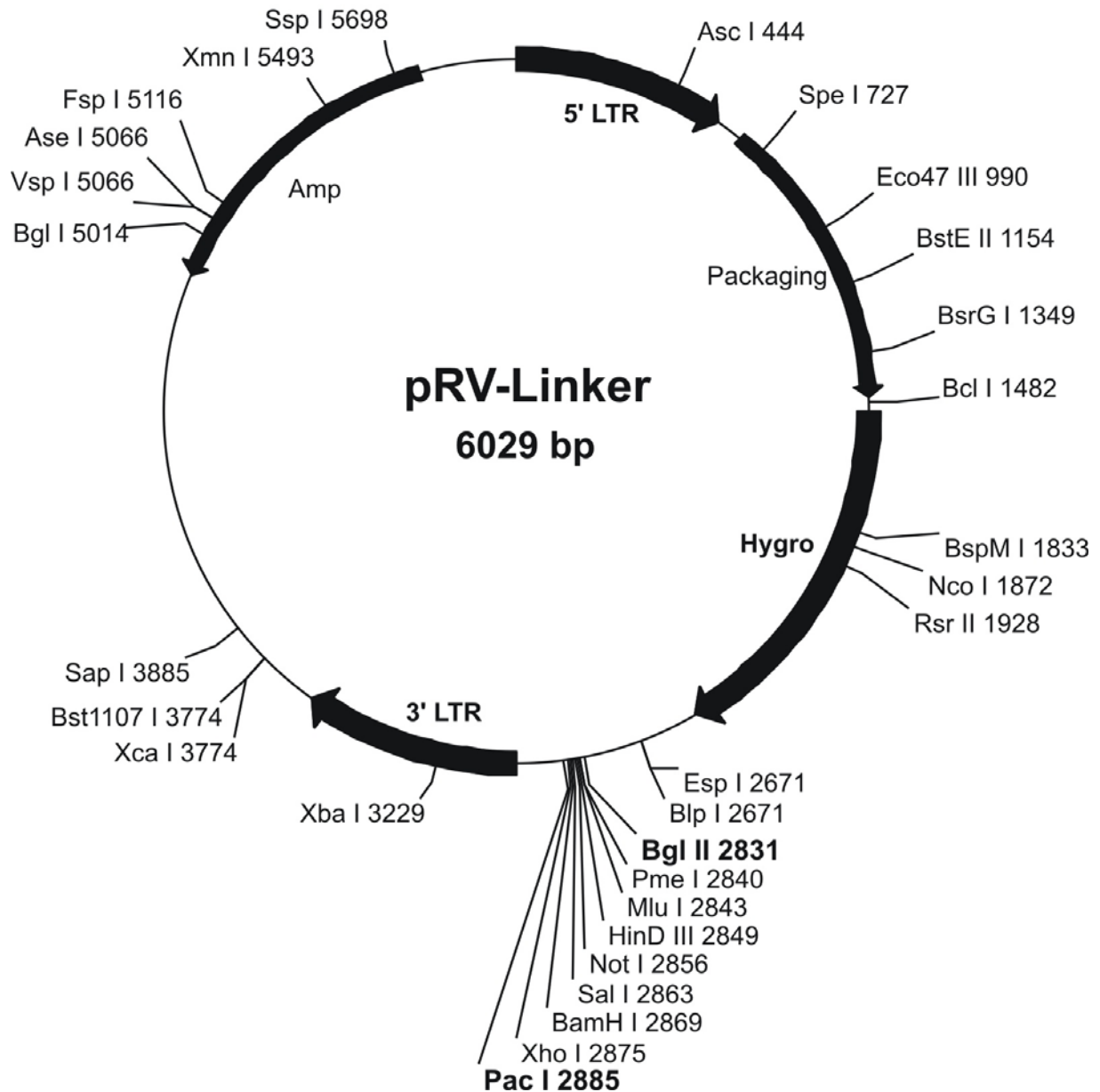


Name of Vector: pRV-Linker
Antibiotic Selection: Amp
Created by: Wei Jiang and Hong Yin
(He Lab @ The University of Chicago)
Date of Creation: February 2005



**pRV-Linker Full-length Sequence
(Derived from pLHCX)**

TTTGAAAGAC CCCACCCGTA GGTGGCAAGC TAGCTTAAGT AACGCCACTT TGCAAGGCAT GGAAAAATAC
ATAACTGAGA ATAGAAAAGT TCAGATCAAG GTCAGGAACA AAGAAACAGC TGAATACCAA ACAGGATATC
TGTGGTAAGC GGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGAGACAG CTGAGTGATG GGCCAAACAG
GATATCTGTG GTAAGCAGTT CCTGCCCCGG CTCGGGGCCA AGAACAGATG GTCCCCAGAT GCGGTCCAGC
CCTCAGCAGT TTCTAGTGAA TCATCAGATG TTTCCAGGGT GCCCCAAGGA CCTGAAAATG ACCCTGTACC
TTATTTGAAC TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC CGCTCTCCGA GCTCAATAAA
AGAGCCCACA ACCCTCACT CGGCGCGCCA GTCTTCCGAT AGACTGCGTC GCCCGGTAC CCGTATTCCC
AATAAAGCCT CTTGCTGTTT GCATCCGAAT CGTGGTCTCG CTGTTCCTTG GGAGGGTCTC CTCTGAGTGA
TTGACTACCC ACGACGGGGG TCTTTTCAITTT GGGGGCTCGT CCGGGATTTG GAGACCCCTG CCCAGGGACC
ACCGACCCAC CACCGGGAGG TAAGCTGGCC AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG
TTTGATGTTA TGCGCCTGCG TCTGTACTAG TTAGCTAATC AGCTCTGTAT CTGGCGGACC CGTGGTGGAA
CTGACGAGTT TGAACACCC GGCCGCAACC CTGGGAGACG TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG
CCCGACCTGA GGAAGGGAGT CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTTCCTGTT AGGAGACGAG
AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTTGGAA CCGAAGCCGC GCGTCTTTGTC
TGCTGCAGCG CTGCAGCATC GTTCTGTGTT GTCTCTGTCT GACTGTGTTT CTGTATTTGT CTGAAAATTA
GGGCCAGACT GTTACCACCT CCTTAAGTTT GACCTTAGGT CACTGGAAAG ATGTCGAGCG GATCGCTCAC
AACCAGTCGG TAGATGTCAA GAAGAGACGT TGGGTTACCT TCTGCTCTGC AGAATGGCCA ACCTTTAACG
TCGGATGGCC GCGAGACGGC ACCTTTAACC GAGACCTCAT CACCCAGGTT AAGATCAAGG TCTTTTCACC
TGGCCCGCAT GGACACCCAG ACCAGTCCC CTACATCGTG ACCTGGGAAG CCTTGGCTTT TGACCCCTT
CCCTGGGTCA AGCCCTTTGT ACACCCTAAG CCTCCGCCTC CTCTTCCTCC ATCCGCCCGG TCTCTCCCC
TTGAACCTCC TCGTTCGACC CCGCCTCGAT CCTCCCTTTA TCCAGCCCTC ACTCCTTCTC TAGGCGCCGG
AATTCGGATC TGATCAGCTT GCCACAACCC GTACCAAAGA TGGATAGATC CGGAAAGCCT GAACTCACCG
CGACGTCTGT CGAGAAGTTT CTGATCGAAA AGTTCGACAG CGTCTCCGAC CTGATGCAGC TCTCGGAGGG
CGAAGAATCT CGTGCTTTCA GCTTCGATGT AGGAGGGCGT GGATATGTCC TGCGGGTAAA TAGCTGCGCC
GATGGTTTCT ACAAAGATCG TTATGTTTAT CGGCACTTTG CATCGGCCGC GCTCCCGATT CCGGAAGTGC
TTGACATTGG GGAATTCAGC GAGAGCCTGA CCTATTGCAT CTCCCGCCGT GCACAGGGTG TCACGTTGCA
AGACCTGCC T GAAACCGAAC TGCCCGCTGT TCTGCAGCCG GTCGCGGAGG CCATGGATGC GATCGCTGCG
GCCGATCTTA GCCAGACGAG CCGGTTCCGG CCATTCCGAG CGCAAGGAAT CCGTCAATAC ACTACATGGC
GTGATTTTCA ATGCGCGATT GCTGATCCCC ATGTGTATCA CTGGCAAACG GTGATGGACG ACACCGCTCAG
TGCGTCCGTC GCGCAGGCTC TCGATGAGCT GATGCTTTGG CCGCAGGACT GCCCCGAAGT CCGGCACCTC
GTGCACGCGG ATTTTCGGCTC CAACAATGTC CTGACGGACA ATGGCCGCAT AACAGCGGTC ATTGACTGGA
GCGAGGCGAT GTTCGGGGAT TCCCAATACG AGGTCGCCAA CATCTTCTTC TGGAGGCCGT GGTGGCTTG
TATGGAGCAG CAGACGCGCT ACTTCGAGCG GAGGCATCCG GAGCTTGACG GATCGCCCGG GCTCCGGGCG
TATATGCTCC GCATTGGTCT TGACCAACTC TATCAGAGCT TGGTTGACGG CAATTTTCGAT GATGCAGCTT
GGGCGCAGGG TCGATGCGAC GCAATCGTCC GATCCGGAGC CGGGACTGTC GGGCGTACAC AAATCGCCCC
CAGAAGCGCG GCCGTCTGGA CCGATGGCTG TGTAGAAGTA CTCGCCGATA GTGGAAACCG ACGCCCCAGC
ACTCGTCCGA GGGCAAAGGA ATAGAGTAGA TGCCGACCGA ACAAGAGCTG ATTTTCGAGAA CGCCTCAGCC
AGCAACTCGC GCGAGCCTAG CAAGGCAAAT GCGAGAGAAC GGCTTACGC TTGGTGGCAC AGTTCCTCGTC
CACAGTTCGC TAAGCTCGCT CGGCTGGGTC GCGGGAGGGC CGGTCGCAGT GATTACAGCC CTTCTGGATT
GTGTTGGTCC CCAGGGCACG ATTTGTCATG CCACGCACCT GGGTGATCTG ACTGATCCCC CAGATTGGAG
ATCGCCGCC GTGCCGCGG ATTTGGGTGCagatctg ttt aaa cgc gta agc ttg cgg ccg cgt cga cgg
atc cct cga gtt aat taa cgATAAAATA AAAGATTTTA TTTAGTCTCC AGAAAAGGG GGGAAATGAAA
GACCCACCT GTAGTTTGG CAAGCTAGCT TAAGTAAACG CATTTTGCAA GGATGGAAA AATACATAAC
TGAGAATAGA GAAGTTCAGA TCAAGGTCAG GAACAGATGG AACAGCTGAA TATGGGCCAA ACAGGATATC
TGTGGTAAGC AGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGGAACAG CTGAATATGG GCCAAACAGG
ATATCTGTGG TAAGCAGTTC CTGCCCCGGC TCAGGGCCAA GAACAGATGG TCCCAGATG CCGTCCAGCC
CTCAGCACTT TCTAGAGAAC CATCAGATGT TTCCAGGTTG CCCC AAGGAC CTGAAAATGAC CCTGTGCTT
ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTTCTGTTTCG CGCGCTTCTG CTCCCCGAGC TCAATAAAAAG
AGCCCACAAC CCCTCACTCG GGGCGCCAGT CCTCCGATTG ACTGAGTTCG CCGGGTACCC GTGTATCCAA
TAAACCTCT TGCAGTTGCA TCCGACTTGT GGTCTCGCTG TTCCTTGGGA GGGTCTCCTC TGAGTGATTG
ACTACCCGTC AGCGGGGGTC TTTCAITTTGG GGGCTCGTCC GGGATCGGGA GACCCCTGCC CAGGGACCAC
CGACCCACCA CCGGGAGGTA AGCTGGCTGC CTCGCGCGTT TCGGTGATGA CCGTGAAAAC CTCTGACACA
TGCAGCTCCC GGAGACGGTC ACAGCTTGTG TGTAAGCGGA TGCCGGGAGC AGACAAGCCC GTCAGGGCGC
GTCAGCGGGT GTTGGCGGGT GTCGGGGCGC AGCCATGACC CAGTCACGTA GCGATAGCGG AGTGTATACT
GGCTTAACTA TGCGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CCGTGTGAAA TACCGCACAG
ATGCGTAAGG AGAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
GTTCCGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG TAATACGGTT ATCCACAGAA TCAGGGGATA

ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAAGGCCG CGTTGCTGGC
GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC
CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA GCTCAGCTG
TAGGTATCTC AGTTCGGTGT AGGTCGTTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC
GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG
CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG
GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC TGCCTCTGCT TGAAGCCAGT TACCTTCGGA
AAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTTT GTTTGCAAGC
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT CTGACGCTCA
GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT
TTAAATTTAA AATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT
GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTCATCC ATAGTTGCCT GACTCCCCGT
CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGCTG CAATGATACC GCGAGACCCA
CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAG CCGGAAGGGC CGAGCGCAGA AGTGGTCCTG
CAACTTTTAT CGCCTCCATC CAGTCTATTA ATTTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
TAGTTTGCGC AACGTTGTTG CCATTGCTGC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA
TTCAGCTCCG GTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCCATGTT GTGCAAAAA GCGGTTAGCT
CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATCA CTCATGGTTA TGGCAGCACT
GCATAATTTCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTG GTGAGTACTC AACCAAGTCA
TTCTGAGAAAT AGTGTATGCG GCGACCGAGT TGCTCTTGCC CGGCGTCAAC ACGGGATAAT ACCGCGCCAC
ATAGCAGAAC TTTAAAAGTG CTCATCATTG GAAAACGTTT TTCGGGGCGA AAACCTCAA GGATCTTACC
GCTGTTGAGA TCCAGTTCGA TGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTACC
AGCGTTTCTG GGTGAGCAAA AACAGGAAG CAAAAATGCC CAAAAAAGG AATAAGGGCG ACACGAAAT
GTTGAATACT CATACTCTTC CTTTTTCAAT ATTTATTGAAG CATTTATCAG GGTTATTGTC TCATGAGCGG
ATACATATTT GAATGTATTT AGAAAAATAA ACAAATAGGG GTTCCGCGCA CATTTCCCCG AAAAGTGCCA
CCTGACGTCT AAGAAACCAT TATTATCATG ACATTAACCT ATAAAAATAG GCGTATCACG AGGCCCTTTC
GTCTTCAAGA ATTCATACCA GATCACCGAA AACTGTCCCT CAAATGTGTC CCCCTCACAC TCCCAAATTC
GCGGGCTTCT GCCTCTTAGA CCACTCTACC CTATTTCCCA CACTCACCGG AGCCAAAGCC GCGGCCCTTC
CGTTTCTTTG CT

Unique enzymes in pRV-Linker:

Asc I	GG ⁺ CGCG,CC	444	Bgl II	(1)	2831		
Spe I	A ⁺ CTAG,T	727	Blp I	(1)	2671		
Eco47 III	AGC GCT	990	Bpm I	(4)	2188	2242	2900 4964
BstE II	G ⁺ GTNAC,C	1154	Bsa I	(8)	531	552	606 1216
BsrG I	T ⁺ GTAC,A	1349			3465	3486	3541 4955
Bcl I	T ⁺ GAATC,A	1482	BsaA I	(1)	3755		
BspM I	ACCTGCG 10/14	1833	BsaH I	(7)	809	1465	1544 2512
Nco I	C ⁺ CAATG,G	1872			3381	5431	5813
Rsr II	AG ⁺ GWC,CG	1928	BsaJ I	(35)	160	236	315 325
Blp I	GC ⁺ TNA,GC	2671			473	537	622 623
Esp I	GC ⁺ TNA,GC	2671			761	800	801 813
Bgl II	A ⁺ GAATC,T	2831			814	1234	1303 1312
Pme I	CTTT AAAC	2840			1332	1333	1872 2073
Mlu I	A ⁺ CGCG,T	2843			2228	2297	2528 2741
Bsg I	GTGCAG 22/20	2848			2742	3097	3172 3251
Hind III	A ⁺ AGCT,T	2849			3261	3408	3471 3557
Not I	GC ⁺ GGCC,GC	2856	BsaW I	(8)	1520	1741	2278 2414
Sal I	G ⁺ TCGA,C	2863			3558	4161	6007
BamH I	G ⁺ GAATC,C	2869	BseR I	(4)	540	1360	1399 3474
PaeR7 I	C ⁺ TCGA,G	2875	Bsg I	(1)	2848		
Xho I	C ⁺ TCGA,G	2875	BsiE I	(13)	794	1728	1863 1884
Pac I	TTA,AT ⁺ TAA	2885			1893	2463	2558 2705
Xba I	T ⁺ CTAG,A	3229			2859	3917	4341 5264
BsaA I	YAC GTR	3755			5413		
Bst1107 I	GTA TAC	3774	BsiHKA I	(8)	414	1804	2106 3349
Xca I	GTA TAC	3774			3821	4319	5480 5565
Sap I	GCTCTTC 8/11	3885	BsmA I	(19)	180	530	551 607
Bgl I	GCCCN,NNN ⁺ NGGC	5014			801	899	1016 1140
Ase I	AT ⁺ TA,AT	5066			1199	1217	1395 1587
Vsp I	AT ⁺ TA,AT	5066			2917	3464	3485 3542
Fsp I	TGC GCA	5116			3645	4956	5730
Xmn I	GAANN NNNTTC	5493	BsmB I	(7)	800	898	1139 1198
Ssp I	AAT ATT	5698			1396	1588	3644
Number of enzymes = 33			BsmF I	(10)	247	640	796 831
					1272	2437	2723 3183
					3575	5911	

The following enzymes do not cut in pRV-Linker:

Age I	Apa I	Avr II	BsaB I	BsiC I	BsoP I	(43)	794	968	984	987
BsiW I	Bsm I	Bsp120 I	Bsp1286 I	BstB I			992	995	1200	1598
BstX I	Cla I	Eco72 I	Fse I	Hpa I			1675	1728	1856	1887
Mun I	Nae I	Ngom I	Nru I	Nsi I			1890	2146	2249	2297
PflM I	Pml I	Sfi I	SnaB I	Sph I			2300	2376	2460	2806
							2856	2859	3595	3641
							3738	3791	3907	3925
							3928	4046	4201	4344
							4409	4412	4618	4946
							5135	5285	5312	5407
							5636	6007	6010	
							4721	5729	5834	
							1833			
							1520	1741	2278	2414
							450	1097	1125	2005
							2170	3385	3749	3780
							4408	4421	4535	4941
							5059	5102	5369	5541
							403	1109	1911	2269
							3934	5735		
							4955	5129		
							1349			
							393	444	3328	
							1620	2099	4174	5558
							5865			
							3774			
							1154			
							316	624	802	815
							1236	1261	1284	1304
							1334	2743	3252	3559
							4029	4150	4163	
							393	395	446	970
							972	1202	1541	1730
							1865	1976	2042	2108
							2257	2299	2459	2600
							2602	2692	2845	2861
							3328	3330	3602	3604
							3707	4048	4629	4959
							5452	5784	5949	6009
							1517	2831	2869	4642
							4653	4739	4751	5519
							5536			
							848	1085		
							28	32	395	446
							657	661	717	1266
							1490	1845	2046	2106
							2286	2449	2591	2604
							2677	2816	2853	2960
							2964	3330	3592	3932
							4018	4055	4615	5006
							5139	5951		
							1858	2700	4974	
							347	478	725	1350
							1502	2436	2489	3413
							3808	5373		
							76	166	192	283
							554	848	1085	1357
							1898	2585	2671	3008
							3103	3178	3219	3400
							3488	3811	4276	4685
							4851	5391	5817	5963
							96	1113	1245	1430
							1479	1484	1519	1565
							1698	1883	1896	1986
							2293	2413	2777	2786
							2802	2833	2871	3028
							3542	4569	4644	4655
							4663	4741	4753	4858
							5199	5217	5263	5521
							5538	5574	5900	
							94	1111	1243	1428
							1477	1482	1517	1563
							1696	1881	1894	1984
							2291	2411	2775	2784
							2800	2831	2869	3026
							3540	4567	4642	4653
							4661	4739	4751	4856
							5197	5215	5261	5519
							5536	5572	5898	
							2840	4760	4779	5471
							1808	2101		
							2024	2405	3696	4109
							761	1872	2228	2297
							6007			
							657	791	1176	1197
							1725	1890	2143	2460

pRV-Linker: sites sorted by name:

		814	1234	1303	1312
		1332	1333	1872	2073
		2228	2297	2528	2741
		2742	3097	3172	3251
		3261	3408	3471	3557
SfaN I	(22)	3558	4161	6007	
		260	520	1005	1585
		1729	1796	1868	2053
		2283	2363	2385	2541
		3196	3454	3668	3801
		3839	3877	4097	5149
		5342	5589		
Sfc I	(8)	984	992	1168	1853
		2947	4266	4457	5135
Sma I	(2)	475	3410		
Spe I	(1)	727			
Ssp I	(1)	5698			
Sty I	(6)	325	537	1312	1872
		3261	3471		
Taq I	(17)	861	1105	1416	1427
		1551	1566	1575	1635
		2052	2265	2367	2392
		2575	2864	2876	4101
		5545			
Tfi I	(9)	299	518	869	1616
		1738	1938	2189	2712
		3976			
Tsp45 I	(7)	1089	1298	1810	3655
		3750	5150	5361	
Tth111 I	(7)	466	878	1284	1580
		2024	3401	3748	
Tth111 II	(10)	144	220	498	691
		1740	3081	3156	4590
		4599	4629		
Vsp I	(1)	5066			
Xba I	(1)	3229			
Xca I	(1)	3774			
Xho I	(1)	2875			
Xho II	(9)	1517	2831	2869	4642
		4653	4739	4751	5519
		5536			
Xma I	(2)	473	3408		
Xma III	(5)	791	1725	1890	2460
		2856			
Xmn I	(1)	5493			

Site usage in prV-Linker:

Aat II	G,ACGT`C	3	Acc I	GT`MK,AC	2
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	71
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	7
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	35
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	4
Apa I	G,GGCC`C	-	Apal I	G`TGCA,C	5
Apo I	R`AATT,Y	5	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	7	Ava II	G`GWC,C	15
Avr II	C`CTAG,C	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,G	9	Ban II	G,RGCY`C	6
Bbe I	G,CGCC`C	2	Bbs I	GAAGAC 8/12	2
Bbv I	GCAAGC 13/17	12	Bbv II	GAAGAC 7/11	2
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	20
Bfa I	C`TA,G	12	Bgl I	GCCN,NNN`NGGC	1
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	1
Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	8
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	-
BsaH I	GR`CG,YC	7	BsaJ I	C`CNGG,G	35
BsaW I	W`CCGG,W	8	Bser I	GAGGAG 16/14	4
Bsg I	GTGGAG 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	19	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	43

Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	1
BspM III	T`CCGG,A	4	Bsr I	ACT,GG`	16
BsrB I	GAG CGG	6	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BssH III	G`CGCG,C	3
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	1
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	15	BstU I	CG CG	32
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	30
Cfr10 I	R`CCGG,Y	3	cla I	AT`CG,AT	-
Csp6 I	G`TA,C	10	Dde I	C`TNA,G	24
Dpn I	GA TC	35	DpnII	`GATC,	35
Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	2
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	5
Eae I	Y`GGCC,R	10	Eag I	C`GGCC,G	5
Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	2	Eco72 I	CAC GTG	1
EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	5
EcoR I	G`AATT,C	3	EcoR II	`CCWGG,	15
EcoR V	GAT ATC	4	Ehe I	GGC GCC	2
Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	43
Fok I	GGATG 14/18	10	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	13
Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	6
Hae II	R,CGCC`Y	5	Hae III	GG CC	36
Hga I	GACGC 9/14	13	HgiA I	G,WGCW`C	8
HgiE III	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	33
Hinc III	GTY RAC	3	Hind II	GTY RAC	3
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	14
Hinf I	GR`CG,YC	7	HinP I	G`CG,C	33
Hpa I	GTT AAC	-	Hpa II	C`CG,G	33
Hph I	GGTGA 12/11	13	Kas I	G`CGCG,C	2
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	12
Mae II	A`CG,T	10	Mae III	`GTNAC,	17
Mbo I	`GATC,	35	Mbo II	GAAGA 12/11	13
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	7
Mnl I	CCTC 10/10	53	Msc I	TGG CCA	2
Mse I	T`TA,A	19	Msl I	CAYNN NNRTG	2
Msp I	C`CG,G	33	MspAl I	CMG CKG	13
Mun I	C`AATT,G	-	Nae I	GCC GGC	-
Nar I	GG`CG,CC	2	Nci I	CC`S,GG	20
Nco I	C`CATG,G	1	Nde I	CA`TA,TG	2
NgoM I	G`CCGG,C	-	Nhe I	G`CTAG,C	2
Nla III	,CATG`	17	Nla IV	GGN NCC	31
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	2
NspB II	CMG CKG	13	NspH I	R,CATG`Y	2
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	1
Pal I	GG CC	36	PflM I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	3	Pme I	CTTT AAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
Pst I	C,TGCA`G	5	Pvu I	CG,AT`CG	2
Pvu I	CAG CTG	4	Rsa I	GT AC	10
Rsr II	CG`GWC,CG	1	Sac I	G,AGTC`C	2
Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	1	Sau3A I	`GATC,	35
Sau96 I	G`GNC,C	34	Sca I	AGT ACT	2
ScrF I	CC`N,GG	35	Sec I	C`CNGG,G	35
SfaN I	GCATC 9/13	22	Sfc I	C`TRYA,G	8
Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	-	Spl I	C`GTAC,G	-
Srf I	GCCC GGGC	-	Ssp I	AAT ATT	1
Stu I	AGG CTT	-	Sty I	C`CWGG,G	6
Taq I	T`CG,A	17	Tfi I	G`AWT,C	9
Tsp45 I	`GTSAC,	7	Tth11 I	GACN`N,NGTC	7
Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	1
Xba I	T`CTAG,A	1	Xca I	GTA TAC	1
Xcm I	CCANNNN,N`NNNNNTGG-	-	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	2
Xma III	C`GGCC,G	5	Xmn I	GAANN NNTTT	1