

10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160

ASN1\_L\_ruvatiilis\_MG434487.1 MDALMKGFSMAKEGVMAAAAEKTKGVSVDAAEKTKEGVVMYMGTKTKE...SVATVAEKTKE...AGGAVVSGVTSVAHKTVEGAENMAAATGLVKKKGPGAKP...EGMPESHMEGMSSP...EAAHEYTEENGY...DYG...ETEQSGGME

ASN1\_P\_marinus\_XM\_032969453.1 MDALMKGFSMAKEGVMAAAAEKTKGVSVDAAEKTKEGVVMYMGTKTKE...SVATVAEKTKE...AGGAVVSGVTSVAHKTVEGAENMAAATGLVKKKGPGAKP...EGMPESHMEGMSSP...EAAHEYTEENGY...DYG...ETEQSGGME

ASN1\_L\_camtchaticum\_WFA01000923.1 MDALMKGFSMAKEGVMAAAAEKTKGVSVDAAEKTKEGVVMYMGTKTKE...SVATVAEKTKE...AGGAVVSGVTSVAHKTVEGAENMAAATGLVKKKGPGAKP...EGMPESHMEGMSSP...EAAHEYTEENGY...DYG...ETEQSGGME

ASN1\_E\_hidentatus\_JAAXJ020004106.1 MDALMKGFSMAKEGVMAAAAEKTKGVSVDAAEKTKEGVVMYMGTKTKE...XVAEKTKE...AGGAVVSGVTSVAHKTVEGAENMAAATGLVKKKGPGAKP...EGMPESHMEGMSSP...EAAHEYTEENGY...DYG...ETEQSGGME

ASN1\_E\_burgeni\_BROF01001137.1 MDVFLKGLSKAKDGVVAAAEKTKGVVADAAEKTKEGVVMYMGTKTKE...AGGAVVSGVTSVAHKTVEGAENMAAATGLVKKKGPGAKP...EGMPESHMEGMSSP...EAAHEYTEENGY...DYN...Q...

SNCA\_A\_radiata\_XM\_033022329.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_R\_typus\_XM\_048601469.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_C\_milii\_XM\_007902527.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_A\_carolinensis\_XM\_00321301.3 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_G\_gallus\_AF293512.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_L\_chalunnae\_XM\_006001527.1 MDMLMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_A\_mississippiensis\_XM\_006261248.3 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_X\_tropicalis\_XM\_031897353.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_H\_sapiens\_CR541653.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_C\_mydas\_XM\_007052739.4 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_P\_senehalus\_XM\_039751128.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_P\_aneetens\_XM\_040661391.1 MDMLMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_T\_rubripes\_XM\_011640510.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_A\_ruthenus\_XM\_034035953.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_C\_milii\_XM\_007906247.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_A\_radiata\_XM\_033029480.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_R\_typus\_XM\_048603711.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_P\_aneetens\_XM\_040663501.1 MDVLMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_X\_tropicalis\_XM\_203541.2 MDVLMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_A\_carolinensis\_XM\_003227782.3 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_H\_sapiens\_XM\_001001502.3 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_Q\_anatinus\_XM\_029052535.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_G\_gallus\_XM\_015293731.4 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_A\_mississippiensis\_LPU01003641 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_C\_mydas\_XM\_037907888.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_L\_chalunnae\_XM\_005993380.1 MDVLMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_P\_senehalus\_XM\_039775673.1 MDVLMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_L\_oculatus\_XM\_006631925.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_T\_rubripes\_XM\_001033846.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCB\_D\_reio\_XM\_200969.1 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKKDLV...KODEDLF...EGMVDSTALQIDPDT...EAFGTADQDEYD...DYE...PEA...

SNCA\_A\_ruthenus\_XM\_034052216.2 MDVFMKGLSKAKDGVVAAAEKTKGVVAAEAGKTKDGLVYGSRTKEGVFHGVSSVAEKTKEQASLVGGAVVTGMSVTAOKTVEGAENIAAATGLVKKK