160
tcaagcacct	gaaagacttc	cctatcctgc	cgggcgaaat	cttcaagtat	aagtggaccg	2220
tcaccgtgga	ggacgggccc	accaagagcg	atcctaggtg	tctgactcgg	tactactcca	2280
gcttcgtgaa	catggaacgg	gacctggcat	cgggactcat	tggaccgctg	ctgatctgct	2340
aaaagagtc	ggtggatcaa	cgcggcaacc	agatcatgtc	cgacaagcgc	aacgtgatcc	2400
tgttctccgt	gtttgatgaa	aacagatcct	ggtacctcac	tgaaaacatc	cagaggttcc	2460
tcccaaacc	cgcaggagtg	caactggagg	accctgagtt	tcaggcctcg	aatatcatgc	2520

actcgattaa	cggttacgtg	ttcgactcgc	tgcaactgag	cgtgtgcctc	catgaagtcg	2580
cttactggta	cattctgtcc	atcggcgccc	agactgactt	cctgagcgtg	ttcttttccg	2640
gttacacctt	taagcacaag	atggtgtacg	aagataccct	gacctgttc	cctttctccg	2700
gcgaaacggt	gttcatgtcg	atggagaacc	cgggtctgtg	gattctggga	tgccacaaca	2760
gcgactttcg	gaaccgcgga	atgactgccc	tgctgaaggt	gtcctcatgc	gacaagaaca	2820
ccggagacta	ctacgaggac	tcctacgagg	atatctcagc	ctacctcctg	tccaagaaca	2880
acgcgatcga	gccgcgcagc	ttcagccaga	acggcgcgcc	aacatcagag	agcgccaccc	2940
ctgaaagtgg	tcccgggagc	gagccagcca	catctgggtc	ggaaacgcca	ggcacaagtg	3000
agtctgcaac	tcccgagtcc	ggacctgggt	ccgagcctgc	cactagcggc	tccgagactc	3060
cgggaacttc	cgagagcgtc	acaccagaaa	gcggaccggg	aaccagtacc	gaacctagcg	3120
agggtctctg	tccgggcagc	ccagccgggt	ctcctacatc	cacggaggag	ggcacttccg	3180
aatccgccac	cccggagtca	gggccaggat	ctgaaccgcg	tacctcaggc	agtgagacgc	3240
caggaacgag	cgagtccgct	acaccggaga	gtgggccagg	gagccctgct	ggatctccta	3300
cgtccactga	ggaaggggtca	ccagcgggct	cggccaccag	cactgaagaa	ggtgcctcga	3360
gcccgcctgt	gctgaagagg	caccagcgag	aaattaccgg	gaccaccctc	caatcggatc	3420
aggaggaaaat	cgactacgac	gacaccatct	cgggtggaaat	gaagaaggaa	gatttcgata	3480
tctacgacga	ggacgaaaat	cagtcccctc	gctcattcca	aaagaaaact	agacactact	3540
ttatcgccgc	ggtggaaaga	ctgtgggact	atggaatgtc	atccagccct	cacgtccttc	3600
ggaaccgggc	ccagagcgga	tcggtgcctc	agttcaagaa	agtgggtgtc	caggagttca	3660
ccgacggcag	cttcacccag	ccgctgtacc	ggggagaact	gaacgaacac	ctgggcctgc	3720
tcggtcccta	catccgcgcg	gaagtggagg	ataacatcat	ggtgaccttc	cgtaaccaag	3780
catccagacc	ttactccttc	tattcctccc	tgatctcata	cgaggaggac	cagcgccaag	3840
gcgccgagcc	ccgcaagaac	ttcgtcaagc	ccaacgagac	taagacctac	ttctggaagg	3900
tccaacacca	tatggccccg	accaaggatg	agtttgactg	caaggcctgg	gcctacttct	3960
ccgacgtgga	ccttgagaag	gatgtccatt	ccggcctgat	cgggccgctg	ctcgtgtgtc	4020
acaccaacac	cctgaaccca	gcgcatggac	gccaggtcac	cgtccaggag	tttgctctgt	4080
tcttcaccat	ttttgacgaa	actaagtcct	ggtacttcac	cgagaatatg	gagcgaaaact	4140
gtagagcgcc	ctgcaatata	cagatggaag	atccgacttt	caaggagaac	tatagattcc	4200
acgccatcaa	cgggtacatc	atggatactc	tgccggggct	ggtcatggcc	caggatcaga	4260
ggattcggtg	gtacttgctg	tcaatgggat	cgaacgaaaa	cattcactcc	attcacttct	4320
ccggtcacgt	gttcaactgtg	cgcaagaagg	aggagtacaa	gatggcgctg	tacaatctgt	4380
accccggggt	gttcgaaact	gtggagatgc	tgccgtccaa	ggccggcatc	tggagagtgg	4440

agtgcctgat	cggagagcac	ctccacgcgg	ggatgtccac	cctcttcctg	gtgtactcga	4500
ataagtgcc	gaccccgctg	ggcatggcct	cgggccacat	cagagacttc	cagatcacag	4560
caagcggaca	atacggccaa	tgggcgccga	agctggcccc	cttgactac	tccggatcga	4620
tcaacgcatg	gtccaccaag	gaaccgttct	cgtggattaa	ggtggacctc	ctggccccta	4680
tgattatcca	cggaattaag	acccagggcg	ccaggcagaa	gttctcctcc	ctgtacatct	4740
cgcaattcat	catcatgtac	agcctggacg	ggaagaagtg	gcagacttac	aggggaaact	4800
ccaccggcac	cctgatggtc	tttttcggca	acgtggattc	ctccggcatt	aagcacaaca	4860
tcttcaaccc	accgatcata	gccagatata	ttaggctcca	ccccactcac	tactcaatcc	4920
gctcaactct	tcggatggaa	ctcatggggg	gcgacctgaa	ctcctgctcc	atgccgttgg	4980
ggatggaatc	aaaggctatt	agcgacgccc	agatcacccg	gagctcctac	ttcactaaca	5040
tgttcgccac	ctggagcccc	tccaaggcca	ggctgcactt	gcagggacgg	tcaaattgcct	5100
ggcggccgca	agtgaacaat	ccgaaggaat	ggcttcaagt	ggatttccaa	aagaccatga	5160
aagtgaccgg	agtcaccacc	cagggagtga	agtcccttct	gacctcgatg	tatgtgaagg	5220
agttcctgat	tagcagcagc	caggacgggc	accagtggac	cctgttcttc	caaaacggaa	5280
aggtcaaggt	gttccagggg	aaccaggact	cgttcacacc	cgtgggtgaac	tccctggacc	5340
ccccactgct	gacgcggtac	ttgaggattc	atcctcagtc	ctgggtccat	cagattgcat	5400
tgcgaatgga	agtcctgggc	tgcgagggcc	aggacctgta	ctgaatcagc	ctgagctcgc	5460
tgatcataat	caacctctgg	attacaaaat	ttgtgaaaga	ttgactggta	ttcttaacta	5520
tgttgctcct	tttacgctat	gtggatacgc	tgctttaatg	cctttgtatc	atgctattgc	5580
ttcccgtatg	gctttcattt	tctcctcctt	gtataaatcc	tggttgctgt	ctctttatga	5640
ggagttgtgg	cccgttgtca	ggcaacgtgg	cgtgggtgtgc	actgtgtttg	ctgacgcaac	5700
ccccactggg	tggggcattg	ccaccacctg	tcagctcctt	tccgggactt	tcgctttccc	5760
cctccctatt	gccacggcgg	aactcatcgc	cgcctgcctt	gcccgcctgct	ggacaggggc	5820
tcggctgttg	ggcactgaca	attccgtggg	gttgctgggg	aaatcatcgt	cctttccttg	5880
gctgctcgcc	tgtgttgcca	cctggattct	gcgcgggacg	tccttctgct	acgtcccttc	5940
ggccctcaat	ccagcggacc	ttccttcccg	cggcctgctg	ccggctctgc	ggcctcttcc	6000
gcgtcttcgc	cttcgccctc	agacgagtcg	gatctccctt	tgggccgcct	ccccgctgat	6060
cagcctcgac	tgtgccttct	agttgccagc	catctgttgt	ttgcccctcc	cccgtgcctt	6120
ccttgaccct	ggaaggtgcc	actcccactg	tcctttccta	ataaaatgag	gaaattgcat	6180
cgcattgtct	gagtaggtgt	cattctattc	tgggggggtg	ggtggggcag	gacagcaagg	6240
gggaggattg	ggaagacaat	agcaggcatg	ctggggatgc	ggtgggctct	atggcttctg	6300
aggcgaaaag	aacgggctcg	agaagcttct	agatatcctc	tcttaaggta	gcatcgagat	6360

ttaaattagg gataacaggg taatggcgcg ggccgcagga acccctagtg atggagttgg	6420
ccactccctc tctgcgcgt cgtcgcgtca ctgaggccgg gcgaccaaag gtcgcccgc	6480
gcccgggctt tgcccgggcg gcctcagtga gcgagcgagc gcgcag	6526

<210> 111
 <211> 130
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5'ITR (5'-end AAV2 inverted terminal repeat)

<400> 111	
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgctc ggcgacctt	60
ggtcgcccgg cctcagttag cgagcgagcg cgcagagagg gaggggccaa ctccatcact	120
aggggttcct	130

<210> 112
 <211> 142
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Plasmid Backbone Sequence (PBS)-1

<400> 112	
gcggcaattc agtcgataac tataacggtc ctaaggtagc gatttaaata cgcgctctct	60
taaggtagcc ccgggacgcg tcaattgaga tctggatccg gtaccgaatt cgcggccgcc	120
tcgacgacta gcgtttaatt aa	142

<210> 113
 <211> 229
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TTPp (liver-specific promoter)

<400> 113	
acgcgtgtct gtctgcacat ttcgtagagc gagggttccg atactctaata ctccctaggc	60
aagggttcata tttgtgtagg ttacttattc tccttttggt gactaagtca ataatacagaa	120
tcagcaggtt tggagtcagc ttggcaggga tcagcagcct ggggttgaag gaggggggtat	180
aaaagcccct tcaccaggag aagccgtcac acagatccac aagctcctg	229

<210> 114
 <211> 2
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Plasmid Backbone Sequence (PBS)-2

<400>	114	
ag		2
<210>	115	
<211>	106	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Synthetic Intron	
<400>	115	
gtaagtgccg tgtgtggttc ccgcgggcct ggcctcttta cgggttatgg cccttgcg		60
ccttgaatta ctgacactga catccacttt ttctttttct ccacag		106
<210>	116	
<211>	11	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Plasmid Backbone Sequence (PBS)-3	
<400>	116	
ctagcgccac c		11
<210>	117	
<211>	4824	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	FVIIIco6XTEN (open reading frame for codon-optimized FVIII version 6 containing XTEN144)	
<400>	117	
atgcagattg agctgtccac ttgtttcttc ctgtgcctcc tgcgcttctg tttctccgcc		60
actcgccggt actaccttgg agccgtggag ctttcatggg actacatgca gagcgacctg		120
ggcgaaactcc ccgtggatgc cagattcccc ccccgcggtgc caaagtcctt cccctttaac		180
acctccgtgg tgtacaagaa aaccctcttt gtcgagttca ctgaccacct gttcaacatc		240
gccaaagccgc gccaccttg gatgggcctc ctgggaccga ccattcaagc tgaagtgtac		300
gacaccgtgg tgatcacctt gaagaacatg gcgtcccacc ccgtgtccct gcatgcggtc		360
ggagtgtcct actggaaggc ctccgaagga gctgagtacg acgaccagac tagccagcgg		420
gaaaaggagg acgataaagt gttcccgggc ggctcgcata cttacgtgtg gcaagtccctg		480
aaggaaaacg gacctatggc atccgatcct ctgtgcctga cttactccta cttttcccat		540
gtggacctcg tgaaggacct gaacagcggg ctgattggtg cacttctcgt gtgccgcgaa		600
ggttcgctcg ctaaggaaaa gaccagacc ctccataagt tcatcctttt gttcgctgtg		660
ttcgaatgaag gaaagtcatg gcattccgaa actaagaact cgctgatgca ggaccgggat		720

gccgcctcag	cccgcgcctg	gcctaaaatg	catacagtca	acggatacgt	gaatcgggtca	780
ctgcccgggc	tcatacggttg	tcacagaaag	tccgtgtact	ggcacgtcat	cggcatgggc	840
actacgcctg	aagtgcactc	catcttcctg	gaagggcaca	ccttcctcgt	gcgcaaccac	900
cgccaggcct	ctctggaaat	ctccccgatt	acctttctga	ccgcccagac	tctgctcatg	960
gacctggggc	agttccttct	cttctgccac	atctccagcc	atcagcacga	cggaatggag	1020
gcctacgtga	aggtggactc	atgcccggaa	gaacctcagt	tgcggatgaa	gaacaacgag	1080
gaggccgagg	actatgacga	cgatttgact	gactccgaga	tggacgtcgt	gcggttcgat	1140
gacgacaaca	gccccagctt	catccagatt	cgcagcgtgg	ccaagaagca	ccccaaaacc	1200
tgggtgcact	acatcgcggc	cgaggaagaa	gattgggact	acgccccgtt	ggtgctggca	1260
cccgatgacc	ggtcgtacaa	gtcccagtat	ctgaacaatg	gtccgcagcg	gattggcaga	1320
aagtacaaga	aagtgcggtt	catggcgtac	actgacgaaa	cgtttaagac	ccgggaggcc	1380
attcaacatg	agagcggcat	tctgggacca	ctgctgtacg	gagaggtcgg	cgataccctg	1440
ctcatcatct	tcaaaaacca	ggcctcccgg	ccttacaaca	tctaccctca	cggaatcacc	1500
gacgtgcggc	cactctactc	gcggcgcctg	ccgaagggcg	tcaagcacct	gaaagacttc	1560
cctatcctgc	cgggcgaaat	cttcaagtat	aagtggaccg	tcaccgtgga	ggacgggccc	1620
accaagagcg	atcctaggtg	tctgactcgg	tactactcca	gcttcgtgaa	catggaacgg	1680
gacctggcat	cgggactcat	tggaccgctg	ctgatctgct	acaaagagtc	ggtggatcaa	1740
cgcggcaacc	agatcatgtc	cgacaagcgc	aacgtgatcc	tgttctccgt	gtttgatgaa	1800
aacagatcct	ggtacctcac	tgaaaacatc	cagaggttcc	tcccaaacc	cgcaggagtg	1860
caactggagg	accctgagtt	tcaggcctcg	aatatcatgc	actcgattaa	cggttacgtg	1920
ttcgactcgc	tgcaactgag	cgtgtgcctc	catgaagtcg	cttactggta	cattctgtcc	1980
atcggcgccc	agactgactt	cctgagcgtg	ttcttttccg	gttacacctt	taagcacaag	2040
atgggtgtacg	aagataccct	gaccctgttc	cctttctccg	gcgaaacggt	gttcatgtcg	2100
atggagaacc	cgggtctgtg	gattctggga	tgccacaaca	gcgactttcg	gaaccgcgga	2160
atgactgccc	tgctgaaggt	gtcctcatgc	gacaagaaca	ccggagacta	ctacgaggac	2220
tcctacgagg	atatctcagc	ctacctcctg	tccaagaaca	acgcgatcga	gccgcgcagc	2280
ttcagccaga	acggcgcgcc	aacatcagag	agcgccaccc	ctgaaagtgg	tcccgggagc	2340
gagccagcca	catctgggtc	ggaaacgcca	ggcacaagtg	agtctgcaac	tcccgagtcc	2400
ggacctggct	ccgagcctgc	cactagcggc	tccgagactc	cgggaacttc	cgagagcgct	2460
acaccagaaa	gcggacccgg	aaccagtacc	gaacctagcg	agggtctctg	tccgggcagc	2520
ccagccggct	ctcctacatc	cacggaggag	ggcacttccg	aatccgccac	cccggagtca	2580
gggccaggat	ctgaaccgcg	tacctcaggc	agtgagacgc	caggaacgag	cgagtccgct	2640

acaccggaga	gtgggccagg	gagccctgct	ggatctccta	cgccactga	ggaagggta	2700
ccagcgggct	cgcccaccag	cactgaagaa	ggtgcctcga	gcccgcctgt	gctgaagagg	2760
caccagcgag	aaattacccg	gaccaccctc	caatcggtac	aggaggaaat	cgactacgac	2820
gacaccatct	cggtggaaat	gaagaaggaa	gatttcgata	tctacgacga	ggacgaaaat	2880
cagtcccctc	gctcattcca	aaagaaaact	agacactact	ttatcgccgc	ggtggaaaga	2940
ctgtgggact	atggaatgtc	atccagccct	cacgtccttc	ggaaccgggc	ccagagcgga	3000
tcggtgcctc	agttcaagaa	agtgggtgtc	caggagtcca	ccgacggcag	cttcacccag	3060
ccgctgtacc	ggggagaact	gaacgaacac	ctgggcctgc	tcggtcccta	catccgcgcg	3120
gaagtggagg	ataacatcat	ggtgaccttc	cgtaaccaag	catccagacc	ttactccttc	3180
tattcctccc	tgatctcata	cgaggaggac	cagcgccaag	gcgccgagcc	ccgcaagaac	3240
ttcgtcaagc	ccaacgagac	taagacctac	ttctggaagg	tccaacacca	tatggccccg	3300
accaaggatg	agtttgactg	caaggcctgg	gcctacttct	ccgacgtgga	ccttgagaag	3360
gatgtccatt	ccggcctgat	cgggccgctg	ctcgtgtgtc	acaccaacac	cctgaaccca	3420
gcgcatggac	gccaggtcac	cgtccaggag	tttgctctgt	tcttcacat	ttttgacgaa	3480
actaagtcct	ggtacttcac	cgagaatatg	gagcgaaact	gtagagcgcc	ctgcaatata	3540
cagatggaag	atccgacttt	caaggagaac	tatagattcc	acgccatcaa	cgggtacata	3600
atggatactc	tgccggggct	ggtcatggcc	caggatcaga	ggattcggtg	gtacttgctg	3660
tcaatgggat	cgaacgaaaa	cattcactcc	attcacttct	ccggtcacgt	gttcactgtg	3720
cgcaagaagg	aggagtacaa	gatggcgctg	tacaatctgt	accccggggt	gttcgaaact	3780
gtggagatgc	tgccgtccaa	ggccggcatc	tggagagtgg	agtgcctgat	cggagagcac	3840
ctccacgcgg	ggatgtccac	cctcttcctg	gtgtactcga	ataagtcca	gaccccgctg	3900
ggcatggcct	cgggccacat	cagagacttc	cagatcacag	caagcggaca	atacggccaa	3960
tgggcgccga	agctggcccc	cttgacttac	tccggatcga	tcaacgcatg	gtccaccaag	4020
gaaccgttct	cgtggattaa	ggtggacctc	ctggccccta	tgattatcca	cggaattaag	4080
accagggcg	ccaggcagaa	gttctcctcc	ctgtacatct	cgcaattcat	catcatgtac	4140
agcctggacg	ggaagaagtg	gcagacttac	aggggaaact	ccaccggcac	cctgatggtc	4200
tttttcggca	acgtggattc	ctccggcatt	aagcacaaca	tcttcaacct	accgatcata	4260
gccagatata	ttaggctcca	ccccactcac	tactcaatcc	gctcaactct	tcggatggaa	4320
ctcatggggg	gcgacctgaa	ctcctgctcc	atgccgttgg	ggatggaatc	aaaggctatt	4380
agcgacgccc	agatcaccgc	gagctcctac	ttcactaaca	tgttcgccac	ctggagcccc	4440
tccaaggcca	ggctgcactt	gcaggggacg	tcaaatgcct	ggcggccgca	agtgaacaat	4500
ccgaagggaat	ggcttcaagt	ggattttcaa	aagaccatga	aagtgaccgg	agtcaccacc	4560

cagggagtgag agtcccttct gacctcgatg tatgtgaagg agttcctgat tagcagcagc	4620
caggacggggc accagtggac cctgttcttc caaaacggaa aggtcaaggt gttccagggg	4680
aaccaggact cgttcacacc cgtggtgaac tccctggacc cccactgct gacgcggtac	4740
ttgaggattc atcctcagtc ctgggtccat cagattgcat tgcgaatgga agtcctgggc	4800
tgcgaggccc aggacctgta ctga	4824

<210> 118
 <211> 450
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> XTEN144

<400> 118	
ggcgcgccaa catcagagag cgccaccct gaaagtggtc ccgggagcga gccagccaca	60
tctgggtcgg aaacgccagg cacaagtgag tctgcaactc ccgagtccgg acctggctcc	120
gagcctgcca ctagcggctc cgagactccg ggaacttccg agagcgctac accagaaagc	180
ggacccggaa ccagtaccga acctagcgag ggctctgctc cgggcagccc agccggctct	240
cctacatcca cggaggaggg cacttccgaa tccgccacc cggagtcagg gccaggatct	300
gaacccgcta cctcaggcag tgagacgcc ggaacgagcg agtccgctac accggagagt	360
gggccaggga gccctgctgg atctcctacg tccactgagg aagggtcacc agcgggctcg	420
cccaccagca ctgaagaagg tgcctcgagc	450

<210> 119
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Plasmid Backbone Sequence (PBS)-4

<400> 119	
atcagcctga gctcgctga	19

<210> 120
 <211> 595
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> WPRE (mutated woodchuck hepatitis virus post-transcriptional regulatory element)

<400> 120	
tcataatcaa cctctggatt aaaaaatttg tgaaagattg actggtattc ttaactatgt	60
tgctcctttt acgctatgtg gatacgctgc tttaatgcct ttgtatcatg ctattgcttc	120

cogtatggct	ttcattttct	cctccttgta	taaatacctgg	ttgctgtctc	tttatgagga	180
gttgtggccc	gttgtcaggc	aacgtggcgt	ggtgtgcaact	gtgtttgctg	acgcaacccc	240
caactggttgg	ggcattgcc	ccacctgtca	gctcctttcc	gggactttcg	ctttccccct	300
ccctattgcc	acggcggaac	tcatcgccgc	ctgccttgcc	cgctgctgga	caggggctcg	360
gctgttgggc	actgacaatt	ccgtggtgtt	gtcggggaaa	tcatcgtcct	ttccttggct	420
gctcgctgt	gttgccacct	ggattctgcg	cgggacgtcc	ttctgctacg	tcccttcggc	480
cctcaatcca	gcggaccttc	cttcccgcgg	cctgctgccg	gctctgcggc	ctcttcgcgg	540
tcttcgcctt	cgccctcaga	cgagtcggat	ctccctttgg	gccgcctccc	cgctg	595

<210> 121
 <211> 8
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Plasmid Backbone Sequence (PBS)-5

<400> 121	
atcagcct	8

<210> 122
 <211> 211
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> bGHpA (bovine growth hormone polyadenylation signal)

<400> 122						
cgactgtgcc	ttctagttgc	cagccatctg	ttgtttgccc	ctccccctg	ccttccttga	60
ccctggaagg	tgccactccc	actgtccttt	cctaataaaa	tgaggaaatt	gcacgcatt	120
gtctgagtag	gtgtcattct	attctggggg	gtgggggtggg	gcaggacagc	aagggggagg	180
attgggaaga	caatagcagg	catgctgggg	a			211

<210> 123
 <211> 119
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Plasmid Backbone Sequence (PBS)-6

<400> 123						
tgcggtgggc	tctatggctt	ctgaggcgga	aagaacgggc	tcgagaagct	tctagatatc	60
ctctcttaag	gtagcatcga	gatttaaatt	agggataaca	gggtaatggc	gcggggccgc	119

<210> 124
 <211> 130
 <212> DNA

<213> Artificial Sequence

<220>

<223> 3'ITR (3'-end AAV2 inverted terminal repeat)

<400> 124

aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg 60
ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120
gagcgcgagc 130

<210> 125

<211> 415

<212> PRT

<213> Artificial Sequence

<220>

<223> Mature FIX polypeptide

<400> 125

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly
35 40 45

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn

165

170

175

Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
 180 185 190

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly
 195 200 205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
 210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
 225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
 245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
 260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
 275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
 290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
 305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
 325 330 335

Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
 340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
 370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
 385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 405 410 415

<210> 126

<211> 415
<212> PRT
<213> Artificial Sequence

<220>
<223> Mature Padua(R338L)FIX Polypeptide

<400> 126

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly
35 40 45

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg Ala Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu
145 150 155 160

Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn
165 170 175

Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
180 185 190

Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly
195 200 205

Ser Ile Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu
210 215 220

Thr Gly Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu
225 230 235 240

Thr Glu His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His
245 250 255

His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu
260 265 270

Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile
275 280 285

Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser
290 295 300

Gly Tyr Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala
305 310 315 320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
325 330 335

Leu Leu Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
405 410 415

<210> 127

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> FIX Signal Polypeptide and Propeptide

<400> 127

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg
 35 40 45

<210> 128
 <211> 8442
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> human VWF

<400> 128
 atgattcctg ccagatttgc cggggtgctg cttgctctgg ccctcatttt gccagggacc 60
 ctttgtgcag aaggaactcg cggcaggtca tccacggccc gatgcagcct tttcggaagt 120
 gacttcgtca acacctttga tgggagcatg tacagctttg cgggatactg cagttacctc 180
 ctggcagggg gctgccagaa acgctccttc tcgattattg gggacttcca gaatggcaag 240
 agagtgcgcc tctccgtgta tcttggggaa ttttttgaca tccatttggt tgtcaatggg 300
 accgtgacac agggggacca aagagtctcc atgccctatg cctccaaagg gctgtatcta 360
 gaaactgagg ctgggtacta caagctgtcc ggtgaggcct atggctttgt ggccaggatc 420
 gatggcagcg gcaactttca agtcctgctg tcagacagat acttcaacaa gacctgcggg 480
 ctgtgtggca actttaacat ctttgcgtga gatgacttta tgaccaaga agggaccttg 540
 acctcggacc cttatgactt tgccaactca tgggctctga gcagtggaga acagtgggtg 600
 gaacgggcat ctcctcccag cagctcatgc aacatctcct ctggggaaat gcagaagggc 660
 ctgtgggagc agtgccagct tctgaagagc acctcgggtg ttgcccgtg ccacctctg 720
 gtggaccccg agccttttgt ggccctgtgt gagaagactt tgtgtgagtg tgctgggggg 780
 ctggagtgcg cctgccctgc cctcctggag tacgcccgga cctgtgcca ggagggaatg 840
 gtgctgtacg gctggaccga ccacagcgcg tgccagcccag tgtgccctgc tggatatggag 900
 tataggcagt gtgtgtcccc ttgcgccagg acctgccaga gcctgcacat caatgaaatg 960
 tgtcaggagc gatgcgtgga tggctgcagc tgccctgagg gacagctcct ggatgaaggc 1020
 ctctgcgtgg agagcaccga gtgtccctgc gtgcattccg gaaagcgcta ccctcccggc 1080
 acctccctct ctcgagactg caacacctgc atttgccgaa acagccagtg gatctgcagc 1140
 aatgaagaat gtccagggga gtgccttgtc actgggtcaat cccacttcaa gagctttgac 1200
 aacagatact tcaccttcag tgggatctgc cagtacctgc tggcccggga ttgccaggac 1260
 cactccttct ccattgtcat tgagactgtc cagtgtgctg atgaccgca cgctgtgtgc 1320
 acccgctccg tcaccgtccg gctgcctggc ctgcacaaca gccttgtgaa actgaagcat 1380
 ggggcaggag ttgccatgga tggccaggac atccagctcc ccctcctgaa aggtgacctc 1440

cgcatccagc	atacagtac	ggcctccgtg	cgctcagct	acggggagga	cctgcagatg	1500
gactgggatg	gccgcgggag	gctgctggtg	aagctgtccc	ccgtctatgc	cggaagacc	1560
tgcggcctgt	gtgggaatta	caatggcaac	cagggcgacg	acttccttac	cccctctggg	1620
ctggcrgagc	cccgggtgga	ggacttcggg	aacgcctgga	agctgcacgg	ggactgccag	1680
gacctgcaga	agcagcacag	cgatccctgc	gccctcaacc	cgcgcatgac	caggttctcc	1740
gaggaggcgt	gcgcggtcct	gacgtccccc	acattcgagg	cctgccatcg	tgccgtcagc	1800
ccgctgccct	acctgcggaa	ctgccgctac	gacgtgtgct	cctgctcgga	cggccgcgag	1860
tgctgtgctg	gcgccctggc	cagctatgcc	gcggcctgct	cggggagagg	cgtgcgcgtc	1920
gcgtggcgcg	agccaggccg	ctgtgagctg	aactgcccga	aaggccagggt	gtacctgcag	1980
tgcgggaccc	cctgcaacct	gacctgccgc	tctctctctt	acccggatga	ggaatgcaat	2040
gaggcctgcc	tggagggctg	cttctgcccc	ccagggctct	acatggatga	gaggggggac	2100
tgctgcccc	aggcccagtg	cccctgttac	tatgacgggtg	agatcttcca	gccagaagac	2160
atcttctcag	accatcacac	catgtgctac	tgtgaggatg	gcttcatgca	ctgtaccatg	2220
agtggagtcc	ccggaagctt	gctgcctgac	gctgtcctca	gcagtcccct	gtctcatcgc	2280
agcaaaagga	gcctatcctg	tcggccccc	atggtcaagc	tggtgtgtcc	cgctgacaac	2340
ctgcgggctg	aagggtctga	gtgtaccaa	acgtgccaga	actatgacct	ggagtgcagt	2400
agcatgggct	gtgtctctgg	ctgcctctgc	ccccggggca	tggtccggca	tgagaacaga	2460
tgtgtggccc	tggaaggtg	tccctgcttc	catcagggca	aggagtatgc	ccctggagaa	2520
acagtgaaga	ttggctgcaa	cacttgtgtc	tgtcgggacc	ggaagtggaa	ctgcacagac	2580
catgtgtgtg	atgccacgtg	ctccacgac	ggcatggccc	actacctcac	cttcgacggg	2640
ctcaaatacc	tgttccccgg	ggagtgccag	tacgttctgg	tgacaggatta	ctgcggcagt	2700
aaccctggga	cctttcggat	cctagtgggg	aataagggat	gcagccacc	ctcagtga	2760
tgcaagaaac	gggtcaccat	cctggtggag	ggaggagaga	ttgagctgtt	tgacggggag	2820
gtgaatgtga	agaggcccat	gaaggatgag	actcactttg	aggtggtgga	gtctggccgg	2880
tacatcattc	tgctgctggg	caaagccctc	tccgtggtct	gggaccgcca	cctgagcatc	2940
tccgtggtcc	tgaagcagac	ataccaggag	aaagtgtgtg	gcctgtgtgg	gaattttgat	3000
ggcatccaga	acaatgacct	caccagcagc	aacctccaag	tgagggaaga	ccctgtggac	3060
tttgggaaact	cctggaaagt	gagctcgacg	tgtgctgaca	ccagaaaagt	gcctctggac	3120
tcaccccctg	ccacctgcca	taacaacatc	atgaagcaga	cgatggtgga	ttcctcctgt	3180
agaatcctta	ccagtgcagt	cttcaggac	tgcaacaagc	tggtggacc	cgagccatat	3240
ctggatgtct	gcatttacga	cacctgctcc	tgtgagtcca	ttggggactg	cgctgcttc	3300
tgcgacacca	ttgctgccta	tgcccacgtg	tgtgcccagc	atggcaagggt	ggtgacctgg	3360

aggacggcca cattgtgccc ccagagctgc gaggagagga atctccggga gaacgggtat	3420
gagtgtgagt ggcgtataa cagctgtgca cctgcctgtc aagtcacgtg tcagcacctt	3480
gagccactgg cctgcctgtg gcagtgtgtg gagggtgccc atgccactg ccctccaggg	3540
aaaatcctgg atgagctttt gcagacctgc gttgacctg aagactgtcc agtgtgtgag	3600
gtggctggcc ggcgttttgc ctcaggaaag aaagtcacct tgaatcccag tgacctgag	3660
cactgccaga tttgccactg tgatgttgtc aacctacct gtgaagcctg ccaggagccg	3720
ggaggcctgg tggcgcctcc cacagatgcc ccggtgagcc ccaccactct gtatgtggag	3780
gacatctcgg aaccgccgtt gcacgatttc tactgcagca ggctactgga cctggctctc	3840
ctgctggatg gctcctccag gctgtccgag gctgagtttg aagtgtgaa ggcctttgtg	3900
gtggacatga tggagcggct gcgcatctcc cagaagtggg tccgcgtggc cgtggtggag	3960
taccacgacg gctcccacgc ctacatcggg ctcaaggacc ggaagcgacc gtcagagctg	4020
cggcgcattg ccagccaggt gaagtatgcg ggcagccagg tggcctccac cagcgaggtc	4080
ttgaaataca cactgttcca aatcttcagc aagatcgacc gccctgaagc ctcccgcac	4140
gccctgctcc tgatggccag ccaggagccc caacggatgt cccggaactt tgtccgctac	4200
gtccagggcc tgaagaagaa gaaggtcatt gtgatcccgg tgggcattgg gcccacatgc	4260
aacctcaagc agatccgcct catcgagaag caggcccctg agaacaaggc cttcgtgctg	4320
agcagtgtgg atgagctgga gcagcaaagg gacgagatcg ttagctacct ctgtgacctt	4380
gccctgaag cccctcctcc tactctgccc cccgacatgg cacaagtcac tgtgggcccg	4440
gggctcttgg gggtttcgac cctggggccc aagaggaact ccatggttct ggatgtggcg	4500
ttcgtcctgg aaggatcgga caaaattggt gaagccgact tcaacaggag caaggagttc	4560
atggaggagg tgattcagcg gatggatgtg ggccaggaca gcatccacgt cacggtgctg	4620
cagtactcct acatggtgac cgtggagtac cccttcagcg aggcacagtc caaaggggac	4680
atcctgcagc gggcgcgaga gatccgctac cagggcggca acaggaccaa cactgggctg	4740
gccctgcggt acctctctga ccacagcttc ttggtcagcc agggtgaccg ggagcaggcg	4800
cccaacctgg tctacatggt caccggaaat cctgcctctg atgagatcaa gaggtgcct	4860
ggagacatcc aggtggtgcc cattggagtg ggccctaata ccaacgtgca ggagctggag	4920
aggattggct ggcccaatgc ccctatcctc atccaggact ttgagacgct ccccgagag	4980
gtcctgacc tggcgtgca gaggtgctgc tccggagagg ggctgcagat cccaccctc	5040
tcccctgcac ctgactgcag ccagcccctg gacgtgatcc ttctcctgga tggctcctcc	5100
agtttcccag cttcttattt tgatgaaatg aagagtttcg ccaaggcttt catttcaaaa	5160
gccaatatag ggctcgtct cactcagggtg tcagtgtgac agtatggaag catcaccacc	5220
attgacgtgc catggaacgt ggtcccggag aaagccatt tgotgagcct tgtggacgtc	5280

atgcagcggg	agggaggccc	cagccaaatc	ggggatgcct	tgggctttgc	tgtgcgatac	5340
ttgacttcag	aaatgcatgg	tgccaggccg	ggagcctcaa	aggcggtggt	catcctggtc	5400
acggacgtct	ctgtggattc	agtggatgca	gcagctgatg	ccgccaggtc	caacagagtg	5460
acagtgttcc	ctattggaat	tggagatcgc	tacgatgcag	cccagctacg	gatccttgga	5520
ggcccagcag	gcgactccaa	cgtgggtgaag	ctccagcgaa	tcgaagacct	ccctaccatg	5580
gtcaccttgg	gcaattcctt	cctccacaaa	ctgtgctctg	gatttgtag	gatttgcatg	5640
gatgaggatg	ggaatgagaa	gaggcccggg	gacgtctgga	ccttgccaga	ccagtgccac	5700
accgtgactt	gccagccaga	tggccagacc	ttgctgaaga	gtcatcgggt	caactgtgac	5760
cgggggctga	ggccttcgtg	ccctaacagc	cagtcccctg	ttaaagtgga	agagacctgt	5820
ggctgccgct	ggacctgccc	ctgygtgtgc	acaggcagct	ccactcggca	catcgtgacc	5880
tttgatgggc	agaatttcaa	gctgactggc	agctgttctt	atgtcctatt	tcaaaacaag	5940
gagcaggacc	tggaggtgat	tctccataat	ggtgcctgca	gccctggagc	aaggcagggc	6000
tgcataaaat	ccatcgaggt	gaagcacagt	gccctctccg	tcgagstgca	cagtgcacatg	6060
gaggtgacgg	tgaatgggag	actggtctct	gttccttacg	tgggtgggaa	catggaagtc	6120
aacgtttatg	gtgccatcat	gcatgaggtc	agattcaatc	accttgggtca	catcttcaca	6180
ttcactccac	aaaacaatga	gttccaactg	cagctcagcc	ccaagacttt	tgcttcaaag	6240
acgtatggtc	tgtgtgggat	ctgtgatgag	aacggagcca	atgacttcat	gctgagggat	6300
ggcacagtca	ccacagactg	gaaaacactt	gttcaggaat	ggactgtgca	gcggccaggg	6360
cagacgtgcc	agcccatcct	ggaggagcag	tgtcttgtcc	ccgacagctc	ccactgccag	6420
gtcctcctct	taccactgtt	tgctgaatgc	cacaagggtcc	tggctccagc	cacattctat	6480
gccatctgcc	agcaggacag	ttgccaccag	gagcaagtgt	gtgaggtgat	cgcctcttat	6540
gcccacctct	gtcggaccaa	cgggggtctgc	gttgactgga	ggacacctga	tttctgtgct	6600
atgtcatgcc	caccatctct	ggtctacaac	cactgtgagc	atggctgtcc	ccggcactgt	6660
gatggcaacg	tgagctcctg	tggggaccat	ccctccgaag	gctgtttctg	ccctccagat	6720
aaagtcatgt	tggaaggcag	ctgtgtccct	gaagaggcct	gcactcagtg	cattgggtgag	6780
gatggagtcc	agcaccagtt	cctggaagcc	tgggtcccgg	accaccagcc	ctgtcagatc	6840
tgcacatgcc	tcagcgggcg	gaagggtcaac	tgcacaacgc	agccctgccc	cacggccaaa	6900
gtctccacgt	gtggcctgtg	tgaagtagcc	cgcctccgcc	agaatgcaga	ccagtgtctgc	6960
cccagtatg	agtgtgtgtg	tgaccacagt	agctgtgacc	tgccccagct	gcctcactgt	7020
gaacgtggcc	tccagcccac	actgaccaac	cctggcgagt	gcagacccaa	cttcacctgc	7080
gcctgcagga	aggaggagtg	caaaagagtg	tccccaccct	cctgcccccc	gcaccgtttg	7140
cccacccttc	ggaagaccca	gtgctgtgat	gagtatgagt	gtgcctgcaa	ctgtgtcaac	7200

tccacagtga gctgtcccct tgggtacttg gcctcaaccg ccaccaatga ctgtggctgt	7260
accacaacca cctgccttcc cgacaagggtg tgtgtccacc gaagcaccat ctaccctgtg	7320
ggccagttct gggaggaggg ctgcgatgtg tgcacctgca ccgacatgga ggatgccgtg	7380
atgggcctcc gcgtggccca gtgctcccag aagccctgtg aggacagctg tcggtcgggc	7440
ttcacttacg ttctgcatga aggcgagtgc tgtggaagggt gcctgccatc tgcctgtgag	7500
gtggtgactg gctcaccgcg gggggactcc cagtcttcct ggaagagtgt cggctcccag	7560
tgggcctccc cggagaaccc ctgcctcatc aatgagtgtg tccgagtga ggaggaggtc	7620
tttatacaac aaaggaacgt ctccctgcccc cagctggagg tccctgtctg cccctcgggc	7680
tttcagctga gctgtaagac ctcagcgtgc tgcccaagct gtcgctgtga gcgcatggag	7740
gcctgcatgc tcaatggcac tgtcattggg ccggaaga ctgtgatgat cgatgtgtgc	7800
acgacctgcc gctgcatggt gcagggtggg gtcctctctg gattcaagct ggagtgcagg	7860
aagaccacct gcaaccctg cccctgggt tacaaggaag aaaataacac aggtgaatgt	7920
tgtgggagat gtttgcctac ggcttgacc attcagctaa gaggaggaca gatcatgaca	7980
ctgaagcgtg atgagacgct ccaggatggc tgtgatactc acttctgcaa ggtcaatgag	8040
agaggagagt acttctggga gaagagggtc acaggctgcc cacccttga tgaacacaag	8100
tgtcttgctg agggaggtaa aattatgaaa attccaggca cctgctgtga cacatgtgag	8160
gagcctgagt gcaacgacat cactgccagg ctgcagtatg tcaagggtggg aagctgtaag	8220
tctgaagtag aggtggatat ccactactgc cagggcaaat gtgccagcaa agccatgtac	8280
tccattgaca tcaacgatgt gcaggaccag tgctcctgct gctctccgac acggacggag	8340
cccatgcagg tggccctgca ctgcaccaat ggctctgttg tgtacatga ggttctcaat	8400
gccatggagt gcaaatgctc cccaggaag tgcagcaagt ga	8442

<210> 129
 <211> 2809
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human VWF

<220>
 <221> misc_feature
 <222> (540)..(540)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature
 <222> (1944)..(1944)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> misc_feature

<222> (2012)..(2012)

<223> Xaa can be any naturally occurring amino acid

<400> 129

Met Ile Pro Ala Arg Phe Ala Gly Val Leu Leu Ala Leu Ala Leu Ile
1 5 10 15

Leu Pro Gly Thr Leu Cys Ala Glu Gly Thr Arg Gly Arg Ser Ser Thr
20 25 30

Ala Arg Cys Ser Leu Phe Gly Ser Asp Phe Val Asn Thr Phe Asp Gly
35 40 45

Ser Met Tyr Ser Phe Ala Gly Tyr Cys Ser Tyr Leu Leu Ala Gly Gly
50 55 60

Cys Gln Lys Arg Ser Phe Ser Ile Ile Gly Asp Phe Gln Asn Gly Lys
65 70 75 80

Arg Val Ser Leu Ser Val Tyr Leu Gly Glu Phe Phe Asp Ile His Leu
85 90 95

Phe Val Asn Gly Thr Val Thr Gln Gly Asp Gln Arg Val Ser Met Pro
100 105 110

Tyr Ala Ser Lys Gly Leu Tyr Leu Glu Thr Glu Ala Gly Tyr Tyr Lys
115 120 125

Leu Ser Gly Glu Ala Tyr Gly Phe Val Ala Arg Ile Asp Gly Ser Gly
130 135 140

Asn Phe Gln Val Leu Leu Ser Asp Arg Tyr Phe Asn Lys Thr Cys Gly
145 150 155 160

Leu Cys Gly Asn Phe Asn Ile Phe Ala Glu Asp Asp Phe Met Thr Gln
165 170 175

Glu Gly Thr Leu Thr Ser Asp Pro Tyr Asp Phe Ala Asn Ser Trp Ala
180 185 190

Leu Ser Ser Gly Glu Gln Trp Cys Glu Arg Ala Ser Pro Pro Ser Ser
195 200 205

Ser Cys Asn Ile Ser Ser Gly Glu Met Gln Lys Gly Leu Trp Glu Gln
210 215 220

Cys Gln Leu Leu Lys Ser Thr Ser Val Phe Ala Arg Cys His Pro Leu
225 230 235 240

Val	Asp	Pro	Glu	Pro	Phe	Val	Cys	Glu	Lys	Thr	Leu	Cys	Glu	Cys	Ala	
				245					250						255	
Gly	Gly	Leu	Glu	Cys	Ala	Cys	Pro	Ala	Leu	Leu	Glu	Tyr	Ala	Arg	Thr	
			260					265						270		
Cys	Ala	Gln	Glu	Gly	Met	Val	Leu	Tyr	Gly	Trp	Thr	Asp	His	Ser	Ala	
		275					280					285				
Cys	Ser	Pro	Val	Cys	Pro	Ala	Gly	Met	Glu	Tyr	Arg	Gln	Cys	Val	Ser	
	290					295					300					
Pro	Cys	Ala	Arg	Thr	Cys	Gln	Ser	Leu	His	Ile	Asn	Glu	Met	Cys	Gln	
305					310					315					320	
Glu	Arg	Cys	Val	Asp	Gly	Cys	Ser	Cys	Pro	Glu	Gly	Gln	Leu	Leu	Asp	
				325					330					335		
Glu	Gly	Leu	Cys	Val	Glu	Ser	Thr	Glu	Cys	Pro	Cys	Val	His	Ser	Gly	
			340					345					350			
Lys	Arg	Tyr	Pro	Pro	Gly	Thr	Ser	Leu	Ser	Arg	Asp	Cys	Asn	Thr	Cys	
		355					360					365				
Ile	Cys	Arg	Asn	Ser	Gln	Trp	Ile	Cys	Ser	Asn	Glu	Glu	Cys	Pro	Gly	
	370					375					380					
Glu	Cys	Leu	Val	Thr	Gly	Gln	Ser	His	Phe	Lys	Ser	Phe	Asp	Asn	Arg	
385					390					395					400	
Tyr	Phe	Thr	Phe	Ser	Gly	Ile	Cys	Gln	Tyr	Leu	Leu	Ala	Arg	Asp	Cys	
				405					410					415		
Gln	Asp	His	Ser	Phe	Ser	Ile	Val	Ile	Glu	Thr	Val	Gln	Cys	Ala	Asp	
			420					425					430			
Asp	Arg	Asp	Ala	Val	Cys	Thr	Arg	Ser	Val	Thr	Val	Arg	Leu	Pro	Gly	
		435					440					445				
Leu	His	Asn	Ser	Leu	Val	Lys	Leu	Lys	His	Gly	Ala	Gly	Val	Ala	Met	
	450					455					460					
Asp	Gly	Gln	Asp	Ile	Gln	Leu	Pro	Leu	Leu	Lys	Gly	Asp	Leu	Arg	Ile	
465					470					475					480	
Gln	His	Thr	Val	Thr	Ala	Ser	Val	Arg	Leu	Ser	Tyr	Gly	Glu	Asp	Leu	
				485					490					495		

Gln Met Asp Trp Asp Gly Arg Gly Arg Leu Leu Val Lys Leu Ser Pro
 500 505 510

Val Tyr Ala Gly Lys Thr Cys Gly Leu Cys Gly Asn Tyr Asn Gly Asn
 515 520 525

Gln Gly Asp Asp Phe Leu Thr Pro Ser Gly Leu Xaa Glu Pro Arg Val
 530 535 540

Glu Asp Phe Gly Asn Ala Trp Lys Leu His Gly Asp Cys Gln Asp Leu
 545 550 555 560

Gln Lys Gln His Ser Asp Pro Cys Ala Leu Asn Pro Arg Met Thr Arg
 565 570 575

Phe Ser Glu Glu Ala Cys Ala Val Leu Thr Ser Pro Thr Phe Glu Ala
 580 585 590

Cys His Arg Ala Val Ser Pro Leu Pro Tyr Leu Arg Asn Cys Arg Tyr
 595 600 605

Asp Val Cys Ser Cys Ser Asp Gly Arg Glu Cys Leu Cys Gly Ala Ser
 610 615 620

Tyr Ala Ala Ala Cys Ala Gly Arg Gly Val Arg Val Ala Trp Arg Glu
 625 630 635 640

Pro Gly Arg Cys Glu Leu Asn Cys Pro Lys Gly Gln Val Tyr Leu Gln
 645 650 655

Cys Gly Thr Pro Cys Asn Leu Thr Cys Arg Ser Leu Ser Tyr Pro Asp
 660 665 670

Glu Glu Cys Asn Glu Ala Cys Leu Glu Gly Cys Phe Cys Pro Pro Gly
 675 680 685

Leu Tyr Met Asp Glu Arg Gly Asp Cys Val Pro Lys Ala Gln Cys Pro
 690 695 700

Cys Tyr Tyr Asp Gly Glu Ile Phe Gln Pro Glu Asp Ile Phe Ser Asp
 705 710 715 720

His His Thr Met Cys Tyr Cys Glu Asp Gly Phe Met His Cys Thr Met
 725 730 735

Ser Gly Val Pro Gly Ser Leu Leu Pro Asp Ala Val Leu Ser Ser Pro
 740 745 750

Leu	Ser	His	Arg	Ser	Lys	Arg	Ser	Leu	Ser	Cys	Arg	Pro	Pro	Met	Val		
		755					760					765					
Lys	Leu	Val	Cys	Pro	Ala	Asp	Asn	Leu	Arg	Ala	Glu	Gly	Leu	Glu	Cys		
		770				775					780						
Thr	Lys	Thr	Cys	Gln	Asn	Tyr	Asp	Leu	Glu	Cys	Met	Ser	Met	Gly	Cys		
					790					795					800		
Val	Ser	Gly	Cys	Leu	Cys	Pro	Pro	Gly	Met	Val	Arg	His	Glu	Asn	Arg		
				805					810					815			
Cys	Val	Ala	Leu	Glu	Arg	Cys	Pro	Cys	Phe	His	Gln	Gly	Lys	Glu	Tyr		
			820					825					830				
Ala	Pro	Gly	Glu	Thr	Val	Lys	Ile	Gly	Cys	Asn	Thr	Cys	Val	Cys	Arg		
		835					840					845					
Asp	Arg	Lys	Trp	Asn	Cys	Thr	Asp	His	Val	Cys	Asp	Ala	Thr	Cys	Ser		
	850					855					860						
Thr	Ile	Gly	Met	Ala	His	Tyr	Leu	Thr	Phe	Asp	Gly	Leu	Lys	Tyr	Leu		
	865				870					875					880		
Phe	Pro	Gly	Glu	Cys	Gln	Tyr	Val	Leu	Val	Gln	Asp	Tyr	Cys	Gly	Ser		
				885					890					895			
Asn	Pro	Gly	Thr	Phe	Arg	Ile	Leu	Val	Gly	Asn	Lys	Gly	Cys	Ser	His		
			900					905					910				
Pro	Ser	Val	Lys	Cys	Lys	Lys	Arg	Val	Thr	Ile	Leu	Val	Glu	Gly	Gly		
		915					920					925					
Glu	Ile	Glu	Leu	Phe	Asp	Gly	Glu	Val	Asn	Val	Lys	Arg	Pro	Met	Lys		
	930					935					940						
Asp	Glu	Thr	His	Phe	Glu	Val	Val	Glu	Ser	Gly	Arg	Tyr	Ile	Ile	Leu		
	945				950					955					960		
Leu	Leu	Gly	Lys	Ala	Leu	Ser	Val	Val	Trp	Asp	Arg	His	Leu	Ser	Ile		
				965					970					975			
Ser	Val	Val	Leu	Lys	Gln	Thr	Tyr	Gln	Glu	Lys	Val	Cys	Gly	Leu	Cys		
			980					985					990				
Gly	Asn	Phe	Asp	Gly	Ile	Gln	Asn	Asn	Asp	Leu	Thr	Ser	Ser	Asn	Leu		
		995					1000					1005					

Gln Val	Glu Glu Asp Pro	Val Asp Phe Gly Asn Ser	Trp Lys Val
1010		1015	1020
Ser Ser	Gln Cys Ala Asp Thr	Arg Lys Val Pro Leu	Asp Ser Ser
1025		1030	1035
Pro Ala	Thr Cys His Asn Asn	Ile Met Lys Gln Thr	Met Val Asp
1040		1045	1050
Ser Ser	Cys Arg Ile Leu Thr	Ser Asp Val Phe Gln	Asp Cys Asn
1055		1060	1065
Lys Leu	Val Asp Pro Glu Pro	Tyr Leu Asp Val Cys	Ile Tyr Asp
1070		1075	1080
Thr Cys	Ser Cys Glu Ser Ile	Gly Asp Cys Ala Cys	Phe Cys Asp
1085		1090	1095
Thr Ile	Ala Ala Tyr Ala His	Val Cys Ala Gln His	Gly Lys Val
1100		1105	1110
Val Thr	Trp Arg Thr Ala Thr	Leu Cys Pro Gln Ser	Cys Glu Glu
1115		1120	1125
Arg Asn	Leu Arg Glu Asn Gly	Tyr Glu Cys Glu Trp	Arg Tyr Asn
1130		1135	1140
Ser Cys	Ala Pro Ala Cys Gln	Val Thr Cys Gln His	Pro Glu Pro
1145		1150	1155
Leu Ala	Cys Pro Val Gln Cys	Val Glu Gly Cys His	Ala His Cys
1160		1165	1170
Pro Pro	Gly Lys Ile Leu Asp	Glu Leu Leu Gln Thr	Cys Val Asp
1175		1180	1185
Pro Glu	Asp Cys Pro Val Cys	Glu Val Ala Gly Arg	Arg Phe Ala
1190		1195	1200
Ser Gly	Lys Lys Val Thr Leu	Asn Pro Ser Asp Pro	Glu His Cys
1205		1210	1215
Gln Ile	Cys His Cys Asp Val	Val Asn Leu Thr Cys	Glu Ala Cys
1220		1225	1230
Gln Glu	Pro Gly Gly Leu Val	Val Pro Pro Thr Asp	Ala Pro Val
1235		1240	1245

Ser	Pro	Thr	Thr	Leu	Tyr	Val	Glu	Asp	Ile	Ser	Glu	Pro	Pro	Leu
1250						1255					1260			
His	Asp	Phe	Tyr	Cys	Ser	Arg	Leu	Leu	Asp	Leu	Val	Phe	Leu	Leu
1265						1270					1275			
Asp	Gly	Ser	Ser	Arg	Leu	Ser	Glu	Ala	Glu	Phe	Glu	Val	Leu	Lys
1280						1285					1290			
Ala	Phe	Val	Val	Asp	Met	Met	Glu	Arg	Leu	Arg	Ile	Ser	Gln	Lys
1295						1300					1305			
Trp	Val	Arg	Val	Ala	Val	Val	Glu	Tyr	His	Asp	Gly	Ser	His	Ala
1310						1315					1320			
Tyr	Ile	Gly	Leu	Lys	Asp	Arg	Lys	Arg	Pro	Ser	Glu	Leu	Arg	Arg
1325						1330					1335			
Ile	Ala	Ser	Gln	Val	Lys	Tyr	Ala	Gly	Ser	Gln	Val	Ala	Ser	Thr
1340						1345					1350			
Ser	Glu	Val	Leu	Lys	Tyr	Thr	Leu	Phe	Gln	Ile	Phe	Ser	Lys	Ile
1355						1360					1365			
Asp	Arg	Pro	Glu	Ala	Ser	Arg	Ile	Ala	Leu	Leu	Leu	Met	Ala	Ser
1370						1375					1380			
Gln	Glu	Pro	Gln	Arg	Met	Ser	Arg	Asn	Phe	Val	Arg	Tyr	Val	Gln
1385						1390					1395			
Gly	Leu	Lys	Lys	Lys	Lys	Val	Ile	Val	Ile	Pro	Val	Gly	Ile	Gly
1400						1405					1410			
Pro	His	Ala	Asn	Leu	Lys	Gln	Ile	Arg	Leu	Ile	Glu	Lys	Gln	Ala
1415						1420					1425			
Pro	Glu	Asn	Lys	Ala	Phe	Val	Leu	Ser	Ser	Val	Asp	Glu	Leu	Glu
1430						1435					1440			
Gln	Gln	Arg	Asp	Glu	Ile	Val	Ser	Tyr	Leu	Cys	Asp	Leu	Ala	Pro
1445						1450					1455			
Glu	Ala	Pro	Pro	Pro	Thr	Leu	Pro	Pro	Asp	Met	Ala	Gln	Val	Thr
1460						1465					1470			
Val	Gly	Pro	Gly	Leu	Leu	Gly	Val	Ser	Thr	Leu	Gly	Pro	Lys	Arg
1475						1480					1485			

Asn	Ser	Met	Val	Leu	Asp	Val	Ala	Phe	Val	Leu	Glu	Gly	Ser	Asp
1490						1495					1500			
Lys	Ile	Gly	Glu	Ala	Asp	Phe	Asn	Arg	Ser	Lys	Glu	Phe	Met	Glu
1505						1510					1515			
Glu	Val	Ile	Gln	Arg	Met	Asp	Val	Gly	Gln	Asp	Ser	Ile	His	Val
1520						1525					1530			
Thr	Val	Leu	Gln	Tyr	Ser	Tyr	Met	Val	Thr	Val	Glu	Tyr	Pro	Phe
1535						1540					1545			
Ser	Glu	Ala	Gln	Ser	Lys	Gly	Asp	Ile	Leu	Gln	Arg	Val	Arg	Glu
1550						1555					1560			
Ile	Arg	Tyr	Gln	Gly	Gly	Asn	Arg	Thr	Asn	Thr	Gly	Leu	Ala	Leu
1565						1570					1575			
Arg	Tyr	Leu	Ser	Asp	His	Ser	Phe	Leu	Val	Ser	Gln	Gly	Asp	Arg
1580						1585					1590			
Glu	Gln	Ala	Pro	Asn	Leu	Val	Tyr	Met	Val	Thr	Gly	Asn	Pro	Ala
1595						1600					1605			
Ser	Asp	Glu	Ile	Lys	Arg	Leu	Pro	Gly	Asp	Ile	Gln	Val	Val	Pro
1610						1615					1620			
Ile	Gly	Val	Gly	Pro	Asn	Ala	Asn	Val	Gln	Glu	Leu	Glu	Arg	Ile
1625						1630					1635			
Gly	Trp	Pro	Asn	Ala	Pro	Ile	Leu	Ile	Gln	Asp	Phe	Glu	Thr	Leu
1640						1645					1650			
Pro	Arg	Glu	Ala	Pro	Asp	Leu	Val	Leu	Gln	Arg	Cys	Cys	Ser	Gly
1655						1660					1665			
Glu	Gly	Leu	Gln	Ile	Pro	Thr	Leu	Ser	Pro	Ala	Pro	Asp	Cys	Ser
1670						1675					1680			
Gln	Pro	Leu	Asp	Val	Ile	Leu	Leu	Leu	Asp	Gly	Ser	Ser	Ser	Phe
1685						1690					1695			
Pro	Ala	Ser	Tyr	Phe	Asp	Glu	Met	Lys	Ser	Phe	Ala	Lys	Ala	Phe
1700						1705					1710			
Ile	Ser	Lys	Ala	Asn	Ile	Gly	Pro	Arg	Leu	Thr	Gln	Val	Ser	Val
1715						1720					1725			

Leu	Gln	Tyr	Gly	Ser	Ile	Thr	Thr	Ile	Asp	Val	Pro	Trp	Asn	Val
1730						1735					1740			
Val	Pro	Glu	Lys	Ala	His	Leu	Leu	Ser	Leu	Val	Asp	Val	Met	Gln
1745						1750					1755			
Arg	Glu	Gly	Gly	Pro	Ser	Gln	Ile	Gly	Asp	Ala	Leu	Gly	Phe	Ala
1760						1765					1770			
Val	Arg	Tyr	Leu	Thr	Ser	Glu	Met	His	Gly	Ala	Arg	Pro	Gly	Ala
1775						1780					1785			
Ser	Lys	Ala	Val	Val	Ile	Leu	Val	Thr	Asp	Val	Ser	Val	Asp	Ser
1790						1795					1800			
Val	Asp	Ala	Ala	Ala	Asp	Ala	Ala	Arg	Ser	Asn	Arg	Val	Thr	Val
1805						1810					1815			
Phe	Pro	Ile	Gly	Ile	Gly	Asp	Arg	Tyr	Asp	Ala	Ala	Gln	Leu	Arg
1820						1825					1830			
Ile	Leu	Ala	Gly	Pro	Ala	Gly	Asp	Ser	Asn	Val	Val	Lys	Leu	Gln
1835						1840					1845			
Arg	Ile	Glu	Asp	Leu	Pro	Thr	Met	Val	Thr	Leu	Gly	Asn	Ser	Phe
1850						1855					1860			
Leu	His	Lys	Leu	Cys	Ser	Gly	Phe	Val	Arg	Ile	Cys	Met	Asp	Glu
1865						1870					1875			
Asp	Gly	Asn	Glu	Lys	Arg	Pro	Gly	Asp	Val	Trp	Thr	Leu	Pro	Asp
1880						1885					1890			
Gln	Cys	His	Thr	Val	Thr	Cys	Gln	Pro	Asp	Gly	Gln	Thr	Leu	Leu
1895						1900					1905			
Lys	Ser	His	Arg	Val	Asn	Cys	Asp	Arg	Gly	Leu	Arg	Pro	Ser	Cys
1910						1915					1920			
Pro	Asn	Ser	Gln	Ser	Pro	Val	Lys	Val	Glu	Glu	Thr	Cys	Gly	Cys
1925						1930					1935			
Arg	Trp	Thr	Cys	Pro	Xaa	Val	Cys	Thr	Gly	Ser	Ser	Thr	Arg	His
1940						1945					1950			
Ile	Val	Thr	Phe	Asp	Gly	Gln	Asn	Phe	Lys	Leu	Thr	Gly	Ser	Cys
1955						1960					1965			

Ser 1970	Tyr	Val	Leu	Phe	Gln	Asn 1975	Lys	Glu	Gln	Asp	Leu 1980	Glu	Val	Ile
Leu 1985	His	Asn	Gly	Ala	Cys	Ser 1990	Pro	Gly	Ala	Arg	Gln 1995	Gly	Cys	Met
Lys 2000	Ser	Ile	Glu	Val	Lys	His 2005	Ser	Ala	Leu	Ser	Val 2010	Glu	Xaa	His
Ser 2015	Asp	Met	Glu	Val	Thr	Val 2020	Asn	Gly	Arg	Leu	Val 2025	Ser	Val	Pro
Tyr 2030	Val	Gly	Gly	Asn	Met	Glu 2035	Val	Asn	Val	Tyr	Gly 2040	Ala	Ile	Met
His 2045	Glu	Val	Arg	Phe	Asn	His 2050	Leu	Gly	His	Ile	Phe 2055	Thr	Phe	Thr
Pro 2060	Gln	Asn	Asn	Glu	Phe	Gln 2065	Leu	Gln	Leu	Ser	Pro 2070	Lys	Thr	Phe
Ala 2075	Ser	Lys	Thr	Tyr	Gly	Leu 2080	Cys	Gly	Ile	Cys	Asp 2085	Glu	Asn	Gly
Ala 2090	Asn	Asp	Phe	Met	Leu	Arg 2095	Asp	Gly	Thr	Val	Thr 2100	Thr	Asp	Trp
Lys 2105	Thr	Leu	Val	Gln	Glu	Trp 2110	Thr	Val	Gln	Arg	Pro 2115	Gly	Gln	Thr
Cys 2120	Gln	Pro	Ile	Leu	Glu	Glu 2125	Gln	Cys	Leu	Val	Pro 2130	Asp	Ser	Ser
His 2135	Cys	Gln	Val	Leu	Leu	Leu 2140	Pro	Leu	Phe	Ala	Glu 2145	Cys	His	Lys
Val 2150	Leu	Ala	Pro	Ala	Thr	Phe 2155	Tyr	Ala	Ile	Cys	Gln 2160	Gln	Asp	Ser
Cys 2165	His	Gln	Glu	Gln	Val	Cys 2170	Glu	Val	Ile	Ala	Ser 2175	Tyr	Ala	His
Leu 2180	Cys	Arg	Thr	Asn	Gly	Val 2185	Cys	Val	Asp	Trp	Arg 2190	Thr	Pro	Asp
Phe 2195	Cys	Ala	Met	Ser	Cys	Pro 2200	Pro	Ser	Leu	Val	Tyr 2205	Asn	His	Cys

Glu	His	Gly	Cys	Pro	Arg	His	Cys	Asp	Gly	Asn	Val	Ser	Ser	Cys
2210						2215					2220			
Gly	Asp	His	Pro	Ser	Glu	Gly	Cys	Phe	Cys	Pro	Pro	Asp	Lys	Val
2225						2230					2235			
Met	Leu	Glu	Gly	Ser	Cys	Val	Pro	Glu	Glu	Ala	Cys	Thr	Gln	Cys
2240						2245					2250			
Ile	Gly	Glu	Asp	Gly	Val	Gln	His	Gln	Phe	Leu	Glu	Ala	Trp	Val
2255						2260					2265			
Pro	Asp	His	Gln	Pro	Cys	Gln	Ile	Cys	Thr	Cys	Leu	Ser	Gly	Arg
2270						2275					2280			
Lys	Val	Asn	Cys	Thr	Thr	Gln	Pro	Cys	Pro	Thr	Ala	Lys	Ala	Pro
2285						2290					2295			
Thr	Cys	Gly	Leu	Cys	Glu	Val	Ala	Arg	Leu	Arg	Gln	Asn	Ala	Asp
2300						2305					2310			
Gln	Cys	Cys	Pro	Glu	Tyr	Glu	Cys	Val	Cys	Asp	Pro	Val	Ser	Cys
2315						2320					2325			
Asp	Leu	Pro	Pro	Val	Pro	His	Cys	Glu	Arg	Gly	Leu	Gln	Pro	Thr
2330						2335					2340			
Leu	Thr	Asn	Pro	Gly	Glu	Cys	Arg	Pro	Asn	Phe	Thr	Cys	Ala	Cys
2345						2350					2355			
Arg	Lys	Glu	Glu	Cys	Lys	Arg	Val	Ser	Pro	Pro	Ser	Cys	Pro	Pro
2360						2365					2370			
His	Arg	Leu	Pro	Thr	Leu	Arg	Lys	Thr	Gln	Cys	Cys	Asp	Glu	Tyr
2375						2380					2385			
Glu	Cys	Ala	Cys	Asn	Cys	Val	Asn	Ser	Thr	Val	Ser	Cys	Pro	Leu
2390						2395					2400			
Gly	Tyr	Leu	Ala	Ser	Thr	Ala	Thr	Asn	Asp	Cys	Gly	Cys	Thr	Thr
2405						2410					2415			
Thr	Thr	Cys	Leu	Pro	Asp	Lys	Val	Cys	Val	His	Arg	Ser	Thr	Ile
2420						2425					2430			
Tyr	Pro	Val	Gly	Gln	Phe	Trp	Glu	Glu	Gly	Cys	Asp	Val	Cys	Thr
2435						2440					2445			

Cys	Thr	Asp	Met	Glu	Asp	Ala	Val	Met	Gly	Leu	Arg	Val	Ala	Gln
2450						2455					2460			
Cys	Ser	Gln	Lys	Pro	Cys	Glu	Asp	Ser	Cys	Arg	Ser	Gly	Phe	Thr
2465						2470					2475			
Tyr	Val	Leu	His	Glu	Gly	Glu	Cys	Cys	Gly	Arg	Cys	Leu	Pro	Ser
2480						2485					2490			
Ala	Cys	Glu	Val	Val	Thr	Gly	Ser	Pro	Arg	Gly	Asp	Ser	Gln	Ser
2495						2500					2505			
Ser	Trp	Lys	Ser	Val	Gly	Ser	Gln	Trp	Ala	Ser	Pro	Glu	Asn	Pro
2510						2515					2520			
Cys	Leu	Ile	Asn	Glu	Cys	Val	Arg	Val	Lys	Glu	Glu	Val	Phe	Ile
2525						2530					2535			
Gln	Gln	Arg	Asn	Val	Ser	Cys	Pro	Gln	Leu	Glu	Val	Pro	Val	Cys
2540						2545					2550			
Pro	Ser	Gly	Phe	Gln	Leu	Ser	Cys	Lys	Thr	Ser	Ala	Cys	Cys	Pro
2555						2560					2565			
Ser	Cys	Arg	Cys	Glu	Arg	Met	Glu	Ala	Cys	Met	Leu	Asn	Gly	Thr
2570						2575					2580			
Val	Ile	Gly	Pro	Gly	Lys	Thr	Val	Met	Ile	Asp	Val	Cys	Thr	Thr
2585						2590					2595			
Cys	Arg	Cys	Met	Val	Gln	Val	Gly	Val	Ile	Ser	Gly	Phe	Lys	Leu
2600						2605					2610			
Glu	Cys	Arg	Lys	Thr	Thr	Cys	Asn	Pro	Cys	Pro	Leu	Gly	Tyr	Lys
2615						2620					2625			
Glu	Glu	Asn	Asn	Thr	Gly	Glu	Cys	Cys	Gly	Arg	Cys	Leu	Pro	Thr
2630						2635					2640			
Ala	Cys	Thr	Ile	Gln	Leu	Arg	Gly	Gly	Gln	Ile	Met	Thr	Leu	Lys
2645						2650					2655			
Arg	Asp	Glu	Thr	Leu	Gln	Asp	Gly	Cys	Asp	Thr	His	Phe	Cys	Lys
2660						2665					2670			
Val	Asn	Glu	Arg	Gly	Glu	Tyr	Phe	Trp	Glu	Lys	Arg	Val	Thr	Gly
2675						2680					2685			

Cys Pro Pro Phe Asp Glu His Lys Cys Leu Ala Glu Gly Gly Lys
2690 2695 2700

Ile Met Lys Ile Pro Gly Thr Cys Cys Asp Thr Cys Glu Glu Pro
2705 2710 2715

Glu Cys Asn Asp Ile Thr Ala Arg Leu Gln Tyr Val Lys Val Gly
2720 2725 2730

Ser Cys Lys Ser Glu Val Glu Val Asp Ile His Tyr Cys Gln Gly
2735 2740 2745

Lys Cys Ala Ser Lys Ala Met Tyr Ser Ile Asp Ile Asn Asp Val
2750 2755 2760

Gln Asp Gln Cys Ser Cys Cys Ser Pro Thr Arg Thr Glu Pro Met
2765 2770 2775

Gln Val Ala Leu His Cys Thr Asn Gly Ser Val Val Tyr His Glu
2780 2785 2790

Val Leu Asn Ala Met Glu Cys Lys Cys Ser Pro Arg Lys Cys Ser
2795 2800 2805

Lys

<210> 130
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> AE36
<400> 130

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
20 25 30

Ser Glu Thr Pro
35

<210> 131
<211> 42
<212> PRT
<213> Artificial Sequence

<220>

<223> AE42

<400> 131

Gly Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Ala Ser Ser
35 40

<210> 132

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> AE72

<400> 132

Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1 5 10 15

Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
20 25 30

Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu
35 40 45

Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr
50 55 60

Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala Ser Ser
65 70 75

<210> 133

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> AE78

<400> 133

Gly Ala Pro Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser
1 5 10 15

Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala
20 25 30

Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu
35 40 45

Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr
50 55 60

Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ala Ser Ser
65 70 75

<210> 134

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144

<400> 134

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
20 25 30

Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
50 55 60

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly
65 70 75 80

Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
85 90 95

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
100 105 110

Ser Ala Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
115 120 125

Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
130 135 140

<210> 135

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AE144_6B

<400> 135

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
50 55 60

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
65 70 75 80

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
85 90 95

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro Ala
100 105 110

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 136

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144

<400> 136

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
1 5 10 15

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr
20 25 30

Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
35 40 45

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro

50

55

60

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
65 70 75 80

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
85 90 95

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
100 105 110

Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala
115 120 125

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
130 135 140

<210> 137

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> AG144_A

<400> 137

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1 5 10 15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
20 25 30

Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65 70 75 80

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
85 90 95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
100 105 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

<210> 138
<211> 288
<212> PRT
<213> Artificial Sequence

<220>
<223> AE288

<400> 138

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
1 5 10 15

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
20 25 30

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
35 40 45

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
50 55 60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
65 70 75 80

Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
85 90 95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu
100 105 110

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr
115 120 125

Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
130 135 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu
145 150 155 160

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro
165 170 175

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
180 185 190

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro

195

200

205

Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr
 210 215 220

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 225 230 235 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
 245 250 255

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
 260 265 270

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 275 280 285

<210> 139

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> AE288_2

<400> 139

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
 1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
 20 25 30

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 50 55 60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
 65 70 75 80

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 85 90 95

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 100 105 110

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
 115 120 125

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
130 135 140

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
145 150 155 160

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
165 170 175

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
180 185 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
195 200 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
210 215 220

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
225 230 235 240

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
245 250 255

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
260 265 270

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
275 280 285

<210> 140

<211> 288

<212> PRT

<213> Artificial Sequence

<220>

<223> AG288

<400> 140

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
1 5 10 15

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
20 25 30

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
35 40 45

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser

50

55

60

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr
65 70 75 80

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
85 90 95

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
100 105 110

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser
115 120 125

Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
130 135 140

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
145 150 155 160

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser
165 170 175

Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
180 185 190

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
195 200 205

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly
210 215 220

Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
225 230 235 240

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser
245 250 255

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
260 265 270

Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
275 280 285

<210> 141

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> AE576

<400> 141

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
1 5 10 15

Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu
20 25 30

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
50 55 60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
65 70 75 80

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
85 90 95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala
100 105 110

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
115 120 125

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
130 135 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala
145 150 155 160

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
165 170 175

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
180 185 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
195 200 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
210 215 220

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
225 230 235 240

Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Thr	245	250	255	
Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	260	265	270	
Glu	Ser	Gly	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	275	280	285	
Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu	290	295	300	
Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	305	310	315	320
Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	325	330	335	
Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Thr	340	345	350	
Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	355	360	365	
Gly	Ser	Ala	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	370	375	380	
Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Thr	385	390	395	400
Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	405	410	415	
Ser	Thr	Glu	Glu	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	420	425	430	
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	435	440	445	
Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	450	455	460	
Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	465	470	475	480
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	485	490	495	

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
500 505 510

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
515 520 525

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
530 535 540

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
545 550 555 560

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
565 570 575

<210> 142

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> AG576

<400> 142

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser
1 5 10 15

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser
20 25 30

Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly
35 40 45

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
50 55 60

Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
65 70 75 80

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
85 90 95

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
100 105 110

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser
115 120 125

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser

130

135

140

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser
 145 150 155 160

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr
 165 170 175

Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
 180 185 190

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser
 195 200 205

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly
 210 215 220

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
 225 230 235 240

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro
 245 250 255

Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly
 260 265 270

Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser
 275 280 285

Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser
 290 295 300

Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser
 305 310 315 320

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
 325 330 335

Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser
 340 345 350

Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser
 355 360 365

Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser
 370 375 380

Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro

385		390		395		400									
Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro	Gly	Ser	Ser	Thr	Pro	Ser	Gly
				405					410					415	
Ala	Thr	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser
			420					425					430		
Pro	Gly	Ser	Ser	Thr	Pro	Ser	Gly	Ala	Thr	Gly	Ser	Pro	Gly	Thr	Pro
		435					440					445			
Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser	Pro	Gly	Ser	Ser	Thr	Pro	Ser	Gly
	450					455					460				
Ala	Thr	Gly	Ser	Pro	Gly	Ser	Ser	Thr	Pro	Ser	Gly	Ala	Thr	Gly	Ser
465					470					475					480
Pro	Gly	Ser	Ser	Pro	Ser	Ala	Ser	Thr	Gly	Thr	Gly	Pro	Gly	Ser	Ser
				485					490					495	
Pro	Ser	Ala	Ser	Thr	Gly	Thr	Gly	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser
			500					505					510		
Ser	Thr	Gly	Ser	Pro	Gly	Thr	Pro	Gly	Ser	Gly	Thr	Ala	Ser	Ser	Ser
		515					520					525			
Pro	Gly	Ser	Ser	Thr	Pro	Ser	Gly	Ala	Thr	Gly	Ser	Pro	Gly	Ser	Ser
	530					535					540				
Pro	Ser	Ala	Ser	Thr	Gly	Thr	Gly	Pro	Gly	Ser	Ser	Pro	Ser	Ala	Ser
545					550					555					560
Thr	Gly	Thr	Gly	Pro	Gly	Ala	Ser	Pro	Gly	Thr	Ser	Ser	Thr	Gly	Ser
				565					570					575	

<210> 143
 <211> 864
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AE864

<400> 143

Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu
1				5					10					15	
Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu
			20					25					30		

Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
 35 40 45

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 50 55 60

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
 65 70 75 80

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 85 90 95

Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala
 100 105 110

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro
 115 120 125

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 130 135 140

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala
 145 150 155 160

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
 165 170 175

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 180 185 190

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
 195 200 205

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
 210 215 220

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 225 230 235 240

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 245 250 255

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
 260 265 270

Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 275 280 285

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
 290 295 300

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
 305 310 315 320

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 325 330 335

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 340 345 350

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
 355 360 365

Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 370 375 380

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr
 385 390 395 400

Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr
 405 410 415

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 420 425 430

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
 435 440 445

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
 450 455 460

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 465 470 475 480

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
 485 490 495

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro
 500 505 510

Glu Ser Gly Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu
 515 520 525

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
 530 535 540

Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	545	550	555	560
Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	565	570	575	
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	580	585	590	
Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	595	600	605	
Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	610	615	620	
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	625	630	635	640
Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	645	650	655	
Ser	Thr	Glu	Glu	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	660	665	670	
Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	675	680	685	
Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	690	695	700	
Ser	Thr	Glu	Glu	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu	705	710	715	720
Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Thr	Ser	Glu	725	730	735	
Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	740	745	750	
Glu	Ser	Gly	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	755	760	765	
Gly	Ser	Glu	Pro	Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Ser	Glu	Pro	770	775	780	
Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Ser	Pro	Ala	Gly	Ser	Pro	Thr	785	790	795	800

Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
805 810 815

Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Glu Pro
820 825 830

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
835 840 845

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
850 855 860

<210> 144

<211> 864

<212> PRT

<213> Artificial Sequence

<220>

<223> AG864

<400> 144

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Pro
1 5 10 15

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
20 25 30

Gly Thr Gly Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
35 40 45

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
50 55 60

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
65 70 75 80

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
85 90 95

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
100 105 110

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
115 120 125

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
130 135 140

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr

145		150		155		160
Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser						
		165		170		175
Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro						
		180		185		190
Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro						
		195		200		205
Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr						
		210		215		220
Gly Thr Gly Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro						
		225		230		235
Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ala Ser Pro						
		245		250		255
Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser						
		260		265		270
Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro						
		275		280		285
Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro						
		290		295		300
Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser						
		305		310		315
Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro						
		325		330		335
Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly						
		340		345		350
Ser Gly Thr Ala Ser Ser Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser						
		355		360		365
Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro						
		370		375		380
Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr						
		385		390		395
Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala						

405

410

415

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 420 425 430

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 435 440 445

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
 450 455 460

Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
 465 470 475 480

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro
 485 490 495

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
 500 505 510

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
 515 520 525

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro
 530 535 540

Gly Thr Ser Ser Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser
 545 550 555 560

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 565 570 575

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 580 585 590

Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala
 595 600 605

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
 610 615 620

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 625 630 635 640

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
 645 650 655

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro

660

665

670

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro
 675 680 685

Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala
 690 695 700

Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
 705 710 715 720

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
 725 730 735

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
 740 745 750

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 755 760 765

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
 770 775 780

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
 785 790 795 800

Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro
 805 810 815

Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr
 820 825 830

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
 835 840 845

Thr Gly Ser Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
 850 855 860

<210> 145

<211> 72

<212> PRT

<213> Artificial Sequence

<220>

<223> XTEN_AE72_2A_1

<400> 145

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
 1 5 10 15

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 146
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_2A_2

<400> 146

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser
50 55 60

Ala Thr Pro Glu Ser Gly Pro Gly
65 70

<210> 147
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_3B_1

<400> 147

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 148
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_3B_2

<400> 148

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
1 5 10 15

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
35 40 45

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 149
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_4A_2

<400> 149

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly
1 5 10 15

Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser
20 25 30

Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 150
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_5A_2

<400> 150

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly
50 55 60

Ser Pro Thr Ser Thr Glu Glu Gly
65 70

<210> 151
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_6B_1

<400> 151

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
20 25 30

Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
35 40 45

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
50 55 60

Thr Ser Gly Ser Glu Thr Pro Gly
65 70

<210> 152
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_6B_2

<400> 152

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu
1 5 10 15

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 153
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_1A_1

<400> 153

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 154
<211> 72
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE72_1A_2

<400> 154

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
1 5 10 15

Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
20 25 30

Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly
65 70

<210> 155
<211> 144
<212> PRT
<213> Artificial Sequence

<220>
<223> XTEN_AE144_1A

<400> 155

Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser
1 5 10 15

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
20 25 30

Ser Ala Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly
35 40 45

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu
50 55 60

Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
65 70 75 80

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
85 90 95

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly
100 105 110

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
115 120 125

Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
130 135 140

<210> 156

<211> 150

<212> PRT

<213> Artificial Sequence

<220>

<223> AE150

<400> 156

Gly Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
1 5 10 15

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
20 25 30

Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly Ser Pro Thr Ser
35 40 45

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
50 55 60

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala
65 70 75 80

Thr Ser Gly Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
85 90 95

Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
100 105 110

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala
115 120 125

Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly
130 135 140

Ser Ala Pro Ala Ser Ser
145 150

<210> 157

<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> G150

<400> 157

Gly Ala Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro Gly
1 5 10 15

Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser
20 25 30

Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly
35 40 45

Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly
50 55 60

Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr Pro
65 70 75 80

Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr Gly
85 90 95

Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly
100 105 110

Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly Ser
115 120 125

Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr
130 135 140

Gly Ser Pro Ala Ser Ser
145 150

<210> 158
<211> 294
<212> PRT
<213> Artificial Sequence

<220>
<223> AE294

<400> 158

Gly Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
1 5 10 15

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser

20

25

30

Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser
 35 40 45

Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly
 50 55 60

Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly Ser Pro Ala Gly
 65 70 75 80

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu Ser Ala Thr Pro Glu
 85 90 95

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
 100 105 110

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Pro Ala Gly
 115 120 125

Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala Gly Ser Pro Thr Ser
 130 135 140

Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
 145 150 155 160

Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser
 165 170 175

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu
 180 185 190

Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly
 195 200 205

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Ser Pro Ala Gly
 210 215 220

Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu Gly
 225 230 235 240

Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro Gly
 245 250 255

Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser
 260 265 270

Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly

275

280

285

Ser Ala Pro Ala Ser Ser
290

<210> 159

<211> 294

<212> PRT

<213> Artificial Sequence

<220>

<223> AG294

<400> 159

Gly Ala Pro Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
1 5 10 15

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Thr Pro Gly
20 25 30

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
35 40 45

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
50 55 60

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Thr Pro Gly
65 70 75 80

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
85 90 95

Thr Gly Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro
100 105 110

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro
115 120 125

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser
130 135 140

Thr Gly Ser Pro Gly Thr Pro Gly Ser Gly Thr Ala Ser Ser Ser Pro
145 150 155 160

Gly Ser Ser Thr Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro
165 170 175

Ser Ala Ser Thr Gly Thr Gly Pro Gly Ser Ser Pro Ser Ala Ser Thr
180 185 190

Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
195 200 205

Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro Gly Ser Ser Thr
210 215 220

Pro Ser Gly Ala Thr Gly Ser Pro Gly Ser Ser Pro Ser Ala Ser Thr
225 230 235 240

Gly Thr Gly Pro Gly Ala Ser Pro Gly Thr Ser Ser Thr Gly Ser Pro
245 250 255

Gly Ser Ser Pro Ser Ala Ser Thr Gly Thr Gly Pro Gly Thr Pro Gly
260 265 270

Ser Gly Thr Ala Ser Ser Ser Pro Gly Ser Ser Thr Pro Ser Gly Ala
275 280 285

Thr Gly Ser Ala Ser Ser
290

<210> 160
<211> 1016
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX-Linker-Albumin

<400> 160

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly
35 40 45

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr

100					105					110					
Glu	Gly	Tyr	Arg	Leu	Ala	Glu	Asn	Gln	Lys	Ser	Cys	Glu	Pro	Ala	Val
		115					120					125			
Pro	Phe	Pro	Cys	Gly	Arg	Val	Ser	Val	Ser	Gln	Thr	Ser	Lys	Leu	Thr
	130					135					140				
Arg	Ala	Glu	Thr	Val	Phe	Pro	Asp	Val	Asp	Tyr	Val	Asn	Ser	Thr	Glu
145					150					155					160
Ala	Glu	Thr	Ile	Leu	Asp	Asn	Ile	Thr	Gln	Ser	Thr	Gln	Ser	Phe	Asn
				165					170					175	
Asp	Phe	Thr	Arg	Val	Val	Gly	Gly	Glu	Asp	Ala	Lys	Pro	Gly	Gln	Phe
			180					185					190		
Pro	Trp	Gln	Val	Val	Leu	Asn	Gly	Lys	Val	Asp	Ala	Phe	Cys	Gly	Gly
		195					200					205			
Ser	Ile	Val	Asn	Glu	Lys	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu
	210					215					220				
Thr	Gly	Val	Lys	Ile	Thr	Val	Val	Ala	Gly	Glu	His	Asn	Ile	Glu	Glu
225					230					235					240
Thr	Glu	His	Thr	Glu	Gln	Lys	Arg	Asn	Val	Ile	Arg	Ile	Ile	Pro	His
				245					250					255	
His	Asn	Tyr	Asn	Ala	Ala	Ile	Asn	Lys	Tyr	Asn	His	Asp	Ile	Ala	Leu
			260					265					270		
Leu	Glu	Leu	Asp	Glu	Pro	Leu	Val	Leu	Asn	Ser	Tyr	Val	Thr	Pro	Ile
		275					280					285			
Cys	Ile	Ala	Asp	Lys	Glu	Tyr	Thr	Asn	Ile	Phe	Leu	Lys	Phe	Gly	Ser
	290					295					300				
Gly	Tyr	Val	Ser	Gly	Trp	Gly	Arg	Val	Phe	His	Lys	Gly	Arg	Ser	Ala
305					310					315					320
Leu	Val	Leu	Gln	Tyr	Leu	Arg	Val	Pro	Leu	Val	Asp	Arg	Ala	Thr	Cys
				325					330					335	
Leu	Arg	Ser	Thr	Lys	Phe	Thr	Ile	Tyr	Asn	Asn	Met	Phe	Cys	Ala	Gly
			340					345					350		
Phe	His	Glu	Gly	Gly	Arg	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro

355

360

365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
 370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
 385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Pro
 405 410 415

Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Thr Val Phe Pro Asp
 420 425 430

Val Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly
 435 440 445

Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu
 450 455 460

Gln Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr
 465 470 475 480

Glu Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp
 485 490 495

Lys Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr
 500 505 510

Leu Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu
 515 520 525

Pro Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn
 530 535 540

Leu Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe
 545 550 555 560

His Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala
 565 570 575

Arg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys
 580 585 590

Arg Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala
 595 600 605

Ala Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala

610

615

620

Ser Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly
 625 630 635 640

Glu Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe
 645 650 655

Pro Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr
 660 665 670

Lys Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp
 675 680 685

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile
 690 695 700

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser
 705 710 715 720

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro
 725 730 735

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr
 740 745 750

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala
 755 760 765

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys
 770 775 780

Thr Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Phe Cys
 785 790 795 800

Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro Gln
 805 810 815

Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu Tyr
 820 825 830

Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro Gln
 835 840 845

Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys Val
 850 855 860

Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys Ala

865		870		875		880
Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His Glu						
	885			890		895
Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser Leu						
	900			905		910
Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr						
	915			920		925
Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp Ile						
	930			935		940
Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu						
	945			950		955
						960
Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys						
	965			970		975
Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys Ala						
	980			985		990
Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val Ala						
	995			1000		1005
Ala Ser Gln Ala Ala Leu Gly Leu						
	1010			1015		
<210>	161					
<211>	424					
<212>	PRT					
<213>	Artificial Sequence					
<220>						
<223>	FIX					
<400>	161					
Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg						
1	5			10		15
Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe						
	20			25		30
Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly						
	35			40		45
Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp						
	50			55		60

Asp	Ile	Asn	Ser	Tyr	Glu	Cys	Trp	Cys	Pro	Phe	Gly	Phe	Glu	Gly	Lys	65	70	75	80
Asn	Cys	Glu	Leu	Asp	Val	Thr	Cys	Asn	Ile	Lys	Asn	Gly	Arg	Cys	Glu	85	90	95	
Gln	Phe	Cys	Lys	Asn	Ser	Ala	Asp	Asn	Lys	Val	Val	Cys	Ser	Cys	Thr	100	105	110	
Glu	Gly	Tyr	Arg	Leu	Ala	Glu	Asn	Gln	Lys	Ser	Cys	Glu	Pro	Ala	Val	115	120	125	
Pro	Phe	Pro	Cys	Gly	Arg	Val	Ser	Val	Ser	Gln	Thr	Ser	Lys	Leu	Thr	130	135	140	
Arg	Ala	Glu	Thr	Val	Phe	Pro	Asp	Val	Asp	Tyr	Val	Asn	Ser	Thr	Glu	145	150	155	160
Ala	Glu	Thr	Ile	Leu	Asp	Asn	Ile	Thr	Gln	Ser	Thr	Gln	Ser	Phe	Asn	165	170	175	
Asp	Phe	Thr	Arg	Val	Val	Gly	Gly	Glu	Asp	Ala	Lys	Pro	Gly	Gln	Phe	180	185	190	
Pro	Trp	Gln	Val	Val	Leu	Asn	Gly	Lys	Val	Asp	Ala	Phe	Cys	Gly	Gly	195	200	205	
Ser	Ile	Val	Asn	Glu	Lys	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	210	215	220	
Thr	Gly	Val	Lys	Ile	Thr	Val	Val	Ala	Gly	Glu	His	Asn	Ile	Glu	Glu	225	230	235	240
Thr	Glu	His	Thr	Glu	Gln	Lys	Arg	Asn	Val	Ile	Arg	Ile	Ile	Pro	His	245	250	255	
His	Asn	Tyr	Asn	Ala	Ala	Ile	Asn	Lys	Tyr	Asn	His	Asp	Ile	Ala	Leu	260	265	270	
Leu	Glu	Leu	Asp	Glu	Pro	Leu	Val	Leu	Asn	Ser	Tyr	Val	Thr	Pro	Ile	275	280	285	
Cys	Ile	Ala	Asp	Lys	Glu	Tyr	Thr	Asn	Ile	Phe	Leu	Lys	Phe	Gly	Ser	290	295	300	
Gly	Tyr	Val	Ser	Gly	Trp	Gly	Arg	Val	Phe	His	Lys	Gly	Arg	Ser	Ala	305	310	315	320

Leu Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys
 325 330 335

Leu Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly
 340 345 350

Phe His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 355 360 365

His Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser
 370 375 380

Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys
 385 390 395 400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Pro
 405 410 415

Val Ser Gln Thr Ser Lys Leu Thr
 420

<210> 162
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 162

Arg Ala Glu Thr Val Phe Pro Asp Val
 1 5

<210> 163
 <211> 585
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Albumin

<400> 163

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
 1 5 10 15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
 20 25 30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
 35 40 45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50 55 60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65 70 75 80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
85 90 95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
100 105 110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
115 120 125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130 135 140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 164
<211> 763
<212> PRT
<213> Artificial Sequence

<220>
<223> FIX(XTEN)-Fc

<400> 164

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145 150 155 160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
165 170 175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala

180							185							190						
Glu	Thr	Val	Phe	Pro	Asp	Val	Asp	Tyr	Val	Asn	Ser	Thr	Glu	Ala	Glu					
		195					200					205								
Thr	Ile	Leu	Asp	Gly	Pro	Ser	Pro	Gly	Ser	Pro	Thr	Ser	Thr	Glu	Glu					
	210					215					220									
Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro	Glu	Ser	Gly	Pro	Gly	Ser	Glu	Pro					
225					230					235					240					
Ala	Thr	Ser	Gly	Ser	Glu	Thr	Pro	Gly	Thr	Ser	Glu	Ser	Ala	Thr	Pro					
				245					250					255						
Glu	Ser	Gly	Pro	Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro					
			260					265					270							
Gly	Thr	Ser	Thr	Glu	Pro	Ser	Glu	Gly	Ser	Ala	Pro	Gly	Ala	Ser	Ser					
		275					280					285								
Asn	Ile	Thr	Gln	Ser	Thr	Gln	Ser	Phe	Asn	Asp	Phe	Thr	Arg	Val	Val					
	290					295					300									
Gly	Gly	Glu	Asp	Ala	Lys	Pro	Gly	Gln	Phe	Pro	Trp	Gln	Val	Val	Leu					
305					310					315					320					
Asn	Gly	Lys	Val	Asp	Ala	Phe	Cys	Gly	Gly	Ser	Ile	Val	Asn	Glu	Lys					
				325					330					335						
Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Thr	Gly	Val	Lys	Ile	Thr					
			340					345					350							
Val	Val	Ala	Gly	Glu	His	Asn	Ile	Glu	Glu	Thr	Glu	His	Thr	Glu	Gln					
		355					360					365								
Lys	Arg	Asn	Val	Ile	Arg	Ile	Ile	Pro	His	His	Asn	Tyr	Asn	Ala	Ala					
	370					375					380									
Ile	Asn	Lys	Tyr	Asn	His	Asp	Ile	Ala	Leu	Leu	Glu	Leu	Asp	Glu	Pro					
385					390					395					400					
Leu	Val	Leu	Asn	Ser	Tyr	Val	Thr	Pro	Ile	Cys	Ile	Ala	Asp	Lys	Glu					
				405					410					415						
Tyr	Thr	Asn	Ile	Phe	Leu	Lys	Phe	Gly	Ser	Gly	Tyr	Val	Ser	Gly	Trp					
		420						425					430							
Gly	Arg	Val	Phe	His	Lys	Gly	Arg	Ser	Ala	Leu	Val	Leu	Gln	Tyr	Leu					

435

440

445

Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Leu Ser Thr Lys Phe
 450 455 460

Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg
 465 470 475 480

Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu
 485 490 495

Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala
 500 505 510

Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser Arg Tyr Val Asn
 515 520 525

Trp Ile Lys Glu Lys Thr Lys Leu Thr Asp Lys Thr His Thr Cys Pro
 530 535 540

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 545 550 555 560

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 565 570 575

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 580 585 590

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 595 600 605

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 610 615 620

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 625 630 635 640

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 645 650 655

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 660 665 670

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 675 680 685

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro

690

695

700

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
705 710 715 720

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
725 730 735

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
740 745 750

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
755 760

<210> 165

<211> 712

<212> PRT

<213> Artificial Sequence

<220>

<223> FIX-FXIa-AE288

<400> 165

Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg
1 5 10 15

Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe
20 25 30

Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly
35 40 45

Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp
50 55 60

Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys
65 70 75 80

Asn Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu
85 90 95

Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr
100 105 110

Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val
115 120 125

Pro Phe Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr
130 135 140

Arg	Ala	Glu	Thr	Val	Phe	Pro	Asp	Val	Asp	Tyr	Val	Asn	Ser	Thr	Glu	145	150	155	160
Ala	Glu	Thr	Ile	Leu	Asp	Asn	Ile	Thr	Gln	Ser	Thr	Gln	Ser	Phe	Asn	165	170	175	
Asp	Phe	Thr	Arg	Val	Val	Gly	Gly	Glu	Asp	Ala	Lys	Pro	Gly	Gln	Phe	180	185	190	
Pro	Trp	Gln	Val	Val	Leu	Asn	Gly	Lys	Val	Asp	Ala	Phe	Cys	Gly	Gly	195	200	205	
Ser	Ile	Val	Asn	Glu	Lys	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	210	215	220	
Thr	Gly	Val	Lys	Ile	Thr	Val	Val	Ala	Gly	Glu	His	Asn	Ile	Glu	Glu	225	230	235	240
Thr	Glu	His	Thr	Glu	Gln	Lys	Arg	Asn	Val	Ile	Arg	Ile	Ile	Pro	His	245	250	255	
His	Asn	Tyr	Asn	Ala	Ala	Ile	Asn	Lys	Tyr	Asn	His	Asp	Ile	Ala	Leu	260	265	270	
Leu	Glu	Leu	Asp	Glu	Pro	Leu	Val	Leu	Asn	Ser	Tyr	Val	Thr	Pro	Ile	275	280	285	
Cys	Ile	Ala	Asp	Lys	Glu	Tyr	Thr	Asn	Ile	Phe	Leu	Lys	Phe	Gly	Ser	290	295	300	
Gly	Tyr	Val	Ser	Gly	Trp	Gly	Arg	Val	Phe	His	Lys	Gly	Arg	Ser	Ala	305	310	315	320
Leu	Val	Leu	Gln	Tyr	Leu	Arg	Val	Pro	Leu	Val	Asp	Arg	Ala	Thr	Cys	325	330	335	
Leu	Arg	Ser	Thr	Lys	Phe	Thr	Ile	Tyr	Asn	Asn	Met	Phe	Cys	Ala	Gly	340	345	350	
Phe	His	Glu	Gly	Gly	Arg	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	355	360	365	
His	Val	Thr	Glu	Val	Glu	Gly	Thr	Ser	Phe	Leu	Thr	Gly	Ile	Ile	Ser	370	375	380	
Trp	Gly	Glu	Glu	Cys	Ala	Met	Lys	Gly	Lys	Tyr	Gly	Ile	Tyr	Thr	Lys	385	390	395	400

Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Gly
 405 410 415

Lys Leu Thr Arg Ala Glu Thr Gly Gly Thr Ser Glu Ser Ala Thr Pro
 420 425 430

Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 435 440 445

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro
 450 455 460

Ala Thr Ser Gly Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro
 465 470 475 480

Glu Ser Gly Pro Gly Thr Ser Thr Glu Pro Ser Glu Gly Ser Ala Pro
 485 490 495

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Glu
 500 505 510

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
 515 520 525

Ser Glu Thr Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 530 535 540

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Ser Pro Ala
 545 550 555 560

Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr Glu Pro Ser Glu
 565 570 575

Gly Ser Ala Pro Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro
 580 585 590

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Glu
 595 600 605

Ser Ala Thr Pro Glu Ser Gly Pro Gly Ser Glu Pro Ala Thr Ser Gly
 610 615 620

Ser Glu Thr Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
 625 630 635 640

Gly Ser Pro Ala Gly Ser Pro Thr Ser Thr Glu Glu Gly Thr Ser Thr
 645 650 655

Glu Pro Ser Glu Gly Ser Ala Pro Gly Thr Ser Thr Glu Pro Ser Glu
660 665 670

Gly Ser Ala Pro Gly Ser Glu Pro Ala Thr Ser Gly Ser Glu Thr Pro
675 680 685

Gly Thr Ser Glu Ser Ala Thr Pro Glu Ser Gly Pro Gly Thr Ser Thr
690 695 700

Glu Pro Ser Glu Gly Ser Ala Pro
705 710

<210> 166

<211> 944

<212> PRT

<213> Artificial Sequence

<220>

<223> FIX-Fc-Fc

<400> 166

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr
1 5 10 15

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20 25 30

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
35 40 45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
50 55 60

Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65 70 75 80

Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
85 90 95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
100 105 110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
115 120 125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
130 135 140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly

145		150		155		160
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe	165			170		175
Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala	180		185			190
Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu	195		200		205	
Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe	210		215		220	
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp	225		230		235	240
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile	245		250			255
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly	260		265			270
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu	275		280		285	
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn	290		295		300	
Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu	305		310		315	320
Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile	325			330		335
Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr	340		345		350	
Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val	355		360		365	
Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg	370		375		380	
Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His	385		390		395	400
Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val						

405

410

415

Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
 420 425 430

Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
 435 440 445

Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr Asp Lys Thr
 450 455 460

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 465 470 475 480

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 485 490 495

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 500 505 510

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 515 520 525

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 530 535 540

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 545 550 555 560

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 565 570 575

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 580 585 590

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 595 600 605

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 610 615 620

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 625 630 635 640

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 645 650 655

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

660

665

670

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 675 680 685

Arg Arg Arg Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 690 695 700

Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg Arg Arg Arg Asp Lys Thr
 705 710 715 720

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 725 730 735

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 740 745 750

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 755 760 765

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 770 775 780

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val
 785 790 795 800

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
 805 810 815

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
 820 825 830

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
 835 840 845

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 850 855 860

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
 865 870 875 880

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 885 890 895

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 900 905 910

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 930 935 940

<210> 167
 <211> 383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus B19 KY940273.1

<400> 167
 ccaaattcaga tgccgcccgtt cgccgcccgtt aggcgggact tccggtacaa gatggcggac 60
 aattacgtca tttcctgtga cgtcatttcc tgtgacgtca cttccggtgg gcgggacttc 120
 cggaattagg gttggctctg ggccagcttg cttggggttg ccttgacact aagacaagcg 180
 gcgcgcccgtt tgatcttagt ggcacgtcaa cccaagcgc tggcccagag ccaaccctaa 240
 ttccggaagt cccgcccacc ggaagtgcg tcacaggaaa tgacgtcaca ggaaatgacg 300
 taattgtccg ccatcttgta ccggaagtcc cgcctaccgg cggcgaccgg cggcatctga 360
 tttggtgtct tcttttaaat ttt 383

<210> 168
 <211> 248
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus B19 d135

<400> 168
 ctctggggcca gcttgcttgg ggttgccctt acactaagac aagcggcgcg ccgcttgatc 60
 ttagtggcac gtcaacccca agcgttggcc cagagccaac cctaattccg gaagtcccg 120
 ccaccggaag tgacgtcaca ggaaatgacg tcacaggaaa tgacgtaatt gtccgccatc 180
 ttgtaccgga agtccgcct accggcggcg accggcggca tctgatttgg tgtcttcttt 240
 taaatttt 248

<210> 169
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus v1 AAV2

<400> 169
 cggcgcgccg cttgatctta gtggcacgtc aaccagcgtt ggcccagagc caaccctaatt 60
 tccggaagtc ctacgtccgc catcttgccc gcctaccggc ggcgaccggc ggcacatctt 120

<210> 170
 <211> 113
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus V2

<400> 170
 ctctgggcca gcttgcttgg ggttgccttg acactaagac aagcggcgcg ccgcttgatc 60
 ttagtggcac gtcaacccca agcgctggcc cagagtgtct tcttttaaatt ttt 113

<210> 171
 <211> 340
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus V3

<400> 171
 caaatcagat gccgccggtc gccgccggta ggcgggactt ccggtacaag atggcggaca 60
 attacgtcat ttctgtgac gtatttcctg tgacgtactt ccggtggcgg gacttccgga 120
 attttggtc tgggccagct tgcttggggt tgccttgacc aagcgcgcgc cgcttgatca 180
 cccaagcgc tggccagag ccacctaacc ggaagtcccc ccaccggaag tgacgtcaca 240
 ggaaagacgt cacaggaagt aattgtccgc catcttgtag cggaagtccc gcaccggcgg 300
 cgaccggcgg catctgattt ggtgtcttct tttaaatttt 340

<210> 172
 <211> 444
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Parvovirus U25749.1

<400> 172
 ctcataggag ggttcgttcg ttcgaaccag ccaatcaggg gagggggaag tgacgcaagt 60
 tccggtcaca tgcttccggt gacgcacatc cggtgacgta gttccggtca cgtgcttcct 120
 gtcacgtgtt tccggtcacg tgacttccgg tcatgtgact tccggtgacg tgtttccggc 180
 tgtaggttg accacgcgca tgccgcgcgg tcagcccaat agttaagccg gaaacacgtc 240
 accggaagtc acatgaccgg aagtcacgtg accggaacac cgtgacagga agcacgtgac 300
 cggaactacg tcaccgatg tgcgtcaccg gaagcatgtg accggaactt gcgtcacttc 360
 cccctcccct gattggctgg ttcgaacgaa cgaaccctcc aatgagactc aaggacaaga 420
 ggatatatttg cgcgccagga agtg 444

<210> 173
<211> 282
<212> DNA
<213> Artificial Sequence

<220>
<223> Parvovirus GPV AAV2 V1

<400> 173
cggtgacgtg tttccggctg ttaggttgac cacgcgcatg ccgcgcggtc agcccaatag 60
ttaagccgga aacacgtcac cggaagtcac atgaccggaa gtcacgtgac cggaaacacg 120
tgacaggaag cacgtgaccg gaactacgtc accggatgtg cgtcaccgga agcatgtgac 180
cggaacttgc gtcacttccc cctcccctga ttggctgggt cgaacgaacg aaccctccaa 240
tgagactcaa ggacaagagg atattttgcg cgccaggaag tg 282

<210> 174
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Parvovirus GPV AAV2 V1

<400> 174
ttgaccacgc gcatgccgcg cggtcagccc aatagttaag ccgggtgacc acacgtgaca 60
ggaagcacgg gatgtgcgtc accggaagca gtgaccgggc tggttcgaac gaacgaaccc 120
tccaactcaa ggacaagagg atatt 145

<210> 175
<211> 120
<212> DNA
<213> Artificial Sequence

<220>
<223> Parvovirus GPV V2

<400> 175
cggtgacgtg tttccggctg ttaggttgac cacgcgcatg ccgcgcggtc agcccaatag 60
ttaagccgga aacacgtcac cgactcaagg acaagaggat attttgcgcg ccaggaagtg 120

<210> 176
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> Parvovirus GPV V3

<400> 176
gggaacaatc aggggaagtg accggtgacg tcatgtaact tgcgtcactt cccgttcgaa 60
cgaacgaacg agactcaagg acaagaggcg cgccaggaag tg 102

<210> 177
<211> 145
<212> DNA
<213> Artificial Sequence

<220>
<223> Parvovirus AAV2 NC_001401.2

<400> 177
ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60
cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg 120
gccaactcca tcactagggg ttcct 145

<210> 178
<211> 130
<212> DNA
<213> Artificial Sequence

<220>
<223> Parvovirus Gtx

<400> 178
ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgctc ggcgaccttt 60
ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagtggccaa ctccatcact 120
agggggttcct 130

<210> 179
<211> 6762
<212> DNA
<213> Artificial Sequence

<220>
<223> B19-FVIII construct

<400> 179
ctctgggcca gcttgcttgg ggttgccttg aactaagac aagcggcgcg ccgcttgatc 60
ttagtggcac gtcaaccca agcgtggcc cagagccaac cctaattccg gaagtcccgc 120
ccaccggaag tgacgtcaca ggaaatgacg tcacaggaaa tgacgtaatt gtccgccatc 180
ttgtaccgga agtcccgcct accggcgggc accggcggca tctgatttgg tgtcttcttt 240
taaattttgc ggcaattcag tcgataacta taacggtcct aaggtagcga tttaaatacg 300
cgctctctta aggtagcccc gggacgcgtc aattgagatc tggatccggt accgaattcg 360
cggccgcctc gacgactagc gtttaattaa acgcgtgtct gtctgcacat ttcgtagagc 420
gagtgttccg atactcta atctccctaggc aaggttcata tttgtgtagg ttacttattc 480
tcctttttgtt gactaagtca ataatacaga tcagcagggt tggagtcagc ttggcagggg 540
tcagcagcct gggttggaag gaggggggat aaaagcccct tcaccaggag aagccgtcac 600
acagatccac aagctcctga ggtaagtgcc gtgtgtgggt cccgcggggc tggcctcttt 660

acggggttatg gcccttgcg	gccttgaatt actgacactg	acatccactt tttctttttc	720
tccacagcta gcgccaccat	gcagattgag ctgtccactt	gtttcttcct gtgcctcctg	780
cgtttctgtt tctccgccac	tcgccggtac taccttggag	ccgtggagct ttcattggag	840
tacatgcaga gcgacctggg	cgaactcccc gtggatgcca	gattcccccc ccgcgtgcca	900
aagtccttcc cctttaacac	ctccgtggtg tacaagaaaa	ccctctttgt cgagttcact	960
gaccacctgt tcaacatcgc	caagccgcgc ccaccttga	tgggcctcct gggaccgacc	1020
attcaagctg aagtgtacga	caccgtggtg atcacctga	agaacatggc gtcccacccc	1080
gtgtccctgc atgcggtcgg	agtgtcctac tggaaggcct	ccgaaggagc tgagtacgac	1140
gaccagacta gccagcggga	aaaggaggac gataaagtgt	tcccgggcgg ctgcataact	1200
tacgtgtggc aagtcctgaa	ggaaaacgga cctatggcat	ccgatcctct gtgcctgact	1260
tactcctacc tttcccatgt	ggacctcgtg aaggacctga	acagcgggct gattggtgca	1320
cttctcgtgt gccgcgaagg	ttcgctcgtc aaggaaaaga	cccagaccct ccataagttc	1380
atccttttgt tcgctgtgtt	cgatgaagga aagtcatggc	attccgaaac taagaactcg	1440
ctgatgcagg accgggatgc	cgcctcagcc cgcgcctggc	ctaaaatgca tacagtcaac	1500
ggatacgtga atcggtcact	gcccgggctc atcggttgtc	acagaaagtc cgtgtactgg	1560
cacgtcatcg gcatgggcac	tacgcctgaa gtgcactcca	tcttcctgga agggcacacc	1620
ttcctcgtgc gcaaccaccg	ccaggcctct ctggaaatct	ccccgattac ctttctgacc	1680
gcccagactc tgctcatgga	cctggggcag ttccttctct	tctgccacat ctccagccat	1740
cagcacgacg gaatggaggc	ctacgtgaag gtggactcat	gcccgggaaga acctcagttg	1800
cggatgaaga acaacgagga	ggccgaggac tatgacgacg	atgtgactga ctccgagatg	1860
gacgtcgtgc ggttcgatga	cgacaacagc cccagcttca	tccagattcg cagcgtggcc	1920
aagaagcacc ccaaaacctg	ggtgcactac atcgcggccg	aggaagaaga ttgggactac	1980
gccccgttgg tgctggcacc	cgatgaccgg tcgtacaagt	cccagtatct gaacaatggt	2040
ccgcagcggg	ttggcagaaa gtacaagaaa	gtgcggttca tggcgtagac	2100
tgacgaaaacg	tttaagaccc gggaggccat	tcaacatgag agcggcattc	2160
gctgtacgga	gaggtcggcg ataccttct	catcatcttc aaaaaccagg	2220
cctcccggcc	ttacaacatc	tacctcacg gaatcaccga	2280
cgtgcggcca	ctctactcgc ggcgcctgcc	gaagggcgtc	2340
aagcacctga	aagacttccc tatcctgccg	ggcgaaatct tcaagtataa	2400
gtggaccgtc	accgtggagg acgggcccac	caagagcgat cctaggtgtc	2460
tgactcggta	ctactccagc	ttcgtgaaca tggaacggga	2520
cctggcatcg	ggactcattg gaccgctgct	gatctgctac	2580
aaagagtcgg	tggtatcaacg cggcaaccag	atcatgtccg acaagcgcaa	
cgtgatcctg	ttctccgtgt ttgatgaaaa	cagatcctgg tacctcactg	
aaaacatcca	gaggttcctc		

ccaaacccccg	caggagtgca	actggaggac	cctgagtttc	aggcctcgaa	tatcatgcac	2640
tcgattaacg	gttacgtggt	cgactcgctg	caactgagcg	tgtgcctcca	tgaagtcgct	2700
tactgggtaca	ttctgtccat	cggcgcccag	actgacttcc	tgagcgtggt	cttttccggt	2760
tacaccttta	agcacaagat	ggtgtacgaa	gataccctga	ccctgttccc	tttctccggc	2820
gaaacgggtgt	tcatgtcgat	ggagaacccg	ggtctgtgga	ttctgggatg	ccacaacagc	2880
gacttttcgga	accgcggaat	gactgccctg	ctgaagggtgt	cctcatgcga	caagaacacc	2940
ggagactact	acgaggactc	ctacgaggat	atctcagcct	acctcctgtc	caagaacaac	3000
gcgatcgagc	cgcgagctt	cagccagaac	ggcgcgccaa	catcagagag	cgccaccctt	3060
gaaagtgggtc	ccgggagcga	gccagccaca	tctgggtcgg	aaacgccagg	cacaagtgag	3120
tctgcaactc	ccgagtccgg	acctggctcc	gagcctgcca	ctagcggctc	cgagactccg	3180
ggaacttccg	agagcgctac	accagaaagc	ggaccgggaa	ccagtaccga	acctagcgag	3240
ggctctgctc	cgggcagccc	agccggctct	cctacatcca	cggaggaggg	cacttccgaa	3300
tccgccaccc	cggagtccag	gccaggatct	gaaccgcgta	cctcaggcag	tgagacgcca	3360
ggaacgagcg	agtccgctac	accggagagt	gggccaggga	gccctgctgg	atctcctacg	3420
tccactgagg	aagggtcacc	agcgggctcg	cccaccagca	ctgaagaagg	tgctctgagc	3480
ccgcctgtgc	tgaagaggca	ccagcgagaa	attaccggga	ccaccctcca	atcggatcag	3540
gaggaaatcg	actacgacga	caccatctcg	gtggaaatga	agaaggaaga	tttcgatatc	3600
tacgacgagg	acgaaaatca	gtcccctcgc	tcattccaaa	agaaaactag	acactacttt	3660
atcgccgcgg	tggaaagact	gtgggactat	ggaatgtcat	ccagccctca	cgtccttcgg	3720
aaccgggccc	agagcggatc	ggtgcctcag	ttcaagaaag	tggtgttcca	ggagttcacc	3780
gacggcagct	tcaccagacc	gctgtaccgg	ggagaactga	acgaacacct	gggcctgctc	3840
ggtccctaca	tccgcgcgga	agtggaggat	aacatcatgg	tgaccttccg	taaccaagca	3900
tccagacctt	actccttcta	ttcctccctg	atctcatacg	aggaggacca	gcgccaaggc	3960
gccgagcccc	gcaagaactt	cgtcaagccc	aacgagacta	agacctactt	ctggaagggtc	4020
caacaccata	tggtcccgac	caaggatgag	tttgactgca	aggcctgggc	ctactttctcc	4080
gacgtggacc	ttgagaagga	tgtccattcc	ggcctgatcg	ggccgctgct	cgtgtgtcac	4140
accaacaccc	tgaaccagac	gcatggacgc	caggtcaccg	tccaggagtt	tgctctgttc	4200
ttcaccatth	ttgacgaaac	taagtcctgg	tacttcaccg	agaatatgga	gcgaaactgt	4260
agagcgccct	gcaatatcca	gatggaagat	ccgactttca	aggagaacta	tagattccac	4320
gccatcaacg	ggtacatcat	ggatactctg	ccggggctgg	tcatggccca	ggatcagagg	4380
attcgggtgg	acttgctgtc	aatgggatcg	aacgaaaaca	ttcactccat	tcactttctcc	4440
ggtcacgtgt	tcactgtgcg	caagaaggag	gagtacaaga	tggtcgctgta	caatctgtac	4500

cccggggtgt	tcgaaactgt	ggagatgctg	ccgtccaagg	ccggcatctg	gagagtggag	4560
tgcttgatcg	gagagcacct	ccacgcgggg	atgtccaccc	tcttcctggt	gtactcgaat	4620
aagtgccaga	ccccgctggg	catggcctcg	ggccacatca	gagacttcca	gatcacagca	4680
agcggacaat	acggccaatg	ggcgccgaag	ctggcccgcg	tgcactactc	cggatcgatc	4740
aacgcatggt	ccaccaagga	accgttctcg	tggattaagg	tggacctcct	ggcccctatg	4800
attatccacg	gaattaagac	ccagggcgcc	aggcagaagt	tctcctccct	gtacatctcg	4860
caattcatca	tcatgtacag	cctggacggg	aagaagtggc	agacttacag	gggaaactcc	4920
accggcaccc	tgatggtctt	tttcggcaac	gtggattcct	ccggcattaa	gcacaacatc	4980
ttcaaccac	cgatcatagc	cagatatatt	aggctccacc	ccactcacta	ctcaatccgc	5040
tcaactcttc	ggatggaact	catgggggtgc	gacctgaact	cctgctccat	gccgttgggg	5100
atggaatcaa	aggctattag	cgacgcccag	atcacgcgca	gctcctactt	cactaacatg	5160
ttcgccacct	ggagcccctc	caaggccagg	ctgcacttgc	agggacggtc	aaatgcctgg	5220
cggccgcaag	tgaacaatcc	gaaggaatgg	cttcaagtgg	atttccaaaa	gaccatgaaa	5280
gtgaccggag	tcaccaccca	gggagtgaag	tcccttctga	cctcgatgta	tgtgaaggag	5340
ttcctgatta	gcagcagcca	ggacgggcac	cagtggaccc	tgttcttcca	aaacggaaa	5400
gtcaaggtgt	tccaggggaa	ccaggactcg	ttcacacccg	tggtgaaactc	cctggacccc	5460
ccactgctga	cgcggtactt	gaggattcat	cctcagtcct	gggtccatca	gattgcattg	5520
cgaatggaag	tcctgggctg	cgaggcccag	gacctgtact	gaatcagcct	gagctcgctg	5580
atcataatca	acctctggat	tacaaaatth	gtgaaagatt	gactggtatt	cttaactatg	5640
ttgctccttt	tacgctatgt	ggatacgctg	ctttaatgcc	tttgtatcat	gctattgctt	5700
ccgctatggc	tttcattttc	tcctccttgt	ataaatcctg	gttgctgtct	ctttatgagg	5760
agttgtggcc	cgttgtcagg	caacgtggcg	tgggtgtgcac	tgtgtttgct	gacgcaaccc	5820
ccactggttg	gggcattgcc	accacctgtc	agctcctttc	cgggactttc	gctttccccc	5880
tccttattgc	cacggcgga	ctcatcgccg	cctgccttgc	ccgctgctgg	acaggggctc	5940
ggctgttggg	cactgacaat	tccgtggtgt	tgtcggggaa	atcatcgctc	tttccttggc	6000
tgctcgctg	tggtgccacc	tggattctgc	gcgggacgtc	cttctgctac	gtcccttcgg	6060
ccctcaatcc	agcggacctt	ccttcccgcg	gcctgctgcc	ggctctgcgg	cctcttccgc	6120
gtcttcgcct	tcgccctcag	acgagtcgga	tctccctttg	ggccgcctcc	ccgctgatca	6180
gcctcgactg	tgcttcttag	ttgccagcca	tctgttgtht	gcccctcccc	cgtgccttcc	6240
ttgaccctgg	aagggtccac	tcccactgtc	ctttccta	aaaatgagga	aattgcatcg	6300
cattgtctga	gtaggtgtca	ttctattctg	gggggtgggg	tggggcagga	cagcaagggg	6360
gaggattggg	aagacaatag	caggcatgct	ggggatgcgg	tgggctctat	ggcttctgag	6420

gcggaaagaa cgggctcgag aagcttctag atatacctctc ttaaggtagc atcgagatctt	6480
aaattaggga taacagggtta atggcgcggg ccgcaaaatt taaaagaaga caccaaatca	6540
gatgccgccg gtcgccgccg gtaggcggga cttccgggtac aagatggcgg acaattacgt	6600
catttcctgt gacgtcattt cctgtgacgt cacttccgggt gggcgggact tccggaatta	6660
gggttggctc tgggccagcg cttgggggtg acgtgccact aagatcaagc ggcgcgccgc	6720
ttgtcttagt gtcaaggcaa cccaagcaa gctggcccag ag	6762

<210> 180
 <211> 248
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' ITR

<400> 180	
ctctggggcca gcttgcttgg ggttgccttg acactaagac aagcggcgcg ccgcttgatc	60
ttagtggcac gtcaacccca agcgttgcc cagagccaac cctaattccg gaagtccgcg	120
ccaccggaag tgacgtcaca ggaaatgacg tcacaggaaa tgacgtaatt gtccgccatc	180
ttgtaccgga agtcccgctt accggcgggc accggcggca tctgatttgg tgtcttcttt	240
taaatttt	248

<210> 181
 <211> 248
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' ITR inverted terminal repeat

<400> 181	
ctctggggcca gcttgcttgg ggttgccttg acactaagac aagcggcgcg ccgcttgatc	60
ttagtggcac gtcaacccca agcgttgcc cagagccaac cctaattccg gaagtccgcg	120
ccaccggaag tgacgtcaca ggaaatgacg tcacaggaaa tgacgtaatt gtccgccatc	180
ttgtaccgga agtcccgctt accggcgggc accggcggca tctgatttgg tgtcttcttt	240
taaatttt	248

<210> 182
 <211> 6830
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GPV-FVIII construct

<400> 182	
cggtgacgtg tttccggctg ttaggttgac cacgcgcatg ccgcgcggtc agcccaatag	60

ttaagccgga	aacacgtcac	cggaagtcac	atgaccggaa	gtcacgtgac	cggaaacacg	120
tgacaggaag	cacgtgaccg	gaactacgtc	accggatgtg	cgtcaccgga	agcatgtgac	180
cggaacttgc	gtcacttccc	cctcccctga	ttggctgggt	cgaacgaacg	aaccctccaa	240
tgagactcaa	ggacaagagg	atattttgcg	cgccaggaag	tggcggcaat	tcagtcgata	300
actataacgg	tcctaaggta	gcgatttaaa	tacgcgctct	cttaaggtag	ccccgggacg	360
cgtcaattga	gatctggatc	cggtagccga	ttcgcggccg	cctcgacgac	tagcgtttaa	420
ttaaacgcgt	gtctgtctgc	acatttcgta	gagcgagtgt	tccgatactc	taatctccct	480
aggcaagggt	catatttgtg	taggttactt	attctccttt	tgttgactaa	gtcaataatc	540
agaatcagca	ggtttgaggt	cagcttggca	gggatcagca	gcctggggtg	gaaggagggg	600
gtataaaagc	cccttcacca	ggagaagccg	tcacacagat	ccacaagctc	ctgaggtaag	660
tgccgtgtgt	ggttcccgcg	ggcctggcct	ctttacgggt	tatggccctt	gcgtgccttg	720
aattactgac	actgacatcc	actttttctt	tttctccaca	gctagcgcca	ccatgcagat	780
tgagctgtcc	acttgtttct	tcctgtgcct	cctgcgcttc	tgtttctccg	ccactcgccg	840
gtactacctt	ggagccgtgg	agctttcatg	ggactacatg	cagagcgacc	tgggcgaact	900
ccccgtggat	gccagattcc	ccccccgcgt	gcaaagtc	ttccccttta	acacctccgt	960
gggtgtacaag	aaaaccctct	ttgtcgagtt	cactgaccac	ctgttcaaca	tcgccaagcc	1020
gcgcccacct	tggatgggccc	tcctgggacc	gaccattcaa	gctgaagtgt	acgacaccgt	1080
ggtgatcacc	ctgaagaaca	tggcgtccca	ccccgtgtcc	ctgcatgcgg	tcggagtgtc	1140
ctactggaag	gcctccgaag	gagctgagta	cgacgaccag	actagccagc	gggaaaagga	1200
ggacgataaa	gtgttcccgg	gcggctcgca	tacttacgtg	tggcaagtcc	tgaaggaaaa	1260
cggacctatg	gcatccgatc	ctctgtgcct	gacttactcc	tacctttccc	atgtggacct	1320
cgtgaaggac	ctgaacagcg	ggctgattgg	tgcatttctc	gtgtgccgcg	aaggttcgct	1380
cgctaaggaa	aagaccaga	ccctccataa	gttcatcctt	ttgttcgctg	tgttcgatga	1440
aggaaagtca	tggcattccg	aaactaagaa	ctcgctgatg	caggaccggg	atgccgcctc	1500
agcccgcgcc	tggcctaaaa	tgcatacagt	caacggatac	gtgaatcggg	cactgcccgg	1560
gctcatcggt	tgtcacagaa	agtccgtgta	ctggcacgtc	atcggcattg	gcactacgcc	1620
tgaagtgcac	tccatcttcc	tgggaaggga	caccttcctc	gtgcgcaacc	accgccaggc	1680
ctctctggaa	atctccccga	ttacctttct	gaccgcccag	actctgctca	tggacctggg	1740
gcagttcctt	ctcttctgcc	acatctccag	ccatcagcac	gacggaatgg	aggcctacgt	1800
gaaggtggac	tcatgcccgg	aagaacctca	gttgccgatg	aagaacaacg	aggaggccga	1860
ggactatgac	gacgatttga	ctgactccga	gatggacgtc	gtgcggttcg	atgacgacaa	1920
cagccccagc	ttcatccaga	ttcgcagcgt	ggccaagaag	cacccccaaa	cctgggtgca	1980

ctacatcgcg gccgaggaag aagattggga ctacgccccg ttggtgctgg caccgatga	2040
ccggtcgtac aagtcccagt atctgaacaa tgggtccgcag cggattggca gaaagtacaa	2100
gaaagtgcgg ttcatggcgt aactgacga aacgtttaag acccgggagg ccattcaaca	2160
tgagagcggc attctgggac cactgctgta cggagaggtc ggcgataccc tgctcatcat	2220
cttcaaaaac caggcctccc ggccttacaa catctaccct cacggaatca ccgacgtgcg	2280
gccactctac tcgcggcgcc tgccgaaggg cgtcaagcac ctgaaagact tccctatcct	2340
gccgggcgaa atcttcaagt ataagtggac cgtcaccgtg gaggacgggc ccaccaagag	2400
cgatcctagg tgtctgactc ggtactactc cagcttcgtg aacatggaac gggacctggc	2460
atcgggactc attggaccgc tgctgatctg ctacaaagag tcggtggatc aacgcggcaa	2520
ccagatcatg tccgacaagc gcaacgtgat cctgttctcc gtgtttgatg aaaacagatc	2580
ctggtacctc actgaaaaca tccagaggtt cctcccaaac cccgcaggag tgcaactgga	2640
ggaccctgag tttcaggcct cgaatatcat gcactcgatt aacggttacg tgttcgactc	2700
gctgcaactg agcgtgtgcc tccatgaagt cgcttactgg tacattctgt ccatcggcgc	2760
ccagactgac ttcttgagcg tgttcttttc cggttacacc tttaagcaca agatggtgta	2820
cgaagatacc ctgaccctgt tccctttctc cggcgaaacg gtgttcatgt cgatggagaa	2880
cccggtctg tggattctgg gatgccacaa cagcgacttt cggaaccgcg gaatgactgc	2940
cctgctgaag gtgtcctcat gcgacaagaa caccggagac tactacgagg actcctacga	3000
ggatatctca gcctacctc tgtccaagaa caacgcgatc gagccgcgca gcttcagcca	3060
gaacggcgcg ccaacatcag agagcgccac ccctgaaagt ggtcccggga gcgagccagc	3120
cacatctggg tcggaaacgc caggcacaag tgagtctgca actcccagat ccggacctgg	3180
ctccgagcct gccactagcg gctccgagac tccgggaact tccgagagcg ctacaccaga	3240
aagcggaccc ggaaccagta ccgaacctag cgagggctct gctccgggca gccagccgg	3300
ctctcctaca tccacggagg agggcacttc cgaatccgcc accccggagt cagggccagg	3360
atctgaaccc gctacctcag gcagtgagac gccaggaacg agcgagtccg ctacaccgga	3420
gagtgggcca gggagccctg ctggatctcc tacgtccact gaggaagggc caccagcggg	3480
ctcgcaccac agcactgaag aaggtgcctc gagccgcct gtgctgaaga ggcaccagcg	3540
agaaattacc cggaccaccc tccaatcgga tcaggaggaa atcgactacg acgacaccat	3600
ctcggtgga atgaagaagg aagatttcga tatctacgac gaggacgaaa atcagtcccc	3660
tcgctcattc caaaagaaaa ctagacacta ctttatcgcc gcggtggaag gactgtggga	3720
ctatggaatg tcatccagcc ctacagtcct tcggaaccgg gccagagcg gatcgggtgc	3780
tcagttcaag aaagtgggtg tccaggagtt caccgacggc agcttcaccc agccgctgta	3840
ccggggagaa ctgaacgaac acctgggcct gctcggctcc tacatccgcg cggaagtgga	3900

ggataacatc	atggtgacct	tccgtaacca	agcatccaga	ccttactcct	tctattcctc	3960
cctgatctca	tacgaggagg	accagcgcca	aggcgccgag	ccccgcaaga	acttcgtcaa	4020
gccaacgag	actaagacct	acttctggaa	ggtccaacac	catatggccc	cgaccaagga	4080
tgagtttgac	tgcaaggcct	gggcctactt	ctccgacgtg	gaccttgaga	aggatgtcca	4140
ttccggcctg	atcggggccg	tgctcgtgtg	tcacaccaac	accctgaacc	cagcgcatgg	4200
acgccaggtc	accgtccagg	agtttgctct	gttcttcacc	atttttgacg	aaactaagtc	4260
ctggtacttc	accgagaata	tggagcgaaa	ctgtagagcg	ccctgcaata	tccagatgga	4320
agatccgact	ttcaaggaga	actatagatt	ccacgccatc	aacgggtaca	tcatggatac	4380
tctgccgggg	ctgggtcatgg	cccaggatca	gaggattcgg	tggtacttgc	tgtcaatggg	4440
atcgaacgaa	aacattcact	ccattcactt	ctccggtcac	gtgttcactg	tgcgcaagaa	4500
ggaggagtac	aagatggcgc	tgtacaatct	gtaccccggg	gtgttcgaaa	ctgtggagat	4560
gctgccgtcc	aaggccggca	tctggagagt	ggagtgcctg	atcggagagc	acctccacgc	4620
ggggatgtcc	accctcttcc	tggtgtactc	gaataagtgc	cagaccccg	tgggcatggc	4680
ctcgggccac	atcagagact	tccagatcac	agcaagcgga	caatacggcc	aatgggcgcc	4740
gaagctggcc	cgcttgcact	actccggatc	gatcaacgca	tggtccacca	aggaaccgtt	4800
ctcgtggatt	aaggtggacc	tcctggcccc	tatgattatc	cacggaatta	agaccaggg	4860
cgccaggcag	aagttctcct	ccctgtacat	ctcgcaattc	atcatcatgt	acagcctgga	4920
cgggaagaag	tggcagactt	acaggggaaa	ctccaccggc	accctgatgg	tctttttcgg	4980
caacgtggat	tcctccggca	ttaagcacia	catcttcaac	ccaccgatca	tagccagata	5040
tattaggctc	caccctactc	actactcaat	ccgctcaact	cttcggatgg	aactcatggg	5100
gtgcgacctg	aactcctgct	ccatgccgtt	ggggatggaa	tcaaaggcta	ttagcgacgc	5160
ccagatcacc	gcgagctcct	acttcactaa	catgttcgcc	acctggagcc	cctccaaggc	5220
caggctgcac	ttgcagggac	ggtcaaattgc	ctggcgggccg	caagtgaaca	atccgaagga	5280
atggcttcaa	gtggattttcc	aaaagaccat	gaaagtgacc	ggagtcacca	cccagggagt	5340
gaagtccctt	ctgacctcga	tgtatgtgaa	ggagttcctg	attagcagca	gccaggacgg	5400
gcaccagtgg	accctgttct	tccaaaacgg	aaaggtcaag	gtgttccagg	ggaaccagga	5460
ctcgttcaca	cccgtgggtga	actccctgga	ccccccactg	ctgacgcggt	acttgaggat	5520
tcatacctcag	tcctgggtcc	atcagattgc	attgcgaatg	gaagtcctgg	gctgcgaggc	5580
ccaggacctg	tactgaatca	gcctgagctc	gctgatcata	atcaacctct	ggattacaaa	5640
atthgtgaaa	gattgactgg	tattcttaac	tatgttgctc	cttttacgct	atgtggatac	5700
gctgctttta	tgcccttgta	tcatgctatt	gcttcccgta	tggttttcat	tttctcctcc	5760
ttgtataaat	cctgggttgc	gtctctttat	gaggagtgtg	ggcccgttgt	caggcaacgt	5820

ggcgtggtgt	gactgtgtt	tgctgacgca	acccccactg	gttggggcat	tgccaccacc	5880
tgtcagctcc	tttccgggac	tttcgctttc	cccctcccta	ttgccacggc	ggaactcatc	5940
gccgcctgcc	ttgcccgtg	ctggacaggg	gctcggctgt	tgggcactga	caattccgtg	6000
gtgttgctcg	ggaaatcatc	gtcctttcct	tggtgctcg	cctgtgttgc	cacctggatt	6060
ctgcgcggga	cgctccttctg	ctacgtccct	tcggccctca	atccagcgga	ccttccttcc	6120
cgcggcctgc	tgccggctct	gcggcctctt	ccgcgtcttc	gccttcgccc	tcagacgagt	6180
cggatctccc	tttggggcgc	ctccccgtg	atcagcctcg	actgtgcctt	ctagttgcca	6240
gccatctgtt	gtttgcccct	cccccgctgc	ttccttgacc	ctggaagggtg	ccactcccac	6300
tgctcctttcc	taataaaatg	aggaaaattgc	atcgcatgtt	ctgagtaggt	gtcattctat	6360
tctggggggt	ggggtggggc	aggacagcaa	gggggaggat	tggaagaca	atagcaggca	6420
tgctggggat	gcggtgggct	ctatggcttc	tgaggcgga	agaacgggct	cgagaagctt	6480
ctagatatcc	tctcttaagg	tagcatcgag	atttaaatta	gggataacag	ggtaatggcg	6540
cgggccgcca	cttcctggcg	cgcaaaatat	cctcttgctc	ttgagtctca	ttggagggtt	6600
cgttcgttcg	aaccagccaa	tcaggggagg	gggaagtgac	gcaagttccg	gtcacatgct	6660
tccggtgacg	cacatccggt	gacgtagttc	cggtcacgtg	cttcctgtca	cgtgtttccg	6720
gtcacgtgac	ttccggtcat	gtgacttccg	gtgacgtgtt	tccggcttaa	ctattgggct	6780
gaccgcgcgg	catgcgcgtg	gtcaacctaa	cagccggaaa	cacgtcacccg		6830

<210> 183
 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' ITR

<400>	183					
cggtgacgtg	tttccggctg	ttagggtgac	cacgcgcatg	ccgcgcggtc	agcccaatag	60
ttaagccgga	aacacgtcac	cggaaagtcac	atgaccggaa	gtcacgtgac	cggaaacacg	120
tgacaggaag	cacgtgaccg	gaactacgtc	accggatgtg	cgtcaccgga	agcatgtgac	180
cggaaacttg	gtcacttccc	cctcccctga	ttggctgggt	cgaacgaacg	aaccctccaa	240
tgagactcaa	ggacaagagg	atatthttg	cgccaggaag	tg		282

<210> 184
 <211> 282
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 3' ITR inverted terminal repeat

<400> 184

cggtgacgtg tttccggctg ttaggttgac cacgcgcatg ccgcgcggtc agcccaatag	60
ttaagccgga aacacgtcac cggaagtcac atgaccggaa gtcacgtgac cggaaacacg	120
tgacaggaag cacgtgaccg gaactacgtc accggatgtg cgtcaccgga agcatgtgac	180
cggaacttgc gtcacttccc cctcccctga ttggctgggt cgaacgaacg aaccctccaa	240
tgagactcaa ggacaagagg atatatttgcg cgccaggaag tg	282