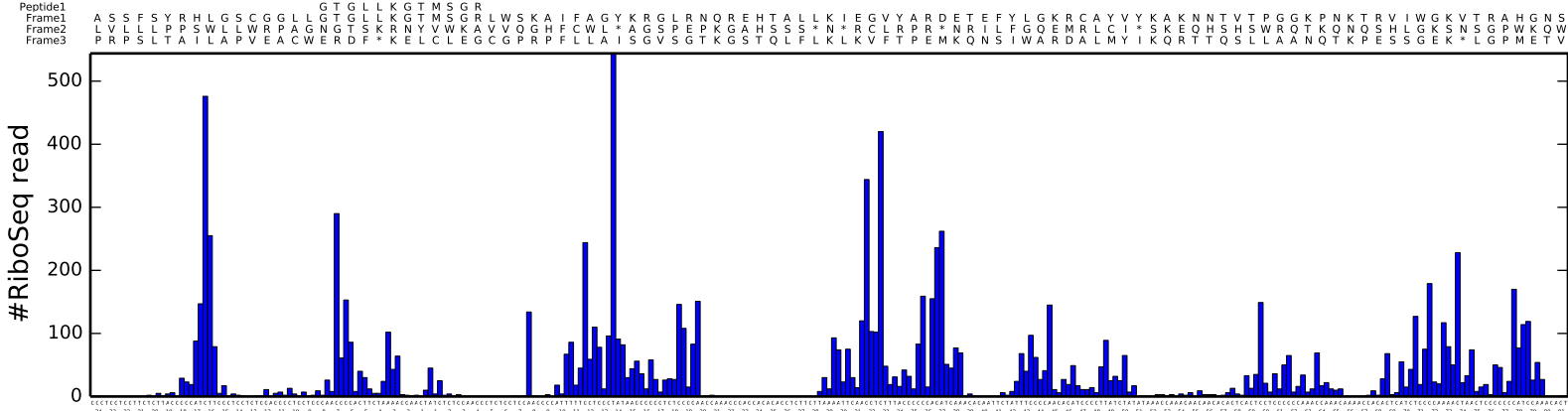
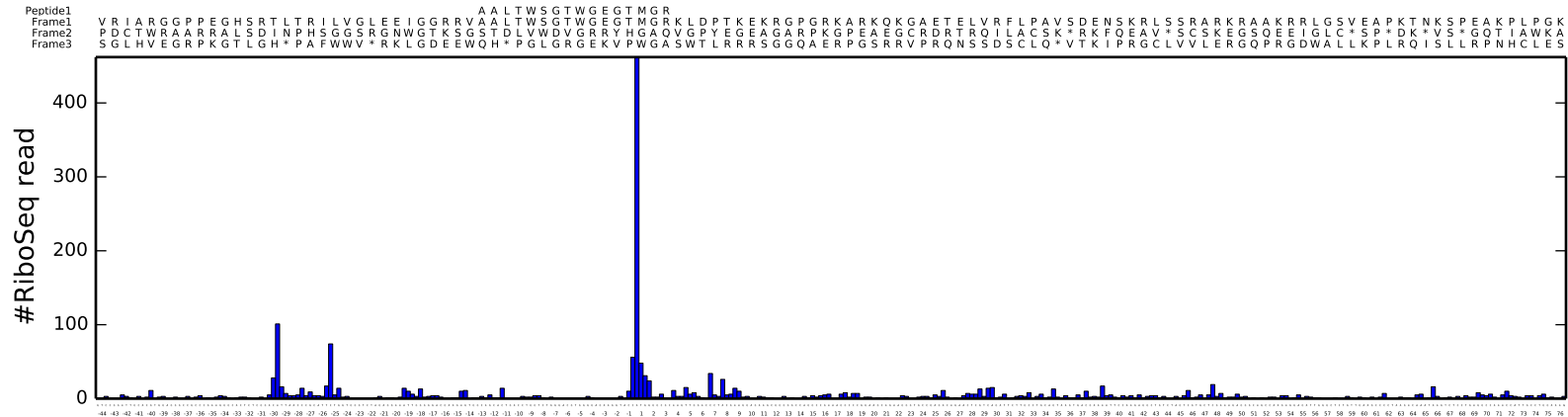


Supplemental Figure S3

NM_000996 Ac-GTGLLKGTMSG R

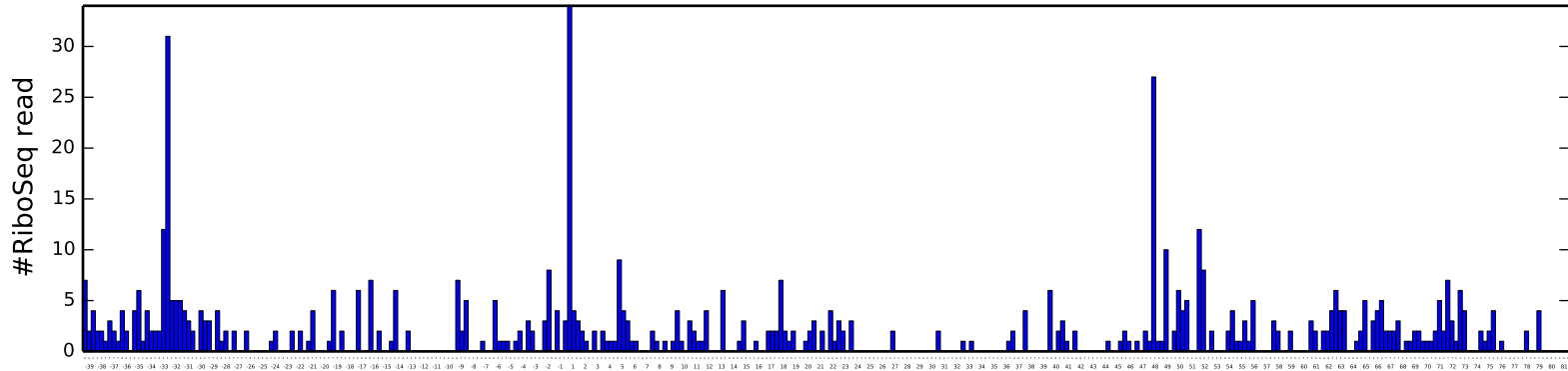


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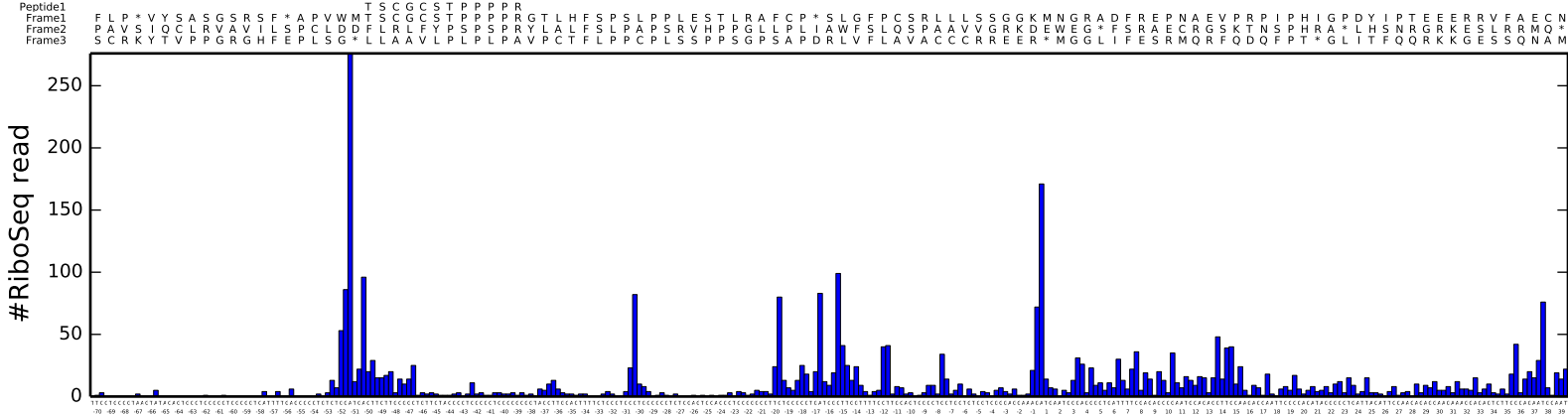


NM_001039591 Ac-AKICPVSSMTATTR

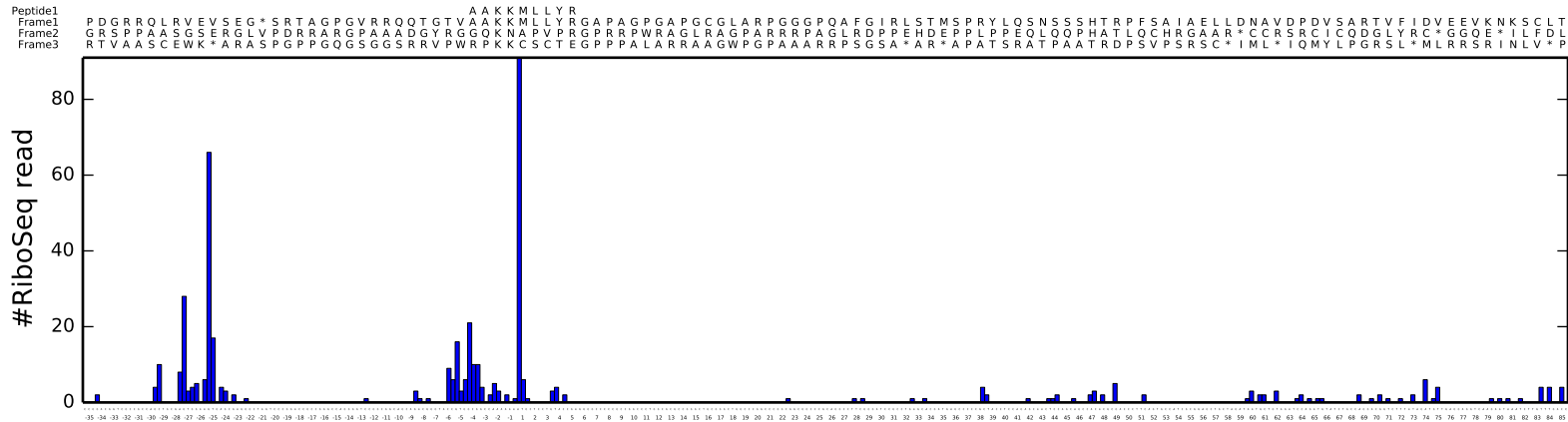
Peptide1 AKICPVSSMTATTR
 Frame1 DLFKTDKCWYFIFYKWTIISFLKTTT*ADKIAKICPVSSMTATTRGSPVGGNDNQGOAPDGQSQPPLQQNQTSSPDSSNENSPATPPDEQGQGDAPPQLEDEEPAFPHTDLAKLDDMINR
 Frame2 PF*D*QMLVLHLL*VDYNFFSQDNYISRONCKDLPCVEYDSHDSWLSGRRE*QPGPGS*WTVSAPPPTESDFIA*FFQ*KFPGNspr*ARSr*CPTTA*R*GTCISTY*LGQVG*HDQQA
 Frame3 TFLRLTNAGTSSSISGL*FLFSRQLHKQTKLQRSALCRV*QPRLVALRSEGMTTRARLLMDSLSPPSNRIRLHRLILPMKIPRQLPQMSKVKVMPHHS LKMRNLHFHILTWPSWMT*STG



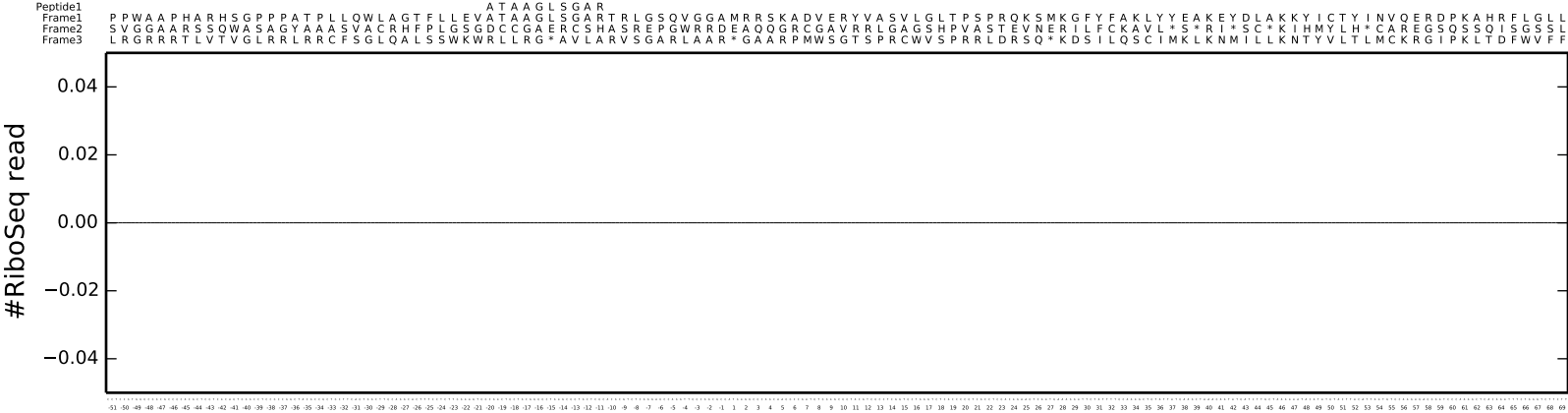
NM_001079840 Ac-TSCGCSTPPPPR



NM_001085354 Ac-AAKKMLLYR



NM_001123363 Ac-ATAAGLSGAR



NM_001142726 Ac-AATAALIPLHR

Peptide1

Frame1

Frame2

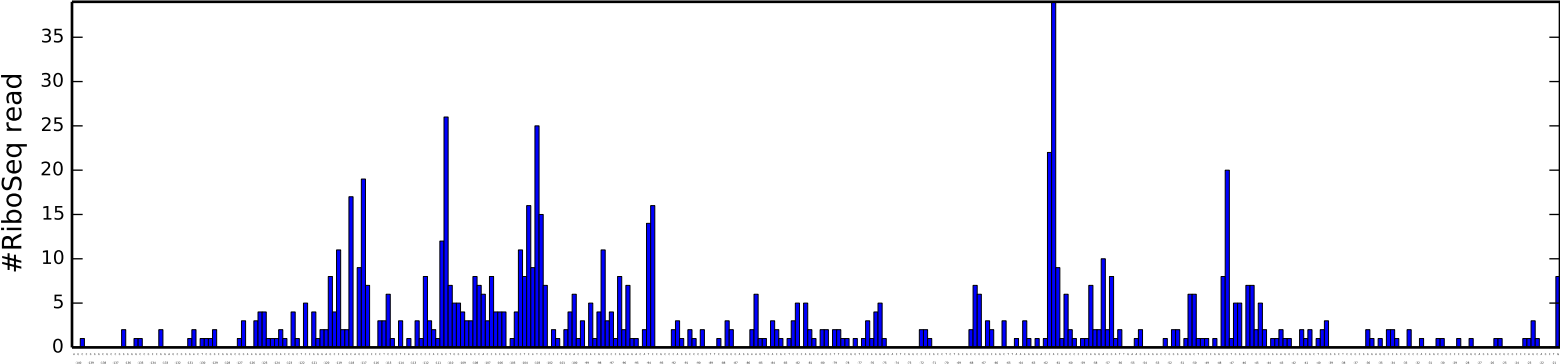
Frame3

AATAALIPLHR

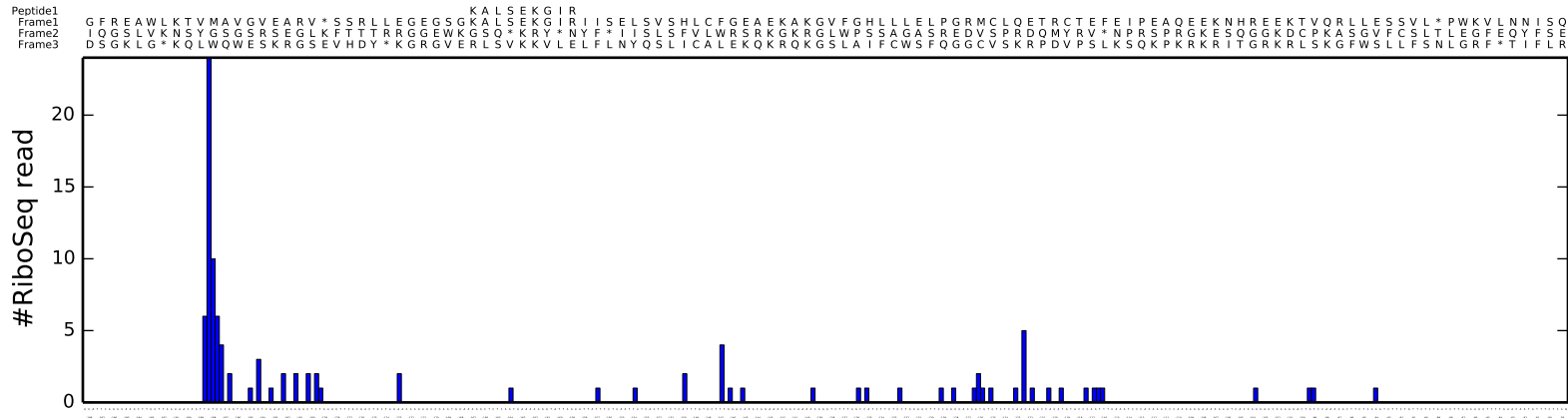
SRAPGAAGAGLGGRKRRPLREPAGPSLNPTLAATAALIPLHRRAGDIRPGPLPGGSDAPSQLPVQETRPRLCAGQLKGTTPRRIEGDREAAGVDRGKAGLGGLGGRPPPPQPPREERAQQL

PGAGGRRSGTRRAEEATAPGASRPLAQPHAGSHRGPHPPAPTTRRRHPPRPASGRK*RSQPASGPGDSAPPLRRAA*RDHDPQED*RRPGGCRRGPREGGAGARREATPTAAPGGARPAAA

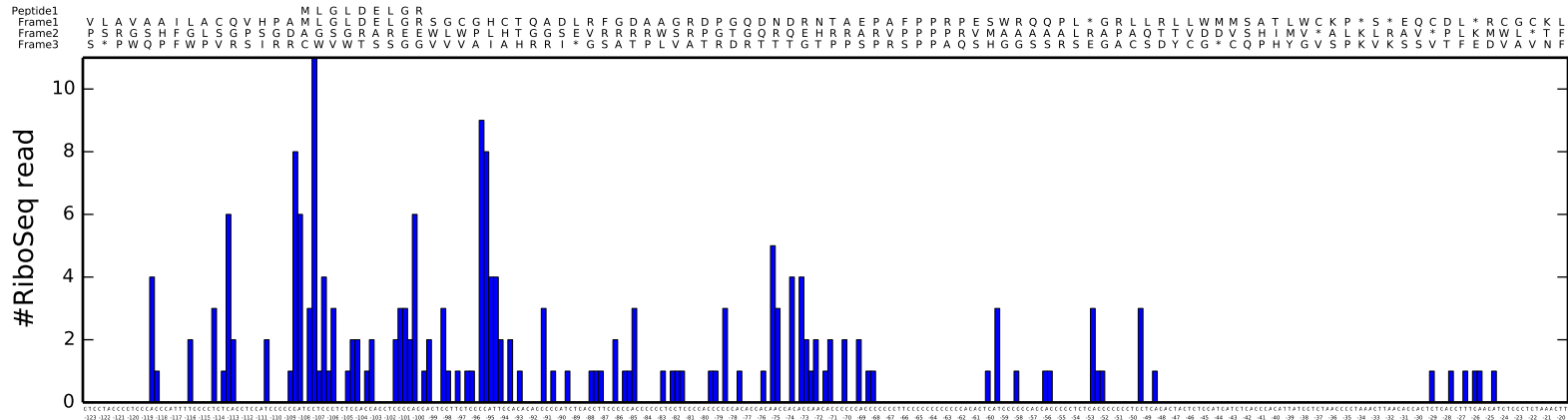
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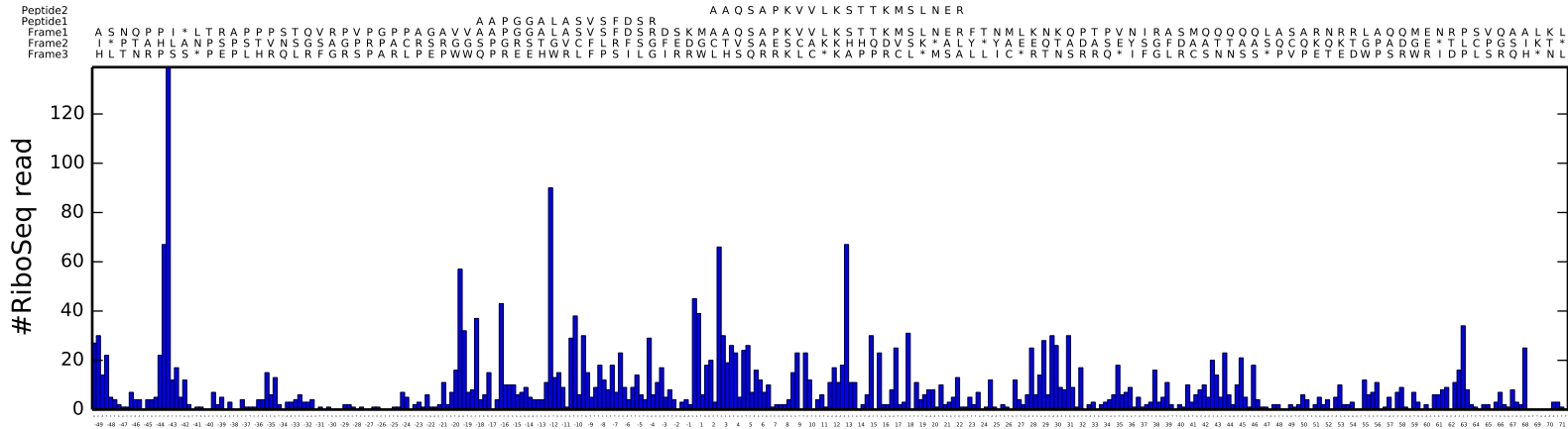
NM_001204173 Ac-KALSEKGIR



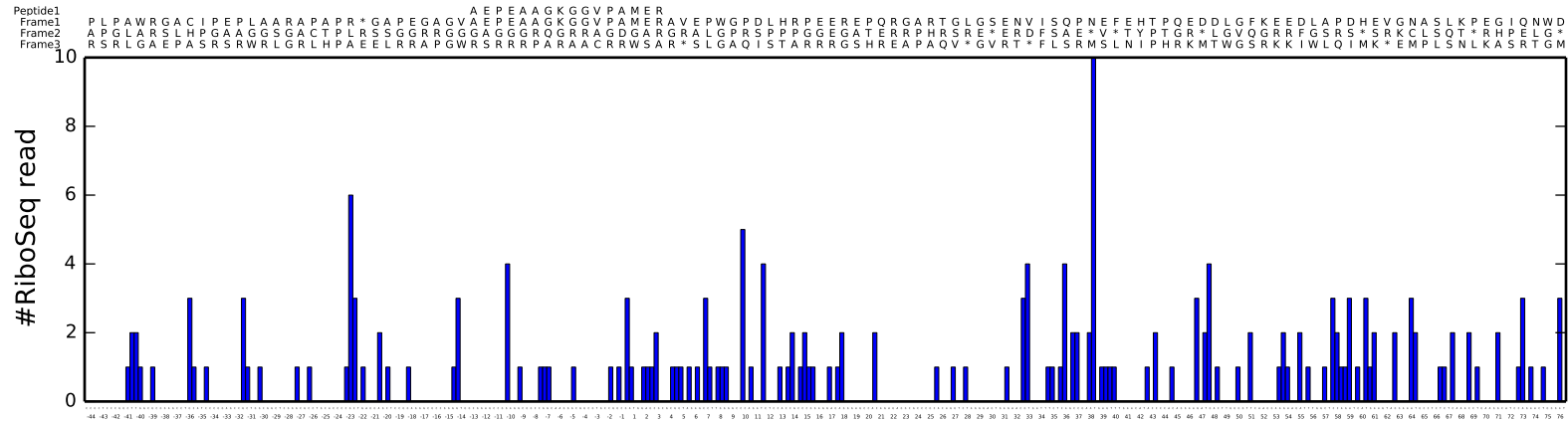
NM_001204814 Ac-MLGLDELGR



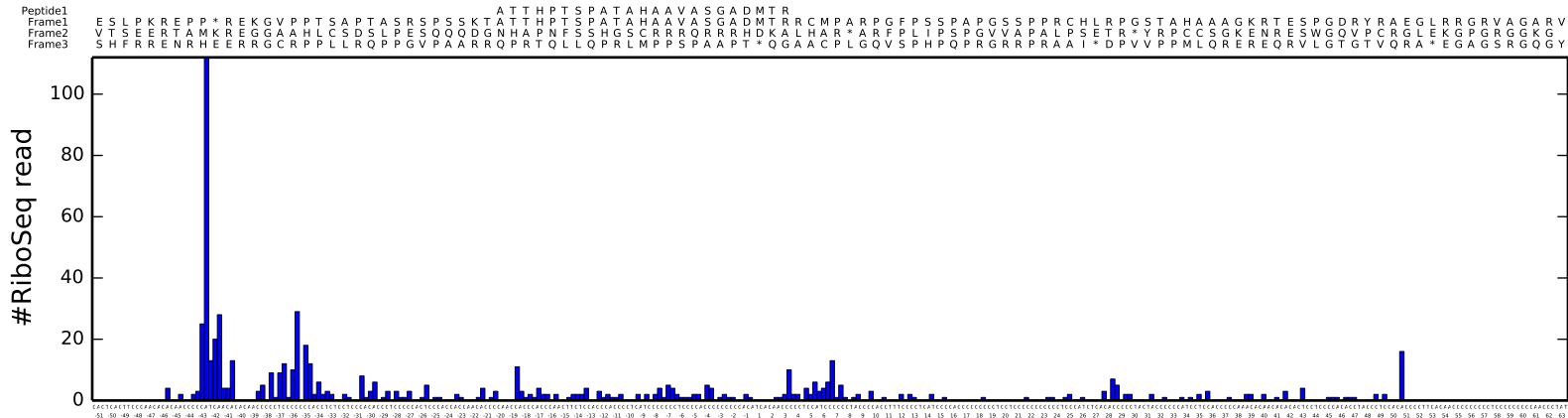
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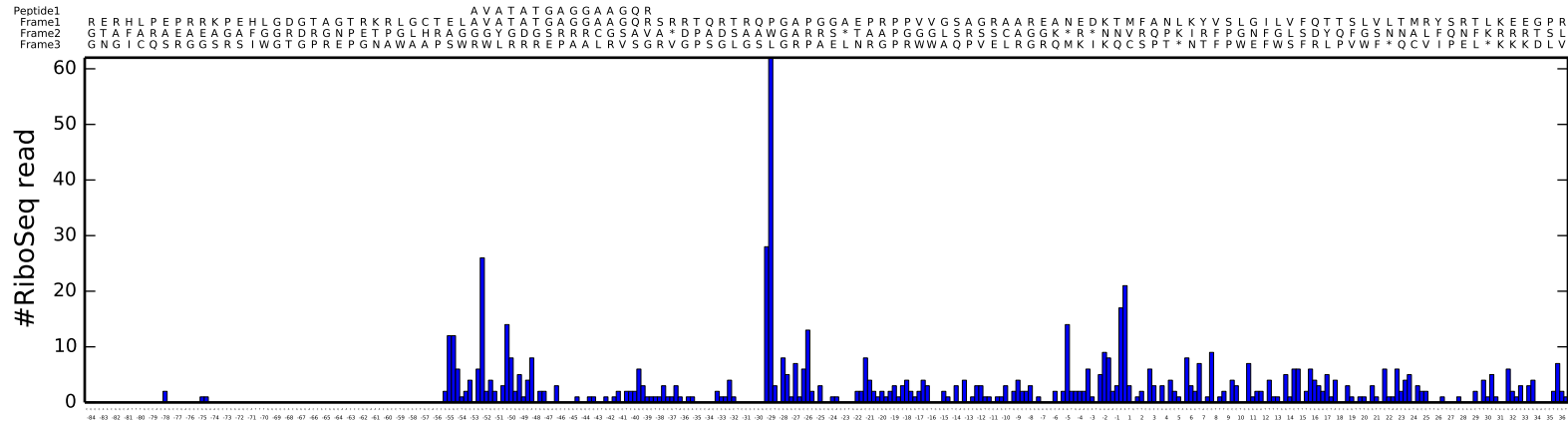
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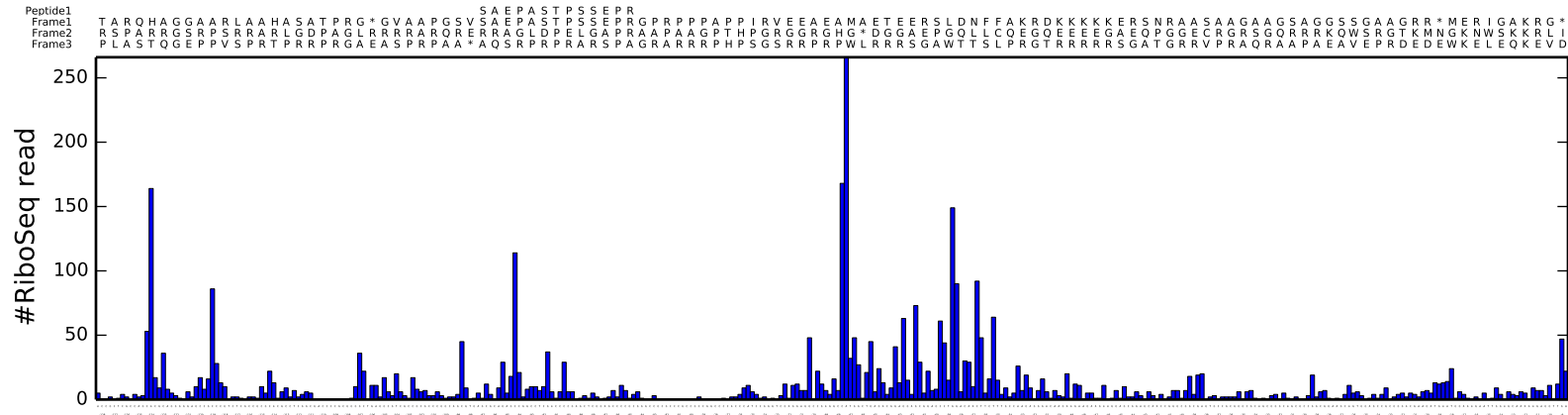
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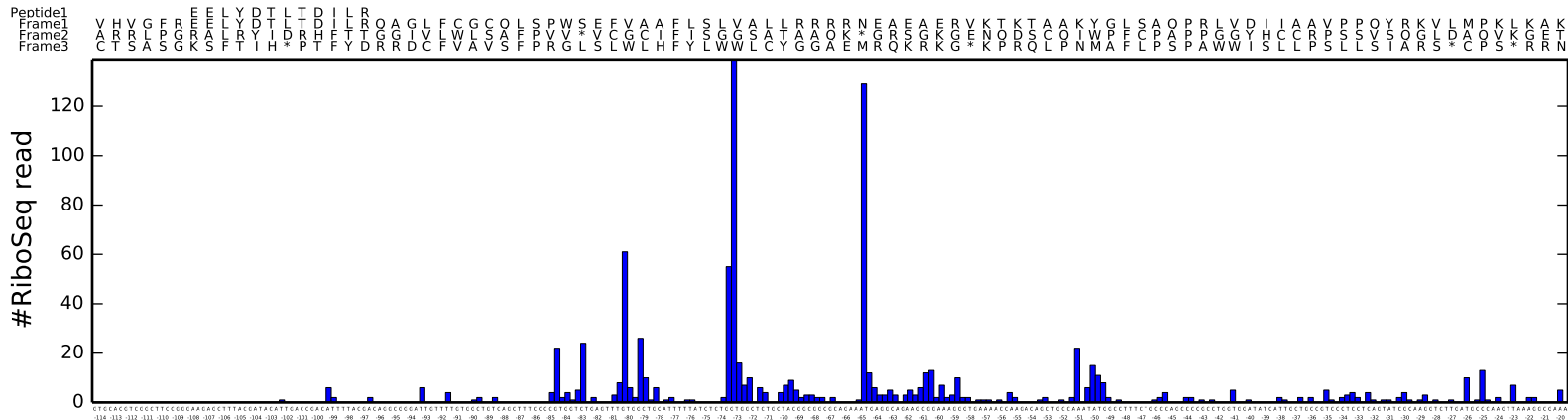
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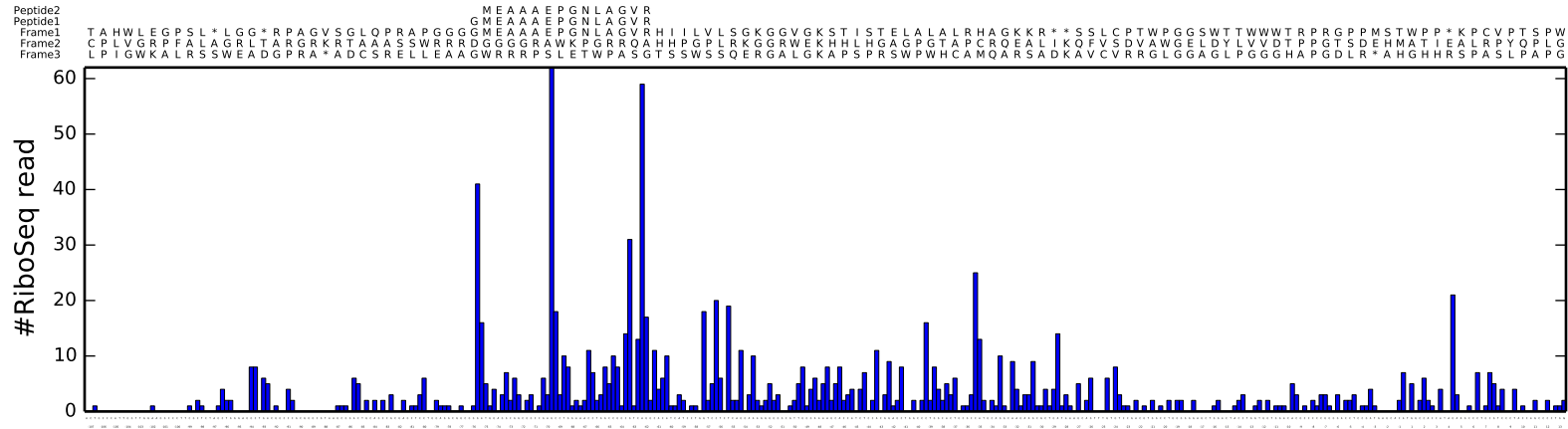
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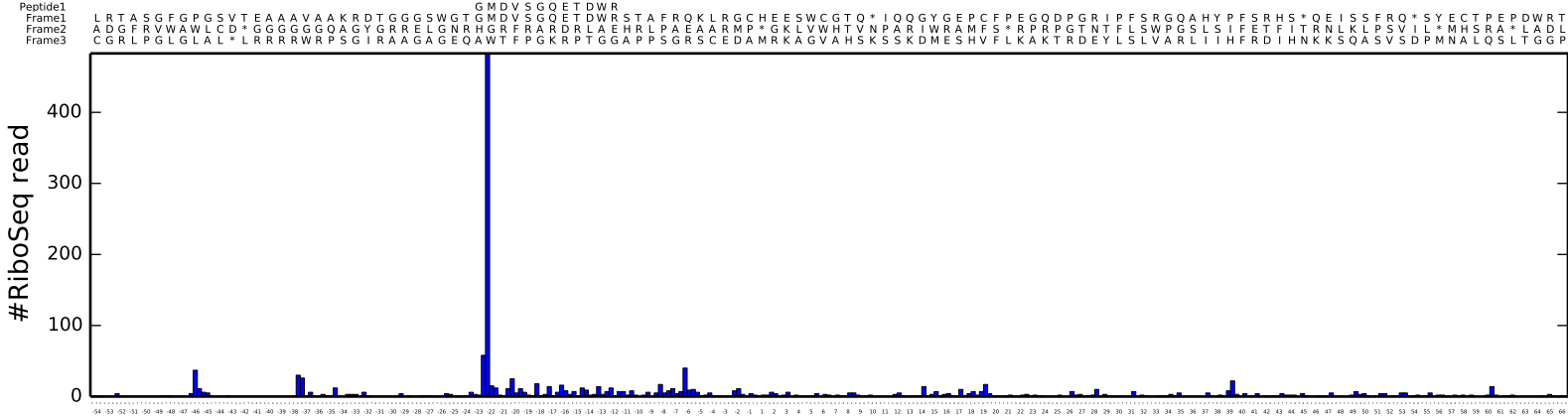
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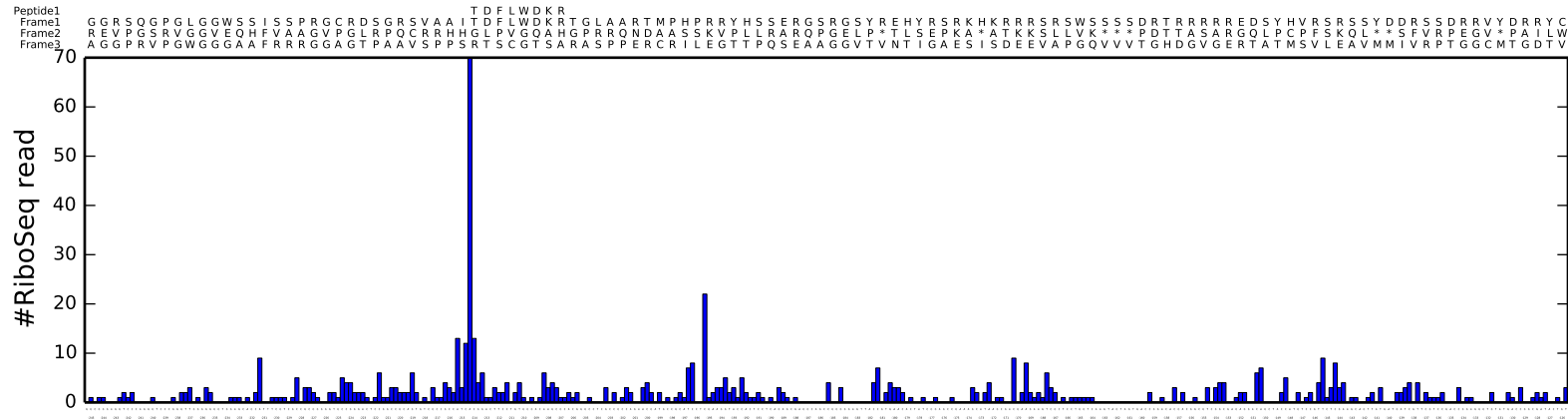
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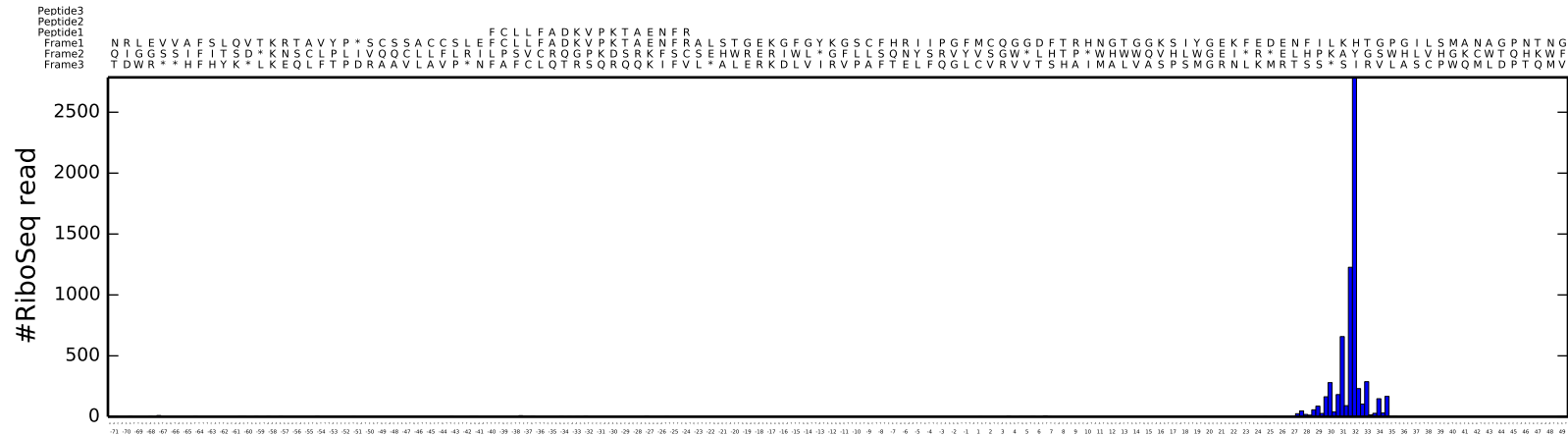
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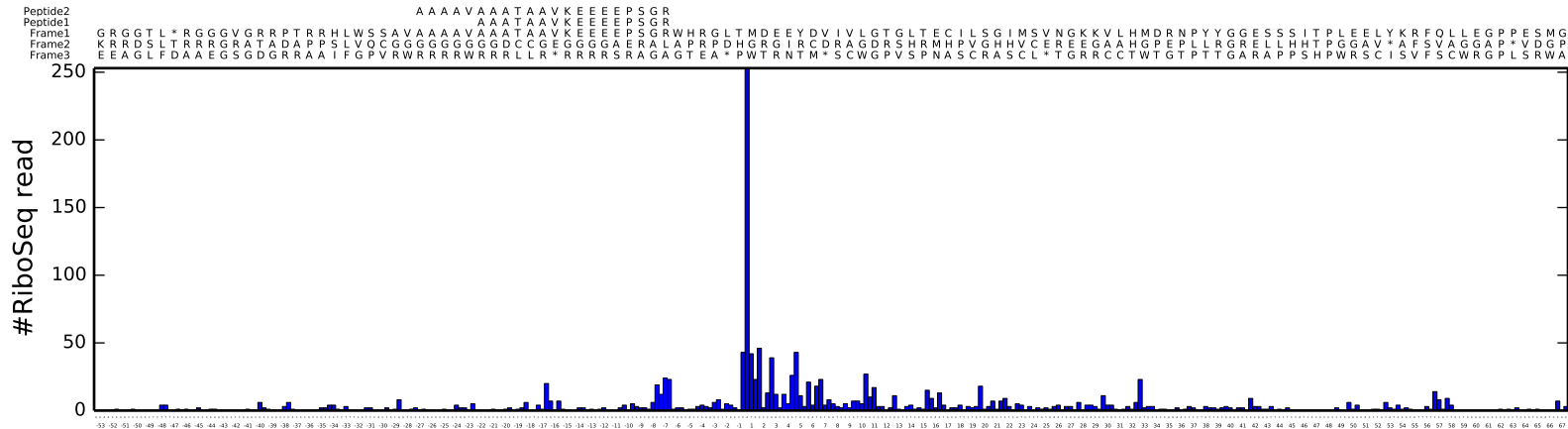
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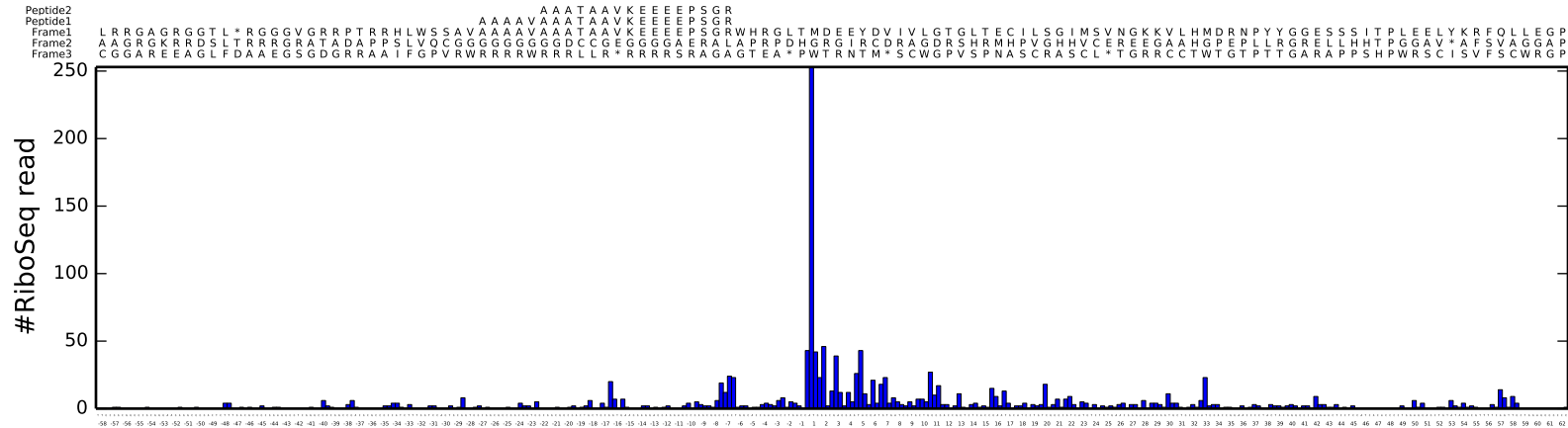
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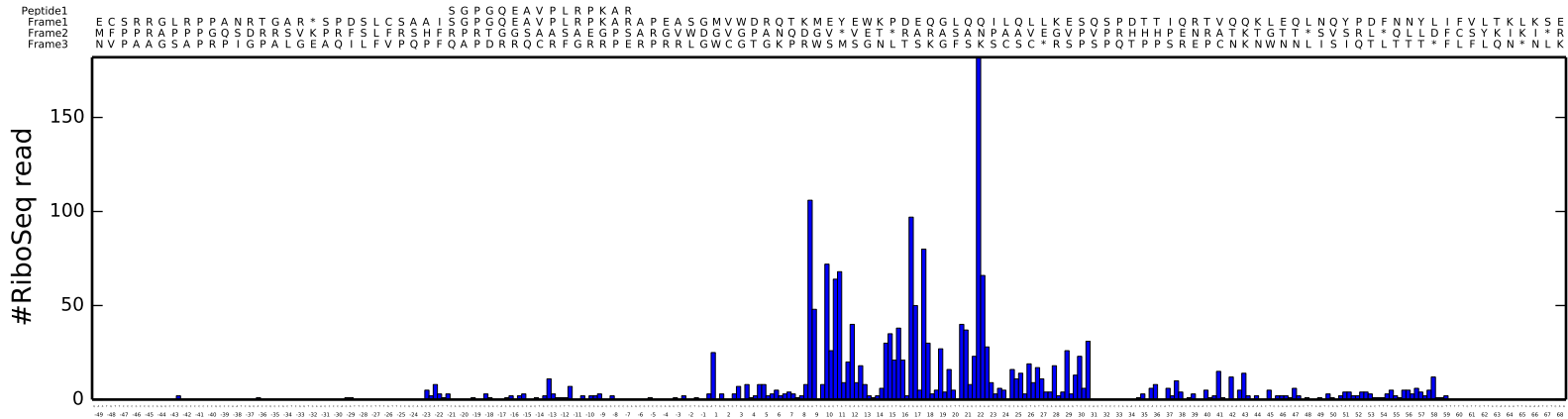
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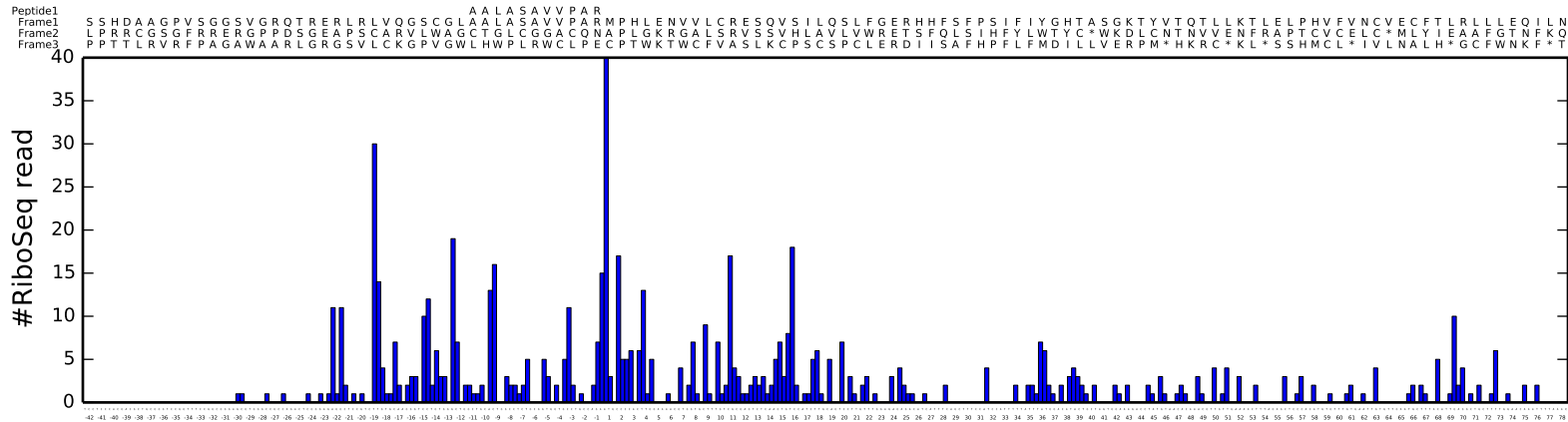
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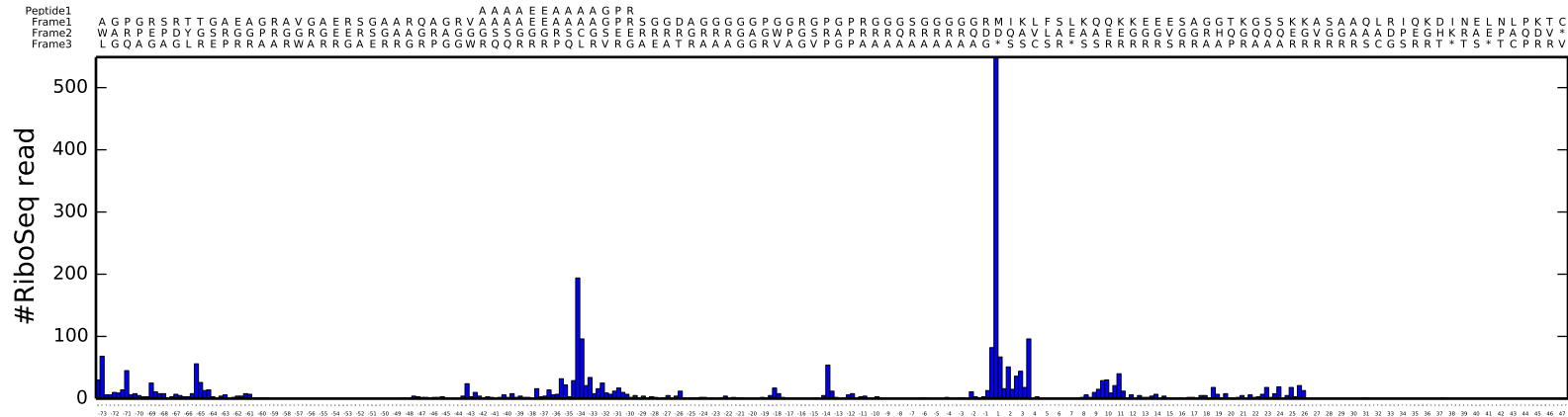
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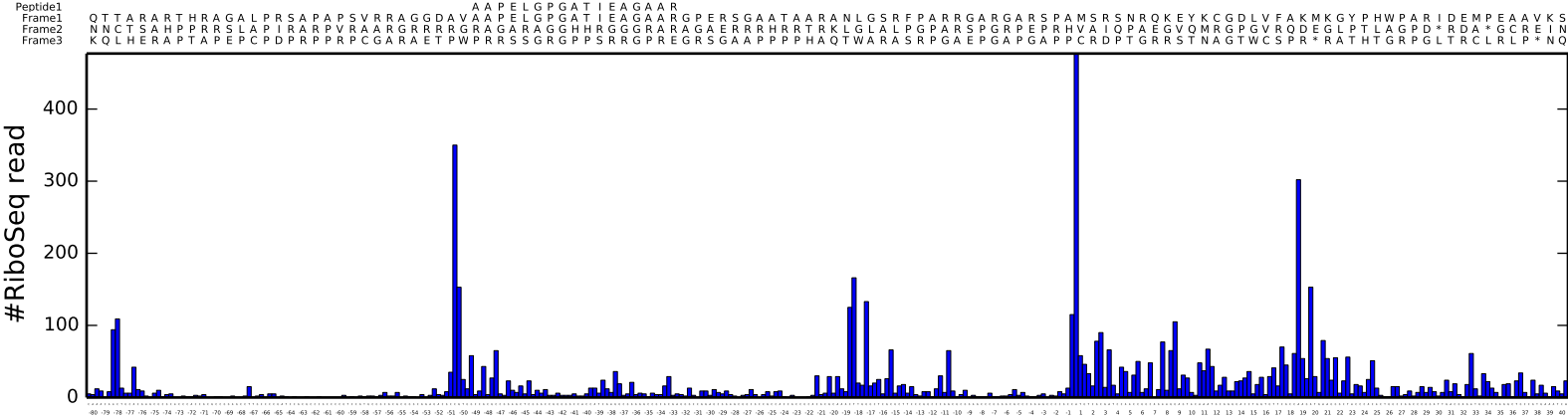
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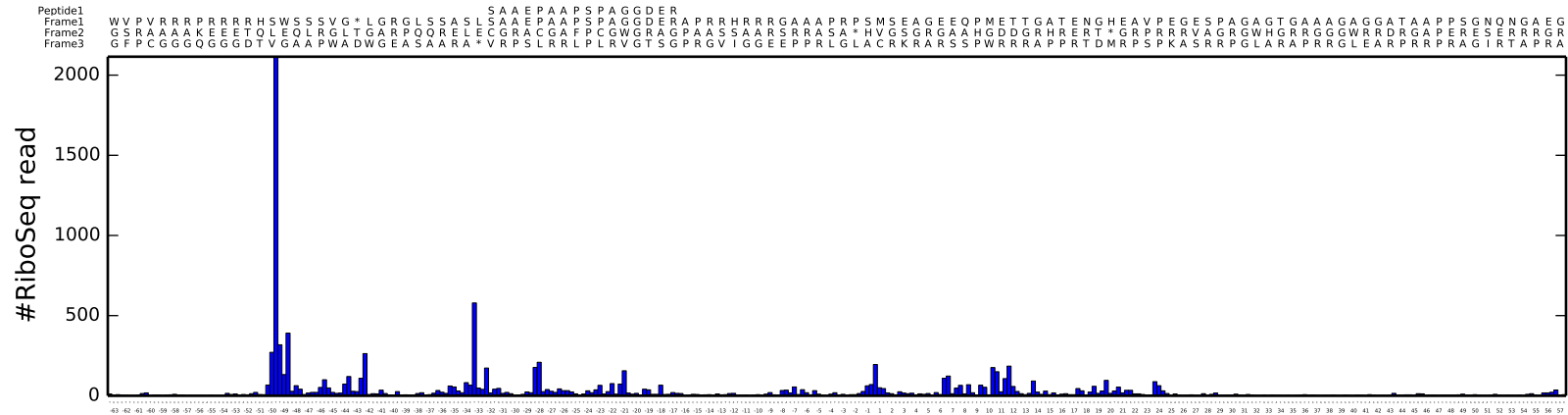
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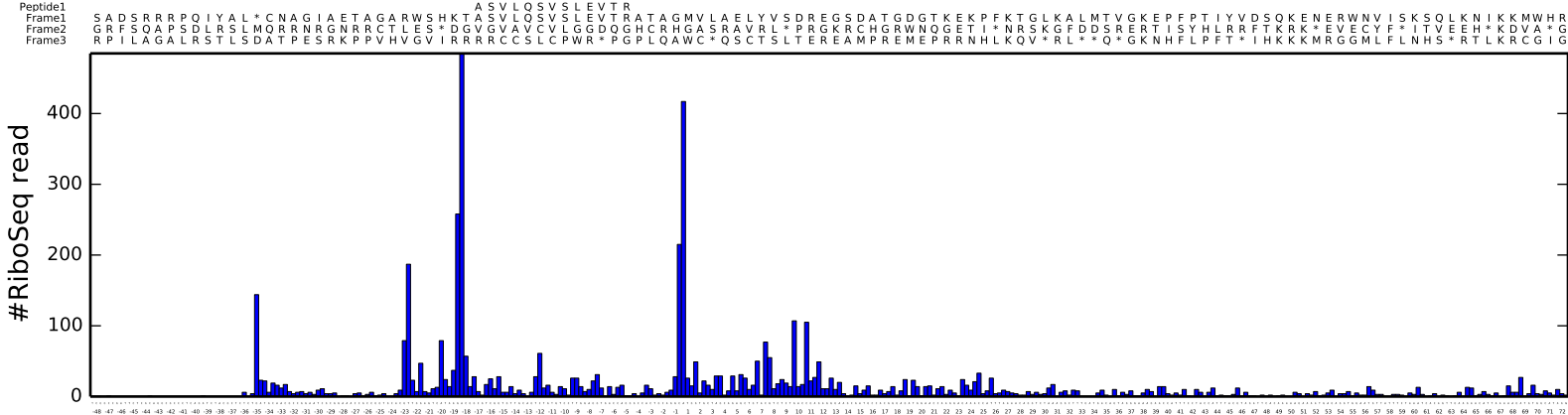
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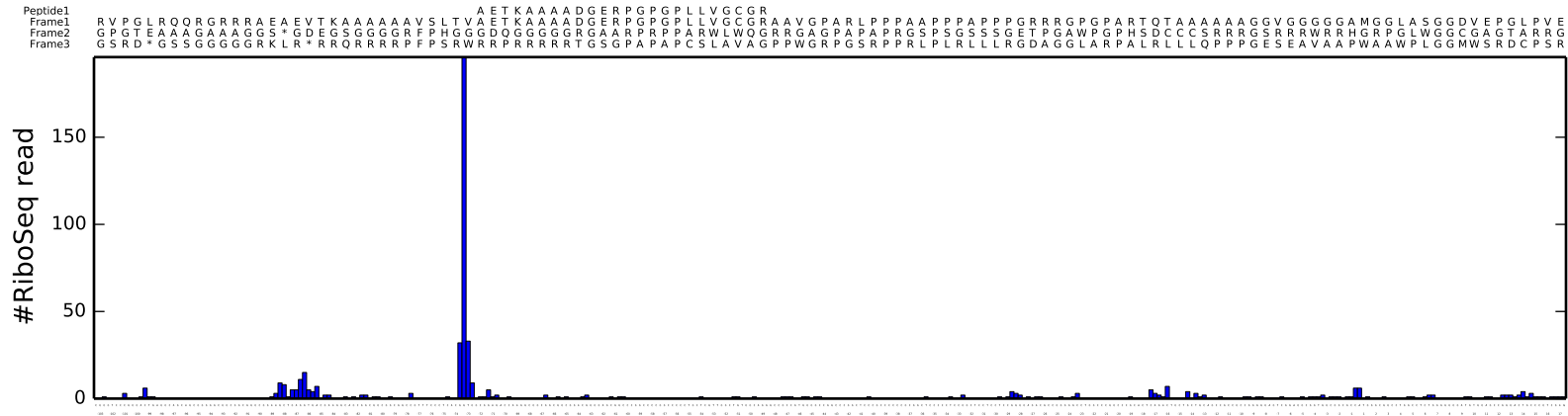
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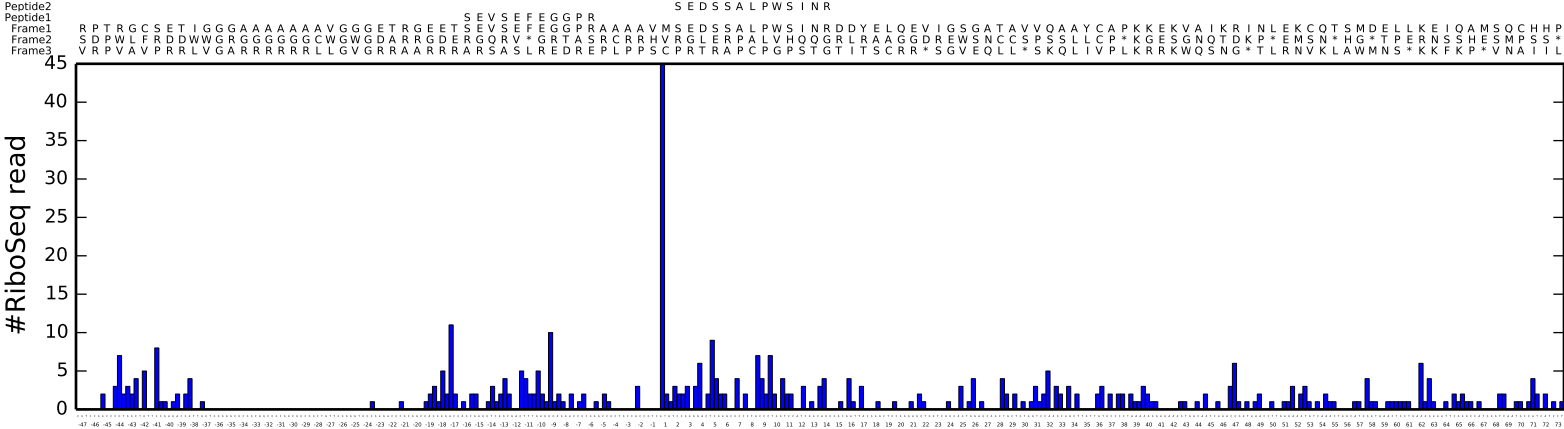
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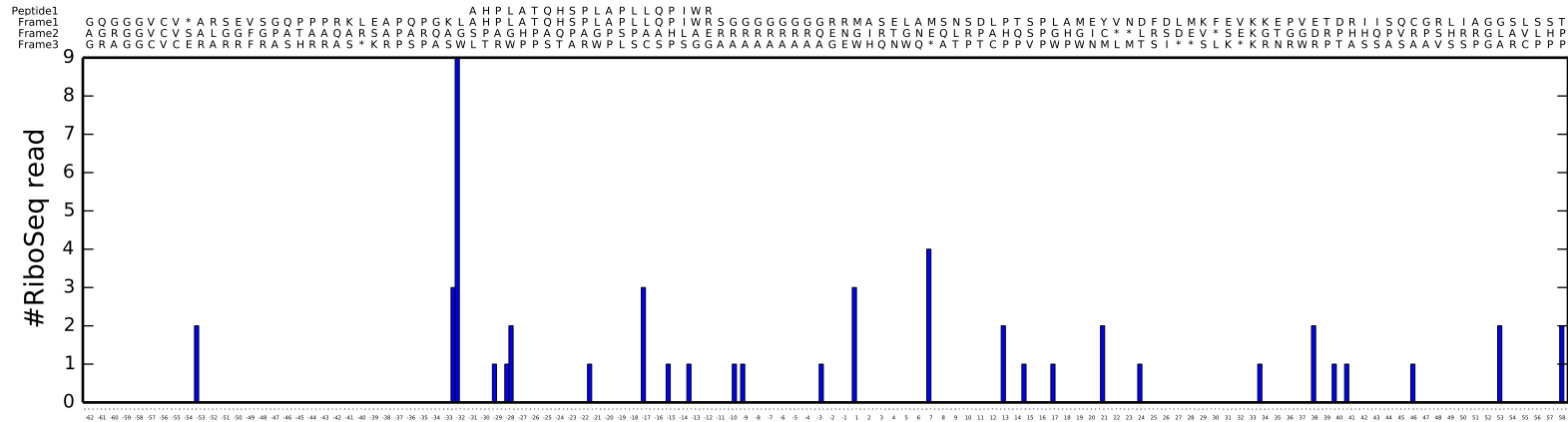
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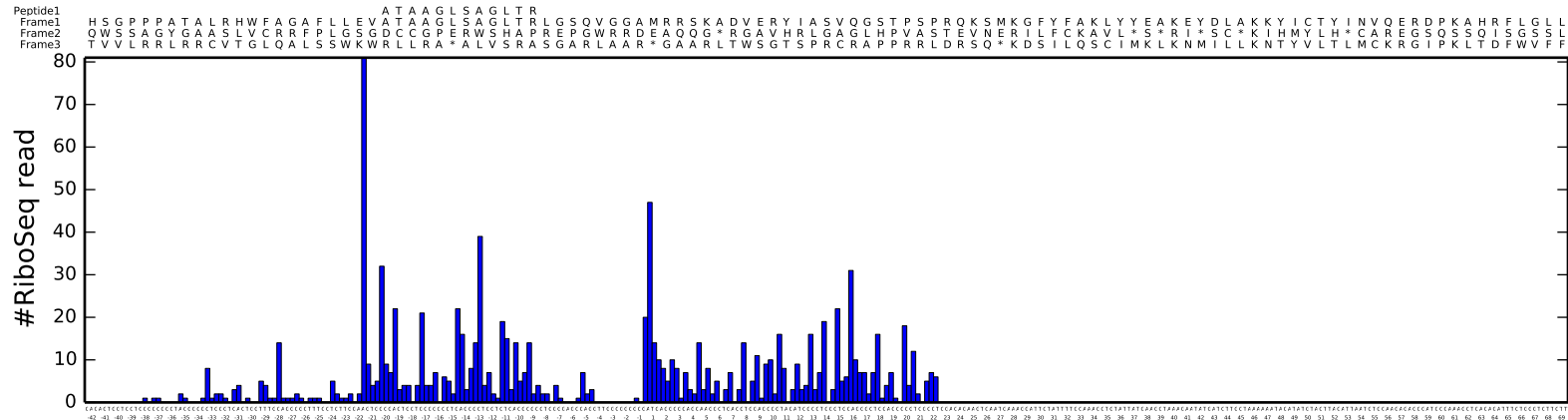
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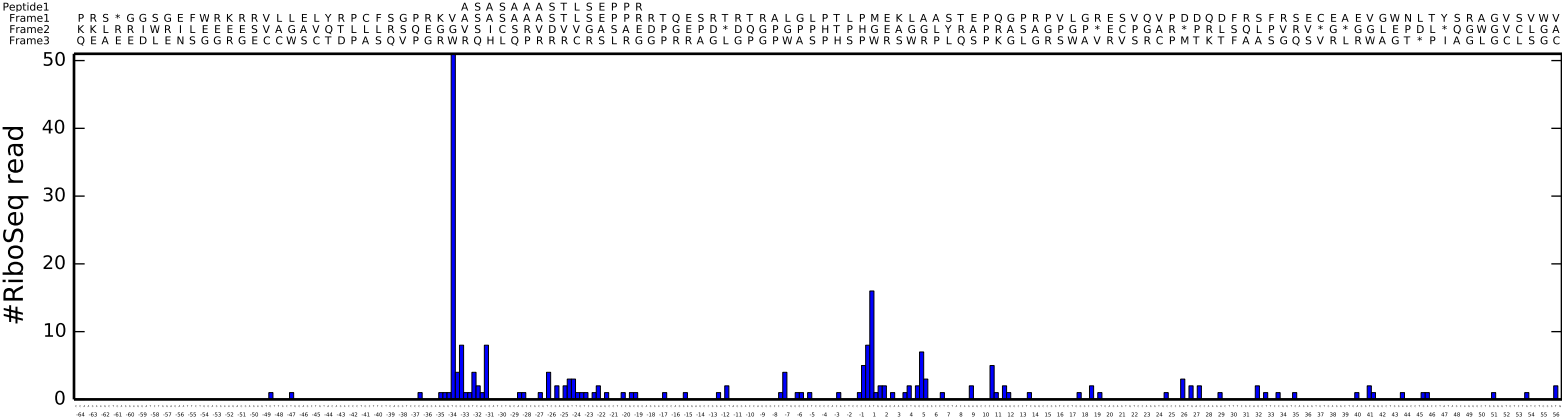
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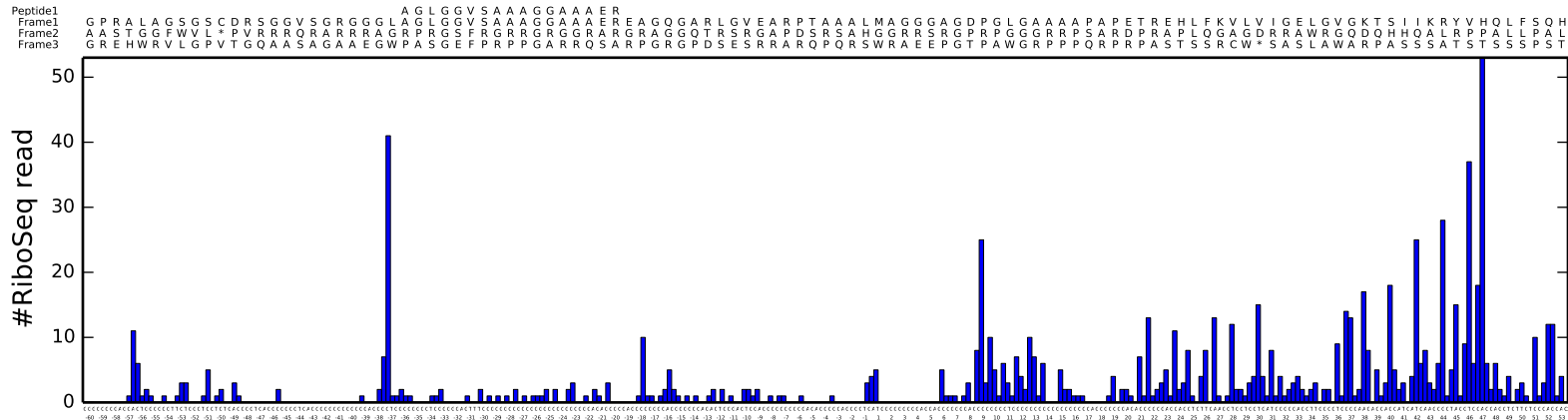
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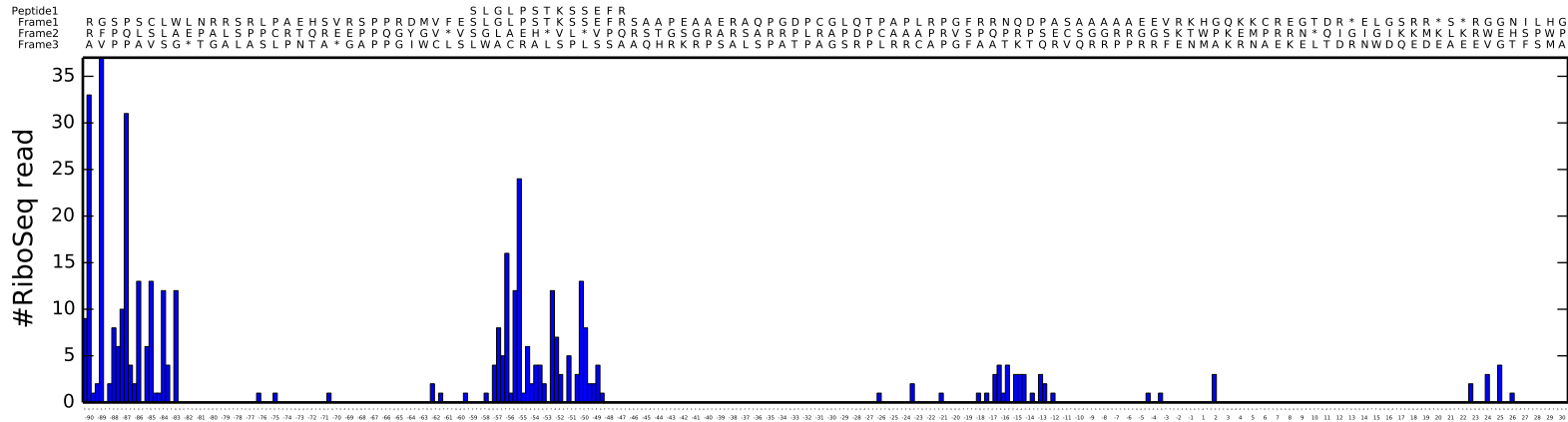
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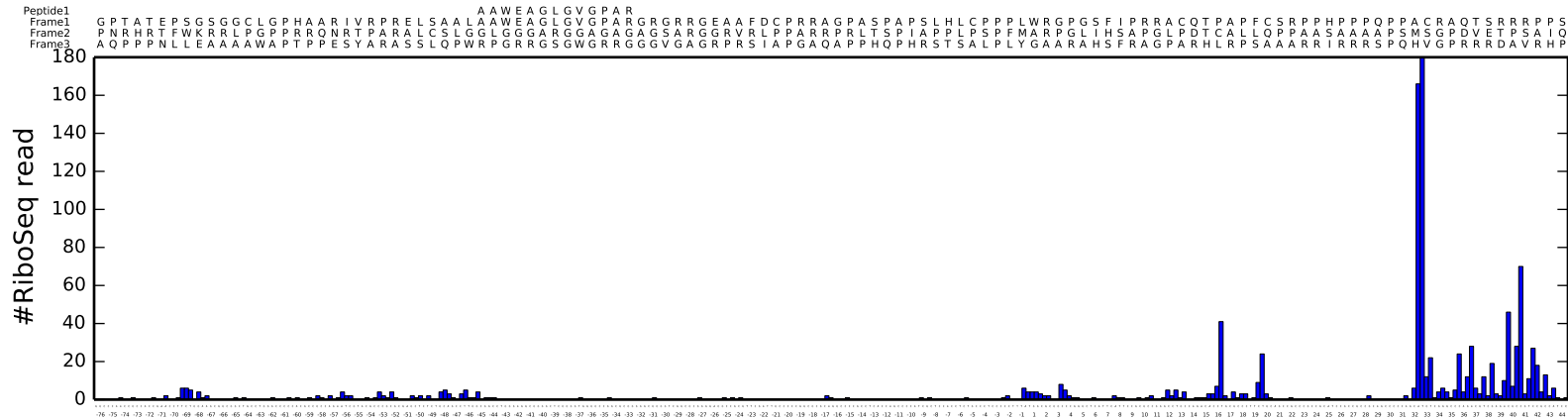
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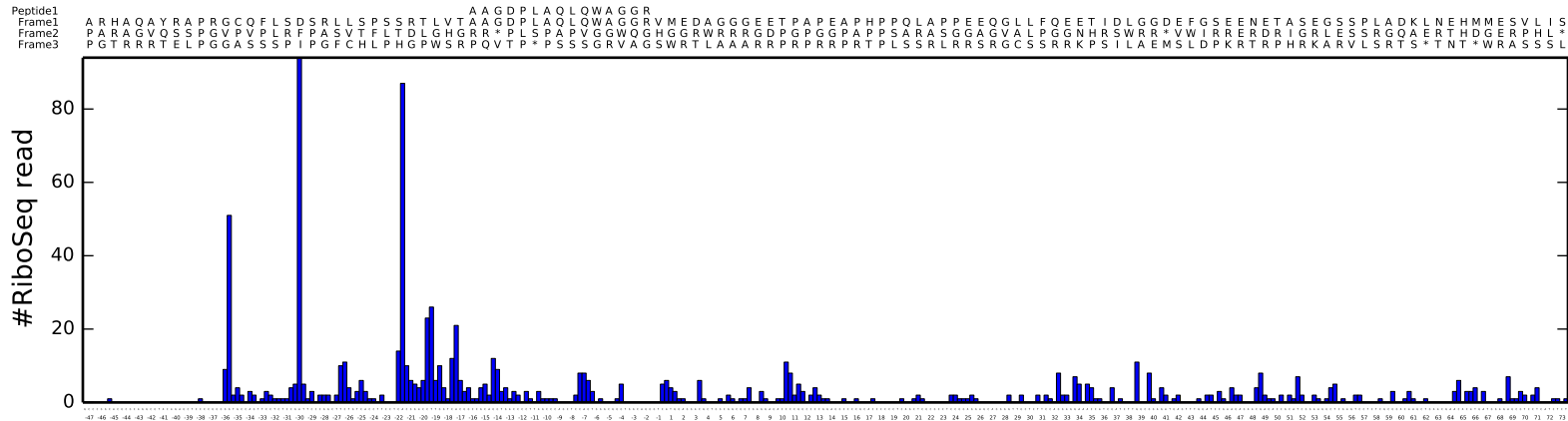
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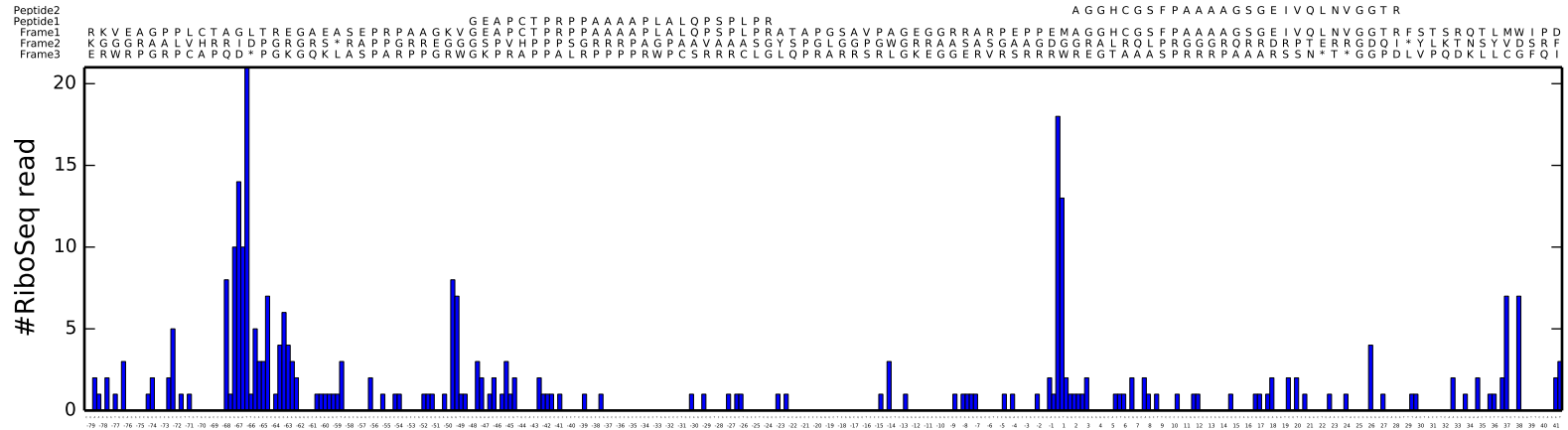
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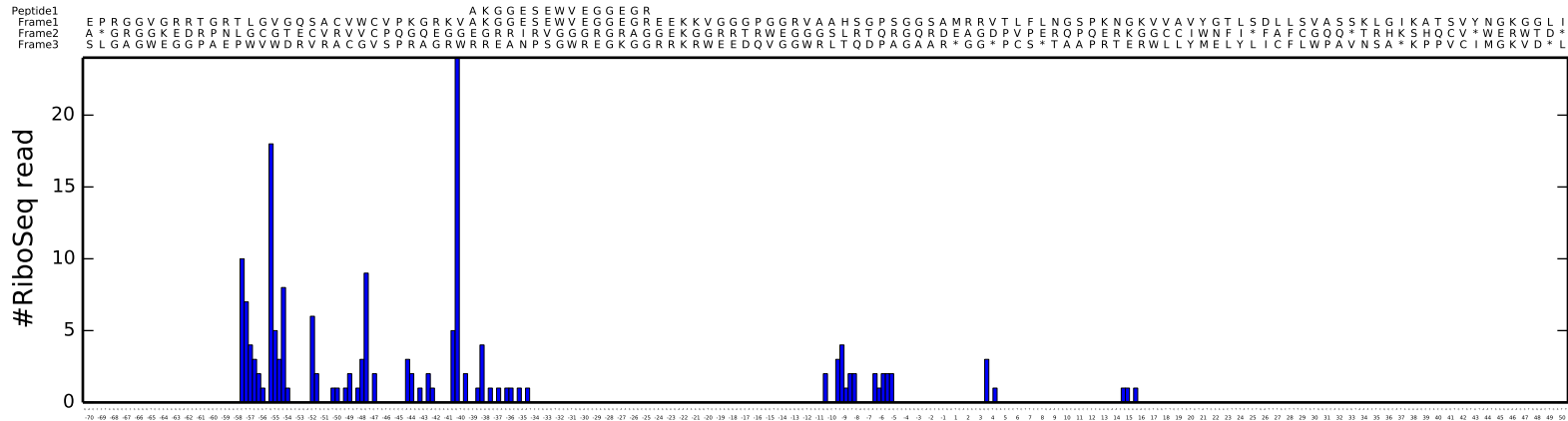
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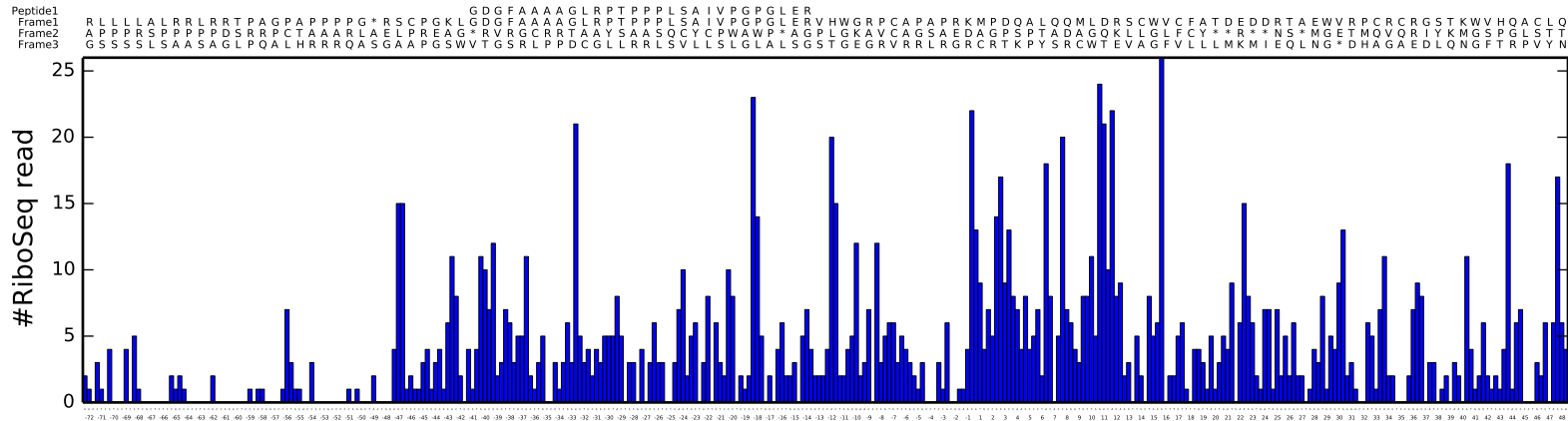
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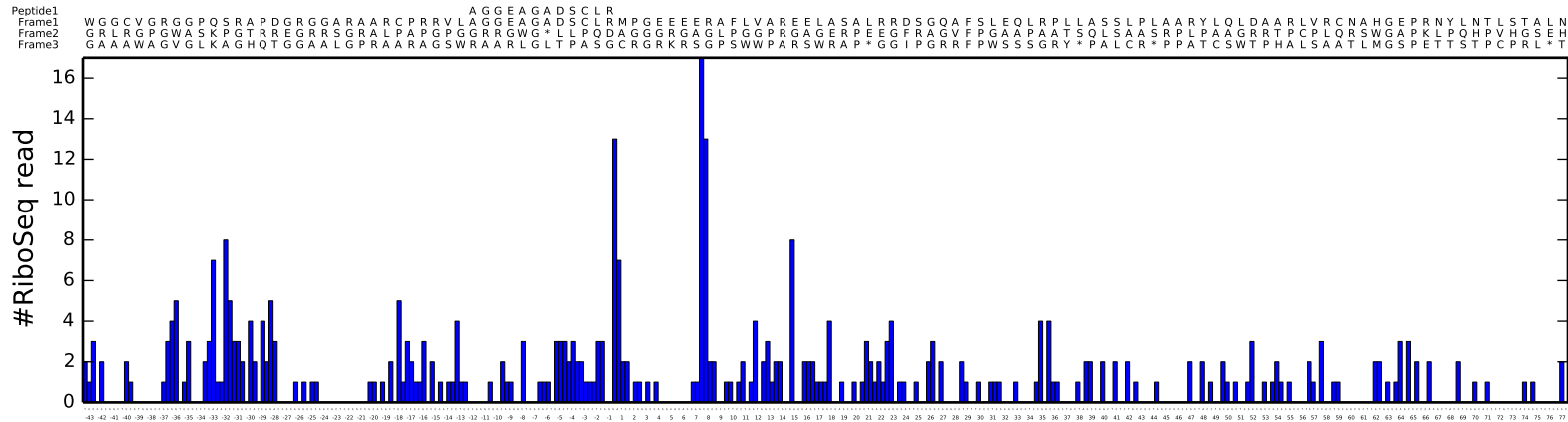
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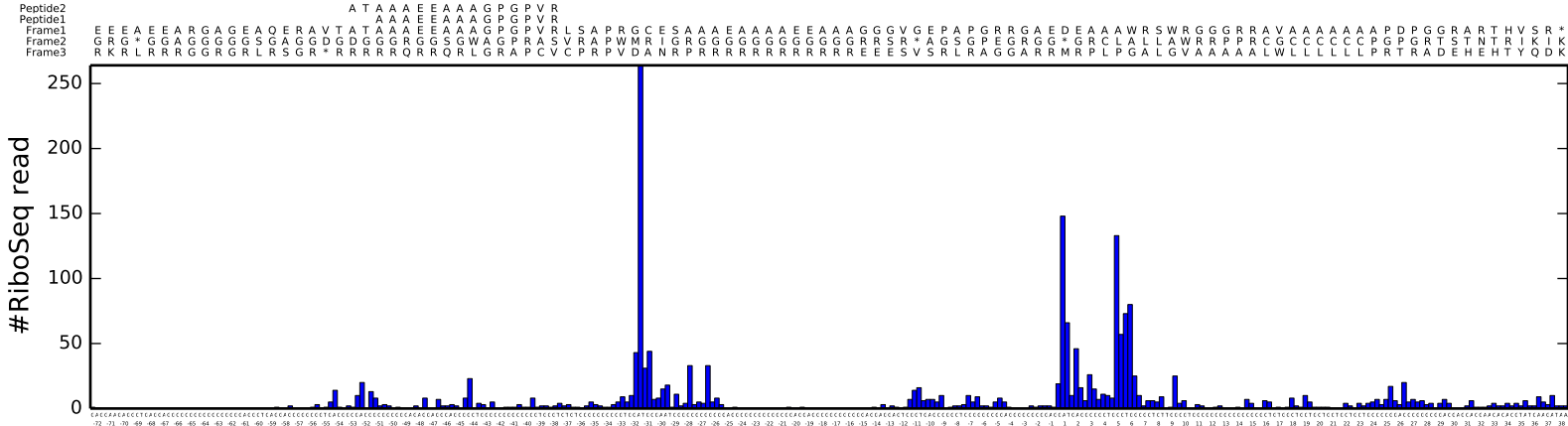
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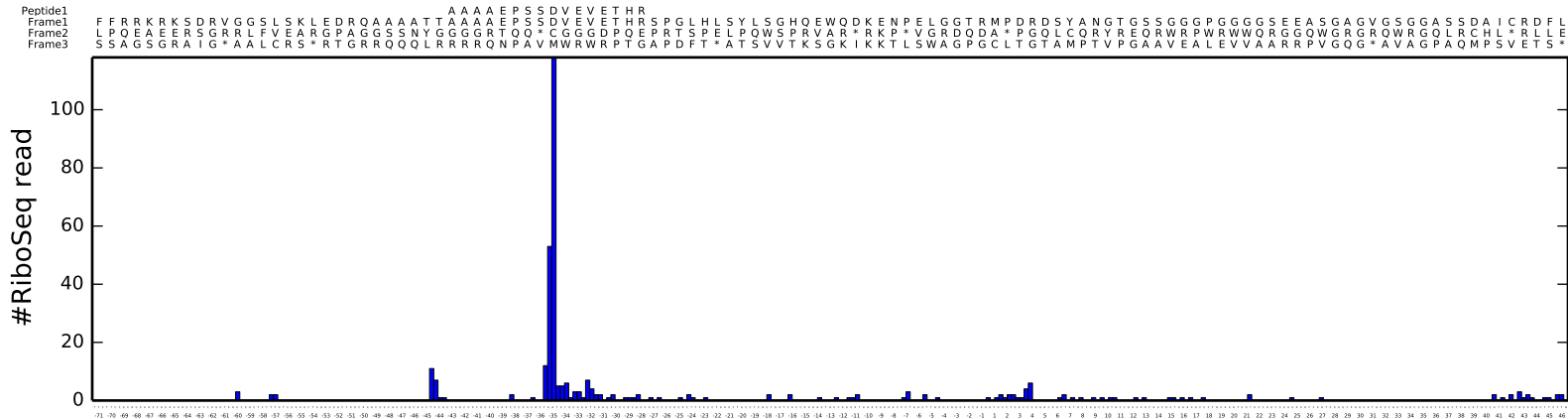
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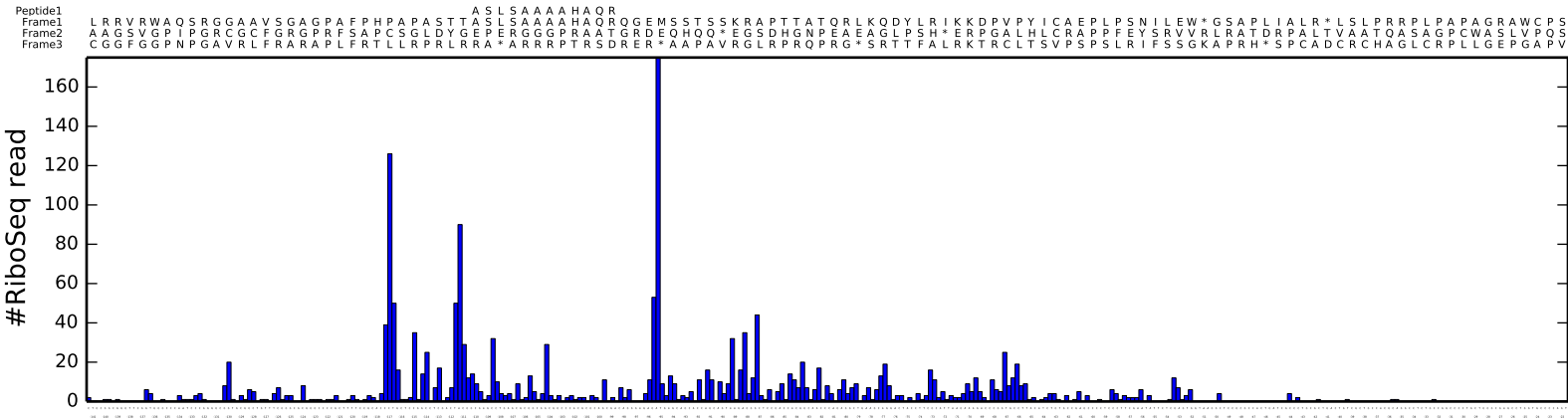
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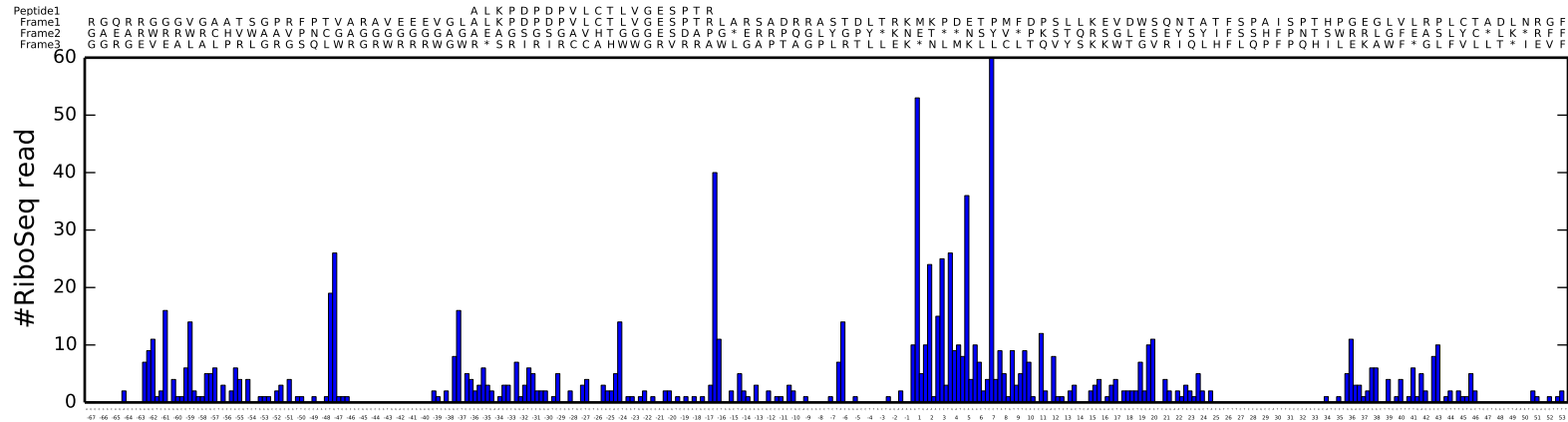
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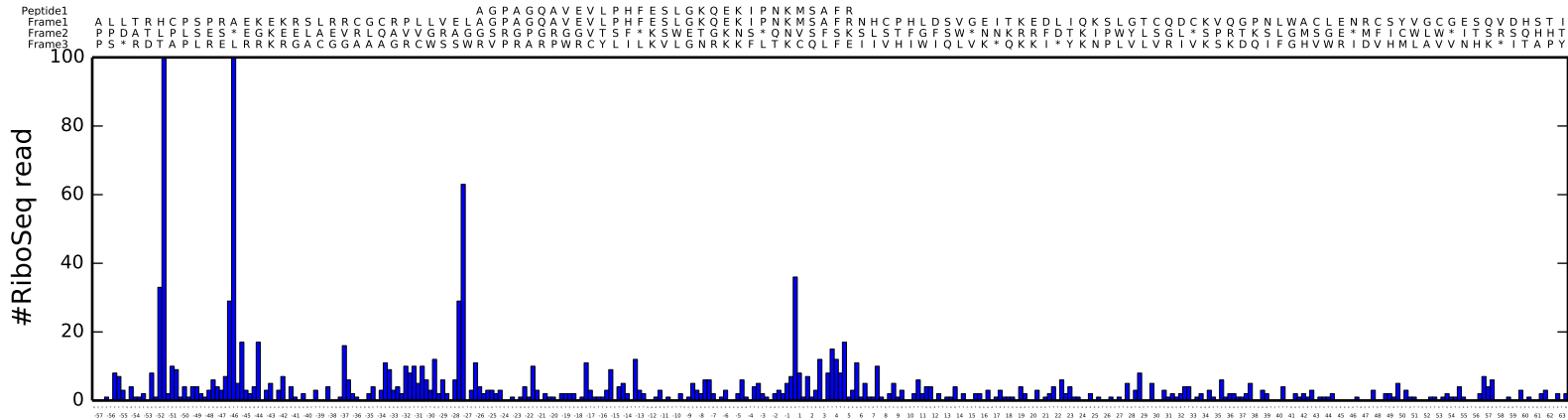
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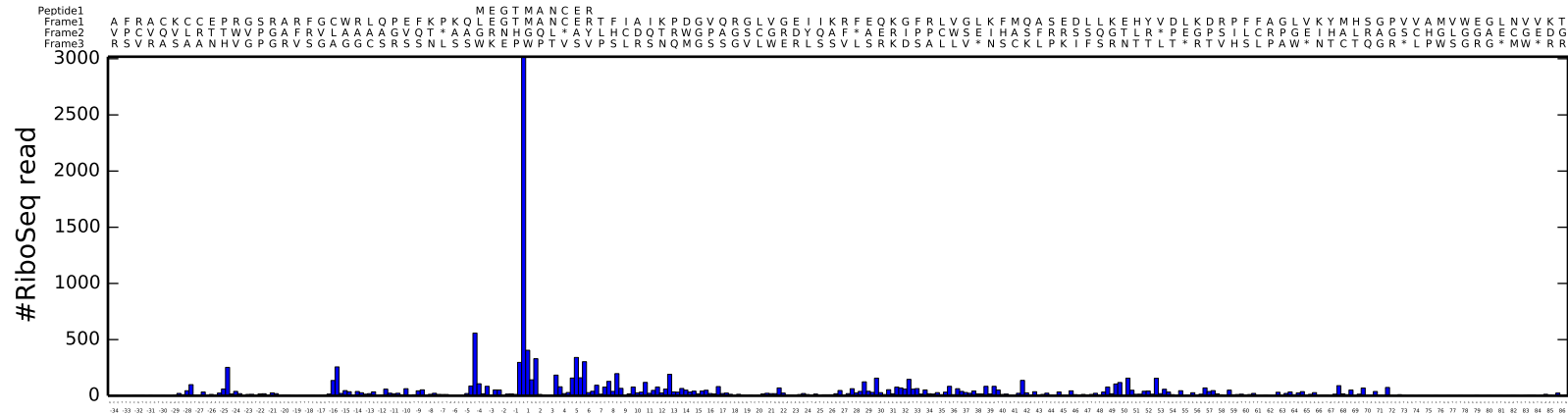
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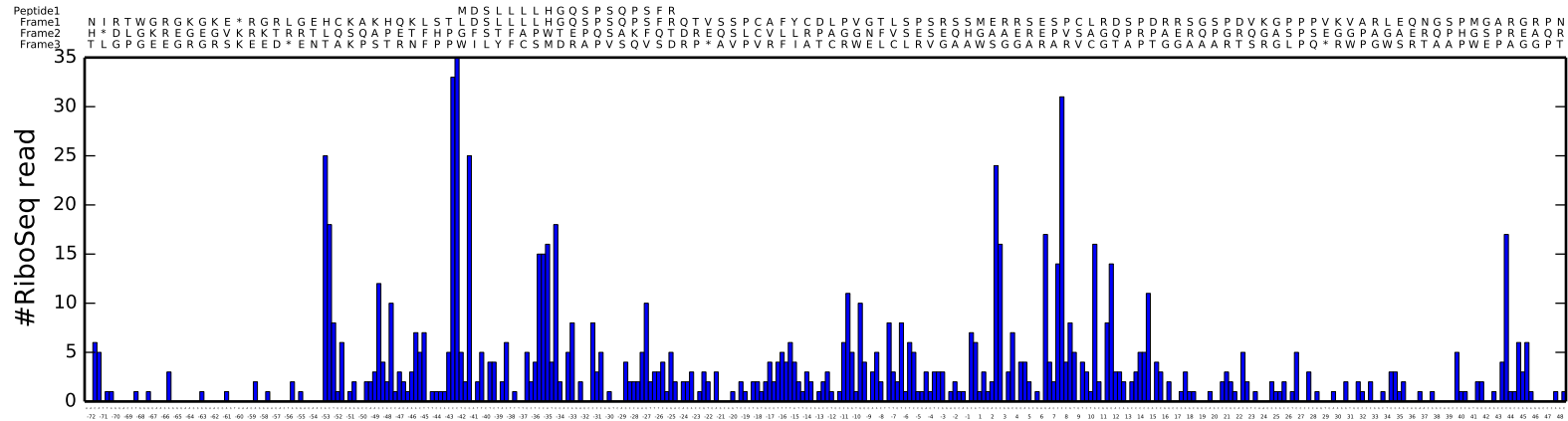
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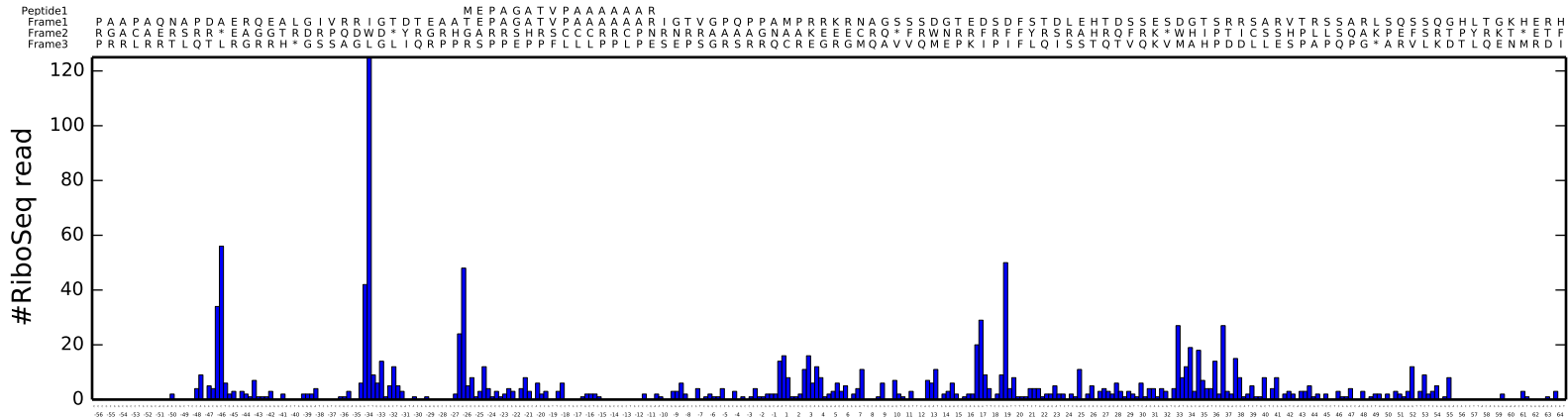
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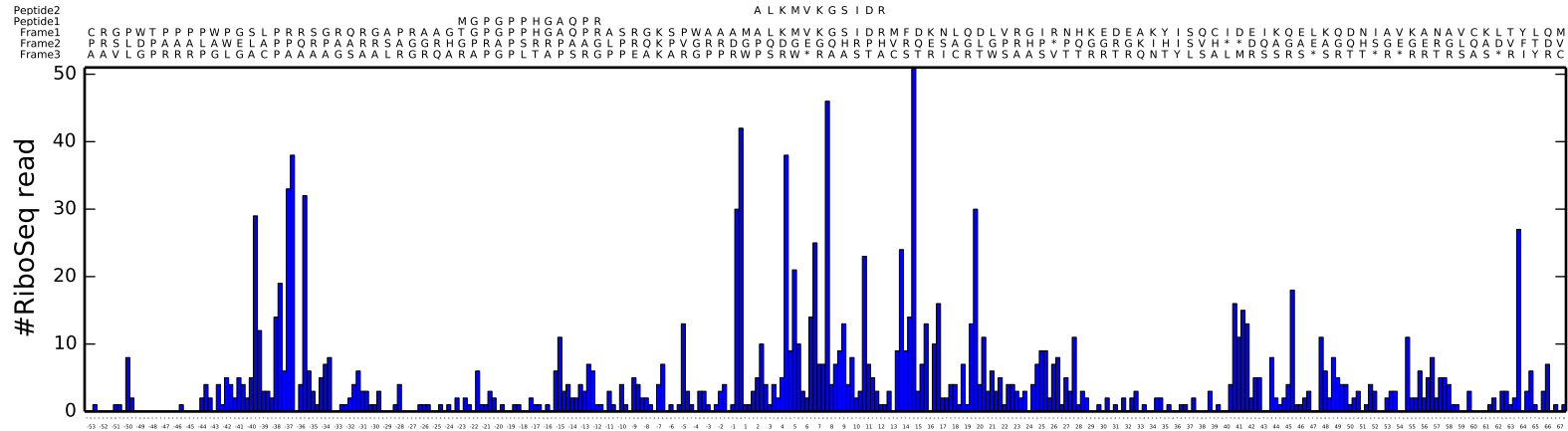
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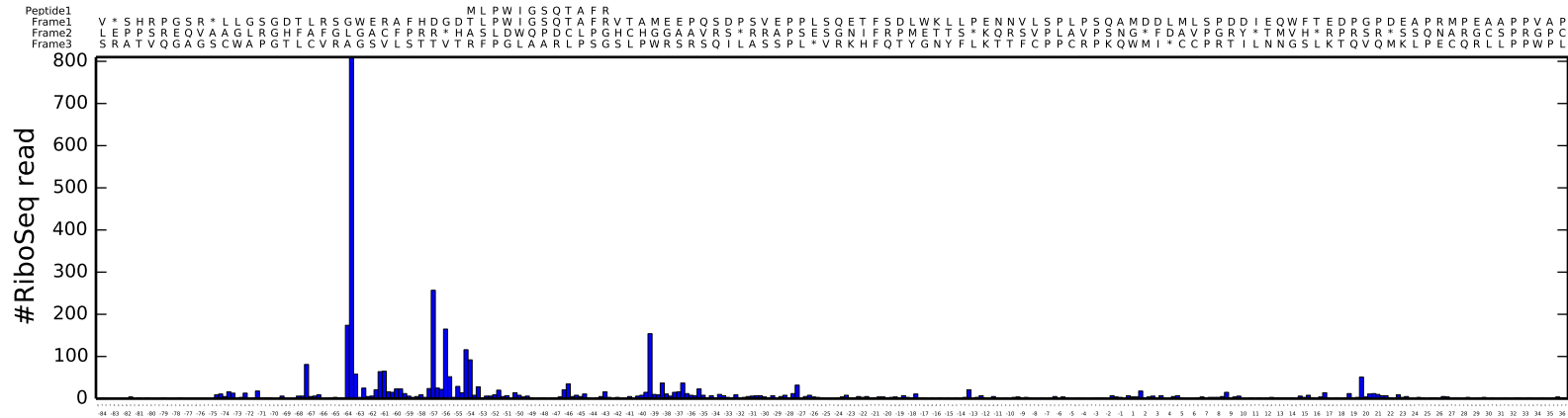
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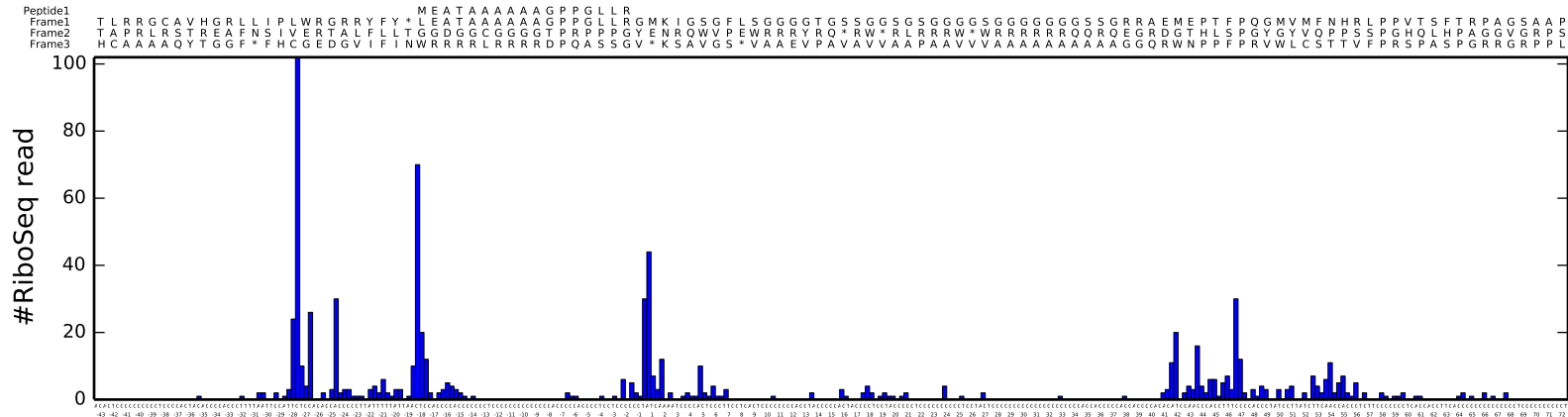
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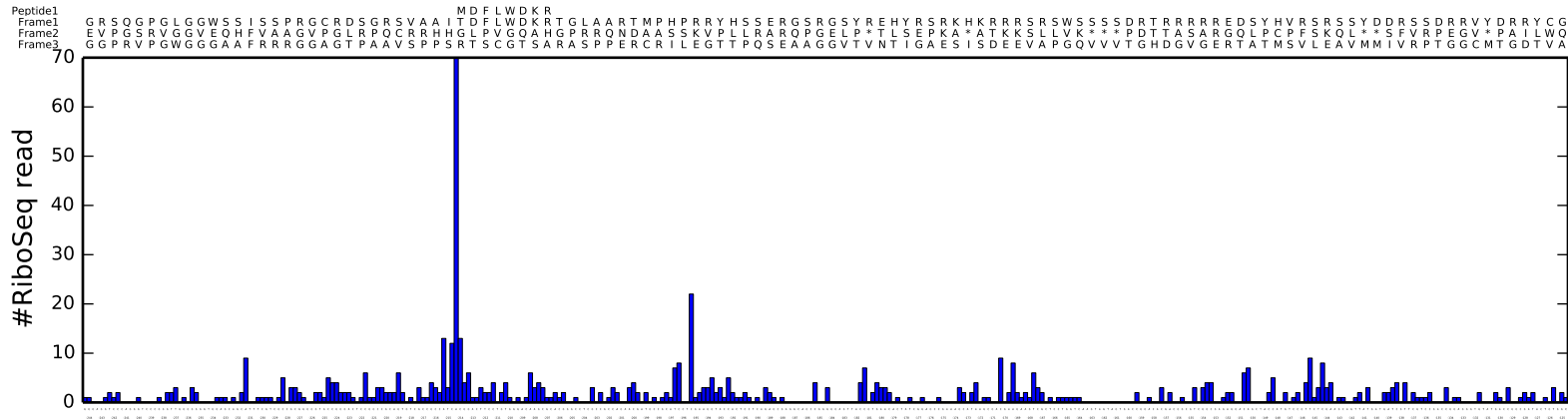
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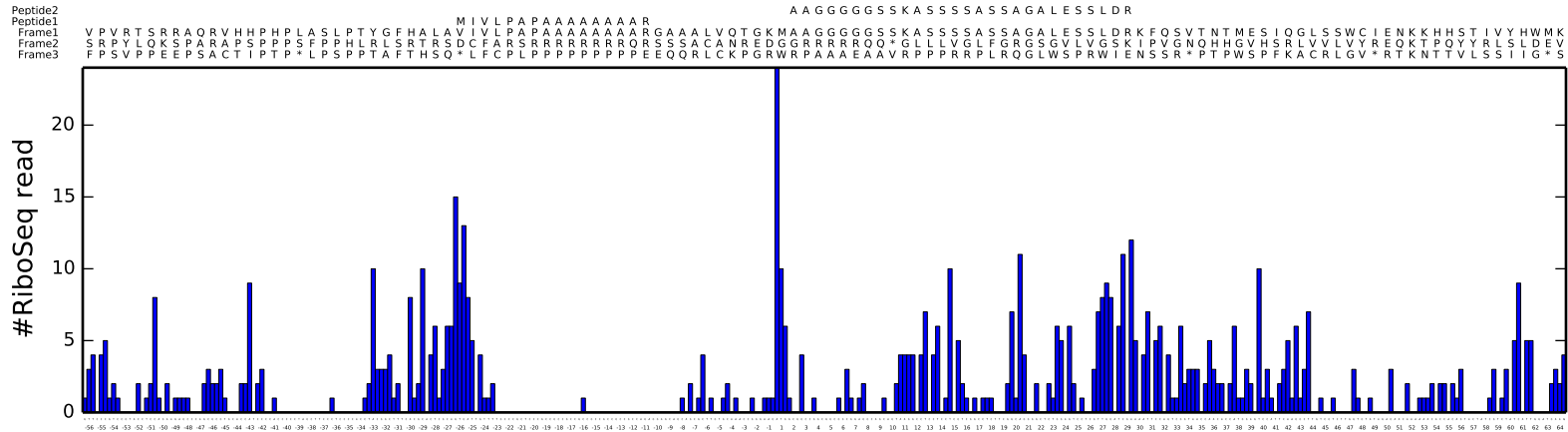
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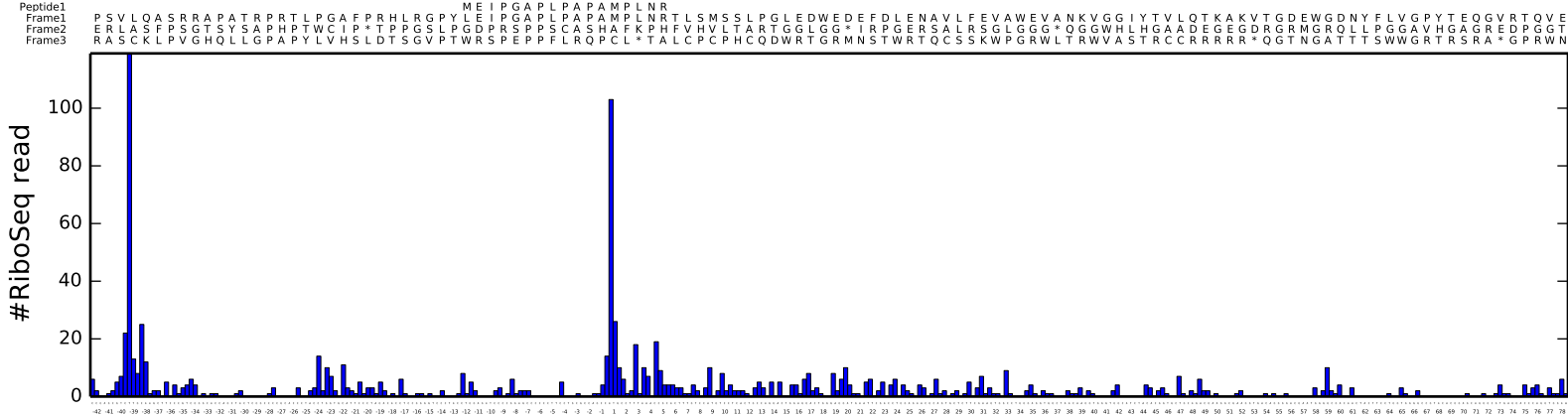
NM_001294339 Ac-MDFLWDKR



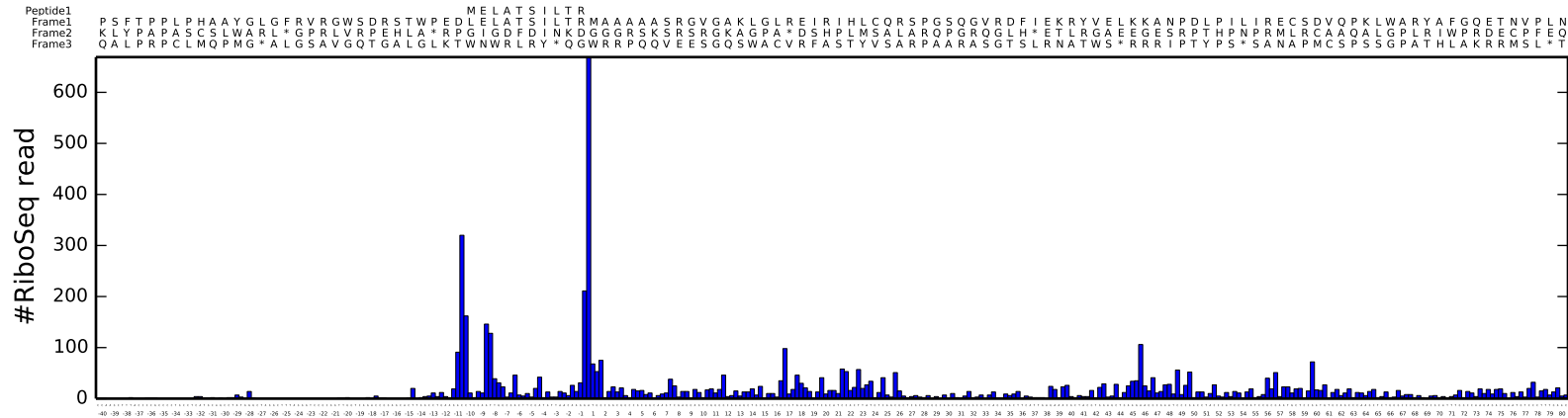
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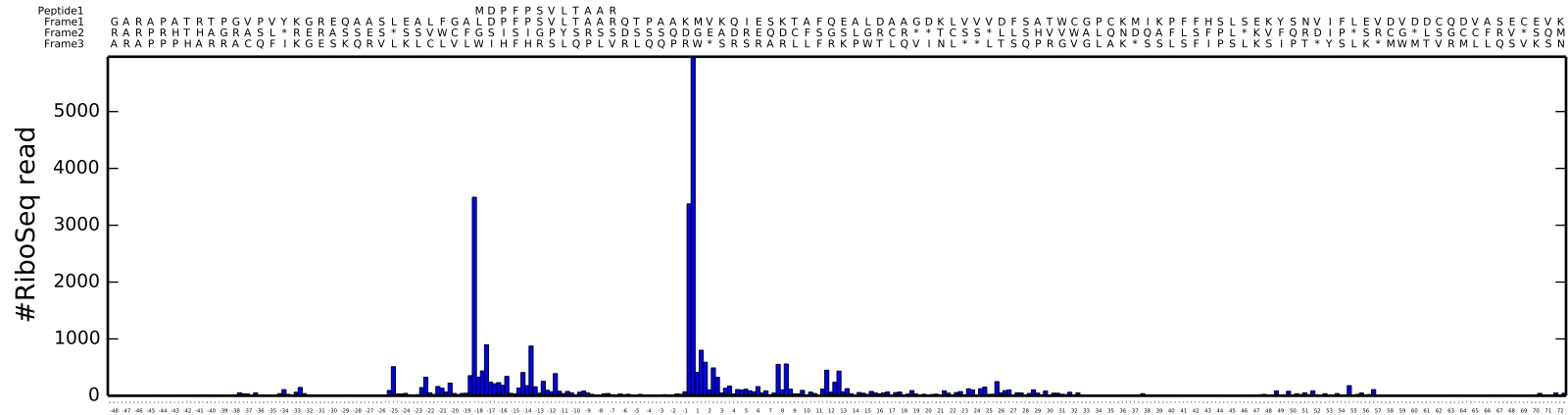
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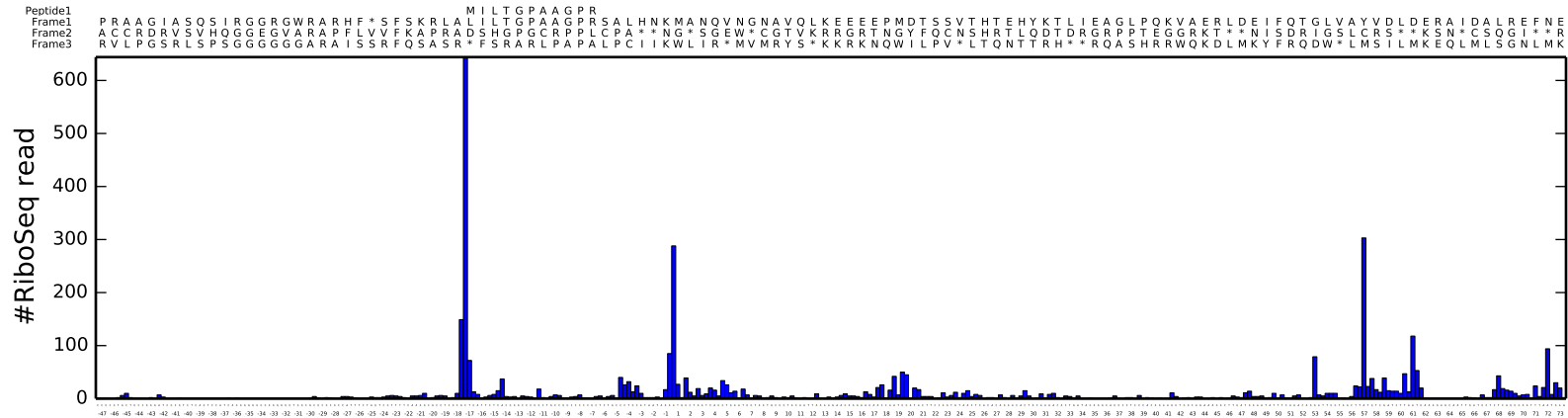
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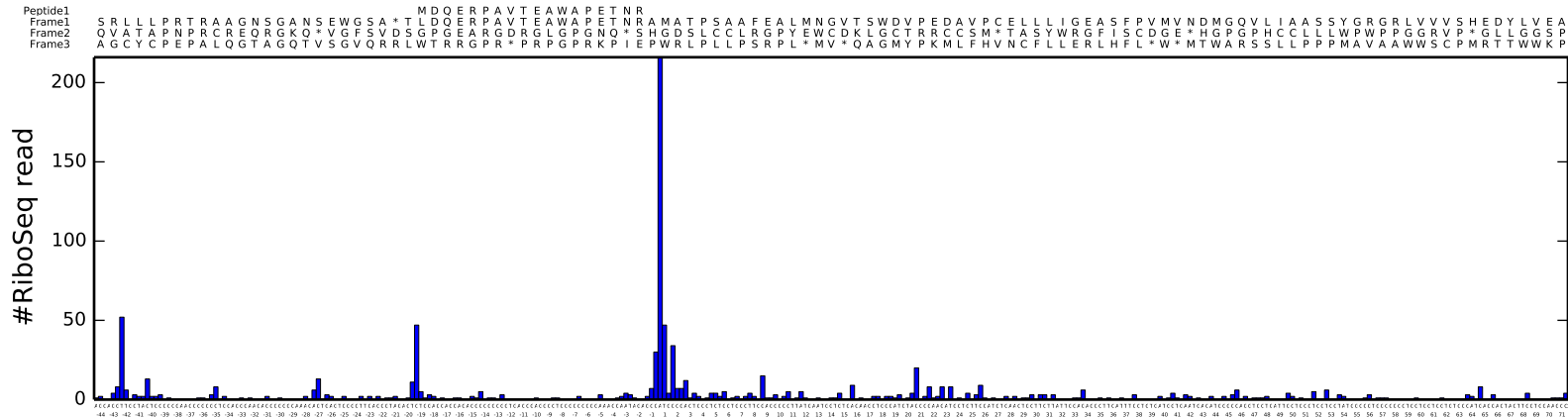
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NM_005826 MILTGPAAGPR



NM_014719 Ac-MDQERPAVTEAWAPETNR

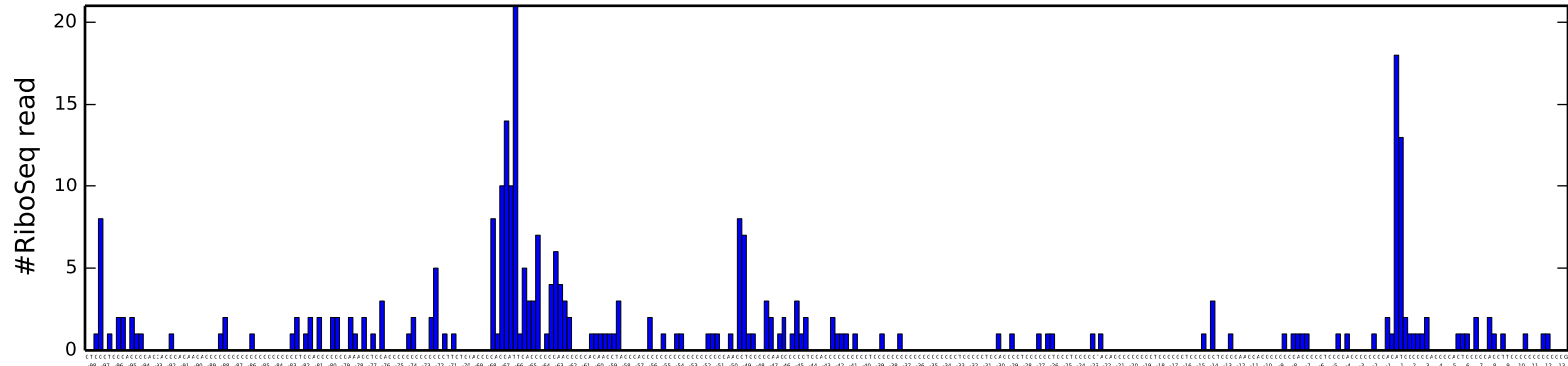


NM_016121 Ac-MEAGPPLCTAGLTR

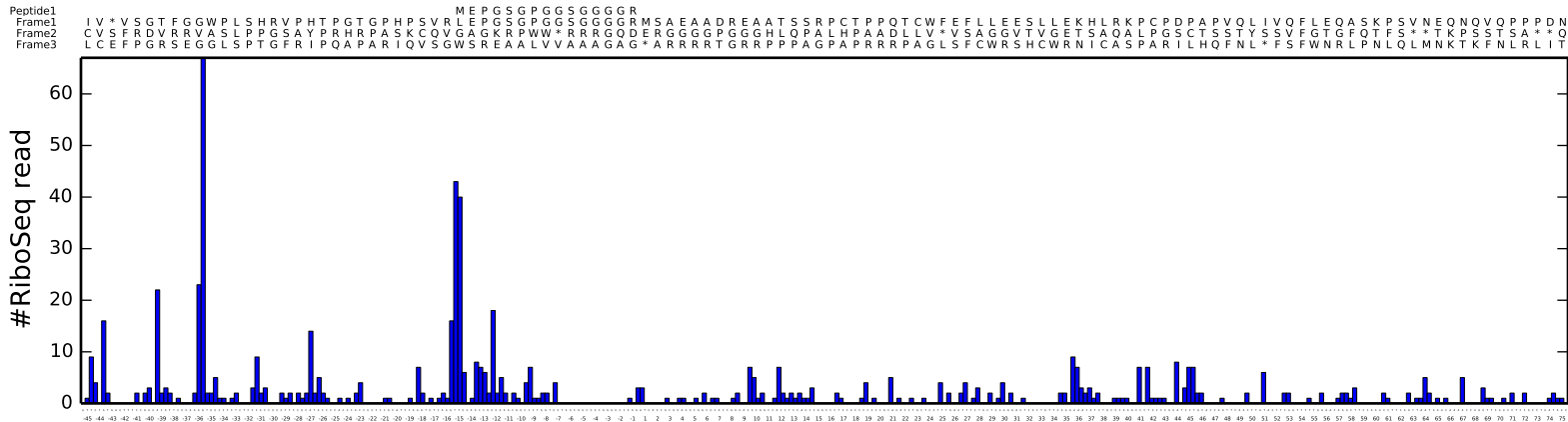
Peptide3
Peptide2
Peptide1
Frame1
Frame2
Frame3

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GEAPCTPRPPAAAAPLALQPSPLPR
AGGHCGSFPAAA

VGGSGARRRGPGGPAAWRPVKVEAGPPLCTAGLTLREGAEASEPRPAAGKVGEAPCTPRPPAAAAPLALQPSPLPRATAPGSAPVAPAGEGRRRARPEPPEMAGGHCGSFPAAA
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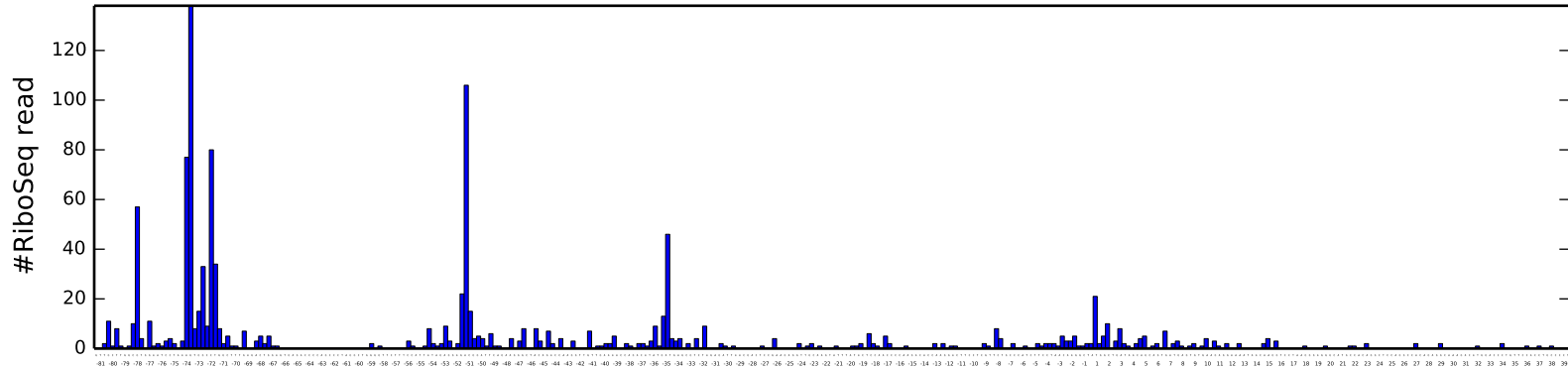


NM_017864 Ac-MEPGSGPGGSGGGGR

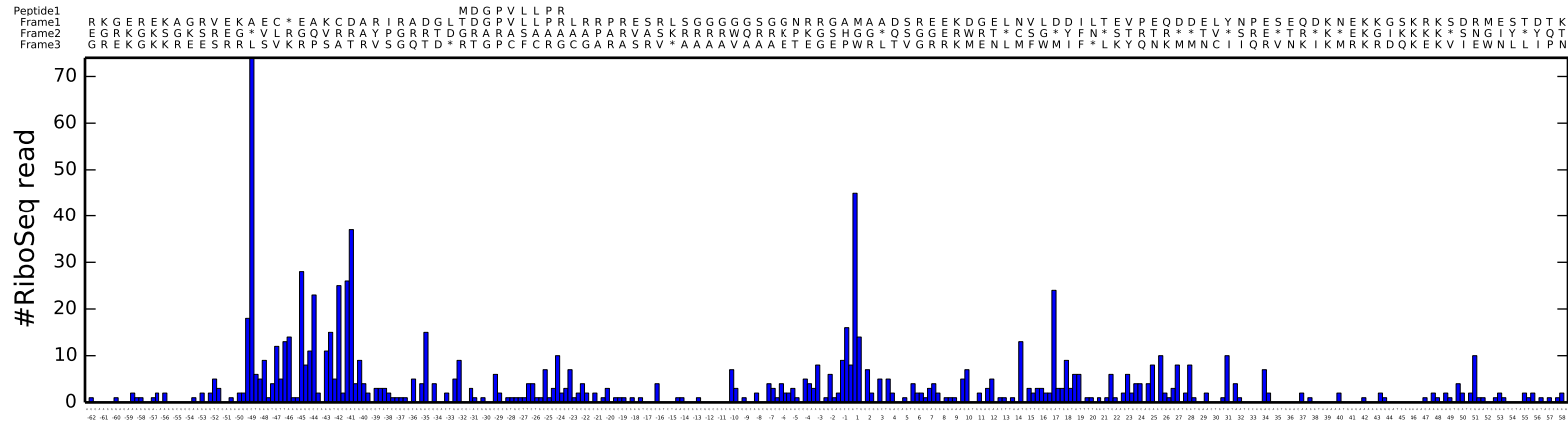


NM_020153 Ac-MDSEGLQTKVVENQTYDER

Peptide1 MDSEGLQTKVVENQTYDER
 Frame1 VAWRGILKWPGFETGVRPQP*AGVLSII EETDSEGLQTKVVENQTYDERLEINDSEEVASIYTPTPRHQGLPRSAHLPNKAMADNSSDECEEEENNKVLRREGMPQAPGHRGKDMDPVPPAP
 Frame2 CLAWNPKVAWL*DWSETPALGWGSFHYRGDGFRRATDQGC*KPDI**ASRD*RLRRGCKYLYSNPKTPRTSSFCPSS*QGYG**QQ**V*RGK*QGPKGGHATGSRPQRQRHGPCSTCPC
 Frame3 LLGVES*SGLALRLE*DPS PRLGFFPL*RRRIQKGYRPRL LKTRHMSV*RLTTPKRLQVFILQPQDTKDFLVLP IFLTRLWLITAVMSVKRKITRS*GRACHRLQATEAKTWT L FHLPL



NM_133370 Ac-MDGPVLLPR



Supplemental Figure S3. Alignment of TISs identified by mass spectrometry with TISs identified by a ribosome profiling study

TISs identified by TAILS method followed by mass spectrometry analysis were aligned with the putative TISs identified by ribosome profiling to estimate the overlap between the TISs annotated by two different approaches. The Y axis of the bar graph is the read number of Ribo-Seq. The apexes of the bar graph can be considered as the TIS annotated by ribosome profiling.