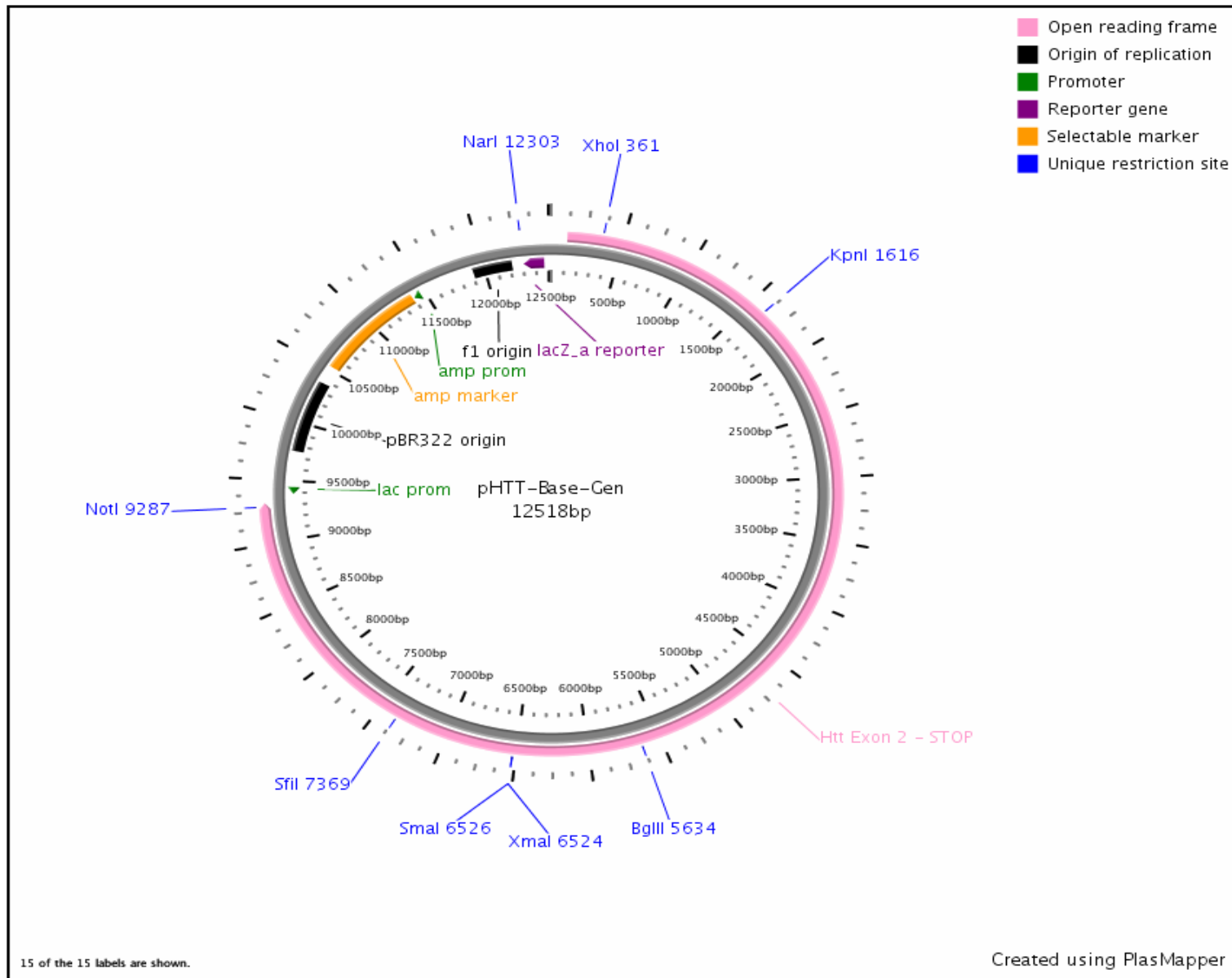


# pHtt-Base-gen (Blue Heron)

Htt wt ORF at bp 114 (CAC) aa 88 to STOP at bp 9317



# pHtt-Base-gen

Flanking vector sequence in **BLACK**, Htt wt ORF at bp 114 (CAC) aa 88 to STOP at bp 9317 in **GREEN**

```
1 GACTCTCTTA AGGTAGCAAA TATTAGCACA GGTGGGTAGT TTTGAAGACA CACTCATGCG GAGACGTCGA TCGATCGAAG TCAGTCAGTC CAAATTGGCC
101 AATTGGCGTC TCACACCGAC CAAAGAAAGA ACTTTCAGCT ACCAAGAAAG ACCGTGTGAA TCATTGTCTG ACAATATGTG AAAACATAGT GGCACAGTCT
201 GTCAGAAATT CTCCAGAATT TCAGAAACTT CTGGGCATCG CTATGGAAC TTTTCTGCTG TGCAGTGATG ACGCAGAGTC AGATGTCAGG ATGGTGGCTG
301 ACGAATGCCT CAACAAAGTT ATCAAAGCTT TGATGGATTC TAATCTTCCA AGGTTACAGC TCGAGCTCTA TAAGGAAATT AAAAAGAATG GTGCCCTCG
401 GAGTTTGCGT GCTGCCCTGT GGAGGTTTGC TGAGCTGGCT CACCTGGTTC GGCCTCAGAA ATGCAGGCCT TACCTGGTGA ACCTTCTGCC GTGCCGACT
501 CGAACAAAGCA AGAGACCCGA AGAATCAGTC CAGGAGACCT TGGCTGCAGC TGTTCCCAA ATTATGGCTT CTTTTGGCAA TTTTGCAAAT GACAATGAAA
601 TTAAGTTTTT GTTAAAGGCC TTCATAGCGA ACCTGAAGTC AAGCTCCCC ACCATTCCGC GGACAGCGGC TGGATCAGCA GTGAGCATCT GCCAGCACTC
701 AAGAAGGACA CAATATTTCT ATAGTTGGCT ACTAAATGTG CTCTTAGGCT TACTCGTTCC TGTCGAGGAT GAACACTCCA CTCTGCTGAT TCTTGGCGTG
801 CTGCTCACCC TGAGGTATTT GGTGCCCTTG CTGCAGCAGC AGGTCAAGGA CACAAGCCTG AAAGGCAGCT TCGGAGTGAC AAGGAAAGAA ATGGAAGTCT
901 CTCCTTCTCG AGAGCAGCTT GTCCAGGTTT ATGAACTGAC GTTACATCAT ACACAGCACC AAGACCACAA TGTTGTGACC GGAGCCCTGG AGCTGTTGCA
1001 GCAGCTTTC AGAACGCCTC CACCCGAGT TCTGCAAACC CTGACCCGAG TCGGGGGCTC TGGGCGACTC ACCGCTGCTA AGGAGCCGCA TGGTGGCCGA
1101 AGCCGTAGTG AGAGTATTGT GGAACCTATA GCTGGAGGGG GTTCTCATG CAGCCCTGTCT CTTTCAAGAA AACAAAAAGG CAAAGTGCTC TTAGGGAAG
1201 AAGAAGCCTT GGAGGATGAC TCTGAATCGA GATCGGATGT CAGCAGCTCT GCCTTAACAG CCTCAGTGAA GGATGAGATC AGTGGAGAGC TGGCTGCTTC
1301 TTCAGGGGTT TCCACTCCAG GGTGAGCAGG TCATGACATC ATCACAGAAC AGCCACGGTC ACAGCACACA CTGCAGGCGG ACTCAGTGA TCTGGCCAGC
1401 TGTGACTTGA CAAGCTCTGC CACTGATGGG GATGAGGAGG ATATCTTGAG CCACAGCTCC AGCCAGGTCA GCGCCGTCCC ATCTGACCTT GCCATGGACC
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1601 TGTGTTAGAC GGTACCGACA ACCAGTATTT GGGCCTGCAG ATTGGACAGC CCCAGGATGA AGATGAGGAA GCCACAGGTA TTCTTCTGTA TGAAGCCTCG
1701 GAGGCCTTCA GAACTCTTC CATGGCCCTT CAACAGGCAC AATTTATTGAA AACTGATGAGT CACTGCAGGC AGCCTTCTGA CAGCAGGATT GATAAATTTG
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2001 GCCCTCAGCT GTGTGGGAGC AGCTGTGGCC CTCACCCCGG AATCTTTCTT CAGCAAACCT TATAAAGTTC CTCTTGACAC CACGGAATAC CCTGAGGAAC
2101 AGTATGTCTC AGACATCTTG AACTACATCG ATCATGGAGA CCCACAGGTT CGAGGAGCCA CTGCCATTCT CTGTGGGACC CTCATCTGCT CCATCCTCAG
2201 CAGGTCCCGC TTCCACGTGG GAGATTGGAT GGGCACCATT AGAACCTCA CAGGAAATAC ATTTTCTTTG GCGGATTGCA TTCCTTTGCT GCGGAAAAACA
2301 CTGAAGGATG AGTCTTCTGT TACTTGCAAG TTAGCTTGTA CAGCTGTGAG GAAGTGTGTC ATGAGTCTCT GCAGCAGCAG CTACAGTGAG TTAGGACTGC
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3101 GGATCTCTCA CCCCATCAAG ATGCTTTGAT TTTGGCCGGA AACTTGTCTG CAGCCAGTGC TCCCAAATCT CTGAGAAGTT CATGGGCTC TGAAGAAGAA
3201 GCCAACCAG CAGCCACCAA GCAAGAGGAG GTCTGGCCAG CCCTGGGGGA CCGGGCCCTG GTGCCATGG TGGAGCAGCT CTTCTCTCAC CTGCTGAAGG
3301 TGATTAACAT TTGTGCCAC GTCCTGGATG ACGTGGCTCC TGGACCCGCA ATAAAGGCAG CCTTGCCTTC TCTAACAAAC CCCCCTTCTC TAAGTCCCAT
3401 CCGACGAAAG GGGAAGGAGA AAGAACCAGG AGAACAAGCA TCTGTACCGT TGAGTCCCAA GAAAGGCAGT GAGGCCAGTG CAGCTTCTAG ACAATCTGAT
3501 ACCTCAGGTC CTGTTACAAC AAGTAAATCC TCATCACTGG GGAGTTTCTA TCATTTCTCT TCATACCTCA AACTGCATGA TGTCCTGAAA GCTACACAGC
3601 CTAACACTAA GGTACAGCTG GATCTTCA GAAGTATTGA ACAGCACGGA AAAGTATTGA GGGTCTTCTC GCTCAGCTT GGATGTTCT TCTCAGATAC TAGAGCTGGC
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3901 CCAGTGTGAG GCCAGGCTTG TACCACTACT GCTTCATGGC CCCGTACACC CACTTCACCC AGGCCCTCGC TGACGCCAGC CTGAGGAACA TGGTGCAGGC
4001 GGAGCAGGAG AACGACACCT CGGGATGGTT TGATGTCCTC CAGAAAGTGT CTACCCAGTT GAAGACAAAC CTCACGAGTG TCACAAAGAA CCGTGCAGAT
4101 AAGAATGCTA TTCATAATCA CATTGTTTTG TTTGAACCTC TTGTTATAAA AGCTTTAAAA CAGTACACGA CTACAACATG TGTGCAGTTA CAGAAGCAGG
4201 TTTTAGATTT GCTGGCGCAG CTGGTTCACT TACGGGTTAA TTAAGTGTCT CTGGATTGAG ATCAGGTGTT TATTGGCTTT GTATTGAAAC AGTTTGAATA
4301 CATTGAAGTG GGCCAGTTCA GGAATCAGA GGCAATCATT CCAAACATCT TTTTCTTCTT GGTATTACTA TCTTATGAAC GCTATCATTC AAAACAGATC
4401 ATTGGAATTC CTAATAATCAT TCAGCTCTGT GATGGCATCA TGGCCAGTGG AAGGAAGGCT GTGACACATG CCATACCGGC TCTGCAGCCC ATAGTCCACG
```

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4701 CTCCCAATGT TAGCCAAACA GCAGATGCAC ATTGACTCTC ATGAAGCCCT TGGAGTGTTA AATACATTAT TTGAGATTTT GGCCCCTTCC TCCCTCCGTC  
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9001 CGGTGCGCAT GGCCACGTGG AGCCTCTCCT GCTTCTTTGT CAGCGCTCC ACCAGCCCGT GGGTCCGCGC GATCCTCCA CATGTCTATC GCAGGATGGG  
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12501 CTCTCTTAAAG GTAGCAAA

## RESTRICTION MAP: ALL ENZYMES

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Enzyme      Cuts    [ ----- Base 5' to Cleave Sites ----- ]
=====
AatII      3        67  2845 11525
AccI       3        4050 4804 5881
AclI       3        10829 11202 11786
AcyI       10       64   106  2842  3973  4848  7792  8212 1114011522 12302
AflII      3         7   6302 12505

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AflIII	7	2630	4176	6118	7083	7085	9080	9710	
AgeI	0								
AhaIII	5	2560	4156	10469	10488	11180			
AluI	91	138	327	359	365	434	549	643	868
		917	992	1004	1028	1067	1131	1246	1289
		1399	1414	1456	1540	1572	1815	2008	2022
		2334	2343	2380	2402	2459	2500	2669	2697
		2940	3040	3087	3278	3483	3591	3695	4152
		4220	4424	4530	4547	4689	4952	5135	5250
		5308	5817	6221	6294	6404	6437	6719	6833
		7078	7109	7425	7432	7470	7496	7646	7676
		7690	7918	8012	8106	8261	8528	8561	9104
		9176	9294	9353	9375	9470	9534	9652	9878
		9968	10014	10271	10792	10892	10955	11634	11653
		11831	12088	12374					
AlwNI	11	669	3510	5250	5375	6198	6509	6542	7900
		8081	8924	10126					
ApaBI	3	1371	3157	7881					
ApaI	3	3257	6530	8999					
ApaLI	7	5849	6789	8046	8583	10024	11270	11767	
ApoI	12	206	216	1794	4405	4882	5057	5924	6322
		6609	8406	11803	11814				
AscI	0								
AsuI	48	1496	1510	1560	1631	1724	1994	2000	2027
		2176	2203	3184	3248	3253	3254	3342	3507
		3938	3962	4310	4781	5348	5942	6184	6377
		6521	6526	6527	6632	6710	7055	7231	7261
		7342	7930	8400	8599	8615	8951	8995	8996
		9187	10645	10724	10741	10963	11579	11992	12352
AsuII	0								
AvaI	7	360	1023	4019	6432	6523	7665	11890	
AvaII	14	1496	1510	2176	2203	3248	3342	3507	6184
		7231	7342	7930	8951	10741	10963		

AvrII	2	3737	6308							
BalI	11	98 8787	1395 8895	3057 9012	3236	3699	4443	4890	6334	
BamHI	4	5794	7589	7903	8791					
BclI	5	1829	2404	5332	5638	7945				
BetI	8	978	1964	4799	5233	6140	9916	10063	10894	
BglI	7	862	1701	4476	7368	8607	10723	12317		
BglII	1	5633								
BsaAI	6	2216	6119	7086	8342	9016	12001			
BsaBI	3	340	4258	5211						
BseMII	24	468 3517 7933	1276 3676 7993	1396 3696 8088	2018 5816 8183	2122 6018 8507	2210 7046 9999	3034 7257 10408	3121 7403 10574	
BsePI	0									
BsiYI	64	421 1628 3462 4897 6530 7670 8828 9732	655 1733 3907 5351 6548 7754 8891 9750	658 2036 3982 5408 6640 7128 8116 8953 9916	1051 3243 4024 5689 7184 8120 9058 10195	1318 3257 4319 5867 7184 8120 9167 11643	1426 3296 4450 6101 7301 8156 9167 11896	1493 3323 4562 6105 7413 8597 9295 11897	1558 3407 4799 6181 7486 8603 9558 12223	
Bsp1407I	4	2337	4980	7891	8635					
BspHI	9	1331	2359	2888	4739	6259	8836	10430	11438	11543
BspLU11I	4	2630	4176	9080	9710					
BspMII	3	1964	5233	6140						
BstEII	2	7117	9272							
BstXI	7	563	2604	3843	5478	7102	8783	12464		
Cac8I	53	409	436	465	693	798	1291	1375	1397	

1635	1767	3148	3238	3697	3977	3997	4213
5320	5705	5869	5873	5997	6001	6288	6292
6442	6451	6770	7008	7012	7058	7062	7369
7415	8089	8154	8166	8334	8592	9102	9503
9532	9641	9727	9764	10324	10715	11728	12104
12147	12161	12352	12372	12376			

CauII	22	1825	2037	3252	5346	5901	6524	6525	7129
		7451	7845	7935	8268	8598	8662	8936	8955
		9000	10090	10786	11137	11638	11673		

Cfr10I	7	4475	6449	7010	7413	9238	10683	12102	
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CfrI	23	96	1094	1393	2710	3055	3133	3234	3697
		4441	4888	6332	7360	7411	7700	7936	8785
		8893	9010	9286	9297	9549	10991	12454	

ClaI	3	71	2128	2410					
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CviJI	290	98	138	297	327	359	365	434	438
		452	467	543	549	567	618	643	669
		728	748	856	868	917	984	992	1004
		1028	1067	1096	1102	1131	1153	1206	1246
		1260	1289	1293	1352	1395	1399	1414	1450
		1456	1462	1518	1540	1562	1572	1633	1649
		1671	1695	1704	1725	1772	1815	1844	1995
		2001	2008	2022	2028	2157	2334	2343	2380
		2402	2444	2459	2492	2500	2538	2555	2657
		2669	2697	2712	2768	2815	2940	3040	3057
		3087	3111	3135	3153	3186	3201	3213	3236
		3240	3255	3278	3336	3360	3474	3483	3591
		3666	3695	3699	3831	3847	3877	3895	3911
		3916	3939	3963	3979	4152	4220	4276	4312
		4424	4443	4458	4479	4487	4530	4547	4689
		4713	4746	4782	4890	4952	5135	5250	5261
		5278	5308	5322	5349	5508	5550	5612	5644
		5657	5710	5806	5817	5843	5871	5919	5943
		5999	6020	6221	6286	6294	6307	6334	6360
		6378	6404	6431	6437	6449	6456	6522	6528
		6633	6692	6711	6719	6727	6807	6821	6833
		6870	6933	6981	7051	7056	7078	7109	7228
		7263	7292	7318	7362	7371	7413	7425	7432
		7448	7460	7470	7496	7614	7636	7646	7676
		7690	7702	7727	7788	7848	7897	7918	7923
		7938	8012	8106	8130	8141	8149	8179	8202
		8261	8332	8402	8500	8528	8561	8590	8601
		8610	8617	8691	8761	8775	8787	8876	8895

8997	9012	9022	9055	9104	9176	9189	9219
9229	9242	9288	9294	9299	9337	9353	9375
9427	9448	9470	9534	9551	9633	9652	9725
9736	9754	9780	9878	9968	10014	10019	10044
10123	10188	10199	10242	10271	10634	10646	10687
10713	10717	10726	10792	10882	10892	10955	10993
11580	11634	11653	11686	11726	11730	11831	11851
11889	11993	12074	12088	12102	12320	12354	12374
12456	12471						

CviRI	73	262	463	546	585	833	909	998	1034
		1150	1373	1637	1765	1893	2278	2326	2371
		2399	2475	2567	2756	2877	2974	3150	3480
		3575	3707	3995	4095	4184	4484	4536	4634
		4727	5420	5524	5851	5922	6059	6201	6216
		6398	6444	6495	6575	6716	6791	6813	6818
		6930	6968	7367	7395	7800	8048	8098	8207
		8544	8585	8632	8688	8927	9216	9537	10026
		10322	10657	10747	10940	11028	11272	11631	11769 12396

DdeI	51	430	454	743	810	1078	1190	1262	1382
		2004	2092	2108	2196	2424	3012	3020	3107
		3171	3390	3503	3662	3682	3981	4584	5463
		5802	6004	6069	6282	6586	6669	6837	6916
		7032	7156	7243	7389	7497	7749	7919	7979
		8074	8169	8493	8521	8562	9985	10394	10560
		11100	11526	11761					

DpnI	52	70	74	674	1232	1278	1390	1831	2131
		2406	2701	2725	3103	3622	3735	4261	4398
		5208	5334	5635	5640	5796	6478	6651	6663
		6679	6898	7161	7350	7591	7659	7905	7947
		7964	8067	8307	8751	8793	9072	10278	10353
		10364	10372	10450	10462	10567	10908	10926	10972
		11230	11247	11283	12344				

DraII	16	1510	1560	1994	2176	2203	3254	3507	3962
		6527	6632	7342	7930	8995	8996	9187	11579

DraIII	4	3015	7721	8318	12001				
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DrdI	3	9818	11687	11956					
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DsaI	13	1353	1492	1720	2080	2713	3265	7165	8131
		8602	8899	8947	9007	9057			

Eam1105I	3	275	8702	10603					
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Eco47IIII	0									
EcoNI	3	1731	3294	7752						
EcoRI	2	4405	4882							
EcoRII	52	442	472	529	922	985	1316	1462	1513	
		1651	1996	2619	3241	3256	3322	3338	3425	
		3911	3958	5176	5299	5350	5719	5974	6186	
		6529	6541	6639	6682	6706	6722	6799	6821	
		7051	7177	7279	7357	7479	7702	7833	7923	
		8080	8500	8536	8787	8827	9133	9221	9448	
		9736	9857	9870	12419					
EcoRV	2	1442	4876							
EspI	4	430	3662	7497	7919					
Fnu4HI	110	412	544	547	667	801	831	834	837	
		866	915	999	1002	1065	1075	1151	1244	
		1294	1770	1850	2020	2289	2372	2375	2378	
		2400	2638	2641	2766	2878	3151	3211	3276	
		3358	3481	4218	4485	4635	5157	5248	5251	
		5285	5358	5379	5421	5506	5701	5708	5920	
		5936	5993	6358	6389	6399	6402	6438	6454	
		6493	6701	6704	6717	6720	6819	6831	6931	
		7004	7290	7433	7443	7446	7647	7650	7898	
		8104	8107	8150	8177	8259	8337	8526	8608	
		8689	8874	9067	9217	9243	9286	9289	9292	
		9535	9616	9634	9637	9755	9910	10053	10118	
		10121	10327	10655	10994	11021	11116	11345	11632	
		11741	12181	12203	12217	12321	12394			
FnuDII	17	9045	9066	9285	9557	9559	9757	10338	10668	
		11161	11493	11593	11595	11698	11809	12185	12205	12229
FseI	0									
HaeI	25	98	467	618	1395	1518	1704	3057	3236	
		3474	3699	3831	3911	4443	4890	6334	6727	
		6981	7371	8500	8787	8895	9012	9725	9736	10188
HaeII	8	1474	3890	8510	9588	9958	12152	12160	12305	
HaeIII	77	98	452	467	618	1096	1395	1518	1562	
		1633	1704	1725	1995	2001	2028	2712	3057	

3135	3186	3236	3255	3474	3699	3831	3877
3911	3939	3963	4312	4443	4782	4890	5349
5710	5943	6334	6378	6456	6522	6528	6633
6711	6727	6807	6981	7056	7263	7362	7371
7413	7702	7788	7938	8130	8402	8500	8601
8617	8787	8895	8997	9012	9189	9288	9299
9551	9725	9736	9754	10188	10646	10726	10993
11580	11851	11993	12354	12456			

HgiAI	22	367	742	1189	2581	2918	3161	3884	4860
		4954	5602	5824	5853	6793	7390	8050	8166
		8587	9178	10028	11189	11274	11771		

HgiCI	12	390	821	1611	2232	3260	6390	7623	8084
		9454	10551	12038	12301				

HgiJII	14	367	986	2540	3257	4954	5324	5552	6001
		6530	7320	8204	8999	9178	12076		

HhaI	30	1473	3889	4217	7999	8509	9045	9285	9494
		9559	9587	9620	9890	9957	10057	10231	10340
		10733	10826	11163	11495	11595	11698	12151	12159
		12185	12207	12216	12229	12304	12325		

HincII	6	4918	5387	5882	7073	7829	7856		
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HindIII	4	325	2938	4150	7107				
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HinfI	55	1	158	276	336	497	522	788	1086
		1218	1224	1380	1566	1757	1887	2040	2310
		2363	2420	3027	3065	3452	3809	4254	4323
		4588	4734	5239	5493	5592	5971	6063	6137
		6195	6227	6233	6371	6671	6911	6960	7529
		8460	8547	8703	8921	9545	9610	9685	10081
		10598	11588	11641	11928	11950	12489	12499	

HpaI	0								
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HpaII	42	979	1824	1965	2037	3136	3251	4476	4800
		5234	5346	5900	6141	6450	6524	7011	7128
		7414	7451	7611	7844	7935	8268	8403	8597
		8661	8935	8954	9000	9239	9428	9917	10064
		10090	10280	10684	10718	10785	10895	11137	11638
		11672	12103						

KpnI	1	1615							
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MaeI	16	3031	3487	3690	3738	5025	5184	5257	6291
		6309	7224	7971	8808	10205	10458	10793	12152
MaeII	27	64	939	2215	2842	3319	3331	5607	6118
		6157	7085	7354	8341	8395	8581	9015	9118
		10413	10829	11202	11522	11786	11945	11957	12000
		12110	12248	12440					
MaeIII	44	352	875	940	974	1357	1401	1574	1758
		1860	2318	2682	2843	3512	3611	3868	4079
		4186	4228	4460	4579	4829	5123	5458	6121
		6368	6758	7117	7283	7807	8021	9272	10066
		10129	10245	10528	10859	10917	11070	11258	11646
		12174	12186	12413	12433				
MboI	52	68	72	672	1230	1276	1388	1829	2129
		2404	2699	2723	3101	3620	3733	4259	4396
		5206	5332	5633	5638	5794	6476	6649	6661
		6677	6896	7159	7348	7589	7657	7903	7945
		7962	8065	8305	8749	8791	9070	10276	10351
		10362	10370	10448	10460	10565	10906	10924	10970
		11228	11245	11281	12342				
McrI	10	71	75	9004	9182	9289	9626	10050	10973
		11122	12345						
MfeI	2	100	3798						
MluI	0								
MseI	38	8	379	601	612	1254	2559	3304	4155
		4237	4512	4758	4971	4990	4998	5604	6303
		7195	9481	9540	10416	10468	10473	10487	10540
		10775	10814	11179	11551	11732	11789	11800	11812
		11823	11840	11938	12209	12405	12506		
MslI	13	53	240	2412	2927	3118	4305	7086	7100
		8631	8901	10855	11014	11373			
MstI	2	10825	12324						
MwoI	62	435	624	675	830	836	862	998	1257
		1370	1468	1701	2025	2206	2340	2377	2762
		3156	3207	3354	3480	3597	4001	4217	4476
		5275	5284	6437	6446	6450	6665	6733	6827
		7057	7368	7880	8045	8506	8513	8522	8558
		8591	8607	9003	9028	9097	9291	9454	9498



PpuMI	6	1510	2176	2203	3507	7342	7930		
PshAI	1	1047							
PstI	16	548	835	911	1375	1639	1767	2373	2401
		3709	4486	4636	6446	6718	6932	6970	8690
PvuI	4	71	75	10973	12345				
PvuII	15	549	1399	1572	2008	2022	2343	2402	4220
		5135	5250	6719	7425	8106	9534	12374	
RsaI	22	1613	2339	3044	3445	3921	3945	4164	4599
		4982	5015	5539	5665	6156	6540	7241	7893
		8079	8344	8637	11083	11759	12232		
RsrII	0								
SacI	3	367	4954	9178					
SacII	0								
SalI	1	5880							
SanDI	2	1510	2176						
SauI	5	810	2092	3503	3981	7749			
ScaI	2	5015	11083						
ScrFI	74	444	474	531	924	987	1318	1464	1515
		1653	1825	1998	2037	2621	3243	3252	3258
		3324	3340	3427	3913	3960	5178	5301	5346
		5352	5721	5901	5976	6188	6524	6525	6531
		6543	6641	6684	6708	6724	6801	6823	7053
		7129	7179	7281	7359	7451	7481	7704	7835
		7845	7925	7935	8082	8268	8502	8538	8598
		8662	8789	8829	8936	8955	9000	9135	9223
		9450	9738	9859	9872	10090	10786	11137	11638
		11673	12421						
SduI	43	367	395	742	826	986	1189	2235	2540
		2581	2918	3161	3257	3265	3317	3884	4860
		4954	5324	5552	5602	5824	5853	6001	6118
		6347	6530	6793	7093	7320	7390	7628	8050
		8166	8204	8492	8587	8999	9178	10028	11189
		11274	11771	12076					

SecI	51	348	396	538	985	1207	1317	1353	1492
		1513	1651	1696	1720	1996	2080	2619	2620
		2687	2713	3241	3242	3256	3265	3667	3737
		3890	3958	4018	4748	5299	5350	6308	6523
		6529	6982	7165	7271	7449	7933	8114	8131
		8602	8827	8899	8947	8998	9007	9057	9221
		9449	9870	12420					
SexAI	6	442	472	6186	6541	7479	8080		
SfeI	26	544	719	831	907	1371	1635	1763	2369
		2381	2397	3705	4482	4632	6442	6714	6928
		6966	7618	7653	8686	9152	9975	10166	10844
		12220	12472						
SfiI	1	7368							
SgfI	0								
SgrAI	0								
SmaI	1	6525							
SmlI	13	7	360	698	1445	6302	6627	7884	9204
		9816	10078	10355	11223	12505			
SnaBI	0								
SpeI	0								
SphI	0								
SplI	0								
SrfI	1	6525							
Sse8387I	0								
Sse8647I	1	3507							
SspI	5	21	714	7559	11407	11793			
StuI	5	467	618	1518	1704	8500			
StyI	18	348	538	1207	1492	1720	2687	3265	3667
		3737	3890	4748	6308	6982	7271	8114	8602

		8947	9007							
SwaI	0									
TaqI	19	67	71	75	361	500	763	1227	2128	
		2150	2410	3764	4679	5881	7474	9178	9810	
		11254	11586	12034						
TatI	9	2337	4162	4980	5013	5663	7891	8635	11081	11757
TfiI	22	158	336	522	788	1224	1566	2040	3065	
		4254	4323	5239	5493	5971	6195	6227	6233	
		6911	7529	8547	9545	9685	12489			
TseI	87	411	543	546	800	830	833	836	865	
		914	998	1001	1064	1074	1150	1243	1293	
		1769	2019	2288	2371	2374	2377	2399	2640	
		2765	2877	3150	3210	3275	3357	3480	4217	
		4484	4634	5156	5247	5250	5357	5378	5420	
		5505	5700	5919	5935	5992	6357	6398	6401	
		6437	6492	6700	6703	6716	6719	6818	6830	
		6930	7289	7432	7442	7445	7646	7649	8103	
		8106	8176	8258	8336	8525	8688	8873	9216	
		9242	9291	9534	9615	9633	10052	10117	10120	
		10326	10654	11020	11631	12180	12320	12393		
Tsp45I	26	875	974	1357	1401	1758	1860	2682	2843	
		3611	3868	4079	4460	4829	6121	6368	6758	
		7117	7283	7807	8021	9272	10859	11070	11646	
		12174	12433							
Tsp4CI	42	153	196	1357	1590	1611	1873	2101	2355	
		2385	2433	2997	3047	3448	3785	4092	4162	
		4245	4291	4675	4862	4870	4985	5013	5037	
		5442	6134	6395	6499	6538	6786	7403	8487	
		8900	9674	9745	10215	10528	11043	11611	11976	
		12330	12476							
TspEI	32	92	100	206	216	376	559	578	598	
		1597	1794	2650	3798	4238	4405	4882	4987	
		5057	5725	5924	6322	6609	8406	9390	9407	
		9482	10470	10776	11031	11777	11803	11814	12462	
TspRI	59	269	685	1270	1286	1375	1390	1427	1767	
		1790	1883	2165	2305	2390	2738	2963	3000	
		3016	3161	3473	3482	3541	3709	3908	4451	
		4644	4865	5042	5197	5276	5684	5787	6130	

6139	6183	6208	6502	6820	6932	7102	7387
7397	7955	8255	8319	8366	8490	8713	9314
9503	9612	10118	10131	10402	10551	10656	11003
11030	12464	12485					

Tth111I	3	5440	6188	8961					
VspI	4	4990	9481	9540	10775				
XbaI	2	3486	8807						
XcmI	3	2974	7379	8609					
XhoI	1	360							
XhoII	21	1388	3101	3620	3733	5633	5794	6661	6677
		6896	7159	7589	7903	7962	8065	8791	10351
		10362	10448	10460	11228	11245			
XmaIII	1	9286							
XmnI	6	250	5911	5983	6255	9126	11202		

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