

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

TGAAAGACC CACCTGTAGG TTTGGCAAGC TAGCTTAAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAAGCAGTTCCCTCCCGGTCAGGGCCAAAGACAGATGGTCCCAGATGCGGTCCC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTCCCAAGGACCTGAAATGACCTTGTGCCCTATTGGAACTAACCAATCGATTCGCTTCTCGCTTCT
 GTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATTTCCCAAT
 AAAGCCTCTTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG
 GTTCCACCAG GATTTGGAGACCCTGCCCA GGGACCACCGACCCCGCCG CGGGAGGTAA GCTGGCCAGC GGTGTTTCTGTCTGTCTC TGTCTTTGTG
 CGTGTTTGTGCCGGCATCTAATGTTTGGCCTGCGCTCTGTAAGTCTAGTCTAGTAACTAGCTCTGTATCTGGCGGACCCGTTGGTGAAGTCTGTAACACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT
 CTGGTAGGACGACGAAACCT AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTCGGTT TGGAAACCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA
 GCATCGTTCT GTGTTGTCT TGTCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTGCACCTTAGGTCAGT
 GAAAGATGTCGAGCCGATCG CTCACAACCA GTCGGTAGAT GTCAAGAAAGAGACGTTGGGT TACTTCTGCT TCTGCAGAAAT GGCCAAACCTTAAACCGCGGA
 TGGCCCGGAGACGGCACCTT TAACCGAGAC CTCATCACCC AGGTTAAGAT CAAGGTCTTT TCACCTGGCCCGCATGGACA CCCAGACCAGGTCCCCTACA
 TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT
 CCCCTTGAACCTCTCGTTCGACCCCGCTCGATCTCCCTTTATCCAGCCCTCACTCTCTCTAGGCGCCGGAATTCaccatgggcATGATTGAACAAGATGG
 ATTGCAGCGAGTTCTCCGCGCTTCCGAGGCTATTCGGTGTAGCTAGCTGACCTCAACAGACAATCGGCTGCTCTGATGCGCCGCTGCTGATGCGGCTGCTGAGC
 CAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCGGTGCCTGAAATGAACTGCAGGACGAGGCGAGCGCGGCTATCGTGGCTGGCCACGACGGGCTTCTT
 GCGCAGCTGTGCTCGACGTTGTCAAGCGGGAAGGGACTGGTGTCTATTGGCGCAAGTGCCGGGCGAGGATCTCCTGTCTCATCTACCTTGTCTCTGCGGAGAA
 AGTATCCATCATGGCTGATGCAATCGCGCGGCTGCATACGCTGTATCCGGTACCTGCCATTCGACCACCAAGCGAAACATCGCATCGAGCGACGACTACTCGG
 ATGGAAGCCGCTTGTGCTGATCAGGATGATCTGGACGAGAGCATCAGGGCTCGCGCCAGGCAACTGTTCGCCAGGCTCAAGCGCGCATCCGACCGCGGAGG
 ATCTCGTCTGACCCATGGCGATGCTGCTTCCGCAATATCATGGTGGAAAATGGCCGTTTTTCTGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTA
 TCAGGACATAGCGTTGGCTACCCGATGATTTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCCCTGCTGTTTACGGTATCGCCGCTCCCGATTCGCGACGC
 ATCGCCCTTATCGCCTTCTTACGAGTTCCTTCTGAGgtttaaacatgacgCGTCCGCTGCGCCGTCAGTGGGCGAGAGCGCACATCGCCACAGTCCCAGAGAGTT
 GGGGGGAGGTTCCGCAATTTGAACCGTGTCCAGGAGTGGCGGGGTAACCTGGGAAGATGTGCTGTACTGGCTCCGCTTTTCCGAGGGTGGGGA
 GAACCGTATATAAGTGCAGTGTGCGCCGTGAACGTTCTTTTTCGCAACGGGTTTCCCGCCAGAACACAGCTGAAGCTAGCTTCGAGGGGCTCGCATCTCTCTTCA
 CGCGCCCGCCGCTACCTGAGGCGCCATCCACGCCGTTGAGTGTGCTTCTGCGCCCTCCGCGCTGTGGTGCCTCCTGAACCTGCGTCCGCGCTTAGTAAGTT
 TAAAGCTCAGGTCGAGACCGGCTTTGTCCGCGCTCCCTGGAGCTACCTAGACTACCGCGGCTCTCCACGCTTTGCTGACCCGCTGTCTCAACTCTACGTT
 CTTTGTCTTCTGTTTCTGTTCTGCTGCGCGTTACAGACTCCAAGCTGACCGCGCTCAT atcgat cgcgag AGAtcgaagtt cggc cgc cgt cga cgg
 atccACGCGTGGGCCGgagggcggcattacaaggtatgacgagatgataAGAttc ttaattaaCGATAAAAATAAAAGATTATTTAGTCTCCGAAAAAAGG
 GGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAAGTAAAGCCATTTTGCAGGCATGGAAAATACATAACTGAGAAATAGAGAAGTTCAGATCAAGG
 TTAGGAACAGAGAGACGAGAATATGGGCCAAACAGGATATCTGTGGTAAAGCAGTTCCCTGCCCGGCTCAGGGCCAAAGAACAGATGGTCCCAGATGCTCCGCG
 CCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTGACCAAGGACCTGAAATGACCTGTGCTTATTTGAACCAACCAATCAGTTCCGCTTCTCGTCTC
 TGTTCGCGCCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGCGCGCCAGTCTCCCGATAGACTGCGTCCGATAGACTGCGTCCGCGGATTCGTA
 TAAACCTCTTGCAGTTGCATCCGACTTGTGCTGCTGTTCCCTGGGAGGCTCCTCTGAGTATTGACTACCCGTCAGCGGGGCTTTTTCATGGGTAACAGT
 TTCCTGAAAGTTGGAGAACAACATTTCTGAGGTTAGGAGTCAATATAAGTAACTGACTCAATTAGCCACTGTTTGAATCCACATCTCAATACTCCTGAAAT
 AGTTCATTATGGACAGCGCAGAGAGCTGGGAGAAATTAATTCGTAATCATGGTCAATAGCTGTTTCTGTTGAAATGTTTATCCGCTCACAATTCACACAACAT
 ACGAGCCGGAACCATAAAGTGAATAAGCTTGGGGTCCCTAATGAGTGAAGTAACTCATATTAATTG CGTTCGCTCACTCCCGCTTTCCAGTCCGGAAACGCTGTC
 GTGCCAGTGCATTAATGAA TCGGCCAACG CGCGGGGAGA GCGGTTTTCGCTATTGGGCG CTCTCCGCT TCCTCGCTCA CTGACTCGTGCCTCGGTC
 GTTCCGCTGCGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAAATCCGTTATCCACAGAA TCAGGGGATAACGCAGGAAA GAACATGTGAGCAAAAGGCC
 AGCAAAAGGC CAGAACCGT AAAAAGCCCGCTTGTCTGGC GTTTTCCATAGGCTCCGCC CCCCTGACCA GCATCAGAAA AATCGACGCTCAAGTACAGAG
 GTGGCGAAAC CCGACAGGAT TATAAAGATACACAGCCGTTTT CCCCCTGGAAGCTCCCTCGT GCGCTCCTCT GTTCCGACCC TGCCGCTTACCAGGATACCTG
 TCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAAC
 CCCC CGTTCAGCCC GACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTTAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAAACAGG
 ATTACGACGCGAGGATATGAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGC
 CAGT TACTTCCGAAAAAGGATTG GTAGCTCTTGTATCCGCAACAAACCCGCTGAGTACGCGTGGTGTGTTTTTTTGTGAAGCAGCATTAACCGCAGAAA
 AAAGGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGT CTGACGCTCA GTGGAACGAA AACTCACGTTAAGGGATTTT GGTCAATGAGATTATCAAAAA
 GGATCTTCC CAGATCCCTT TTAATTAATAAATGAAGTTT TAAATCAATCTAAGATATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAATGCTTAATCAG
 TGAGGCACT ATCTCAGCA CTGTCTATTTCGTTTCACTC ATAGTTGCTGACTCCCGCT CGTGTAGATA ACTACGATA GGGAGGGCTTACCATCTGGC
 CCCAGTCTGCAATGATACC GCGAGCCACCGTCAACCGG CTCCAGATT ATCAGCAATA AACACGCGAGCCGGAAGGGC CGAGCGCAGAAGTGGTCTCTG
 CAACCTTATC CGCTCCATC CAGTCTATTAATTTGTTGCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAATAGTTTGGCG AACGTTGTTGCCATTGCTAC
 AGGCATCGT GTGTACCGT CTGCTGTTTGGTATGGCTTCA TTCAGTCCGTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCATATTTGTGCAAAAAA
 GCGGTTAGCTCCTTCGGTCC TCCGATGTTGTGAGAAGTA AGTTGGCCG AGTGTATCA CTCATGGTTATGGCAGCACT GCATAATTTCT CTACTGTCA
 TGCCATCCGTAAGATGCTTT TCTGTGACTGGTGTAGTACTC AACCAAGTCA TCTGAGAAT AGTGTATGCG GCGAGCAGT TGCCTTGGCCGCGCTCAAT
 ACGGGATAATACCGCCACATAGCAGAATTTAAAGTGTCTCATCATTTGAAAACGTTCTTCCGGGCGAAAACCTCAAGGATCTTACCCTGTTGAGATCCAGT
 TCGATGTAACCCAC TCGTGCACCC AACTGATCTTCAGCATCTTTACTTTCCACAGCGTTCCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGG
 AATAAGGGCGACACGAAATGTTGAATACTCATACTCTTCTTTTCAATATATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT
 ATTT AGAAAAATAAACAATAGGG GTTCCGCGCACATTTCCCGAAAAGTGCCACCTGACGCTCAAGAAAACCATTATATCATGACATTAACCTATAAAAAATAG
 GCGTATCACGAGGCCCTTCTGCTCGCGCTTTCGGTGTAGCGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTACAGCTTGTCTGTAAGCGGATGCC
 GGGAGCAGACAAGCCGCTCAGGCGCGCTCAGCGGGTGTGGCGGGTGTGCGGGCTGGCTTAACTATCGCGCATCAGAGCAGGATTGACTGAGAGTGCACCCATATGC
 GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTTCCGCTTACAGGTCGCGCACTGTTGGGAGGGGCGATCGGTGCCGCTCTC
 GC TATTACGCCA GCTGGCGAAA GGGGATGTGCTGCAGAGCG ATTAAGTTTGGCTAACGCCAGGGTTTCCAGTCAACAGCTGTGTAACCAAGCAGCGCGCAAGG
 AATGGTGCAT GCAAGGAGAT GCGCCCAACAGTCCCCCG CCACGGGCTGCCACCATA CCCACGCCA AACAGCGCT CATGAGCCCGAAGTGGCGAG
 CCCGATCTTCCCATCGGTG ATGTCGGCGA TATAGGCGCC AGCAACCGCA CCGTGTGGCG CGGTGATGCCGCGCCAGATG CGTCCGCGCTAGAGGCGATT
 AGTCCAATTT GTTAAAGACA GGATATCAGTGGTCCAGGCT CTAGTTTTGA CTCAACAATA TCACCAGCTGAAGCCTATAG AGTACGAGCCATAGATAAAA
 TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAA

Unique enzymes in pSEN-Flag:

Spe I	A`CTAG,T	660	Bsp I	GTGCAG 22/20	2424
BstE II	G`GTNAC,C	1087	Cla I	AT`CG,AT	2766
BsrG I	T`GTAC,A	1282	Sac II	CC,GC`GG	2774
Bsp1286 I	G, DGCH`C	1850	Bgl II	A`GATC,T	2777
BsaA I	YAC GTR	1851	HinD III	A`AGCT,T	2783
Rsr II	CG`GWC,CG	2063	Not I	GC`GGCC,GC	2790
Pme I	CTTT AACC	2217	Sal I	G`TCGA,C	2797
Mun I	C`AATT,G	2299	Acc I	GT`MK,AC	2798
Age I	A`CCGG,T	2306	HinC II	GTY RAC	2799
			Hind II	GTY RAC	2799
			BamH I	G`GATC,C	2803
			Mlu I	A`CGCG,T	2809

		5330	5756	5991		Hinf I	(17)	442	450	791	802
Dpn I	(30)	94	459	1046	1178			2032	2166	2537	2656
		1363	1720	1798	1879			3475	3497	3518	3775
		1888	1966	2741	2769			3840	3915	4311	4828
		2779	2805	3010	4508			6466			
		4583	4594	4602	4680	HinI I	(10)	742	1398	1547	2757
		4692	4797	5138	5156			5370	5752	6056	6239
		5202	5460	5477	5513			6353	6374		
		6098	6322			HinP I	(50)	317	319	368	370
DpnII	(30)	92	457	1044	1176			646	903	922	1398
		1361	1718	1796	1877			1539	1547	1611	1648
		1886	1964	2739	2767			1914	1944	1946	2174
		2777	2803	3008	4506			2227	2254	2326	2497
		4581	4592	4600	4678			2634	2729	2757	3234
		4690	4795	5136	5154			3236	3285	3287	3562
		5200	5458	5475	5511			3722	3787	3815	3848
		6096	6320					4118	4185	4285	4459
Dra I	(5)	2217	2602	4699	4718			4568	4961	5054	5391
		5410						5723	5823	5926	6056
Drd I	(3)	1574	4048	5917				6077	6210	6239	6293
Dsa I	(5)	694	1411	1979	2771			6353	6374		
		6258				Hpa II	(40)	163	398	569	630
Eae I	(13)	582	724	1109	1130			723	1401	1452	1529
		1453	1627	2018	2045			1551	1579	1710	1800
		2790	3779	5221	6255			1867	2048	2232	2307
		6387						2531	2619	2631	2663
Eag I	(3)	724	1453	2790				2754	2819	3080	3315
Ear I	(8)	1070	1311	1891	2101			3658	4147	4294	4320
		3562	3824	5628	6116			4510	4914	4948	5015
Eco47 III	(3)	923	2228	6294				5125	5367	5868	5902
Eco57 I	(6)	1692	2124	2479	4487			6254	6377	6386	6401
		5501	6505			Hph I	(14)	1157	1183	1401	1726
EcoN I	(4)	784	1392	2317	2512			4677	4904	5318	5526
EcoO109 I	(5)	254	1219	3171	5809			5559	5843	5852	6345
		6263						6390	6471		
EcoR I	(2)	1404	2858			Kas I	(7)	1397	1546	2756	6055
EcoR II	(17)	239	546	733	746			6238	6352	6373	
		1167	1192	1215	1235	Kpn I	(2)	405	3322		
		1265	1932	3156	3678	Mae I	(15)	31	219	661	673
		3966	4087	4100	6173			1394	2314	2465	2591
		6450						2653	2946	3136	4435
EcoR V	(3)	140	3056	6441				4688	5023	6458	
Ehe I	(7)	1399	1548	2758	6057	Mae II	(12)	742	1081	1122	1663
		6240	6354	6375				1850	2421	2704	4643
Fnu4H I	(48)	727	901	917	920			5059	5432	5752	6194
		925	928	1133	1456	Mae III	(22)	39	994	1022	1087
		1508	1519	1609	1614			1231	1667	1973	2733
		1651	1692	1779	1782			2749	2954	3432	4296
		1785	2021	2117	2158			4359	4475	4758	5089
		2172	2225	2445	2504			5147	5300	5488	5876
		2519	2550	2790	2793			6167	6187		
		2826	3765	3846	3864	Mbo I	(30)	92	457	1044	1176
		3867	3985	4140	4283			1361	1718	1796	1877
		4348	4351	4557	4885			1886	1964	2739	2767
		5224	5251	5346	5575			2777	2803	3008	4506
		5862	5971	6075	6148			4581	4592	4600	4678
Fok I	(13)	423	1140	1300	1871			4690	4795	5136	5154
		1896	2509	2851	3339			5200	5458	5475	5511
		4799	4980	5267	5910			6096	6320		
		6154				Mbo II	(14)	1086	1299	1907	2117
Fsp I	(3)	1649	5055	6078				2199	3578	3812	4601
Gdi II	(13)	723	725	1129	1452			4674	5429	5507	5616
		1454	2017	2044	2789			6104	6316		
		2791	3780	5220	6256	Mlu I	(1)	2809			
		6388				Mme I	(6)	829	1106	3379	3431
Gsu I	(3)	2884	4904	6522				4154	4338		
Hae I	(6)	584	1111	1629	3955	Mnl I	(54)	167	216	368	387
		3966	4418					432	460	484	506
Hae II	(13)	925	1401	1550	2230			510	566	776	872
		2637	2760	3818	4188			1168	1271	1304	1310
		6059	6242	6296	6356			1313	1319	1349	1352
		6377						1367	1374	1390	1462
Hae III	(33)	129	173	584	726			1598	1955	2147	2282
		762	774	987	1111			2371	2466	2508	2562
		1132	1197	1455	1629			2578	2815	3133	3285
		2020	2047	2518	2623			3304	3349	3376	3400
		2792	2817	3045	3090			3460	3789	3838	4048
		3781	3955	3966	3984			4121	4372	4772	4853
		4418	4876	4956	5223			4999	5205	5800	5858
		5810	6108	6257	6265			6118	6402		
		6389				Msc I	(3)	584	1111	1629	
Hga I	(11)	381	642	895	2570	Mse I	(26)	36	1007	1119	1149
		2785	3298	4050	4628			1173	2216	2601	2864
		5360	5918	6387				2868	2951	3485	3583
HgiA I	(8)	338	1660	1850	3255			3711	3770	4646	4698
		4258	5419	5504	6001			4703	4717	4770	5005
HgiE II	(2)	4519	5999					5044	5409	5781	5962
Hha I	(50)	319	321	370	372			6159	6429		
		648	905	924	1400	Msl I	(4)	1416	1984	5085	5244
		1541	1549	1613	1650	Msp I	(40)	163	398	569	630
		1916	1946	1948	2176			723	1401	1452	1529
		2229	2256	2328	2499			1551	1579	1710	1800
		2636	2731	2759	3236			1867	2048	2232	2307
		3238	3287	3289	3564			2531	2619	2631	2663
		3724	3789	3817	3850			2754	2819	3080	3315
		4120	4187	4287	4461			3658	4147	4294	4320
		4570	4963	5056	5393			4510	4914	4948	5015
		5725	5825	5928	6058			5125	5367	5868	5902
		6079	6212	6241	6295			6254	6377	6386	6401
		6355	6376			MspAl I	(12)	588	1653	2458	2773
HinC II	(1)	2799						3416	3764	4282	4527
Hind II	(1)	2799						5468	5934	6128	6484
HinD III	(1)	2783				Mun I	(1)	2299			

Nae I	(4)	631	2049	2664	6387		6057	6373	6385	
Nar I	(7)	1398	1547	2757	6056	Sfc I	(10)	15	917	1101
		6239	6353	6374				1596	2930	4396
Nci I	(18)	163	398	399	570			5074	6492	
		723	1551	1711	2620	Sma I	(2)	399	3316	
		2819	3080	3315	3316	Spe I	(1)	660		
		4320	5016	5367	5868	Sph I	(2)	1952	6228	
		5903	6254			Ssp I	(2)	3483	5637	
Nco I	(2)	1411	1979			Sty I	(8)	250	461	1411
Nde I	(1)	6004						1979	2640	3377
NgoM I	(4)	629	2047	2662	6385	Taq I	(16)	794	1038	1349
Nhe I	(3)	30	2464	2945				1660	1816	1840
Nla III	(23)	62	1205	1415	1421			2038	2471	2613
		1766	1952	1983	2009			2798	3478	4040
		2224	2977	3431	3598	Tfi I	(7)	442	802	2032
		3944	4664	5155	5165			3518	3775	3915
		5243	5279	5672	5777	Tsp45 I	(9)	1022	1231	1667
		5861	6228	6301				2749	5089	5300
Nla IV	(39)	188	201	246	403			6187		5876
		521	552	692	761	Tth111 I	(5)	390	811	1217
		893	1144	1221	1399			3307		1665
		1548	1583	2236	2311	Tth111 II	(10)	146	422	613
		2363	2567	2646	2758			1983	2680	3062
		2805	2817	3105	3118			4538	4568	4529
		3163	3320	3686	3972	Vsp I	(4)	3583	3711	3770
		4011	4783	4877	4918	Xba I	(2)	218	3135	5005
		5129	5719	6057	6240	Xho II	(11)	1718	1964	2739
		6264	6354	6375				2803	4581	2777
Not I	(1)	2790						4690	4581	4678
Nsp7524 I	(5)	1948	2220	3940	5857	Xma I	(2)	397	3314	
		6224				Xma III	(3)	724	1453	2790
NspB II	(12)	588	1653	2458	2773	Xmn I	(3)	3546	3584	5432
		3416	3764	4282	4527					
		5468	5934	6128	6484					
NspH I	(5)	1952	2224	3944	5861					
		6228								
Pac I	(1)	2868								
Pal I	(33)	129	173	584	726					
		762	774	987	1111					
		1132	1197	1455	1629					
		2020	2047	2518	2623					
		2792	2817	3045	3090					
		3781	3955	3966	3984					
		4418	4876	4956	5223					
		5810	6108	6257	6265					
		6389								
Ple I	(4)	799	2545	3483	4319					
Pme I	(1)	2217								
PpuM I	(3)	254	1219	3171						
Psp1406 I	(3)	2421	5059	5432						
PspA I	(2)	397	3314							
Pst I	(4)	921	929	1105	1600					
Pvu I	(2)	5203	6099							
Pvu II	(5)	1653	2458	3764	6128					
		6484								
Rsa I	(9)	403	659	1284	1853					
		2357	3320	5313	5989					
		6500								
Rsr II	(1)	2063								
Sac I	(2)	338	3255							
Sac II	(1)	2774								
Sal I	(1)	2797								
Sap I	(4)	1891	2101	3562	3824					
Sau3A I	(30)	92	457	1044	1176					
		1361	1718	1796	1877					
		1886	1964	2739	2767					
		2777	2803	3008	4506					
		4581	4592	4600	4678					
		4690	4795	5136	5154					
		5200	5458	5475	5511					
		6096	6320							
Sau96 I	(29)	127	171	186	199					
		254	551	690	760					
		773	985	1196	1219					
		2063	2621	2815	2816					
		3043	3088	3103	3116					
		3171	4875	4954	4971					
		5193	5809	6106	6263					
		6448								
Sca I	(1)	5313								
ScrF I	(35)	163	241	398	399					
		548	570	723	735					
		748	1169	1194	1217					
		1237	1267	1551	1711					
		1934	2620	2819	3080					
		3158	3315	3316	3680					
		3968	4089	4102	4320					
		5016	5367	5868	5903					
		6175	6254	6452						
Sec I	(34)	161	240	250	397					
		461	497	546	547					
		694	733	734	746					
		747	1167	1236	1245					
		1265	1266	1411	1710					
		1979	2376	2640	2771					
		3078	3157	3167	3314					
		3377	3679	4100	6174					
		6252	6258							
SfaN I	(23)	185	444	641	938					
		1506	1761	1845	1909					
		1977	2184	2490	3102					
		3360	4036	5088	5281					
		5528	5889	5981	6019					

Site usage in pSEN-Flag:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Act I	C`CG,C	78
Afl I	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	10
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	33
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	3	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	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	18	Ban II	G,RGCY`C	9
Bbe I	G,CGCC`C	7	Bbs I	GAAGAC 8/12	-
bbv I	GCAGC 13/17	11	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	2
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	-
BsaH I	GR`CG,YC	10	BsaJ I	C`CNNG,G	34
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	9	BsiHKA I	G,WGCW`C	8
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	21	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	48
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	2
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	3
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	5
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	17	BstU I	CG CG	28
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	11
Bsu36 I	CC`TNA,GC	3	Cac8 I	GCN NGC	45
Cfr1 I	R`CCGG,Y	10	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	23
Dpn I	GA TC	30	DpnII	`GATC,	30
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	5
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	3
Ear I	CTCTTC 7/10	8	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	4	EcoI019 I	RG`GNC,CY	5
EcoR I	G`AATT,C	2	EcoR II	`CCWGG,	17
EcoR V	GAT ATC	3	Ehe I	GGC GCC	7
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	48
Fok I	GGATG 14/18	13	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	13
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	6
Hae II	R,CGCC`Y	13	Hae III	GG CC	33
Hga I	GACGC 9/14	11	HgiA I	G,WGCW`C	8
HgiE II	ACNNNNNNNGGT -1/132	-	Hha I	G,CG`C	50
Hinc II	GTY RAC	1	Hind II	GTY RAC	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	17
HinI	GR`CG,YC	10	HinP I	G`CG,C	50
Hpa I	GTT ARC	-	Hpa II	C`CG,G	40
Hph I	GGTGA 12/11	14	Kas I	G`GGCC,C	7
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	15
Mae II	A`CG,T	12	Mae III	`GTNAC,	22
Mbo I	`GATC,	30	Mbo II	GAAGA 12/11	14
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	54	Msc I	TGG CCA	3
Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	4
Msp I	C`CG,G	40	MspAl I	CMG CKG	12
Mun I	C`AATT,G	1	Nae I	GCC GGC	4
Nar I	GG`CG,CC	7	Nci I	CC`S,GG	18
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	4	Nhe I	G`CTAG,C	3
Nla III	,CATG`	23	Nla IV	GGN NCC	39
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Nsi I	A,TCGA`T	-	Nsp7524 I	R`CATG,Y	5
NspB II	CMG CKG	12	NspH I	R,CTGY`Y	5
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-
Pal I	GG CC	33	Pf1M I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	-
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
Pst I	C,TCGA`G	4	Pvu I	CG,AT`CG	2
Pvu II	CAG CTG	5	Rsa I	GT AC	9

Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1	Stu I	AGG CCT	-	Sty I	C`CWWG,G	8
Sap I	GCTCTTC 8/11	4	Sau3A I	`GATC,	30	Taq I	T`CG,A	16	Tfi I	G`AWT,C	7
Sau96 I	G`GNC,C	29	Sca I	AGT ACT	1	Tsp45 I	`GTSAC,	9	Tth111 I	GACN`N,NGTC	5
ScrF I	CC`N,GG	35	Sec I	C`CNNG,G	34	Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	4
SfaN I	GCATC 9/13	23	Sfc I	C`TRYA,G	10	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2	Xcm I	CCANNNN,N`NNNTGG-	-	Xho I	C`TCGA,G	-
SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1	Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	2
Sph I	G,CATG`C	2	Spl I	C`GTAC,G	-	Xma III	C`GGCC,G	3	Xmm I	GAANN NNTTC	3