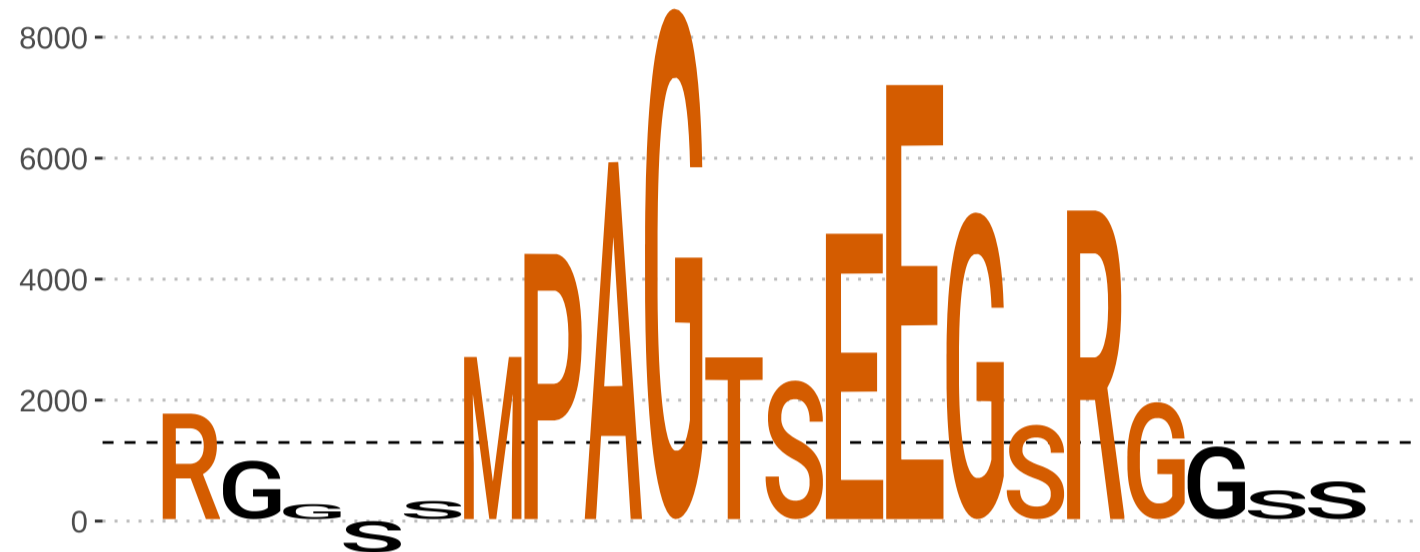
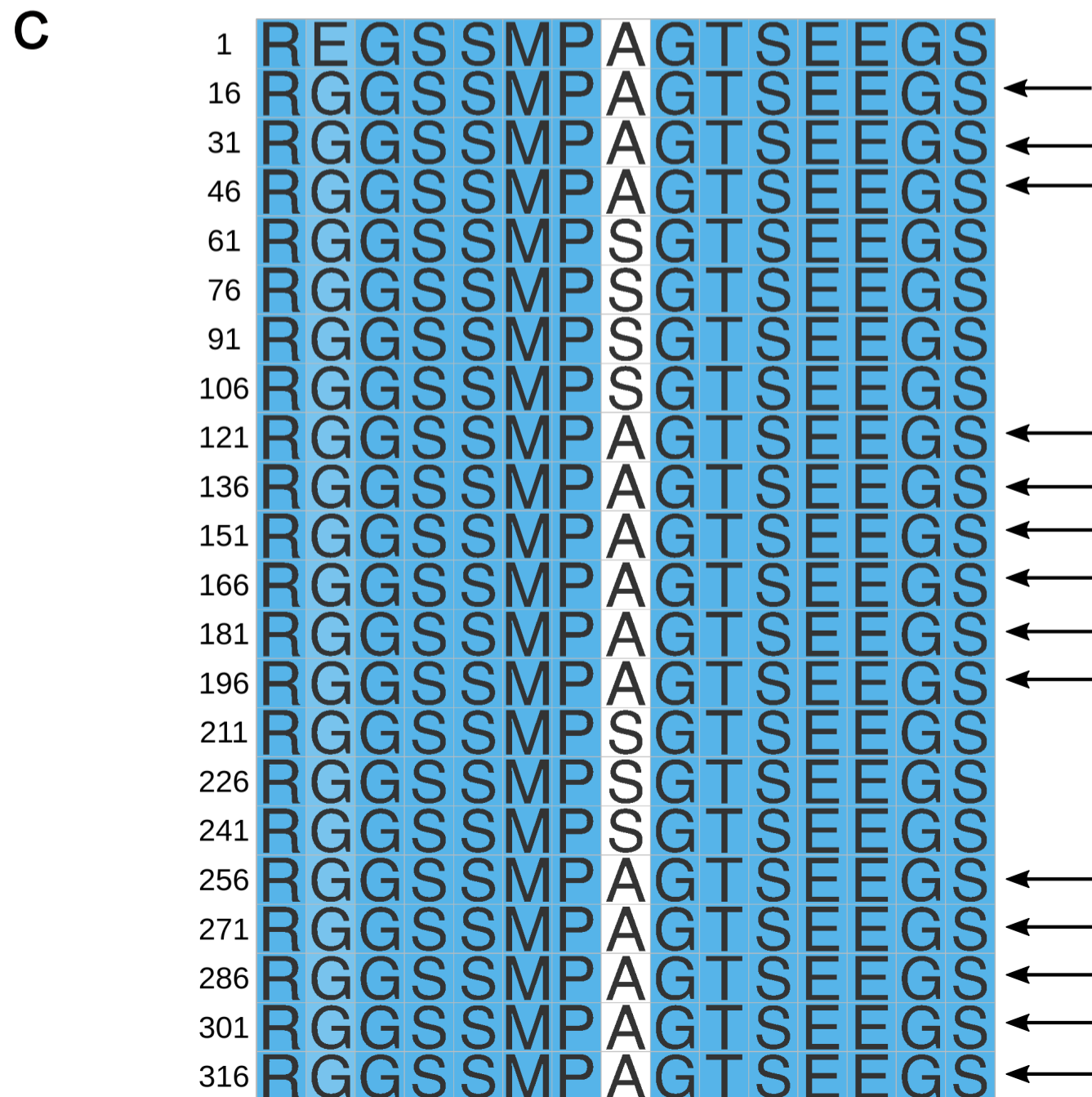


Single-residue mutagenesis of repetitive T. cruzi antigens. The figure summarizes the key epitope residues in repetitive antigens. When repeats alignments have dashed lines at the beginning or at the end it represents a sequence too long to be displayed. **A)** Sequence logo depicting the effect of mutations on antibody-binding (colors as in Figure 6 main manuscript). **B)** Original 20mer sequence selected for mutagenesis (showing the best 16mer identified at CHAGASTOPE-V1 screening). **C)** Multiple sequence alignment of repeats identified by Xstream (AM Newman 2007), with their positions in the cognate protein. Arrows indicate the repeats matching the original sequence in B.

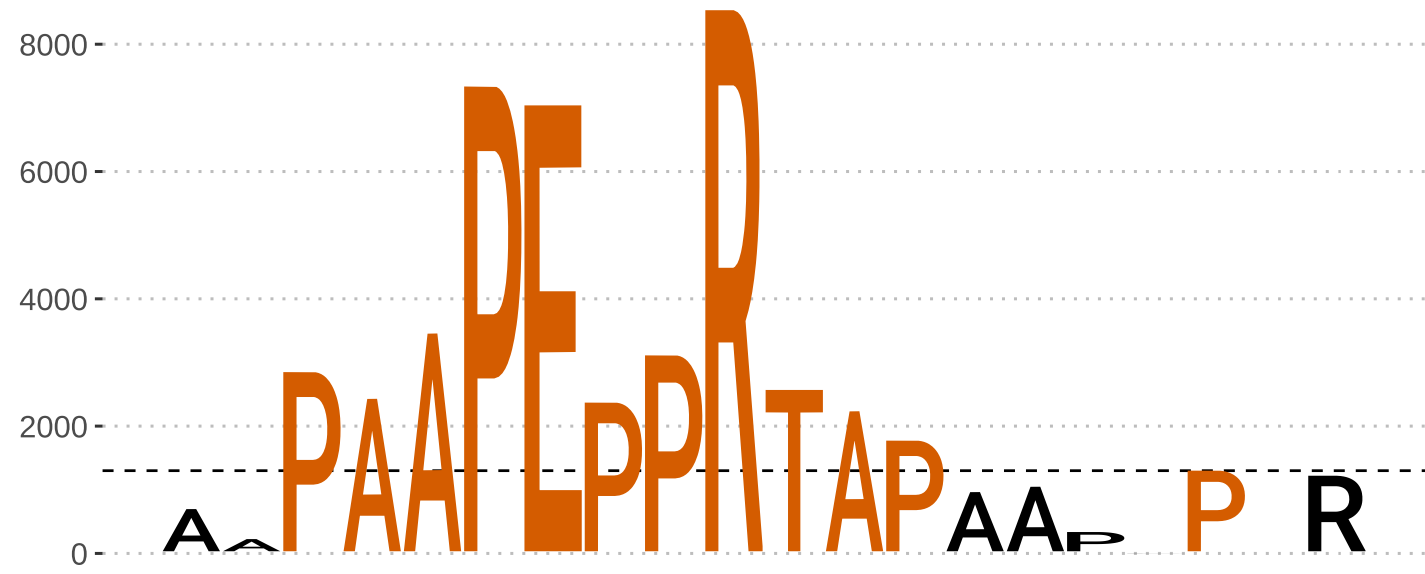
A TcCLB.499233.10 | Trans-sialidase | Repeat: 15aa | Number of repeats: 22



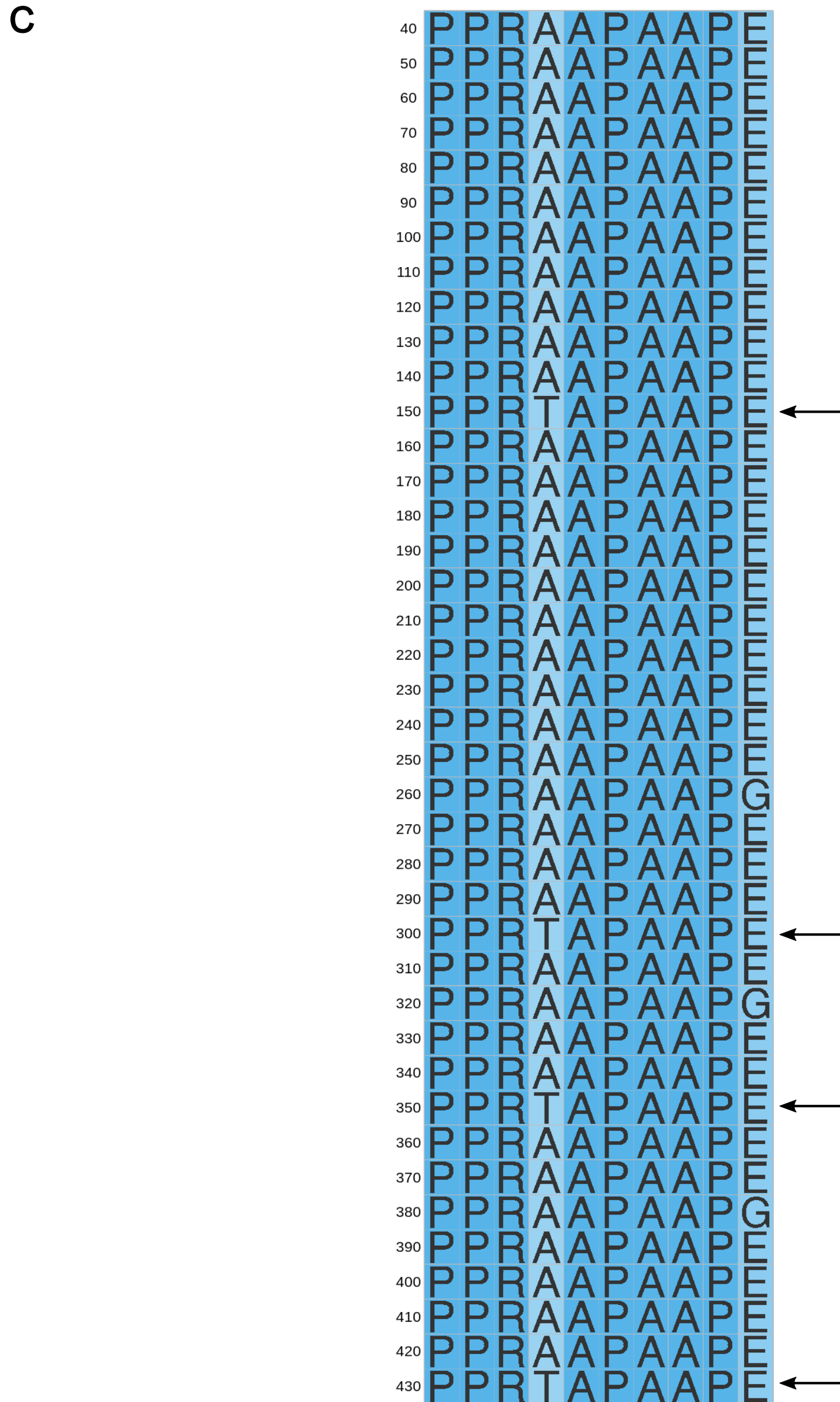
B RGGSSMPAGTSEEGSRGGSS
Best 16mer →

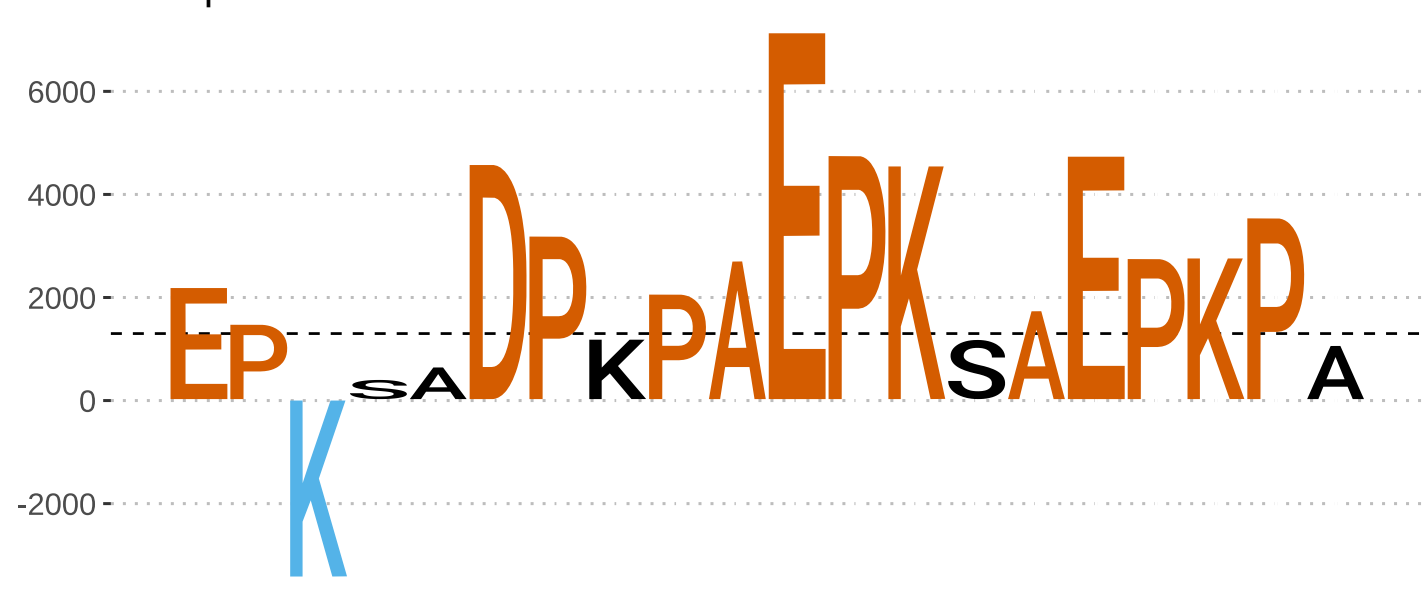


A TcCLB.503453.70 | hypothetical protein, conserved, repetitive | Repeat: 10aa |
Number of repeats: 40

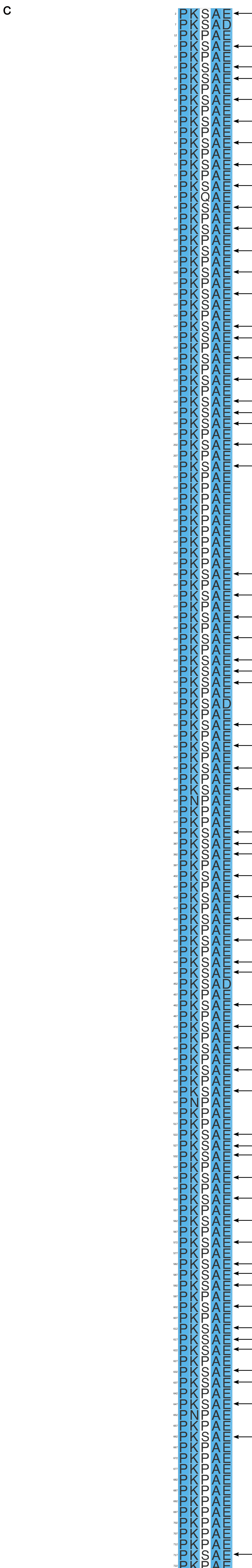


B A A P A A P E P P R T A P A A P E P P R
Best 16mer →

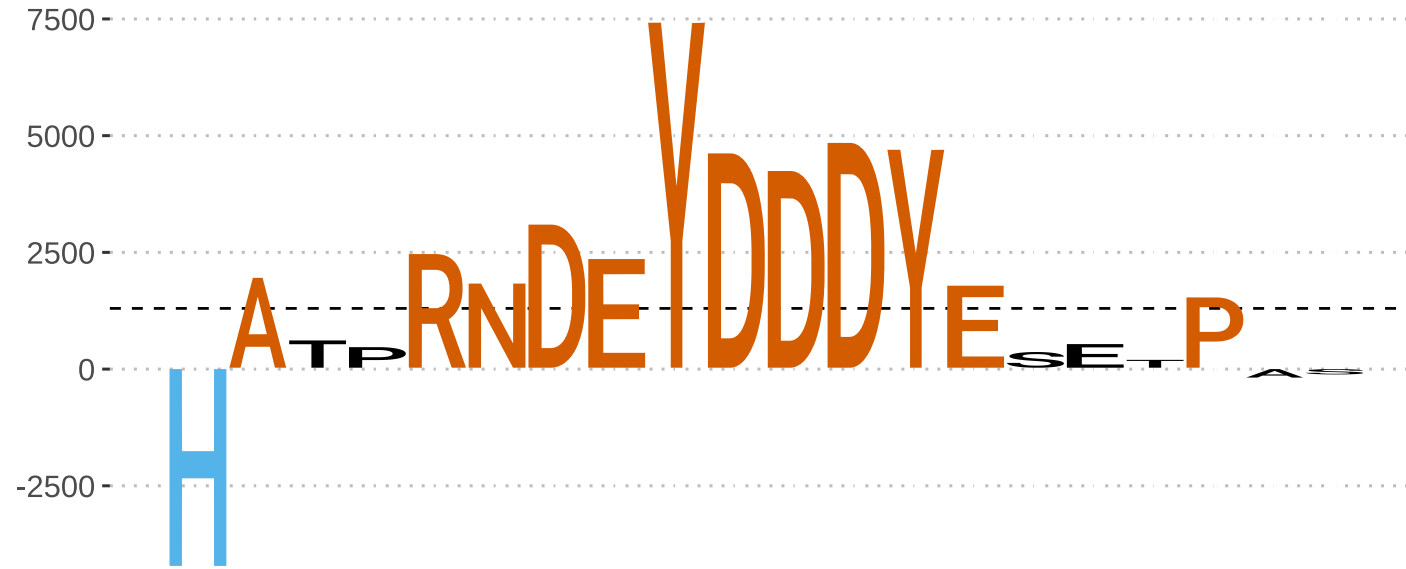




B EPKSADPKPAEPKSAEPKPA
Best 16mer →



A TcCLB.506041.60 | hypothetical protein, conserved | Repeat: 40aa |
 Number of repeats: 10

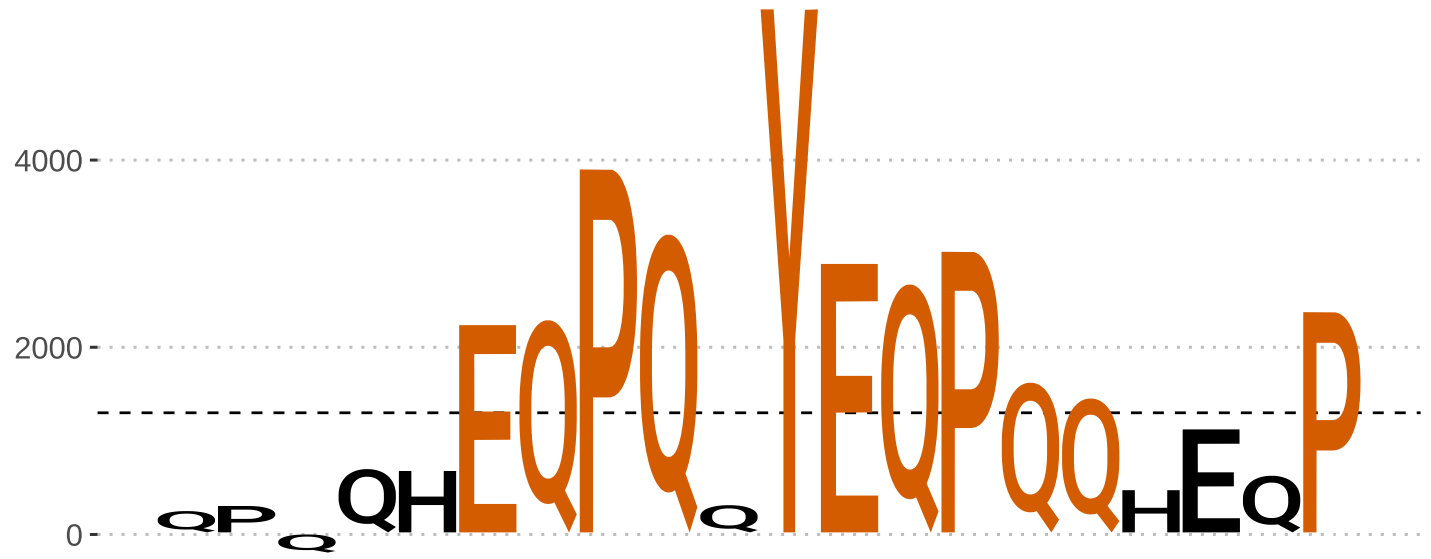


B HATPRNDEYDDDDYESETPAS
 Best 16mer →

C



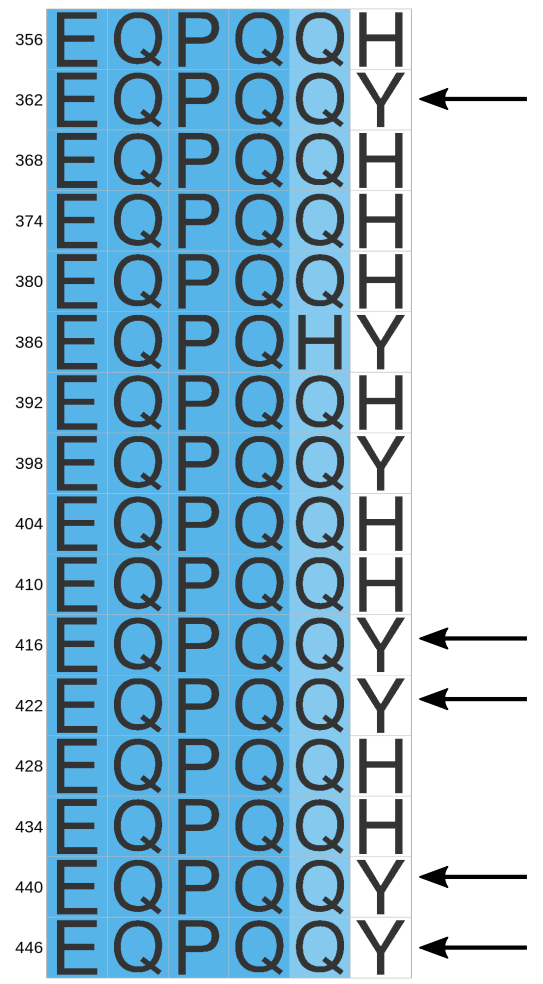
A TcCLB.506177.20 | lectin, putative | Repeat: 6aa | Number of repeats: 16



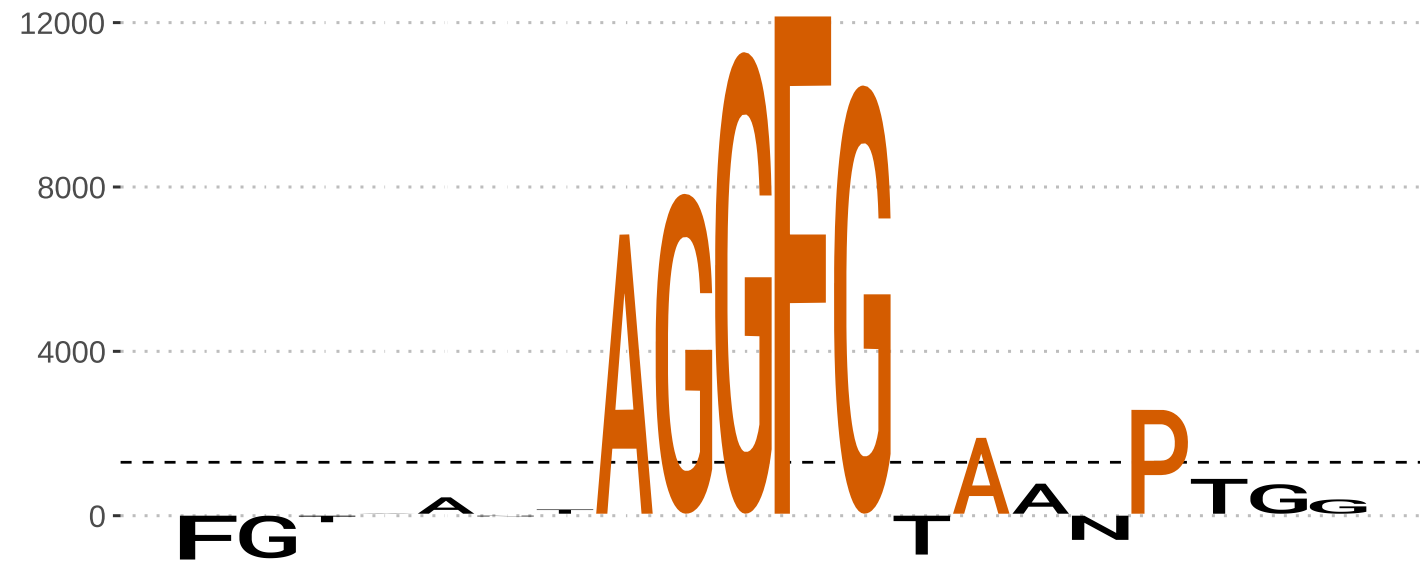
B

QPQQHEQPQQYEQPQQHEQP
Best 16mer → QPQQHEQPQQYEQPQQHEQP

C



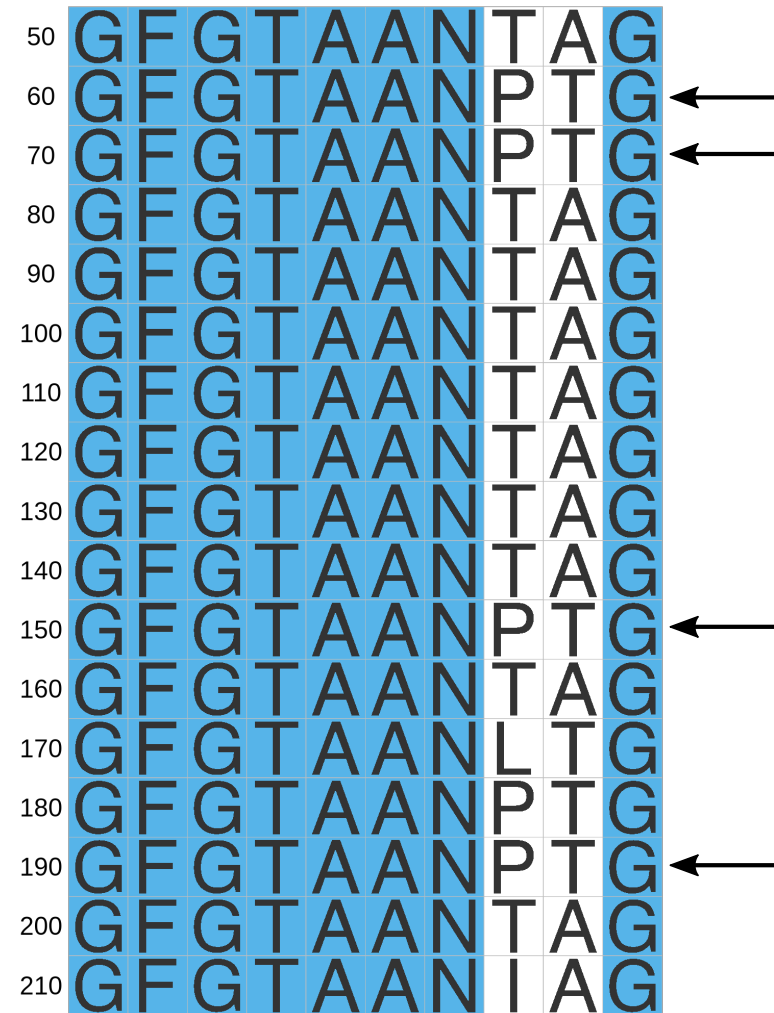
A TcCLB.506419.60 | Nucleoporin NUP62 | Repeat: 10aa | Number of repeats: 17



B FGTAANTAGGFGTAANPTGG

Best 16mer →

C



A TcCLB.506441.20 | cytoskeleton associated protein | Repeat: 21aa | Number of repeats: 10



B GREGRERGYP E E K E D S R R E R
Best 16mer → GREGRERGYP E E K E D S R R E R

C

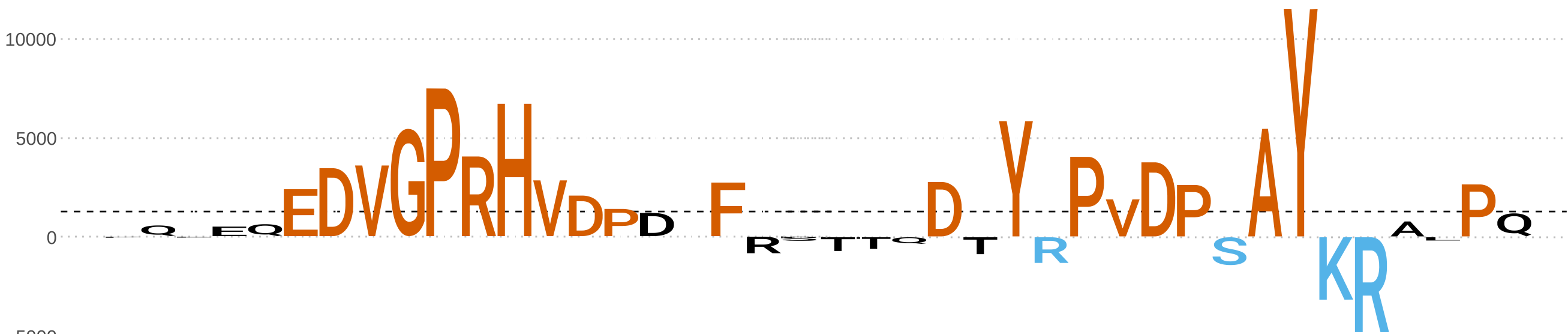
→ 665	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 686	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 707	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 728	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 749	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 770	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 791	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 812	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 833	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	S	G	R	E	G	R	E
→ 854	R	G	Y	P	E	E	K	E	D	S	R	R	E	R	D	H	P	E	E	G	L



B VAEAEKQRAAEATKVAEAEK
 Best 16mer →

C

184	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
198	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
212	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	
226	A	E	A	E	R	Q	R	A	A	E	A	T	K	A	
240	V	E	T	E	K	R	K	A	A	E	A	T	K	V	
254	A	E	A	E	K	Q	R	A	A	A	A	T	K	A	
268	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
282	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
296	A	E	A	E	K	Q	R	A	A	A	A	T	K	A	
310	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
324	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
338	A	E	A	E	K	Q	K	A	A	E	A	T	K	A	
352	V	E	T	E	K	R	K	A	A	E	A	T	K	V	
366	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
380	A	E	A	E	K	Q	R	A	A	E	A	T	K	D	
394	V	E	T	E	K	Q	R	A	A	E	A	T	K	V	
408	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
422	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	
436	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
450	V	E	T	E	K	R	K	A	A	E	A	T	K	V	
464	A	E	A	E	K	Q	R	A	A	E	A	T	K	D	
478	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
492	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
506	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
520	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
534	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
548	A	E	A	E	K	Q	K	A	A	E	A	T	K	A	
562	V	E	T	E	K	R	K	A	A	E	A	T	K	V	
576	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
590	A	E	A	E	K	Q	R	A	A	E	A	T	K	D	
604	V	E	T	E	K	Q	R	A	A	E	A	T	K	V	
618	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
632	A	E	A	E	K	Q	K	A	A	E	A	T	K	A	
646	V	E	T	E	K	R	K	A	A	E	A	T	K	V	
660	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
674	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	←
688	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
702	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
716	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
730	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
744	V	E	T	E	K	Q	K	A	A	E	A	T	K	V	
758	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
772	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
786	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	←
800	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
814	V	E	T	E	K	Q	R	A	A	E	A	T	K	V	
828	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	←
842	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
856	V	E	T	E	K	R	K	A	A	E	A	T	K	V	
870	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
884	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	←
898	A	E	A	E	K	R	K	A	A	E	A	T	K	V	
912	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
926	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	
940	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	
954	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
968	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
982	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
996	A	E	A	E	K	Q	R	A	A	E	A	T	K	V	←
1010	A	E	A	E	K	Q	K	A	A	E	A	T	K	V	
1024	A	E	A	E	K	Q	R	A	A	E	A	T	K	A	
1038	V	E	T	E	K	R	K	A	A	E	A	T	K	I	



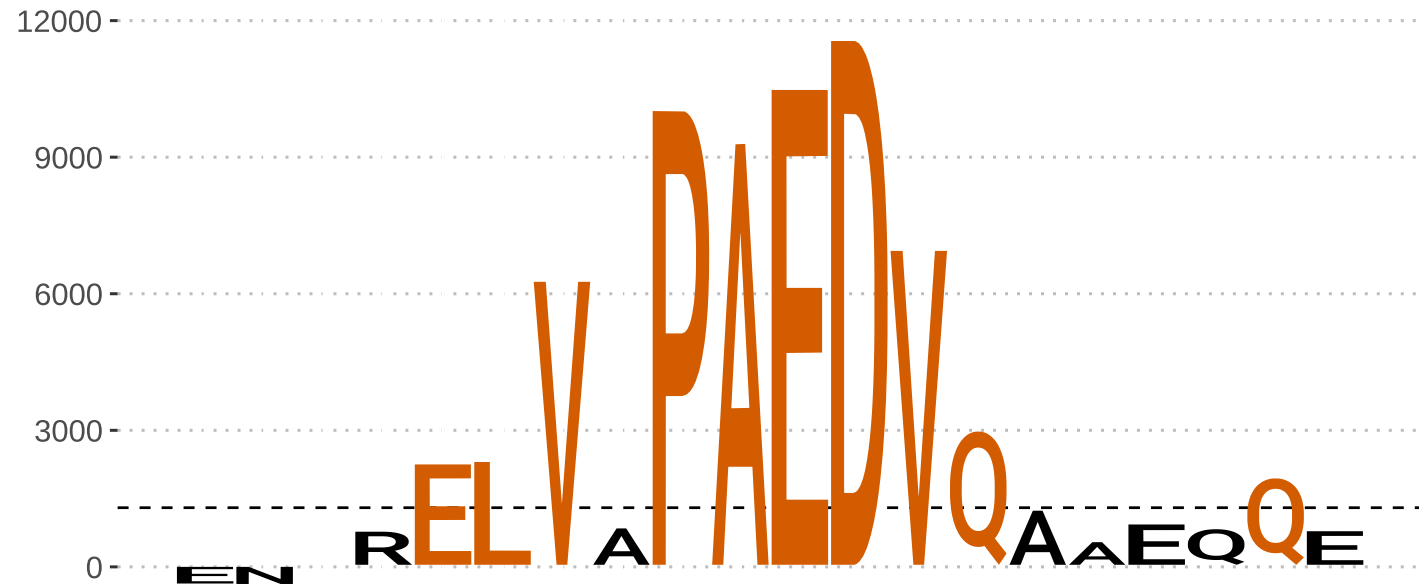
B PQEEQEDVVGPRRHVDPDHFRRSTTTQD TYR PVDP S AYKRALPQ

Best 16mer →

C

12	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
50	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
88	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
126	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	L	E
164	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
202	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	L	E
240	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	L	L	E
278	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	L	E
316	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
354	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
392	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	T	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
430	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
468	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
506	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	L	E
544	E	E	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
582	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
620	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
658	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E
696	E	Q	E	D	V	G	P	R	H	V	D	P	D	H	F	R	S	T	T	Q	D	A	Y	R	P	V	D	P	S	A	Y	K	R	A	L	P	Q	E

A TcCLB.507711.250 | nucleolar RNA-binding protein | Repeat: 39aa | Number of repeats: 21



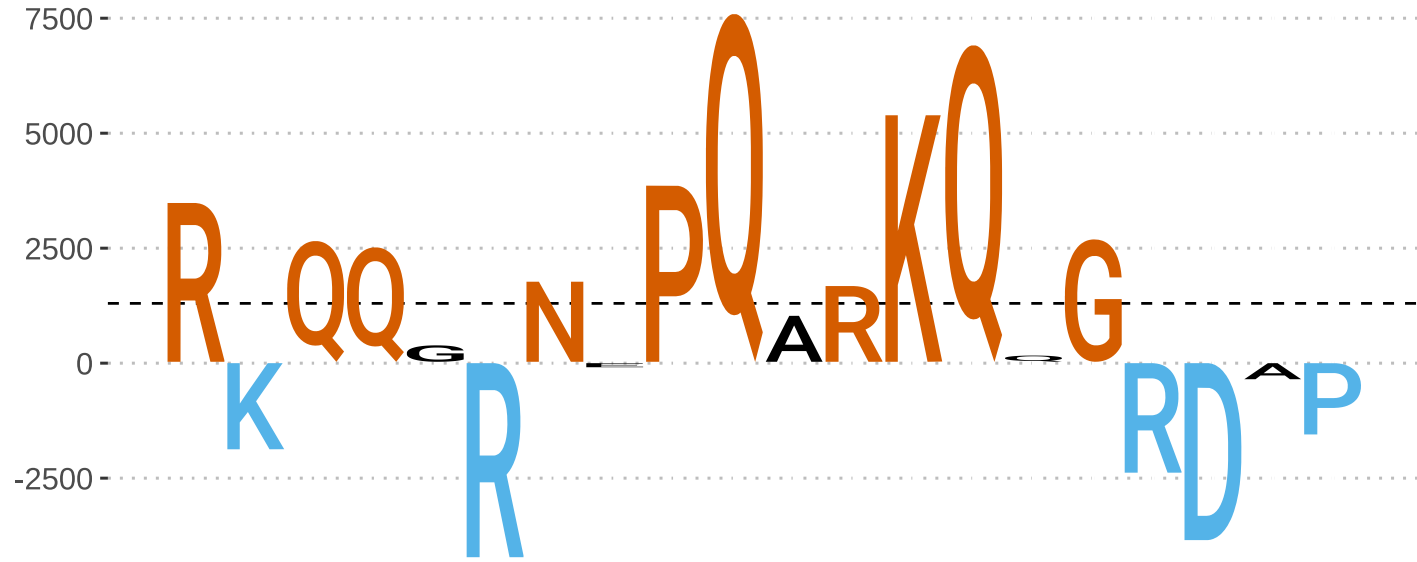
B ENVREL VAPAE DVQAAEQQE

Best 16mer →

C



A TcCLB.507765.60 | Ribosomal S21 | Repeat: 11aa | Number of repeats: 4



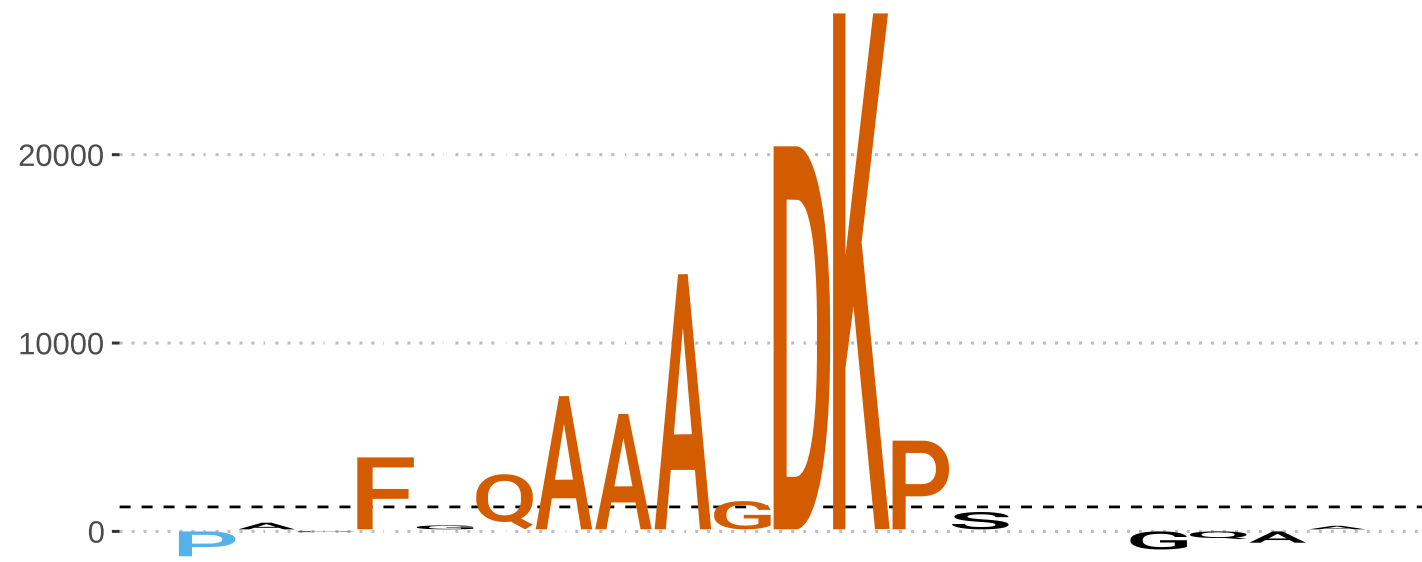
B

Best 16mer → RKQQGRNEPQARKQQGRDAP

C



A TcCLB.508831.140 | Ag2 | CA-2 | Repeat: 12aa | Number of repeats: 34

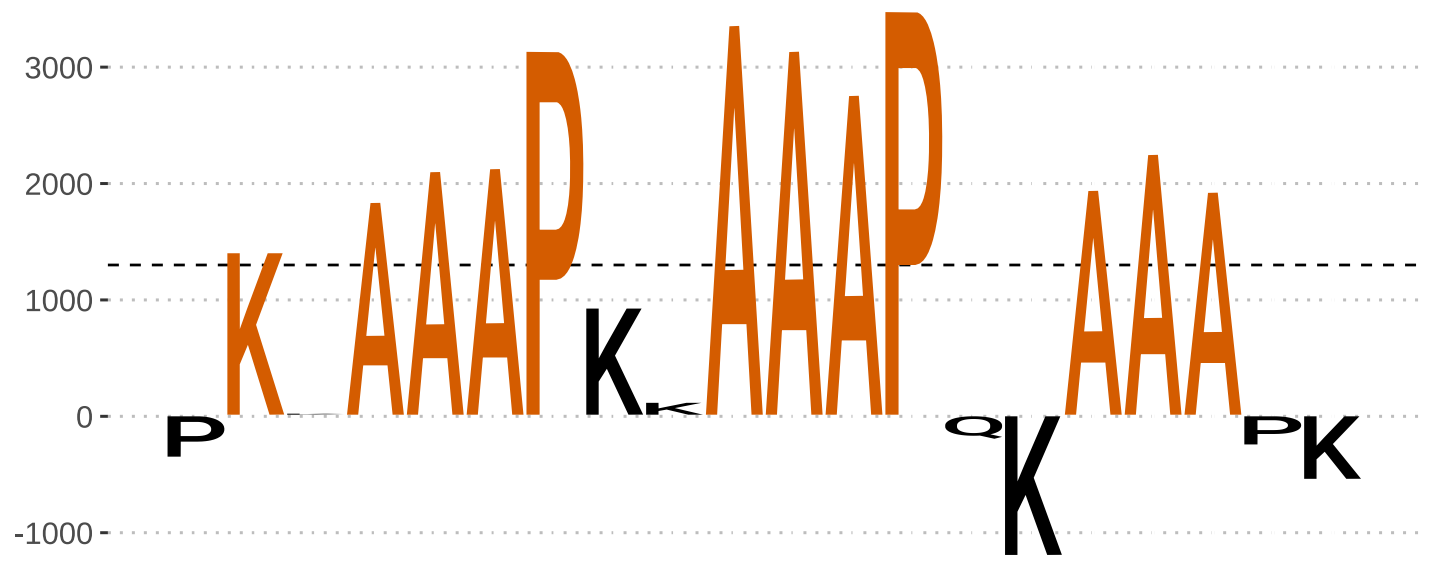


B PAPFGQAAAGDKPSPFGQAA
Best 16mer →

C

209	P	F	G	Q	A	A	A	G	D	K	P	S	←
221	P	F	G	Q	A	A	A	G	D	K	P	P	←
233	P	F	G	Q	A	A	A	G	D	K	P	S	←
245	P	F	G	Q	A	A	A	G	D	K	P	P	←
257	P	F	G	Q	A	A	A	G	D	K	P	P	←
269	P	F	G	Q	A	A	A	G	D	K	L	S	←
281	L	F	G	Q	A	A	A	G	D	K	P	A	←
293	P	F	G	Q	A	A	A	G	D	K	P	S	←
305	P	F	G	Q	A	A	A	G	D	K	P	P	←
317	P	F	G	Q	A	A	A	G	D	K	P	S	←
329	P	F	G	Q	A	A	A	G	D	K	P	P	←
341	P	F	G	Q	A	A	A	G	D	K	P	S	←
353	P	F	G	Q	A	A	A	G	D	K	P	P	←
365	P	F	G	Q	A	A	A	G	D	K	P	P	←
377	P	F	G	Q	A	A	A	G	D	K	P	P	←
389	P	F	G	Q	A	A	A	G	D	K	P	S	←
401	L	F	G	Q	A	A	A	G	D	K	P	S	←
413	P	F	G	Q	A	A	A	G	D	K	P	P	←
425	P	F	G	Q	A	A	E	G	D	K	P	P	←
437	P	F	G	Q	A	A	A	G	D	K	P	A	←
449	P	F	G	Q	A	A	A	G	D	K	P	A	←
461	P	F	G	Q	A	A	A	A	D	K	P	S	←
473	L	F	G	Q	A	A	A	G	D	K	P	P	←
485	P	F	G	Q	A	A	A	G	D	K	P	A	←
497	P	F	G	Q	A	A	A	G	D	K	L	S	←
509	L	F	G	Q	A	A	A	G	D	K	P	S	←
521	P	F	G	Q	A	A	A	G	D	K	P	S	←
533	L	F	G	Q	A	A	A	G	D	K	P	S	←
545	P	F	G	Q	A	A	A	G	G	K	P	S	←
557	P	F	G	Q	A	A	A	G	G	K	P	S	←
569	P	F	G	Q	A	A	A	G	D	K	P	S	←
581	P	F	G	Q	A	A	A	G	G	K	P	S	←
593	P	F	G	Q	A	A	A	G	D	K	P	S	←
605	P	F	G	Q	G	T	A	F	D	A	S	R	←

A TcCLB.509151.140 | Ribosomal L23a | Repeat: 6aa | Number of repeats: 6



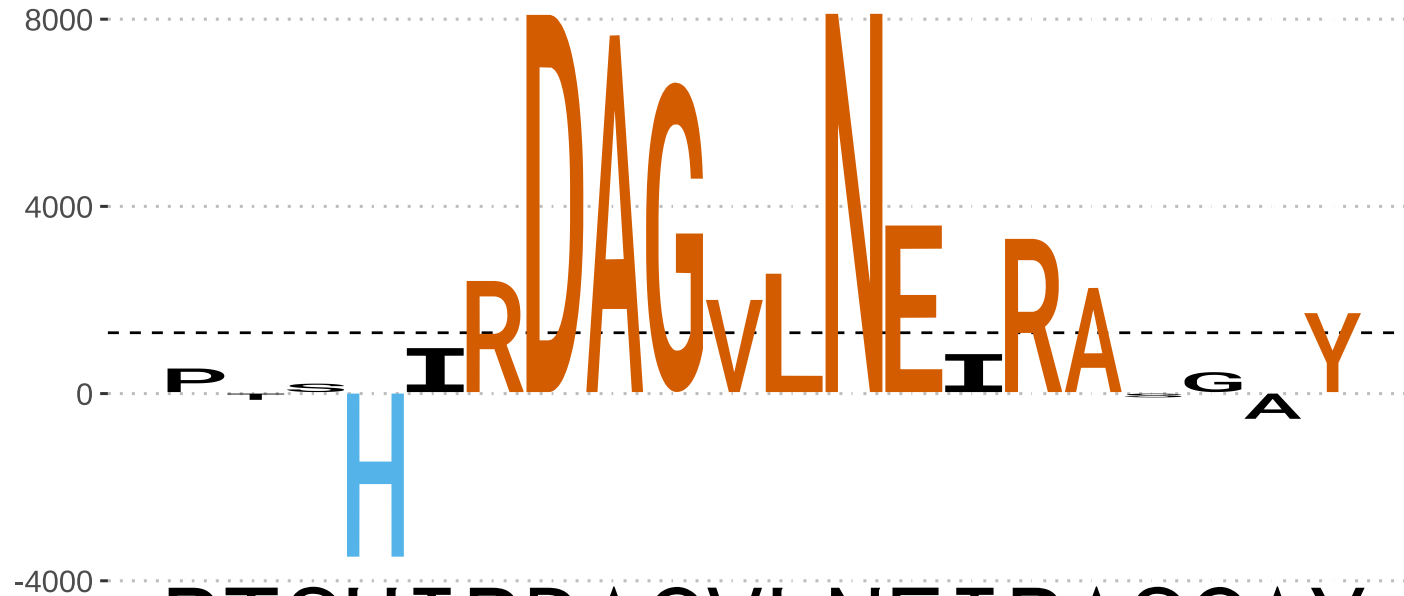
B

PKKAAAPKKAAPQKAAAPK
Best 16mer →

C

35	K	A	A	A	P	K	
41	K	A	A	A	P	K	
47	K	A	A	A	P	Q	←
53	K	A	A	A	P	K	
59	K	T	A	A	P	K	
65	K	A	A	A	P	Q	←

A TcCLB.509219.20 | nretrotransposon hot spot (RHS) protein | Repeat: 145aa | Number of repeats: 3



B PTSHIRDAGV LNEIRASGAY

Best 16mer →

C

→ 138	---	PTSHIRDAGV LNEIRASGAY	---
→ 283	---	PTSHIRDAGV LNEIRASGAY	---
428	---	PTSHIRDAGV LGEIQTTGAY	---

A TCSYLVIO_003468 | Trans-sialidase | SAPA | Repeat: 12aa | Number of repeats: 6



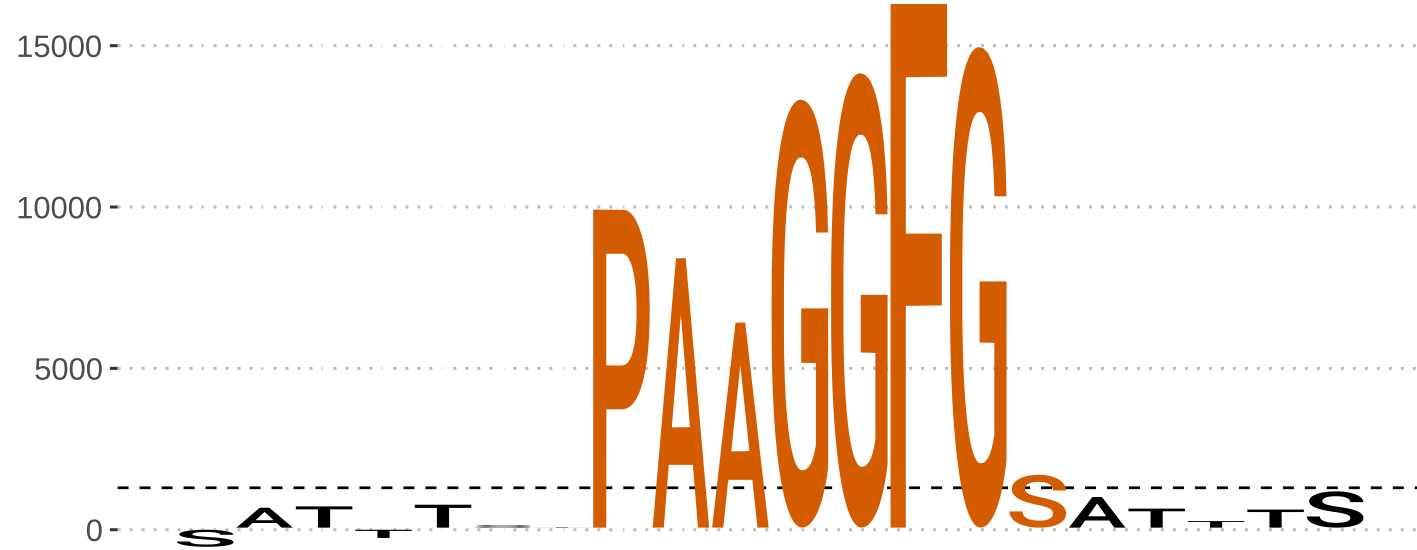
B

SSAHGTPTVDSSAHGTPS
 Best 16mer →

C



A TCSYLVIO_004056 | Nucleoporin NUP53a | Repeat: 14aa | Number of repeats: 3



B

SATTTSTPAAGGFGSATTTT

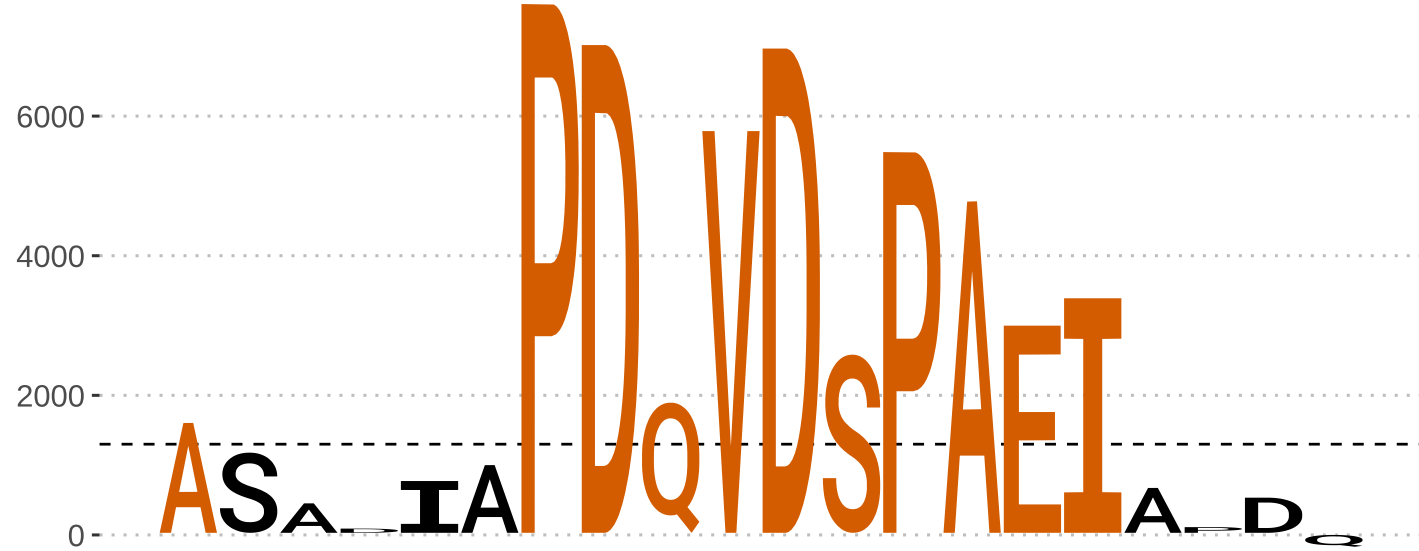
Best 16mer →



C

84	G	F	G	S	A	T	T	T	S	T	P	A	A	G	←
98	G	F	G	S	A	T	T	T	S	A	P	A	V	G	
112	G	F	G	S	A	A	H	T	S	T	P	A	A	G	

A TCSYLVI0_009198 | hypothetical protein | Repeat: 11aa | Number of repeats: 3



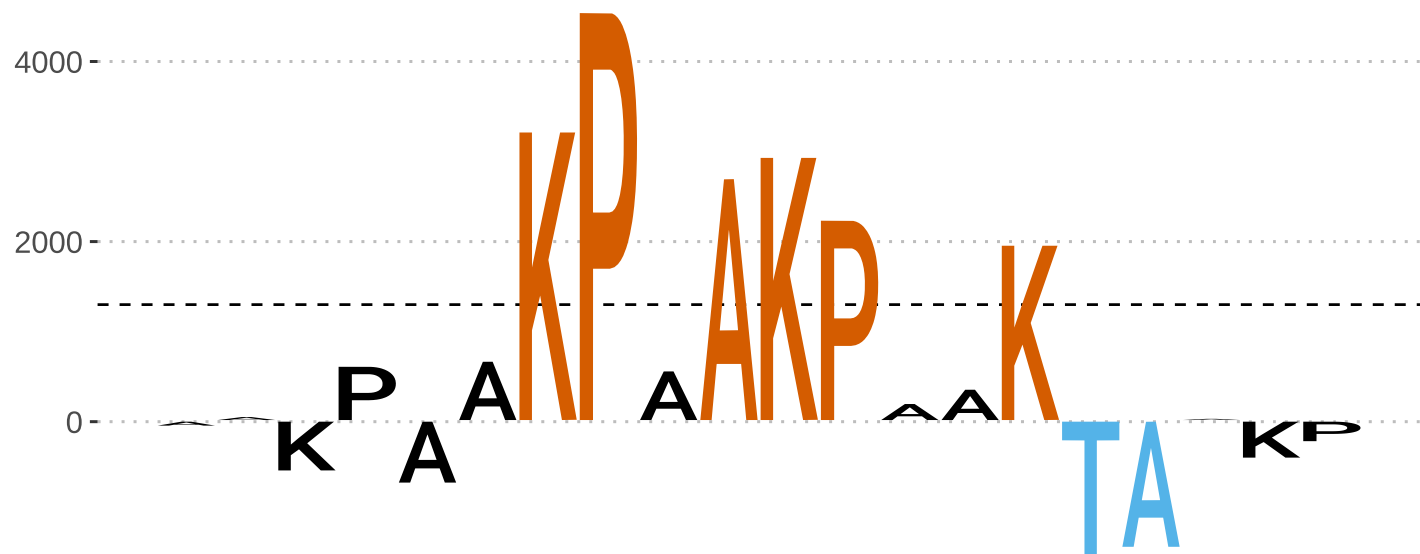
B

ASADIAPDQVDSPAEIAPDQ
Best 16mer →

C

677	I	A	P	D	Q	V	D	S	P	A	E	←
680	I	A	P	D	Q	V	D	S	P	A	E	←
699	I	A	P	D	Q	V	D	S	P	A	E	←

A TCSYLVIQ_009765 | Ribosomal L7a | RNA binding protein | Repeat: 8aa | Number of repeats: 4



B

AAKPAAKPAAKPAAKTAAKP
Best 16mer →

C

