

Clustering Polypeptide motifs using the Hammock hidden Markov model peptide clustering of organoid samples

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Thu Nov 5 16:47:50 2020

This script clusters Polypeptide motifs using the Hammock hidden Markov model peptide clustering fo Organoid samples.

```
suppressPackageStartupMessages(library(knitr))
```

Loading samples

```
all.samples <- readRDS("data/allSamplesDataTable.RDS")
all.samples[, `:=`(Peptide, as.character(Peptide)), ]

setkey(all.samples, Group)

select.samples <- all.samples[J(c("mRNA_30cpc_Organoid_MD114", "mRNA_3000cpc_Organoid_MD101"))]

select.samples[, `:=`(BCcount, as.integer(mclapply(BC, function(x) length(table(strsplit(paste(t(x),
collapse = ","), ","))), mc.cores = detectCores())))]
select.samples[Animals == "mRNA_30cpc_Organoid_MD114", `:=`(BCcount, as.integer(BCcount *
10)), ] # Introduces bias toward the 30cpc
select.samples[, `:=`(Animalcount, as.integer(mclapply(Animals, function(x) length(table(strsplit(paste(t(x),
collapse = ","), ","))), mc.cores = detectCores())))]
select.samples <- select.samples[BCcount > 4]
select.samples[, `:=`(Score, BCcount + Animalcount - 1), ]
select.samples.trsp <- unique(select.samples, by = c("Animals", "BC", "LUTnrs"))

fasta.names <- paste(1:nrow(select.samples.trsp), select.samples.trsp$Score,
select.samples.trsp$Group, sep = "|")
write.fasta(as.list(select.samples.trsp$Peptide), fasta.names, "data/organoidPeptides.fasta",
open = "w", nbchar = 60, as.string = TRUE)

# Generate Scoring table for Weblogo Weighting
select.samples.pepMerge <- select.samples.trsp[, sum(Score), by = c("Peptide")]
setnames(select.samples.pepMerge, "V1", "Score")
```

Executing Hammock Clustering

```
Sys.setenv(PATH = paste("/root/HMMER/binaries", Sys.getenv("PATH"), sep = ":"),
HHLIB = "/home/rstudio/Hammock_v_1.2.0/hhsuite-2.0.16/lib/hh/")
unlink("/home/rstudio/data/HammockOrganoids", recursive = TRUE, force = FALSE)
sys.out <- system(paste("java -jar /home/rstudio/Hammock_v_1.2.0/dist/Hammock.jar full -i /home/rstudio/data/
detectCores(), sep = ""), intern = TRUE, ignore.stdout = TRUE)
# Alternative parameters --use_clinkage --alignment_threshold 23 --max_shift
# 13 --max_aln_length 37 --count_threshold 50 --max_inner_gaps 0
# --assign_thresholds 14.1,10.5,7.0
hammock.log <- data.table(readLines("data/HammockOrganoids/run.log"))
```

```
colnames(hammock.log) <- c("Hammock log file")
knitr::kable(hammock.log, longtable = T)
```

Hammock log file

2020-11-05 16:48:02.206:

Hammock version 1.2.0 Run with `-help` for a brief description of command line parameters.

2020-11-05 16:48:02.348: Program started in mode “full”.

Command-line arguments:

full -i /home/rstudio/data/organoidPeptides.fasta -d /home/rstudio/data/HammockOrganoids -max_shift 7 -c 65 -t 48

Complete list of input/output parameters:

-i, -input /home/rstudio/data/organoidPeptides.fasta
 -d, -output_directory /home/rstudio/data/HammockOrganoids
 -t, -thread 48
 -l, -labels null

Complete list of linkage clustering parameters:

-f, -file_format fasta
 -m, -matrix /home/rstudio/Hammock_v_1.2.0/matrices/blosum62.txt
 -g, -alignment_threshold (-greedy_threshold)null
 -x, -max_shift 7
 -p, -gap_penalty 0
 -C, -cache_size_limit 1

2020-11-05 16:48:02.349: Loading input sequences...

2020-11-05 16:48:02.385: 1934 unique sequences loaded.

2020-11-05 16:48:02.388: 18040 total sequences loaded.

2020-11-05 16:48:02.388: 1934 unique sequences after non-specified labels filtered out

2020-11-05 16:48:02.393: 18040 total sequences after non-specified labels filtered out

2020-11-05 16:48:02.394: Shortest sequence: 14 AA. Longest sequence: 22 AA.

2020-11-05 16:48:02.394: Up to 10 000 unique sequences. Using linkage clustering. Use `-use_greedy` to force greedy clustering

2020-11-05 16:48:02.400: Generating input statistics...

2020-11-05 16:48:02.406: Linkage clustering threshold not set. Setting automatically to: 26

2020-11-05 16:48:02.408: Linkage clustering...

2020-11-05 16:48:11.127: Ready. Clustering time: 8718

2020-11-05 16:48:11.129: Resulting clusters: 1025

2020-11-05 16:48:11.129: Building MSAs...

2020-11-05 16:48:11.508: Ready. Total time: 9100

2020-11-05 16:48:11.508: Saving results to output files...

2020-11-05 16:48:11.650: Linkage clustering results in: /home/rstudio/data/HammockOrganoids/initial_clusters.tsv

2020-11-05 16:48:11.650: and: /home/rstudio/data/HammockOrganoids/initial_clusters_sequences.tsv

2020-11-05 16:48:11.650: and:

/home/rstudio/data/HammockOrganoids/initial_clusters_sequences_original_order.tsv

2020-11-05 16:48:11.651:

Loading clusters...

2020-11-05 16:48:11.671: Maximal alignment length not set. Setting automatically to: 30

2020-11-05 16:48:11.672: Minimal number of match states not set. Setting automatically to: 5

2020-11-05 16:48:11.737: Assign threshold not set. Setting automatically to:

2020-11-05 16:48:11.742: 14.36,11.34,8.31

2020-11-05 16:48:11.742: Overlap threshold not set. Setting automatically to:

2020-11-05 16:48:11.743: 10.58,6.05,0.0

Hammock log file

2020-11-05 16:48:11.743: Merge threshold not set. Setting automatically on the basis of average sequence length to:
2020-11-05 16:48:11.744: 15.12,13.61,12.09
2020-11-05 16:48:11.744: Initial extension threshold not set. Setting automatically on the basis of merge threshold
sequence to: 16.632

Complete list of HMM-based clustering parameters:

-a, -part_threshold null
-s, -size_threshold null
-c, -count_threshold 65
-n, -assign_thresholds 14.36,11.34,8.31,
-v, -overlap_thresholds 10.58,6.05,0.0,
-r, -merge_thresholds 15.12,13.61,12.09,
-e, -relative_thresholds false
-b, -absolute_thresholds true
-h, -min_conserved_positions 5
-y, -max_gap_proportion 0.2
-k, -min_ic 1.2
-j, -max_aln_length 30
-u, -max_inner_gaps 0
-q, -extension_increase_length false

2020-11-05 16:48:11.827: Initial cluster extension...
2020-11-05 16:48:37.107:
Clustering in 3 rounds...
2020-11-05 16:48:37.108:
2020-11-05 16:48:37.108: Round 1:

2020-11-05 16:48:37.109: 65 clusters remaining
2020-11-05 16:48:37.109: Building hmms and searching database...
2020-11-05 16:48:37.272: Extending clusters...
2020-11-05 16:48:37.274: 15 sequences to be inserted into clusters
2020-11-05 16:48:37.275: 13 clusters to be extended
2020-11-05 16:48:37.285: 13 sequences rejected
2020-11-05 16:48:37.286: 1 cluster pairs to check and merge.
2020-11-05 16:48:37.286: Merging clusters from 1 groups...
2020-11-05 16:48:37.295: Buiding hhs...
2020-11-05 16:48:37.295: HH clustering...
2020-11-05 16:48:37.535:
2020-11-05 16:48:37.535: Round 2:

2020-11-05 16:48:37.536: 65 clusters remaining
2020-11-05 16:48:37.536: Building hmms and searching database...
2020-11-05 16:48:37.591: Extending clusters...
2020-11-05 16:48:37.593: 21 sequences to be inserted into clusters
2020-11-05 16:48:37.593: 17 clusters to be extended
2020-11-05 16:48:37.603: 20 sequences rejected
2020-11-05 16:48:37.604: 22 cluster pairs to check and merge.
2020-11-05 16:48:37.604: Merging clusters from 6 groups...
2020-11-05 16:48:37.612: Buiding hhs...
2020-11-05 16:48:37.623: HH clustering...
2020-11-05 16:48:37.964:
2020-11-05 16:48:37.964: Round 3:

2020-11-05 16:48:37.964: 65 clusters remaining
2020-11-05 16:48:37.964: Building hmms and searching database...
2020-11-05 16:48:38.019: Extending clusters...

Hammock log file

2020-11-05 16:48:38.020: 58 sequences to be inserted into clusters
2020-11-05 16:48:38.020: 33 clusters to be extended
2020-11-05 16:48:38.038: 36 sequences rejected
2020-11-05 16:48:38.039: Overlap threshold is 0. Running full cluster merging.
2020-11-05 16:48:38.047: Buiding hhs...
2020-11-05 16:48:38.064: HH clustering...
2020-11-05 16:48:42.760:
Ready. Clustering time : 5652
2020-11-05 16:48:42.760: Resulting clusers: 55
2020-11-05 16:48:42.760: Containing 319 unique sequences and 3415 total sequences.
2020-11-05 16:48:42.761: Unique sequences not assigned: 1056, total sequences not assigned: 9304
2020-11-05 16:48:42.761: Saving results to outupt files...
2020-11-05 16:48:42.795: Results in: /home/rstudio/data/HammockOrganoids/final_clusters_sequences.tsv
2020-11-05 16:48:42.795: and: /home/rstudio/data/HammockOrganoids/final_clusters.tsv
2020-11-05 16:48:42.795: and: /home/rstudio/data/HammockOrganoids/final_clusters_sequences_original_order.tsv
2020-11-05 16:48:42.795:
Calculating KLD...
2020-11-05 16:48:42.908: Final system KLD over match state MSA positions: 14.25595141691389
2020-11-05 16:48:42.909: Final system KLD over all MSA positions: 16.17814917306265
2020-11-05 16:48:42.909: Program successfully ended.

Generation of Weblogo visualization

```
ham.clusters <- data.table(read.table("/home/rstudio/data/HammockOrganoids/final_clusters.tsv",
  header = TRUE, skip = 0, sep = "\t", stringsAsFactors = FALSE, fill = TRUE))
id.order <- as.list(ham.clusters$cluster_id)
ham.clusters.all <- data.table(read.table("/home/rstudio/data/HammockOrganoids/final_clusters_sequences.tsv",
  header = TRUE, skip = 0, sep = "\t", stringsAsFactors = FALSE, fill = TRUE))
ham.clusters.all[, `:=`(alignment, gsub("\\-", "\\_", alignment))]
setkey(select.samples, Peptide)
setkey(select.samples.trsp, Peptide)

unlink("/home/rstudio/data/WEBlogosOrganoids", recursive = TRUE, force = FALSE)
dir.create(file.path("/home/rstudio/data/", "WEBlogosOrganoids"), showWarnings = FALSE)
dir.create(file.path("/home/rstudio/data/HammockOrganoids/", "alignments_final_Scored"),
  showWarnings = FALSE)

setkey(ham.clusters.all, cluster_id)
setkey(ham.clusters, cluster_id)
setkey(select.samples.pepMerge, Peptide)

opts_chunk$set(out.width = "100%", fig.align = "center")
generateWeblogo <- function(in.name) {
  # in.name <- ham.clusters$cluster_id[2] in.name <- 4352
  print(in.name)
  this.fa <- read.fasta(file = paste("/home/rstudio/data/HammockOrganoids/alignments_final/",
    in.name, ".aln", sep = ""))
  allSeqs <- unlist(getSequence(this.fa, as.string = TRUE))
  allSeqs <- data.table(unlist(lapply(allSeqs, function(x) gsub("([ -])", "",
    toupper(x)))))
  allSeqs.out <- select.samples.pepMerge[J(allSeqs)]
  allSeqs.out$Annot <- data.table(getName(this.fa))
  allSeqs.out[, `:=`(Annot, paste(Annot, "_", Score, sep = ""))]
```

```

allSeqs.out$Alignment <- data.table(toupper(unlist(getSequence(this.fa,
  as.string = TRUE))))

allSeqs.out <- allSeqs.out[rep(1:.N, Score)][, `:=`(Indx, 1:.N), by = Peptide]
allSeqs.out[, `:=`(Annot, paste(Annot, "_", Indx, sep = ""))]

write.fasta(as.list(allSeqs.out$Alignment), allSeqs.out$Annot, nbchar = 60,
  paste("/home/rstudio/data/HamcockOrganoids/alignments_final_Scored/",
    in.name, ".aln", sep = ""), open = "w")

this.main <- ham.clusters[J(in.name)]
main.gene <- select.samples.trsp[J(this.main$main_sequence)]$GeneName[1]
this.title <- paste("## Peptide", this.main$main_sequence, "from", main.gene,
  "with cluster number", in.name, sep = " ")

tmp <- system(paste("weblgo --format PDF --sequence-type protein --size large --errorbars NO --resolution",
  this.title, "' < /home/rstudio/data/HamcockOrganoids/alignments_final_Scored/",
  in.name, ".aln > /home/rstudio/data/WEBlogosOrganoids/", in.name, ".pdf",
  sep = ""), intern = TRUE, ignore.stdout = FALSE)

cat("\n")
cat(this.title, "\n")
cat("\n")
cat("\n")
cat(paste0("[Peptide: ", this.main$main_sequence, " from ", main.gene,
  " with cluster number ", in.name, "](/home/rstudio/data/WEBlogosOrganoids/",
  in.name, ".pdf)"))
cat("\n")
out.table <- knitr::kable(this.main, format = "latex")
print(column_spec(out.table, 1:ncol(this.main), monospace = TRUE) %>% kable_styling(latex_options = c("striped",
  "scale_down", "repeat_header"))))
cat("\n")
this.cluster <- ham.clusters.all[J(in.name)]
out.table <- knitr::kable(this.cluster, format = "latex")
print(column_spec(out.table, 1:ncol(this.cluster), monospace = TRUE) %>%
  kable_styling(latex_options = c("striped", "scale_down", "repeat_header"))))

this.found <- select.samples[J(this.cluster$sequence)]
setnames(this.cluster, "sequence", "Peptide")
this.found <- merge(this.found, this.cluster[, 2:3], by = "Peptide", all = FALSE)
cat("\n")
cat("\n")
output.order <- c("alignment", "LUTnrs", "GeneName", "start", "structure",
  "Group", "Score")
if (nrow(this.found) >= 48) {
  this.found.p1 <- this.found[1:47, ]
  out.table <- knitr::kable(this.found.p1[, ..output.order], format = "latex")
  print(column_spec(out.table, 1, monospace = TRUE) %>% kable_styling(latex_options = c("striped",
    "scale_down", "repeat_header"))))
  cat("\n")
  cat("\n\n\\pagebreak\n")
  cat("\n\n\\clearpage\n")
  this.found <- this.found[48:nrow(this.found), ]
  if (nrow(this.found) >= 48) {
    this.found.p2 <- this.found[1:47, ]
    out.table <- knitr::kable(this.found.p2[, ..output.order], format = "latex")
    print(column_spec(out.table, 1, monospace = TRUE) %>% kable_styling(latex_options = c("striped",

```

```

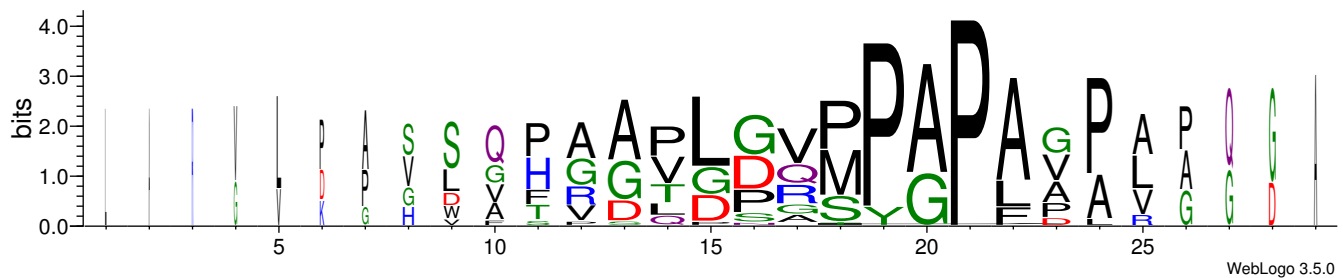
      "scale_down", "repeat_header"))))
cat("\n")
cat("\n\n\\pagebreak\n")
cat("\n\n\\clearpage\n")
this.found <- this.found[48:nrow(this.found), ]
}
if (nrow(this.found) >= 48) {
  this.found.p2 <- this.found[1:47, ]
  out.table <- knitr::kable(this.found.p2[, ..output.order], format = "latex")
  print(column_spec(out.table, 1, monospace = TRUE) %>% kable_styling(latex_options = c("striped",
    "scale_down", "repeat_header"))))
  cat("\n")
  cat("\n\n\\pagebreak\n")
  cat("\n\n\\clearpage\n")
  this.found <- this.found[48:nrow(this.found), ]
}
out.table <- knitr::kable(this.found[, ..output.order], format = "latex")
print(column_spec(out.table, 1, monospace = TRUE) %>% kable_styling(latex_options = c("striped",
  "scale_down", "repeat_header"))))
cat("\n")
cat("\n\n\\clearpage\n")
cat("\n")
} else {
  out.table <- knitr::kable(this.found[, ..output.order], format = "latex")
  print(column_spec(out.table, 1, monospace = TRUE) %>% kable_styling(latex_options = c("striped",
    "scale_down", "repeat_header"))))
  cat("\n")
  cat("\n\n\\pagebreak\n")
  cat("\n\n\\clearpage\n")
}
}
invisible(lapply(id.order, generateWeblogo))

```

[1] 2778

Peptide SQHAGPLGVMPAPA from HSV-1-pUL36 with cluster number 2778

Peptide SQHAGPLGVMPAPA from HSV-1-pUL36 with cluster number 2778



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2778	SQHAGPLGVMPAPA	199	90	109

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2778	SQHAGPLGVMPAPA	-----SQHAGPLGVMPAPA-----	20	10	10
2778	AVGDRPPAPLAPVG	-----AVGDRPPAPLAPVG-----	18	10	8
2778	SLVPGAQDSAPPGP	-----SLVPGAQDSAPPGP-----	17	10	7
2778	GVMPAPAGAAPQGA	-----GVMPAPAGAAPQGA-----	15	10	5
2778	AGPLGVMPAPAGAA	-----AGPLGVMPAPAGAA-----	15	10	5
2778	VLPPHWAPGALDDGPYAPFPPR	___VLPPHWAPGALDDGPYAPFPPR___	10	10	0
2778	RDTLPQSPGPAVPL	-----RDTLPQSPGPAVPL-----	10	10	0
2778	LPQSPGPAVPLAGD	-----LPQSPGPAVPLAGD-----	10	10	0
2778	AVSQHAGPLGVMPA	-----AVSQHAGPLGVMPA-----	10	10	0
2778	LGVMAPAGAAPQG	-----LGVMAPAGAAPQG-----	7	0	7
2778	GTRDTLPQSPGPAV	-----GTRDTLPQSPGPAV-----	7	0	7
2778	FVAVGDRPPAPLAP	-----FVAVGDRPPAPLAP-----	7	0	7
2778	SPSVNPPTPGADL	-----SPSVNPPTPGADL-----	6	0	6
2778	LARGVDAVSQHAGPLGVMPAPA	LARGVDAVSQHAGPLGVMPAPA-----	6	0	6
2778	APGALDDGPYAPFP	-----APGALDDGPYAPFP-----	6	0	6
2778	VFFVAVGDRPPAPA	-----VFFVAVGDRPPAPA-----	5	0	5
2778	VAVGDRPPAPLAPV	-----VAVGDRPPAPLAPV-----	5	0	5
2778	TLPQSPGPAVPLAG	-----TLPQSPGPAVPLAG-----	5	0	5
2778	PGALDDGPYAPFPP	-----PGALDDGPYAPFPP-----	5	0	5
2778	LKGGDGTRDTLPQSPGPAVPLA	-----LKGGDGTRDTLPQSPGPAVPLA-----	5	0	5
2778	GDGTRDTLPQSPGP	-----GDGTRDTLPQSPGP-----	5	0	5
2778	FVAVGDRPPAPADP	-----FVAVGDRPPAPADP-----	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
-----AGPLGVMPAPAGAA-----	X44054	HSV-1-pUL36	744	14aa	mRNA_30cpc_Organoid_MD114	10
-----AGPLGVMPAPAGAA-----	X44054	HSV-1-pUL36	744	14aa	mRNA_3000cpc_Organoid_MD101	5
-----APGALDDGPYAPFP-----	X41944	HSV-2-pUS4	301	14aa	mRNA_3000cpc_Organoid_MD101	6
-----AVGDRPPAPLAPVG-----	X44646	PRV-Becker-gE	205	14aa	mRNA_30cpc_Organoid_MD114	10
-----AVGDRPPAPLAPVG-----	X44646	PRV-TJ-gE	206	14aa	mRNA_30cpc_Organoid_MD114	10
-----AVGDRPPAPLAPVG-----	X44646	PRV-Becker-gE	205	14aa	mRNA_3000cpc_Organoid_MD101	8
-----AVGDRPPAPLAPVG-----	X44646	PRV-TJ-gE	206	14aa	mRNA_3000cpc_Organoid_MD101	8
-----AVSQHAGPLGVMPA-----	X56752	HSV-1-pUL36	739	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----FVAVGDRPPAPADP-----	X76192	PRV-Becker-gE	203	14aa	mRNA_3000cpc_Organoid_MD101	5
-----FVAVGDRPPAPADP-----	X76192	PRV-TJ-gE	204	14aa	mRNA_3000cpc_Organoid_MD101	5
-----FVAVGDRPPAPLAP-----	X76191	PRV-Becker-gE	203	14aa	mRNA_3000cpc_Organoid_MD101	7
-----FVAVGDRPPAPLAP-----	X76191	PRV-TJ-gE	204	14aa	mRNA_3000cpc_Organoid_MD101	7
-----GDGTRDTLPQSPGP-----	X57646	HSV-1-pUS4	97	14aaA5	mRNA_3000cpc_Organoid_MD101	5
-----GTRDTLPQSPGPAV-----	X61567	HSV-1-pUS4	99	14aa	mRNA_3000cpc_Organoid_MD101	7
-----GVMPAPAGAAPQGA-----	X57955	HSV-1-pUL36	748	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----GVMPAPAGAAPQGA-----	X57955	HSV-1-pUL36	748	14aaA5	mRNA_3000cpc_Organoid_MD101	5
LARGVDAVSQHAGPLGVMPAPA	X31969	HSV-1-pUL36	733	22aa	mRNA_3000cpc_Organoid_MD101	6
-----LGVMAPAGAAPQG-----	X32660	HSV-1-pUL36	747	14aa	mRNA_3000cpc_Organoid_MD101	7
___LKGGDGTRDTLPQSPGPAVPLA___	X28727	HSV-1-pUS4	94	22aa	mRNA_3000cpc_Organoid_MD101	5
-----LPQSPGPAVPLAGD-----	X30196	HSV-1-pUS4	104	14aa	mRNA_30cpc_Organoid_MD114	10
-----PGALDDGPYAPFPP-----	X23987	HSV-2-pUS4	302	14aa	mRNA_3000cpc_Organoid_MD101	5
-----RDTLPQSPGPAVPL-----	X26647	HSV-1-pUS4	101	14aa	mRNA_30cpc_Organoid_MD114	10
-----SLVPGAQDSAPPGP-----	X12339	HSV-1-pUL21	269	14aa	mRNA_30cpc_Organoid_MD114	10
-----SLVPGAQDSAPPGP-----	X12339	HSV-1-pUL21	269	14aa	mRNA_3000cpc_Organoid_MD101	7
-----SPSVNPPTPGADL-----	X11538	HSV-1-pUL36	2499	14aa	mRNA_3000cpc_Organoid_MD101	6
-----SQHAGPLGVMPAPA-----	X11365	HSV-1-pUL36	741	14aa	mRNA_30cpc_Organoid_MD114	10
-----SQHAGPLGVMPAPA-----	X11365	HSV-1-pUL36	741	14aa	mRNA_3000cpc_Organoid_MD101	10
-----TLPQSPGPAVPLAG-----	X7811	HSV-1-pUS4	103	14aa	mRNA_3000cpc_Organoid_MD101	5
-----VAVGDRPPAPLAPV-----	X68849	PRV-Becker-gE	204	14aa	mRNA_3000cpc_Organoid_MD101	5
-----VAVGDRPPAPLAPV-----	X68849	PRV-TJ-gE	205	14aa	mRNA_3000cpc_Organoid_MD101	5
-----VFFVAVGDRPPAPA-----	X59346	PRV-Becker-gE	201	14aaA5	mRNA_3000cpc_Organoid_MD101	5
-----VFFVAVGDRPPAPA-----	X59346	PRV-TJ-gE	202	14aaA5	mRNA_3000cpc_Organoid_MD101	5
___VLPPHWAPGALDDGPYAPFPPR___	X67733	HSV-2-pUS4	295	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2833

Peptide PDPEALTFPRGDNV from HSV-1-pUL22 with cluster number 2833

Peptide PDPEALTFPRGDNV from HSV-1-pUL22 with cluster number 2833



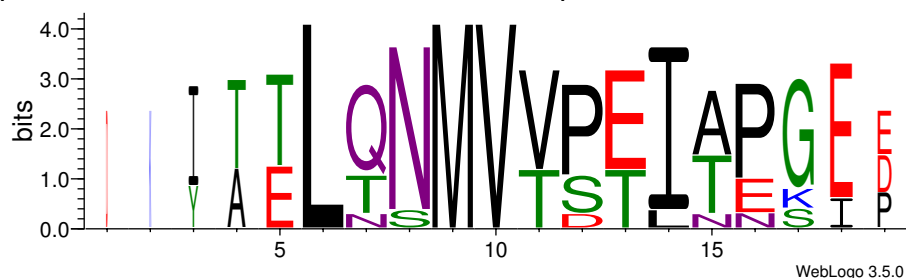
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2833	PDPEALTFPRGDNV	158	120	38

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2833	PDPEALTFPRGDNV	_____PDPEALTFPRGDNV_____	26	20	6
2833	LALPWTSPSSTA	_____LALPWTSPSSTA_____	20	20	0
2833	SSQPRGDSGTPTES	_____SSQPRGDSGTPTES_____	15	10	5
2833	VPDPEALTFPRGDN	_____VPDPEALTFPRGDN_____	10	10	0
2833	PWSSAGSTTWRNRE	_____PWSSAGSTTWRNRE_____	10	10	0
2833	PSSQPRGDSGTPT	_____PSSQPRGDSGTPT_____	10	10	0
2833	PEALTFPRGDNVATASHPSGPR	_____PEALTFPRGDNVATASHPSGPR_____	10	10	0
2833	KQPSSQPRGDSGT	_____KQPSSQPRGDSGT_____	10	10	0
2833	HDSLPLWTSPSSTA	_____HDSLPLWTSPSSTA_____	10	10	0
2833	DPEALTFPRGDNVA	_____DPEALTFPRGDNVA_____	10	10	0
2833	TQASPPGPGTGPS	_____TQASPPGPGTGPS_____	6	0	6
2833	SAVPDPEALTFPRG	_____SAVPDPEALTFPRG_____	6	0	6
2833	QPSSQPRGDSGTPT	_____QPSSQPRGDSGTPT_____	5	0	5
2833	PEALTFPRGDNVAT	_____PEALTFPRGDNVAT_____	5	0	5
2833	IDPWNQPGSQPKTA	_____IDPWNQPGSQPKTA_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
_____DPEALTFPRGDNVA_____	X34957	HSV-1-pUL22	168	14aa	mRNA_30cpc_Organoid_MD114	10
HDSLPLWTSPSSTA	X17861	JEV-E-KE-093	219	14aa	mRNA_30cpc_Organoid_MD114	10
HDSLPLWTSPSSTA	X17861	JEV-E-SA14-5-3	219	14aa	mRNA_30cpc_Organoid_MD114	10
HDSLPLWTSPSSTA	X17861	JEV-E-ThCMAR4492	219	14aa	mRNA_30cpc_Organoid_MD114	10
_____IDPWNQPGSQPKTA_____	X15965	HIV-tat-GR17	8	14aa	mRNA_3000cpc_Organoid_MD101	5
_____KQPSSQPRGDSGT_____	X3874	HIV-tat	71	14aa	mRNA_30cpc_Organoid_MD114	10
_____LALPWTSPSSTA_____	X31994	JEV-E-BN19	221	14aa	mRNA_30cpc_Organoid_MD114	20
_____LALPWTSPSSTA_____	X31994	JEV-E-KE-093	221	14aa	mRNA_30cpc_Organoid_MD114	20
_____LALPWTSPSSTA_____	X31994	JEV-E-SA14-5-3	221	14aa	mRNA_30cpc_Organoid_MD114	20
_____LALPWTSPSSTA_____	X31994	JEV-E-ThCMAR4492	221	14aa	mRNA_30cpc_Organoid_MD114	20
_____PDPEALTFPRGDNV_____	X22953	HSV-1-pUL22	167	14aa	mRNA_30cpc_Organoid_MD114	20
_____PDPEALTFPRGDNV_____	X22953	HSV-1-pUL22	167	14aa	mRNA_3000cpc_Organoid_MD101	6
_____PEALTFPRGDNVAT_____	X23217	HSV-1-pUL22	169	14aa	mRNA_3000cpc_Organoid_MD101	5
_____PEALTFPRGDNVATASHPSGPR_____	X23218	HSV-1-pUL22	169	22aa	mRNA_30cpc_Organoid_MD114	10
_____PSSQPRGDSGTPT_____	X21128	HIV-tat	73	14aa	mRNA_30cpc_Organoid_MD114	10
_____PWSSAGSTTWRNRE_____	X24556	WNV-E-AZ10-918	224	14aa	mRNA_30cpc_Organoid_MD114	10
_____PWSSAGSTTWRNRE_____	X24556	WNV-E-ArD76104	220	14aa	mRNA_30cpc_Organoid_MD114	10
_____PWSSAGSTTWRNRE_____	X24556	WNV-E-H-442	224	14aa	mRNA_30cpc_Organoid_MD114	10
_____QPSSQPRGDSGTPT_____	X19191	HIV-tat	72	14aa	mRNA_3000cpc_Organoid_MD101	5
_____SAVPDPEALTFPRG_____	X13061	HSV-1-pUL22	164	14aa	mRNA_3000cpc_Organoid_MD101	6
_____SSQPRGDSGTPTES_____	X10707	HIV-tat	74	14aa	mRNA_30cpc_Organoid_MD114	10
_____SSQPRGDSGTPTES_____	X10707	HIV-tat	74	14aa	mRNA_3000cpc_Organoid_MD101	5
_____TQASPPGPGTGPS_____	X7067	Tau	275	14aa	mRNA_3000cpc_Organoid_MD101	6
_____VPDPEALTFPRGDN_____	X67221	HSV-1-pUL22	166	14aa	mRNA_30cpc_Organoid_MD114	10

Peptide TLQNMVVPEIAPGE from HSV-1-pUL19 with cluster number 2140

ptide TLQNMVVPEIAPGE from HSV-1-pUL19 with cluster number



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2140	TLQNMVVPEIAPGE	157	100	57

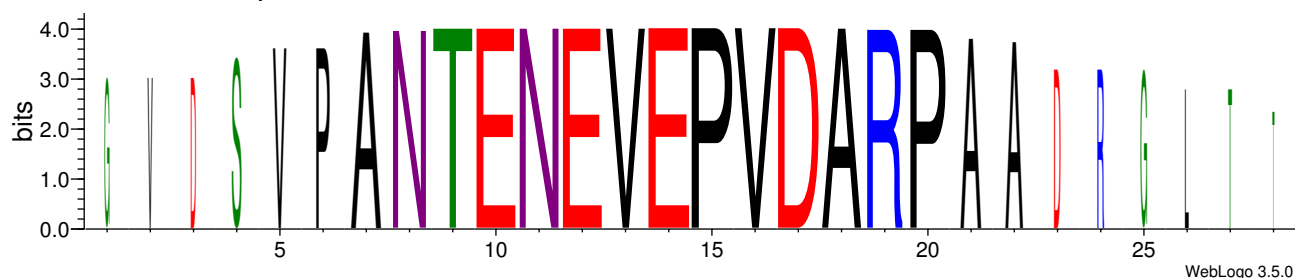
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2140	TLQNMVVPEIAPGE	___TLQNMVVPEIAPGE_	34	20	14
2140	LQNMVVPEIAPGEE	____LQNMVVPEIAPGEE	20	20	0
2140	ITELTNMVTSTITE	__ITELTNMVTSTITE__	20	20	0
2140	LQNMVVPEITPGED	____LQNMVVPEITPGED	17	10	7
2140	ATLQNMVVPEIAPG	___ATLQNMVVPEIAPG__	17	10	7
2140	TELTNMVTSTITEK	___TELTNMVTSTITEK__	16	10	6
2140	LNSMVTDTLNSIP	____LNSMVTDTLNSIP	16	10	6
2140	YATLQNMVVPEITP	__YATLQNMVVPEITP__	11	0	11
2140	DKITELTNMVTSTI	DKITELTNMVTSTI_____	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
___ATLQNMVVPEIAPG__	X40328	HSV-1-pUL19	837	14aa	mRNA_30cpc_Organoid_MD114	10
___ATLQNMVVPEIAPG__	X40328	HSV-2-pUL19	837	14aa	mRNA_30cpc_Organoid_MD114	10
___ATLQNMVVPEIAPG__	X40328	HSV-1-pUL19	837	14aa	mRNA_3000cpc_Organoid_MD101	7
___ATLQNMVVPEIAPG__	X40328	HSV-2-pUL19	837	14aa	mRNA_3000cpc_Organoid_MD101	7
DKITELTNMVTSTI_____	X33879	PV1-VP1	474	14aa	mRNA_3000cpc_Organoid_MD101	6
__ITELTNMVTSTITE__	X14645	PV1-VP1	476	14aa	mRNA_30cpc_Organoid_MD114	20
____LNSMVTDTLNSIP	X28344	BoNT-E-Hc	31	14aa	mRNA_30cpc_Organoid_MD114	10
____LNSMVTDTLNSIP	X28344	BoNT-E-Hc	31	14aa	mRNA_3000cpc_Organoid_MD101	6
____LQNMVVPEIAPGEE	X29938	HSV-1-pUL19	839	14aa	mRNA_30cpc_Organoid_MD114	20
____LQNMVVPEIAPGEE	X29938	HSV-2-pUL19	839	14aa	mRNA_30cpc_Organoid_MD114	20
____LQNMVVPEITPGED	X29937	HSV-1-pUL19	839	14aa	mRNA_30cpc_Organoid_MD114	10
____LQNMVVPEITPGED	X29937	HSV-2-pUL19	839	14aa	mRNA_30cpc_Organoid_MD114	10
____LQNMVVPEITPGED	X29937	HSV-1-pUL19	839	14aa	mRNA_3000cpc_Organoid_MD101	7
____LQNMVVPEITPGED	X29937	HSV-2-pUL19	839	14aa	mRNA_3000cpc_Organoid_MD101	7
___TELTNMVTSTITEK__	X8305	PV1-VP1	477	14aa	mRNA_30cpc_Organoid_MD114	10
___TELTNMVTSTITEK__	X8305	PV1-VP1	477	14aa	mRNA_3000cpc_Organoid_MD101	6
____TLQNMVVPEIAPGE_	X7795	HSV-1-pUL19	838	14aa	mRNA_30cpc_Organoid_MD114	10
____TLQNMVVPEIAPGE_	X47264	HSV-1-pUL19	838	14aaA5	mRNA_30cpc_Organoid_MD114	10
____TLQNMVVPEIAPGE_	X7795	HSV-2-pUL19	838	14aa	mRNA_30cpc_Organoid_MD114	10
____TLQNMVVPEIAPGE_	X47264	HSV-2-pUL19	838	14aaA5	mRNA_30cpc_Organoid_MD114	10
____TLQNMVVPEIAPGE_	X7795	HSV-1-pUL19	838	14aa	mRNA_3000cpc_Organoid_MD101	5
____TLQNMVVPEIAPGE_	X47264	HSV-1-pUL19	838	14aaA5	mRNA_3000cpc_Organoid_MD101	9
____TLQNMVVPEIAPGE_	X7795	HSV-2-pUL19	838	14aa	mRNA_3000cpc_Organoid_MD101	5
____TLQNMVVPEIAPGE_	X47264	HSV-2-pUL19	838	14aaA5	mRNA_3000cpc_Organoid_MD101	9
__YATLQNMVVPEITP__	X71450	HSV-1-pUL19	836	14aa	mRNA_3000cpc_Organoid_MD101	11
__YATLQNMVVPEITP__	X71450	HSV-2-pUL19	836	14aa	mRNA_3000cpc_Organoid_MD101	11

[1] 2504

Peptide ANTENEVEPVDARP from APP with cluster number 2504

Peptide ANTENEVEPVDARP from APP with cluster number 2504



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2504	ANTENEVEPVDARP	118	40	78

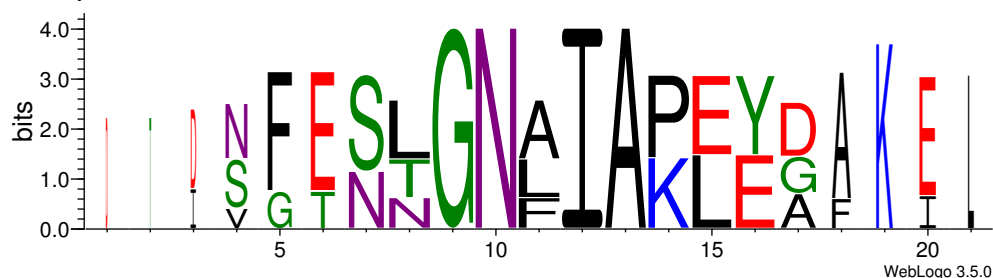
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2504	ANTENEVEPVDARP	-----ANTENEVEPVDARP-----	42	30	12
2504	TENEVEPVDARPA	-----TENEVEPVDARPA-----	17	10	7
2504	GVDSVPANTENEVEPVDARPA	GVDSVPANTENEVEPVDARPA-----	15	0	15
2504	VPANTENEVEPVDA	-----VPANTENEVEPVDA-----	11	0	11
2504	NTENEVEPVDARPA	-----NTENEVEPVDARPA-----	9	0	9
2504	SVPANTENEVEPVDARPAADRG	---SVPANTENEVEPVDARPAADRG---	8	0	8
2504	ANTENEVEPVDARPAADRGLTT	-----ANTENEVEPVDARPAADRGLTT	6	0	6
2504	SVPANTENEVEPVD	---SVPANTENEVEPVD-----	5	0	5
2504	EPVDARPAADRGLT	-----EPVDARPAADRGLT---	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
-----ANTENEVEPVDARP-----	X39803	APP	631	14aa	mRNA_30cpc_Organoid_MD114	10
-----ANTENEVEPVDARP-----	X55577	APP	631	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----ANTENEVEPVDARP-----	X86867	APP	631	14aaG4S	mRNA_30cpc_Organoid_MD114	10
-----ANTENEVEPVDARP-----	X39803	APP	631	14aa	mRNA_3000cpc_Organoid_MD101	12
-----ANTENEVEPVDARPAADRGLTT	X39804	APP	631	22aa	mRNA_3000cpc_Organoid_MD101	6
-----EPVDARPAADRGLT---	X37901	APP	638	14aa	mRNA_3000cpc_Organoid_MD101	5
GVDSVPANTENEVEPVDARPA-----	X64911	APP	625	22aa	mRNA_3000cpc_Organoid_MD101	15
-----NTENEVEPVDARPA-----	X524	APP	632	14aa	mRNA_3000cpc_Organoid_MD101	9
---SVPANTENEVEPVD-----	X48790	APP	628	14aaA5	mRNA_3000cpc_Organoid_MD101	5
---SVPANTENEVEPVDARPAADRG---	X13535	APP	628	22aa	mRNA_3000cpc_Organoid_MD101	8
-----TENEVEPVDARPA-----	X8197	APP	633	14aa	mRNA_30cpc_Organoid_MD114	10
-----TENEVEPVDARPA-----	X8197	APP	633	14aa	mRNA_3000cpc_Organoid_MD101	7
-----VPANTENEVEPVDA-----	X67260	APP	629	14aa	mRNA_3000cpc_Organoid_MD101	11

[1] 2792

Peptide NFESNGNFIAP EYA from H5N1-HA with cluster number 2792

Peptide NFESNGNFIAP EYA from H5N1-HA with cluster number 2792



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2792	NFESNGNFIAP EYA	113	60	53

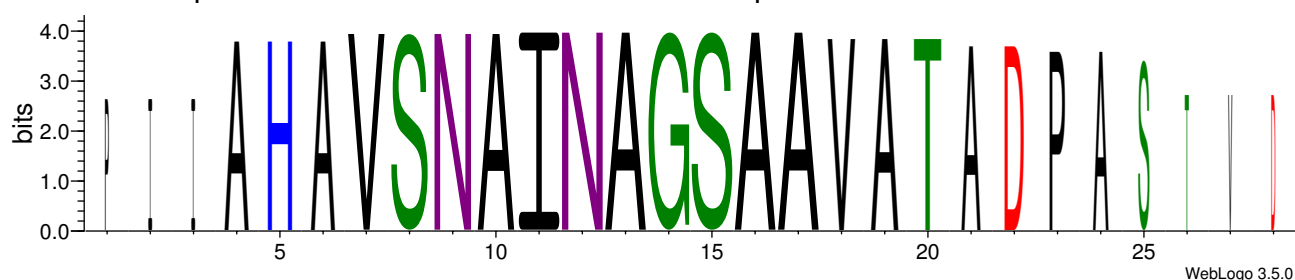
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2792	NFESNGNFIAP EYA	__NFESNGNFIAP EYA__	27	10	17
2792	NLGNAIAKLEDAKE	____NLGNAIAKLEDAKE_	20	10	10
2792	SFESTGNLIAPEYG	___SFESTGNLIAPEYG___	19	10	9
2792	LGNAIAKLEDAKEL	____LGNAIAKLEDAKEL	16	10	6
2792	STGNLIAPEYGFKI	____STGNLIAPEYGFKI_	10	10	0
2792	DVGTNLGNAIAKLE	__DVGTNLGNAIAKLE__	10	10	0
2792	GTNLGNAIAKLEDA	____GTNLGNAIAKLEDA__	6	0	6
2792	DTISFESTGNLIAP	DTISFESTGNLIAP_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
DTISFESTGNLIAP_____	X34028	H2N2-HA	251	14aa	mRNA_3000cpc_Organoid_MD101	5
__DVGTNLGNAIAKLE__	X36365	MV-F-CAM-70	461	14aa	mRNA_30cpc_Organoid_MD114	10
__DVGTNLGNAIAKLE__	X36365	MV-F-Edmonston	461	14aa	mRNA_30cpc_Organoid_MD114	10
__DVGTNLGNAIAKLE__	X36365	MV-F-Halle	461	14aa	mRNA_30cpc_Organoid_MD114	10
____GTNLGNAIAKLEDA__	X57096	MV-F-CAM-70	463	14aaA5	mRNA_3000cpc_Organoid_MD101	6
____GTNLGNAIAKLEDA__	X57096	MV-F-Edmonston	463	14aaA5	mRNA_3000cpc_Organoid_MD101	6
____GTNLGNAIAKLEDA__	X57096	MV-F-Halle	463	14aaA5	mRNA_3000cpc_Organoid_MD101	6
____LGNAIAKLEDAKEL	X32295	MV-F-CAM-70	466	14aa	mRNA_30cpc_Organoid_MD114	10
____LGNAIAKLEDAKEL	X32295	MV-F-Edmonston	466	14aa	mRNA_30cpc_Organoid_MD114	10
____LGNAIAKLEDAKEL	X32295	MV-F-Halle	466	14aa	mRNA_30cpc_Organoid_MD114	10
____LGNAIAKLEDAKEL	X32295	MV-F-CAM-70	466	14aa	mRNA_3000cpc_Organoid_MD101	6
____LGNAIAKLEDAKEL	X32295	MV-F-Edmonston	466	14aa	mRNA_3000cpc_Organoid_MD101	6
____LGNAIAKLEDAKEL	X32295	MV-F-Halle	466	14aa	mRNA_3000cpc_Organoid_MD101	6
___NFESNGNFIAP EYA__	X2967	H5N1-HA	256	14aa	mRNA_30cpc_Organoid_MD114	10
___NFESNGNFIAP EYA__	X2967	H5N1-HA	256	14aa	mRNA_3000cpc_Organoid_MD101	11
___NFESNGNFIAP EYA__	X46009	H5N1-HA	256	14aaA5	mRNA_3000cpc_Organoid_MD101	6
____NLGNAIAKLEDAKE_	X1704	MV-F-CAM-70	465	14aa	mRNA_30cpc_Organoid_MD114	10
____NLGNAIAKLEDAKE_	X1704	MV-F-Edmonston	465	14aa	mRNA_30cpc_Organoid_MD114	10
____NLGNAIAKLEDAKE_	X1704	MV-F-Halle	465	14aa	mRNA_30cpc_Organoid_MD114	10
____NLGNAIAKLEDAKE_	X1704	MV-F-CAM-70	465	14aa	mRNA_3000cpc_Organoid_MD101	10
____NLGNAIAKLEDAKE_	X1704	MV-F-Edmonston	465	14aa	mRNA_3000cpc_Organoid_MD101	10
____NLGNAIAKLEDAKE_	X1704	MV-F-Halle	465	14aa	mRNA_3000cpc_Organoid_MD101	10
___SFESTGNLIAPEYG___	X14087	H2N2-HA	254	14aa	mRNA_30cpc_Organoid_MD114	10
___SFESTGNLIAPEYG___	X14087	H2N2-HA	254	14aa	mRNA_3000cpc_Organoid_MD101	9
____STGNLIAPEYGFKI_	X10468	H2N2-HA	257	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2255

Peptide AHAVSNAINAGSAA from HSV-1-pUL36 with cluster number 2255

Peptide AHAVSNAINAGSAA from HSV-1-pUL36 with cluster number 2255



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2255	AHAVSNAINAGSAA	98	60	38

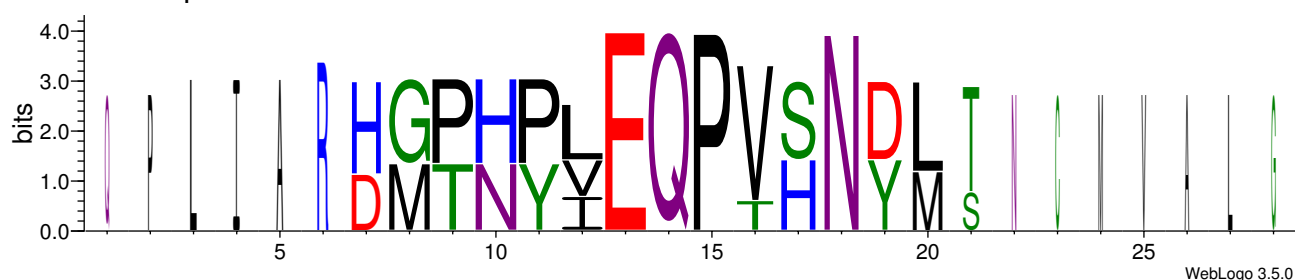
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2255	AHAVSNAINAGSAA	___AHAVSNAINAGSAA_____	32	20	12
2255	VSNAINAGSAAVAT	_____VSNAINAGSAAVAT_____	20	10	10
2255	AHAVSNAINAGSAAVATADPAS	___AHAVSNAINAGSAAVATADPAS___	17	10	7
2255	VSNAINAGSAAVATADPASTVD	_____VSNAINAGSAAVATADPASTVD	10	10	0
2255	INAGSAAVATADPA	_____INAGSAAVATADPA_____	10	10	0
2255	PIIAHAVSNAINAGSAAVATAD	PIIAHAVSNAINAGSAAVATAD_____	9	0	9

alignment	LUThrs	GeneName	start	structure	Group	Score
___AHAVSNAINAGSAA_____	X41348	HSV-1-pUL36	1138	14aa	mRNA_30cpc_Organoid_MD114	20
___AHAVSNAINAGSAA_____	X41348	HSV-1-pUL36	1138	14aa	mRNA_3000cpc_Organoid_MD101	12
___AHAVSNAINAGSAAVATADPAS___	X41349	HSV-1-pUL36	1138	22aa	mRNA_30cpc_Organoid_MD114	10
___AHAVSNAINAGSAAVATADPAS___	X41349	HSV-1-pUL36	1138	22aa	mRNA_3000cpc_Organoid_MD101	7
_____INAGSAAVATADPA_____	X14290	HSV-1-pUL36	1145	14aa	mRNA_30cpc_Organoid_MD114	10
PIIAHAVSNAINAGSAAVATAD_____	X21423	HSV-1-pUL36	1135	22aa	mRNA_3000cpc_Organoid_MD101	9
_____VSNAINAGSAAVAT_____	X66274	HSV-1-pUL36	1141	14aa	mRNA_30cpc_Organoid_MD114	10
_____VSNAINAGSAAVAT_____	X66274	HSV-1-pUL36	1141	14aa	mRNA_3000cpc_Organoid_MD101	10
_____VSNAINAGSAAVATADPASTVD	X66275	HSV-1-pUL36	1141	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2830

Peptide HMTNYLEQPVSN DL from MV-H-CAM-70 with cluster number 2830

Peptide HMTNYLEQPVSN DL from MV-H-CAM-70 with cluster number 2830



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2830	HMTNYLEQPVSN DL	93	70	23

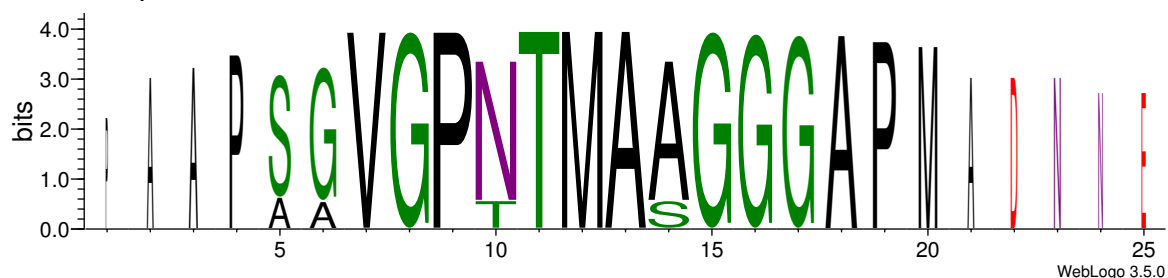
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2830	HMTNYLEQPVSN DL	_____HMTNYLEQPVSN DL_____	31	20	11
2830	GPHPV EQPVHNYMT	_____GPHPV EQPVHNYMT_____	17	10	7
2830	RDGPHPV EQPVHNY	_____RDGPHPV EQPVHNY_____	10	10	0
2830	QPLIARDGPHPIEQ	QPLIARDGPHPIEQ_____	10	10	0
2830	HMTNYLEQPVSN DL SNCMVALG	_____HMTNYLEQPVSN DL SNCMVALG_____	10	10	0
2830	GPHPIEQPTHNYMT	_____GPHPIEQPTHNYMT_____	10	10	0
2830	LIARDGPHPIEQPT	__LIARDGPHPIEQPT_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
_____GPHPIEQPTHNYMT_____	X62586	HSV-1-pUL19	108	14aa	mRNA_30cpc_Organoid_MD114	10
_____GPHPV EQPVHNYMT_____	X62589	HSV-2-pUL19	108	14aa	mRNA_30cpc_Organoid_MD114	10
_____GPHPV EQPVHNYMT_____	X62589	HSV-2-pUL19	108	14aa	mRNA_3000cpc_Organoid_MD101	7
_____HMTNYLEQPVSN DL_____	X17313	MV-H-CAM-70	271	14aa	mRNA_30cpc_Organoid_MD114	20
_____HMTNYLEQPVSN DL_____	X17313	MV-H-Edmonston	271	14aa	mRNA_30cpc_Organoid_MD114	20
_____HMTNYLEQPVSN DL_____	X17313	MV-H-Halle	271	14aa	mRNA_30cpc_Organoid_MD114	20
_____HMTNYLEQPVSN DL_____	X17313	MV-H-CAM-70	271	14aa	mRNA_3000cpc_Organoid_MD101	11
_____HMTNYLEQPVSN DL_____	X17313	MV-H-Edmonston	271	14aa	mRNA_3000cpc_Organoid_MD101	11
_____HMTNYLEQPVSN DL_____	X17313	MV-H-Halle	271	14aa	mRNA_3000cpc_Organoid_MD101	11
_____HMTNYLEQPVSN DL SNCMVALG_____	X17312	MV-H-CAM-70	271	22aa	mRNA_30cpc_Organoid_MD114	10
_____HMTNYLEQPVSN DL SNCMVALG_____	X17312	MV-H-Edmonston	271	22aa	mRNA_30cpc_Organoid_MD114	10
_____HMTNYLEQPVSN DL SNCMVALG_____	X17312	MV-H-Halle	271	22aa	mRNA_30cpc_Organoid_MD114	10
_____HMTNYLEQPVSN DL SNCMVALG_____	X17312	MV-H-MVi-Illinois.USA-50.99	271	22aa	mRNA_30cpc_Organoid_MD114	10
_____HMTNYLEQPVSN DL SNCMVALG_____	X17312	MV-H-MVi-Texas.USA-28.99	271	22aa	mRNA_30cpc_Organoid_MD114	10
__LIARDGPHPIEQPT_____	X29647	HSV-1-pUL19	103	14aa	mRNA_3000cpc_Organoid_MD101	5
QPLIARDGPHPIEQ_____	X19271	HSV-1-pUL19	101	14aa	mRNA_30cpc_Organoid_MD114	10
QPLIARDGPHPIEQ_____	X19271	HSV-2-pUL19	101	14aa	mRNA_30cpc_Organoid_MD114	10
_____RDGPHPV EQPVHNY_____	X26778	HSV-2-pUL19	106	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2783

Peptide VGPNTMAAGGGAPM from AAV8-VP1 with cluster number 2783

Peptide VGPNTMAAGGGAPM from AAV8-VP1 with cluster number 2783



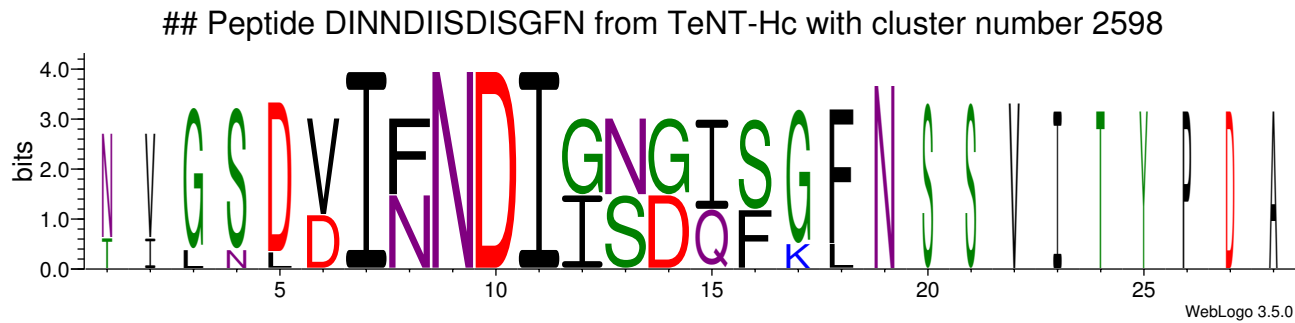
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2783	VGPNTMAAGGGAPM	90	60	30

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2783	VGPNTMAAGGGAPM	-----VGPNTMAAGGGAPM-----	26	20	6
2783	PSGVGPNTMAAGGGAPMADNNE	___PSGVGPNTMAAGGGAPMADNNE	10	10	0
2783	GVGPNTMAAGGGAP	-----GVGPNTMAAGGGAP-----	10	10	0
2783	AAVGPTTMAAGGGA	-----AAVGPTTMAAGGGA-----	10	10	0
2783	AAPSGVGPNTMAAG	___AAPSGVGPNTMAAG_____	10	10	0
2783	SGVGPNTMAAGGGA	-----SGVGPNTMAAGGGA-----	9	0	9
2783	TTMASGGGAPMADN	-----TTMASGGGAPMADN___	5	0	5
2783	PAAPSGVGPNTMAA	PAAPSGVGPNTMAA_____	5	0	5
2783	APSGVGPNTMAAGG	___APSGVGPNTMAAGG_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
___AAPSGVGPNTMAAG_____	X43545	AAV8-VP1	194	14aa	mRNA_30cpc_Organoid_MD114	10
___AAVGPTTMAAGGGA_____	X87907	AAV1-VP1	196	14aaG4S	mRNA_30cpc_Organoid_MD114	10
___AAVGPTTMAAGGGA_____	X87907	AAV6-VP1	196	14aaG4S	mRNA_30cpc_Organoid_MD114	10
___APSGVGPNTMAAGG_____	X41614	AAV8-VP1	195	14aa	mRNA_3000cpc_Organoid_MD101	5
___GVGPNTMAAGGGAP_____	X64974	AAV8-VP1	198	14aa	mRNA_30cpc_Organoid_MD114	10
PAAPSGVGPNTMAA_____	X23600	AAV8-VP1	193	14aa	mRNA_3000cpc_Organoid_MD101	5
___PSGVGPNTMAAGGGAPMADNNE	X21320	AAV1-VP1	195	22aa	mRNA_30cpc_Organoid_MD114	10
___PSGVGPNTMAAGGGAPMADNNE	X21320	AAV6-VP1	195	22aa	mRNA_30cpc_Organoid_MD114	10
___PSGVGPNTMAAGGGAPMADNNE	X21320	AAV8-VP1	196	22aa	mRNA_30cpc_Organoid_MD114	10
___SGVGPNTMAAGGGA_____	X13360	AAV8-VP1	197	14aa	mRNA_3000cpc_Organoid_MD101	9
___TTMASGGGAPMADN___	X5996	AAV1-VP1	201	14aa	mRNA_3000cpc_Organoid_MD101	5
___TTMASGGGAPMADN___	X5996	AAV6-VP1	201	14aa	mRNA_3000cpc_Organoid_MD101	5
___TTMASGGGAPMADN___	X5996	AAV8-VP1	202	14aa	mRNA_3000cpc_Organoid_MD101	5
___TTMASGGGAPMADN___	X5996	AAV9-VP1	202	14aa	mRNA_3000cpc_Organoid_MD101	5
___VGPNTMAAGGGAPM_____	X69003	AAV8-VP1	199	14aa	mRNA_30cpc_Organoid_MD114	20
___VGPNTMAAGGGAPM_____	X69003	AAV8-VP1	199	14aa	mRNA_3000cpc_Organoid_MD101	6

[1] 2598

Peptide DINNDIISDISGFN from TeNT-Hc with cluster number 2598



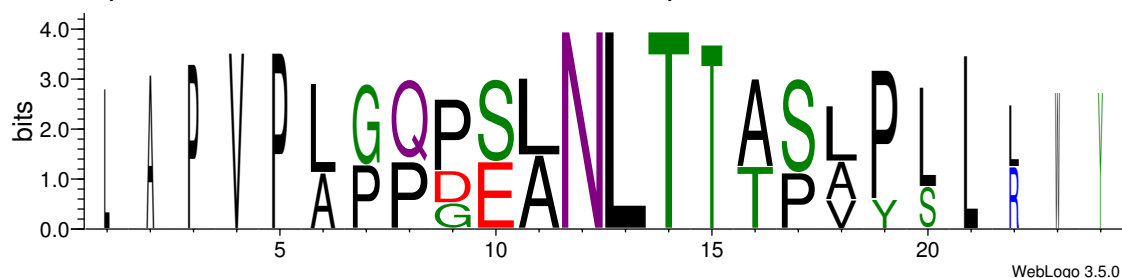
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2598	DINNDIISDISGFN	88	50	38

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2598	GSDVIFNDIGNGQF	__GSDVIFNDIGNGQF_____	20	10	10
2598	DINNDIISDISGFN	____DINNDIISDISGFN_____	20	20	0
2598	INNDIISDISGFNSSVITYPDA	____INNDIISDISGFNSSVITYPDA	18	10	8
2598	NVGSDVIFNDIGNG	NVGSDVIFNDIGNG_____	17	10	7
2598	DVIFNDIGNGQFKL	____DVIFNDIGNGQFKL_____	8	0	8
2598	TILNLDINNDIISDISGFNSSV	TILNLDINNDIISDISGFNSSV_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
____DINNDIISDISGFN_____	X34449	TeNT-Hc	27	14aa	mRNA_30cpc_Organoid_MD114	20
____DVIFNDIGNGQFKL_____	X36259	BoNT-G-Hc	29	14aa	mRNA_3000cpc_Organoid_MD101	8
__GSDVIFNDIGNGQF_____	X61902	BoNT-G-Hc	27	14aa	mRNA_30cpc_Organoid_MD114	10
__GSDVIFNDIGNGQF_____	X61902	BoNT-G-Hc	27	14aa	mRNA_3000cpc_Organoid_MD101	10
____INNDIISDISGFNSSVITYPDA	X14169	TeNT-Hc	28	22aa	mRNA_30cpc_Organoid_MD114	10
____INNDIISDISGFNSSVITYPDA	X14169	TeNT-Hc	28	22aa	mRNA_3000cpc_Organoid_MD101	8
NVGSDVIFNDIGNG_____	X45919	BoNT-G-Hc	25	14aaA5	mRNA_30cpc_Organoid_MD114	10
NVGSDVIFNDIGNG_____	X45919	BoNT-G-Hc	25	14aaA5	mRNA_3000cpc_Organoid_MD101	7
TILNLDINNDIISDISGFNSSV_____	X6634	TeNT-Hc	22	22aa	mRNA_3000cpc_Organoid_MD101	5

Peptide APPGELNLTTASVP from HSV-1-pUL22 with cluster number 2182

Peptide APPGELNLTTASVP from HSV-1-pUL22 with cluster number 2182



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2182	APPGELNLTTASVP	86	30	56

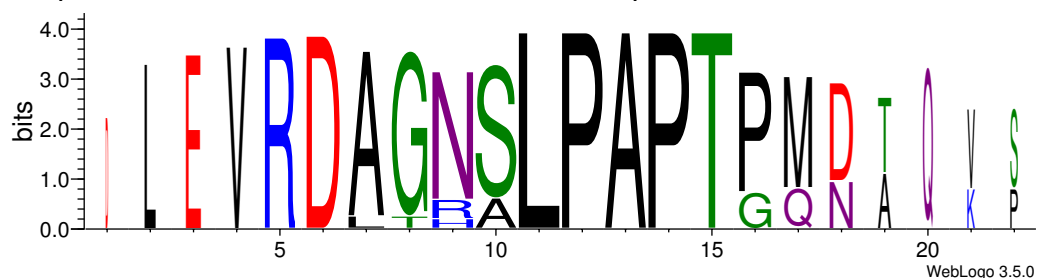
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2182	APPGELNLTTASVP	____APPGELNLTTASVP____	15	10	5
2182	LAPVPLGQPSANLT	LAPVPLGQPSANLT_____	11	0	11
2182	VPLGQPSANLTTPA	___VPLGQPSANLT_TPA_____	10	0	10
2182	QPSANLTTPAYSL	_______QPSANLT_TPAYSL___	10	10	0
2182	LNLTASLPLLRWY	_______LNLTASLPLLRWY____	10	10	0
2182	PDELNLTTASLPL	_______PDELNLTTASLPL____	9	0	9
2182	PVPLGQPSANLTTP	___PVPLGQPSANLT_TP_____	6	0	6
2182	PPDELNLTTASLPL	_______PPDELNLTTASLPL____	5	0	5
2182	APVPLGQPSANLTT	_APVPLGQPSANLT_T_____	5	0	5
2182	APPDELNLTTASLP	_______APPDELNLTTASLP____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
____APPDELNLTTASLP____	X41723	HSV-1-pUL22	67	14aa	mRNA_3000cpc_Organoid_MD101	5
____APPDELNLTTASLP____	X41723	HSV-2-pUL22	67	14aa	mRNA_3000cpc_Organoid_MD101	5
____APPGELNLTTASVP____	X56090	HSV-1-pUL22	67	14aaA5	mRNA_30cpc_Organoid_MD114	10
____APPGELNLTTASVP____	X56090	HSV-2-pUL22	67	14aaA5	mRNA_30cpc_Organoid_MD114	10
____APPGELNLTTASVP____	X41744	HSV-1-pUL22	67	14aa	mRNA_3000cpc_Organoid_MD101	5
____APPGELNLTTASVP____	X41744	HSV-2-pUL22	67	14aa	mRNA_3000cpc_Organoid_MD101	5
_APVPLGQPSANLT_T_____	X41962	HSV-1-pUL37	206	14aa	mRNA_3000cpc_Organoid_MD101	5
LAPVPLGQPSANLT_____	X31942	HSV-1-pUL37	205	14aa	mRNA_3000cpc_Organoid_MD101	5
LAPVPLGQPSANLT_____	X53552	HSV-1-pUL37	205	14aaA5	mRNA_3000cpc_Organoid_MD101	6
_______LNLTASLPLLRWY____	X28419	HSV-1-pUL22	72	14aa	mRNA_30cpc_Organoid_MD114	10
_______LNLTASLPLLRWY____	X28419	HSV-2-pUL22	72	14aa	mRNA_30cpc_Organoid_MD114	10
_______PDELNLTTASLPL____	X22994	HSV-1-pUL22	69	14aa	mRNA_3000cpc_Organoid_MD101	9
_______PDELNLTTASLPL____	X22994	HSV-2-pUL22	69	14aa	mRNA_3000cpc_Organoid_MD101	9
_______PPDELNLTTASLPL____	X22100	HSV-1-pUL22	68	14aa	mRNA_3000cpc_Organoid_MD101	5
_______PPDELNLTTASLPL____	X22100	HSV-2-pUL22	68	14aa	mRNA_3000cpc_Organoid_MD101	5
___PVPLGQPSANLT_TP_____	X24172	HSV-1-pUL37	207	14aa	mRNA_3000cpc_Organoid_MD101	6
_______QPSANLT_TPAYSL___	X19197	HSV-1-pUL37	212	14aa	mRNA_30cpc_Organoid_MD114	10
___VPLGQPSANLT_TPA_____	X67210	HSV-1-pUL37	208	14aa	mRNA_3000cpc_Organoid_MD101	10

[1] 2424

Peptide RDAGNSLPAPTPMD from HSV-1-pUL37 with cluster number 2424

Peptide RDAGNSLPAPTPMD from HSV-1-pUL37 with cluster number 2424



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2424	RDAGNSLPAPTPMD	81	40	41

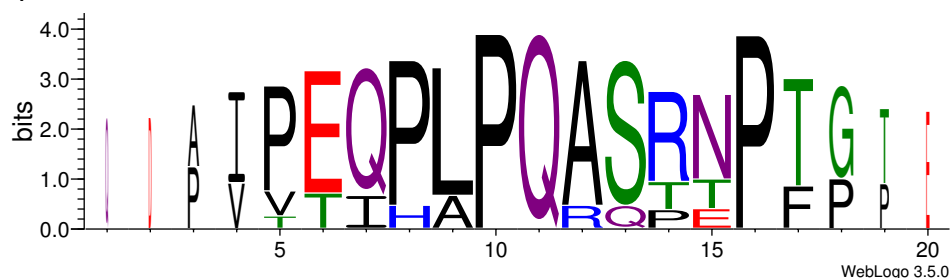
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2424	RDAGNSLPAPTPMD	____RDAGNSLPAPTPMD____	20	10	10
2424	LEVRDAGNSLPAPT	_LEVRDAGNSLPAPT_____	17	10	7
2424	VRDAGNSLPAPTPM	___VRDAGNSLPAPTPM_____	10	10	0
2424	RALPAPTGGNTQVS	____RALPAPTGGNTQVS_____	10	10	0
2424	EVRDAGNSLPAPTP	__EVRDAGNSLPAPTP_____	8	0	8
2424	DAGNSLPAPTPMDA	____DAGNSLPAPTPMDA_____	6	0	6
2424	LTHALPAPTGGNTQ	____LTHALPAPTGGNTQ____	5	0	5
2424	DLEVRDAGNSLPAPTPMDAQKP	DLEVRDAGNSLPAPTPMDAQKP	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
____DAGNSLPAPTPMDA____	X35985	HSV-1-pUL37	1062	14aa	mRNA_3000cpc_Organoid_MD101	6
DLEVRDAGNSLPAPTPMDAQKP	X35377	HSV-1-pUL37	1057	22aa	mRNA_3000cpc_Organoid_MD101	5
__EVRDAGNSLPAPTP_____	X39316	HSV-1-pUL37	1059	14aa	mRNA_3000cpc_Organoid_MD101	8
_LEVRDAGNSLPAPT_____	X31743	HSV-1-pUL37	1058	14aa	mRNA_30cpc_Organoid_MD114	10
_LEVRDAGNSLPAPT_____	X31743	HSV-1-pUL37	1058	14aa	mRNA_3000cpc_Organoid_MD101	7
____LTHALPAPTGGNTQ____	X28893	EV71-VP1-1095-Japan-97	20	14aa	mRNA_3000cpc_Organoid_MD101	5
____LTHALPAPTGGNTQ____	X28893	EV71-VP1-FY23	20	14aa	mRNA_3000cpc_Organoid_MD101	5
____LTHALPAPTGGNTQ____	X28893	EV71-VP1-cx2011-016	20	14aa	mRNA_3000cpc_Organoid_MD101	5
____RALPAPTGGNTQVS_____	X27174	EV71-VP1-1095-Japan-97	22	14aa	mRNA_30cpc_Organoid_MD114	10
____RALPAPTGGNTQVS_____	X27174	EV71-VP1-FY23	22	14aa	mRNA_30cpc_Organoid_MD114	10
____RALPAPTGGNTQVS_____	X27174	EV71-VP1-cx2011-016	22	14aa	mRNA_30cpc_Organoid_MD114	10
____RDAGNSLPAPTPMD_____	X26767	HSV-1-pUL37	1061	14aa	mRNA_30cpc_Organoid_MD114	10
____RDAGNSLPAPTPMD_____	X26767	HSV-1-pUL37	1061	14aa	mRNA_3000cpc_Organoid_MD101	10
____VRDAGNSLPAPTPM_____	X67519	HSV-1-pUL37	1060	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2791

Peptide PEQPLPQASRNPTG from HIV-tat-GR17 with cluster number 2791

peptide PEQPLPQASRNPTG from HIV-tat-GR17 with cluster number 2791



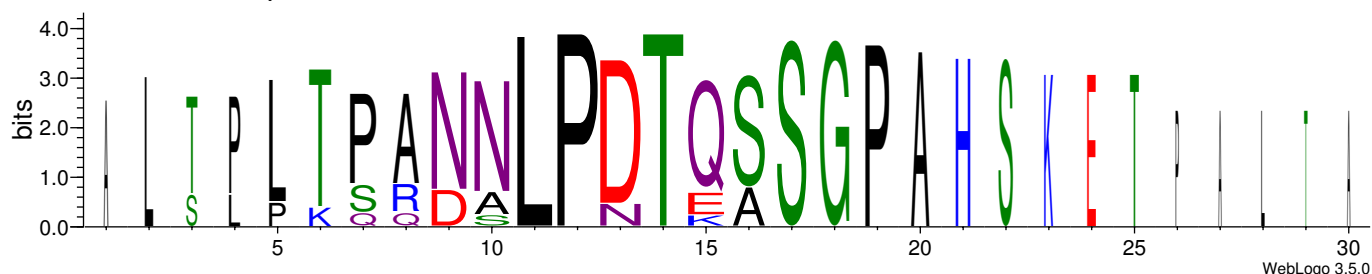
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2791	PEQPLPQASRNPTG	73	40	33

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2791	PEQPLPQASRNPTG	___PEQPLPQASRNPTG__	22	10	12
2791	TIPAPQASTTTPFPT	____TIPAPQASTTTPFPT_	10	10	0
2791	IPEQPLPQASRNPT	___IPEQPLPQASRNPT___	10	10	0
2791	AVVEQHLPQRQPEP	__AVVEQHLPQRQPEP____	10	10	0
2791	QPLPQASRNPTGPE	____QPLPQASRNPTGPE	6	0	6
2791	TTIPAPQASTTTPFP	____TTIPAPQASTTTPFP__	5	0	5
2791	QDPIPEQPLPQASR	QDPIPEQPLPQASR_____	5	0	5
2791	PIPEQPLPQASRNP	__PIPEQPLPQASRNP____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
__AVVEQHLPQRQPEP____	X56833	HSV-2-pUS8	379	14aaA5	mRNA_30cpc_Organoid_MD114	10
___IPEQPLPQASRNPT___	X15454	HIV-tat-GR17	69	14aa	mRNA_30cpc_Organoid_MD114	10
____PEQPLPQASRNPTG__	X23115	HIV-tat-GR17	70	14aa	mRNA_30cpc_Organoid_MD114	10
____PEQPLPQASRNPTG__	X23115	HIV-tat-GR17	70	14aa	mRNA_3000cpc_Organoid_MD101	5
____PEQPLPQASRNPTG__	X51225	HIV-tat-GR17	70	14aaA5	mRNA_3000cpc_Organoid_MD101	7
__PIPEQPLPQASRNP____	X21435	HIV-tat-GR17	68	14aa	mRNA_3000cpc_Organoid_MD101	5
QDPIPEQPLPQASR_____	X19677	HIV-tat-GR17	66	14aa	mRNA_3000cpc_Organoid_MD101	5
____QPLPQASRNPTGPE	X19276	HIV-tat-GR17	72	14aa	mRNA_3000cpc_Organoid_MD101	6
____TIPAPQASTTTPFPT_	X6623	HSV-1-pUS7	220	14aa	mRNA_30cpc_Organoid_MD114	10
____TTIPAPQASTTTPFP__	X5986	HSV-1-pUS7	219	14aa	mRNA_3000cpc_Organoid_MD101	5

Peptide LTPANNLPDTQSSG from PV2-VP1 with cluster number 2628

Peptide LTPANNLPDTQSSG from PV2-VP1 with cluster number 2628



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2628	LTPANNLPDTQSSG	73	30	43

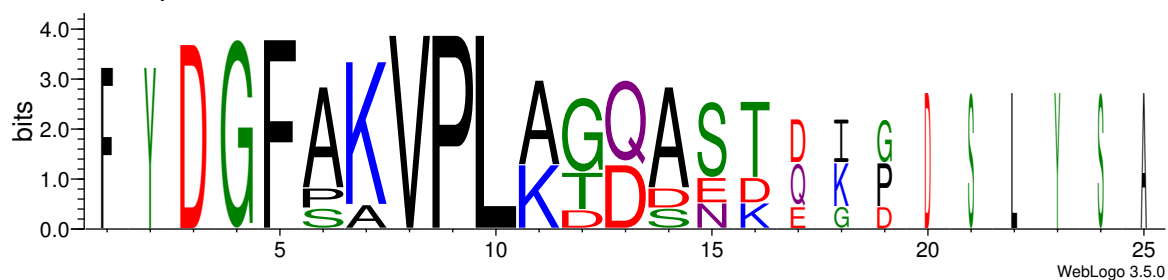
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2628	TSRDALPNTASGP	____TSRDALPNTASGP_____	10	10	0
2628	PDTQSSGPAHSKET	____PDTQSSGPAHSKET_____	10	10	0
2628	NNLPDTQSSGPAHS	____NNLPDTQSSGPAHS_____	10	10	0
2628	LTPANNLPDTQSSG	____LTPANNLPDTQSSG_____	10	0	10
2628	ALTPLTPANNLPDT	ALTPLTPANNLPDT_____	8	0	8
2628	PANNLPDTQSSGPA	____PANNLPDTQSSGPA_____	7	0	7
2628	LTPLTPANNLPDTQ	____LTPLTPANNLPDTQ_____	7	0	7
2628	NNLPDTQSSGPAHSKETPALTA	____NNLPDTQSSGPAHSKETPALTA_____	6	0	6
2628	SLPKQQDSLPTKA	____SLPKQQDSLPTKA_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
ALTPLTPANNLPDT_____	X42333	PV2-VP1	17	14aa	mRNA_3000cpc_Organoid_MD101	8
____LTPANNLPDTQSSG_____	X28917	PV2-VP1	21	14aa	mRNA_3000cpc_Organoid_MD101	10
____LTPLTPANNLPDTQ_____	X28902	PV2-VP1	18	14aa	mRNA_3000cpc_Organoid_MD101	7
____NNLPDTQSSGPAHS_____	X142	PV2-VP1	25	14aa	mRNA_30cpc_Organoid_MD114	10
____NNLPDTQSSGPAHSKETPALTA_____	X141	PV2-VP1	25	22aa	mRNA_3000cpc_Organoid_MD101	6
____PANNLPDTQSSGPA_____	X23293	PV2-VP1	23	14aa	mRNA_3000cpc_Organoid_MD101	7
____PDTQSSGPAHSKET_____	X22894	PV2-VP1	28	14aa	mRNA_30cpc_Organoid_MD114	10
____SLPKQQDSLPTKA_____	X12153	PV3-VP1	595	14aa	mRNA_3000cpc_Organoid_MD101	5
____TSRDALPNTASGP_____	X6352	PV1-VP1	22	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2650

Peptide DGFAKVPLAGQAST from PV2-VP1 with cluster number 2650

Peptide DGFAKVPLAGQAST from PV2-VP1 with cluster number 2650



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2650	DGFAKVPLAGQAST	70	60	10

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2650	DGFAKVPLAGQAST	__DGFAKVPLAGQAST_____	25	20	5
2650	PAVPLAGDDEKDKP	____PAVPLAGDDEKDKP_____	10	10	0
2650	GFAKVPLKTDANDQIGDSLYSA	___GFAKVPLKTDANDQIGDSLYSA	10	10	0
2650	FYDGFSAKVPLKDKS	FYDGFSAKVPLKDKS_____	10	10	0
2650	FYDGFSAKVPLKTD	FYDGFSAKVPLKTD_____	10	10	0
2650	AKVPLAGQASTEGD	____AKVPLAGQASTEGD_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
____AKVPLAGQASTEGD_____	X40095	PV2-VP1	213	14aa	mRNA_3000cpc_Organoid_MD101	5
__DGFAKVPLAGQAST_____	X36211	PV2-VP1	210	14aa	mRNA_30cpc_Organoid_MD114	20
__DGFAKVPLAGQAST_____	X36211	PV2-VP1	210	14aa	mRNA_3000cpc_Organoid_MD101	5
FYDGFSAKVPLKDKS_____	X60984	PV3-VP1	784	14aaA5	mRNA_30cpc_Organoid_MD114	10
FYDGFSAKVPLKDKS_____	X76306	PV1-VP1	208	14aa	mRNA_30cpc_Organoid_MD114	10
___GFAKVPLKTDANDQIGDSLYSA	X65528	PV3-VP1	787	22aa	mRNA_30cpc_Organoid_MD114	10
____PAVPLAGDDEKDKP_____	X23690	HSV-1-pUS4	110	14aa	mRNA_30cpc_Organoid_MD114	10

Peptide AVGLLVLAGLVAAF from HSV-1-pUL27 with cluster number 2829

Peptide AVGLLVLAGLVAAF from HSV-1-pUL27 with cluster number 2829



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2829	AVGLLVLAGLVAAF	67	60	7

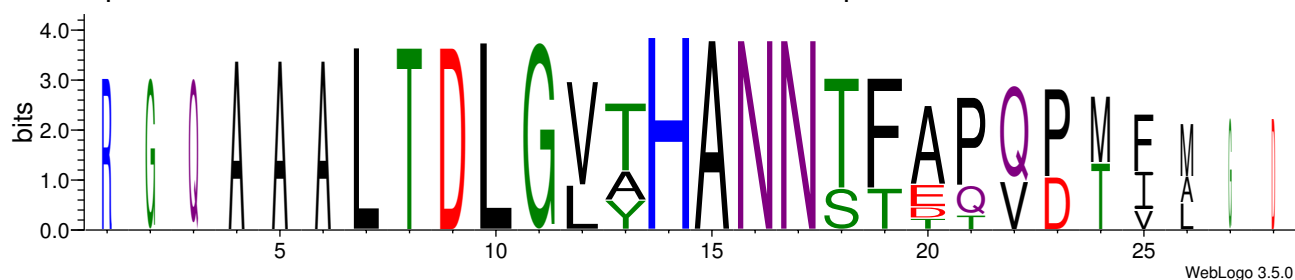
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2829	QTGVRVALALVAAFALAMAVLR	QTGVRVALALVAAFALAMAVLR__	10	10	0
2829	QTGVRVALALVAAF	QTGVRVALALVAAF_____	10	10	0
2829	ICALVVGALVAASAAAPA	_ICALVVGALVAASAAAPA_	10	10	0
2829	GLLVLAGLVAAFFAFRYVLQLQ	__GLLVLAGLVAAFFAFRYVLQLQ	10	10	0
2829	GLLVLAGLVAAFFA	__GLLVLAGLVAAFFA_____	10	10	0
2829	AVGLLVLAGLVAAF	AVGLLVLAGLVAAF_____	10	10	0
2829	NENDVLVALVASSP	_NENDVLVALVASSP_____	7	0	7

alignment	LUThrs	GeneName	start	structure	Group	Score
AVGLLVLAGLVAAF_____	X44643	HSV-1-pUL27	779	14aa	mRNA_30cpc_Organoid_MD114	10
AVGLLVLAGLVAAF_____	X44643	HSV-2-pUL27	776	14aa	mRNA_30cpc_Organoid_MD114	10
__GLLVLAGLVAAFFA_____	X57542	HSV-1-pUL27	781	14aaA5	mRNA_30cpc_Organoid_MD114	10
__GLLVLAGLVAAFFA_____	X57542	HSV-2-pUL27	778	14aaA5	mRNA_30cpc_Organoid_MD114	10
__GLLVLAGLVAAFFAFRYVLQLQ	X63279	HSV-1-pUL27	781	22aa	mRNA_30cpc_Organoid_MD114	10
__GLLVLAGLVAAFFAFRYVLQLQ	X63279	HSV-2-pUL27	778	22aa	mRNA_30cpc_Organoid_MD114	10
ICALVVGALVAASAAAPA	X16834	HSV-2-pUL27	7	22aa	mRNA_30cpc_Organoid_MD114	10
_NENDVLVALVASSP_____	X45739	HSV-1-pUL36	2098	14aaA5	mRNA_3000cpc_Organoid_MD101	7
QTGVRVALALVAAF_____	X50108	HSV-1-pUL10	319	14aaA5	mRNA_30cpc_Organoid_MD114	10
QTGVRVALALVAAF_____	X50108	HSV-2-pUL10	319	14aaA5	mRNA_30cpc_Organoid_MD114	10
QTGVRVALALVAAFALAMAVLR__	X18706	HSV-1-pUL10	319	22aa	mRNA_30cpc_Organoid_MD114	10
QTGVRVALALVAAFALAMAVLR__	X18706	HSV-2-pUL10	319	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2012

Peptide AAALTDLGVTHANNTFAPQPMF from HSV-1-pUL35 with cluster number 2012

Peptide AAALTDLGVTHANNTFAPQPMF from HSV-1-pUL35 with cluster number 2012



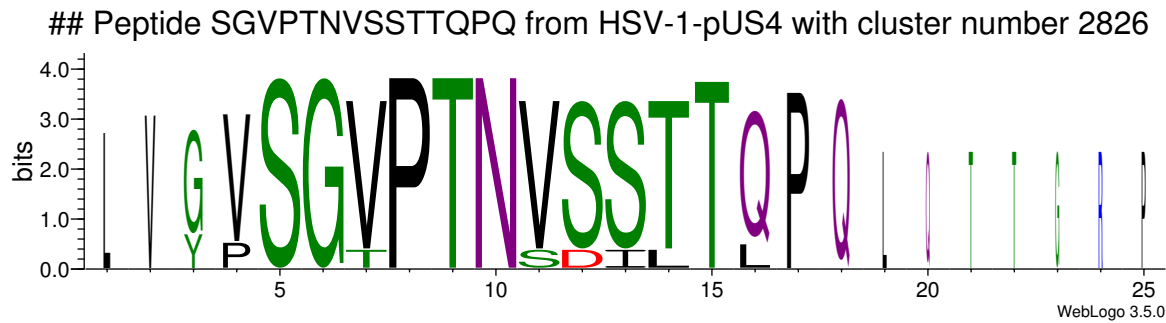
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2012	AAALTDLGVTHANNTFAPQPMF	65	40	25

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2012	YHANNSTEQVDTIM	-----YHANNSTEQVDTIM--	10	10	0
2012	RGQAAALTDLGLAH	RGQAAALTDLGLAH-----	10	10	0
2012	LGVTHANNTFAPQP	-----LGVTHANNTFAPQP--	10	10	0
2012	AAALTDLGVTHANNTFAPQPMF	___AAALTDLGVTHANNTFAPQPMF___	10	10	0
2012	YHANNSTDIVDTVL	-----YHANNSTDIVDTVL--	5	0	5
2012	RGQAAALTDLGVTHANNTFAPQ	RGQAAALTDLGVTHANNTFAPQ-----	5	0	5
2012	LTDLGVTHANNTFAPQPMFAGD	-----LTDLGVTHANNTFAPQPMFAGD-----	5	0	5
2012	LTDLGVTHANNTFA	-----LTDLGVTHANNTFA-----	5	0	5
2012	LTDLGLAHANNTFT	-----LTDLGLAHANNTFT-----	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
___AAALTDLGVTHANNTFAPQPMF___	X43752	HSV-1-pUL35	58	22aa	mRNA_30cpc_Organoid_MD114	10
___AAALTDLGVTHANNTFAPQPMF___	X43752	HSV-2-pUL34	58	22aa	mRNA_30cpc_Organoid_MD114	10
-----LGVTHANNTFAPQP-----	X32656	HSV-2-pUL34	64	14aa	mRNA_30cpc_Organoid_MD114	10
-----LTDLGLAHANNTFT-----	X28986	HSV-1-pUL35	61	14aa	mRNA_3000cpc_Organoid_MD101	5
-----LTDLGVTHANNTFA-----	X52773	HSV-2-pUL34	61	14aaA5	mRNA_3000cpc_Organoid_MD101	5
-----LTDLGVTHANNTFAPQPMFAGD-----	X28987	HSV-1-pUL35	61	22aa	mRNA_3000cpc_Organoid_MD101	5
-----LTDLGVTHANNTFAPQPMFAGD-----	X28987	HSV-2-pUL34	61	22aa	mRNA_3000cpc_Organoid_MD101	5
RGQAAALTDLGLAH-----	X27444	HSV-1-pUL35	55	14aa	mRNA_30cpc_Organoid_MD114	10
RGQAAALTDLGLAH-----	X27444	HSV-2-pUL34	55	14aa	mRNA_30cpc_Organoid_MD114	10
RGQAAALTDLGVTHANNTFAPQ-----	X27447	HSV-1-pUL35	55	22aa	mRNA_3000cpc_Organoid_MD101	5
RGQAAALTDLGVTHANNTFAPQ-----	X27447	HSV-2-pUL34	55	22aa	mRNA_3000cpc_Organoid_MD101	5
-----YHANNSTDIVDTVL--	X70760	H1N1-HA	24	14aa	mRNA_3000cpc_Organoid_MD101	5
-----YHANNSTEQVDTIM--	X70763	H2N2-HA	22	14aa	mRNA_30cpc_Organoid_MD114	10
-----YHANNSTEQVDTIM--	X70763	H5N1-HA	23	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2826

Peptide SGVPTNVSSTTQPQ from HSV-1-pUS4 with cluster number 2826



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2826	SGVPTNVSSTTQPQ	61	30	31

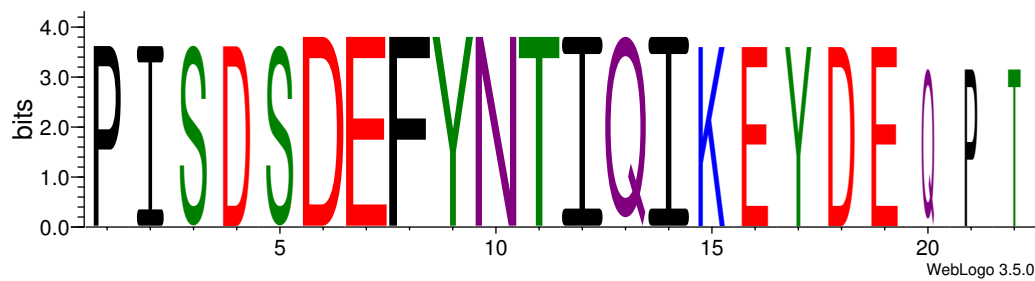
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2826	SGVPTNVSSTTQPQ	___SGVPTNVSSTTQPQ_____	20	20	0
2826	LVGVSGVPTNVSST	LVGVSGVPTNVSST_____	10	10	0
2826	YPSGTPTNSDILTL	__YPSGTPTNSDILTL_____	7	0	7
2826	VSGVPTNVSSTTQP	___VSGVPTNVSSTTQP_____	7	0	7
2826	VSGVPTNVSSTTQQLQTTGRP	___VSGVPTNVSSTTQQLQTTGRP	6	0	6
2826	VGVSGVPTNVSSTT	_VGVSGVPTNVSSTT_____	6	0	6
2826	GVSGVPTNVSSTTQ	__GVSGVPTNVSSTTQ_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
__GVSGVPTNVSSTTQ_____	X64803	HSV-1-pUS4	21	14aa	mRNA_3000cpc_Organoid_MD101	5
LVGVSGVPTNVSST_____	X33077	HSV-1-pUS4	19	14aa	mRNA_30cpc_Organoid_MD114	10
___SGVPTNVSSTTQPQ_____	X13347	HSV-1-pUS4	23	14aa	mRNA_30cpc_Organoid_MD114	20
_VGVSGVPTNVSSTT_____	X69188	HSV-1-pUS4	20	14aa	mRNA_3000cpc_Organoid_MD101	6
___VSGVPTNVSSTTQP_____	X66506	HSV-1-pUS4	22	14aa	mRNA_3000cpc_Organoid_MD101	7
___VSGVPTNVSSTTQQLQTTGRP	X66505	HSV-1-pUS4	22	22aa	mRNA_3000cpc_Organoid_MD101	6
__YPSGTPTNSDILTL_____	X70871	TMEV-VP3	198	14aa	mRNA_3000cpc_Organoid_MD101	7

[1] 2579

Peptide PISDSDEFYNTIQI from BoNT-B-Hc with cluster number 2579

Peptide PISDSDEFYNTIQI from BoNT-B-Hc with cluster number 2579



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2579	PISDSDEFYNTIQI	59	40	19

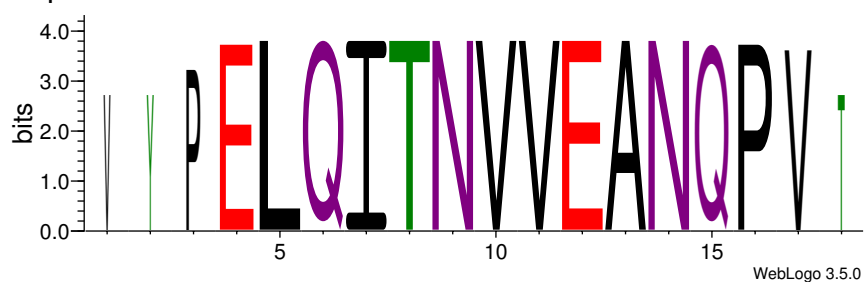
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2579	PISDSDEFYNTIQI	PISDSDEFYNTIQI_____	21	10	11
2579	DEFYNTIQIKEYDE	____DEFYNTIQIKEYDE__	20	20	0
2579	PISDSDEFYNTIQIKEYDEQPT	PISDSDEFYNTIQIKEYDEQPT	18	10	8

alignment	LUThrs	GeneName	start	structure	Group	Score
____DEFYNTIQIKEYDE__	X35767	BoNT-B-Hc	378	14aa	mRNA_30cpc_Organoid_MD114	20
PISDSDEFYNTIQI_____	X21416	BoNT-B-Hc	373	14aa	mRNA_30cpc_Organoid_MD114	10
PISDSDEFYNTIQI_____	X50793	BoNT-B-Hc	373	14aaA5	mRNA_3000cpc_Organoid_MD101	11
PISDSDEFYNTIQIKEYDEQPT	X21415	BoNT-B-Hc	373	22aa	mRNA_30cpc_Organoid_MD114	10
PISDSDEFYNTIQIKEYDEQPT	X21415	BoNT-B-Hc	373	22aa	mRNA_3000cpc_Organoid_MD101	8

[1] 2551

Peptide ELQITNVVEANQPV from APP with cluster number 2551

Peptide ELQITNVVEANQPV from APP with cluster number 25



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2551	ELQITNVVEANQPV	59	50	9

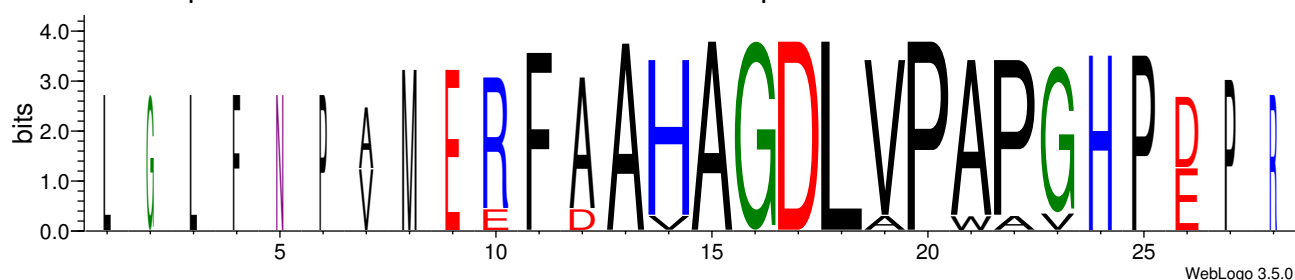
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2551	ELQITNVVEANQPV	___ELQITNVVEANQPV_	29	20	9
2551	VYPELQITNVVEAN	VYPELQITNVVEAN_____	10	10	0
2551	PELQITNVVEANQP	__PELQITNVVEANQP__	10	10	0
2551	LQITNVVEANQPVT	____LQITNVVEANQPVT	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
___ELQITNVVEANQPV_	X38162	APP	79	14aa	mRNA_30cpc_Organoid_MD114	10
___ELQITNVVEANQPV_	X86438	APP	79	14aaG4S	mRNA_30cpc_Organoid_MD114	10
___ELQITNVVEANQPV_	X38162	APP	79	14aa	mRNA_3000cpc_Organoid_MD101	9
____LQITNVVEANQPVT	X29973	APP	80	14aa	mRNA_30cpc_Organoid_MD114	10
__PELQITNVVEANQP__	X23144	APP	78	14aa	mRNA_30cpc_Organoid_MD114	10
VYPELQITNVVEAN_____	X59232	APP	76	14aaA5	mRNA_30cpc_Organoid_MD114	10

[1] 2831

Peptide AHAGDLVPAPGHPE from HSV-1-pUL19 with cluster number 2831

Peptide AHAGDLVPAPGHPE from HSV-1-pUL19 with cluster number 2831



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2831	AHAGDLVPAPGHPE	57	40	17

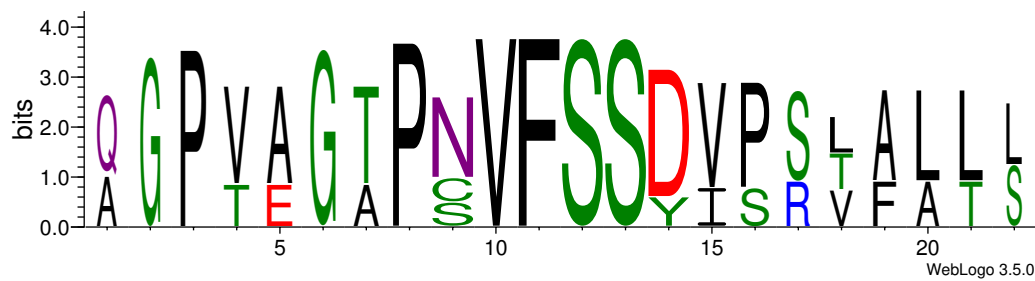
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2831	VMERFAAHAGDLVPAPGHPDPR	-----VMERFAAHAGDLVPAPGHPDPR	10	10	0
2831	RFAAHAGDLVPAPG	-----RFAAHAGDLVPAPG-----	10	10	0
2831	LGLFNPAMERFAAHAGDLVPAP	LGLFNPAMERFAAHAGDLVPAP-----	10	10	0
2831	AHAGDLVPAPGHPE	-----AHAGDLVPAPGHPE-----	10	10	0
2831	AHAGDLVPAPGHPD	-----AHAGDLVPAPGHPD-----	7	0	7
2831	HAGDLVPAPGHPEP	-----HAGDLVPAPGHPEP-----	5	0	5
2831	EFDVAGDLAPWAV	-----EFDVAGDLAPWAV-----	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
-----AHAGDLVPAPGHPD-----	X41345	HSV-1-pUL19	418	14aa	mRNA_3000cpc_Organoid_MD101	7
-----AHAGDLVPAPGHPD-----	X41345	HSV-2-pUL19	418	14aa	mRNA_3000cpc_Organoid_MD101	7
-----AHAGDLVPAPGHPE-----	X55989	HSV-1-pUL19	418	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----AHAGDLVPAPGHPE-----	X55989	HSV-2-pUL19	418	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----EFDVAGDLAPWAV-----	X39707	HSV-1-pUL36	1845	14aa	mRNA_3000cpc_Organoid_MD101	5
-----HAGDLVPAPGHPEP-----	X18063	HSV-1-pUL19	419	14aa	mRNA_3000cpc_Organoid_MD101	5
-----HAGDLVPAPGHPEP-----	X18063	HSV-2-pUL19	419	14aa	mRNA_3000cpc_Organoid_MD101	5
LGLFNPAMERFAAHAGDLVPAP-----	X32520	HSV-1-pUL19	406	22aa	mRNA_30cpc_Organoid_MD114	10
LGLFNPAMERFAAHAGDLVPAP-----	X32520	HSV-2-pUL19	406	22aa	mRNA_30cpc_Organoid_MD114	10
-----RFAAHAGDLVPAPG-----	X28278	HSV-1-pUL19	415	14aa	mRNA_30cpc_Organoid_MD114	10
-----RFAAHAGDLVPAPG-----	X28278	HSV-2-pUL19	415	14aa	mRNA_30cpc_Organoid_MD114	10
-----VMERFAAHAGDLVPAPGHPDPR	X66824	HSV-1-pUL19	412	22aa	mRNA_30cpc_Organoid_MD114	10
-----VMERFAAHAGDLVPAPGHPDPR	X66824	HSV-2-pUL19	412	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2825

Peptide QGPVAGTPNVFSSD from HSV-2-pUL22 with cluster number 2825

Peptide QGPVAGTPNVFSSD from HSV-2-pUL22 with cluster number 2825



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2825	QGPVAGTPNVFSSD	53	40	13

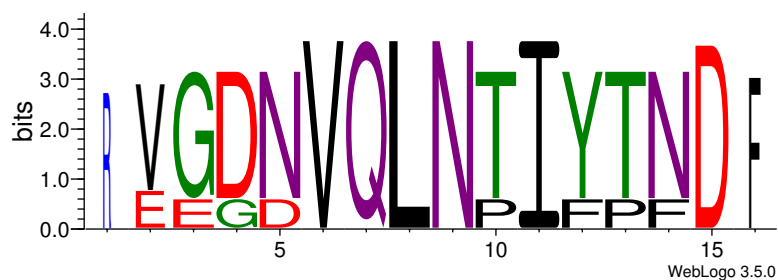
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2825	QGPVAGTPNVFSSD	QGPVAGTPNVFSSD_____	16	10	6
2825	PNVFSSDVPSTALL	_____PNVFSSDVPSTALL	10	10	0
2825	CVFSSYISRLFATS	_____CVFSSYISRLFATS	10	10	0
2825	AGPTEGAPSVFSSDVPSTALL	AGPTEGAPSVFSSDVPSTALL	10	10	0
2825	PVAGTPNVFSSDVP	__PVAGTPNVFSSDVP_____	7	0	7

alignment	LUTnrs	GeneName	start	structure	Group	Score
AGPTEGAPSVFSSDVPSTALL	X44043	HSV-1-pUL22	760	22aa	mRNA_30cpc_Organoid_MD114	10
_____CVFSSYISRLFATS	X73281	HSV-1-pUL16	343	14aa	mRNA_30cpc_Organoid_MD114	10
_____PNVFSSDVPSTALL	X20600	HSV-1-pUL22	767	14aa	mRNA_30cpc_Organoid_MD114	10
_____PNVFSSDVPSTALL	X20600	HSV-2-pUL22	767	14aa	mRNA_30cpc_Organoid_MD114	10
__PVAGTPNVFSSDVP_____	X24297	HSV-2-pUL22	762	14aa	mRNA_3000cpc_Organoid_MD101	7
QGPVAGTPNVFSSD_____	X50456	HSV-2-pUL22	760	14aaA5	mRNA_30cpc_Organoid_MD114	10
QGPVAGTPNVFSSD_____	X50456	HSV-2-pUL22	760	14aaA5	mRNA_3000cpc_Organoid_MD101	6

[1] 2585

Peptide VGDNVQLNTIYTND from BoNT-D-Hc with cluster number 2585

le VGDNVQLNTIYTND from BoNT-D-Hc with cluster num



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2585	VGDNVQLNTIYTND	53	40	13

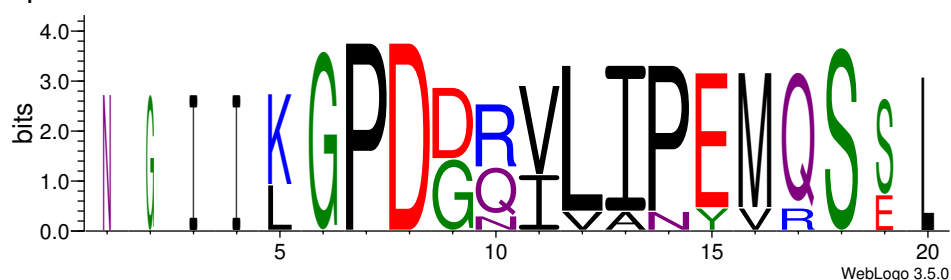
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2585	VGDNVQLNTIYTND	_VGDNVQLNTIYTND_	18	10	8
2585	GDNVQLNTIYTND	__GDNVQLNTIYTND	15	10	5
2585	RVGDNVQLNTIYT	RVGDNVQLNTIYT__	10	10	0
2585	EEGDVQLNPIFPD	_EEGDVQLNPIFPD_	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
EEGDVQLNPIFPD	X38657	BoNT-C-Hc	35	14aa	mRNA_30cpc_Organoid_MD114	10
__GDNVQLNTIYTND	X63483	BoNT-D-Hc	29	14aa	mRNA_30cpc_Organoid_MD114	10
__GDNVQLNTIYTND	X63483	BoNT-D-Hc	29	14aa	mRNA_3000cpc_Organoid_MD101	5
RVGDNVQLNTIYT__	X27836	BoNT-D-Hc	27	14aa	mRNA_30cpc_Organoid_MD114	10
VGDNVQLNTIYTND	X69090	BoNT-D-Hc	28	14aa	mRNA_30cpc_Organoid_MD114	10
VGDNVQLNTIYTND	X69090	BoNT-D-Hc	28	14aa	mRNA_3000cpc_Organoid_MD101	8

[1] 2671

Peptide KGPDPGQILIPMQS from RV-G-Mocala with cluster number 2671

Peptide KGPDPGQILIPMQS from RV-G-Mocala with cluster number 2



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2671	KGPDPGQILIPMQS	52	40	12

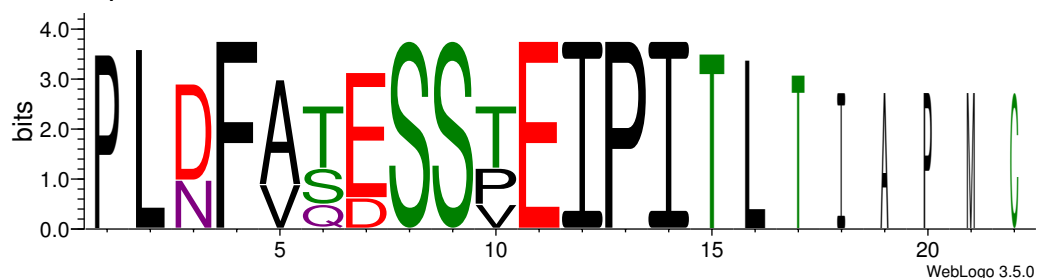
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2671	KGPDPGQILIPMQS	___KGPDPGQILIPMQS__	20	20	0
2671	PDDRVLIPEMQSSL	_____PDDRVLIPEMQSSL	10	10	0
2671	NGIILGPDDRVLIP	NGIILGPDDRVLIP_____	10	10	0
2671	PDDRVVANYVRSEL	_____PDDRVVANYVRSEL	6	0	6
2671	GPDGNVLIPEMQSS	_____GPDGNVLIPEMQSS_	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
_____GPDGNVLIPEMQSS_	X62680	RV-G-B19	366	14aa	mRNA_3000cpc_Organoid_MD101	6
_____GPDGNVLIPEMQSS_	X62680	RV-G-B2c	366	14aa	mRNA_3000cpc_Organoid_MD101	6
_____GPDGNVLIPEMQSS_	X62680	RV-G-N2c	385	14aa	mRNA_3000cpc_Organoid_MD101	6
_____GPDGNVLIPEMQSS_	X62680	RV-G-PV	366	14aa	mRNA_3000cpc_Organoid_MD101	6
___KGPDPGQILIPMQS__	X4926	RV-G-Mocala	365	14aa	mRNA_30cpc_Organoid_MD114	20
NGIILGPDDRVLIP_____	X45853	RV-G-B19	361	14aaA5	mRNA_30cpc_Organoid_MD114	10
NGIILGPDDRVLIP_____	X45853	RV-G-B2c	361	14aaA5	mRNA_30cpc_Organoid_MD114	10
NGIILGPDDRVLIP_____	X45853	RV-G-N2c	380	14aaA5	mRNA_30cpc_Organoid_MD114	10
NGIILGPDDRVLIP_____	X45853	RV-G-PV	361	14aaA5	mRNA_30cpc_Organoid_MD114	10
_____PDDRVLIPEMQSSL	X82482	RV-G-B19	367	14aaG4S	mRNA_30cpc_Organoid_MD114	10
_____PDDRVLIPEMQSSL	X82482	RV-G-B2c	367	14aaG4S	mRNA_30cpc_Organoid_MD114	10
_____PDDRVLIPEMQSSL	X82482	RV-G-N2c	386	14aaG4S	mRNA_30cpc_Organoid_MD114	10
_____PDDRVLIPEMQSSL	X82482	RV-G-PV	367	14aaG4S	mRNA_30cpc_Organoid_MD114	10
_____PDDRVVANYVRSEL	X22978	HSV-1-pUL21	59	14aa	mRNA_3000cpc_Organoid_MD101	6

[1] 2752

Peptide PLDFAQDSSVEIPI from PV3-VP1 with cluster number 2752

Peptide PLDFAQDSSVEIPI from PV3-VP1 with cluster number 2752



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2752	PLDFAQDSSVEIPI	51	30	21

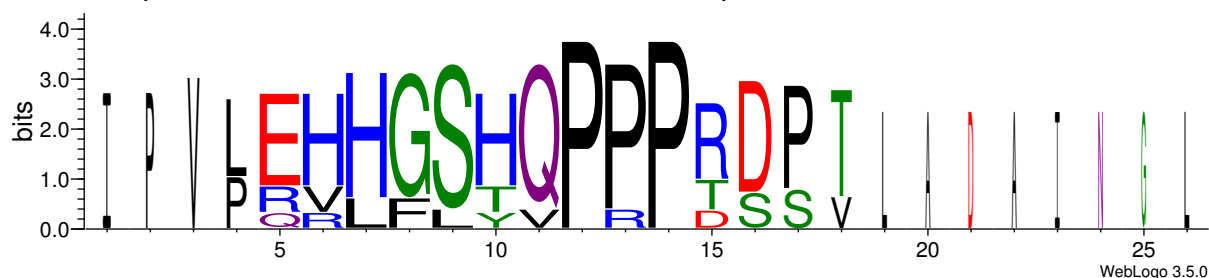
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2752	PLDFATESSTEIPITLTIAPMC	PLDFATESSTEIPITLTIAPMC	10	10	0
2752	PLDFATESSTEIPI	PLDFATESSTEIPI_____	10	10	0
2752	PLDFAQDSSVEIPI	PLDFAQDSSVEIPI_____	10	10	0
2752	NFVSESSPEIPITL	__NFVSESSPEIPITL_____	9	0	9
2752	LNFSSESSPEIPIT	_LNFSSESSPEIPIT_____	6	0	6
2752	FATESSTEIPITLT	___FATESSTEIPITLT_____	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
___FATESSTEIPITLT_____	X75762	PV1-VP2	238	14aa	mRNA_3000cpc_Organoid_MD101	6
___FATESSTEIPITLT_____	X75762	PV2-VP2	238	14aa	mRNA_3000cpc_Organoid_MD101	6
_LNFSSESSPEIPIT_____	X28523	PV1-VP2	236	14aa	mRNA_3000cpc_Organoid_MD101	6
__NFVSESSPEIPITL_____	X2982	PV1-VP2	237	14aa	mRNA_3000cpc_Organoid_MD101	9
PLDFAQDSSVEIPI_____	X82418	PV3-VP1	304	14aaG4S	mRNA_30cpc_Organoid_MD114	10
PLDFATESSTEIPI_____	X22728	PV2-VP2	235	14aa	mRNA_30cpc_Organoid_MD114	10
PLDFATESSTEIPITLTIAPMC	X22727	PV1-VP2	235	22aa	mRNA_30cpc_Organoid_MD114	10
PLDFATESSTEIPITLTIAPMC	X22727	PV2-VP2	235	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2738

Peptide EHHGSHQPPPRDPT from HSV-1-pUL44 with cluster number 2738

Peptide EHHGSHQPPPRDPT from HSV-1-pUL44 with cluster number 2738



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2738	EHHGSHQPPPRDPT	51	40	11

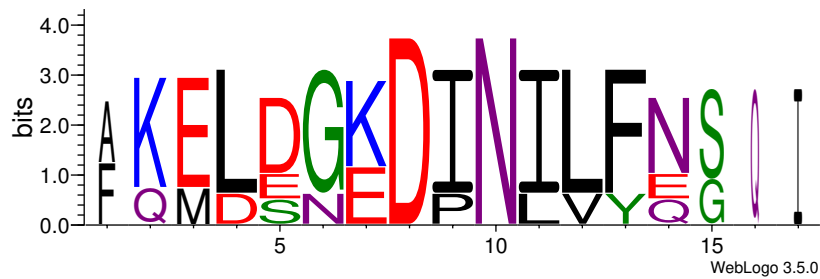
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2738	EHHGSHQPPPRDPT	___EHHGSHQPPPRDPT_____	20	20	0
2738	PRVLFSTQPPPTSS	___PRVLFSTQPPPTSS_____	10	10	0
2738	IPVLEHHGSHQPPP	IPVLEHHGSHQPPP_____	10	10	0
2738	QRHGLYVPRPDDPVLADAINGL	___QRHGLYVPRPDDPVLADAINGL	6	0	6
2738	VLEHHGSHQPPPRD	__VLEHHGSHQPPPRD_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
___EHHGSHQPPPRDPT_____	X54998	HSV-1-pUL44	455	14aaA5	mRNA_30cpc_Organoid_MD114	10
___EHHGSHQPPPRDPT_____	X86288	HSV-1-pUL44	455	14aaG4S	mRNA_30cpc_Organoid_MD114	10
___EHHGSHQPPPRDPT_____	X54998	HSV-2-pUL44	424	14aaA5	mRNA_30cpc_Organoid_MD114	10
___EHHGSHQPPPRDPT_____	X86288	HSV-2-pUL44	424	14aaG4S	mRNA_30cpc_Organoid_MD114	10
IPVLEHHGSHQPPP_____	X80594	HSV-1-pUL44	451	14aaG4S	mRNA_30cpc_Organoid_MD114	10
IPVLEHHGSHQPPP_____	X80594	HSV-2-pUL44	420	14aaG4S	mRNA_30cpc_Organoid_MD114	10
___PRVLFSTQPPPTSS_____	X22500	NGF	67	14aa	mRNA_30cpc_Organoid_MD114	10
___QRHGLYVPRPDDPVLADAINGL	X19358	HSV-1-pUL21	376	22aa	mRNA_3000cpc_Organoid_MD101	6
__VLEHHGSHQPPPRD_____	X67856	HSV-1-pUL44	453	14aa	mRNA_3000cpc_Organoid_MD101	5
__VLEHHGSHQPPPRD_____	X67856	HSV-2-pUL44	422	14aa	mRNA_3000cpc_Organoid_MD101	5

[1] 2803

Peptide KELDGKDINILFNS from BoNT-C-Hc with cluster number 2803

tide KELDGKDINILFNS from BoNT-C-Hc with cluster numbe



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2803	KELDGKDINILFNS	50	40	10

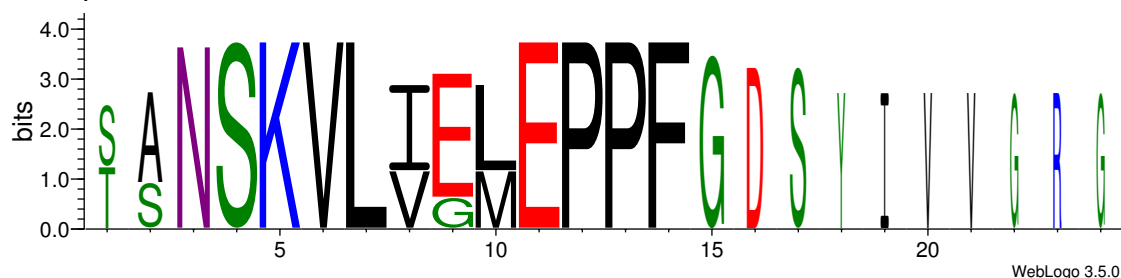
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2803	KELDGKDINILFNS	_KELDGKDINILFNS__	20	20	0
2803	LSNEDINIVYEGQI	___LSNEDINIVYEGQI	10	0	10
2803	FQMDEGEDPNLLFQ	FQMDEGEDPNLLFQ___	10	10	0
2803	AKELDGKDINILFN	AKELDGKDINILFN___	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
AKELDGKDINILFN___	X40071	BoNT-C-Hc	217	14aa	mRNA_30cpc_Organoid_MD114	10
FQMDEGEDPNLLFQ___	X75093	RV-P	81	14aa	mRNA_30cpc_Organoid_MD114	10
_KELDGKDINILFNS__	X4632	BoNT-C-Hc	218	14aa	mRNA_30cpc_Organoid_MD114	20
___LSNEDINIVYEGQI	X29122	BoNT-D-Hc	204	14aa	mRNA_3000cpc_Organoid_MD101	10

[1] 2491

Peptide ANSKVLIELEPPFG from WNV-E-ArD76104 with cluster number 2491

Peptide ANSKVLIELEPPFG from WNV-E-ArD76104 with cluster number 2491



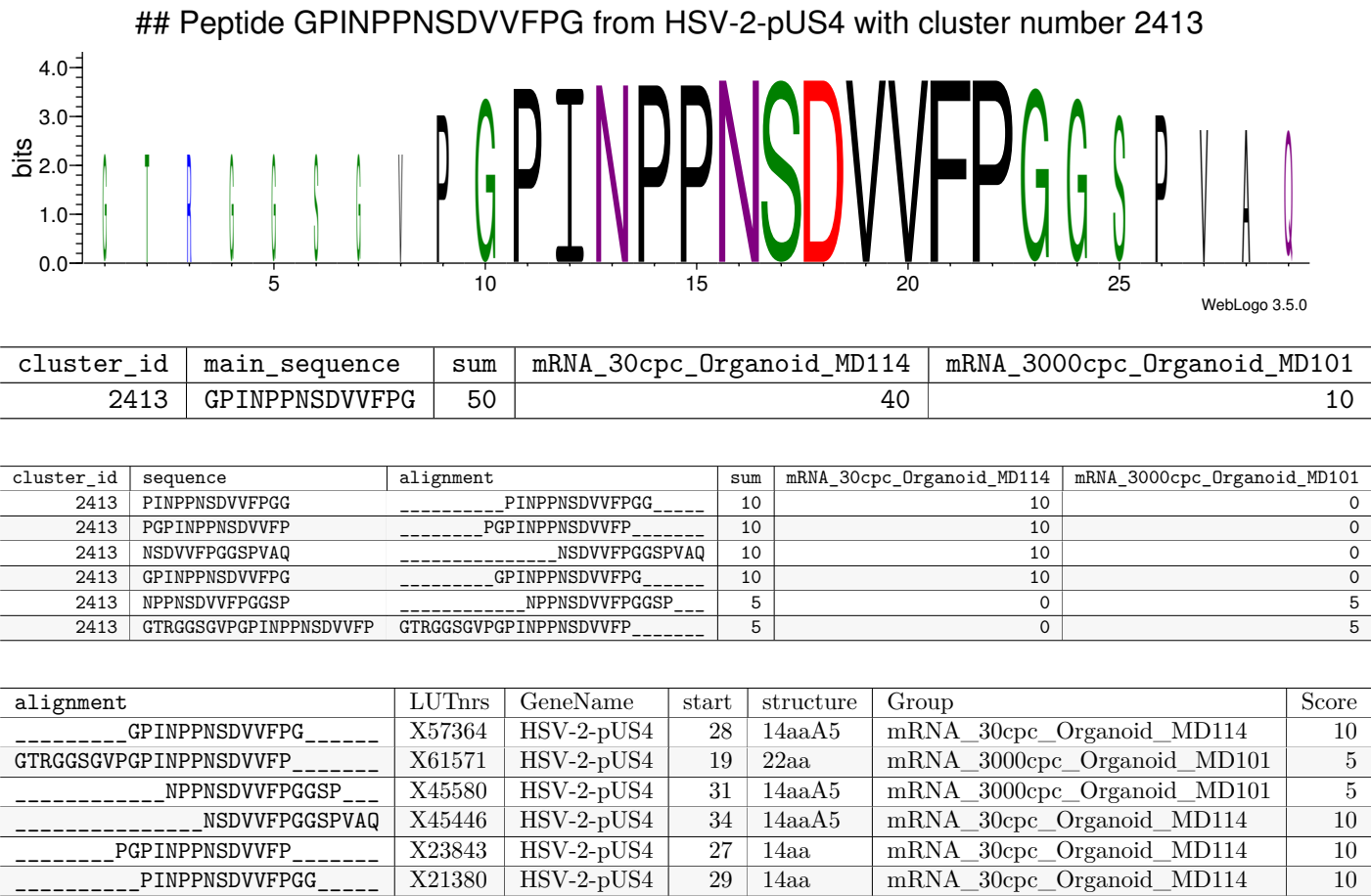
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2491	ANSKVLIELEPPFG	50	50	0

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2491	TANSKVLIELEPPF	TANSKVLIELEPPF_____	10	10	0
2491	SSNSKVLVGMEPPF	SSNSKVLVGMEPPF_____	10	10	0
2491	SKVLVEMEPPFGDS	__SKVLVEMEPPFGDS_____	10	10	0
2491	NSKVLIELEPPFGDSYIVVGRG	__NSKVLIELEPPFGDSYIVVGRG	10	10	0
2491	ANSKVLIELEPPFG	_ANSKVLIELEPPFG_____	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
_ANSKVLIELEPPFG_____	X39811	WNV-E-ArD76104	363	14aa	mRNA_30cpc_Organoid_MD114	10
_ANSKVLIELEPPFG_____	X39811	WNV-E-H-442	367	14aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	JEV-E-BN19	367	22aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	JEV-E-KE-093	367	22aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	JEV-E-SA14-5-3	367	22aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	JEV-E-ThCMAr4492	367	22aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	WNV-E-AZ10-918	368	22aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	WNV-E-ArD76104	364	22aa	mRNA_30cpc_Organoid_MD114	10
__NSKVLIELEPPFGDSYIVVGRG	X594	WNV-E-H-442	368	22aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	JEV-E-BN19	368	14aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	JEV-E-KE-093	368	14aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	JEV-E-SA14-5-3	368	14aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	JEV-E-ThCMAr4492	368	14aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	WNV-E-AZ10-918	369	14aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	WNV-E-ArD76104	365	14aa	mRNA_30cpc_Organoid_MD114	10
___SKVLVEMEPPFGDS_____	X10181	WNV-E-H-442	369	14aa	mRNA_30cpc_Organoid_MD114	10
SSNSKVLVGMEPPF_____	X10547	JEV-E-KE-093	365	14aa	mRNA_30cpc_Organoid_MD114	10
SSNSKVLVGMEPPF_____	X10547	JEV-E-ThCMAr4492	365	14aa	mRNA_30cpc_Organoid_MD114	10
TANSKVLIELEPPF_____	X8387	WNV-E-ArD76104	362	14aa	mRNA_30cpc_Organoid_MD114	10
TANSKVLIELEPPF_____	X8387	WNV-E-H-442	366	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2413

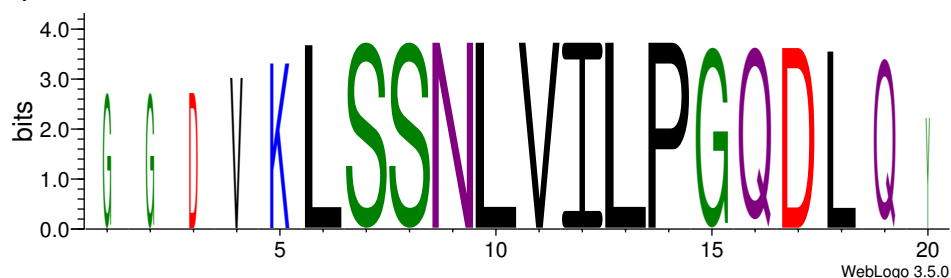
Peptide GPINPPNSDVVFPG from HSV-2-pUS4 with cluster number 2413



[1] 2545

Peptide LSSNLVILPGQDLQ from MV-H-CAM-70 with cluster number 2545

Peptide LSSNLVILPGQDLQ from MV-H-CAM-70 with cluster number 2



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2545	LSSNLVILPGQDLQ	49	20	29

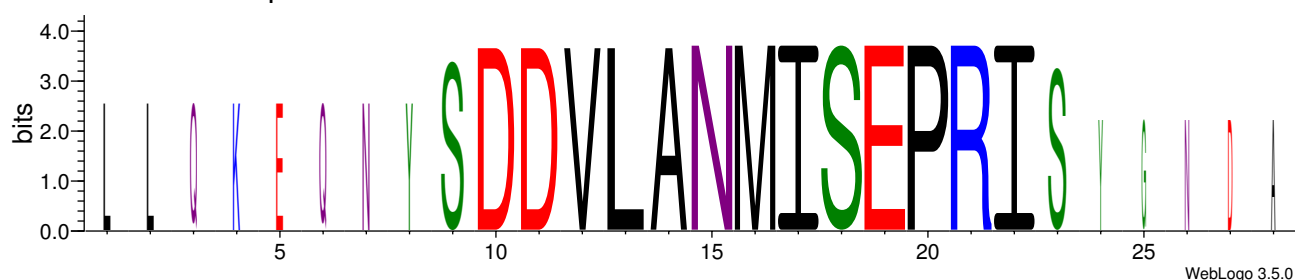
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2545	LSSNLVILPGQDLQ	_____LSSNLVILPGQDLQ_	21	10	11
2545	GGDVKLSSNLVILP	GGDVKLSSNLVILP_____	10	10	0
2545	KLSSNLVILPGQDL	____KLSSNLVILPGQDL__	8	0	8
2545	VKLSSNLVILPGQD	___VKLSSNLVILPGQD___	5	0	5
2545	SSNLVILPGQDLQY	____SSNLVILPGQDLQY	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
GGDVKLSSNLVILP_____	X89184	MV-H-CAM-70	505	14aaG4S	mRNA_30cpc_Organoid_MD114	10
GGDVKLSSNLVILP_____	X89184	MV-H-Edmonston	505	14aaG4S	mRNA_30cpc_Organoid_MD114	10
GGDVKLSSNLVILP_____	X89184	MV-H-Halle	505	14aaG4S	mRNA_30cpc_Organoid_MD114	10
GGDVKLSSNLVILP_____	X89184	MV-H-MVi-Illinois.USA-50.99	505	14aaG4S	mRNA_30cpc_Organoid_MD114	10
GGDVKLSSNLVILP_____	X89184	MV-H-MVi-Texas.USA-28.99	505	14aaG4S	mRNA_30cpc_Organoid_MD114	10
____KLSSNLVILPGQDL__	X4231	MV-H-CAM-70	509	14aa	mRNA_3000cpc_Organoid_MD101	8
____KLSSNLVILPGQDL__	X4231	MV-H-Edmonston	509	14aa	mRNA_3000cpc_Organoid_MD101	8
____KLSSNLVILPGQDL__	X4231	MV-H-Halle	509	14aa	mRNA_3000cpc_Organoid_MD101	8
____KLSSNLVILPGQDL__	X4231	MV-H-MVi-Illinois.USA-50.99	509	14aa	mRNA_3000cpc_Organoid_MD101	8
____KLSSNLVILPGQDL__	X4231	MV-H-MVi-Texas.USA-28.99	509	14aa	mRNA_3000cpc_Organoid_MD101	8
____LSSNLVILPGQDLQ_	X29170	MV-H-CAM-70	510	14aa	mRNA_30cpc_Organoid_MD114	10
____LSSNLVILPGQDLQ_	X29170	MV-H-Edmonston	510	14aa	mRNA_30cpc_Organoid_MD114	10
____LSSNLVILPGQDLQ_	X29170	MV-H-Halle	510	14aa	mRNA_30cpc_Organoid_MD114	10
____LSSNLVILPGQDLQ_	X29170	MV-H-MVi-Illinois.USA-50.99	510	14aa	mRNA_30cpc_Organoid_MD114	10
____LSSNLVILPGQDLQ_	X29170	MV-H-MVi-Texas.USA-28.99	510	14aa	mRNA_30cpc_Organoid_MD114	10
____LSSNLVILPGQDLQ_	X29170	MV-H-CAM-70	510	14aa	mRNA_3000cpc_Organoid_MD101	11
____LSSNLVILPGQDLQ_	X29170	MV-H-Edmonston	510	14aa	mRNA_3000cpc_Organoid_MD101	11
____LSSNLVILPGQDLQ_	X29170	MV-H-Halle	510	14aa	mRNA_3000cpc_Organoid_MD101	11
____LSSNLVILPGQDLQ_	X29170	MV-H-MVi-Illinois.USA-50.99	510	14aa	mRNA_3000cpc_Organoid_MD101	11
____LSSNLVILPGQDLQ_	X29170	MV-H-MVi-Texas.USA-28.99	510	14aa	mRNA_3000cpc_Organoid_MD101	11
____SSNLVILPGQDLQY	X10561	MV-H-CAM-70	511	14aa	mRNA_3000cpc_Organoid_MD101	5
____SSNLVILPGQDLQY	X10561	MV-H-Edmonston	511	14aa	mRNA_3000cpc_Organoid_MD101	5
____SSNLVILPGQDLQY	X10561	MV-H-Halle	511	14aa	mRNA_3000cpc_Organoid_MD101	5
____SSNLVILPGQDLQY	X10561	MV-H-MVi-Illinois.USA-50.99	511	14aa	mRNA_3000cpc_Organoid_MD101	5
____SSNLVILPGQDLQY	X10561	MV-H-MVi-Texas.USA-28.99	511	14aa	mRNA_3000cpc_Organoid_MD101	5
___VKLSSNLVILPGQD___	X65861	MV-H-CAM-70	508	14aa	mRNA_3000cpc_Organoid_MD101	5
___VKLSSNLVILPGQD___	X65861	MV-H-Edmonston	508	14aa	mRNA_3000cpc_Organoid_MD101	5
___VKLSSNLVILPGQD___	X65861	MV-H-Halle	508	14aa	mRNA_3000cpc_Organoid_MD101	5
___VKLSSNLVILPGQD___	X65861	MV-H-MVi-Illinois.USA-50.99	508	14aa	mRNA_3000cpc_Organoid_MD101	5
___VKLSSNLVILPGQD___	X65861	MV-H-MVi-Texas.USA-28.99	508	14aa	mRNA_3000cpc_Organoid_MD101	5

[1] 2798

Peptide SDDVLANMISEPRI from APP with cluster number 2798

Peptide SDDVLANMISEPRI from APP with cluster number 2798



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2798	SDDVLANMISEPRI	47	20	27

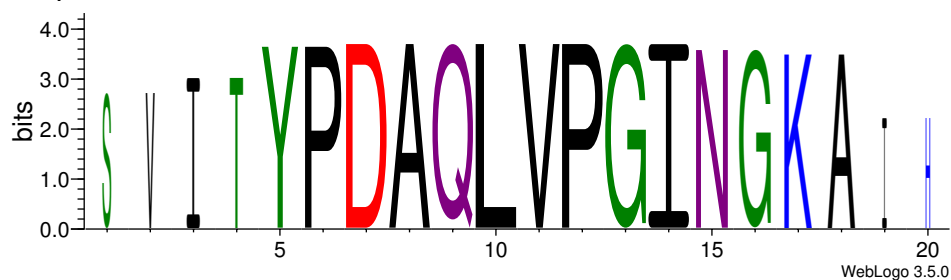
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2798	SDDVLANMISEPRI	-----SDDVLANMISEPRI-----	18	10	8
2798	DDVLANMISEPRIS	-----DDVLANMISEPRIS-----	16	10	6
2798	LLQKEQNYSDVLANMISEPRI	LLQKEQNYSDVLANMISEPRI-----	8	0	8
2798	NMISEPRISYGND	-----NMISEPRISYGND-----	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
-----DDVLANMISEPRIS-----	X54506	APP	574	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----DDVLANMISEPRIS-----	X35610	APP	574	14aa	mRNA_3000cpc_Organoid_MD101	6
LLQKEQNYSDVLANMISEPRI-----	X30879	APP	565	22aa	mRNA_3000cpc_Organoid_MD101	8
-----NMISEPRISYGND-----	X963	APP	579	14aa	mRNA_3000cpc_Organoid_MD101	5
-----SDDVLANMISEPRI-----	X12510	APP	573	14aa	mRNA_30cpc_Organoid_MD114	10
-----SDDVLANMISEPRI-----	X12510	APP	573	14aa	mRNA_3000cpc_Organoid_MD101	8

[1] 2804

Peptide YPDAQLVPGINGKA from TeNT-Hc with cluster number 2804

Peptide YPDAQLVPGINGKA from TeNT-Hc with cluster number 280



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2804	YPDAQLVPGINGKA	46	30	16

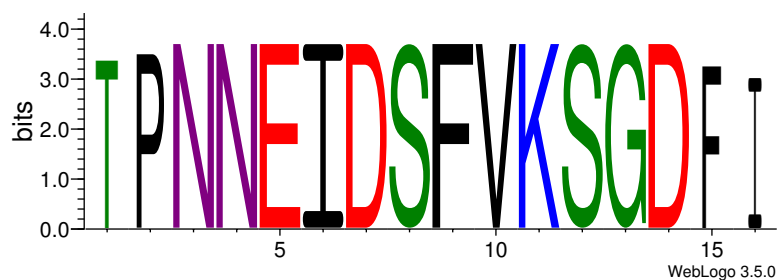
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2804	YPDAQLVPGINGKA	____YPDAQLVPGINGKA__	26	20	6
2804	SVITYPDAQLVPGI	SVITYPDAQLVPGI_____	10	10	0
2804	ITYPDAQLVPGING	__ITYPDAQLVPGING____	5	0	5
2804	DAQLVPGINGKAIH	____DAQLVPGINGKAIH	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
_____DAQLVPGINGKAIH	X35832	TeNT-Hc	48	14aa	mRNA_3000cpc_Organoid_MD101	5
__ITYPDAQLVPGING_____	X14700	TeNT-Hc	44	14aa	mRNA_3000cpc_Organoid_MD101	5
SVITYPDAQLVPGI_____	X13484	TeNT-Hc	42	14aa	mRNA_30cpc_Organoid_MD114	10
____YPDAQLVPGINGKA__	X70921	TeNT-Hc	46	14aa	mRNA_30cpc_Organoid_MD114	10
____YPDAQLVPGINGKA__	X59590	TeNT-Hc	46	14aaA5	mRNA_30cpc_Organoid_MD114	10
____YPDAQLVPGINGKA__	X59590	TeNT-Hc	46	14aaA5	mRNA_3000cpc_Organoid_MD101	6

[1] 2604

Peptide TPNNEIDSFVKSGD from TeNT-Hc with cluster number 2604

ide TPNNEIDSFVKSGD from TeNT-Hc with cluster numb



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2604	TPNNEIDSFVKSGD	46	30	16

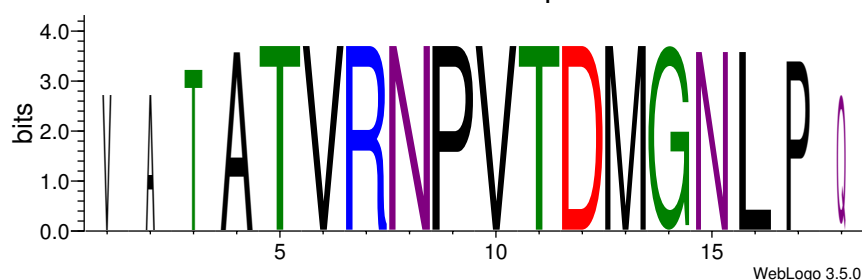
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2604	TPNNEIDSFVKSGD	TPNNEIDSFVKSGD__	25	20	5
2604	NNEIDSFVKSGDFI	__NNEIDSFVKSGDFI	15	10	5
2604	PNNEIDSFVKSGDF	_PNNEIDSFVKSGDF_	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
__NNEIDSFVKSGDFI	X169	TeNT-Hc	320	14aa	mRNA_30cpc_Organoid_MD114	10
__NNEIDSFVKSGDFI	X169	TeNT-Hc	320	14aa	mRNA_3000cpc_Organoid_MD101	5
PNNEIDSFVKSGDF	X20476	TeNT-Hc	319	14aa	mRNA_3000cpc_Organoid_MD101	6
TPNNEIDSFVKSGD__	X7129	TeNT-Hc	318	14aa	mRNA_30cpc_Organoid_MD114	20
TPNNEIDSFVKSGD__	X7129	TeNT-Hc	318	14aa	mRNA_3000cpc_Organoid_MD101	5

[1] 2021

Peptide ATVRNPVTDMGNLP from HSV-1-pUL19 with cluster number 2021

ide ATVRNPVTDMGNLP from HSV-1-pUL19 with cluster numb



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2021	ATVRNPVTDMGNLP	46	40	6

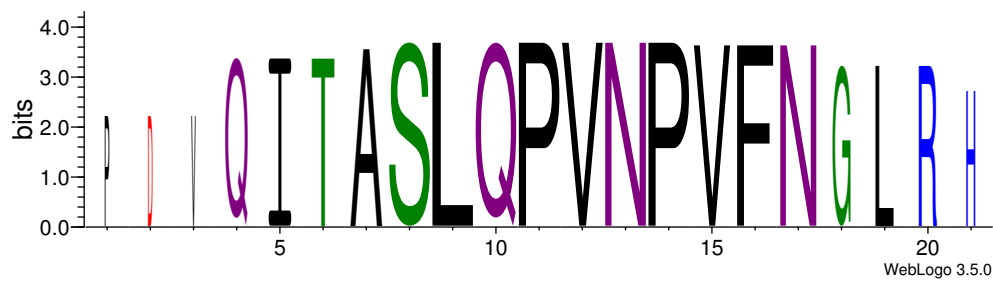
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2021	ATVRNPVTDMGNLP	___ATVRNPVTDMGNLP_	16	10	6
2021	VATATVRNPVTDMG	VATATVRNPVTDMG_____	10	10	0
2021	TVRNPVTDMGNLPQ	_____TVRNPVTDMGNLPQ	10	10	0
2021	TATVRNPVTDMGNL	__TATVRNPVTDMGNL__	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
___ATVRNPVTDMGNLP_	X40482	HSV-1-pUL19	1113	14aa	mRNA_30cpc_Organoid_MD114	10
___ATVRNPVTDMGNLP_	X40482	HSV-2-pUL19	1113	14aa	mRNA_30cpc_Organoid_MD114	10
___ATVRNPVTDMGNLP_	X40482	HSV-1-pUL19	1113	14aa	mRNA_3000cpc_Organoid_MD101	6
___ATVRNPVTDMGNLP_	X40482	HSV-2-pUL19	1113	14aa	mRNA_3000cpc_Organoid_MD101	6
__TATVRNPVTDMGNL__	X8426	HSV-1-pUL19	1112	14aa	mRNA_30cpc_Organoid_MD114	10
__TATVRNPVTDMGNL__	X8426	HSV-2-pUL19	1112	14aa	mRNA_30cpc_Organoid_MD114	10
_____TVRNPVTDMGNLPQ	X9157	HSV-1-pUL19	1114	14aa	mRNA_30cpc_Organoid_MD114	10
_____TVRNPVTDMGNLPQ	X9157	HSV-2-pUL19	1114	14aa	mRNA_30cpc_Organoid_MD114	10
VATATVRNPVTDMG_____	X68514	HSV-1-pUL19	1110	14aa	mRNA_30cpc_Organoid_MD114	10
VATATVRNPVTDMG_____	X68514	HSV-2-pUL19	1110	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2844

Peptide QITASLQPVNPVFN from TMEV-VP2 with cluster number 2844

Peptide QITASLQPVNPVFN from TMEV-VP2 with cluster number 284



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2844	QITASLQPVNPVFN	45	40	5

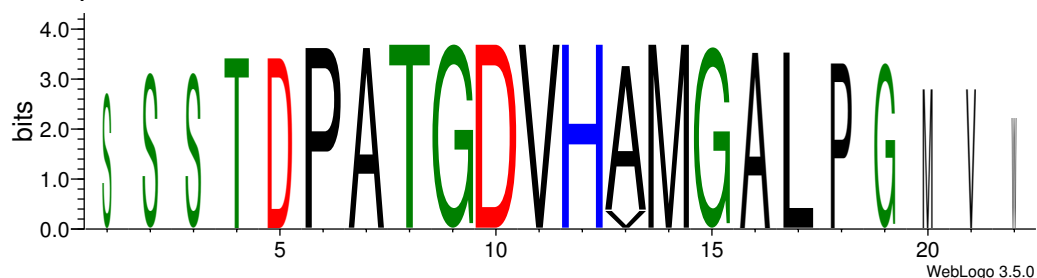
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2844	QITASLQPVNPVFN	___QITASLQPVNPVFN___	20	20	0
2844	SLQPVNPVFNGLRH	_____SLQPVNPVFNGLRH	10	10	0
2844	ASLQPVNPVFNGLR	_____ASLQPVNPVFNGLR_	10	10	0
2844	PDVQITASLQPVNP	PDVQITASLQPVNP_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
_____ASLQPVNPVFNGLR_	X87108	TMEV-VP2	247	14aaG4S	mRNA_30cpc_Organoid_MD114	10
PDVQITASLQPVNP_____	X23042	TMEV-VP2	241	14aa	mRNA_3000cpc_Organoid_MD101	5
___QITASLQPVNPVFN___	X18890	TMEV-VP2	244	14aa	mRNA_30cpc_Organoid_MD114	20
_____SLQPVNPVFNGLRH	X12143	TMEV-VP2	248	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2819

Peptide PATGDVHAMGALPG from AAV1-VP1 with cluster number 2819

Peptide PATGDVHAMGALPG from AAV1-VP1 with cluster number 2819



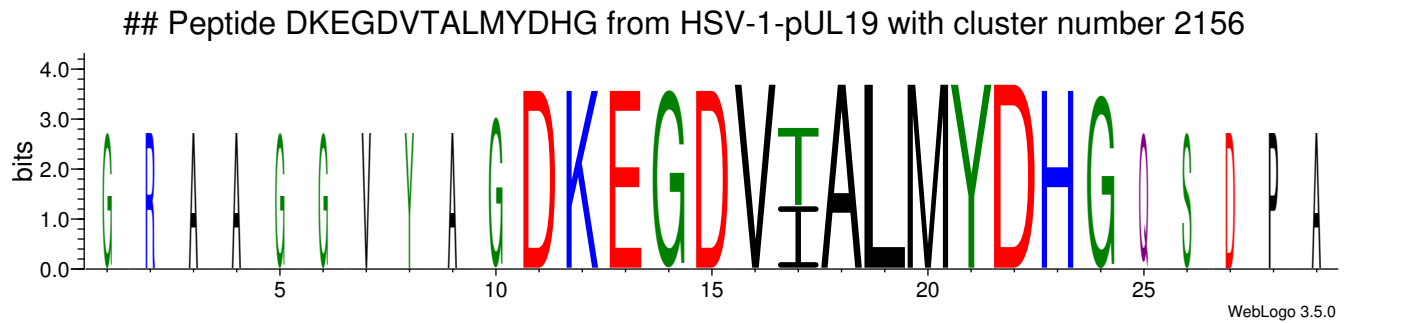
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2819	PATGDVHAMGALPG	45	10	35

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2819	PATGDVHAMGALPG	____PATGDVHAMGALPG__	12	0	12
2819	TDPATGDVHAMGAL	___TDPATGDVHAMGAL___	10	10	0
2819	SSTDPATGDVHAMG	_SSTDPATGDVHAMG_____	7	0	7
2819	TGDVHAMGALPGMV	_____TGDVHAMGALPGMV_	6	0	6
2819	SSSTDPATGDVHVM	SSSTDPATGDVHVM_____	5	0	5
2819	SSSTDPATGDVHAMGALPGMVW	SSSTDPATGDVHAMGALPGMVW	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
____PATGDVHAMGALPG__	X23344	AAV1-VP1	591	14aa	mRNA_3000cpc_Organoid_MD101	12
____PATGDVHAMGALPG__	X23344	AAV6-VP1	591	14aa	mRNA_3000cpc_Organoid_MD101	12
SSSTDPATGDVHAMGALPGMVW	X10627	AAV1-VP1	586	22aa	mRNA_3000cpc_Organoid_MD101	5
SSSTDPATGDVHAMGALPGMVW	X10627	AAV6-VP1	586	22aa	mRNA_3000cpc_Organoid_MD101	5
SSSTDPATGDVHVM_____	X10628	AAV1-VP1	586	14aa	mRNA_3000cpc_Organoid_MD101	5
SSSTDPATGDVHVM_____	X10628	AAV6-VP1	586	14aa	mRNA_3000cpc_Organoid_MD101	5
_SSTDPATGDVHAMG_____	X10606	AAV1-VP1	587	14aa	mRNA_3000cpc_Organoid_MD101	7
_SSTDPATGDVHAMG_____	X10606	AAV6-VP1	587	14aa	mRNA_3000cpc_Organoid_MD101	7
___TDPATGDVHAMGAL___	X78635	AAV1-VP1	589	14aaG4S	mRNA_30cpc_Organoid_MD114	10
___TDPATGDVHAMGAL___	X78635	AAV6-VP1	589	14aaG4S	mRNA_30cpc_Organoid_MD114	10
_____TGDVHAMGALPGMV_	X8895	AAV1-VP1	593	14aa	mRNA_3000cpc_Organoid_MD101	6
_____TGDVHAMGALPGMV_	X8895	AAV6-VP1	593	14aa	mRNA_3000cpc_Organoid_MD101	6

[1] 2156

Peptide DKEGDVTALMYDHG from HSV-1-pUL19 with cluster number 2156



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2156	DKEGDVTALMYDHG	45	30	15

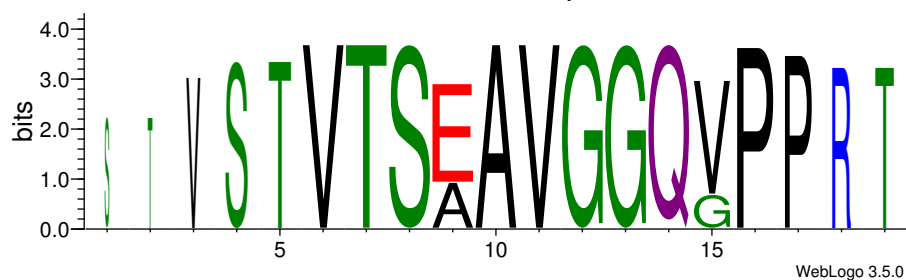
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2156	DKEGDVTALMYDHG	-----DKEGDVTALMYDHG-----	20	10	10
2156	VIALMYDHGQSDPA	-----VIALMYDHGQSDPA-----	10	10	0
2156	GRAAGGVYAGDKEGDVIALMYD	GRAAGGVYAGDKEGDVIALMYD-----	10	10	0
2156	GDKEGDVTALMYDH	-----GDKEGDVTALMYDH-----	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
-----DKEGDVTALMYDHG-----	X33947	HSV-1-pUL19	1217	14aa	mRNA_30cpc_Organoid_MD114	10
-----DKEGDVTALMYDHG-----	X33947	HSV-2-pUL19	1217	14aa	mRNA_30cpc_Organoid_MD114	10
-----DKEGDVTALMYDHG-----	X33947	HSV-1-pUL19	1217	14aa	mRNA_3000cpc_Organoid_MD101	10
-----DKEGDVTALMYDHG-----	X33947	HSV-2-pUL19	1217	14aa	mRNA_3000cpc_Organoid_MD101	10
-----GDKEGDVTALMYDH-----	X57601	HSV-1-pUL19	1216	14aaA5	mRNA_3000cpc_Organoid_MD101	5
-----GDKEGDVTALMYDH-----	X57601	HSV-2-pUL19	1216	14aaA5	mRNA_3000cpc_Organoid_MD101	5
GRAAGGVYAGDKEGDVIALMYD-----	X62981	HSV-1-pUL19	1207	22aa	mRNA_30cpc_Organoid_MD114	10
GRAAGGVYAGDKEGDVIALMYD-----	X62981	HSV-2-pUL19	1207	22aa	mRNA_30cpc_Organoid_MD114	10
-----VIALMYDHGQSDPA-----	X66720	HSV-1-pUL19	1222	14aa	mRNA_30cpc_Organoid_MD114	10
-----VIALMYDHGQSDPA-----	X66720	HSV-2-pUL19	1222	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2832

Peptide VTSEAVGGQVPPRT from HSV-1-pUL44 with cluster number 2832

Peptide VTSEAVGGQVPPRT from HSV-1-pUL44 with cluster number



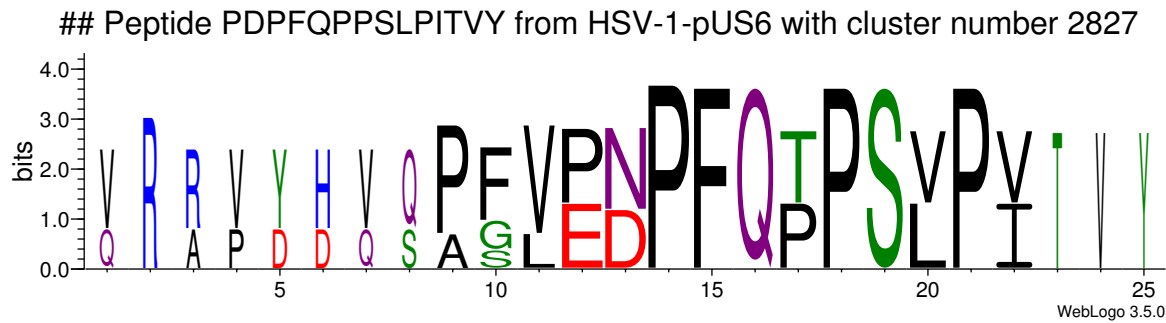
cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2832	VTSEAVGGQVPPRT	44	30	14

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2832	VTSEAVGGQVPPRT	-----VTSEAVGGQVPPRT	20	20	0
2832	VSTVTSEAVGGQVP	--VSTVTSEAVGGQVP---	10	10	0
2832	STVTSAAVGGQGPP	___STVTSAAVGGQGPP__	9	0	9
2832	STVSTVTSAAVGGQ	STVSTVTSAAVGGQ-----	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
STVSTVTSAAVGGQ-----	X10489	HSV-1-pUL44	326	14aa	mRNA_3000cpc_Organoid_MD101	5
STVSTVTSAAVGGQ-----	X10489	HSV-2-pUL44	295	14aa	mRNA_3000cpc_Organoid_MD101	5
___STVTSAAVGGQGPP__	X10486	HSV-2-pUL44	298	14aa	mRNA_3000cpc_Organoid_MD101	9
--VSTVTSEAVGGQVP---	X66304	HSV-1-pUL44	328	14aa	mRNA_30cpc_Organoid_MD114	10
-----VTSEAVGGQVPPRT	X58274	HSV-1-pUL44	331	14aaA5	mRNA_30cpc_Organoid_MD114	10
-----VTSEAVGGQVPPRT	X89564	HSV-1-pUL44	331	14aaG4S	mRNA_30cpc_Organoid_MD114	10

[1] 2827

Peptide PDPFQPPSLPITVY from HSV-1-pUS6 with cluster number 2827



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2827	PDPFQPPSLPITVY	43	30	13

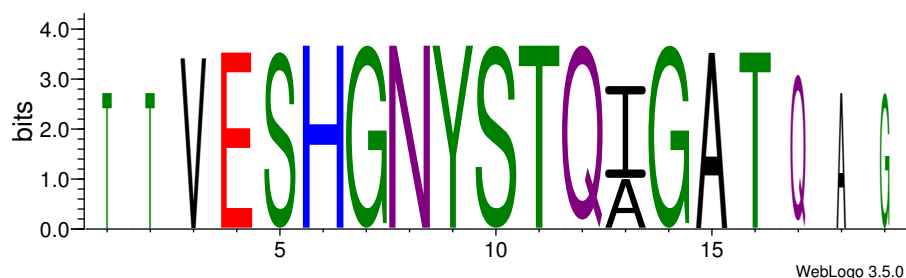
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2827	VRRVYHVQPFVENPFQTPSPVPV	VRRVYHVQPFVENPFQTPSPVPV___	10	10	0
2827	PFVENPFQTPSPVPV	_____PFVENPFQTPSPVPV___	10	10	0
2827	PDPFQPPSLPITVY	_____PDPFQPPSLPITVY	10	10	0
2827	AGLPDPFQPPSLPI	_____AGLPDPFQPPSLPI___	8	0	8
2827	QRAPDDQSPSVNP	QRAPDDQSPSVNP_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
_____AGLPDPFQPPSLPI___	X44094	HSV-1-pUS6	67	14aa	mRNA_3000cpc_Organoid_MD101	8
_____PDPFQPPSLPITVY	X22957	HSV-1-pUS6	70	14aa	mRNA_30cpc_Organoid_MD114	10
_____PFVENPFQTPSPVPV___	X24692	BV-G	66	14aa	mRNA_30cpc_Organoid_MD114	10
QRAPDDQSPSVNP_____	X19424	HSV-1-pUL36	2492	14aa	mRNA_3000cpc_Organoid_MD101	5
VRRVYHVQPFVENPFQTPSPVPV___	X67496	BV-G	58	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2715

Peptide VESHGNYSTQIGAT from WNV-E-AZ10-918 with cluster number 2715

Peptide VESHGNYSTQIGAT from WNV-E-AZ10-918 with cluster number 2715



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2715	VESHGNYSTQIGAT	43	20	23

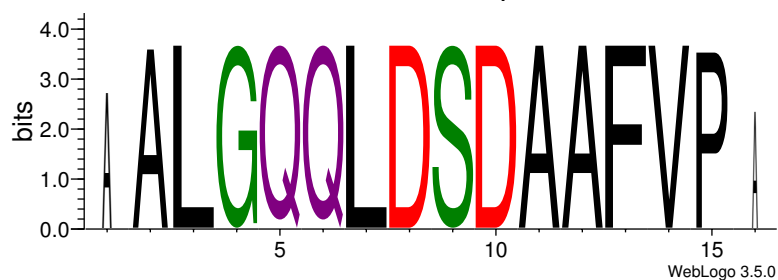
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2715	VESHGNYSTQIGAT	__VESHGNYSTQIGAT__	12	0	12
2715	TTVESHGNYSTQAG	TTVESHGNYSTQAG_____	10	10	0
2715	HGNYSTQIGATQAG	____HGNYSTQIGATQAG	10	10	0
2715	ESHGNYSTQIGATQ	___ESHGNYSTQIGATQ__	6	0	6
2715	VESHGNYSTQAGAT	__VESHGNYSTQAGAT__	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
___ESHGNYSTQIGATQ__	X37279	WNV-E-AZ10-918	150	14aa	mRNA_3000cpc_Organoid_MD101	6
___ESHGNYSTQIGATQ__	X37279	WNV-E-H-442	150	14aa	mRNA_3000cpc_Organoid_MD101	6
____HGNYSTQIGATQAG	X18087	WNV-E-AZ10-918	152	14aa	mRNA_30cpc_Organoid_MD114	10
____HGNYSTQIGATQAG	X18087	WNV-E-H-442	152	14aa	mRNA_30cpc_Organoid_MD114	10
TTVESHGNYSTQAG_____	X6160	WNV-E-AZ10-918	147	14aa	mRNA_30cpc_Organoid_MD114	10
TTVESHGNYSTQAG_____	X6160	WNV-E-H-442	147	14aa	mRNA_30cpc_Organoid_MD114	10
__VESHGNYSTQAGAT__	X68262	WNV-E-AZ10-918	149	14aa	mRNA_3000cpc_Organoid_MD101	5
__VESHGNYSTQAGAT__	X68262	WNV-E-H-442	149	14aa	mRNA_3000cpc_Organoid_MD101	5
__VESHGNYSTQIGAT__	X68261	WNV-E-AZ10-918	149	14aa	mRNA_3000cpc_Organoid_MD101	12
__VESHGNYSTQIGAT__	X68261	WNV-E-H-442	149	14aa	mRNA_3000cpc_Organoid_MD101	12

[1] 2250

Peptide ALGQQLDSDAAFVP from HSV-1-pUL36 with cluster number 2250

ALGQQLDSDAAFVP from HSV-1-pUL36 with cluster nu



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2250	ALGQQLDSDAAFVP	43	30	13

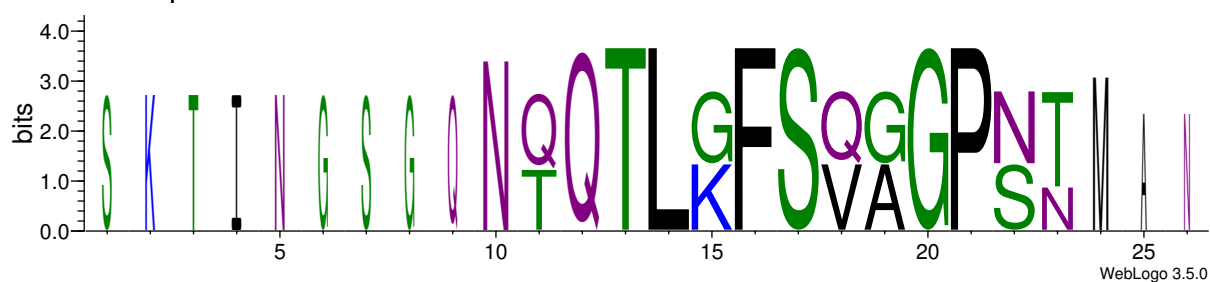
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2250	ALGQQLDSDAAFVP	_ALGQQLDSDAAFVP_	27	20	7
2250	AALGQQLDSDAAAFV	AALGQQLDSDAAAFV_	10	10	0
2250	LGQQLDSDAAAFVPA	__LGQQLDSDAAAFVPA	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
AALGQQLDSDAAAFV_	X43643	HSV-1-pUL36	933	14aa	mRNA_30cpc_Organoid_MD114	10
ALGQQLDSDAAFVP	X42683	HSV-1-pUL36	934	14aa	mRNA_30cpc_Organoid_MD114	10
ALGQQLDSDAAFVP	X56327	HSV-1-pUL36	934	14aaA5	mRNA_30cpc_Organoid_MD114	10
ALGQQLDSDAAFVP	X56327	HSV-1-pUL36	934	14aaA5	mRNA_3000cpc_Organoid_MD101	7
__LGQQLDSDAAAFVPA	X32402	HSV-1-pUL36	935	14aa	mRNA_3000cpc_Organoid_MD101	6

[1] 2821

Peptide NQQLKFSVAGPSN from AAV9-VP1 with cluster number 2821

Peptide NQQLKFSVAGPSN from AAV9-VP1 with cluster number 2821



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2821	NQQLKFSVAGPSN	42	30	12

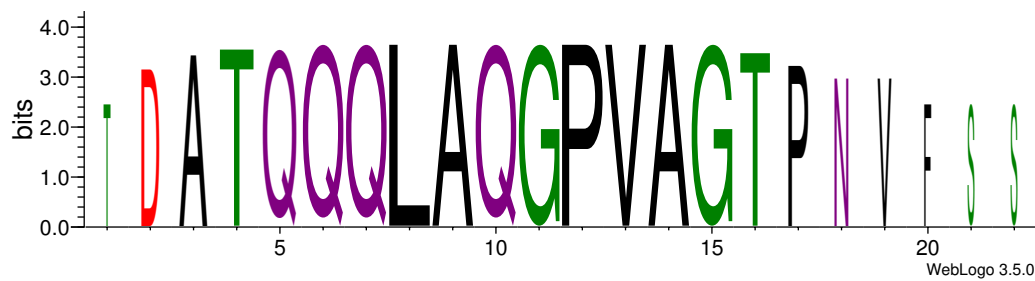
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2821	TQTLGFSQGGPNTM	-----TQTLGFSQGGPNTM--	10	10	0
2821	SKTINGSGQNQQTLKFSVAGPS	SKTINGSGQNQQTLKFSVAGPS_	10	10	0
2821	NQQLKFSVAGPSN	-----NQQLKFSVAGPSN--	10	10	0
2821	TLGFSQGGPNTMAN	-----TLGFSQGGPNTMAN	6	0	6
2821	NTQTLGFSQGGPNT	-----NTQTLGFSQGGPNT--	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
-----NQQLKFSVAGPSN--	X1142	AAV9-VP1	457	14aa	mRNA_30cpc_Organoid_MD114	10
-----NTQTLGFSQGGPNT--	X463	AAV8-VP1	459	14aa	mRNA_3000cpc_Organoid_MD101	6
SKTINGSGQNQQTLKFSVAGPS	X10032	AAV9-VP1	448	22aa	mRNA_30cpc_Organoid_MD114	10
-----TLGFSQGGPNTMAN	X7945	AAV8-VP1	462	14aa	mRNA_3000cpc_Organoid_MD101	6
-----TQTLGFSQGGPNTM--	X6974	AAV8-VP1	460	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2824

Peptide DATQQQLAQGPVAG from HSV-2-pUL22 with cluster number 2824

Peptide DATQQQLAQGPVAG from HSV-2-pUL22 with cluster number 2824



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2824	DATQQQLAQGPVAG	41	10	31

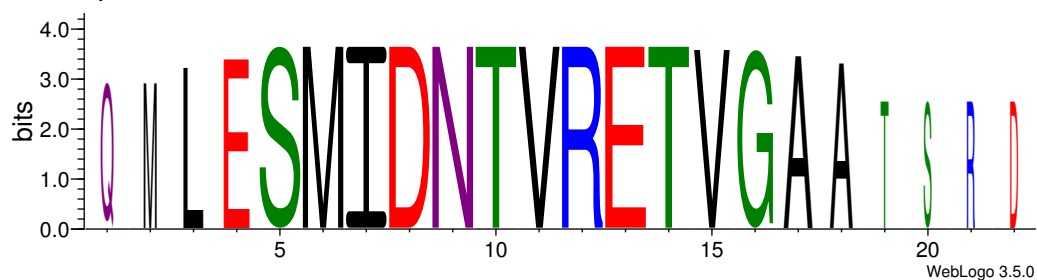
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2824	DATQQQLAQGPVAG	_DATQQQLAQGPVAG_	11	0	11
2824	ATQQQLAQGPVAGT	_ATQQQLAQGPVAGT_	10	10	0
2824	TDATQQQLAQGPVAGTPNVFSS	TDATQQQLAQGPVAGTPNVFSS	7	0	7
2824	QQLAQGPVAGTPNV	____QQLAQGPVAGTPNV__	7	0	7
2824	TQQQLAQGPVAGTP	___TQQQLAQGPVAGTP_____	6	0	6

alignment	LUTnrs	GeneName	start	structure	Group	Score
ATQQQLAQGPVAGT	X40235	HSV-2-pUL22	753	14aa	mRNA_30cpc_Organoid_MD114	10
DATQQQLAQGPVAG	X35790	HSV-2-pUL22	752	14aa	mRNA_3000cpc_Organoid_MD101	11
____QQLAQGPVAGTPNV__	X19148	HSV-2-pUL22	756	14aa	mRNA_3000cpc_Organoid_MD101	7
TDATQQQLAQGPVAGTPNVFSS	X8153	HSV-2-pUL22	751	22aa	mRNA_3000cpc_Organoid_MD101	7
___TQQQLAQGPVAGTP_____	X7009	HSV-2-pUL22	754	14aa	mRNA_3000cpc_Organoid_MD101	6

[1] 2621

Peptide SMIDNTVRETVGAA from PV1-VP1 with cluster number 2621

Peptide SMIDNTVRETVGAA from PV1-VP1 with cluster number 2621



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2621	SMIDNTVRETVGAA	41	10	31

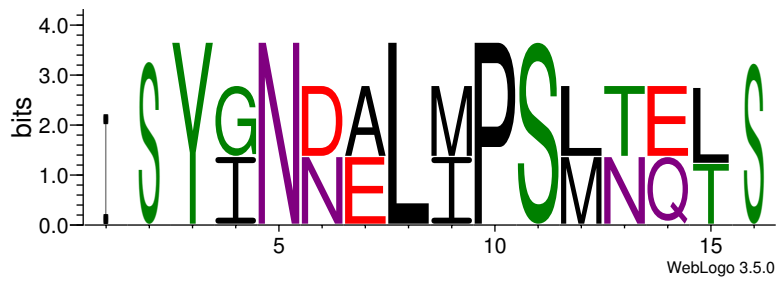
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2621	SMIDNTVRETVGAA	___SMIDNTVRETVGAA___	15	10	5
2621	QMLES MIDNTVRETVGAATSRD	QMLES MIDNTVRETVGAATSRD	8	0	8
2621	LES MIDNTVRETVG	__LES MIDNTVRETVG____	7	0	7
2621	ES MIDNTVRETVGA	___ES MIDNTVRETVGA___	6	0	6
2621	QMLES MIDNTVRET	QMLES MIDNTVRET_____	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
___ES MIDNTVRETVGA___	X37273	PV1-VP1	7	14aa	mRNA_3000cpc_Organoid_MD101	6
__LES MIDNTVRETVG____	X31535	PV1-VP1	6	14aa	mRNA_3000cpc_Organoid_MD101	7
QMLES MIDNTVRET_____	X50196	PV1-VP1	4	14aaA5	mRNA_3000cpc_Organoid_MD101	5
QMLES MIDNTVRETVGAATSRD	X19027	PV1-VP1	4	22aa	mRNA_3000cpc_Organoid_MD101	8
___SMIDNTVRETVGAA___	X11154	PV1-VP1	8	14aa	mRNA_30cpc_Organoid_MD114	10
___SMIDNTVRETVGAA___	X11154	PV1-VP1	8	14aa	mRNA_3000cpc_Organoid_MD101	5

[1] 2525

Peptide YINNELIPSMNQLS from MV-F-CAM-70 with cluster number 2525

» YINNELIPSMNQLS from MV-F-CAM-70 with cluster nur



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2525	YINNELIPSMNQLS	41	30	11

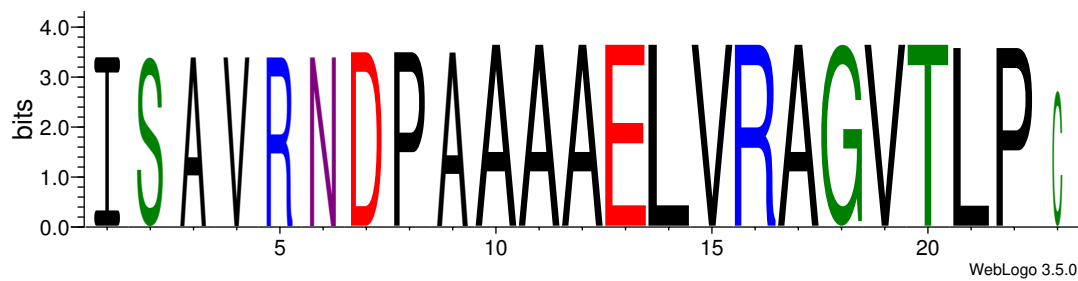
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2525	YINNELIPSMNQLS	__YINNELIPSMNQLS	20	20	0
2525	SYGNDALMPSLTET	_SYGNDALMPSLTET_	16	10	6
2525	ISYGNDALMPSLTE	ISYGNDALMPSLTE__	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
ISYGNDALMPSLTE__	X14903	APP	586	14aa	mRNA_3000cpc_Organoid_MD101	5
SYGNDALMPSLTET	X13829	APP	587	14aa	mRNA_30cpc_Organoid_MD114	10
SYGNDALMPSLTET	X13829	APP	587	14aa	mRNA_3000cpc_Organoid_MD101	6
__YINNELIPSMNQLS	X59499	MV-F-CAM-70	184	14aaA5	mRNA_30cpc_Organoid_MD114	10
__YINNELIPSMNQLS	X90789	MV-F-CAM-70	184	14aaG4S	mRNA_30cpc_Organoid_MD114	10
__YINNELIPSMNQLS	X59499	MV-F-Edmonston	184	14aaA5	mRNA_30cpc_Organoid_MD114	10
__YINNELIPSMNQLS	X90789	MV-F-Edmonston	184	14aaG4S	mRNA_30cpc_Organoid_MD114	10
__YINNELIPSMNQLS	X59499	MV-F-Halle	184	14aaA5	mRNA_30cpc_Organoid_MD114	10
__YINNELIPSMNQLS	X90789	MV-F-Halle	184	14aaG4S	mRNA_30cpc_Organoid_MD114	10

[1] 2263

Peptide ISAVRNDPAAAAELVRAGVTLP from HSV-1-pUL36 with cluster number 2263

Peptide ISAVRNDPAAAAELVRAGVTLP from HSV-1-pUL36 with cluster number



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2263	ISAVRNDPAAAAELVRAGVTLP	41	20	21

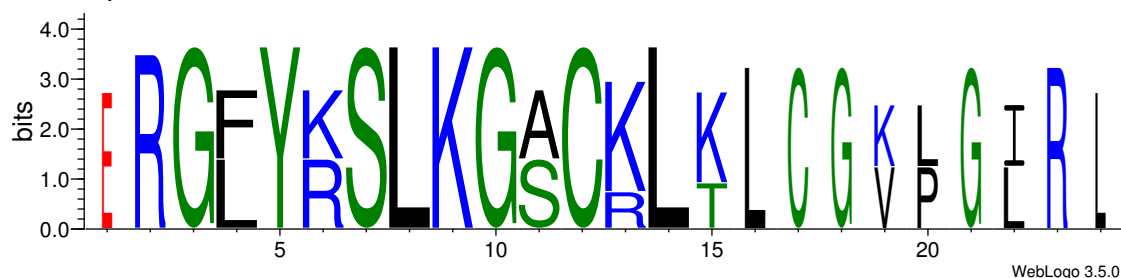
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2263	ISAVRNDPAAAAELVRAGVTLP	ISAVRNDPAAAAELVRAGVTLP_	26	10	16
2263	AAAELVRAGVTLP	-----AAAELVRAGVTLP	10	10	0
2263	DPAAAAELVRAGVT	-----DPAAAAELVRAGVT---	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
-----AAAELVRAGVTLP	X43771	HSV-1-pUL36	1534	14aa	mRNA_30cpc_Organoid_MD114	10
-----DPAAAAELVRAGVT---	X34988	HSV-1-pUL36	1531	14aa	mRNA_3000cpc_Organoid_MD101	5
ISAVRNDPAAAAELVRAGVTLP_	X14875	HSV-1-pUL36	1525	22aa	mRNA_30cpc_Organoid_MD114	10
ISAVRNDPAAAAELVRAGVTLP_	X14875	HSV-1-pUL36	1525	22aa	mRNA_3000cpc_Organoid_MD101	16

[1] 2842

Peptide ERGFYRSLKGSKL from RV-G-Mocala with cluster number 2842

Peptide ERGFYRSLKGSKL from RV-G-Mocala with cluster number 2842



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2842	ERGFYRSLKGSKL	40	40	0

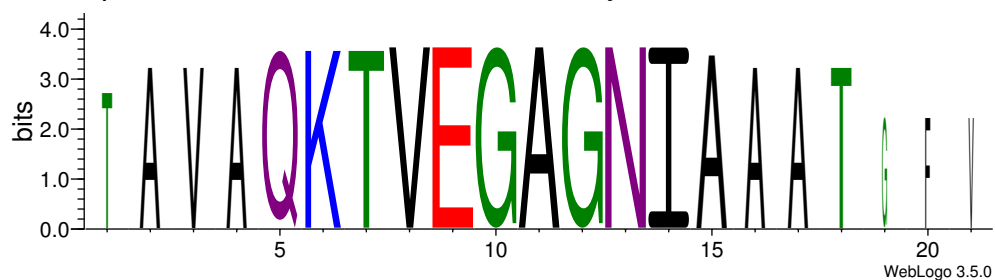
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2842	RGLYKSLKGACRLKCGVLGLR	_RGLYKSLKGACRLKCGVLGLR_	10	10	0
2842	RGLYKSLKGACKLK	_RGLYKSLKGACKLK_	10	10	0
2842	GFYRSLKGSKLTLCGKPGIRL	_GFYRSLKGSKLTLCGKPGIRL	10	10	0
2842	ERGFYRSLKGSKL	ERGFYRSLKGSKL_	10	10	0

alignment	LUTnrs	GeneName	start	structure	Group	Score
ERGFYRSLKGSKL_	X38042	RV-G-Mocala	212	14aa	mRNA_30cpc_Organoid_MD114	10
_GFYRSLKGSKLTLCGKPGIRL	X65576	RV-G-Mocala	214	22aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACKLK	X27501	RV-G-B19	213	14aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACKLK	X27501	RV-G-B2c	213	14aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACKLK	X27501	RV-G-N2c	232	14aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACKLK	X27501	RV-G-PV	213	14aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACRLKCGVLGLR	X27502	RV-G-B19	213	22aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACRLKCGVLGLR	X27502	RV-G-B2c	213	22aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACRLKCGVLGLR	X27502	RV-G-N2c	232	22aa	mRNA_30cpc_Organoid_MD114	10
RGLYKSLKGACRLKCGVLGLR	X27502	RV-G-PV	213	22aa	mRNA_30cpc_Organoid_MD114	10

[1] 2841

Peptide QKTVEGAGNIAAAT from a-Syn with cluster number 2841

Peptide QKTVEGAGNIAAAT from a-Syn with cluster number 2841



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2841	QKTVEGAGNIAAAT	40	30	10

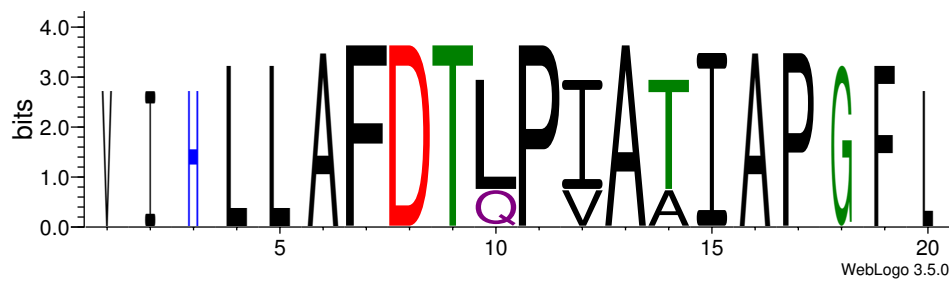
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2841	QKTVEGAGNIAAAT	____QKTVEGAGNIAAAT____	15	10	5
2841	TAVAQKTVEGAGNI	TAVAQKTVEGAGNI_____	10	10	0
2841	AVAQKTVEGAGNIA	_AVAQKTVEGAGNIA_____	10	10	0
2841	VEGAGNIAAATGFV	_______VEGAGNIAAATGFV	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
_AVAQKTVEGAGNIA_____	X56806	a-Syn	76	14aaA5	mRNA_30cpc_Organoid_MD114	10
____QKTVEGAGNIAAAT____	X18521	a-Syn	79	14aa	mRNA_30cpc_Organoid_MD114	10
____QKTVEGAGNIAAAT____	X18521	a-Syn	79	14aa	mRNA_3000cpc_Organoid_MD101	5
TAVAQKTVEGAGNI_____	X8664	a-Syn	75	14aa	mRNA_30cpc_Organoid_MD114	10
_______VEGAGNIAAATGFV	X68412	a-Syn	82	14aa	mRNA_3000cpc_Organoid_MD101	5

[1] 2835

Peptide AFDTQPVA AIAPGF from HSV-1-pUL22 with cluster number 2835

Peptide AFDTQPVA AIAPGF from HSV-1-pUL22 with cluster number 2



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2835	AFDTQPVA AIAPGF	40	40	0

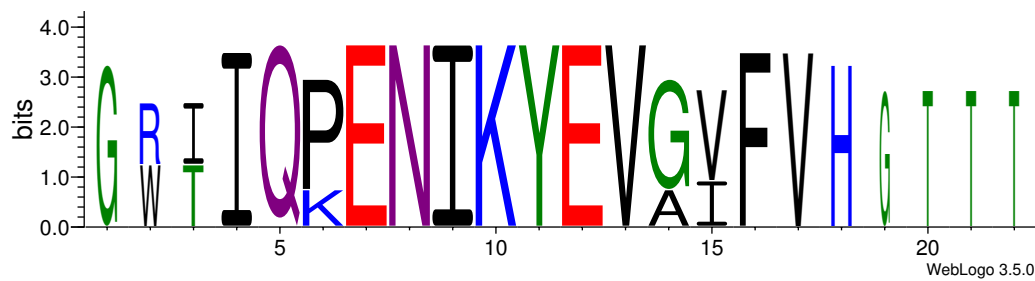
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2835	VIHLLAFDTLPIAT	VIHLLAFDTLPIAT_	10	10	0
2835	LLAFDTLPIATIAP	_LLAFDTLPIATIAP_	10	10	0
2835	FDTLPIATIAPGFL	_FDTLPIATIAPGFL	10	10	0
2835	AFDTQPVA AIAPGF	_AFDTQPVA AIAPGF_	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
AFDTQPVA AIAPGF	X45187	HSV-1-pUL22	792	14aa	mRNA_30cpc_Organoid_MD114	10
_FDTLPIATIAPGFL	X60782	HSV-2-pUL22	793	14aaA5	mRNA_30cpc_Organoid_MD114	10
LLAFDTLPIATIAP	X31095	HSV-2-pUL22	790	14aa	mRNA_30cpc_Organoid_MD114	10
VIHLLAFDTLPIAT_	X66654	HSV-1-pUL22	787	14aa	mRNA_30cpc_Organoid_MD114	10
VIHLLAFDTLPIAT_	X66654	HSV-2-pUL22	787	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2716

Peptide GRTIQPENIKYEVGVFVHGTTT from JEV-E-BN19 with cluster number 2716

Peptide GRTIQPENIKYEVGVFVHGTTT from JEV-E-BN19 with cluster number 2716



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2716	GRTIQPENIKYEVGVFVHGTTT	40	40	0

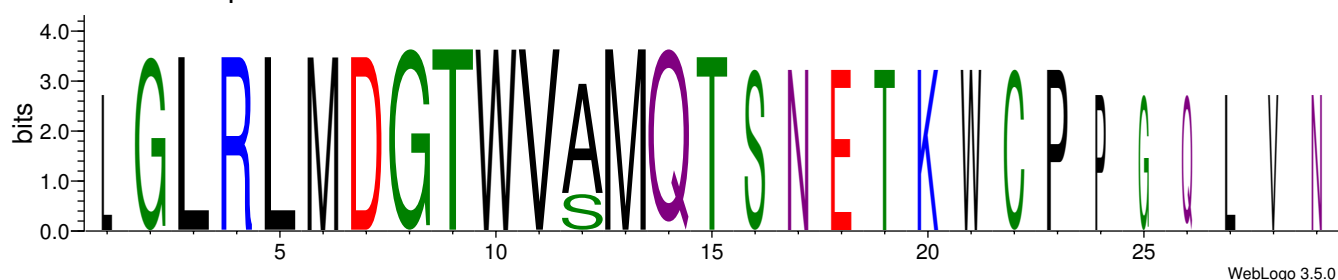
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2716	QPENIKYEVGVFVH	____QPENIKYEVGVFVH____	10	10	0
2716	IQPENIKYEVGIFV	___IQPENIKYEVGIFV_____	10	10	0
2716	GWIIQKENIKYEVA	GWIIQKENIKYEVA_____	10	10	0
2716	GRTIQPENIKYEVGVFVHGTTT	GRTIQPENIKYEVGVFVHGTTT	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
GRTIQPENIKYEVGVFVHGTTT	X62833	JEV-E-BN19	127	22aa	mRNA_30cpc_Organoid_MD114	10
GRTIQPENIKYEVGVFVHGTTT	X62833	JEV-E-KE-093	127	22aa	mRNA_30cpc_Organoid_MD114	10
GRTIQPENIKYEVGVFVHGTTT	X62833	JEV-E-SA14-5-3	127	22aa	mRNA_30cpc_Organoid_MD114	10
GRTIQPENIKYEVGVFVHGTTT	X62833	JEV-E-ThCMAr4492	127	22aa	mRNA_30cpc_Organoid_MD114	10
GWIIQKENIKYEVA_____	X58105	WNV-E-AZ10-918	127	14aaA5	mRNA_30cpc_Organoid_MD114	10
GWIIQKENIKYEVA_____	X58105	WNV-E-ArD76104	127	14aaA5	mRNA_30cpc_Organoid_MD114	10
GWIIQKENIKYEVA_____	X58105	WNV-E-H-442	127	14aaA5	mRNA_30cpc_Organoid_MD114	10
___IQPENIKYEVGIFV_____	X15275	JEV-E-BN19	130	14aa	mRNA_30cpc_Organoid_MD114	10
___IQPENIKYEVGIFV_____	X15275	JEV-E-KE-093	130	14aa	mRNA_30cpc_Organoid_MD114	10
___IQPENIKYEVGIFV_____	X15275	JEV-E-SA14-5-3	130	14aa	mRNA_30cpc_Organoid_MD114	10
___IQPENIKYEVGIFV_____	X15275	JEV-E-ThCMAr4492	130	14aa	mRNA_30cpc_Organoid_MD114	10
____QPENIKYEVGVFVH_____	X19292	JEV-E-BN19	131	14aa	mRNA_30cpc_Organoid_MD114	10
____QPENIKYEVGVFVH_____	X19292	JEV-E-KE-093	131	14aa	mRNA_30cpc_Organoid_MD114	10
____QPENIKYEVGVFVH_____	X19292	JEV-E-SA14-5-3	131	14aa	mRNA_30cpc_Organoid_MD114	10
____QPENIKYEVGVFVH_____	X19292	JEV-E-ThCMAr4492	131	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2517

Peptide GLRLMDGTWVAMQT from RV-G-B19 with cluster number 2517

Peptide GLRLMDGTWVAMQT from RV-G-B19 with cluster number 2517



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2517	GLRLMDGTWVAMQT	40	40	0

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2517	LGLRLMDGTWVAMQ	LGLRLMDGTWVAMQ_____	10	10	0
2517	GTWVAMQTSNETKWCPPGQLVN	_____GTWVAMQTSNETKWCPPGQLVN	10	10	0
2517	GLRLMDGTWVSMQTSNETKWCP	_GLRLMDGTWVSMQTSNETKWCP_____	10	10	0
2517	GLRLMDGTWVAMQT	_GLRLMDGTWVAMQT_____	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
_GLRLMDGTWVAMQT_____	X57527	RV-G-B19	232	14aaA5	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVAMQT_____	X57527	RV-G-B2c	232	14aaA5	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVAMQT_____	X57527	RV-G-N2c	251	14aaA5	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVAMQT_____	X57527	RV-G-PV	232	14aaA5	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVSMQTSNETKWCP_____	X63218	RV-G-B19	232	22aa	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVSMQTSNETKWCP_____	X63218	RV-G-B2c	232	22aa	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVSMQTSNETKWCP_____	X63218	RV-G-N2c	251	22aa	mRNA_30cpc_Organoid_MD114	10
_GLRLMDGTWVSMQTSNETKWCP_____	X63218	RV-G-PV	232	22aa	mRNA_30cpc_Organoid_MD114	10
_____GTWVAMQTSNETKWCPPGQLVN	X61707	RV-G-B19	238	22aa	mRNA_30cpc_Organoid_MD114	10
_____GTWVAMQTSNETKWCPPGQLVN	X61707	RV-G-B2c	238	22aa	mRNA_30cpc_Organoid_MD114	10
_____GTWVAMQTSNETKWCPPGQLVN	X61707	RV-G-N2c	257	22aa	mRNA_30cpc_Organoid_MD114	10
_____GTWVAMQTSNETKWCPPGQLVN	X61707	RV-G-PV	238	22aa	mRNA_30cpc_Organoid_MD114	10
LGLRLMDGTWVAMQ_____	X32500	RV-G-B19	231	14aa	mRNA_30cpc_Organoid_MD114	10
LGLRLMDGTWVAMQ_____	X32500	RV-G-B2c	231	14aa	mRNA_30cpc_Organoid_MD114	10
LGLRLMDGTWVAMQ_____	X32500	RV-G-N2c	250	14aa	mRNA_30cpc_Organoid_MD114	10
LGLRLMDGTWVAMQ_____	X32500	RV-G-PV	231	14aa	mRNA_30cpc_Organoid_MD114	10

[1] 2446

Peptide LVLLVSLGAISFWM from H1N1-HA with cluster number 2446

Peptide LVLLVSLGAISFWM from H1N1-HA with cluster number 2446



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2446	LVLLVSLGAISFWM	40	40	0

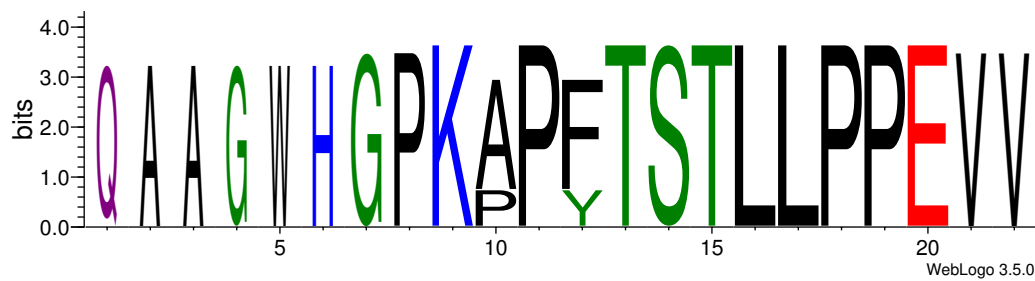
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2446	VLLVSLGAISFWMC	___VLLVSLGAISFWMC_____	10	10	0
2446	SSLVLLVSLGAISFWMCNGL	SSLVLLVSLGAISFWMCNGL	10	10	0
2446	SLVLLVSLGAISFW	_SLVLLVSLGAISFW_____	10	10	0
2446	LVLLVSLGAISFWM	__LVLLVSLGAISFWM_____	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
__LVLLVSLGAISFWM_____	X32923	H1N1-HA	540	14aa	mRNA_30cpc_Organoid_MD114	10
_SLVLLVSLGAISFW_____	X12341	H1N1-HA	539	14aa	mRNA_30cpc_Organoid_MD114	10
SSLVLLVSLGAISFWMCNGL	X10767	H1N1-HA	538	22aa	mRNA_30cpc_Organoid_MD114	10
___VLLVSLGAISFWMC_____	X58757	H1N1-HA	541	14aaA5	mRNA_30cpc_Organoid_MD114	10

[1] 2081

Peptide QAAGWHGPKAPFTSTLLPPEVV from BV-G with cluster number 2081

Peptide QAAGWHGPKAPFTSTLLPPEVV from BV-G with cluster number 2081



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2081	QAAGWHGPKAPFTSTLLPPEVV	40	40	0

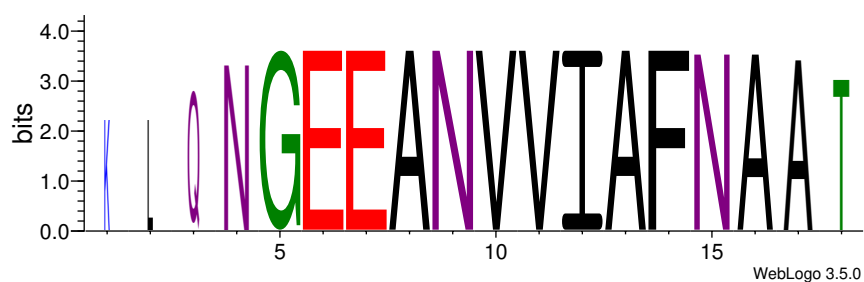
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2081	QAAGWHGPKAPFTSTLLPPEVV	QAAGWHGPKAPFTSTLLPPEVV	20	20	0
2081	KAPFTSTLLPPEVV	-----KAPFTSTLLPPEVV	10	10	0
2081	GPKPPYTSTLLPPE	-----GPKPPYTSTLLPPE__	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
-----GPKPPYTSTLLPPE__	X62510	BV-G	268	14aa	mRNA_30cpc_Organoid_MD114	10
-----GPKPPYTSTLLPPE__	X62510	HSV-1-pUS6	268	14aa	mRNA_30cpc_Organoid_MD114	10
-----GPKPPYTSTLLPPE__	X62510	HSV-2-pUS6	268	14aa	mRNA_30cpc_Organoid_MD114	10
-----KAPFTSTLLPPEVV	X4768	BV-G	270	14aa	mRNA_30cpc_Organoid_MD114	10
QAAGWHGPKAPFTSTLLPPEVV	X19942	BV-G	262	22aa	mRNA_30cpc_Organoid_MD114	20

[1] 2795

Peptide GEEANVVIAFNAAT from PSA-Chain-C with cluster number 2795

Peptide GEEANVVIAFNAAT from PSA-Chain-C with cluster number 2795



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2795	GEEANVVIAFNAAT	38	10	28

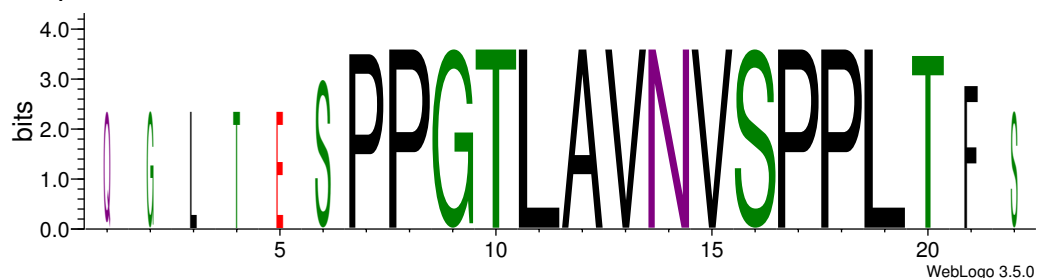
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2795	GEEANVVIAFNAAT	___GEEANVVIAFNAAT	15	10	5
2795	NGEEANVVIAFNAA	___NGEEANVVIAFNAA_	12	0	12
2795	QNGEEANVVIAFNA	__QNGEEANVVIAFNA__	6	0	6
2795	KLQNGEEANVVIAF	KLQNGEEANVVIAF___	5	0	5

alignment	LUThrs	GeneName	start	structure	Group	Score
___GEEANVVIAFNAAT	X63883	PSA-Chain-C	157	14aa	mRNA_30cpc_Organoid_MD114	10
___GEEANVVIAFNAAT	X57709	PSA-Chain-C	157	14aaA5	mRNA_3000cpc_Organoid_MD101	5
KLQNGEEANVVIAF___	X4253	PSA-Chain-C	153	14aa	mRNA_3000cpc_Organoid_MD101	5
__NGEEANVVIAFNAA_	X2412	PSA-Chain-C	156	14aa	mRNA_3000cpc_Organoid_MD101	12
__QNGEEANVVIAFNA__	X18495	PSA-Chain-C	155	14aa	mRNA_3000cpc_Organoid_MD101	6

[1] 2727

Peptide PPGTLAVNVSPPLT from CAV-2-F-SH01 with cluster number 2727

Peptide PPGTLAVNVSPPLT from CAV-2-F-SH01 with cluster number 2727



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2727	PPGTLAVNVSPPLT	37	10	27

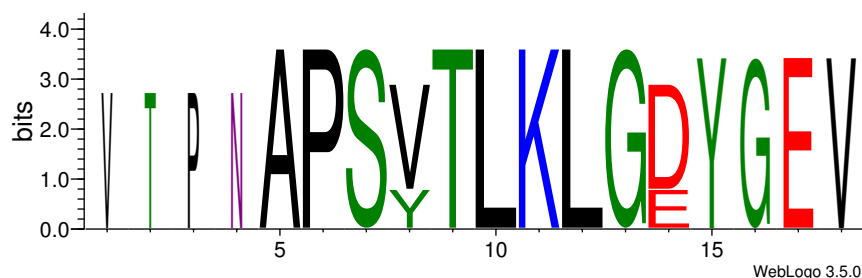
cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2727	PPGTLAVNVSPPLT	_____PPGTLAVNVSPPLT__	17	10	7
2727	SPPGTLAVNVSPPL	_____SPPGTLAVNVSPPL__	8	0	8
2727	QGLTESPPGTLAVNVSPPLTFS	QGLTESPPGTLAVNVSPPLTFS	6	0	6
2727	PGTLAVNVSPPLTF	_____PGTLAVNVSPPLTF_	6	0	6

alignment	LUThrs	GeneName	start	structure	Group	Score
_____PGTLAVNVSPPLTF_	X23756	CAV-2-F-SH01	41	14aa	mRNA_3000cpc_Organoid_MD101	6
_____PGTLAVNVSPPLTF_	X23756	CAV-2-F-Toronto-A26-61	41	14aa	mRNA_3000cpc_Organoid_MD101	6
_____PPGTLAVNVSPPLT__	X22192	CAV-2-F-SH01	40	14aa	mRNA_30cpc_Organoid_MD114	10
_____PPGTLAVNVSPPLT__	X22192	CAV-2-F-Toronto-A26-61	40	14aa	mRNA_30cpc_Organoid_MD114	10
_____PPGTLAVNVSPPLT__	X22192	CAV-2-F-SH01	40	14aa	mRNA_3000cpc_Organoid_MD101	7
_____PPGTLAVNVSPPLT__	X22192	CAV-2-F-Toronto-A26-61	40	14aa	mRNA_3000cpc_Organoid_MD101	7
QGLTESPPGTLAVNVSPPLTFS	X20051	CAV-2-F-SH01	34	22aa	mRNA_3000cpc_Organoid_MD101	6
QGLTESPPGTLAVNVSPPLTFS	X20051	CAV-2-F-Toronto-A26-61	34	22aa	mRNA_3000cpc_Organoid_MD101	6
_____SPPGTLAVNVSPPL__	X11599	CAV-2-F-SH01	39	14aa	mRNA_3000cpc_Organoid_MD101	8
_____SPPGTLAVNVSPPL__	X11599	CAV-2-F-Toronto-A26-61	39	14aa	mRNA_3000cpc_Organoid_MD101	8

[1] 2485

Peptide APSVTLKLG DYGEV from JEV-E-BN19 with cluster number 2485

Peptide APSVTLKLG DYGEV from JEV-E-BN19 with cluster number



cluster_id	main_sequence	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2485	APSVTLKLG DYGEV	37	30	7

cluster_id	sequence	alignment	sum	mRNA_30cpc_Organoid_MD114	mRNA_3000cpc_Organoid_MD101
2485	APSVTLKLG DYGEV	___APSVTLKLG DYGEV	17	10	7
2485	VTPNAPSVTLKLGD	VTPNAPSVTLKLGD___	10	10	0
2485	APSYTLKLGEYGEV	___APSYTLKLGEYGEV	10	10	0

alignment	LUThrs	GeneName	start	structure	Group	Score
___APSVTLKLG DYGEV	X41617	JEV-E-BN19	173	14aa	mRNA_30cpc_Organoid_MD114	10
___APSVTLKLG DYGEV	X41617	JEV-E-KE-093	173	14aa	mRNA_30cpc_Organoid_MD114	10
___APSVTLKLG DYGEV	X41617	JEV-E-SA14-5-3	173	14aa	mRNA_30cpc_Organoid_MD114	10
___APSVTLKLG DYGEV	X41617	JEV-E-ThCMAr4492	173	14aa	mRNA_30cpc_Organoid_MD114	10
___APSVTLKLG DYGEV	X41617	JEV-E-BN19	173	14aa	mRNA_3000cpc_Organoid_MD101	7
___APSVTLKLG DYGEV	X41617	JEV-E-KE-093	173	14aa	mRNA_3000cpc_Organoid_MD101	7
___APSVTLKLG DYGEV	X41617	JEV-E-SA14-5-3	173	14aa	mRNA_3000cpc_Organoid_MD101	7
___APSVTLKLG DYGEV	X41617	JEV-E-ThCMAr4492	173	14aa	mRNA_3000cpc_Organoid_MD101	7
___APSYTLKLGEYGEV	X41628	WNV-E-AZ10-918	173	14aa	mRNA_30cpc_Organoid_MD114	10
___APSYTLKLGEYGEV	X41628	WNV-E-ArD76104	169	14aa	mRNA_30cpc_Organoid_MD114	10
___APSYTLKLGEYGEV	X41628	WNV-E-H-442	173	14aa	mRNA_30cpc_Organoid_MD114	10
VTPNAPSVTLKLGD___	X58291	JEV-E-BN19	169	14aaA5	mRNA_30cpc_Organoid_MD114	10
VTPNAPSVTLKLGD___	X58291	JEV-E-KE-093	169	14aaA5	mRNA_30cpc_Organoid_MD114	10
VTPNAPSVTLKLGD___	X58291	JEV-E-SA14-5-3	169	14aaA5	mRNA_30cpc_Organoid_MD114	10
VTPNAPSVTLKLGD___	X58291	JEV-E-ThCMAr4492	169	14aaA5	mRNA_30cpc_Organoid_MD114	10

```
# setkey(select.samples.trsp,Peptide) select.samples.trsp.select <-
# select.samples.trsp[J(c('PPDELNLTTASLPL'))]
```

```
print("Total analysis time:")
```

```
[1] "Total analysis time:"
```

```
print(Sys.time() - strt1)
```

```
Time difference of 1.549723 mins
```

```
devtools::session_info()
```

```
Session info -----
```

```
setting  value
version  R version 3.4.2 (2017-09-28)
system   x86_64, linux-gnu
ui        X11
language (EN)
collate   en_US.UTF-8
tz        UTC
date      2020-11-05
```

```
Packages -----
```

package	* version	date	source
ade4	1.7-8	2017-08-09	CRAN (R 3.4.2)
backports	1.1.1	2017-09-25	CRAN (R 3.4.2)
base	* 3.4.2	2017-10-06	local
compiler	3.4.2	2017-10-06	local
data.table	* 1.10.4-2	2017-10-12	url
datasets	* 3.4.2	2017-10-06	local
devtools	* 1.13.3	2017-08-02	CRAN (R 3.4.2)
digest	0.6.12	2017-01-27	CRAN (R 3.4.2)
evaluate	0.10.1	2017-06-24	CRAN (R 3.4.2)
formatR	1.5	2017-04-25	CRAN (R 3.4.2)
graphics	* 3.4.2	2017-10-06	local
grDevices	* 3.4.2	2017-10-06	local
highr	0.6	2016-05-09	CRAN (R 3.4.2)
hms	0.3	2016-11-22	CRAN (R 3.4.2)
htmltools	0.3.6	2017-04-28	CRAN (R 3.4.2)
httr	1.3.1	2017-08-20	CRAN (R 3.4.2)
kableExtra	* 0.5.2	2017-09-15	url
knitr	* 1.17	2017-08-10	CRAN (R 3.4.2)
magrittr	1.5	2014-11-22	CRAN (R 3.4.2)
memoise	1.1.0	2017-04-21	CRAN (R 3.4.2)
methods	3.4.2	2017-10-06	local
parallel	* 3.4.2	2017-10-06	local
plyr	1.8.4	2016-06-08	CRAN (R 3.4.2)
R6	2.2.2	2017-06-17	CRAN (R 3.4.2)
Rcpp	0.12.13	2017-09-28	url
readr	1.1.1	2017-05-16	CRAN (R 3.4.2)
reshape2	* 1.4.2	2016-10-22	CRAN (R 3.4.2)
rlang	0.1.2	2017-08-09	CRAN (R 3.4.2)
rmarkdown	1.6	2017-06-15	url
rprojroot	1.2	2017-01-16	CRAN (R 3.4.2)
rvest	0.3.2	2016-06-17	CRAN (R 3.4.2)
seqinr	* 3.4-5	2017-08-01	CRAN (R 3.4.2)

stats	* 3.4.2	2017-10-06	local
stringi	1.1.5	2017-04-07	url
stringr	1.2.0	2017-02-18	CRAN (R 3.4.2)
tibble	1.3.4	2017-08-22	CRAN (R 3.4.2)
tools	3.4.2	2017-10-06	local
utils	* 3.4.2	2017-10-06	local
withr	2.0.0	2017-07-28	url
xml2	1.1.1	2017-01-24	CRAN (R 3.4.2)
yaml	2.1.14	2016-11-12	CRAN (R 3.4.2)