

A) ECR1

Hs-ECR1 CTGACATTTGCAGGCTGCCCTCCTGATTGGTCCCCTCGCCGAGCTGCTCACGGGTTCATT
 Cm-ECR1 CTGACATTTGCAGCGTTGGGTTTTGATTGGCCCTGATTTGGAGCTGCTCATGGGTCATT
 Lc-ECR1 CTGACATTTGCAGCCTTCCAATCTGATTGGTCTCATTTGGAGCAGCTCATGGGTTCATT
 Dr-ECR1 CTGACACCTCCAGGCTTCAACGCTGATTGGCTCTTATTTGAAGGAGTCATGGGTTCATT
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Hs-ECR1 CAACTGTTAAGCACCTCCCCGTCTCTCTAAAGGACATTATAATGCAAGAAGCCCCCTTTT
 Cm-ECR1 CAACTGTTAAGCACCCCGTCCCTCTAAAGGAGATTATAATGCAGGAGACCCCTTTT
 Lc-ECR1 CAACTGTTAAGCACCTCCAGTCTCTCTAAAGGACATTATAATGCAAGAAGCCCCCTTTT
 Dr-ECR1 CAACTATTAAGCGCCTCCAGTCTCTCTAAAGGACATTATAATGCAAGAAGCCCCCTTTT
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Hs-ECR1 TAACCACAAACCGAA
 Cm-ECR1 --ACAACAAACAGAA
 Lc-ECR1 TAACCACAAACCGAA
 Dr-ECR1 TAACCACAAACCGAA
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Sequence 1: Hs-ECR1	135 bp	Sequences (1:2) Aligned. Score: 88
Sequence 2: Lc-ECR1	135 bp	Sequences (1:3) Aligned. Score: 78
Sequence 3: Dr-ECR1	135 bp	Sequences (1:4) Aligned. Score: 80
Sequence 4: Cm-ECR1	133 bp	Sequences (2:3) Aligned. Score: 85
		Sequences (2:4) Aligned. Score: 87
		Sequences (3:4) Aligned. Score: 78

B) ECR2

Hs-ECR2 CAGCCAAGTCTAAAC-AGTAGTAAATTAGTACAAATTTATACTGATTTACTCTAATAAT
 Cm-ECR2 CAGCCAAGTCTAAACCAGGAGTAAATTAGTACACATTTATACTGATTTATTTAATAAT
 Lc-ECR2 CAGCCAAGTCTAAAC-ACTAGTAAATTAGTACAAATTTATACTGATTTACTCTAATAAT
 Dr-ECR2 CAGTCAGGCCTAAAC-ACTACTAAATCAGCCCTAATTTATACTGATCTCGC--TAATAAT
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Hs-ECR2 CGTAATAAAA-GCTTATAGATTTGGCACTAATTACATAAATGCCTAATGATCTTGAAAAAT
 Cm-ECR2 CGTAATAAAA-GCTTATAGATTTGGCACTAATTAGATAAATGCCTAATGATCTTGAAAAAT
 Lc-ECR2 CGTAATAAAA-GCTTATAGATTTGGCACTAATTACATAAATGCCTAATGATCTTGAAAAAT
 Dr-ECR2 CGTAATAAAAAGCTTATAGATTTGGCACTAATTACATAAAGCCCTAATGATGTTGAAAAAT
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Sequence 1: Hs-ECR2	118 bp	Sequences (1:2) Aligned. Score: 99
Sequence 2: Lc-ECR2	118 bp	Sequences (1:3) Aligned. Score: 88
Sequence 3: Dr-ECR2	117 bp	Sequences (1:4) Aligned. Score: 95
Sequence 4: Cm-ECR2	119 bp	Sequences (2:3) Aligned. Score: 88
		Sequences (2:4) Aligned. Score: 94
		Sequences (3:4) Aligned. Score: 83

C) ECR3

Hs-ECR3 TGTTTATACTGCTATAAAAAATCAAGACCAATAGAAAAGTCATAAAAATGAAGCGGGCTATC
 Lc-ECR3 TGTTTATACTGCTATAAAAAATCAAGACCAATAGAAAAGTCATAAAAATGAAGAGCGCTATA
 Dr-ECR3 TGTTTGTACAGCTATAAAAAGGATCGAGCTATTGAAAAGTCGTAATAATGAAGCGCGCTATC
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Hs-ECR3 AATCATGCCGCAACATTGTT
 Lc-ECR3 AATCAGCCAGCAATCTCGTT
 Dr-ECR3 AATCAGCTGTAACCGTGT
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Sequence 1: Hs-ECR3	80 bp	Sequences (1:2) Aligned. Score: 82
Sequence 2: Lc-ECR3	80 bp	Sequences (1:3) Aligned. Score: 78
Sequence 3: Dr-ECR3	80 bp	Sequences (2:3) Aligned. Score: 72

D) **ECR4**

Hs-ECR4 CAGAATTACATTTGTTTTCTTGTGATTTTATTTAAAAGTCACTCCTCATCTCCAGAATGC
 Lc-ECR4 CAGAATTACATTTGTTTTCTTGTGATTTTATTTAAAAGTCACTCCTCATCTCCAGAATGC
 Cm-ECR4 TAGAATTACATTTGTTTT-CTTGTGATATTATTTAAAAGTCTATCCTCATCTCCAGAGTGC
 Dr-ECR4 CAGAATTACATTTGTTTTCTTGTGATTTTATTTAAAAGTCACTCCTCATCTCCAGAGCGC

Hs-ECR4 GTGAAAATATCTACTTTCCACTCAGATACACCGCATTAACCTGTTGGAGGCGAATTTGTT
 Lc-ECR4 GTGAAAATATCTACTTTCCACTCAGATACACCGCATTAACCTGTTGGAGGCGAATTTGTT
 Cm-ECR4 GTGAAAATATCTACTTTCCACTCAGATACACCGCATTAACCTGTTGGAGGCGAATTTGTT
 Dr-ECR4 GTGAAAATGTCTACTTTCCACTCAGATGCGCCGATTAACCTGCGAGGCGCGAGTTTGT

Hs-ECR4 TGTTTGTCTATTTT-ATTTATTTGCTAGAT---AAGATTGATGCGAGTCTTATTAGC
 Lc-ECR4 TGT---CTATTTT-ATTTATTTGCTGGAT---AAGATTGATGCGAGTCTTATTAGC
 Cm-ECR4 TGTTTGTCTATTTTATTTATTTGGGGAGGCGAAGATTGATGTGTTGTTATTATC
 Dr-ECR4 TGTTTGTCTATTTTATTTATATGCGAGTGT---AAGATTGATGCGAGTCTTATTATC
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Sequence 1: Hs-ECR4	172 bp	Sequences (1:2) Aligned. Score: 98
Sequence 2: Lc-ECR4	168 bp	Sequences (1:3) Aligned. Score: 88
Sequence 3: Dr-ECR4	173 bp	Sequences (1:4) Aligned. Score: 90
Sequence 4: Cm-ECR4	175 bp	Sequences (2:3) Aligned. Score: 88
		Sequences (2:4) Aligned. Score: 90
		Sequences (3:4) Aligned. Score: 85

E) **ECR5**

Hs-ECR5 CTGTCACCAAATCACCTGCACGAAACAAGAATCTAATTTGTTAAGCTGGCATGCTGCAG
 Lc-ECR5 CTGTCACCAAATCACCTGCACGAAACAAGAATCTAATTTGTTAAGCTGGCATTTCTGCAG
 Cm-ECR5 CTCTCACAAAATCACCTGCACGAAACAAGAATCTAATTTGTTAAGCTGGCATTTCTGTAG
 Dr-ECR5 CTGTCACCGCATCACCTGCGGAAACAAGAATCTAATTTGTTAAGCTGGCATTTCTGCAG
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Hs-ECR5 ATGGAAGATCGATCTTCTCTGTAGATTTCTCTAATTGAGTGAATATAGACGCC
 Lc-ECR5 ATGGAAGATCGATTTTCTCTTTAGATTTCTCTAATTGAGTGAATATAGACGCC
 Cm-ECR5 ATGGAAGATCGATTTTCTCTTTAGAAATTTCTCTAATTGAGTGAATATAGACGCC
 Dr-ECR5 ATGGACGATCGATTTTCTCTTTAGAAATTTCTCTAATTGAGTGAATATAGACGCC

Sequence 1: Hs-ECR5	114 bp	Sequences (1:2) Aligned. Score: 97
Sequence 2: Lc-ECR5	114 bp	Sequences (1:3) Aligned. Score: 92
Sequence 3: Dr-ECR5	114 bp	Sequences (1:4) Aligned. Score: 92
Sequence 4: Cm-ECR5	114 bp	Sequences (2:3) Aligned. Score: 94
		Sequences (2:4) Aligned. Score: 95
		Sequences (3:4) Aligned. Score: 92

6) **ECR6**

Hs-ECR6 AATGAGACCCCTTTACTCCGTGACGTGCAGCCGCTCCATCTCATTAAGGAAATCGCTCTT
 Lc-ECR6 AACGAGACCCCTTTACTCCGTGACGTGCAACCGCTCCATCTTATTAAGGAAATCGCTCTT
 Cm-ECR6 AATGAGACCCCGGACTCCGTGACATGCAGCCGCTCCATCTCATTAAGGAAATCGCTCTT
 Dr-ECR6 AATGAGGCGCCGACTCCGTGACACCAACCGCTCCATCTCGTTAAGGAAATCGCTCTT
 Dr-ECR6b AATGGAGGCCAGCTACTCCGTGACTTGCCAAAGCTCATTTCATTACGGTAATCGCCGTC
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Hs-ECR6 CAATGCTGATTATTTTATTTGAGCCATAATTATATTTCTTTCCGGTAAATCACGGTTTA
 Lc-ECR6 CAATGCTGATTATTTTATTTGAGCTATAATTATATTTCTTTCCGGTAAATCACGGTTTA
 Cm-ECR6 CAATGCTGATTATTTTATTTGGAACCCATAATTATATTTCTTTCCGGTAAATCACGGTTTA
 Dr-ECR6 CAATGCTGATTATTTTATTTGAGCCATAATTATATTTCTTTCCGGTAAATCACGGTCTA
 Dr-ECR6b CATTGCTGATTATTTTATTTAG-GCCATAATTGTATTCTCCAGATAAATCACGGTTGAA
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Hs-ECR6 ATCGAGCCACAT--GGAGGGCAGCAGCTAAT
 Lc-ECR6 ATCGAGCCACAT--GGAGGGCAACTGGTTTAAAT
 Cm-ECR6 ATAGAGCACACGTTTCGGGGGCAAAGCGCTGTAAT
 Dr-ECR6 ATCGAGTCCGTTC--GGAGGGCAGCGCTCTAAT
 Dr-ECR6b ATCGGGTCCACAT--GGAGGGCACCAAGTCTAAT
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Sequence 1: Hs-ECR6	152 bp	Sequences (1:2) Aligned. Score: 94
Sequence 2: Lc-ECR6	152 bp	Sequences (1:3) Aligned. Score: 86
Sequence 3: Dr-ECR6	152 bp	Sequences (1:4) Aligned. Score: 70
Sequence 4: Dr-ECR6b	151 bp	Sequences (1:5) Aligned. Score: 84
Sequence 5: Cm-ECR6	154 bp	Sequences (2:3) Aligned. Score: 83
		Sequences (2:4) Aligned. Score: 69
		Sequences (2:5) Aligned. Score: 80
		Sequences (3:4) Aligned. Score: 72
		Sequences (3:5) Aligned. Score: 84
		Sequences (4:5) Aligned. Score: 59