

CDS 16116	1	MQAKAPMYPNEPFLVFWNAPTTCQCRMRYKVDLDLKTFFHIVTNANDSLSGSAVTIFYPNHL	60
A3QVN3	24	MQAKAPMY NEPFLVFWNAPTTCQR+RYKVDLDLKTFFHIV+NANDSLSGSAVTIFYPNHL	83
CDS 16116	61	GVYPHIDDRGHFFHGIIPQNESLTKHLDKSKSDINRIIPLNTFHGLGVIDWENWRPQWDR	120
A3QVN3	84	GVYPHIDDRGHFFHGIIPQNESLTKHL+KSKSDINRIIPL FHGLGVIDWENWRPQWDR	143
CDS 16116	121	NWGSKNVYRNRSIQFAKVLHPQLSEDKIRRLAKKQYEKAAKSFMRDTLLLAEMRPNGYW	180
A3QVN3	144	NWGSKNVYRNRSIQFA+ LHP+LSEDKIRRLAKK+YEKAAKSFMRDTLLLAEMRP+GYW	203
CDS 16116	181	GYLYPDCQNYDYKTKGDQYTGKCP EIEMSRNDQLLWLRDSTALFPNVYLEIILRSSN	240
A3QVN3	204	GYLYPDCQNYDYKTKGDQYTGKCP EIEMSRNDQLLWLRDSTALFPNVYLEIILRSS+N	263
CDS 16116	241	ALKFVHHLKESMRIASMAREDYALPVFAYARPFYAYTFEPLTQ	284
A3QVN3	264	ALKFVHHLKESMRIASMAREDYALPVFAYARPFYAYTFEPLTQ	307

E-value: 0.0  
 Score: 1494  
 Ident.: 95.4%  
 Positives : 98.6%  
 Query Length: 290  
 Match Length: 449

**Figure S2.** Pairwise alignment of hyaluronidase-1 proteins.