

CodonCode Aligner

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	16136	16146	16156	16166	16176	16186	16196	16206	16216	16226
<< AE1155 F1r (2)	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG	AAGTACAGGA	ATCAACCCTC	AACTATCACA
<< AE1155 B1r	TAAATAC									
<< AE1155 B2r	TAAATAC									
AE1155 B1f	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATC					
AE1155 B2f	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATC					
AE1155 F1f	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG	AAGTACAGGA	ATCAACCCTC	AACTATCACA
<< AE1155 C1-2r	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG	AA		
<< AE1155 C2r	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG			
AE1155 C1f			GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG	AAGTACAGGA	ATCAACCCTC	AACTATCACA
AE1155 C2f			GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG	AAGTACAGGA	ATCAACCCTC	AACTATCACA
<< AE1155 G1-2r						CCAT	GTTTACAAGG	AAGTACAGGA	ATCAACCCTC	AACTATCACA
<< AE1155 D1-2r								AAGTACAGGA	ATCAACCCTC	AACTATCACA
<< AE1155 D2r								AAGTACAGGA	ATCAACCCTC	AACTATCACA
NC_012920_3 (r...	taaaatacttg	accacctgta	gtatataaaaa	acccaatcca	catcaaaaac	ccctgcccat	gtttacaagg	aagtacagga	atcaaccctc	aactatcaca
AE1155_HVR	TAAATACTTG	ACCACCTGTA	GTAATATAAAA	ACCCAATCCA	CATCAAAAAC	CCCTGCCCAT	GTTTACAAGG	AAGTACAGGA	ATCAACCCTC	AACTATCACA

CodonCode Aligner: AE1155, AE1155_HVR

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<< AE1155 F1r (2)	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	A
AE1155 F1f	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1155 C1f	CATCAACTGC	AA								
AE1155 C2f	CATCAACTGC	AA								
<< AE1155 G1-2r	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
<< AE1155 D1-2r	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CA		
<< AE1155 D2r	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACC					
AE1155 G1f	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1155 D2f			G TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1155 D1-2f				CCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT
<< AE1155 E1r						ACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
<< AE1155 E2r						ACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA
AE1155 E2f										ACATA
NC_012920_3 (r...	Catcaactgc	aaCTCCAAAG	TCACCCCTCA	cccattagga	taccaacaaa	cctaccacc	cttaacagta	catagtacat	aaagccattt	accgtacata
	16236	16246	16256	16266	16276	16286	16296	16306	16316	16326
AE1155_HVR	CATCAACTGC	AACTCCAAAG	TCACCCCTCA	CCCATTAGGA	TACCAACAAA	CCTACCCACC	CTTAACAGTA	CATAGTACAT	AAAGGCATTT	ACCGTACATA

AE1155 F1f	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC						
<< AE1155 G1-2r	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC	CCCCCTCAGA	TAGGG				
AE1155 G1f	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC	CCCCCTCAGA	TAGGGGTCCC	TTGGCCACCA	TCTTCCGTGA	AATCAATATC	C
AE1155 D2f	GACATTAGA	G								
AE1155 D1-2f	GACATTAGA	G								
<< AE1155 E1r	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC	CCCCCTCAGA	TAGGG				
<< AE1155 E2r	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC	CCCCCTCAGA	TAGG				
AE1155 E2f	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC	CCCCCTCAGA	TAGGGGTCCC	TTGGCCACCA	TCTTCCGTGA	AATCAATATC	
AE1155 E1f					CCCCCTCAGA	TAGGGGTCCC	TTGGCCACCA	TCTTCCGTGA	AATCAATATC	
NC_012920_3 (r...	gacattaga	gtcaaatccc	tttctgtccc	catggatgac	ccccctcaga	taggggtccc	ttggccacca	tcttccgtga	aatcaatata	c
	16336	16346	16356	16366	16376	16386	16396	16406	16416	16426
AE1155_HVR	GACATTAGA	GTCAAATCCC	TTTCTGTC	CATGGATGAC	CCCCCTCAGA	TAGGGGTCCC	TTGGCCACCA	TCTTCCGTGA	AATCAATATC	C