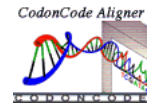


# CodonCode Aligner: AE1004, AE1004\_HVR

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<< AE1004 F1r	GAAGCAGATT	TGGGTACCAG	CCAAGTATTG	ACTCAGCCAT	CAACAACCGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG	TACGGTACCA
<< AE1004 B1r		T TGGGTACCAG	CCAAGTATTG	ACTCAGCCAT	CAACAACCGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG	TACGGTACCA
<< AE1004 B2-2r		T TGGGTACCAG	CCAAGTATTG	ACTCAGCCAT	CAACAACCGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG	TACGGTACCA
AE1004 B1f						CGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG
AE1004 B2f						CGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG
AE1004 F1f						CGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG
<< AE1004 C1r									CACC	ATGAATATTG
<< AE1004 C2r									CACC	ATGAATATTG
NC_012920_2 (r...	gaagcagatt	gggtaccag	ccaagtattg	actcagccat	caacaacggg	tatgtatttc	gtacattact	gccagccacc	atgaatattg	tacggtacca
	16036	16046	16056	16066	16076	16086	16096	16106	16116	16126
AE1004_HVR	GAAGCAGATT	TGGGTACCAG	CCAAGTATTG	ACTCAGCCAT	CAACAACCGG	TATGTATTTC	GTACATTACT	GCCAGCCACC	ATGAATATTG	TACGGTACCA

<< AE1004 F1r	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	GTTACAAGC	AAGTACAGTA	ATCAACCCTC	AACTATCACA
<< AE1004 B1r	TAAATACT									
<< AE1004 B2-2r	TAAATACT									
AE1004 B1f	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATC					
AE1004 B2f	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATC					
AE1004 F1f	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	GTTACAAGC	AAGTACAGTA	ATCAACCCTC	AACTATCACA
<< AE1004 C1r	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	G			
<< AE1004 C2r	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	GTTACAAG			
AE1004 C2f (2)			GTACATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	GTTACAAGC	AAGTACAGTA	ATCAACCCTC	AACTATCACA
AE1004 C1f			ATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	GTTACAAGC	AAGTACAGTA	ATCAACCCTC	AACTATCACA
<< AE1004 D1r								AAGTACAGTA	ATCAACCCTC	AACTATCACA
<< AE1004 D2-2r								AAGTACAGTA	ATCAACCCTC	AACTATCACA
<< AE1004 G1r									TC	AACTATCACA
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	16136	16146	16156	16166	16176	16186	16196	16206	16216	16226
AE1004_HVR	TAAATACTTG	ACCACCTGTA	GTACATAAAA	ACCCAATCCA	CATCAAAACC	CCCTCCCCAT	GTTACAAGC	AAGTACAGTA	ATCAACCCTC	AACTATCACA

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<< AE1004 F1r	CATCAACTGC	AACTCCAAAG	CCACCCCTCA	CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
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AE1004 C2f (2)	CATCAACTGC	AA								
AE1004 C1f	CATCAACTGC	AA								
<< AE1004 D1r	CATCAACTGC	AACTCCAAAG	CCACCCCTCA	CCCAGTAGGA	TACCAAGAAA	CCTA				
<< AE1004 D2-2r	CATCAACTGC	AACTCCAAAG	CCACCCCTCA	CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CA		
<< AE1004 G1r	CATCAACTGC	AACTCCAAAG	CCACCCCTCA	CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1004 G1f	CATCAACTGC	AACTCCAAAG	CCACCCCTCA	CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1004 D1f				CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1004 D2f				CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
<< AE1004 E1r						ACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
<< AE1004 E2r						ACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1004 E2f										CCGTACATA
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	16236	16246	16256	16266	16276	16286	16296	16306	16316	16326
AE1004_HVR	CATCAACTGC	AACTCCAAAG	CCACCCCTCA	CCCAGTAGGA	TACCAAGAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA

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<< AE1004 G1r	GACATTAGA	GTCAAATCCC	TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TAGGG				
AE1004 G1f	GACATTAGA	GTCAAATCCC	TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TAGGGGTCCC	TTGACCACCA	TCTTCCGTGA	AATCAATATC	C
AE1004 D1f	GACATTAGA	G								
AE1004 D2f	GACATTAGA									
<< AE1004 E1r	GACATTAGA	GTCAAATCCC	TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TAGGG				
<< AE1004 E2r	GACATTAGA	GTCAAATCCC	TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TA				
AE1004 E2f	GACATTAGA	GTCAAATCCC	TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TAGGGGTCCC	TTGACCACCA	TCTTCCGTGA	AATCAATATC	
AE1004 E1f			TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TAGGGGTCCC	TTGACCACCA	TCTTCCGTGA	AATCAATATC	
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	16336	16346	16356	16366	16376	16386	16396	16406	16416	16426
AE1004_HVR	GACATTAGA	GTCAAATCCC	TTTCTGGTCCG	CATGGATGAG	CCCCCTCAGA	TAGGGGTCCC	TTGACCACCA	TCTTCCGTGA	AATCAATATC	C