

protein domains	5'-splice donor consensus (A/C)AG//gt(a/g)agt	Intron size (kb)	3'-splice acceptor consensus YYYYYYYYYncag//G
CTCF: ZF1+ZF2	.CAC.ACA.G//gtgctg H T G	4.000	ctttctctag//GT.ACT.CGC.CCT. T R P
BORIS: ZF1+ZF2	.CAC.ACA.G//gtaaaa H T G	0.316	gattttacag//GA.ACC.AGG.CCC. T R P
CTCF: ZF3 + 1/2 ZF4	.AGT.GTA.GAA.//gtgagt S V E	4.0	cgtatttcag//.GTC.AGC.AAA.TTA. V S K L
BORIS: ZF3 + 1/2 ZF4	.AGT.GTG.GAG.//gtaaa S V E	2.9	tatttattag//.GCA.AGC.AAA.TTG. A S K L
CTCF: 1/2 ZF4 + ZF5	.CAT.TCA.G//gtagga H S G	0.7	ttttctttaag//GG.GAA.AAG.CCT. E K P
BORIS: 1/2 ZF4 + ZF5	.CAC.TCA.G//gtaagg H S G	0.97	tctgcatctcag//GT.GAG.AAG.CCT. E K P
CTCF: ZF6 + 1/2 ZF7	.GAT.TTG.G//gtaagt D L G	5.0	tgctttcag//GT.GTC.CAC.TTG. V H L
BORIS: ZF6 + 1/2 ZF7	.GAC.CTA.C//gtgagt D L R	1.839	ccatttttag//GT.GTG.CAT.ATG. V H M
CTCF: 1/2 ZF7 + ZF8 + 1/2 ZF9	.TGT.AGA.CAG.//gtagga C R Q	1.8	ccgtttcag//.GAG.AGG.CAC. E R H
BORIS: 1/2 ZF7 + ZF8 + 1/2 ZF9	.TGC.AAG.CAG.//gtattg C K Q	3.814	ccctcttag//.GAA.CGT.CAT. E R H
CTCF: 1/2 ZF9 + ZF10 + 1/2 ZF11	.ACA.CGT.CGG.//gtaagg T R R	1.0	ctttttgtag//.AAT.ACC.ATG.GCA. I N M A
BORIS: 1/2 ZF9 + ZF10 + 1/2 ZF11	.TCC.CGC.TGG.//gtaagc S R W	5.004	ttctccgacag//.ATT.AAC.CTG.CAC. I N L H