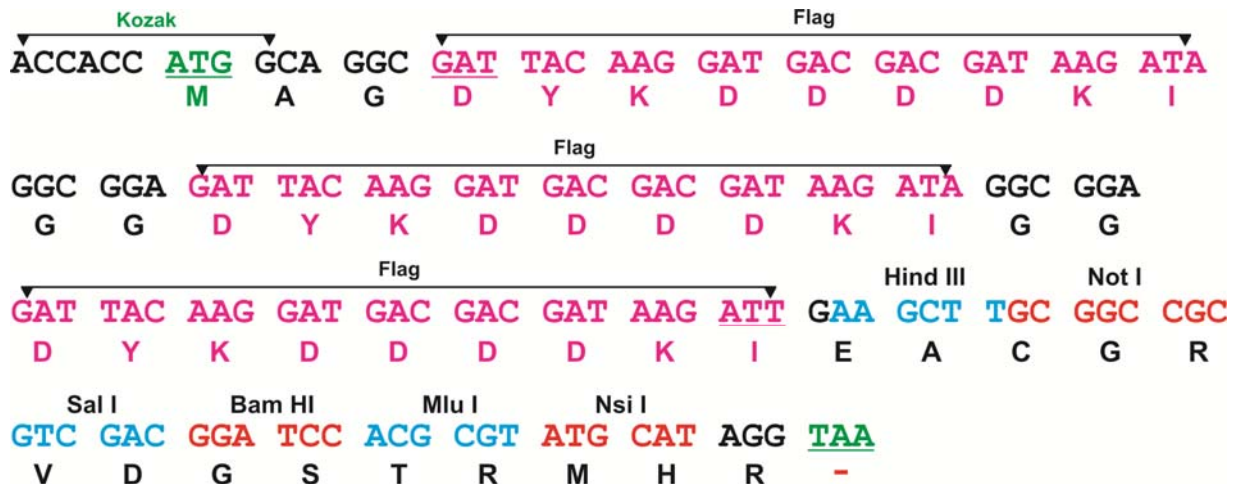
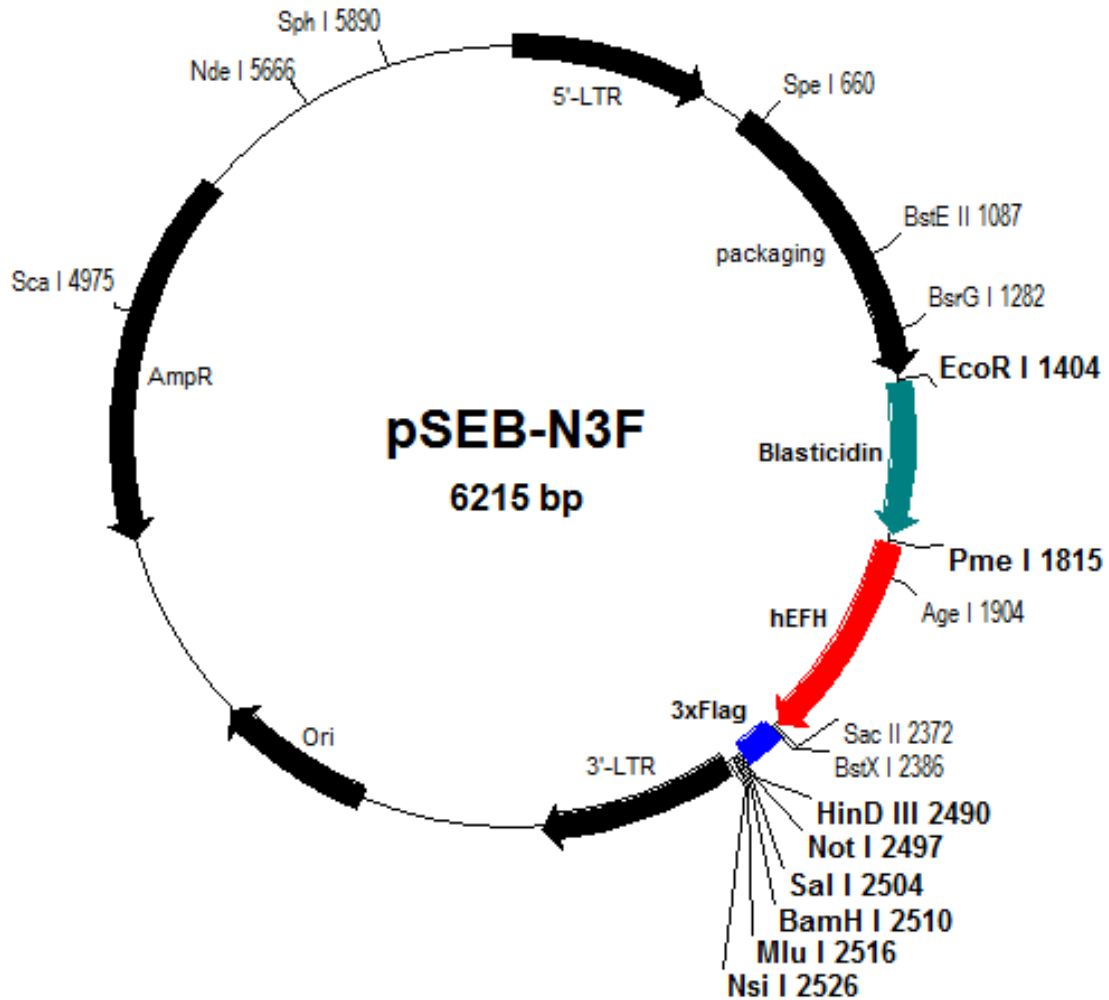


Vector: pSEB-N3F (N-terminal 3xFlag tags)

Antibiotic Selection: Amp

Creator(s): Enyi Huang, Molecular Oncology Lab of The University of Chicago

Date of Construction: November, 2010



pSEB-N3F (human EF1a/HLTV hybrid promoter) Full-Length Sequence

TGAAAGACACG CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGAACGGCATGGAAAATACATAACTGAGAA TAGAGAAGT AGATCAAGG
 TTAGAAGACAGACGACGAGATAATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCGGCTCAGGGCCAAGAACAGATGGTCCCAGATGCGGTCCCGC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTCCCAAGGACCTGAAATGACCTGTGCCATTATTGAACATAACCAACTCAGTTCGCTTCTCGCTTCT
 GTTCGCGCGTCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATTTCCCAAT
 AAAGCCTCTTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG
 GTTCCACCGA GATTTGGAGACCCTGCCCA GGGACCACCGACCCCGCCG CGGGAGGTAA GCTGGCCAGC GGTGTTTCGTGTCTGTCTC TGTCTTTGTG
 CTGTGTTGTGCCGGCATCTAATGTTTGGCGCTGCGTCTGTACTAGTCTAGCTAAGCTCTGTATCTGGCGGACCCGTGGTGAAGTACGAGTTCGTAACACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT
 CTGGTAGGAGACGAGAACC AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTCCGGTT TGAACCCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA
 GCATCGTTCT GTGTTGTCTC TGTCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTTCAGCTTAGGTCAGT
 GAAAGATGTCGAGCCGATCG CTCACAACCA GTCGGTAGAT GTCAAGAGAGAGCTTGGGT TACCTTCTGC TCTGCAAAAT GGCCAACCTTAAACGTCGGA
 TGGCCGCGAGACGGCACCT TAACCGAGAC CTCATCACCC AGGTTAAGAT CAAGGTCTTT TCACCTGGCCCGCATGGACA CCCAGACCAGGTCCCTACA
 TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT
 CCCCCTGAACCTCCTCGTTCGACCCCGCTCGATCCTCCCTTATTCACGCCCTCACTCCTTCTTAGGCGCCGGAATTCACCATG GCCAAGCCTTTGTCTCAAGA
 AGAATCCACCCTCATTGAAAGAGCAACGGTACAATCAACAGCATCCCATCTCTGAAGACTACAGCTCGCCAGCGCAGCTCTCTTAGCCAGCGCCGATCTTC
 ACTGTTGTCATGATATATCATTTTACTGGGGACCTTGTGCAGAATCTGTGTGCTGGGCACTGCTGCTGCGGACAGTGGCAACCTGACTTGTATCGTCGGA
 TCGGAATGAGAACAGGGCATCTTGGACCCCTGCGGACGGTCCGACAGGTGCTTCTCGATCTGCATCTGGGATCAAAGCCATAGTGAAGACAGTGTAGGACA
 GCCGACGGCAGTTGGGATTCTGTAATTGCTGCCCTCTGTTATGTGTGGAGGGCtaagttaaactatgagCGTCCCGTGGCGTCCGTCAGTGGGCGAGCGCACAT
 CGCCACAGTCCCGAGAAGTTGGGGGAGGGTCCGCAATTGAACCGGTGCTTAGAGAAGGTGGCGGGGTAACCTGGGAAGTATGTCGTGTACTGGTCCG
 CTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCCCGTGAACGTTCTTTTCGCAACGGGTTGGCCGAGAACACAGCTGAGCTAGCTTCG
 AGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGCGCCCATCCACCGGGTTGAGTCCGCTTCTGCGCCTCCCGCTGTGGTCCCTCTGAAT
 CGCTCCGCGTCAAGTAAAGTCTTAAAGCTCAGGTCCGAGACCGGGCTTTGTCCGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCCACGCTTTCGCTGA
 CCTGTCTCTCAACTCAGCTCTTGTCTTGTCTGCGCGTTACAGATCCAAGCTGTGACCCGCGCTAC atcgat ccgccc A
GATCCACCAC ATC GCA GGC GAT TAC AAG GAT GAC GAC GAT AAG ATA GGC GGA GAT TAC AAG GAT GAC GAC GAT AAG ATA
GGC GGA GAT TAC AAG GAT GAC GAC GAT AAG ATT GAA GCT GC GGC CGC GTC GAC GGA TCC ACG CGT ATG CAT AGG TAA
CGATAAAAATAAAGATTTTTATTTAGTCTCCAGAAAAGGGGGGAATGAAAGACCCACCTGTAGTGTGGCAAGCTAGCTTAAAGTAAACGCCATTTTGCAGGCATG
GAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGTTTAGGAACAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG
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GCCTTATTTGAACATAACCAATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTC
CTCCGATAGACTGCTGCGCCGGGTACCCGTGTATCCAATAAACCCCTTTCGAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAGTGA
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CCACTGTTTTGAATCCACACTCCCAATACTCCTGAAATCTCCTGAAATGATTCATATGAGACCGCAGAAAGAGCTGGGAGAAATTAATTCGTAATCATGTTGCTGTTTTCC
TGTGTGAAATGTTATCCGCTCACAATCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTCCCTAATGAGTGAAGTCAACTCACATTAATTGGC
TTGGCTCAGTCCCGCTTTCAGTCCGGAACCTGTCTGTCGACCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTTCGCTATTGGGGC
CTCTCCCGCT TCCCTCGTCA CTGACTCGCTCGCTCGGTC GTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAA
TACAGGGATAAACGCAGGAA GAACATGTGAGCAAAAAGCC AGCAAAAAGC CAGGAACCGT AAAAAAGCCGCTTGTCTGGC GTTTTTTCCATAGGCTCCGCC
CCCCTGACGA GCATCACAAA AATCGACGCTCAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATACCAGGCGTTT CCCCTGGAAGCTCCCTCGT
GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCTTTCTCCCTTCGCGG AAGCGTGGCGCTTTTCTCATA GCTCAGCTGTAGTATCTC
AGTTCGGTGTAGGTCGTTCC TCCAAGCTGGGCTGTGTG ACGAACCCCT CGTTCAGCC GACCGTGGCGCTTATCCGG TAACATCTGT CTTGAGTCCA
ACCCGTAAGACACGACTTA TCGCCACTGGCAGCAGCCAC TGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGATCTTCTGAAAGTGTG
GCCTAACTACGGCTACACTA GAAGGACAGT ATTTGGTATC TCGCTCTGTGAAGCCAGT TACCTTCGAAAAAGAGTTG GTAGCTCTTG ATCCGGCAAA
CAAACCACCGCTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTACGCGCAGAAAA AAAGGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGT
CTGACGCTCA GTGGAACGAA AACTCACGTTAAGGGATTTT GGTATGAGATTATCAAAA GGATCTTAC CTAGATCTTT TTAATTAATAAATAAGATTT
TAAATCAATCTAAAGTATAT ATGACTAAAC TTGGTCTGAC AGTTACCAAGTTTAACTCAG TGAAGCAGCT ATCTCAGCGA TGTGCTATTTCTGTTACTC
ATAGTTGCCCTGACTCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGTGCAATGATACC GCGAGACCCACGCTCACCGG
CTCCAGATTT ATCAGCAATA AACAGCCAGCCGGAAGGGC CGAGCGCAGAAGTGGTCTG CAACTTATC CGCTCCATC CAGTCTATTAATTGTTGCCG
GGAAGCTAGA GTAAGTAGTT CGCCAGTTAATAGTTTGGCG AACCTGTGTGCCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGGTATGGCTTCA
TTCAGCTCCGGTCCCAAGC ATCAAGCGA GTTACATGAT CCCCATGTT GTGCAAAAAA CCGGTTAGCTCCTCGGTC TCCGATCGTTGTCCAGAGTA
AGTTGGCCCG AGTGTATCA CTCATGTTTATGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGTAAGATGCTTT TCTGTGACTGGTGAAGTACTC
AACCAAGTCA TTCTGAGAAT AGTGTATCG GCGACCGAGT TGCTTTGCCCGCGCTCAAT ACGGGATAAT ACCGCGCCACATAGCAGAACTTTAAAAGT
CTCATCATTTGAAAACGTTT TCCGGGGCGAAAACCTCTCAA GGATCTTACC GCTGTTGGA TCCAGTTCCGATGTAACCCAC TCGTGCACCC AACTGATCTT
CAGCATCTTTACTTTTACC AGCGTCTTCTGGGTGAGCAAA AACAGGAAG CAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGAAATGTTGAAATCT
CATACCTTCT CTTTTTCAAT ATTATTGAAG CATTATCAG GGTATTGTCTCATGAGCG ATACATATTTGAATGTATTT AGAAAAATAAACAATAAGGG
GTTCGCGCACATTTCCCG AAAAGTGCCA CCTGACGCTT AAGAAACCATTATTATCATG ACATTAACCTATAAAAATAG GCGTATCAC AGGCCCTTTC
GTCTCGCGCG TTTCCGTTGAT GACGGTGAACCTCTGACA CATGCACTC CCGGAGACGG TCACAGCTTG TCTGTAAGCGGATCCGGGAGCAGACAAGC
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CGTCCGCGTATAGGGCGATT AGTCCAATTT GTTAAAGACA GGTATCAAGTGGTCCAGGCT CTAGTTTTGA CTCAACAATA TCACAGCTGAAGCTATAG
AGTACGAGCCATAGATAAAA TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGAA

Unique enzymes in pSEB-N3F:

Spe I	A`CTAG,T	660	Mun I	C`AATT,G	1897
BstE II	G`GTNAC,C	1087	Age I	A`CCGG,T	1904
BsrG I	T`GTAC,A	1282	Cla I	AT`CG,AT	2364
EcoR I	G`AATT,C	1404	Sac II	CC,GC`GG	2372
Bbv II	GAAGAC 7/11	1497	BstX I	CCAN,NNNN`NTGG	2386
Bbs I	GAAGAC 8/12	1498	HinD III	A`AGCT,T	2490
Nru I	TCG CGA	1644	Not I	GC`GGCC,GC	2497
BsaB I	GATNN NNATC	1711	Sal I	G`TCGA,C	2504
Pme I	CTTT AAAC	1815	Acc I	GT`MK,AC	2505
			HinC II	GTY RAC	2506
			Hind II	GTY RAC	2506

BamH I G`GATC,C 2510
 Mlu I A`CGCG,T 2516
 Nsi I A,TGCA`T 2526
 Sca I AGT|ACT 4975
 Nde I CA`TA,TG 5666
 Sph I G,CATG`C 5890
 Number of enzymes = 26

Bsa I (7) 476 530 1149 2207
 3033 3054 4556
 BsaB I (1) 1711
 BsaH I (9) 742 1398 2355 5032
 5414 5718 5901 6015
 6036
 BsaJ I (34) 161 240 250 397
 461 497 546 547
 694 733 734 746
 747 1167 1236 1245
 1265 1266 1411 1716
 1974 2238 2369 2385
 2740 2819 2829 2976
 3039 3341 3762 5836
 5914 5920

The following enzymes do not cut in pSEB-N3F:

Apa I Avr II Bcl I Bgl II Blp I
 BsaA I BsiC I BsiW I Bsm I Bsp120 I
 Bsp1286 I BspM I BspM II Bst1107 I BstB I
 Dra III Eco72 I Esp I Fse I Hpa I
 PaeR7 I PflM I Pml I Rsr II Sfi I
 SnaB I Spl I Srf I Stu I Xca I

BsaW I (5) 1829 1904 3808 3955
 4786
 BseR I (4) 464 1293 1332 3042
 Bsg I (2) 1600 2022
 BsiE I (10) 592 727 1532 1648
 2500 3518 3942 4865
 5014 5761

pSEB-N3F: sites sorted by name:

Aat II (2) 745 5417
 Acc I (1) 2505
 Acc65 I (2) 401 2980
 Aci I (70) 197 203 566 588
 688 727 860 901
 1042 1133 1199 1298
 1317 1355 1532 1614
 1681 1926 1963 2043
 2099 2102 2117 2148
 2155 2182 2369 2371
 2424 2457 2496 2500
 2776 2782 3078 3292
 3395 3451 3461 3485
 3528 3535 3556 3647
 3675 3802 3821 3942
 4052 4187 4196 4558
 4649 4840 4886 5007
 5051 5128 5237 5336
 5383 5557 5596 5606
 5632 5670 5683 5709
 5766 6025
 Afl II (3) 35 1006 2612
 Afl III (2) 2516 3602
 Age I (1) 1904
 Aha II (9) 742 1398 2355 5032
 5414 5718 5901 6015
 6036
 Ahd I (4) 1020 3025 3071 4495
 Alu I (33) 30 34 336 580
 668 676 1515 1620
 2056 2062 2066 2204
 2345 2492 2607 2611
 2915 3234 3267 3362
 3426 3544 3770 3860
 3906 4163 4684 4784
 4847 5526 5545 5790
 6146
 Alw I (17) 453 1051 1357 1727
 2333 2361 2371 2506
 2517 4164 4250 4250
 4347 4348 4812 5127
 5133
 AlwN I (2) 2736 4018
 ApaL I (3) 3916 5162 5659
 Apo I (2) 872 1404
 Asc I (2) 368 2947
 Ase I (4) 3245 3373 3432 4667
 Asp718 (2) 401 2980
 Ava I (7) 331 397 498 1871
 1973 2910 2976
 Ava II (13) 186 199 254 551
 690 1219 1572 2765
 2778 2833 4633 4855
 6110
 BamH I (1) 2510
 Ban I (17) 244 401 1142 1397
 1687 1832 1907 2163
 2354 2823 2980 3346
 4443 5717 5900 6014
 6035
 Ban II (8) 338 351 1677 2078
 2917 2930 5967 5981
 Bbe I (6) 1401 2358 5721 5904
 6018 6039
 Bbs I (1) 1498
 Bbv I (10) 931 939 1524 1629
 1834 4021 4024 4230
 4924 5535
 Bbv II (1) 1497
 Bcn I (15) 164 399 400 571
 724 2219 2743 2978
 2979 3983 4679 5030
 5531 5566 5917
 Bfa I (16) 31 219 661 673
 1394 1522 1912 2063
 2189 2251 2608 2798
 4097 4350 4685 6120
 Bgl I (2) 4615 5733
 Bpm I (3) 2545 4565 6183

BsiHKA I (6) 338 2917 3920 5081
 5166 5663
 BsmA I (22) 107 475 531 609
 734 832 949 1073
 1132 1150 1328 1431
 2208 2562 2685 3032
 3053 4557 5331 5484
 5528 6200
 BsmB I (7) 733 831 1072 1131
 1329 5485 5527
 BsmF I (11) 172 185 564 729
 764 1205 1585 1853
 2751 2764 5896
 BsoF I (41) 727 901 917 920
 925 928 1133 1513
 1532 1606 1609 1612
 1615 1618 1782 1823
 2043 2102 2117 2148
 2497 2500 3427 3508
 3526 3529 3647 3802
 3945 4010 4013 4219
 4547 4886 4913 5008
 5237 5524 5633 5737
 5810
 BspH I (4) 4322 5330 5435 5959
 Bsr I (18) 374 1030 1058 1546
 1570 1939 1960 2953
 3403 4009 4022 4136
 4542 4660 4703 4970
 5142 5848
 BsrB I (4) 1042 3294 3535 5336
 BsrD I (2) 4556 4730
 BsrG I (1) 1282
 BssH II (4) 317 368 2896 2947
 BssS I (4) 1587 3775 5159 5466
 BstE II (1) 1087
 BstN I (17) 241 548 735 748
 1169 1194 1217 1237
 1267 1717 2820 3342
 3630 3751 3764 5837
 6114
 BstU I (26) 317 319 370 903
 905 1135 1644 1926
 2095 2140 2371 2502
 2518 2896 2898 2949
 3449 3451 3649 4230
 4560 5053 5385 5485
 5487 5590
 BstX I (1) 2386
 BstY I (9) 2337 2375 2510 4243
 4254 4340 4352 5120
 5137
 Bsu36 I (3) 781 1018 2111
 Cac8 I (38) 28 32 319 370
 582 586 631 650
 1199 1508 1622 2064
 2078 2099 2262 2290
 2392 2494 2605 2609
 2898 2949 3395 3424
 3533 3619 3656 4216
 4607 5620 5768 5788
 5792 5888 5929 5977
 6019 6049
 Cfr10 I (8) 629 1904 2128 2260
 2351 4575 6038 6047
 Cla I (1) 2364
 Csp6 I (8) 402 658 1283 1954
 2981 4974 5650 6161
 Dde I (22) 75 167 208 476
 781 1018 1290 1808
 2111 2205 2256 2652
 2746 2787 3056 3127
 3877 4286 4452 4992
 5418 5653
 Dpn I (28) 94 459 1046 1178
 1363 1647 1708 1722
 2339 2367 2377 2512
 2672 4170 4245 4256
 4264 4342 4354 4459
 4800 4818 4864 5122
 5139 5175 5760 5984

