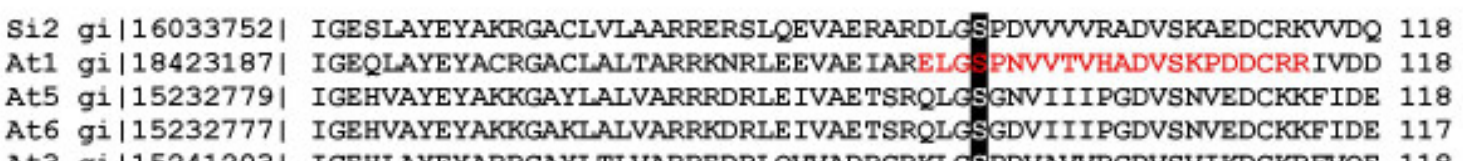
Si2 gi|16033752| IGESLAYEYAKRGACLVLAARRERSLQEVAERARDLGSPDVVVVRADVSKAEDCRKVVDQ 118
At1 gi|18423187| IGEQLAYEYACRGACLALTARRKNRLEEVAEIARELGSPNVVTVHADVSKPDDCRRIVDD 118
At5 gi|15232779| IGEHVAYEYAKKGAYLALVARRRDRLEIVAETSRQLGSGNVIIIPGDVSNVEDCKKFIDE 118
At6 gi|15232777| IGEHVAYEYAKKGAKLALVARRKDRLEIVAETSRQLGSGDVIIIPGDVSNVEDCKKFIDE 117
At3 gi|15241203| IGEHLAYEYARRGAYLTLVARREDRLQVVADRCRKLGSPDVAVVRGDVSVIKDCKRFVQE 118
At2 gi|15241261| IGEALAYEYGKRGAYLALVDIRGEPLFHVAALAELYGSPEVLPLVADVSKLQDCERFIRA 118
At4 gi|15234888| IGEQIAYEYAKRGANLVLVARREQRLRVVSNKAKQIGANHVIIIAADVIKEDDCRRFITQ 120
Si1 gi|21311775| IGEQIAYQYAKRGANLVLVARREHRLRGISENARRLGAPNVLIMAADVVKEEECRRFINE 119