



AVSSPSLFLPLISCGESMDPVTLGCLAKGFLPDSISFSWGDKSNASISTGVKSYKPVMQASGTYASSQV  
10 20 30 40 50 60 70

laev IgM ATSKSPSLFLPLISCGESMDPVTLGCLAKDFLPETISFTWGDKNNASYSTGLKSYKPVMQSSGTYASSQV 70  
trop IgM AVTSPPSLFLPLISCGESMDPVTLGCLAKGFLPDSISFSWEDKSNNTSISNGVKSYPVMQASGTYASSQI 70



NVASAVWDNIEQFYCNAKHLDVIKSVELGKIDSVKPVTPQVVSIHPPSKDALALNESLFFVCLATGFTPT  
80 90 100 110 120 130 140

laev IgM NVASAVWDNIEQFYCNAKHLDTIKSVEL--KKDPVKPVEKPVVSIHPPSKDALALNESLFIIVCLATNFTPT 139  
trop IgM NVDSATWDKSKPFYCNAKHLEVTKRVEIGKIDSLR--TQPVVVIHPPSKDALALNESLYVCLATGFNPK 138



SIVVKWLQNGNQTTDGVTVVEEPPVDKNGGYEATSYLSITRKEWDLDTLYSCVVEHADSGSLQVKNMSKSL  
150 160 170 180 190 200 210

laev IgM HIVIKWLKNGNQTTTEGVRVEEPPVEDKKRGYEATSYLSITRKEWDLDTLYSCVVEHAESGSLQVKNMSKSL 209  
trop IgM SISVKWLQNGKQTTDGVTVVEEPTVDKNGGYETTSYISITRKEWDLDTTYSCVVEHVDSGSLQVKNMSKSL 208



MCDTQTITQTSIQVITIPPSSLESIFEKKSATLTCLVSNMANSEDLRSISWFKISGTQEIQLKTTLGDAIYN  
220 230 240 250 260 270 280

laev IgM MCDTPIPTPTSIIQVITIPPSSLESIFEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYN 279  
trop IgM MCDTQTPQTNIKVITIPPSSLESIFEKKSATLTCLVSNMDNSEDLRSISWFKISGNKEEQKTTLGNDIYH 278



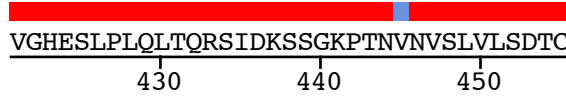
DNRTYSVEGTATVCADEWNNDSFVCKVEHTELASVKEVSLSKEKGAPLISPSVYVFPFPPLEELSLGETAT  
290 300 310 320 330 340 350

laev IgM DNRTYSVKGTTTTVCADEWNNDKFVCKVEHTELASMKEVFLFKEKGE-YNTPSVYVFPFPPLEELSKRETAT 348  
trop IgM DNRTYSKEGTATVCADEWNNKDSFVCKVEHTELASVKEVSLSKEKGAPLISPSVYVFPFPPQEELSLGETAT 348



LTCLVKGFSPSDFVVKWVHKNEAVSKNNYINTSINDELLSNGQKSGKFFLYSLHTIDIKDWDAGDSFSCV  
360 370 380 390 400 410 420

laev IgM LTCLVKGFSPSEIFVKWLHKNEAVPKQNYINTSINDELLPKGQKSGKFFLYSLHTIDIKDWDAGDSFSCV 418  
trop IgM LTCLVKGFSPSDFVVKWVHKNEEVSKNHYTNTNINEELSSNGRKT--FFLYSLFTIDSRNWKDGDGDSFSCV 416



VGHESLPLQLTQRSIDKSSGKPTNVNVSIVLSLSDTC  
430 440 450

laev IgM VGHESLPLQLTQRSIDKSSGKPTNVNVSIVLSLSDTC 453  
trop IgM VGHESLPLQLTQRSIDKSSGKPTNMNVSIVLSLSDTC 451