

pMPB-SOS Full-Length Sequence

CTGCAGAACACGCAGCTAGATTAA**CCCTAGAAA**GATAATCATAT**TGTGACGTACGTTAAAGATAATCATGCGTAAA**ATTGACGCATGTGTT
 TTATCGGTCTGTATATCGAGGTTTATTTTAAATTTGAATAGATATTAAGTTTATTATATTTACTTACATACTAATAATAAAATTC AAC
 AAACAATTTATTTATGTTTATTTATTTATTTAAAAAACA AAAA ACTCAAATTTCTTCTATAAAGTAACAAA ACTTTTATGAGGGACAGC
 CCCCCCAAAGCCCCAGGGATGTAATTACGTCCCTCCCCGCTAGGGGGCAGCAGCGAGCCCGCCGGGGCTCCGCTCCGGTCCGGCGCT
 CCCCCGCATCCCCGAGCCGCAGCGTGC GGGGACAGCCCGGGCAGGGGAAAGTGGCACGGGATCGCTTTCTCTGAACGCTTCTCGCTG
 CTCTTTGAGCCTGCAGACACCTGGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGT**AATGTGTGTCA**GT**TAGGGTGTGGAAAGTCC**
CCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCA
GAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCATCCCGCCCC**TA**ACTCCGCC**CA**GT**TC**CGC
 CCAT**TC**CCGCC**CA**TGGCTGACTA**AT**TTTTTTTATTTATCGAGAGCCGAGGCC**CC**CTCTGCCTCTGAGCTAT**TC**CAGAAGTAGTGAGGA
 GGCTTTTTTGGAGGCCTAGGCTTTT**GCAAAA**AGCTCCCGGGAGCTTGTATATCCATTTT**CG**GATCTGATCAGCACGTGTTGACAATTAATC
 ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAA**ACC**ATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATT
 GAAAGAGCAACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTGC**CC**AGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCA
 CTGGTGTCAATGTATATCATTTTACTGGGGACCTTGTGCAGAACTCGTGGTGTCTGGGC**ACT**GCTGCTGCTGC**GC**CAGCTGGCAACCTGAC
 TTGTATCGT**CG**CATCGGAAATGAGAACAGGGGCATCTT**GAG**CCCCTGCGGACGGTGC**CC**AGCGTCTTCTCGATCTGCATCTTGGGATC
 AAAGCCATAGTGAAGGACAGT**GAT**GGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCTCTGGTTATGTGTGGGAGGGCTAAGCAC
 TTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTT**CG**ATTCCACC**CG**CCCTTCTATGAAAGGTTGGGCTTCGGAAATCGTTTTCC
 GGGACCCGGCTGGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCTT**CG**CCACCCCAACTTGT**TT**ATTGCAGCTTATAATGGTTA
 CAAATAAAGCAATAGCATCACA**AA**TTT**CA**CAAATAAAGC**AT**TTTTTT**CA**CTGCAT**TC**TAGTTGTGGTTTGTCCA**AA**CTCATCAATGTATCT
TATCATGTCTGCGCGCCG**GACGCTCGTAG**g atccagggtcgggcaggaagagggcctatttcccatgattccttcatatttgcataatcga
 tacaaggctgttagagagataattagaattaatttgactgtaaacacaaagatattagtagacaaatacgtgagtagaaagtaataatttct
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 GCAGCGTATTACAGTGACAGTTGACAGCGACAGCTATCAGTTGCTCAAGGCATATATGATGTCAATATCTCCGGTCTGGTAAGCACAA**CC**A
 TGCAGAATGAAGCCCGTCTGCTGCGTGCCGAACGCTGGAAAGCGGAAATCAGGAAGGGATGGCTGAGGTCGCCCGGTTTATTGAAATGAA
 CGGCTCTTTTCTGACGAGAACAGGGGCTGGTGA**ATG**CAGTTTAAAGGTTTACACCTATAAAAAGAGAGAGCCGTTATCGTCTGTTT**GT**GGAA
TGTACAGAGTGATATTAT**GAC**ACGCCCGGGCGACGGATGGT**GAT**CCCCCTGGCCAGTGCACGTCTGCTGTCAGATAAAGTCTCCCGTGAA
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 CTTGTTTATTGCANCTTATAATGGTTACAAATAAAGCAATAGCATCACA**AA**TTT**CA**CAAATAAAGC**AT**TTTTTT**CA**CTGCAT**TC**TAGTTGT
 GGT**TTGT**CCA**AA**CTCATCAATGTATCTTATCATGTCTGGAA**TGACT**CA**AA**TGATGTCA**AT**TAGTCTATCAGAAGCTCATCTGGTCTCC**CT**
 CCGGGGACAAGACATCCCTGTTAATATTTAAACAGCAGTGT**TC**CA**AA**CTGGGTTCTTATATCCCTTGTCTGGTCAACCAGGTTGCAG
 GGTTTCTGTCTCACAGGAACGAAGTCCCTAAAGAAACAGTGGCAGCCAGGTTTAGCCCCGAATTGACTGGATTCTTTT**TT**AGGGCCC
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 GCCCCTAGCGGGGGAGGGACGTA**ATTACAT**CCCTGGGGGCTTTGGGGGGGGCTGTCCCTGATATCTATAACAAGAAAATATATATATAA
 TAAGTTATCACGTAAGTAGAACATGAAATAACAATATAATTATCGTATGAGTTAAATCTTAAAAGTACAGTAAAAGATAATCATGCGT**CA**T
 TTTGACTCACGCGGTGCTTATAGTTCAAATCAGTGACACTTACCGCATTGACAAGCACGCCTCACGGGAGCTCCAAGCGGCGACTGAGAT
 GTCTAAATGCACAGCGACGGATTTCGCGCTATTTAGAAAGAGAGGAATATTTCAAGAAT**G**CAT**GC**GT**CA**ATTT**AC**GCAGACTATCTTT
CTAGGGTTAATCTAGCTGCATCAGGATCATATCGTGGGTCTTTTTT**CA**TCGCCAAGCTGGCGCTATCTGGGCATCGGGGAGGAAGAAGC
 CCGTGCCTTTTCCCGCAGGTTGAAGCGGCATGGAAAGAGTTTGGCAGGATGACTGCTGCTGCATTGACGTTGAGCGAAAACGCACGTTT
 ACCATGATGATTCGGGAAGGTGTGGCCATGCACGCCTTTAACGGTGA**ACT**GTTCGTT**CAG**CCACCTGGGATACCAGTTCGTCGCGGCTTT
 TCCGGACACAGTTCGGATGGTCAGCCGAAGCGCATCAGCA**ACC**GAACAATACCGGCGACAGCCGGA**ACT**GCCGTGCCGGTGTGCAGAT
 TAATGACAGCGGTGCGGCGCTGGGATATTACGT**CAG**CGAGGACGGGTATCTGGCTGGATGCCGAGAAATGGACATGGATACCCCGTGAG
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 CGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT**GAG**CTAACTCACATTAAT**TG**CGTTGCGCTACTGCCC**CT**TTCCAGT**CG**GGGA
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 GGTA**ACT**ATCGTCTT**GAG**TCA**ACC**CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGATG
 TAGCGGTGTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGTGAAGCCAGT
 TACCTTCCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCCCGCTGGTAGCGGTGGTTTTTTTTTGT**TG**CAAGCAGCAGATTACG
 CGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAA**ACT**CACGTTAAGGGATTTTGG

TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAATGAAGTTTTAAATCAATCTAAAGTATATATAGTAAACTTG
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 ACTGGGCAATGGAGCGCTTCGCGCCAGTATCAGCCCCGCTACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGC
 CTCGCGCGCAGATCAGTTGGAAGAATTTGTCCACTACGTGAAAGGCGAGATCACCAAGGTAGTCGGCAAATAACCTCGAGCCACCCATGA
 CCAAAATCCCTTAACGTGAGTTA

Unique enzymes in pMPB-SOS:

BsiI	I	C`GTAC,G	51			1419	1485	1651	1655
Spl	I	C`GTAC,G	51			1941	2136	2475	2732
Sfi	I	GGCCN,NNN`NGGCC	504			2751	2766	3299	3322
Spe	I	A`CTAG,T	512			3344	3356	3377	3561
Avr	II	C`CTAG,G	835			3594	3628	3836	3849
Bbv	II	GAAGAC 7/11	1048			3998	4105	4110	4158
Bbs	I	GAAGAC 8/12	1049			4195	4250	4353	4409
PpuM	I	RG`GWC,CY	1123			4419	4443	4486	4493
Nru	I	TCG CGA	1195			4514	4605	4633	4760
Not	I	GC`GGCC,GC	1652			4779	4900	5010	5145
BamH	I	G`GATC,C	1669			5154	5516	5607	5798
Nde	I	CA`TA,TG	1866	Afl III	(3)	894	1390	4560	
EcoR	I	G`AATT,C	1927	Aha II	(5)	1461	1660	2672	2777
Acc	I	GT`MK,AC	1967			6342			
Bst1107	I	GTA TAC	1968	Ahd I	(1)	5453			
Xca	I	GTA TAC	1968	Alu I	(31)	16	799	853	863
BsrG	I	T`GTAC,A	2277			1066	1171	1535	2036
Hind III		A`AGCT,T	2571			2399	2560	2573	2796
Kas	I	G`GCGC,C	2671			2987	3621	3747	3790
Nar	I	GG`CG,CC	2672			4225	4320	4384	4502
Ehe	I	GGC GCC	2673			4728	4818	4864	5121
Bbe	I	G,GCGC`C	2675			5642	5742	5805	6052
BsiC	I	TT`CG,AA	2787	Alw I	(18)	434	888	1278	1469
BstB	I	TT`CG,AA	2787			1496	1665	1676	2314
EcoN	I	CCTNN`N,NNAGG	3176			3259	3763	5122	5208
EcoR V		GAT ATC	3432			5208	5305	5306	5770
Sac	I	G,AGCT`C	3623	AlwN I	(2)	2212	4976		
Ple	I	GAGTC 9/10	4939	Apa I	(2)	2751	3185		
HgiE	II	ACCNNNNNNGGT -1/135139		ApaL I	(3)	2333	4874	6563	
BspH	I	T`CATG,A	5280	Apo I	(6)	175	233	1570	1927
Ahd	I	GACNN,N`NNGTC	5453			2871	7031		
Fsp	I	TGC GCA	5675	Ase I	(7)	122	906	1759	4096
Psp1406	I	AA`CG,TT	5679			4331	4390	5625	
BstE	II	G`GTNAC,C	6448	Ava I	(10)	339	377	403	856
BspM	I	ACCTGC 10/14	6635			2302	3287	3313	3351
PaeR7	I	C`TCGA,G	7084			6180	7084		
Xho	I	C`TCGA,G	7084	Ava II	(7)	355	1123	3336	5591
						5813	6087	6728	
				Avr II	(1)	835			
				BamH I	(1)	1669			
				Ban I	(4)	1238	2671	4304	5401
				Ban II	(6)	347	1228	2751	3185
						3351	3623		
				Bbe I	(1)	2675			
				Bbs I	(1)	1049			
				Bbv I	(20)	25	337	340	398
						1075	1180	1544	2016
						2569	3151	3250	4979
						4982	5188	5882	6120
						6205	6249	6265	6637
				Bbv II	(1)	1048			
				Bcl I	(2)	886	6486		
				Bcn I	(21)	341	342	405	406
						858	859	1458	2169
						2304	2305	2375	3007
						3156	3289	3290	3353
						3354	4193	4941	5637
						5984			
				Bfa I	(17)	17	28	318	513
						836	1073	1605	1666

The following enzymes do not cut in pMPB-SOS:

Acc65	I	Afe I	Afl II	Age I	Asc I				
Asp718		Bgl II	BsmB I	Bsp1286 I	Bsu36 I				
Cla	I	Eco47 III	Fse I	Hpa I	Kpn I				
Mlu	I	Mun I	Nhe I	Pac I	Pf1M I				
Pme	I	Sac II	Sal I	Sca I	SnaB I				
Swa	I	Tth111 I	Xba I	Xcm I	Xmn I				
pMPB-SOS: sites sorted by name:									
Aat	II	(2)	1663	2780					
Acc	I	(1)	1967						
Acl	I	(72)	315	336	348	370			
			393	683	695	704			
			716	726	737	783			
			1083	1165	1232	1416			

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		2736	2906	3374	3733	Dde I	(9)	795	1359	2158	2467
		3744	5055	5308	5643			3635	4835	5244	5410
		6969						6597			
Bgl I	(3)	504	5573	6920		Dpn I	(33)	429	883	888	1198
Blp I	(2)	1359	6597					1259	1273	1475	1491
Bpm I	(4)	1463	1520	5523	6540			1671	2320	2465	2808
Bsa I	(4)	2442	2583	3001	5514			3265	3758	5128	5203
BsaA I	(6)	895	1393	1798	3470			5214	5222	5300	5312
		3528	7045					5417	5758	5776	5822
BsaB I	(2)	1262	2317					6305	6488	6668	6678
BsaH I	(5)	1461	1660	2672	2777			6753	6771	6999	7020
		6342						7058			
BsaJ I	(40)	289	290	339	340	DpnII	(33)	427	881	886	1196
		403	476	502	547			1257	1271	1473	1489
		619	742	777	835			1669	2318	2463	2806
		856	962	1267	1374			3263	3756	5126	5201
		2302	2324	2706	2759			5212	5220	5298	5310
		3005	3153	3214	3287			5415	5756	5774	5820
		3350	3351	3400	3401			6303	6486	6666	6676
		3868	3979	4299	4720			6751	6769	6997	7018
		5973	5996	6179	6210			7056			
		6517	6581	6720	7062	Dra I	(6)	1839	1852	2802	3035
BsaW I	(9)	352	2073	3338	4006			5319	5338		
		4018	4766	4913	5744	Dra III	(4)	1369	5997	6425	7045
		6754				Drd I	(3)	1051	3639	4668	
BseR I	(2)	831	1391			Dsa I	(6)	502	742	962	5996
Bsg I	(2)	1151	4110					6210	6581		
BsIC I	(1)	2787				Eae I	(11)	505	965	1080	1371
BsIE I	(8)	1083	1199	1655	3565			1652	2327	2423	3937
		4476	4900	5823	6669			4399	5841	6375	
BsIHKA I	(4)	2337	3623	4878	6567	Eag I	(2)	1080	1652		
BsIW I	(1)	51				Ear I	(4)	1681	2571	2703	4444
Bsm I	(3)	1600	2901	3705		Eco57 I	(3)	1060	5107	6433	
BsmA I	(6)	982	2360	2441	2582	Eco72 I	(2)	895	1393		
		3000	5515			EcoN I	(1)	3176			
BsmF I	(15)	281	291	410	529	EcoO109 I	(3)	1123	1691	3181	
		601	665	1136	1472	EcoR I	(1)	1927			
		2670	3023	3106	3280	EcoR II	(21)	289	475	547	602
		3399	3409	6844				619	1266	1672	2324
BsoF I	(59)	14	326	329	336			2705	3084	3142	3214
		387	454	783	1064			3400	3978	4145	4298
		1083	1157	1160	1163			4586	4707	4720	5940
		1166	1169	1333	1419	EcoR V	(1)	3432			
		1533	1652	1655	2005	Ehe I	(1)	2673			
		2558	3140	3239	3306	Esp I	(2)	1359	6597		
		3357	3364	3367	3629	Fnu4H I	(59)	14	326	329	336
		3748	3850	3881	3884			387	454	783	1064
		3999	4111	4158	4385			1083	1157	1160	1163
		4466	4484	4487	4605			1166	1169	1333	1419
		4760	4903	4968	4971			1533	1652	1655	2005
		5177	5505	5844	5871			2558	3140	3239	3306
		5966	6109	6194	6238			3357	3364	3367	3629
		6254	6409	6476	6626			3748	3850	3881	3884
		6735	6815	6912				3999	4111	4158	4385
Bsp120 I	(2)	2747	3181					4466	4484	4487	4605
BspH I	(1)	5280						4760	4903	4968	4971
BspM I	(1)	6635						5177	5505	5844	5871
BspM II	(2)	4006	4018					5966	6109	6194	6238
Bsr I	(23)	721	1097	1121	2331			6254	6409	6476	6626
		2427	2551	2748	3058			6735	6815	6912	
		3168	3989	4361	4967	Fok I	(23)	307	359	686	1015
		4980	5094	5500	5618			1250	1483	2165	2287
		5661	5928	6023	6088			2325	2404	3004	3331
		6826	6922	6944				3383	3885	4034	4166
BsrB I	(5)	350	2766	3344	4252			5419	5600	5887	6019
		4493						6172	6416	6917	
BsrD I	(4)	5514	5688	6637	6930	Fsp I	(1)	5675			
BsrG I	(1)	2277				Gdi II	(9)	506	1079	1081	1370
BssH II	(3)	2717	4199	7012				1651	1653	4400	5840
BssS I	(2)	1138	4733					6374			
Bst1107 I	(1)	1968				Gsu I	(4)	1464	1519	5524	6539
BstB I	(1)	2787				Hae I	(11)	498	834	967	2329
BstE II	(1)	6448						2425	3939	3975	4575
BstN I	(21)	291	477	549	604			4586	5038	7007	
		621	1268	1674	2326	Hae II	(10)	364	2675	3334	3797
		2707	3086	3144	3216			4116	4438	4808	6355
		3402	3980	4147	4300			6785	6934		
		4588	4709	4722	5942	Hae III	(28)	498	507	776	782
		6519						834	967	1082	1373
BstU I	(24)	1195	1485	1657	2477			1654	1693	2329	2425
		2717	2719	2753	3561			2749	3183	3939	3975
		3667	3838	3998	4201			4401	4575	4586	4604
		4407	4409	4607	5188			5038	5496	5576	5843
		5518	6202	6475	6540			6377	6411	6941	7007
		6603	6896	7012	7014	Hga I	(9)	89	1042	1468	3534
BstX I	(2)	2421	3192					3697	4670	5248	5996
BstY I	(8)	881	1489	1669	5201			6332			
		5212	5298	5310	6769	HgiA I	(4)	2337	3623	4878	6567
Cac8 I	(42)	333	384	391	467	HgiE II	(1)	5139			
		562	581	634	653	Hha I	(39)	363	1063	1485	2405
		1059	1173	1465	2119			2674	2713	2719	2721
		2401	2562	2715	2719			3333	3669	3796	4039
		2751	3227	3303	3310			4115	4201	4203	4344
		3361	3608	3705	3792			4409	4437	4470	4740
		3946	4197	4201	4353			4807	4907	5081	5190
		4382	4491	4577	4614			5583	5676	6075	6125
		5174	5565	6198	6375			6202	6354	6542	6603
		6480	6660	6829	6935			6630	6784	6878	6898
		6939	7014					6933	7014	7016	
Cfr10 I	(9)	382	1463	2433	3308	Hinc II	(3)	900	2025	3082	
		4059	4083	5533	6884	Hind I	(3)	900	2025	3082	
		6937				Hind III	(1)	2571			
Csp6 I	(8)	52	1788	2278	5934	Hinf I	(19)	988	1320	1409	1446
		6167	6380	6388	6871						

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	1706	2598	2755	2956			3353	4192	4940	5636
	3168	3554	3662	3923			5983			
	4395	4460	4535	4931		Nco I	(2)	742	962	
	5448	6319	6532			Nde I	(1)	1866		
HinI I	(5)	1461	1660	2672	2777	NgoM I	(4)	382	1463	3308 6937
	6342					Nla III	(29)	71	88	583 655
HinP I	(39)	361	1061	1483	2403			746	966	1498 1646
	2672	2711	2717	2719				1706	2096	2409 2658
	3331	3667	3794	4037				2947	3484	3544 3707
	4113	4199	4201	4342				3856	3920	3944 4174
	4407	4435	4468	4738				4218	4564	5284 5775
	4805	4905	5079	5188				5785	5863	5899 6142
	5581	5674	6073	6123				7098		
	6200	6352	6540	6601		Nla IV	(20)	346	553	625 1124
	6628	6782	6876	6896				1240	1671	2535 2673
	6931	7012	7014					2749	3183	3348 4306
Hpa II	(39)	340	353	358	383			4592	4631	5403 5497
	404	857	1456	1464				5538	5749	6394 6759
	2074	2168	2303	2374		Not I	(1)	1652		
	2434	3005	3155	3288		Nru I	(1)	1195		
	3309	3334	3339	3352		Nsi I	(3)	585	657	3705
	4007	4019	4060	4070		Nsp7524 I	(6)	84	579	651 2654
	4084	4192	4278	4767				3703	4560	
	4914	4940	5130	5534		NspB II	(7)	1171	4105	4384 4902
	5568	5635	5745	5982				5147	6111	6734
	6755	6885	6938			NspH I	(6)	88	583	655 2658
Hph I	(13)	959	2226	2327	2641			3707	4564	
	3968	5297	5524	5938		PaeR7 I	(1)	7084		
	5996	6312	6459	6545		Pal I	(28)	498	507	776 782
	7052							834	967	1082 1373
Kas I	(1)	2671						1654	1693	2329 2425
Mae I	(17)	17	28	318	513			2749	3183	3939 3975
	836	1073	1605	1666				4401	4575	4586 4604
	2736	2906	3374	3733				5038	5496	5576 5843
	3744	5055	5308	5643				6377	6411	6941 7007
	6969					Ple I	(1)	4939		
Mae II	(22)	50	54	304	894	Pml I	(2)	895	1393	
	1392	1660	1797	2337		PpuM I	(1)	1123		
	2622	2777	3388	3469		Psp1406 I	(1)	5679		
	3527	3892	3909	4126		PspA I	(6)	339	403	856 2302
	5263	5679	6368	6854				3287	3351	
	7044	7113				Pst I	(4)	6	471	2559 3227
Mae III	(26)	46	248	1544	1876	Pvu I	(3)	1199	5823	6669
	2016	2738	2845	3523		Pvu II	(2)	1171	4384	
	3583	4186	4916	4979		Rsa I	(8)	53	1789	2279 5935
	5095	5378	5709	5767				6168	6381	6389 6872
	5920	5985	6116	6203		Rsr II	(2)	355	3336	
	6247	6442	6448	6550		Sac I	(1)	3623		
	6880	7118				Sap I	(2)	2571	4444	
Mbo I	(33)	427	881	886	1196	Sau3A I	(33)	427	881	886 1196
	1257	1271	1473	1489				1257	1271	1473 1489
	1669	2318	2463	2806				1669	2318	2463 2806
	3263	3756	5126	5201				3263	3756	5126 5201
	5212	5220	5298	5310				5212	5220	5298 5310
	5415	5756	5774	5820				5415	5756	5774 5820
	6303	6486	6666	6676				6303	6486	6666 6676
	6751	6769	6997	7018				6751	6769	6997 7018
	7056							7056		
Mbo II	(17)	231	996	1053	1081	Sau96 I	(15)	355	1123	1691 2747
	1499	1697	2463	2559				2748	3181	3182 3336
	2691	3827	4432	5221				5495	5574	5591 5813
	5294	6644	7003	7006				6087	6728	6940
	7039					ScrF I	(42)	291	340	341 404
Mme I	(3)	4774	4958	7006				405	477	549 604
Mnl I	(48)	103	258	318	446			621	857	858 1268
	508	766	772	795				1457	1674	2168 2303
	801	809	812	824				2304	2326	2374 2707
	944	1005	1346	1347				3006	3086	3144 3155
	1369	1486	1682	1982				3216	3288	3289 3352
	2153	2697	2705	3115				3353	3402	3980 4147
	3248	3376	3620	3806				4192	4300	4588 4709
	3833	3863	4127	4409				4722	4940	5636 5942
	4458	4668	4741	4992				5983	6519	
	5392	5473	5619	5825		Sec I	(40)	289	290	339 340
	5964	6188	6285	6325				403	476	502 547
	6733	6772	7017	7092				619	742	777 835
Msc I	(4)	967	2329	2425	3939			856	962	1267 1374
Mse I	(32)	22	57	122	138			2302	2324	2706 2759
	212	906	1759	1838				3005	3153	3214 3287
	1851	2228	2501	2792				3350	3351	3400 3401
	2801	3027	3034	3511				3868	3979	4299 4720
	3518	3739	3952	4096				5973	5996	6179 6210
	4331	4390	5266	5318				6517	6581	6720 7062
	5323	5337	5390	5625		SfaN I	(18)	380	591	663 1036
	5664	6281	6797	7110				1093	1225	1271 1571
Msl I	(4)	3190	5705	5864	6560			2872	3310	3758 3813
Msp I	(39)	340	353	358	383			4047	4145	4656 5708
	404	857	1456	1464				5901	6193	
	2074	2168	2303	2374		Sfc I	(9)	2	467	1047 2555
	2434	3005	3155	3288				3223	4825	5016 5694
	3309	3334	3339	3352				6543		
	4007	4019	4060	4070		Sfi I	(1)	504		
	4084	4192	4278	4767		Sma I	(6)	341	405	858 2304
	4914	4940	5130	5534				3289	3353	
	5568	5635	5745	5982		Spe I	(1)	512		
	6755	6885	6938			Sph I	(3)	583	655	3707
MspA1 I	(7)	1171	4105	4384	4902	Spl I	(1)	51		
	5147	6111	6734			Srf I	(3)	405	2304	3289
Nae I	(4)	384	1465	3310	6939	Ssp I	(3)	2663	3031	3691
Nar I	(1)	2672				Stu I	(2)	498	834	
Nci I	(21)	340	341	404	405	Sty I	(7)	742	835	962 2759
	857	858	1457	2168				5973	6720	7062
	2303	2304	2374	3006		Taq I	(14)	108	1256	1407 1893
	3155	3288	3289	3352				2787	4660	5957 6217

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	6317	6348	6360	6654	DpnII	`GATC,	33	Dra I	TTT AAA	6
	6669	7085			Dra III	CAC,NNN`GTG	4	Drd I	GACNN,NN`NNGTC	3
Tfi I	(13) 988	1320	1409	1446	Dsa I	C`CRYG,G	6	Eae I	Y`GGCC,R	11
	1706	2598	2755	3168	Eag I	C`GGCC,G	2	Ear I	CTCTTC 7/10	4
	3662	3923	4395	4535	Eco47 III	AGC GCT	-	Eco57 I	CTGAAG 21/19	3
	6532				Eco72 I	CAC GTG	2	EcoN I	CCTNN`N,NNAGG	1
Tsp45 I	(10) 46	2016	2738	3523	EcoO109 I	RG`GNC,CY	3	EcoR I	G`AATT,C	1
	3583	5709	5920	5985	EcoR II	`CCWGG,	21	EcoR V	GAT ATC	1
	6448	6550			Ehe I	GGC GCC	1	Esp I	GC`TNA,GC	2
Tth111 II	(8) 198	2258	3618	5149	Fnu4H I	GC`N,GC	59	Fok I	GGATG 14/18	23
	5158	5188	6205	6212	Fse I	GG,CCGG`CC	-	Fsp I	TGC GCA	1
Vsp I	(7) 122	906	1759	4096	Gdi II	`YGGC,CG	9	Gsu I	CTGGAG 21/19	4
	4331	4390	5625		Hae I	WGG CCW	11	Hae II	R,GCGC`Y	10
Xca I	(1) 1968				Hae III	GG CC	28	Hga I	GACGC 9/14	9
Xho I	(1) 7084				HgiA I	G,WGCW`C	4	HgiE II	ACCNNNNNNGGT	-1/131
Xho II	(8) 881	1489	1669	5201	Hha I	G,CG`C	39	HinC II	GTY RAC	3
	5212	5298	5310	6769	Hind II	GTY RAC	3	Hind III	A`AGCT,T	1
Xma I	(6) 339	403	856	2302	Hinf I	G`ANT,C	19	HinI I	GR`CG,YC	5
	3287	3351			HinP I	G`CG,C	39	Hpa I	GTT AAC	-
Xma III	(2) 1080	1652			Hpa II	C`CG,G	39	Hph I	GGTGA 12/11	13
					Kas I	G`GCGC,C	1	Kpn I	G,GTAC`C	-
					Mae I	C`TA,G	17	Mae II	A`CG,T	22
					Mae III	`GTNAC,	26	Mbo I	`GATC,	33
					Mbo II	GAAGA 12/11	17	Mlu I	A`CGC,T	-
					Mme I	TCCRAC 25/23	3	Mnl I	CCCT 10/10	48
					Msc I	TGG CCA	4	Mse I	T`TA,A	32
					Msl I	CAYNN NNRTG	4	Msp I	C`CG,G	39
					MspAl I	CMG CKG	7	Mun I	C`AATT,G	-
					Nae I	GCC GGC	4	Nar I	GG`CG,CC	1
					Nci I	CC`S,GG	21	Nco I	C`CATG,G	2
					Nde I	CA`TA,TG	1	NgoM I	G`CCGG,C	4
					Nhe I	G`CTAG,C	-	Nla III	,CATG`	29
					Nla IV	GGN NCC	20	Not I	GC`GGCC,GC	1
					Nru I	TCG CGA	1	Nsi I	A,TGCA`T	3
					Nsp7524 I	R`CATG,Y	6	NspB II	CMG CKG	7
					NspH I	R,CATG`Y	6	Pac I	TTA,AT`TAA	-
					PaeR7 I	C`TCGA,G	1	Pal I	GG CC	28
					PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	1
					Pme I	CTTT AAAC	-	Pml I	CAC GTG	2
					PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	1
					PspA I	C`CCGG,G	6	Pst I	C,TGCA`G	4
					Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	2
					Rsa I	GT AC	8	Rsr II	CG`GWC,CG	2
					Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	-
					Sal I	G`TCGA,C	-	Sap I	GCTCTTC 8/11	2
					Sau3A I	`GATC,	33	Sau96 I	G`GNC,C	15
					Sca I	AGT ACT	-	ScrF I	CC`N,GG	42
					Sec I	C`CNNG,G	40	SfaN I	GCATC 9/13	18
					Sfc I	C`TRYA,G	9	Sfi I	GGCCN,NNN`NGGCC	1
					Sma I	CCC GGG	6	SnaB I	TAC GTA	-
					Spe I	A`CTAG,T	1	Sph I	G,CATG`C	3
					Spl I	C`GTAC,G	1	Srf I	GGCC GGGC	3
					Ssp I	AAT ATT	3	Stu I	AGG CCT	2
					Sty I	C`CWGG,G	7	Swa I	ATTT AAAT	7
					Taq I	T`CG,A	14	Tfi I	G`AWT,C	13
					Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTC	-
					Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	7
					Xba I	T`CTAG,A	-	Xca I	GTA TAC	1
					Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
					Xho II	R`GATC,Y	8	Xma I	C`CCGG,G	6
					Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	-

Site usage in pMPB-SOS:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	-	Aci I	C`CG,C	72
Afe I	AGC GCT	-	Afl II	C`TTAA,G	-
Afl III	A`CRYG,T	3	Age I	A`CCGG,T	-
Aha II	GR`CG,YC	5	Ahd I	GACNN,N`NNGTC	1
Alu I	AG CT	31	Alw I	GGATC 8/9	18
AlwN I	CAG,NNN`CTG	2	Apa I	G,GGCC`C	2
ApaL I	G`TGCA,C	3	Apo I	R`AATT,Y	6
Asc I	GG`CGCG,CC	-	Ase I	AT`TA,AT	7
Asp718	G`GTAC,C	-	Ava I	C`YCGR,G	10
Ava II	G`GWC,C	7	Avr II	C`CTAG,G	1
BamH I	G`GATC,C	1	Ban I	G`GYRC,C	4
Ban II	G,RGCY`C	6	Bbe I	G,GC GC`C	1
Bbs I	GAAGAC 8/12	1	Bbv I	GCAGC 13/17	20
Bbv II	GAAGAC 7/11	1	Bcl I	T`GATC,A	2
Bcn I	CC,S`GG	21	Bfa I	C`TA,G	17
Bgl I	GCCN,NNN`NGGC	3	Bgl II	A`GATC,T	-
Blp I	GC`TNA,GC	2	Bpm I	CTGGAG 22/20	4
Bsa I	GGTCTC 7/11	4	Bsaa I	YAC GTR	6
BsaB I	GATNN NNATC	2	Bsah I	GR`CG,YC	5
BsaJ I	C`CNNG,G	40	Bsaw I	W`CCGG,W	9
BseR I	GAGGAG 16/14	2	Bsg I	GTGCAG 22/20	2
BsiC I	TT`CG,AA	1	Bsie I	CG,RY`CG	8
BsiHKA I	G,WGCW`C	4	BsiW I	C`GTAC,G	1
Bsm I	GAATG,C 7	3	Bsma I	GTCTC`/9	6
BsmB I	CGTCTC 7/11	-	BsmF I	GGGAC 15/19	15
BsoF I	GC`N,GC	59	Bsp120 I	G`GGCC,C	2
Bsp1286 I	G,DGCH`C	-	BspH I	T`CATG,A	1
BspM I	ACCTGC 10/14	1	BspM II	T`CCGG,A	2
Bsr I	ACT,GG`	23	BsrB I	GAG CGG	5
BsrD I	GCAATG, 8	4	BsrG I	T`GTAC,A	1
BssH II	G`CGCG,C	3	Bsss I	C`TCGT,G	2
Bst1107 I	GTA TAC	1	BstB I	TT`CG,AA	1
BstE II	G`GTNAC,C	1	BstN I	CC`W,GG	21
BstU I	CG CG	24	BstX I	CCAN,NNNN`NTGG	2
BstY I	R`GATC,Y	8	Bsu36 I	CC`TNA,GG	-
Cac8 I	GCN NGC	42	Cfr10 I	R`CCGG,Y	9
Cla I	AT`CG,AT	-	Csp6 I	G`TA,C	8
Dde I	C`TNA,G	9	Dpn I	GA TC	33