Metazoan and HGT intronic donor (5') and acceptor (3') sequences

Metazoan 5' Splice sites	**Metazoan 3' Splice sites**	**HGT 5' Splice sites**	**HGT 3' Splice sites**
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Codon usage table

Amino Acid	Codon	Hd_Metazoan	Hd_HGT	N. koreensis	F. taffensis
Ala	GCG	0.28	0.34	0.2	0.12
Ala	GCA	0.18	0.16	0.21	0.38
Ala	GCT	0.22	0.15	0.18	0.39
Ala	GCC	0.32	0.35	0.41	0.11
Cys	TGT	0.37	0.42	0.59	0.72
Cys	TGC	0.63	0.58	0.41	0.28
Asp	GAT	0.43	0.49	0.66	0.79
Asp	GAC	0.57	0.51	0.34	0.21
Glu	GAG	0.49	0.46	0.25	0.23
Glu	GAA	0.51	0.54	0.75	0.77
Phe	TTT	0.44	0.42	0.68	0.63
Phe	TTC	0.56	0.58	0.32	0.37
Gly	GGG	0.17	0.15	0.15	0.1
Gly	GGA	0.29	0.17	0.16	0.53
Gly	GGT	0.21	0.21	0.29	0.29
Gly	GGC	0.33	0.48	0.41	0.08
His	CAT	0.48	0.47	0.64	0.67
His	CAC	0.52	0.53	0.36	0.33
Ile	ATA	0.13	0.08	0.21	0.11
Ile	ATT	0.37	0.32	0.4	0.63
Ile	ATC	0.5	0.6	0.39	0.26
Lys	AAG	0.52	0.57	0.3	0.22
Lys	AAA	0.48	0.43	0.7	0.78
Leu	TTG	0.2	0.24	0.22	0.37
Leu	TTA	0.08	0.06	0.18	0.29
Leu	CTG	0.29	0.35	0.37	0.08
Leu	CTA	0.06	0.04	0.03	0.06
Leu	CTT	0.14	0.11	0.11	0.15
Leu	CTC	0.23	0.2	0.08	0.06
Met	ATG	1	1	1	1
Asn	AAT	0.44	0.41	0.54	0.68
Asn	AAC	0.56	0.59	0.46	0.32
Pro	CCG	0.46	0.43	0.29	0.17
Pro	CCA	0.18	0.16	0.16	0.43
Pro	CCT	0.14	0.13	0.21	0.3
Pro	CCC	0.22	0.29	0.33	0.1
Gln	CAG	0.6	0.65	0.57	0.26
Gln	CAA	0.4	0.35	0.43	0.74
Arg	AGG	0.08	0.05	0.15	0.03

HGT coding sequences used for codon usage calculations.

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Niastella koreensis coding sequences used for codon usage calculations

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