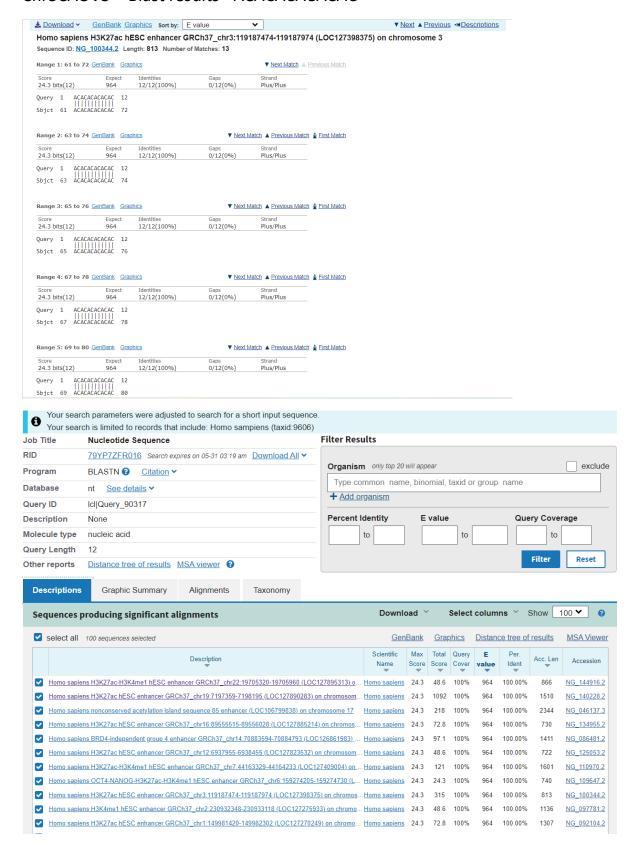
Chr3CAOV3 - Blast results - ACACACACACAC



Chr3HLT -Blast Results – TGTTTGTTTGTT

| | Description | Scientific Name | Max Score | Total Score | | E value | Per. | Acc. Len | Accession |
|--------------|--|--------------------|--------------|----------------|------|------------|---------|----------|-------------|
| ~ | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 18307 | 100% | 964 | 100.00% | 19127894 | OX419549.1 |
| \checkmark | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 17555 | 100% | 964 | 100.00% | 18621146 | OX419651.1 |
| \checkmark | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 17093 | 100% | 964 | 100.00% | 19647028 | OX419546.1 |
| ~ | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 17069 | 100% | 964 | 100.00% | 21334752 | OX419650.1 |
| ~ | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 16948 | 100% | 964 | 100.00% | 20898827 | OX419649.1 |
| \checkmark | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 16826 | 100% | 964 | 100.00% | 21483326 | OX419548.1 |
| \checkmark | Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 15345 | 100% | 964 | 100.00% | 20047005 | OX419547.1 |
| ~ | Homo sapiens Sharpr-MPRA regulatory regions 192 and 10030 (LOC121392918) on chromosome 11 | Homo sapiens | 24.3 | 145 | 100% | 964 | 100.00% | 841 | NG_074575.4 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid active region 18963 (LOC130067363) on chromosome 22 | Homo sapiens | 24.3 | 121 | 100% | 964 | 100.00% | 250 | NG_201778.1 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid silent region 10792 (LOC130064721) on chromosome 19 | Homo sapiens | 24.3 | 97.1 | 100% | 964 | 100.00% | 590 | NG_199138.1 |
| ~ | Homo sapiens ATAC-STARR-seq.lymphoblastoid silent region 7215 (LOC130058513) on chromosome 16 | Homo sapiens | 24.3 | 97.1 | 100% | 964 | 100.00% | 370 | NG_192934.1 |
| \checkmark | Homo sapiens ATAC-STARR-seq.lymphoblastoid active region 3750 (LOC130004313) on chromosome 10 | Homo sapiens | 24.3 | 97.1 | 100% | 964 | 100.00% | 510 | NG_183758.1 |
| ~ | Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr17;74993993-74994533 (LOC12788806 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 776 | NG_137672.2 |
| ~ | Homo sapiens H3K27ac hESC enhancer GRCh37_chr2:120517730-120518354 (LOC127274538) on chro | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 855 | NG_096388.2 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid active region 14100 (LOC130063679) on chromosome 19 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 250 | NG_198096.1 |
| \checkmark | Homo sapiens ATAC-STARR-seq.lymphoblastoid silent region 9559 (LOC130062743) on chromosome 18 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 280 | NG_195635.1 |
| \checkmark | Homo sapiens ATAC-STARR-seq.lymphoblastoid active region 12269 (LOC130061001) on chromosome 17 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 250 | NG_196237.1 |
| ~ | Homo sapiens ATAC-STARR-seq.lymphoblastoid active region 9926 (LOC130057708) on chromosome 15 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 250 | NG_192129.1 |
| ~ | Homo sapiens ATAC-STARR-seq.lymphoblastoid active region 9554 (LOC130057262) on chromosome 15 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 930 | NG_191683.1 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid active region 5707 (LOC130007029) on chromosome 11 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 490 | NG_186473.1 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid active region 4417 (LOC130005287) on chromosome 11 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 350 | NG_184732.1 |
| ~ | Homo sapiens ATAC-STARR-seq.lymphoblastoid active region 4360 (LOC130005219) on chromosome 11 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 250 | NG_184664.1 |
| ~ | Homo sapiens ATAC-STARR-seg lymphoblastoid active region 25763 (LOC129998116) on chromosome 7 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 250 | NG_177557.1 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid active region 25211 (LOC129997365) on chromosome 6 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 900 | NG_176811.1 |
| \checkmark | Homo sapiens H3K4me1 hESC enhancer GRCh37_chr7:65509069-65509569 (LOC127409359) on chrom | . Homo sapiens | 24.3 | 48.6 | 100% | 964 | 100.00% | 751 | NG_111324.2 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid silent region 20893 (LOC130068405) on chromosome X | Homo sapiens | 24.3 | 48.6 | 100% | 964 | 100.00% | 320 | NG_202820.1 |
| ~ | Homo sapiens ATAC-STARR-seq lymphoblastoid active region 18862 (LOC130067256) on chromosome 22 | Homo sapiens | 24.3 | 48.6 | 100% | 964 | 100.00% | 260 | NG_201671.1 |

chr3MFE280-Blast – TTTTTTTTTTT

| Seq | uences producing significant alignments | Downlo | oad Y | S | elect | colum | ns Y | Show | 100 🗸 |
|------------|---|--------------------|--------------|----------------|-------|---------------|---------------|-------------|-------------|
| Z : | select all 100 sequences selected | Gen | <u>Bank</u> | Graph | nics | <u>Distan</u> | ce tree of | result | MSA View |
| | Description | Scientific Name | Max Score | Total Score | | E value | Per. Ident | Acc. Len | Accession |
| ~ | Homo sapiens IFNGR2 promoter region (LOC119266102) on chromosome 21 | Homo sapiens | 24.3 | 704 | 100% | 964 | 100.00% | 1874 | NG_070955.3 |
| ~ | Homo sapiens STAR 5' regulatory region (LOC108863620) on chromosome 8 | Homo sapiens | 24.3 | 704 | 100% | 964 | 100.00% | 3910 | NG_051673.3 |
| ~ | Homo sapiens hESC enhancers GRCh37_chr12:120727716-120728708 and GRCh37_chr12:120728709-120 | Homo sapiens | 24.3 | 631 | 100% | 964 | 100.00% | 2225 | NG_079835.3 |
| ~ | Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr19:2085331-2086056 (LOC127889950) on c | Homo sapiens | 24.3 | 485 | 100% | 964 | 100.00% | 968 | NG_139913.2 |
| ~ | Homo sapiens ReSE screen-validated silencer GRCh37_chr12:34175251-34175437 (LOC129663121) on chr | Homo sapiens | 24.3 | 461 | 100% | 964 | 100.00% | 450 | NG_160127.2 |
| ~ | Homo sapiens NANOG-H3K27ac-H3K4me1 hESC enhancer GRCh37_chr17:27070105-27071105 (LOC11252 | . Homo sapiens | 24.3 | 461 | 100% | 964 | 100.00% | 1383 | NG_056893.3 |
| ~ | Homo sapiens CDK7 strongly-dependent group 2 enhancer GRCh37_chr8:102655529-102656728 (LOC1268 | Homo sapiens | 24.3 | 388 | 100% | 964 | 100.00% | 1405 | NG_084961.2 |
| ~ | Homo sapiens ReSE screen-validated silencer GRCh37_chr15:85924371-85924538 (LOC129663677) on chr | Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 770 | NG_160683.2 |
| ~ | Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr12:120876089-120876610 (LOC127825326) | . Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 858 | NG_126839.2 |
| ~ | Homo sapiens H3K4me1 hESC enhancer GRCh37_chr11:65990246-65990746 (LOC127821528) on chromos | Homo sapiens | 24.3 | 315 | 100% | 964 | 100.00% | 746 | NG_122977.2 |
| ~ | Homo sapiens H3K4me1 hESC enhancer GRCh37_chr10:104192697-104193332 (LOC127819038) on chrom | Homo sapiens | 24.3 | 315 | 100% | 964 | 100.00% | 937 | NG_120510.2 |
| ~ | Homo sapiens H3K27ac hESC enhancer GRCh37_chr17:29036042-29036718 (LOC127886427) on chromoso | . Homo sapiens | 24.3 | 291 | 100% | 964 | 100.00% | 997 | NG_139311.2 |
| ~ | Homo sapiens MPRA-validated peak1891 silencer (LOC129390529) on chromosome 12 | Homo sapiens | 24.3 | 291 | 100% | 964 | 100.00% | 556 | NG_156159.2 |
| ~ | Homo sapiens H3K4me1 hESC enhancer GRCh37_chr7:100751090-100752040 (LOC127457183) on chromo | . Homo sapiens | 24.3 | 291 | 100% | 964 | 100.00% | 1166 | NG_111957.2 |
| ~ | Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr17:2496154-2496882 (LOC127885423) on c | Homo sapiens | 24.3 | 267 | 100% | 964 | 100.00% | 983 | NG_135164.2 |
| ~ | Homo sapiens isolate UA2022tp1237 MHC class II antigen (HLA-DRB5) gene, HLA-DRB5*01:999N allele, co | Homo sapiens | 24.3 | 267 | 100% | 964 | 100.00% | 12554 | OQ059337.1 |
| ~ | Homo sapiens Sharpr-MPRA regulatory region 5179 (LOC113839514) on chromosome 9 | Homo sapiens | 24.3 | 267 | 100% | 964 | 100.00% | 517 | NG_063131.2 |
| ~ | Homo sapiens H3K27ac hESC enhancer GRCh37_chr19:9895653-9896484 (LOC127890392) on chromosom | Homo sapiens | 24.3 | 242 | 100% | 964 | 100.00% | 1085 | NG_140330.2 |
| ~ | Homo sapiens H3K27ac hESC enhancer GRCh37_chr18:12948589-12949190 (LOC127888846) on chromoso | . Homo sapiens | 24.3 | 242 | 100% | 964 | 100.00% | 833 | NG_138411.2 |
| ~ | Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr15:41835695-41836276 (LOC127829362) o | Homo sapiens | 24.3 | 242 | 100% | 964 | 100.00% | 1105 | NG_130844.2 |
| ~ | Homo sapiens NANOG-H3K27ac hESC enhancer GRCh37_chr9:79085403-79086064 (LOC127814962) on c | Homo sapiens | 24.3 | 242 | 100% | 964 | 100.00% | 876 | NG_116480.2 |
| ~ | Homo sapiens H3K27ac hESC enhancer GRCh37_chr9:33043981-33044482 (LOC127814615) on chromoso | Homo sapiens | 24.3 | 242 | 100% | 964 | 100.00% | 876 | NG_116136.2 |
| ~ | Homo sapiens H3K27ac hESC enhancer GRCh37 chr8:61428694-61429554 (LOC127459619) on chromoso | Homo sapiens | 24.3 | 242 | 100% | 964 | 100.00% | 1506 | NG 114388.2 |

chr3MFE319 - Blast - AAGAAAGAAAGA

| Des | criptions | Graphic Summary | Alignments | Taxonomy | | | | | | | | | |
|-----|---------------|----------------------------|--------------------------|-------------------|--------------------|--------------------|--------------|----------------|----------------|---------------|------------|----------|-------------|
| Seq | uences pro | oducing significant al | lignments | | | Downlo | ad Y | S | elect | colum | ns Y | Show 1 | 00 🕶 🔞 |
| ☑ : | select all 10 | 00 sequences selected | | | | <u>Genl</u> | Bank | Graph | nics . | <u>Distan</u> | ce tree of | results | MSA Viewer |
| | | | Description | | | Scientific Name | Max Score | Total Score | Query Cover | E value | Per. | Acc. Len | Accession |
| ~ | Homo sapiens | genome assembly, chromosom | ie: Y | | | Homo sapiens | 24.3 | 20881 | 100% | 964 | 100.00% | 19127894 | OX419549.1 |
| ✓ | Homo sapiens | genome assembly, chromosom | ie: Y | | | Homo sapiens | 24.3 | 19522 | 100% | 964 | 100.00% | 19647028 | OX419546.1 |
| ~ | Homo sapiens | genome assembly, chromosom | ie: Y | | | Homo sapiens | 24.3 | 19497 | 100% | 964 | 100.00% | 21334752 | OX419650.1 |
| ~ | Homo sapiens | genome assembly, chromosom | ie: Y | | | Homo sapiens | 24.3 | 19327 | 100% | 964 | 100.00% | 20898827 | OX419649.1 |
| ✓ | Homo sapiens | genome assembly, chromosom | ie: Y | | | Homo sapiens | 24.3 | 18842 | 100% | 964 | 100.00% | 18621146 | OX419651.1 |
| ~ | Homo sapiens | genome assembly, chromosom | <u>ie: Y</u> | | | Homo sapiens | 24.3 | 18453 | 100% | 964 | 100.00% | 21483326 | OX419548.1 |
| ~ | Homo sapiens | genome assembly, chromosom | ie: Y | | | Homo sapiens | 24.3 | 2986 | 100% | 964 | 100.00% | 20047005 | OX419547.1 |
| ~ | Homo sapiens | H3K27ac-H3K4me1 hESC enh | ancer GRCh37_chr13: | 41019797-41020402 | (LOC127826147) o | Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 915 | NG_127654.2 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 6471 | (LOC130008047) on | chromosome 12 | Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 250 | NG_186712.1 |
| ✓ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 10592 | (LOC130058671) o | n chromosome 16 | Homo sapiens | 24.3 | 267 | 100% | 964 | 100.00% | 330 | NG_193092.1 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 29516 | (LOC130068089) o | n chromosome X | Homo sapiens | 24.3 | 121 | 100% | 964 | 100.00% | 250 | NG_202504.1 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 29515 | (LOC130068088) o | n chromosome X | Homo sapiens | 24.3 | 121 | 100% | 964 | 100.00% | 260 | NG_202503.1 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid silent region 20730 | (LOC130068087) or | chromosome X | Homo sapiens | 24.3 | 121 | 100% | 964 | 100.00% | 330 | NG_202502.1 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 29427 | (LOC130067955) o | n chromosome X | Homo sapiens | 24.3 | 121 | 100% | 964 | 100.00% | 250 | NG_202370.1 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 9253 | (LOC130056860) on | chromosome 15 | Homo sapiens | 24.3 | 121 | 100% | 964 | 100.00% | 250 | NG_191281.1 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid silent region 3512 (| LOC130006000) on | chromosome 11 | Homo sapiens | 24.3 | 97.1 | 100% | 964 | 100.00% | 260 | NG_185445.1 |
| ✓ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 26535 | (LOC129999171) o | n chromosome 7 | Homo sapiens | 24.3 | 97.1 | 100% | 964 | 100.00% | 300 | NG_178617.1 |
| ✓ | Homo sapiens | H3K27ac-H3K4me1 hESC enh | ancer GRCh37_chr19: | 383808-384334 (LO | C127889770) on chr | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 735 | NG_139740.2 |
| ~ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 29466 | (LOC130068007) o | n chromosome X | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 350 | NG_202422.1 |
| ✓ | Homo sapiens | ATAC-STARR-seq lymphoblast | oid active region 13480 | (LOC130062698) o | n chromosome 18 | Homo sapiens | 24.3 | 72.8 | 100% | 964 | 100.00% | 250 | NG_195590.1 |
| | | | | | | | | | | | | | |

chr3SKOV3_OVARY - blast - CACACACACACA

| Graphic Summary Alignments Taxonomy | | | | | | | | |
|--|--------------------|--------------|----------------|-------|------------|---------------|----------|------------|
| equences producing significant alignments | Downlo | ad ~ | S | elect | colum | ns Y | Show 1 | 00 🗸 |
| select all 100 sequences selected | Gen | Bank | Graph | nics | Distan | ce tree of | results | MSA Viewe |
| Description | Scientific Name | Max Score | Total Score | | E value | Per. Ident | Acc. Len | Accession |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 20517 | 100% | 964 | 100.00% | 18621146 | OX419651.1 |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 18890 | 100% | 964 | 100.00% | 19127894 | OX419549.1 |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 17093 | 100% | 964 | 100.00% | 19647028 | OX419546.1 |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 14787 | 100% | 964 | 100.00% | 21334752 | OX419650.1 |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 13403 | 100% | 964 | 100.00% | 21483326 | OX419548.1 |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 11994 | 100% | 964 | 100.00% | 20898827 | OX419649.1 |
| Homo sapiens genome assembly, chromosome: Y | Homo sapiens | 24.3 | 2088 | 100% | 964 | 100.00% | 20047005 | OX419547.1 |
| Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr17:75462088-75462839 (LOC127888118) on | Homo sapiens | 24.3 | 509 | 100% | 964 | 100.00% | 1033 | NG_137725 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 17840 (LOC130065821) on chromosome 20 | Homo sapiens | 24.3 | 485 | 100% | 964 | 100.00% | 270 | NG_200238 |
| Homo sapiens H3K4me1 hESC enhancer GRCh37_chr10:88726172-88726925 (LOC127818706) on chromos | Homo sapiens | 24.3 | 461 | 100% | 964 | 100.00% | 974 | NG_120178 |
| Homo sapiens ATAC-STARR-seg lymphoblastoid silent region 13655 (LOC130067298) on chromosome 22 | Homo sapiens | 24.3 | 461 | 100% | 964 | 100.00% | 280 | NG_201713 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 3263 (LOC130003680) on chromosome 10 | Homo sapiens | 24.3 | 461 | 100% | 964 | 100.00% | 250 | NG_183126 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 3698 (LOC130004248) on chromosome 10 | Homo sapiens | 24.3 | 437 | 100% | 964 | 100.00% | 250 | NG_183694 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid silent region 12869 (LOC130065779) on chromosome 20 | Homo sapiens | 24.3 | 412 | 100% | 964 | 100.00% | 250 | NG_200196 |
| Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr12:129338353-129339004 (LOC127825666) | Homo sapiens | 24.3 | 388 | 100% | 964 | 100.00% | 913 | NG_127178 |
| Homo sapiens H3K4me1 hESC enhancer GRCh37_chr4:109088159-109088660 (LOC127401317) on chromo | Homo sapiens | 24.3 | 388 | 100% | 964 | 100.00% | 819 | NG_103280 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 18995 (LOC130067400) on chromosome 22 | Homo sapiens | 24.3 | 388 | 100% | 964 | 100.00% | 370 | NG_201815 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 4384 (LOC130005244) on chromosome 11 | Homo sapiens | 24.3 | 388 | 100% | 964 | 100.00% | 270 | NG_184689 |
| Homo sapiens Sharpr-MPRA regulatory region 13989 (LOC121740689) on chromosome 7 | Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 590 | NG_075751 |
| Homo sapiens H3K4me1 hESC enhancer GRCh37_chr1:15438940-15439518 (LOC127267588) on chromoso. | Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 789 | NG_089463 |
| Homo sapiens chromosome 10 open reading frame 71 (C10orf71) mRNA, partial cds | Homo sapiens | 24.3 | 364 | 100% | 964 | 100.00% | 2127 | OQ575334. |
| Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr19:45958106-45959072 (LOC127891742) o. | Homo sapiens | 24.3 | 339 | 100% | 964 | 100.00% | 1179 | NG_141595 |
| Homo sapiens H3K27ac hESC enhancer GRCh37_chr15:65134214-65134737 (LOC127829773) on chromoso | Homo sapiens | 24.3 | 339 | 100% | 964 | 100.00% | 971 | NG_131255 |
| Homo sapiens H3K27ac-H3K4me1 hESC enhancer GRCh37_chr2:25500333-25500922 (LOC127272861) on | Homo sapiens | 24.3 | 339 | 100% | 964 | 100.00% | 1322 | NG_094712 |
| Homo sapiens ATAC-STARR-seq lymphoblastoid active region 29644 (LOC130068294) on chromosome X | Homo sapiens | 24.3 | 339 | 100% | 964 | 100.00% | 270 | NG_202709 |