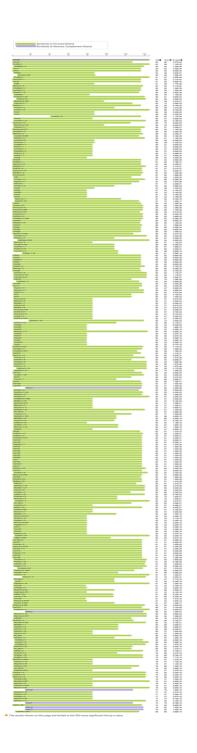
Appendix

A. Results for finding Alu domains

Fig1. Human BC200

Fig2. Gorilla Gorilla BC200



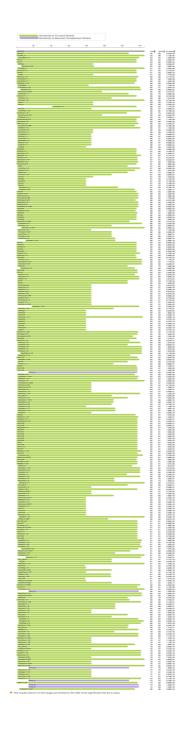
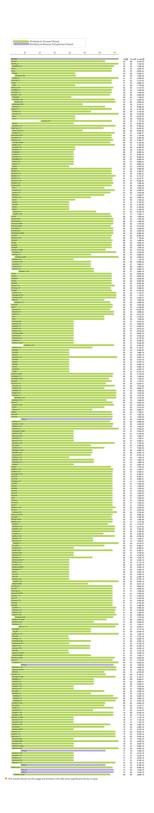
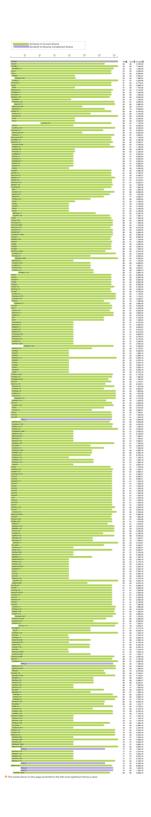


Fig4. Pongo Pygmaeus BC200





B. Multiple Sequence Alignment Result

CLUSTAL O(1.2.4) multiple sequence alignment

AF067780.1	GAAGCCAGCAAGAAGAACATGGTGGACTCTCTGTGAGGCCCCAAACCCCAAATCATGAGC
AF067779.1	${\tt GAAGCCAGCAAGAAGAACATGGTGGACTCTCTGTGAGGCCCCAAACCCCAAATCATGAGC}$
NR_001568.1	
AF067778.1	CCAAACCCCAAATCATGAGC
AF067781.1	CCAAACCCCAAATCATGAGC
AB067700 1	CTCTCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAAAA
AF067780.1 AF067779.1	CTCTGCCCCCTGAACGTATTCCAGGATCTCCAAGGGAG-TATTGGGAGGGGGCCAACGTC CTCCGCCCCCTGAAAGTATTCCAGGATCTCCGAGGGAGGTTTTGGGAGGGGGCCAAGGTC
NR 001568.1	CTCCGCCCCCTGAAAGTATTCCAGGATCTCCGAGGGAGGTTTTGGGAGGGGGCCAAGGTC
AF067778.1	CTCCGCCCCTGAAAGTATTCCAGGATCTCTGAGGGAGGTTTTGGGAGGGGGCCAAGGTC
AF067781.1	$\tt CTCCGCCCCCTGAAAGTATTCCAGGATCTCCGAGGGAGGTTTTGGGAGGGGGCCAAGTTC$
NE067780 1	
AF067780.1 AF067779.1	CTCCAATTGGGTGGGTGGGGCTCCAAGCCATTGTTCTTTGCACATTCATGCCAATGTGAC CTGCAATTGGGTGGGTGGGGCTCCAAGCCATTGTTCTTTGCACATTCATGCCAATGTGAC
NR 001568.1	CIGCANITOGGOGGGCCCAAGCCAITGITCITIGACATICATGCCAATGTGAC
AF067778.1	CTGCAATTGGGTGGGTGGGGCTCCAAGCCATTGTTCTTTGCACATTCATGCCAATGTGAC
AF067781.1	$\tt CTGCAATTGGGTGGGTGGGGCTCCAAGCCATTGTTCTTTGCACATTCTTGCCAATGTGAC$
AB067700 1	
AF067780.1 AF067779.1	CTAATTGGCTAAGCACAGGCTGGAGAAGCTGGATAAACCTATTTAAATTCAGAGCCAAAA TTAATTGGCTAAGCACAGGCTGGAGAAGCTAGATAAACCTATTTAAATTCAGAGCCAAAA
NR_001568.1	TIMATIOCTAMOCACHOCTOMOMACTAGATAMACCTATITAMATICAGACCAAAA
AF067778.1	CTAATTGGCTAAGCACAGGCTGGAGAAGCTAGATAAACCTATTTAAATTCAGAGCCAAAA
AF067781.1	$\tt CTAATTGGCTAAGCACAGGCTGGAGAAGCTAGATAAACCTATTTAAATTCAGAGCCAAAA$
AF067780.1 AF067779.1	AACACTCAAGGATGTTTTCTGAGGGGGCGTGAGGGTTTGGAAAATTATCCTATATTTGATT GACACTCAAGGATGTTTTCTGAGGGGGTGTGAGGGTTTGGAAAATCATCCTATATTTGATT
NR 001568.1	GACACTCAAGGATGTTTTCTGAGGGGTTGGAAAATCATCCTATATTTGATT
AF067778.1	GACACTCAAGGATGTTTTCTGAGGGGGTTGAGGGTTGGAAAATCATCCTATATTTGATT
AF067781.1	GACACTCAAGGATGTTTTCTGAGGGGGTTGGAGGGTTGGAAAATCATCCTATATTTAATT
AF067780.1	TATCTCCCACCTCATGTCGTGAGTCAATTCCTTAGTCTTAGATGAGGGAGAGGACTTGGG
AF067779.1	TATCTCCCACCTCATGTCCTGAGTCAATTCCTTAGTCTTAGATGAGGGAGAGGACTTGGG
NR_001568.1 AF067778.1	TATCTCCCACCTCATGTCCTGAGTCAATTCCTTAGTCTTAGATGAGGGAGAGACTTGGG
AF067781.1	TATCTCCCACCTCATGTCCTGAGTCAATTCCTTAGTCTTAGATGAGGGAGAGGACTTGGG
AF067780.1	AGTCATCCTTGTTTTTGATGAGCTATACAACCCTATGGCCAGCAGAGGGAAGTACTGCAT
AF067779.1	AGTCATCCTTGTTTTTGATGAGCTATACAACCCTATGGCCAGCAGAGGGAAGTACTGCAT
NR_001568.1	2.0mg 2.mg 2.mg 2.mg 2.mg 2.mg 2.mg 2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.
AF067778.1 AF067781.1	AGTCATCCTTGTTTTTGATGAGCTATACAACCCTATGGCCAGCAGAGGGAAGTACTGCAT AGTCATCCTTGTTTTTGATGAGCTATACAACCCTATGGCCAGCAGAGGGAAGTACTGCAT
AF007761.1	AGICATCCTIGITITIGATGAGCTATACAACCCTATGGCCAGCAGAGGGAAGTACTGCAT
AF067780.1	TTCAGAGCGACAATTTGAGATCTATGAAAGAATTTCAATCGAGAATAAGAGGCCGGGCGC
AF067779.1	TTCAGAGCGACAATTTGAGATCTATGAAAGAATTTCAATCGAAAATAAGAGGCCGGGCGC
NR_001568.1	GGCCGGGCGC
AF067778.1	$\tt TTCAGAGCGACAATTTGAGATCTATGAAAGAATTTCAATCGAGAATAAGAGGCCGGGCGC$
AF067781.1	TTCAGAGCGACAATTTGAGATCTATGAAAGAATTTCAATCGAGAATAAGAGGCCGGGCGC *******
AF067780.1	GGTGGCTCACGCCTGTAATCCCAGCTCTCAGGGAGGC-AAGAGGCGGGAGGATAGCTTGA
AF067779.1	GGTGGCTCACGCCTGTAATCCCAGCTCTCAGGGAGGCTAAGAGGCGGGAGGATAGCTTGA
NR_001568.1	GGTGGCTCACGCCTGTAATCCCAGCTCTCAGGGAGGCTAAGAGGCGGGAGGATAGCTTGA
AF067778.1	GGTGGCTCACGCCTGTAATCCCAGCTCTCAGGGAGGCTAAGAGGCGGGAGGATAGCTTGA
AF067781.1	GGTGGCTCACGCCTGTAATCCCAGCTCTCAGGGAGGC-AAGAGGCGGGAGGATAGCTTGA ***********************************
AF067780.1	GCCCAGGAGTTCGAGACCTGCCTGGGCAATATAGCGAGACCCCGTTCTCCAGAAAAAGGA
AF067779.1	GCCCTGGAGTTCGAGACCTACCCGGGCAATATAGTGAGACCCCGTTCTCCAGAAAAATGA
NR_001568.1	GCCCAGGAGTTCGAGACCTGCCTGGGCAATATAGCGAGACCCCGTTCTCCAGAAAAAGGA
AF067778.1	GCCCAGGAGTTCGAGACCTGCCTGGGCAATATAGCGAGACCCCGTTCTCCAGAAAAAGGA
AF067781.1	GCCCAGGAGTTCGAGACCTGCCTGGGCAATATAGCGAGACCCCGTTCTCCCGAAAAAGAA *** ********* ** *************
AF067780.1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AF067779.1	AAAAGAAAAAAAACAAAAGACAAAAAAAAAAAATAAGCGTAACTTCCCTCAAAGCAACAA
NR 001568.1	AAAAAAAAAACAAAAGACAAAAAAAAAAAATAAGCGTAACTTCCCTCAAAGCAACAA
AF067778.1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AF067781.1	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
	*** ************** ********
AF067780.1	CCCCCCCCCCCTTTTCATATTCTTGCCTGGAAGAAAGGCCTTGCTTTCCTCTGCTTC
AF067779.1	$\tt CCCCCCCCCCCTTTTTCATATTCTTGCCTGGAAGAAAGGCCTTGCTTTCCTCTGCTTC$
NR_001568.1	CCCCCC-CCCCCTTT
AF067778.1	CCCCC-CCCCCTTTTCATATTCTTGCTTGGAAGAAAGGCCTTGCTTTCCTCAGCTTC
AF067781.1	CCCCCC-CCCCTTTTTTCATATTCTTGCCTGGAAGAAAGGCCTTGCTTTTCTCTGCTTC ***** * * * *
AF067780.1	TTAAAGCTGGGA-AAGTTAAAGCCATTCTGAAAT
AF067779.1	TTAAAGCTGGGAAAAGTTAAAGCCATTCTGAAAT
NR_001568.1	
AF067778.1	TTAAAGCTGGGAAAAGTTAAAGCCATTCTGAAAT
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