

p83-2
Monday, August 16, 1993 2:27 PM

LOCUS P83-2 8151 BP DS- CIRCULAR ENTERED 12/15/88
COMMENT unpublished construction
by Dean A. Regier, Dept. of Microbiology, New England Regional Primate Research Center, Harvard
Medical School, 1 Pine Hill Drive, Southborough, MA 01772-9102 508-624-8188,
regier@husc.harvard.edu.
p83-2 contains HIV-1 NY5 sequences derived from pNL4-3 (Adachi et al, 1986, J.Virol, 59:284-291).
HIV-1 insert DNA extends from ApaI in flanking cellular DNA (-156bp) to EcoRI in vpr and is
cloned into EcoRI and BstBI sites of pDR8, a derivative of pUC19.

FEATURES

	From	To/Span	Description
frag	< 1	5742	pNL43 proviral DNA (NY-5)
refnumbr	1	1	numbered 1 in [1]
LTR	1	634	5' LTR
revision	182	183	at in [3]; tg in [1]
revision	194	194	g in [3]; c in [1]
rpt	454	550	R repeat 5' copy
binding	636	653	primer (Lys-tRNA) binding site
pept	790	2292	1 gag polyprotein
pept	< 2085	5096	1 pol polyprotein (NH2-terminus uncertain; AA at 2085)
revision	2421	2421	g in [3]; a in [1]
pept	5041	5619	1 vif protein
pept	5559	> 5742	1 vpr protein (partial)
site	7983	7988	NcoI
site	7986	> 7996	Polylinker [Split]
cell	7997	8151	Flanking cellular DNA from pNL4-3

BASE COUNT 2717 A 1645 C 1989 G 1800 T 0 OTHER

ORIGIN bp #1 of NL4-3 proviral DNA

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1 TGGGAAGGGCT AATTGGTTC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA
61 CACAAGGCTA CTTCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC
121 TGACCTTTGG ATGGTGTTC AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA
181 AATAAGGAGA GAAGAACAGC TTGTTACACC CTATGAGCAG GCATGGGATG GAGGACCCGG
241 AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC ATTTCTGTAC ATGGCCCGAG
301 AGCTGCATCC GGAGTACTAC AAAGACTGCT GACATCGAGC GGAGTGGCGA GCCCTCAGAT
361 CTGGGGACTT TCCAGGAGG TGTTGGCTGG CGGGGACTGG GGAGTGGCGA GCCCTCAGAT
421 GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA
481 GCCTGGGAGC TCTCTGGCTA ACTAGGGAAC CCAGTGTCTA AGCCTCAATA AAGCTTGCCT
541 TGAGTGCTCA AAGTAGTGTG TGCCCCGTCT TTGTGTGACT CTGGTAACTA GAGATCCCTC
601 AGACCTTTT AGTCAGTGTG GAAATCTCT AGCAGTGGCG CCCGAACAGG GACTTGAAG
661 CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG GCTTGTCTGA GCCGCCAGG
721 CAAGAGGCGA GGGCGCGCGA CTGGTGAAGA CGCCAAAAT TTTGACTAGC GGAGGCTAGA
781 AGGAGAGAGA TGGGTGCGAG AGCGTCGGTA TTAAGCGGGG GAGAATTAGA TAAATGGCAA
841 AAAATTCGGT TAAGGCCAGG GGGAAAGAAA CAATATAAAC TAAAACATAT AGTATGGGCA
901 AGCAGGGAGC TAGAACGATT CGCAGTTAAT CCTGCCCTTT TAGAGACATC AGAAGGCTGT
961 AGACAAATAC TGGGACAGCT ACAACCATCC CTTCAGACAG GATCAGAAGA ACTTAGATCA
1021 TTATATAATA CAATAGCAGT CCTCTATTGT GTGCATCAAA GGATAGATGT AAAAGACACC
1081 AAGGAAGCCT TAGATAAGAT AGAGGAAGAG CAAACAAAAA GTAAGAAAAA GGCACAGCAA
1141 GCAGCAGCTG ACACAGGAAA TCAGGCCATA TCACCTAGAA CTTTAAATGC ATGGGTAAAA
1201 CTCCAGGGGC AAATGGTACA CAGCCCAGAA GTAATACCCA TGTTTTCAGC ATTATCAGAA
1261 GTAGTAGAAG AGAAGGCTTT AATATACCAT GTAAACACAG TGGGGGGACA TCAAGCAGCC
1321 GGAGCCACCC CACAAGATT CATCAATGAG GAAGCTGCAG AATGGGATAG ATTGCATCCA
1381 ATGCAATATG TAAAGAGAGC ACCAGGCCAG ATGAGAGAAC CAAGGGGAAG TGACATAGCA
1441 GTGCTGCAG GGCCTATTGC ACCAGGCCAG ATGAGAGAAC CAAGGGGAAG TGACATAGCA
1501 GGAATCTACT GTACCTTTCA GGAACAAATA GGATGGATGA CACATAATCC ACCTATCCCA
1561 GTAGGAGAAA TCTATAAAG ATGATAATC CTGGGATTAA ATAAAATAGT AAGAACTGAT
1621 AGCCCTACCA GCATTCTGGA CATAGACAAA GGACCAAAG AACCCCTTAG AGACTATGTA
1681 AGCCGATTCT ATAAACTCT AAGAGCCGAG CAAGCTTCAC AAGAGGTAAA AAATTGGATG
1741 ACAGAAACCT TGTGGTCCA AAATGCGAAC CCAGATTGTA AGACTATTTT AAAAGCAITG
1801 GGACAGGAGG CGACACTAGA AGAAATGATG ACAGCATGTC AGGGAGTGGG GGGACCCGGC
1861 CATAAAGCAA GAGTTTGGC TGAAGCAATG AGCCAAAGTA CAAATCCAGC TACCATAATG
1921 ATACAGAAAG GCAATTTTAG GAACCAAGA AAGACTGTTA AGTGTTCATA TTGTGGCAAA
1981 GAAGGGCACA TAGCCAAAAA TTGCAGGCC CCTAGGAAAA AGGGCTGTGG GAAATGTGGA
2041 AAGGAAGGAC ACCAAATGAA AGATTGTACT GAGAGACAGG CTAATTTTTT AGGGAAGATC
2101 TGCCCTTCCC ACAAGGGAAG GCCAGGGAAT TTTCTTCAGA GCAGACCAGA GCCAACAGCC
2161 CCACAGGAAG AGAGCTTCAG GTTTGGGGA GAGACAACAA CTCCTCTCA CAAGCAGGAG
2221 CCGATAGACA AGGAATGTA TCCTTTAGCT TCCCTCAGAT CACTCTTTGG CAGCGACCCC
2281 TCGTCACAAT AAAGATAGGG GGGCAATTAA AGGAAGCTCT ATTAGATACA GGAGCAGATG
2341 ATACAGTATT AGAAGAAATG AATTGTCCAG GAAGATGGAA ACCAAAAATG ATAGGGGGAA
2401 TTGGAGTTT TATCAAGTA GGACAGTATG ATCAGATACT CATAGAAATC TGCGGACATA
2461 AAGCTATAGG TACAGTATTA GTAGGACCTA CACCTGTCAA CATAATTGGA AGAAATCTGT
2521 TGACTCAGAT TGGTGCACCT TTAATTTTC CCATTAGTCC TATTGAGACT GTACCAGTAA
2581 AATTAAAGCC AGGAATGGAT GGCCCAAAAG TTAAACAAAT GCCATTGACA GAAGAAAAAA
2641 TAAAGCAATT AGTAGAAAT TGTACAGAAA TGGAAAGGGA AGGAAAAATT TCAAAATTTG
2701 GGCTGAAAAA TCCATACAA CTCTCAGTAT TTGCCATAA GAAAAAAGAC AGTACTAAAT
2761 GGAGAAAAAT AGTAGATTTC AGAGAATTAA ATAAGAGAAC TCAAGATTTC TGGGAAGTTC
2821 AATTAGGAAT ACCACATCCT GCAGGGTTAA AACAGAAAAA ATCAGTAACA GTACTGGATG
2881 TGGGCGATGC ATATTTTTC GTTCCCTTAG ATAAAGACT CAGGAAGTAT ACTGCATTTA
2941 CCATACCTAG TATAACAAT GAGACACCAG GCATAGATA TCAGTACAA GTGCTTCCAC
3001 AGGGATGGAA AGGATACCCA CCAATATTCC AGTGTAGCAT GACAAAAATC TTAGAGCCTT
3061 TTAGAAAACA AAATCCAGAG ATAGTCACT ATCAATACAT GGATGATTTG TATGTAGGAT
3121 CTGACTTAGA AATAGGCGAG CATAGAACAA AAATAGAGGA ACTGAGACAA CATCTGTTGA
3181 GGTGGGGATT TACCACACCA GACAAAAAAC ATCAGAAAGA ACCTCCATT CTTTGGATGG
3241 GTTAGAACT CCATCTGAT AATGGACAG TACAGCCTAT AGTGCTGCCA GAAAAGGACA
3301 GCTGGACTGT CAATGACATA CAGAAATTAG TGGGAAATTT GAATTGGGCA AGTCAGATT
3361 ATGCAGGGAT TAAAGTAAAG CAATTATGTA AACTCTTAG GGAACCAA GCACTAACAG
3421 AAGTAGTACC ACTAACAGAA GAAGCAGAGC TAGAAGTGGC AGAAAACAGG GAGATTCTAA
3481 AAGAACCGGT ACATGGAGTG TATTATGACC CATCAAAAGA CTTAATAGCA GAAATCAGAA
3541 AGCAGGGGCA AGGCCAATGG ACATATCAAA TTTATCAAGA GCCATTAAAA AATCTGAAAA
3601 CAGGAAAAAT TGCAAGATG AAGGGTGGCC ACATTAATGA TGTGAACAA TTAACAGAGG
3661 CATACAAAA AATAGCCACA GAAAGCATAG TAATATGGG AAAGACTCCT AAATTTAAAT
3721 TACCATACA AAAGGAAACA TGGGAAGCAT GGTGGACAGA GTATTGGCAA GCCACCTGGA
3781 TTCTGAGTG GAGGTTTGT AATACCCCTC CTTAGTTGAA GTTATGGTAC CAGTTAGAGA
3841 AAGAACCCAT AATAGGAGCA GAACTTTTCT ATGTAGATGG GCCAGCCAAT AGGGAACATA
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3901 AATTAGGAAA AGCAGGATAT GTAAC TGACA GAGGAAGACA AAAAGTTGTC CCCCTAACGG
3961 ACACAACAAA TCAGAAGACT GAGTTACAAG CAATTCATCT AGCTTTGCAG GAITTCGGAT
4021 TAGAAGTAAA CATAGTGACA GACTCACAAT ATGCATTGGG AATCAITCAA GCACAACCAG
4081 ATAAGAGTGA ATCAGAGTTA GTCAGTCAAA TAATAGAGCA GTTAATAAAA AAGGAAAAAG
4141 TCTACCTGGC ATGGGTACCA GCACACAAAG GAATTGGAGG AAATGAACAA GTAGATGGGT
4201 TGGTCAGTGC TGGAAATCAGG AAAGTACTAT TTTTAGATGG AATAGATAAG GCCCAAGAAG
4261 AACATGAGAA ATATCACAGT AATTGGAGAG CAATGGCTAG TGATTTTAAC CTACCACCTG
4321 TAGTAGCAAA AGAAATAGTA GCCAGCTGTG ATAAATGTCA GCTAAAAGGG GAAGCCATGC
4381 ATGGACAAGT AGACTGTAGC CCAGGAATAT GGCAGCTAGA TTGTACACAT TTAGAAGGAA
4441 AAGTTATCTT GGTAGCAGTT CATGTAGCCA GTGGATATAT AGAAGCAGAA GTAAITCCAG
4501 CAGAGACAGG GCAAGAAACA GCATACTTCC TCTTAAATTT AGCAGGAAGA TGGCCAGTAA
4561 AAACAGTACA TACAGACAAT GGCAGCAATT TCACCAGTAC TACAGTTAAG GCCGCTGT
4621 GGTGGCGCGG GATCAAGCAG GAATTTGGCA TTCCCTACAA TCCCAAAAGT CAAGGAGTAA
4681 TAGAATCTAT GAATAAGAA TTAAAGAAAA TTATAGGACA GGTAAGAGAT CAGGCTGAAC
4741 ATCTTAAGAC AGCAGTACAA ATGGCAGTAT TCATCCACAA TTTTAAAGA AAAGGGGGGA
4801 TTGGGGGGTA CAGTGCAGGG GAAAGAATAG TAGACATAAT AGCAACAGAC ATACAAACTA
4861 AAGAATTACA AAAACAAATT AAAAAAATTC AAAATTTTCG GGTTTATTAC AGGGACAGCA
4921 GAGATCCAGT TTGGAAGGGA CCAGCAAAGC TCCTCTGGAA AGGTGAAGGG GCAGTAGTAA
4981 TACAAGATAA TAGTGACATA AAAGTAGTGC CAAGAAGAAA AGCAAAGATC ATCAGGGATT
5041 ATGGAAAAACA GATGGCAGGT GATGATTGTG TGGCAAGTAG ACAGGATGAG GATTACACAA
5101 TGGAAAAGAT TAGTAAACA CCATATGTAT AITTCAGGA AAGCTAAGGA CTGGTTTTAT
5161 AGACATCACT ATGAAAGTAC TAATCCAAAA ATAAGTTTCA AGTACACAT CCCACTAGGG
5221 GATGCTAAAT TAGTAATAAC AACATATTGG GGTCTGCATA CAGGAGAAAG AGACTGGCAT
5281 TTGGGTCAGG GAGTCTCCAT AGAATGGAGG AAAAAGAGAT ATAGCACACA AGTAGACCTT
5341 GACCTAGCAG ACCAACTAAT TCATCTGCAC TATTTTGATT GTTTTTCAGA ATCTGCTATA
5401 AGAAATACCA TATTAGGACG TATAGTTAGT CCTAGGTGTG AATATCAAGC AGGACATAAC
5461 AAGGTAGGAT CTCTACAGTA CTTGGCAGTA GCAGCATTAA TAAACACAAA ACAGATAAAG
5521 CCACCTTTTC CTAGTGTAGG GAAACTGACA GAGGACAGAT GGAACAGGCC CCAGAAGACC
5581 AAGGGCCACA GAGGGAGCCA TACAATGAAT GGACACTAGA GCTTTTAGAG GAACTTAAGA
5641 GTGAAGCTGT TAGACATTTT CCTAGGATAT GGCTCCATAA CTTAGGACAA CATATCTATG
5701 AAACCTACGG GGATACTTGG GCAGGAGTGG AAGCCATAAT AAGAATTCGG TCACCATCCT
5761 CGCTCACTGA CTCGCTGCGC TCGGTCGTTC GGCTGCGGGG AGCGGTATCA GCTCACTCAA
5821 AGCGGTAAT ACGGTTATTC ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA
5881 AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
5941 TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG CGAAACCCGA
6001 CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCCT TCTCCTGTTT
6061 CGACCTGCGC GCTTACCGGA TACCTGTCCG CTTTCTCCCC TTGCGGAAGC GTGGCGCTTT
6121 CTCAATGCTC ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT
6181 GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
6241 AGTCCAACCC GGTAAAGACG GACTTATCGC CACTGCGAGC AGCCACTGGT AACAGGATTA
6301 GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT AACTACGGCT
6361 ACACATAGAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTGCGAAAAA
6421 GAGTTGGTAG CTCTTGATCC GCAAAACAAA CCACCGCTGG TAGCGGTTGT TTTTTTGTTT
6481 GCAAGCAGCA GATTACGGC AGAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
6541 CGGGGTCTGA CGCTCAGTGG AACGAAACT CACGTTAAGG GATTTTGGTC ATGAGATTAT
6601 CAAAAAGGAT CTTACCTTAG ATCTTTTAA ATTAAAAATG AAGTTTTTAA TCAATCTAAA
6661 GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT
6721 CAGCGATCTG TCTATTTCTG TCATCCATAG TTGCTGACT CCCCGTCTGT TAGATACTA
6781 CGATACGGGA GGGCTTACCA TCTGGCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT
6841 CACCGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG
6901 GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAAITG TTGCGGGGAA GCTAGAGTAA
6961 GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTACAGGC ATCGTGGTGT
7021 CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCGGTTT CCAACGATCA AGGCGAGTTA
7081 CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCTCTCG ATCGTTGTCA
7141 GAAGTAAGTT GGCCGCAAGT TTATCACTCA TGGTTATGGC AGCACTGCAT AATCTCTTAA
7201 CTGTCAATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA GTACTCAACC AAGTCATTCT
7261 GAGAATAGTG TATGCCGCGA CCGAGTTGCT CTGCGCCGGC GTCAATACGG GATAATACCG
7321 CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCT GGGCGAAAAA
7381 TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAACT
7441 GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAAACA GGAAGGCAAA
7501 ATGCCGCAAA AAAGGGAATA AGGCGACAC GGAATGTTG AATACTCATA CTCTCTCTTT
7561 TTCAATATTA TTGAAGCAAT TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTGGAAT
7621 GTATTTAGAA AAATAAACAA ATAGGGGTTT CGCGCACATT TCCCGAAAA GTGCCACCTG
7681 ACGTCTAAGA AACCAITATT ATCATGACAT TAACCTATAA AAATAGGCGT ATCACAGGGC
7741 CCTTTCGTCT TCAAGAACTG CCTCGCGCGT TTCGGTGATG ACGGTGAAAA CCTCTGACAC
7801 ATGCAGCTCC CGGAGACGGT CACAGCTTGT CTGTAAGCGG ATGCCGGGAG CAGACAAGCC
7861 CGTCAGGGCG CGTCAGCGGG TGTGGCGGGG TGTCGGGGCG CAGCCATGAC CCAGTCAGCT
7921 AGCGATAGCG GAGTGTAATG GCTTAACATAT GCGGCATCAG AGCAGATTGT ACTGAGAGTG
7981 CACCATGGTG ACCTTCGTGC ACATGGCCGG AGGAACTGCC ATGTCCGAGG TGCAAGCACA
8041 CCTGCGCATC AGAGTCTCTG GTGTGGAGGG AGGGACCAGC GCAGCTTCCA GCCATCCACC
8101 TGATGAACAG AACCTAGGGA AAGCCCCAGT TCTACTTACA CCAGGAAAGG C
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p83-2 Enzyme Cutters
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Sequence Range: 1 to 8151

Enzyme	#Cuts	Positions					
Aat2	1	7684					
AccI	8	960	1679	2928	4141	4390	4831
		5078	5333				
Acc65I	2	3826	4154				
AcII	15	358	4612	5914	5942	6069	6088
		6209	6454	6825	6916	7153	7318
		7395	7504	7650			
Afl2	3	517	4743	5634			
Afl3	1	5869					
AgeI	1	3485					
AluI	36	199	302	339	435	489	533
		909	978	1147	1414	1714	1909
		2174	2248	2316	2463	3301	3449
		4002	4345	4361	4415	4949	5143
		5621	5646	5811	6037	6173	6430
		6951	7051	7114	7806	7825	8084
AlwI	18	29	57	114	587	1008	3020
		3125	4638	4917	5475	6430	6516
		6518	6614	6615	7078	7395	7399
AlwNI	3	1147	5392	6285			
ApaI	1	2010					
ApaLI	4	6183	7429	7978	7997		
ApoI	13	757	842	2127	2360	2543	2656
		2686	3568	3711	4641	4885	4892
		5743					
Asel	2	5497	6934				
Asp700	5	842	1276	2687	4492	7361	
AvaI	1	295					
Ava2	11	16	233	1651	1755	1801	1852
		2484	4938	6900	7122	8073	
Avr2	4	2011	5431	5661	8113		
BanI	5	637	3624	3826	4154	6710	
Ban2	3	413	491	2010			
BbeI	1	641					
BbsI	3	3941	3981	5581			
BbvI	26	289	422	444	1153	1156	1387
		1401	2282	2520	3149	3271	3894
		4424	4594	5503	5761	5779	6198
		6288	6291	6497	6800	7191	7815
		7912	8093				
BcgI	2	6165	7267				
BclI	1	2429					
BfaI	27	276	502	588	629	766	776
		910	1235	1508	1816	2012	2947
		3450	3999	4297	4416	5215	5344
		5432	5488	5531	5616	5662	6364
		6617	6952	8114			
BqlI	1	6882					
Bql2	3	473	679	2096			
BsaI	4	153	461	666	2140		
BsaAI	1	7918					
BsaHI	3	638	7299	7681			
BsaJI	21	96	102	372	386	482	856
		1079	1203	1480	1590	2011	2122
		2967	4400	5431	5579	5661	6029
		7983	8056	8113			
BsqI	2	1213	4834				
BsiEI	4	5785	6209	7132	7281		
BslI	19	102	130	452	647	3236	3492
		3852	3956	4151	4618	4621	5217
		5303	5891	5909	6075	6354	7815
		8062					
BsmI	2	1631	4648				
BsmAI	22	154	461	667	2131	2141	2774
		3439	3649	3751	3923	4087	4495
		4913	5298	5543	5583	5976	6296
		6322	7599	7952	8044		
BspI286I	12	413	491	548	564	1988	2010
		3629	6187	7348	7433	7982	8001
BspEI	1	308					
BspHI	3	6589	7597	7702			
BspMI	2	5046	8049				
BspWI	16	5	543	717	1138	1172	1440
		1449	1628	1711	3281	5491	5526
		5808	5922	6494	6882		
BsrI	17	120	401	456	745	974	2878
		3460	3505	5155	5278	5339	6277
		6290	7238	7906	7942	7988	
BsrFI	2	3485	6842				
BssH2	1	711					
Bst1107I	1	2929					
BstE2	2	5749	7987				
BstNI	23	97	103	373	387	483	857
		932	1168	1204	1463	1591	1805
		2123	2368	2590	2968	3776	4146
		4402	5897	6018	6031	8142	
BstOI	9	713	5916	6497	6827	7320	7652

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BstX1	5	7765	7767	7870			
BstY1	15	1635	2374	3004	3232	4408	
		34	49	473	592	679	2096
		3117	4922	5467	6510	6521	6607
		6619	7387	7404			
Cfr101	2	3485	6842				
Dde1	26	414	477	598	1012	1089	1699
		2069	2207	2254	2524	2906	3050
		3125	3162	3396	3784	3812	3979
		5144	5681	6144	6553	6719	7259
		7685	7972				
Dpn1	32	36	43	51	108	475	594
		681	1002	1017	2098	2259	2431
		3014	3119	4632	4729	4924	5028
		5469	6437	6512	6523	6531	6609
		6621	6726	7067	7085	7131	7389
		7406	7442				
Dpn2	32	34	41	49	106	473	592
		679	1000	1015	2096	2257	2429
		3012	3117	4630	4727	4922	5026
		5467	6435	6510	6521	6529	6607
		6619	6724	7065	7083	7129	7387
		7404	7440				
Dra1	10	1244	1340	1790	2542	3587	3716
		4784	6628	6647	7339		
Drd1	2	5977	7859				
Dsa1	1	7983					
Dsa5	30	95	101	235	371	385	481
		855	930	1166	1202	1461	1589
		1803	1854	2121	2366	2588	2966
		3774	4144	4400	5895	6016	6029
		6247	6943	7294	7808	7843	8140
Eae1	5	1857	2619	4551	7150	8004	
Eam1105I	3	1835	2280	6762			
Ear1	4	184	239	1265	7557		
Ecl136II	1	489					
Eco57I	4	727	1901	2901	6417		
EcoO109I	7	233	1450	1852	2006	2007	2484
		7738					
EcoR1	1	5743					
EcoR1*	51	10	757	823	842	1179	1731
		1932	1968	1998	2082	2127	2304
		2360	2398	2503	2543	2580	2656
		2686	2695	2766	2820	3324	3336
		3341	3381	3568	3648	3711	3717
		3900	3991	4171	4280	4492	4536
		4586	4641	4698	4708	4778	4863
		4876	4885	4892	5227	5357	5743
		6629	6935	7190			
EcoR5	2	114	2979				
EspIII	4	3438	4494	4912	6295		
Fnu4HL	35	303	433	436	735	1142	1145
		1376	1415	2271	2534	3138	3285
		3883	4413	4583	4612	5492	5775
		5793	5796	5914	6069	6212	6277
		6280	6486	6814	7153	7180	7275
		7504	7804	7901	7952	8082	
Fok1	25	142	239	292	972	1421	1544
		1548	1749	2610	2821	2889	3016
		3114	3238	3248	4758	5097	5194
		5233	5741	6728	6909	7196	7852
		8079					
Fsp1	2	6984	8045				
Hae2	2	641	6117				
Hae3	30	101	177	294	385	855	935
		1225	1452	1466	1859	2008	2103
		2121	2602	2621	2702	3553	4251
		4553	4611	5585	5884	5895	5913
		6347	6805	6885	7152	7739	8006
Hga1	6	697	791	5980	6558	7288	7859
HqiA1	7	491	548	6187	7348	7433	7982
		8001					
Hha1	18	640	713	715	5779	6049	6116
		6216	6390	6499	6892	6985	7322
		7654	7767	7870	7900	8046	8081
Hinc2	2	2498	2521				
Hind3	2	531	1712				
Hinf1	21	577	695	917	1685	2522	3473
		3704	3779	4011	4041	4060	4089
		4213	4683	5291	5389	5769	5844
		6240	6757	8052			
HinP1	18	638	711	713	5777	6047	6114
		6214	6388	6497	6890	6983	7320
		7652	7765	7868	7898	8044	8079
Hpa2	16	237	309	1856	3486	6076	6223
		6249	6439	6843	6877	6944	7054
		7296	7810	7844	8007		
Hph1	15	755	1223	3007	4583	4974	5070
		5743	6605	6832	7248	7454	7489
		7786	7795	7999			
Kas1	1	637					

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Kpn1	2	3830	4158				
Mae2	6	5418	6572	6988	7361	7681	7917
Mae3	24	202	285	574	583	1489	1896
		2282	2864	3920	3982	4034	4992
		5749	6225	6288	6404	6687	7018
		7076	7229	7417	7818	7913	7987
Mbo1	32	34	41	49	106	473	592
		679	1000	1015	2096	2257	2429
		3012	3117	4630	4727	4922	5026
		5467	6435	6510	6521	6529	6607
		6619	6724	7065	7083	7129	7387
		7404	7440				
Mbo2	27	183	203	1018	1117	1279	1831
		2106	2125	2179	2200	2364	2383
		2521	2643	3450	3946	3986	4269
		4558	5026	5586	6531	6602	7357
		7435	7544	7740			
Mnl1	50	166	223	232	282	369	423
		533	607	667	716	721	764
		1051	1094	1210	1400	1715	2214
		2263	2289	2396	3148	3171	3232
		3649	3817	3923	4169	4539	4962
		5080	5299	5543	5583	5620	5768
		5976	6051	6300	6700	6781	6929
		7135	7728	7771	7801	8002	8019
		8058	8062				
MscI	2	2621	4553				
MseI	41	518	811	850	926	1243	1339
		1390	1597	1789	1958	2307	2541
		2583	2611	2788	2847	3370	3522
		3586	3651	3715	4122	4306	4533
		4606	4701	4744	4783	5093	5497
		5635	6575	6627	6632	6646	6699
		6934	6973	7338	7710	7943	
Msp1	16	237	309	1856	3486	6076	6223
		6249	6439	6843	6877	6944	7054
		7296	7810	7844	8007		
MunI	1	1968					
NarI	1	638					
NciI	7	237	1856	6249	6945	7296	7810
		7845					
NcoI	1	7983					
NdeI	1	5123					
Nla3	32	225	293	1253	1302	1350	1383
		1447	1838	3041	3101	3495	3742
		3751	4153	4266	4379	4383	4464
		5102	5873	6593	7084	7094	7172
		7208	7601	7706	7803	7908	7987
		8005	8023				
Nla4	27	18	235	508	639	1323	1661
		1802	1853	1854	1942	2008	2009
		2219	3404	3626	3828	4156	5596
		5673	5901	5940	6712	6806	6847
		7058	7648	8074			
NsiI	4	1251	2891	4055	4381		
NspB2	9	360	435	1147	3301	4345	6211
		6456	7397	7876			
NspH1	4	1447	1838	5873	7803		
PflM1	1	5303					
PleI	10	571	689	2516	3698	4035	5299
		5763	6248	6751	8060		
PpuM1	3	233	1852	2484			
PstI	2	1419	2843				
PvuI	1	7132					
Pvu2	4	435	1147	3301	4345		
RmaI	27	276	502	588	629	766	776
		910	1235	1508	1816	2012	2947
		3450	3999	4297	4416	5215	5344
		5432	5488	5531	5616	5662	6364
		6617	6952	8114			
RsaI	31	148	315	450	749	1217	1512
		2067	2471	2572	2663	2753	2872
		2985	3271	3427	3490	3664	3828
		4156	4225	4424	4567	4598	4756
		4809	5178	5204	5479	7242	7936
		7970					
SacI	1	491					
SapI	1	1100					
Sau3A1	32	34	41	49	106	473	592
		679	1000	1015	2096	2257	2429
		3012	3117	4630	4727	4922	5026
		5467	6435	6510	6521	6529	6607
		6619	6724	7065	7083	7129	7387
		7404	7440				
Sau96I	23	16	99	233	293	1450	1651
		1755	1801	1852	2006	2007	2484
		2601	2700	4250	4938	5583	6804
		6883	6900	7122	7738	8073	
ScaI	8	315	2753	2872	4225	4598	5178
		5479	7242				
ScrF1	30	97	103	237	373	387	483

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		857	932	1168	1204	1463	1591
		1805	1856	2123	2368	2590	2968
		3776	4146	4402	5897	6018	6031
		6249	6945	7296	7810	7845	8142
SfaNI	13	314	408	1062	1443	2876	5211
		5966	7018	7209	7458	7830	7963
		8055					
SfcI	13	957	1187	1415	2464	2839	3277
		4318	4394	4600	5473	6134	6325
		7003					
SpeI	1	1507					
SphI	1	1447					
SspI	2	3025	7566				
StyI	9	1079	1480	2011	5431	5579	5661
		7983	8056	8113			
Swal	2	1340	3716				
TaqI	4	335	686	5969	7413		
TaqII	5	1697	5737	5771	7110	7295	
TfiI	11	917	1685	3473	3779	4011	4060
		4089	4213	4683	5389	5844	
Tth111I	2	3081	7911				
XcmI	1	5605					
XmnI	5	842	1276	2687	4492	7361	

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AscI
BamHI
BbrPI
BpmI
Bpu1102I
BsaBI
BsiWI
BspOI
BstBI
Bsu36I
ClaI
Dra3
EaqI
Eco47III
Eco81I
EcoNI
HpaI
MluI
NaeI
NcoMI
NheI
NotI
NruI
PacI
PaeR7I
PmeI
PmlI
Rsr2
Sac2
SalI
SceI
SfiI
SgrAI
SmaI
SnaBI
StuI
XbaI
XhoI
XmaI

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Sequence Range: 1 to 8151

#Cuts	Enzyme	Positions				
1	Aat2	7684				
1	Afl3	5869				
1	AgeI	3485				
1	Apal	2010				
1	Aval	295				
1	BbeI	641				
1	BclI	2429				
1	BglI	6882				
1	BsaAI	7918				
1	BspEI	308				
1	BssH2	711				
1	Bst1107I	2929				
1	DsaI	7983				
1	Ecl136II	489				
1	EcoRI	5743				
1	KasI	637				
1	MunI	1968				
1	NarI	638				
1	NcoI	7983				
1	NdeI	5123				
1	PflMI	5303				
1	PvuI	7132				
1	SacI	491				
1	SapI	1100				
1	SpeI	1507				
1	SphI	1447				
1	XcmI	5605				
2	Acc65I	3826	4154			
2	AseI	5497	6934			
2	BogI	6165	7267			
2	BsqI	1213	4834			
2	BsmI	1631	4648			
2	BspMI	5046	8049			
2	BsrFI	3485	6842			
2	BstE2	5749	7987			
2	Cfr101	3485	6842			
2	DrdI	5977	7859			
2	EcoRS	114	2979			
2	FspI	6984	8045			
2	Hae2	641	6117			
2	Hinc2	2498	2521			
2	Hind3	531	1712			
2	KpnI	3830	4158			
2	MscI	2621	4553			
2	PstI	1419	2843			
2	SspI	3025	7566			
2	Swal	1340	3716			
2	Tth1111I	3081	7911			
3	Afl2	517	4743	5634		
3	AlwNI	1147	5392	6285		
3	Ban2	413	491	2010		
3	BbsI	3941	3981	5581		
3	Bgl2	473	679	2096		
3	BsaHI	638	7299	7681		
3	BspHI	6589	7597	7702		
3	Eam1105I	1835	2280	6762		
3	PpuMI	233	1852	2484		
4	ApaLI	6183	7429	7978	7997	
4	Avr2	2011	5431	5661	8113	
4	BsaI	153	461	666	2140	
4	BsiEI	5785	6209	7132	7281	
4	EarI	184	239	1265	7557	
4	Eco57I	727	1901	2901	6417	
4	EspIII	3438	4494	4912	6295	
4	NsiI	1251	2891	4055	4381	
4	NspHI	1447	1838	5873	7803	
4	Pvu2	435	1147	3301	4345	
4	TaqI	335	686	5969	7413	
5	Asp700	842	1276	2687	4492	7361
5	BanI	637	3624	3826	4154	6710
5	BstXI	1635	2374	3004	3232	4408
5	EaeI	1857	2619	4551	7150	8004
5	TaqII	1697	5737	5771	7110	7295
5	XmnI	842	1276	2687	4492	7361
6	HgaI	697	791	5980	6558	7288
6	Mae2	5418	6572	6988	7361	7859
6						7917
7	EcoO109I	233	1450	1852	2006	2484
7		7738				
7	HqIAI	491	548	6187	7348	7433
7		8001				7982
7	NciI	237	1856	6249	6945	7296
7		7845				7810
8	AccI	960	1679	2928	4141	4390
8		5078	5333			4831
8	ScaI	315	2753	2872	4225	4598
8		5479	7242			5178
9	BstUI	713	5916	6497	6827	7320
9						7652

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9	NspB2	7765	7767	7870			
		360	435	1147	3301	4345	6211
		6456	7397	7876			
9	Styl	1079	1480	2011	5431	5579	5661
		7983	8056	8113			
10	Dra1	1244	1340	1790	2542	3587	3716
		4784	6628	6647	7339		
10	Ple1	571	689	2516	3698	4035	5299
		5763	6248	6751	8060		
11	Ava2	16	233	1651	1755	1801	1852
		2484	4938	6900	7122	8073	
11	Tf11	917	1685	3473	3779	4011	4060
		4089	4213	4683	5389	5844	
12	Bsp1286I	413	491	548	564	1988	2010
		3629	6187	7348	7433	7982	8001
13	ApoI	757	842	2127	2360	2543	2656
		2686	3568	3711	4641	4885	4892
		5743					
13	SfaNI	314	408	1062	1443	2876	5211
		5966	7018	7209	7458	7830	7963
		8055					
13	SfcI	957	1187	1415	2464	2839	3277
		4318	4394	4600	5473	6134	6325
		7003					
15	AcII	358	4612	5914	5942	6069	6088
		6209	6454	6825	6916	7153	7318
		7395	7504	7650			
15	BstYI	34	49	473	592	679	2096
		3117	4922	5467	6510	6521	6607
		6619	7387	7404			
15	HphI	755	1223	3007	4583	4974	5070
		5743	6605	6832	7248	7454	7489
		7786	7795	7999			
16	BspWI	5	543	717	1138	1172	1440
		1449	1628	1711	3281	5491	5526
		5808	5922	6494	6882		
16	Hpa2	237	309	1856	3486	6076	6223
		6249	6439	6843	6877	6944	7054
		7296	7810	7844	8007		
16	MspI	237	309	1856	3486	6076	6223
		6249	6439	6843	6877	6944	7054
		7296	7810	7844	8007		
17	BsrI	120	401	456	745	974	2878
		3460	3505	5155	5278	5339	6277
		6290	7238	7906	7942	7988	
18	AlwI	29	57	114	587	1008	3020
		3125	4638	4917	5475	6430	6516
		6518	6614	6615	7078	7395	7399
18	HhaI	640	713	715	5779	6049	6116
		6216	6390	6499	6892	6985	7322
		7654	7767	7870	7900	8046	8081
18	HinPI	638	711	713	5777	6047	6114
		6214	6388	6497	6890	6983	7320
		7652	7765	7868	7898	8044	8079
19	BslI	102	130	452	647	3236	3492
		3852	3956	4151	4618	4621	5217
		5303	5891	5909	6075	6354	7815
		8062					
21	BsaJI	96	102	372	386	482	856
		1079	1203	1480	1590	2011	2122
		2967	4400	5431	5579	5661	6029
		7983	8056	8113			
21	HinfI	577	695	917	1685	2522	3473
		3704	3779	4011	4041	4060	4089
		4213	4683	5291	5389	5769	5844
		6240	6757	8052			
22	BsmAI	154	461	667	2131	2141	2774
		3439	3649	3751	3923	4087	4495
		4913	5298	5543	5583	5976	6296
		6322	7599	7952	8044		
23	BstNI	97	103	373	387	483	857
		932	1168	1204	1463	1591	1805
		2123	2368	2590	2968	3776	4146
		4402	5897	6018	6031	8142	
23	Sau96I	16	99	233	293	1450	1651
		1755	1801	1852	2006	2007	2484
		2601	2700	4250	4938	5583	6804
		6883	6900	7122	7738	8073	
24	Mae3	202	285	574	583	1489	1896
		2282	2864	3920	3982	4034	4992
		5749	6225	6288	6404	6687	7018
		7076	7229	7417	7818	7913	7987
25	FokI	142	239	292	972	1421	1544
		1548	1749	2610	2821	2889	3016
		3114	3238	3248	4758	5097	5194
		5233	5741	6728	6909	7196	7852
		8079					
26	BbvI	289	422	444	1153	1156	1387
		1401	2282	2520	3149	3271	3894
		4424	4594	5503	5761	5779	6198
		6288	6291	6497	6800	7191	7815

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26	Dde1	7912	8093				
		414	477	598	1012	1089	1699
		2069	2207	2254	2524	2906	3050
		3125	3162	3396	3784	3812	3979
		5144	5681	6144	6553	6719	7259
27	BfaI	7685	7972				
		276	502	588	629	766	776
		910	1235	1508	1816	2012	2947
		3450	3999	4297	4416	5215	5344
		5432	5488	5531	5616	5662	6364
27	Mbo2	6617	6952	8114			
		183	203	1018	1117	1279	1831
		2106	2125	2179	2200	2364	2383
		2521	2643	3450	3946	3986	4269
		4558	5026	5586	6531	6602	7357
27	Nla4	7435	7544	7740			
		18	235	508	639	1323	1661
		1802	1853	1854	1942	2008	2009
		2219	3404	3626	3828	4156	5596
		5673	5901	5940	6712	6806	6847
27	Rma1	7058	7648	8074			
		276	502	588	629	766	776
		910	1235	1508	1816	2012	2947
		3450	3999	4297	4416	5215	5344
		5432	5488	5531	5616	5662	6364
30	Dsa5	6617	6952	8114			
		95	101	235	371	385	481
		855	930	1166	1202	1461	1589
		1803	1854	2121	2366	2588	2966
		3774	4144	4400	5895	6016	6029
30	Hae3	6247	6943	7294	7808	7843	8140
		101	177	294	385	855	935
		1225	1452	1466	1859	2008	2103
		2121	2602	2621	2702	3553	4251
		4553	4611	5585	5884	5895	5913
30	ScrF1	6347	6805	6885	7152	7739	8006
		97	103	237	373	387	483
		857	932	1168	1204	1463	1591
		1805	1856	2123	2368	2590	2968
		3776	4146	4402	5897	6018	6031
31	Rsa1	6249	6945	7296	7810	7845	8142
		148	315	450	749	1217	1512
		2067	2471	2572	2663	2753	2872
		2985	3271	3427	3490	3664	3828
		4156	4225	4424	4567	4598	4756
32	Dpn1	4809	5178	5204	5479	7242	7936
		7970					
		36	43	51	108	475	594
		681	1002	1017	2098	2259	2431
		3014	3119	4632	4729	4924	5028
32	Dpn2	5469	6437	6512	6523	6531	6609
		6621	6726	7067	7085	7131	7389
		7406	7442				
		34	41	49	106	473	592
		679	1000	1015	2096	2257	2429
32	Mbo1	3012	3117	4630	4727	4922	5026
		5467	6435	6510	6521	6529	6607
		6619	6724	7065	7083	7129	7387
		7404	7440				
		34	41	49	106	473	592
32	Nla3	679	1000	1015	2096	2257	2429
		3012	3117	4630	4727	4922	5026
		5467	6435	6510	6521	6529	6607
		6619	6724	7065	7083	7129	7387
		7404	7440				
32	Sau3A1	225	293	1253	1302	1350	1383
		1447	1838	3041	3101	3495	3742
		3751	4153	4266	4379	4383	4464
		5102	5873	6593	7084	7094	7172
		7208	7601	7706	7803	7908	7987
32	Fnu4H1	8005	8023				
		34	41	49	106	473	592
		679	1000	1015	2096	2257	2429
		3012	3117	4630	4727	4922	5026
		5467	6435	6510	6521	6529	6607
35	Alu1	6619	6724	7065	7083	7129	7387
		7404	7440				
		303	433	436	735	1142	1145
		1376	1415	2271	2534	3138	3285
		3883	4413	4583	4612	5492	5775
36	Mse1	5793	5796	5914	6069	6212	6277
		6280	6486	6814	7153	7180	7275
		7504	7804	7901	7952	8082	
		199	302	339	435	489	533
		909	978	1147	1414	1714	1909
41	Mse1	2174	2248	2316	2463	3301	3449
		4002	4345	4361	4415	4949	5143
		5621	5646	5811	6037	6173	6430
		6951	7051	7114	7806	7825	8084
		518	811	850	926	1243	1339
		1390	1597	1789	1958	2307	2541

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		2583	2611	2788	2847	3370	3522
		3586	3651	3715	4122	4306	4533
		4606	4701	4744	4783	5093	5497
		5635	6575	6627	6632	6646	6699
		6934	6973	7338	7710	7943	
50	Mnl1	166	223	232	282	369	423
		533	607	667	716	721	764
		1051	1094	1210	1400	1715	2214
		2263	2289	2396	3148	3171	3232
		3649	3817	3923	4169	4539	4962
		5080	5299	5543	5583	5620	5768
		5976	6051	6300	6700	6781	6929
		7135	7728	7771	7801	8002	8019
		8058	8062				
51	EcoRI*	10	757	823	842	1179	1731
		1932	1968	1998	2082	2127	2304
		2360	2398	2503	2543	2580	2656
		2686	2695	2766	2820	3324	3336
		3341	3381	3568	3648	3711	3717
		3900	3991	4171	4280	4492	4536
		4586	4641	4698	4708	4778	4863
		4876	4885	4892	5227	5357	5743
		6629	6935	7190			