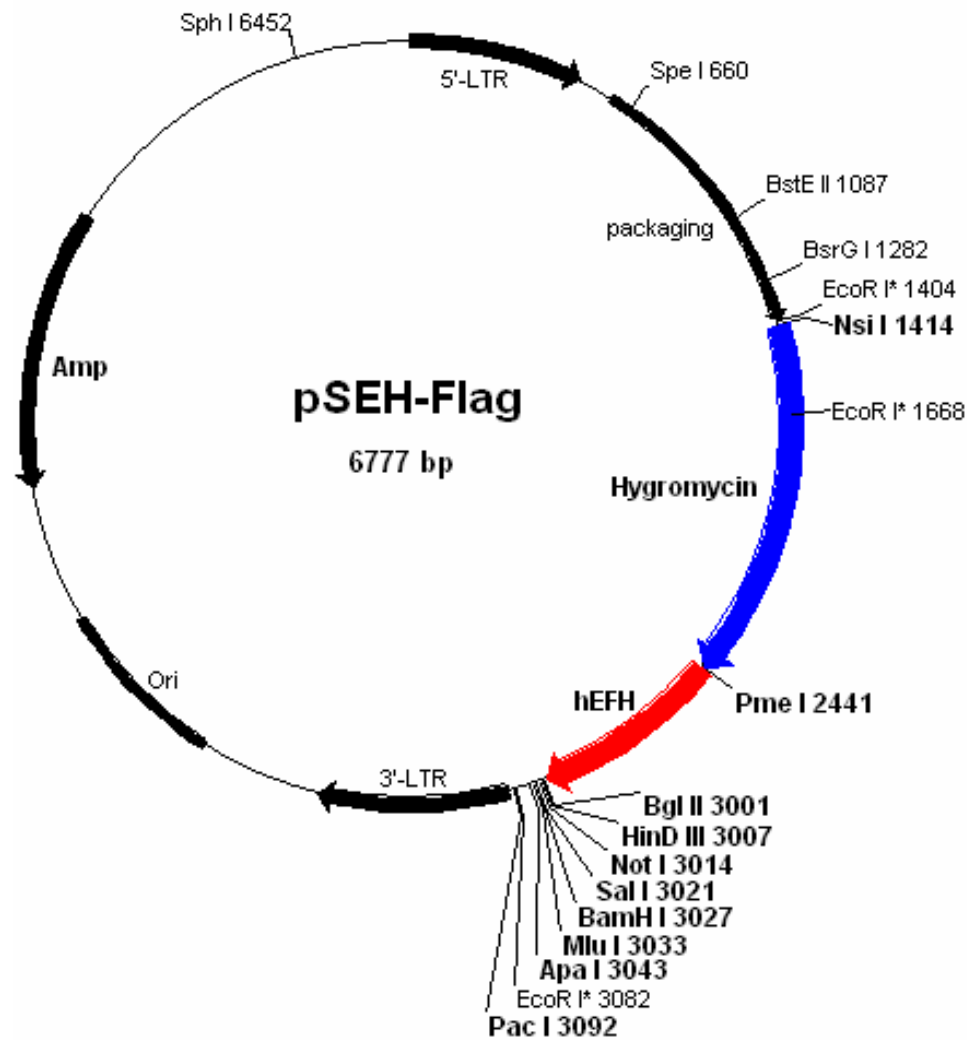


Vector: pSEH-Flag

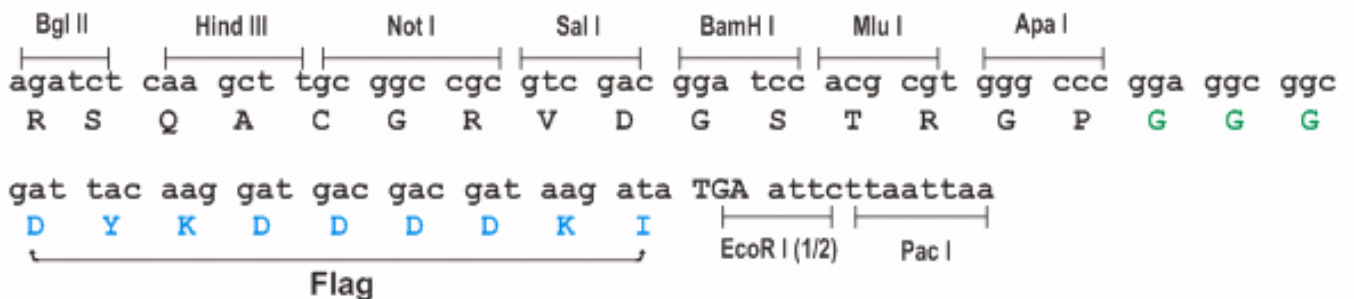
Antibiotic Selection: Amp

Creator(s): Hong Yin & Xiaoji Luo, Molecular Oncology Lab of The University of Chicago

Date of Construction: Feb, 2006



Linker Sequence



pSEH-Flag (human EF1a/HLTV hybrid promoter) Full-Length Sequence

TGAAAGACC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGGACACAGACGACAGCAGATAATGGGCAACAGCAGTAACTCTGTGGTAAGCAGTTCCCTCCCGGTCAGGGCCAAAGAACAGATGGTCCCAGATGCGGTCCCGC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTCCCAAGGACCTGAAATGACCTTGTGCCATTATTGAACTAACCAATCAGTTCGCTTCTCGCTTCT
 GTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATATCCCAAT
 AAAGCCTCTTG CTGTTTGCAT CCGAATCGTG GACTCCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCAATTTGGAG
 GTTCCACCAG GATTTGGAGACCCTGCCCA GGGACCACCGACCCCGCCG CGGGAGGTA GCTGGCCAGC GGTGTTTCGTGTCTGTCTC TGCTTTGTG
 CGTGTGTTGCGCGCATCTAATGTTTGGCCTGCGCTGTGTACTAGTTAGTAACTAGCTCTGTATCTGGCGGACCCGTTGGAACTGACGAGTTCTGAACACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTT
 CTGGTAGGAGACGAGAACC AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTCGGTT TGGAAACCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA
 GCATCGTTCT GTGTTGTCT TGTCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTACCTTAGGTCAGT
 GAAAGATGTCGAGCGGATCG CTCACAACA GTCCGTAGAT GTCAAGAAGAGACGTTGGGT TACCTTCTGC TCTGCAGAAAT GGCCAACTTTAAGTCGGA
 TGGCCGCGAGACGGCACCT TAACCGAGAC CTCATCACCC AGGTTAAGAT CAAGGTCTTT TCACTGGCCCGCATGGACA CCCAGACCAGGTCCCTACA
 TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCGTCTCT
 CCCCTTGAACCTCTCGTTCGACCCCGCTCGATCCTCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCatgcatACCATGGCATGAAAAAGCC
 TGAACTCACCGGACGCTGTGAGAAAGTTCTGATCGAAAAGTTTCGACAGCGCTCCGACCTGATGCAGCTCTCGAGGGCGAAGAATCTCGTGGCTTTACGTTCC
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 AGGCATCCGAGCTTGCAGGATCGCCGCGCTCCGGCGTATATCTCCGATCGCATTTGCTTTCGACCAACTTATCAGAGCTTGGTTGACGGCAATTTGCATGATGAG
 CTTGGGCGCAGGTCGATGCGACCAACTGTCGATCCGAGCCGGACTGTCGGCGGTACACAAATCCGCCGCAAGAGCGCGCGCTGGACCCGATGGCTGTGT
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 CCCCAGAAAGTTGGGGGAGGGGTTCGCAATTGAACCGGTGCCTAGAGAAGGTGGCGCGGGTAAACTGGGAAGTGATGTCGTACTGGCTCCGCTTTTCC
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 cgt cga cgg atc cA CGC GT GGGCCC gga ggc ggc gat tac aag gat gac gac gat aag ata TGA attc ttaattaa
 CGATAAAATAAAGATTTTATTAGTCTCCAGAAAAGGGGGAATGAAAGACCCACCTGTAGTTTGGCAAGCTAGCTTAAGTAAACGCATTTTGAAGGCATG
 GAAAATACATAAAGTGAAGATAGAGAAGTTCAGATCAAGTTAGGAACAGAGAGACAGCAGAGAATGGGCCAAACAGGATATCTGTGTTAGGATTCCTGCCCGG
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 CCCTGTTTTGAATCCACATACTCCAATACTCTGAAATAGTTTATTATGGACAGCGCAGAAGAGCTGGGGAGAATTAATTCGTAATCATGGTCAATGCTGTTTCC
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 CGTTGCGCTC ACTGCCGCT TCCAGTCCGGAACCTGTC GTGCGACTGCATTAAGAA TCGGCCAACG CGCGGGGAGA GCGCGTTTTCGCTATTGGGCG
 CTCTTCGCT TCTCTGCTCA CTGACTCGTGCCTCGTGC GTTCGGTTCGCGGATGGGT ACCTAGCTCAC TCAAAGCGGA TAATACGGTTATCCACAGAA
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 CGCTCTCTCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCTTTCTCCCTTCGGG AAGCGTGGGCTTTCTCATAG CTCAAGCTGTAGGATCTC
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 ACCCGGTAAGACACGACTTA TCGCCACTGGCAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCTTGAAGTGGTG
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 CAAACCACCGCTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTACGCGCAAAAA AAAGGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGT
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 GGAAGCTTA GTAAGTAGTT CGCCAGTTAATAGTTTGGCG AACGTTGTTGCCATGTGACT AGGCATCGTG GTGTCACGCT CGTGGTTGGTATGGCTTCA
 TTCAGCTCCGGTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAAA GCGGTTAGCTCCTTCGCTCC TCCGATCGTTGTGAGAAGTA
 AGTTGGCCG AGTGTATCA CTCATGGTTATGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGTAAGATGCTTT TCTGTGACTGGTGGTACTC
 AACCAGTCA TTTGAGAAAT AGTGTATGCG GCGACCGAGT TGCTCTTCCCGCGCTCAAT ACCGGATAAT ACCGCGCCACATGACGAACTTTAAAAGT
 CTCATCATTTGGAAAAGCTT TTCGGGGCAAAACTCTCAA GGATCTTACC GCTGTTGAGA TCCAGTTCGATGTAACCCAC TCGTGACCC AACTGACTCTT
 CAGCATCTTTTACTTTTACC AGCGTTTCTGGGTGAGCAAA AACAGGAAG CAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGGAATGTTGAATACT
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 GTCTCGCGC TTTCCGTGAT GACGGTGAACCTCTGACA CATGACGCT CCGGACAGCG TCACAGCTTG TCTGTAAGCGGATCCGCGGACGACGCAAGC
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 AATGGTGCAT CAAAGGAGAT GCGCCCAACAGTCCCGCG CCACGGGGCTGCCACCATA CCCAGCCGA AACAAGCGCT CATGAGCCCGAAGGTGCGGAG
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 TAAAAGATTT TATTAGTCT CCAGAAAAG GGGGAA

Unique enzymes in pSEH-Flag:

Spe I	A ¹ CTAG,T	660	Rsr II	CG ¹ GWC,CG	1833
BstE II	G ¹ TNAC,C	1087	Pme I	CTTT AAAC	2441
BsrG I	T ¹ TAC,A	1282	Mun I	C ¹ AATT,G	2523
Nsi I	A,TGCA ¹ T	1414	Age I	A ¹ CCGG,T	2530
BspM I	ACCTGC 10/14	1738	Bsg I	GTGCAG 22/20	2648
			Clal I	AT ¹ CG,AT	2990
			Bgl II	A ¹ GATC,T	3001
			Hind III	A ¹ AGCT,T	3007
			Not I	GC ¹ GGCC,GC	3014

Sal I G`TCGA,C 3021
 Acc I GT`MK,AC 3022
 BamH I G`GATC,C 3027
 Mlu I A`CGCG,T 3033
 Bsp120 I G`GGCC,C 3039
 Apa I G,GGCC`C 3043
 Pac I TTA,AT`TAA 3092
 Sph I G,CATG`C 6452
 Number of enzymes = 22

Bgl I (2) 4912 5247 6682
 Bgl II (1) 5177 6295
 Bpm I (5) 3001 2147 3107 5127
 2093 6745
 Bsa I (7) 476 530 1149 2833
 3595 3616 5118
 BsaH I (11) 742 1398 1449 2417
 2981 5594 5976 6280
 6463 6577 6598
 BsaJ I (36) 161 240 250 397
 461 497 546 547
 694 733 734 746
 747 1167 1236 1245
 1265 1266 1417 1777
 1978 2133 2202 2600
 2864 2995 3302 3381
 3391 3538 3601 3903
 4324 6398 6476 6482
 BsaW I (8) 1646 2183 2319 2455
 2530 4370 4517 5348
 BseR I (4) 464 1293 1332 3604
 Bsg I (1) 2648
 BsiE I (13) 592 727 1633 1768
 1789 1798 2368 3017
 4080 4504 5427 5576
 6323
 BsiHKA I (8) 338 1709 2011 3479
 4482 5643 5728 6225
 BsmA I (22) 107 475 531 609
 734 832 949 1073
 1132 1150 1328 1492
 2834 3124 3247 3594
 3615 5119 5893 6046
 6090 6762
 BsmB I (8) 733 831 1072 1131
 1329 1493 6047 6089
 BsmF I (11) 172 185 564 729
 764 1205 2342 2479
 3313 3326 6458
 BsoF I (46) 727 901 917 920
 925 928 1133 1503
 1580 1633 1761 1792
 1795 2051 2154 2202
 2205 2281 2365 2449
 2669 2728 2743 2774
 3014 3017 3050 3989
 4070 4088 4091 4209
 4364 4507 4572 4575
 4781 5109 5448 5475
 5570 5799 6086 6195
 6299 6372
 Bsp120 I (1) 3039
 BspH I (4) 4884 5892 5997 6521
 BspM I (1) 1738
 BspM II (3) 1646 2183 2319 1910
 Bsr I (18) 374 1030 1058 3515
 2075 2565 2586 4698
 3965 4571 4584 5532
 5104 5222 5265 5532
 5704 6410
 BsrB I (6) 1042 1816 2174 3856
 4097 5898
 BsrD I (2) 5118 5292
 BsrG I (1) 1282
 BssH II (4) 317 368 3458 3509
 BssS I (5) 1525 2004 4337 5721
 6028
 BstE II (1) 1087
 BstN I (16) 241 548 735 748
 1169 1194 1217 1237
 1267 3382 3904 4192
 4313 4326 6399 6676
 BstU I (34) 317 319 370 903
 905 1135 1446 1635
 1770 1881 1947 2013
 2162 2204 2364 2552
 2721 2766 2997 3019
 3035 3458 3460 3511
 4011 4013 4211 4792
 5122 5615 5947 6047
 6049 6152
 BstY I (9) 2963 3001 3027 4805
 4816 4902 4914 5682
 5699
 Bsu36 I (3) 781 1018 2737
 Cac8 I (40) 28 32 319 370
 582 586 631 650
 1199 1750 1951 2011
 2191 2354 2690 2704
 2725 2888 2916 3011
 3167 3171 3460 3511
 3957 3986 4095 4181
 4218 4778 5169 6182
 6330 6350 6354 6450
 6491 6539 6581 6611
 Cfr10 I (9) 629 1763 2530 2754
 2886 2977 5137 6600
 6609
 Cla I (1) 2990
 Csp6 I (10) 402 658 1283 2341
 2394 2580 3543 5536
 6212 6723

The following enzymes do not cut in pSEH-Flag:

Avr II Bbs I Bbv II Bcl I Blp I
 BsaA I BsaB I BsiC I BsiW I Bsm I
 Bsp1286 I Bst1107 I BstB I BstX I Eco72 I
 Esp I Fse I Hpa I Nru I PaeR7 I
 PflM I Pml I Sfi I SnaB I Spl I
 Srf I Stu I Xca I Xcm I Xho I

pSEH-Flag: sites sorted by name:

Aat II (3) 745 1452 5979
 Acc I (1) 3022
 Acc65 I (2) 401 3542
 Aci I (84) 197 203 566 588
 688 727 860 901
 1042 1133 1199 1298
 1317 1355 1444 1568
 1633 1700 1750 1770
 1794 1816 1836 2013
 2051 2061 2174 2202
 2204 2225 2354 2364
 2552 2589 2669 2725
 2728 2743 2774 2781
 2808 2995 2997 3013
 3017 3049 3338 3344
 3640 3854 3957 4013
 4023 4047 4090 4097
 4118 4209 4237 4364
 4383 4504 4614 4749
 4758 5120 5211 5402
 5448 5569 5613 5690
 5799 5898 5945 6119
 6158 6168 6194 6232
 6245 6271 6328 6587
 Afl II (3) 35 1006 3174
 Afl III (2) 3033 4164
 Age I (1) 2530
 Aha II (11) 742 1398 1449 2417
 2981 5594 5976 6280
 6463 6577 6598
 Ahd I (4) 1020 3587 3633 5057
 Alu I (38) 30 34 336 580
 668 676 1505 1537
 1579 1964 2189 2254
 2283 2682 2688 2692
 2830 2971 3009 3169
 3173 3477 3796 3829
 3924 3988 4106 4332
 4422 4468 4725 5246
 5346 5409 6088 6107
 6352 6708
 Alw I (18) 453 1051 1357 1885
 2203 2312 2959 2987
 3023 3034 4726 4812
 4812 4909 4910 5374
 5689 5695
 AlwN I (2) 3298 4580
 Apa I (1) 3043
 ApaL I (5) 1705 2007 4478 5724
 6221
 Apo I (4) 872 1404 1668 3082
 Asc I (2) 368 3509
 Ase I (4) 3807 3935 3994 5229
 Asp718 (2) 401 3542
 Ava I (7) 331 397 498 2497
 2599 3472 3538
 Ava II (14) 186 199 254 551
 690 1219 1833 2374
 3327 3340 3395 5195
 5417 6672
 BamH I (1) 3027
 Ban I (17) 244 401 1142 1397
 1999 2458 2533 2789
 2980 3385 3542 3908
 5005 6279 6462 6576
 6597
 Ban II (8) 338 351 2704 3043
 3479 3492 6529 6543
 Bbe I (6) 1401 2984 6283 6466
 6580 6601
 Bbv I (12) 931 939 1514 1772
 2165 2292 2460 4583
 4586 4792 5486 6097
 Bcn I (18) 164 399 400 571
 724 2212 2328 2845
 3044 3305 3540 3541
 4545 5241 5592 6093
 6128 6479
 Bfa I (15) 31 219 661 673
 1394 2538 2689 2815
 2877 3170 3360 4659

Dde I	(23)	75	167	208	476	5187	5280	5617	5949
		781	1018	1290	1803	6049	6152	6282	6303
		2737	2831	2882	3005	6436	6465	6519	6579
		3214	3308	3349	3618	6600			
		3689	4439	4848	5014				
		5554	5980	6215		HinC II (2)	2261	3023	
Dpn I	(32)	94	459	1046	1178	Hind II (2)	2261	3023	
		1363	1470	1603	1788	HinD III (1)	3007		
		1801	1891	2198	2318	Hinf I (19)	442	450	791
		2965	2993	3003	3029		1521	1643	1843
		3234	4732	4807	4818		2761	2880	3699
		4826	4904	4916	5021		3742	3999	4064
		5362	5380	5426	5684		4535	5052	6690
		5701	5737	6322	6546	HinI I (11)	742	1398	1449
DpnII	(32)	92	457	1044	1176		2981	5594	5976
		1361	1468	1601	1786	HinP I (49)	6463	6577	6598
		1799	1889	2196	2316		317	319	368
		2963	2991	3001	3027		646	903	922
		3232	4730	4805	4816		1582	1635	1879
		4824	4902	4914	5019		2162	2289	2362
		5360	5378	5424	5682		2478	2550	2721
		5699	5735	6320	6544		2953	2981	3458
Dra I	(5)	2441	2826	4923	4942		3509	3511	3786
		5634					4011	4039	4072
		1713	2006				4409	4509	4683
Dra III	(2)	1929	2310	4272	6141		5185	5278	5615
Drd I	(4)	694	1417	1777	2133		6047	6150	6280
Dsa I	(7)	2202	2995	6482			6434	6463	6517
		582	724	1109	1130	Hpa II (39)	6598	163	398
Eae I	(13)	1630	1795	2048	2365		723	1401	1647
		3014	4003	5445	6479		1997	2184	2210
		6611					2326	2456	2531
Eag I	(5)	724	1630	1795	2365		2843	2855	2887
		3014					3043	3304	3539
Ear I	(6)	1070	1311	3786	4048		4371	4518	4544
		5852	6340				5138	5172	5239
Eco47 III	(3)	923	2452	6518			5591	6092	6126
Eco57 I	(4)	2703	4711	5725	6729		6601	6610	6625
EcoN I	(4)	784	1392	2541	2736	Hph I (13)	1157	1183	1434
EcoO109 I	(5)	254	1219	3395	6033		5128	5542	5750
		6487					6067	6076	6569
EcoR I	(3)	1404	1668	3082			6695		
EcoR II	(16)	239	546	733	746	Kas I (6)	1397	2980	6279
		1167	1192	1215	1235		6576	6597	
		1265	3380	3902	4190	Kpn I (2)	405	3546	
		4311	4324	6397	6674	Mae I (15)	31	219	661
EcoR V	(3)	140	3280	6665			1394	2538	2689
Ehe I	(6)	1399	2982	6281	6464		2877	3170	3360
		6578	6599				4912	5247	6682
Fnu4H I	(46)	727	901	917	920	Mae II (12)	742	1081	1122
		925	928	1133	1503		1719	2645	2928
		1580	1633	1761	1792		5283	5656	5976
		1795	2051	2154	2202	Mae III (21)	39	994	1022
		2205	2281	2365	2449		1231	1715	2957
		2669	2728	2743	2774		3178	3656	4520
		3014	3017	3050	3989		4699	4982	5313
		4070	4088	4091	4209		5524	5712	6100
		4364	4507	4572	4575		6411		
		4781	5109	5448	5475	Mbo I (32)	92	457	1044
		5570	5799	6086	6195		1361	1468	1601
		6299	6372				1799	1889	2196
Fok I	(13)	423	1140	1300	1794		2963	2991	3001
		2167	2733	3075	3563		3232	4730	4805
		5023	5204	5491	6134		4824	4902	4914
		6378					5360	5378	5424
Fsp I	(2)	5279	6302				5699	5735	6320
Gdi II	(16)	723	725	1129	1629	Mbo II (14)	1086	1299	1529
		1631	1794	1796	2047		2115	3802	4036
		2364	2366	3013	3015		4898	5653	5731
		4004	5444	6480	6612		6328	6540	
Gsu I	(5)	2092	2146	3108	5128	Mlu I (1)	3033		
		6746				Mme I (8)	829	1106	1515
Hae I	(6)	584	1111	1776	4179		3603	3655	4378
		4190	4642				167	216	368
Hae II	(12)	925	1401	2454	2861	Mnl I (59)	432	460	484
		2984	4042	4412	6283		510	566	776
		6466	6520	6580	6601		1168	1271	1304
Hae III	(37)	129	173	584	726		1313	1319	1349
		762	774	987	1111		1367	1374	1390
		1132	1197	1632	1776		1542	1766	1973
		1797	1825	1977	2050		2072	2099	2122
		2132	2367	2742	2847		2506	2595	2690
		3016	3041	3269	3314		2786	2802	3039
		4005	4179	4190	4208		3509	3528	3573
		4642	5100	5180	5447		3624	3684	4013
		6034	6332	6481	6489		4272	4345	4596
		6613					5077	5223	5429
Hga I	(16)	381	642	895	1476		6082	6342	6626
		1928	2167	2312	2424	Msc I (2)	584	1111	
		2794	3009	3522	4274	Mse I (26)	36	1007	1119
		4852	5584	6142	6611		1173	2440	2825
HgiA I	(8)	338	1709	2011	3479		3092	3175	3709
		4482	5643	5728	6225		3935	3994	4870
HgiE II	(2)	4743	6223				4927	4941	4994
Hha I	(49)	319	321	370	372		5268	5633	6005
		648	905	924	1400		6383	6653	
		1584	1637	1881	1949	Msl I (3)	1422	5309	5468
		2164	2291	2364	2453	Msp I (39)	163	398	569
		2480	2552	2723	2860		723	1401	1647
		2955	2983	3460	3462		1997	2184	2210
		3511	3513	3788	3948		2326	2456	2531
		4013	4041	4074	4344		2843	2855	2887
		4411	4511	4685	4794		3043	3304	3539

		4371	4518	4544	4734			1265	1266	1417	1777
		5138	5172	5239	5349			1978	2133	2202	2600
		5591	6092	6126	6478			2864	2995	3302	3381
		6601	6610	6625				3391	3538	3601	3903
MspAl I	(14)	588	1752	2061	2204			4324	6398	6476	6482
		2682	2997	3640	3988	SfaN I	(25)	185	444	641	938
		4506	4751	5692	6158			1490	1634	1701	1773
		6352	6708					1958	2188	2268	2290
Mun I	(1)	2523						2714	3326	3584	4260
Nae I	(3)	631	2888	6611				5312	5505	5752	6113
Nar I	(6)	1398	2981	6280	6463			6205	6243	6281	6597
		6577	6598					6609			
Nci I	(18)	163	398	399	570	Sfc I	(10)	15	917	925	1101
		723	2211	2327	2844			1758	3154	4429	4620
		3043	3304	3539	3540			5298	6716		
		4544	5240	5591	6092						
		6127	6478			Sma I	(2)	399	3540		
Nco I	(2)	1417	1777			Spe I	(1)	660			
Nde I	(2)	1875	6228			Sph I	(1)	6452			
NgoM I	(3)	629	2886	6609		Ssp I	(2)	3707	5861		
Nhe I	(3)	30	2688	3169		Sty I	(8)	250	461	1245	1417
Nla III	(23)	62	1205	1412	1421			1777	2864	3391	3601
		1427	1781	1864	1899	Taq I	(19)	794	1038	1349	1360
		2448	3201	3655	3822			1456	1471	1480	1540
		4168	4888	5379	5389			1957	2170	2272	2297
		5467	5503	5896	6001			2695	2837	2990	3022
		6085	6452	6525		Tfi I	(9)	3702	4264	5708	
Nla IV	(41)	188	201	246	403			442	802	1521	1643
		521	552	692	761			1843	2094	3742	3999
		893	1144	1221	1399			4139			
		2001	2024	2208	2324	Tsp45 I	(8)	1022	1231	1715	2973
		2460	2535	2587	2791			5313	5524	6100	6411
		2870	2982	3029	3041	Tth111 I	(6)	390	811	1217	1485
		3329	3342	3387	3544			1929	3531		
		3910	4196	4235	5007	Tth111 II	(10)	146	422	613	632
		5101	5142	5353	5943			1645	2904	3286	4753
		6281	6464	6488	6578			4762	4792		
		6599				Vsp I	(4)	3807	3935	3994	5229
Not I	(1)	3014				Xba I	(2)	218	3359		
Nsi I	(1)	1414				Xho II	(9)	2963	3001	3027	4805
Nsp7524 I	(4)	2444	4164	6081	6448			4816	4902	4914	5682
NspB II	(14)	588	1752	2061	2204			5699			
		2682	2997	3640	3988	Xma I	(2)	397	3538		
		4506	4751	5692	6158	Xma III	(5)	724	1630	1795	2365
		6352	6708					3014			
NspH I	(4)	2448	4168	6085	6452	Xmn I	(3)	3770	3808	5656	
Pac I	(1)	3092									
Pal I	(37)	129	173	584	726						
		762	774	987	1111						
		1132	1197	1632	1776						
		1797	1825	1977	2050						
		2132	2367	2742	2847						
		3016	3041	3269	3314						
		4005	4179	4190	4208						
		4642	5100	5180	5447						
		6034	6332	6481	6489						
		6613									
Ple I	(4)	799	2769	3707	4543						
Pme I	(1)	2441									
PpuM I	(3)	254	1219	3395							
Psp1406 I	(3)	2645	5283	5656							
PspA I	(2)	397	3538								
Pst I	(4)	921	929	1105	1762						
Pvu I	(3)	1789	5427	6323							
Pvu II	(4)	2682	3988	6352	6708						
Rsa I	(10)	403	659	1284	2342						
		2395	2581	3544	5537						
		6213	6724								
Rsr II	(1)	1833									
Sac I	(2)	338	3479								
Sac II	(2)	2205	2998								
Sal I	(1)	3021									
Sap I	(2)	3786	4048								
Sau3A I	(32)	92	457	1044	1176						
		1361	1468	1601	1786						
		1799	1889	2196	2316						
		2963	2991	3001	3027						
		3232	4730	4805	4816						
		4824	4902	4914	5019						
		5360	5378	5424	5682						
		5699	5735	6320	6544						
Sau96 I	(32)	127	171	186	199						
		254	551	690	760						
		773	985	1196	1219						
		1824	1833	1975	2374						
		2845	3039	3040	3267						
		3312	3327	3340	3395						
		5099	5178	5195	5417						
		6033	6330	6487	6672						
Sca I	(2)	2395	5537								
ScrF I	(34)	163	241	398	399						
		548	570	723	735						
		748	1169	1194	1217						
		1237	1267	2211	2327						
		2844	3043	3304	3382						
		3539	3540	3904	4192						
		4313	4326	4544	5240						
		5591	6092	6127	6399						
		6478	6676								
Sec I	(36)	161	240	250	397						
		461	497	546	547						
		694	733	734	746						
		747	1167	1236	1245						

Site usage in pSEH-Flag:

Aat II	G,ACGT`C	3	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	84
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	11
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	38
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
Apa I	G,GC`C`C	1	ApaL I	G`TGCA,C	5
Apo I	R`AATT,Y	4	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	7	Ava II	G`GWC,C	14
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	17	Ban II	G,RCGY`C	8
Bbe I	G,CGC`C	6	Bbs I	GAAGAC 8/12	-
Bbv I	GCAGC 13/17	12	Bbv II	GAAGAC 7/11	-
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	18
Bfa I	C`TA,G	15	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	7
Bsa I	YAC GTR	-	BsaB I	GATNN NNATC	-
BsaH I	GR`CG,YC	11	BsaJ I	C`C`NNG,G	36
BsaW I	W`CCGG,W	8	BseI I	GAGGAG 16/14	4
Bsg I	GTCCAG 22/20	1	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	13	BsiHKA I	G,WGCW`C	8
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	8
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	46
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	1
BspM II	T`CCGG,A	3	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	6	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	-	BstE II	G`GTINAC,C	1
BstN I	CC`W,GG	16	BstU I	CG CG	34
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	40
Cfr10 I	R`CCGG,Y	9	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	10	Dde I	C`TNA,G	23
Dpn I	GA TC	32	DpnII	`GATC,	32
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	2
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	7
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	5
Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-
EcoN I	CCTTN`N,NNAGG	4	EcoO109 I	RG`GNC,CY	5
EcoR I	G`AATT,C	3	EcoR II	`CCWGG,	16
EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	46
Fok I	GGATG 14/18	13	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	16
Gau I	CTGGAG 21/19	5	Hae I	WGG CCW	6
Hae II	R,CGC`Y	12	Hae III	GG CC	37
Hga I	GACGC 9/14	16	HgiA I	G,WGCW`C	8
HgiE II	ACNNNNNNNGGT	-1/132	Hha I	G,CG`C	49

HinC II	GTY RAC	2	Hind II	GTY RAC	2	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	19	Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
HinI I	GR`CG,YC	11	HinP I	G`CG,C	49	Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Hpa I	GTT AAC	-	Hpa II	C`CG,G	39	Pvu II	CAG CTG	4	Rsa I	GT AC	10
Hph I	GGTGA 12/11	13	Kas I	G`GCGC,C	6	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	15	Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
Mae II	A`CG,T	12	Mae III	`GTNAC,	21	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	32
Mbo I	`GATC,	32	Mbo II	GAAGA 12/11	14	Sau96 I	G`GNC,C	32	Sca I	AGT ACT	2
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	8	ScrF I	CC`N,GG	34	Sec I	C`CNNG,G	36
Mnl I	CCTC 10/10	59	Msc I	TGG CCA	2	SfaN I	GCATC 9/13	25	Sfc I	C`TRYA,G	10
Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	3	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
Msp I	C`CG,G	39	MspAl I	CMG CKG	14	SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Mun I	C`AATT,G	1	Nae I	GCC GGC	3	Sph I	G,CATG`C	1	SpI I	C`GTAC,G	-
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	18	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2	Stu I	AGG CCT	-	Sty I	C`CWWG,G	8
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	3	Taq I	T`CG,A	19	Tfi I	G`AWT,C	9
Nla III	,CATG`	23	Nla IV	GGN NCC	41	Tsp45 I	`GTSAC,	8	Tth111 I	GACN`N,NGTC	6
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-	Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	4
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	4	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
NspB II	CMG CKG	14	NspH I	R,CATG`Y	4	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-	Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	2
Pal I	GG CC	37	PflM I	CCAN,NNN`NTGG	-	Xma III	C`GGCC,G	5	Xmn I	GAANN NNTTC	3
Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1						