

pSOHU Full-Length Sequence

TGAAAGACCCACCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTA
GATCAAGGTTAGGAACAGAGACAGCAGAAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCCGGCTCAGGGCCAAGAACAG
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GAAGCCTATAGAGTACGGCATAGATAAAAATAAAAGATTTTATTTAGTCTCCAGAAAAGGGGGAA

Unique enzymes in pSOHU:

Spe I	A`CTAG,T	660			2633	2688	4498	4720	
BstE II	G`GTNAC,C	1087			5975				
BsrG I	T`GTAC,A	1282		Ban I	(14)	244	401	1142	1397
EcoR I	G`AATT,C	1404				1751	2007	2678	2835
Nco I	C`CATG,G	1475				3201	4308	5582	5765
Bbv II	GAAGAC 7/11	1561		Ban II	(8)	5879	5900		
Bbs I	GAAGAC 8/12	1562				338	351	1741	1934
Bsg I	GTGCAG 22/20	1664		Bbe I	(6)	2772	2785	5832	5846
Nru I	TCG CGA	1708				1401	2011	5586	5769
BsaB I	GATNN NNATC	1775		Bbs I	(1)	5883	5904		
Pme I	CTTT AAAC	1879		Bbv I	(9)	1562			
BsiC I	TT`CG,AA	1892				931	939	1588	1693
BstB I	TT`CG,AA	1892		Bcn I	(14)	3886	3889	4095	4789
Bsp120 I	G`GGCC,C	1930				5400			
Apa I	G,GGCC`C	1934		Bbv II	(1)	1561			
HinD III	A`AGCT,T	2106		Bcn I	(14)	164	399	400	571
Mlu I	A`CGCG,T	2112				724	2598	2833	2834
Stu I	AGG CCT	2120				3848	4544	4895	5396
Sal I	G`TCGA,C	2124		Bfa I	(13)	5431	5782		
Acc I	GT`MK,AC	2125				31	219	661	673
BsaA I	YAC GTR	2257		Bgl I	(2)	1394	1586	1943	2463
Sca I	AGT ACT	4840		Bpm I	(3)	2653	3962	4215	4550
Sph I	G,CATG`C	5755		Bsa I	(6)	5985			
Number of enzymes = 23									
				BsaA I	(1)	4480	5598		
				BsaB I	(1)	2400	4430	6048	
				BsaH I	(10)	476	530	1149	2888
						2909	4421		
				BsaJ I	(32)	161	240	250	397
						461	497	546	547
						694	733	734	746
						747	1167	1236	1245
						1265	1266	1475	1780
						1918	1971	2595	2674
						2684	2831	2894	3196
						3617	5701	5779	5785
				BsaW I	(3)	3673	3820	4651	
				BseR I	(4)	464	1293	1332	2897
				Bsg I	(1)	1664			
				BsiC I	(1)	1892			
				BsiE I	(9)	592	727	1596	1712
						3373	3807	4730	4879
						5626			
				BsiHKA I	(6)	338	2772	3785	4946
						5031	5528		
				BsmA I	(22)	107	475	531	609
						734	832	949	1073
						1132	1150	1328	1495
						2096	2417	2540	2887
						2908	4422	5196	5349
						5393	6065		
				BsmB I	(7)	733	831	1072	1131
						1329	5350	5392	
				BsmF I	(11)	172	185	564	729
						764	1205	1649	2008
						2606	2619	5761	
				BsoF I	(34)	727	901	917	920
						925	928	1133	1577
						1596	1670	1673	1676
						1679	1682	1846	3282
						3363	3381	3384	3502
						3667	3810	3875	3878
						4084	4412	4751	4778
						4873	5102	5389	5498
						5602	5675		
				Bsp120 I	(1)	1930			
				BspH I	(4)	4187	5195	5300	5824
				Bsr I	(17)	374	1030	1058	1610
						1634	1935	2808	3258
						3874	3887	4001	4407
						4525	4568	4835	5007
						5713			
				BsrB I	(5)	1042	1915	3149	3390
						5201			
				BsrD I	(2)	4421	4595		
				BsrG I	(1)	1282			
				BssH II	(5)	317	368	1960	2751
						2802			
				BssS I	(4)	1651	3640	5024	5331
				BstB I	(1)	1892			
				BstE II	(1)	1087			
				BstN I	(18)	241	548	735	748
						1169	1194	1217	1237
						1267	1781	1973	2675
						3197	3485	3606	3619
						5702	5979		
				BstU I	(24)	317	319	370	903
						905	1135	1708	1928
						1962	1964	2114	2751
						2753	2804	3304	3306
						3504	4095	4425	4918
						5250	5350	5352	5455
				BstY I	(6)	4108	4119	4205	4217
						4985	5002		
				Bsu36 I	(2)	781	1018		
				Cac8 I	(34)	28	32	319	370
						582	586	631	650
						1199	1572	1686	1930

The following enzymes do not cut pSOHU:

Age I	Avr II	BamH I	Bcl I						
Bgl II									
Blp I	BsiW I	Bsm I	Bsp1286 I						
BspM I				BsaW I	(3)	3673	3820	4651	
BspM II	Bst1107 I	BstX I	Cla I	BseR I	(4)	464	1293	1332	2897
Dra III				Bsg I	(1)	1664			
Eco72 I	Esp I	Fse I	Hpa I	BsiC I	(1)	1892			
Mun I				BsiE I	(9)	592	727	1596	1712
Not I	Nsi I	PaeR7 I	PflM I			3373	3807	4730	4879
Pml I						5626			
Rsr II	Sac II	Sfi I	SnaB I	BsiHKA I	(6)	338	2772	3785	4946
Spl I						5031	5528		
				BsmA I	(22)	107	475	531	609
						734	832	949	1073
						1132	1150	1328	1495
						2096	2417	2540	2887
						2908	4422	5196	5349
						5393	6065		
				BsmB I	(7)	733	831	1072	1131
						1329	5350	5392	
				BsmF I	(11)	172	185	564	729
						764	1205	1649	2008
						2606	2619	5761	
				BsoF I	(34)	727	901	917	920
						925	928	1133	1577
						1596	1670	1673	1676
						1679	1682	1846	3282
						3363	3381	3384	3502
						3667	3810	3875	3878
						4084	4412	4751	4778
						4873	5102	5389	5498
						5602	5675		
				Bsp120 I	(1)	1930			
				BspH I	(4)	4187	5195	5300	5824
				Bsr I	(17)	374	1030	1058	1610
						1634	1935	2808	3258
						3874	3887	4001	4407
						4525	4568	4835	5007
						5713			
				BsrB I	(5)	1042	1915	3149	3390
						5201			
				BsrD I	(2)	4421	4595		
				BsrG I	(1)	1282			
				BssH II	(5)	317	368	1960	2751
						2802			
				BssS I	(4)	1651	3640	5024	5331
				BstB I	(1)	1892			
				BstE II	(1)	1087			
				BstN I	(18)	241	548	735	748
						1169	1194	1217	1237
						1267	1781	1973	2675
						3197	3485	3606	3619
						5702	5979		
				BstU I	(24)	317	319	370	903
						905	1135	1708	1928
						1962	1964	2114	2751
						2753	2804	3304	3306
						3504	4095	4425	4918
						5250	5350	5352	5455
				BstY I	(6)	4108	4119	4205	4217
						4985	5002		
				Bsu36 I	(2)	781	1018		
				Cac8 I	(34)	28	32	319	370
						582	586	631	650
						1199	1572	1686	1930

		1962	1966	2460	2464			4897	5279	5583	5766
		2753	2804	3250	3279			5880	5901		
		3388	3474	3511	4081	HinP I	(40)	317	319	368	370
		4472	5485	5633	5653			646	903	922	1398
		5657	5753	5794	5842			1574	1960	1962	1968
		5884	5914					2008	2751	2753	2802
Cfr10 I	(4)	629	4440	5903	5912			2804	3079	3239	3304
Csp6 I	(8)	402	658	1283	2265			3332	3365	3645	3712
		2836	4839	5515	6026			3812	3986	4095	4488
Dde I	(19)	75	167	208	476			4581	4918	5250	5350
		781	1018	1290	1872			5453	5583	5604	5737
		2507	2601	2642	2911			5766	5820	5880	5901
		2982	3742	4151	4317	Hpa II	(24)	163	398	569	630
		4857	5283	5518				723	1401	2597	2832
Dpn I	(24)	94	459	1046	1178			3175	3674	3821	3847
		1363	1711	1772	1786			4037	4441	4475	4542
		2527	4035	4110	4121			4652	4894	5395	5429
		4129	4207	4219	4324			5781	5904	5913	5928
		4665	4683	4729	4987	Hph I	(14)	1157	1183	1472	2042
		5004	5040	5625	5849			4204	4431	4845	5053
DpnII	(24)	92	457	1044	1176			5086	5370	5379	5872
		1361	1709	1770	1784			5917	5998		
		2525	4033	4108	4119	Kas I	(6)	1397	2007	5582	5765
		4127	4205	4217	4322			5879	5900		
		4663	4681	4727	4985	Kpn I	(2)	405	2839		
		5002	5038	5623	5847	Mae I	(13)	31	219	661	673
Dra I	(6)	1879	2202	2215	4226			1394	1586	1943	2463
		4245	4937					2653	3962	4215	4550
								5985			
Drd I	(3)	1564	3565	5444				742	1081	1122	1902
Dsa I	(3)	694	1475	5785		Mae II	(12)	2058	2251	2256	4170
Eae I	(10)	582	724	1109	1130			4586	4959	5279	5721
		1478	1593	3296	4748			39	994	1022	1087
		5782	5914			Mae III	(21)	1231	1938	2173	2252
Eag I	(2)	724	1593					2471	2949	3823	3886
Ear I	(7)	1070	1311	2371	3079			4002	4285	4616	4674
		3341	5155	5643				4827	5015	5403	5694
Eco47 III	(2)	923	5821					5714			
Eco57 I	(4)	1573	4014	5028	6032			92	457	1044	1176
EcoN I	(2)	784	1392			Mbo I	(24)	1361	1709	1770	1784
EcoO109 I	(7)	254	1219	1636	2361			2525	4033	4108	4119
		2688	5336	5790				4127	4205	4217	4322
EcoR I	(1)	1404						4663	4681	4727	4985
EcoR II	(18)	239	546	733	746			5002	5038	5623	5847
		1167	1192	1215	1235	Mbo II	(16)	1086	1299	1509	1566
		1265	1779	1971	2673			1594	1991	2359	3095
		3195	3483	3604	3617			3329	4128	4201	4956
		5700	5977					5034	5143	5631	5843
EcoR V	(3)	140	2573	5968				2112			
Ehe I	(6)	1399	2009	5584	5767	Mlu I	(1)	829	1106	2896	2948
		5881	5902			Mme I	(6)	3681	3865		
Fnu4H I	(34)	727	901	917	920			167	216	368	387
		925	928	1133	1577	Mnl I	(49)	432	460	484	506
		1596	1670	1673	1676			510	566	776	872
		1679	1682	1846	3282			1168	1271	1304	1310
		3363	3381	3384	3502			1313	1319	1349	1352
		3667	3810	3875	3878			1367	1374	1390	1457
		4084	4412	4751	4778			1518	1859	1860	1985
		4873	5102	5389	5498			2373	2650	2802	2821
Fok I	(11)	5602	5675					2866	2893	2917	2977
		423	1140	1300	1528			3306	3355	3565	3648
		1763	2856	4326	4507			3899	4299	4380	4526
		4794	5437	5681				4732	5327	5385	5645
Fsp I	(2)	4582	5605					5929			
Gdi II	(9)	723	725	1129	1592	Msc I	(3)	584	1111	1480	
		1594	3297	4747	5783	Mse I	(29)	36	1007	1119	1149
		5915						1173	1419	1878	1887
Gsu I	(3)	2401	4431	6049				2201	2214	2294	2385
Hae I	(7)	584	1111	1480	2120			2468	3002	3100	3228
		3472	3483	3945				3287	4173	4225	4230
Hae II	(10)	925	1401	2011	3335			4244	4297	4532	4571
		3715	5586	5769	5823			4936	5308	5489	5686
		5883	5904					5956			
Hae III	(30)	129	173	584	726			2057	4612	4771	
		762	774	987	1111	Msl I	(3)	163	398	569	630
		1132	1197	1480	1595	Msp I	(24)	723	1401	2597	2832
		1932	2120	2362	2562			3175	3674	3821	3847
		2607	3298	3472	3483			4037	4441	4475	4542
		3501	3945	4403	4483			4652	4894	5395	5429
		4750	5337	5635	5784			5781	5904	5913	5928
		5792	5916					588	1684	2933	3281
Hga I	(10)	381	642	895	1555	MspAl I	(10)	3809	4054	4995	5461
		2815	3567	4155	4887			5655	6011		
		5445	5914			Nae I	(2)	631	5914		
HgiA I	(6)	338	2772	3785	4946	Nar I	(6)	1398	2008	5583	5766
		5031	5528					5880	5901		
HgiE II	(2)	4046	5526					163	398	399	570
Hha I	(40)	319	321	370	372	Nci I	(14)	723	2597	2832	2833
		648	905	924	1400			3847	4543	4894	5395
		1576	1962	1964	1970			5430	5781		
		2010	2753	2755	2804			1475			
		2806	3081	3241	3306	Nco I	(1)	2186	5531		
		3334	3367	3647	3714	Nde I	(2)	629	5912		
		3814	3988	4097	4490	NgoM I	(2)	30	2462		
		4583	4920	5252	5352	Nhe I	(2)	62	1205	1479	2028
		5455	5585	5606	5739	Nla III	(19)	2353	2494	2948	3115
		5768	5822	5882	5903			3461	4191	4682	4692
HinC II	(2)	1413	2126					4770	4806	5199	5304
Hind II	(2)	1413	2126					5388	5755	5828	
HinD III	(1)	2106						188	201	246	403
Hinf I	(18)	442	450	791	802	Nla IV	(33)	521	552	692	761
		1501	1833	1923	2081			893	1144	1221	1399
		2346	2992	3014	3035			1637	1753	1932	2009
		3292	3357	3432	3838			2622	2635	2680	2837
		4355	5993					3203	3489	3528	4310
HinI I	(10)	742	1398	1902	2008						

Sca I	AGT ACT	1	SerF I	CC`N,GG	Sty I	C`CWWG,G	7	Taq I	T`CG,A	
32					11					
Sec I	C`CNNG,G	32	SfaN I	GCATC 9/13	Tfi I	G`AWT,C	10	Tsp45 I	`GTSAC,	8
20					Tth111 I	GACN`N,NGTC	4	Tth111 II	CAARCA 16/14	8
Sfc I	C`TRYA,G	10	Sfi I	GGCCN,NNN`NGGCC -	Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	2
Sma I	CCC GGG	2	SnaB I	TAC GTA -	Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNNTGG-	
Spe I	A`CTAG,T	1	Sph I	G,CATG`C 1	Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	6
Sp1 I	C`GTAC,G	-	Srf I	GCCC GGGC -	Xma I	C`CCGG,G	2	Xma III	C`GGCC,G	2
Ssp I	AAT ATT	3	Stu I	AGG CCT 1						