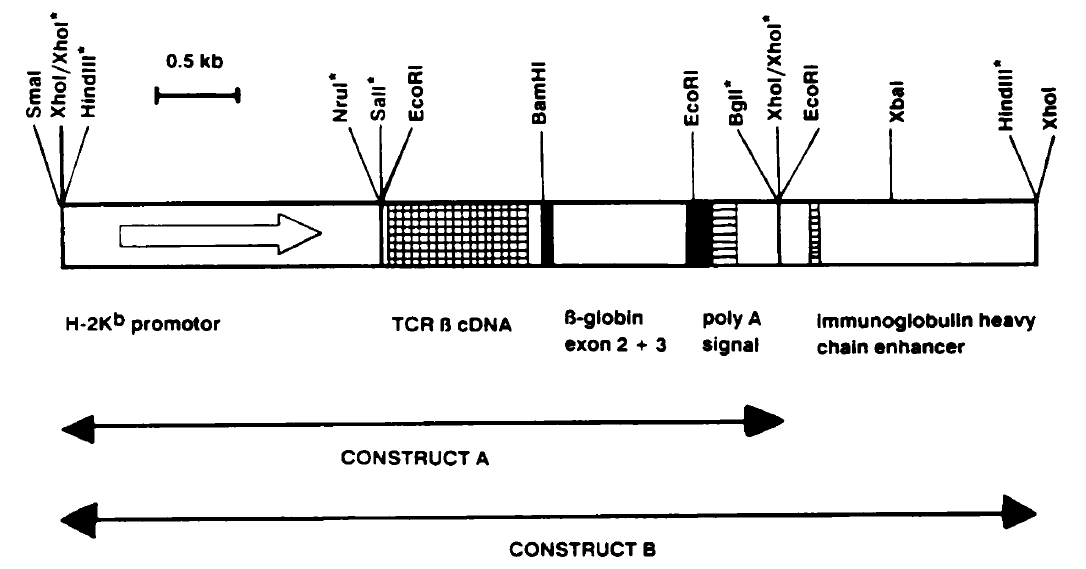
Figure 1. Annotated A-Tram dnRAG1 transgene sequence assembly

dnRAG1 mouse F56

>1\_NODE\_1\_length\_8614\_cov\_14.111397\_REV iteration=1 contig\_id=NODE\_1\_length\_8614\_cov\_14.111397 score=14041.2

**ACTCTGGGGCCAACTCAATTATCAGAACCCGTGTCCCACACAGCTGTGACATTCATGTCCCTCACCTCATCAGC**TCAAAAGTGTGAGTGAAGGTCAGGGAGGGAGGGAGAGGGTCAGAGATTACATAACTTCTACCACACTAGCATCCTTATTCTGTGTTATAGTTGGTGACAGCTCCTCTCCTACTGTGATTGAGTCACTAAAGCAACTGCACCATGGAAGTGCAGACACAGAGAAGTCCAGTGGAGACAGGGATCAGTGCCCTGCTGTCTGTGGTCTGCACGGGGTCTCTCTTCAGTGGACAAGGGGGTCTCCTGTGCTGAGACAATGTCCCAGATCCACAGAGACAAACTCAGGACTCAGAATGAAGATCCTTGTTTCAAATACACACACACACACATACACACACACACACACACACACACACACACACACACACACCTGCAGCCACAGACTTTTCATCTAGGAATTAACACAAGGAATCTGTGTCTCAGCACAGGGCTGAGAAGACAGATCCTGAGGGGAGAGGCAAAGTCTACACTTAACAGATGAGAGTCCTGCACTCAGGCTTGGCAGTGTGAGCCGCCCATTGCAGGTGAACAGAGCCTGGTCTCTGTGGGGTCCCTGTGGGGCTTGCAGCCCAGCGCCTTGACTTTAAGGAAAAGCCTCTCTCTCCACTGCATCCCTAAGCGCTTGTGTCGCCATTGTATTCCCGGAAGAGGCTTTTCTTCTAGAAGACTCCAGGGTCTGACTTCTGAAGAGAAGAAGAAAGAGGAAGAGTGGAAGAGAGGACACAGAGAGTCTGGCCTGCGGGTCTCTCCTGGTGTTTTGAGAGTTTCTGGATCAGAACTCGGAGACGACAGCACAGGGTTCAGGCAAAGTCTTAGTCGCCAGGCAGTGAGGTCAGGGGTGGGGAAGCCCAGGGCTGGGGATTCCCCATCTCCACAGTTTCACTTCTGCACCTAACCTGGGTCAGGTCCTTCTGTCCGGACACTGTTGACGCGCAGTCAGCTCTTACCCCCATTGGGTGGCGCGATCACCAAGAACCAATCAGTGTCGCCGCGGACGCTGGATATAAAGTCCACGCAGCCCGCAGAACTCAGAAGTCGTG**GTCGACTCTAGAGGATCC**AC**ATG**GCTGCCTCCTTGCCGTCTACCCTGAGCTTCAGTTCTGCACCCGATGAAATTCAACACCCACAAATCAAATTTTCCGAGTGGAAATTTAAGCTGTTTAGGGTGAGATCCTTTGAAAAGGCACCCGAAGAAGCACAGAAGGAGAAGGATTCCTCAGAGGGGAAACCTTACCTAGAACAGTCTCCAGTAGTTCCAGAGAAGCCTGGTGGTCAGAACTCAATTCTGACTCAACGAGCACTGAAACTCCATCCTAAATTTTCAAAGAAATTCCATGCTGATGGGAAGTCAAGCGACAAAGCAGTTCACCAAGCCAGGCTTAGACACTTCTGCCGCATCTGTGGGAATCGTTTCAAGAGTGACGGGCACAGCCGGAGATACCCAGTCCACGGGCCCGTGGACGCTAAAACCCAAAGTCTTTTCCGAAAGAAGGAAAAAAGAGTCACTTCCTGGCCAGACCTCATTGCCAGGATTTTCCGGATCGACGTGAAGGCAGATGTTGACTCCATCCACCCGACGGAATTCTGCCATGACTGTTGGAGCATCATGCACAGAAAGTTCAGCAGTTCCCACAGTCAGGTCTACTTCCCAAGGAAAGTGACCGTGGAGTGGCACCCCCACACACCGTCCTGTGACATCTGTTTTACTGCCCATCGGGGACTCAAGAGGAAGAGACATCAGCCCAATGTGCAGCTCAGCAAGAAACTAAAAACTGTGCTCAACCACGCGAGACGGGACCGTCGCAAGAGAACTCAGGCTAGGGTCAGCAGCAAGGAAGTCCTGAAGAAGATCTCCAACTGCAGTAAGATTCATCTCAGTACCAAGCTTCTTGCCGTGGACTTCCCAGCACACTTTGTGAAATCCATCTCCTGCCAGATATGCGAACACATTCTGGCTGATCCCGTGGAGACCAGCTGCAAGCATCTATTCTGTAGGATCTGCATTCTCAGATGTCTCAAAGTCATGGGCAGCTATTGTCCCTCTTGCCGATATCCGTGCTTCCCTACTGACCTGGAGAGCCCAGTGAAGTCCTTTCTGAACATCTTGAATTCTCTCATGGTCAAGTGTCCCGCGCAAGATTGCAATGAGGAAGTGAGTCTGGAAAAATATAACCACCATGTGTCAAGCCACAAAGAATCTAAAGAGACTTTGGTGCATATCAATAAAGGGGGACGGCCTCGCCAGCATCTCCTGTCACTGACGAGAAGGGCGCAGAAACATCGGCTGAGGGAGCTCAAGATTCAAGTCAAAGAATTTGCTGACAAAGAAGAAGGTGGAGATGTGAAGGCTGTCTGCTTGACATTGTTTCTCCTGGCACTGAGGGCGAGGAATGAGCACAGGCAAGCTGATGAATTAGAGGCCATCATGCAAGGCAGGGGCTCCGGGCTTCAACCAGCTGTTTGCTTGGCCATCCGTGTCAATACCTTCCTCAGCTGTAGCCAATACCATAAGATGTACAGGACTGTGAAAGCTATCACTGGGAGGCAGATTTTTCAACCTTTGCATGCTCTTCGGAATGCCGAGAAAGTCCTTCTGCCAGGCTACCATCCCTTTGAGTGGCAGCCCCCACTGAAGAATGTGTCCTCCAGAACTGATGTTGGAATTATTGATGGGCTGTCTGGACTTGCCTCCTCTGTGGATGAGTACCCAGTAGATACCATTGCGAAGAGGTTCCGCTACGACTCTGCTTTGGTGTCTGCTTTGATGGACATGGAAGAAGACATCTTGGAAGGCATGAGATCCCAAGATCTTGATGACTACCTGAATGGTCCCTTCACAGTGGTGGTAAAGGAGTCTTGC**GCA**GGAATGGGGGATGTGAGTGAGAAGCACGGGAGTGGGCCCGCAGTTCCAGAAAAGGCCGTTCGTTTCTCTTTCACAGTCATGAGAATTACGATAGAGCATGGTTCACAGAACGTGAAGGTGTTTGAGGAACCCAAGCCCAATTCTGAACTGTGTTGCAAGCCGTTGTGTCTTATGCTGGCAGATGAGTCTGACCATGAGACCCTTACTGCTATTCTAAGCCCCCTCATTGCCGAGAGGGAGGCCATGAAGAGCAGTGAATTAACGCTGGAGATGGGAGGCATCCCCAGGACTTTTAAATTCATCTTCAGGGGCACCGGTTAC**GCT**GAAAAACTTGTCCGGGAAGTAGAAGGCTTGGAAGCTTCTGGCTCAGTCTACATCTGTACACTCTGTGACACCACCCGTTTGGAAGCCTCTCAGAATCTTGTCTTCCACTCCATAACCAGAAGCCACGCCGAGAACCTGCAGCGCTATGAGGTCTGGCGGTCCAATCCGTATCATGAGTCCGTGGAAGAGCTCCGGGACCGGGTGAAAGGGGTCTCTGCCAAACCTTTCATCGAGACAGTCCCTTCCATAGATGCGCTTCACTGTGACATTGGCAATGCAGCTGAATTCTATAAGATTTTCCAGCTGGAGATAGGGGAAGTGTATAAACATCCCAATGCCTCTAAAGAGGAAAGGAAGAGATGGCAGGCCACGCTGGACAAACATCTCCGGAAAAGGATGAACTTAAAACCAATCATGAGGATGAATGGCAACTTTGCCCGGAAGCTTATGACCCAAGAGACTGTAGACGCAGTTTGTGAGTTAATTCCTTCTGAGGAGAGGCATGAAGCTCTCAGGGAGCTCATGGACCTTTACCTGAAGATGAAACCCGTGTGGCGCTCTTCATGTCCCGCTAAAGAGTGTCCAGAGTCCCTCTGTCAGTACAGTTTCAACTCACAGCGTTTCGCGGAACTCCTCTCCACCAAGTTCAAATATAGATACGAGGGCAAAATCACCAATTACTTTCACAAAACCTTGGCACATGTCCCTGAAATTATTGAAAGGGATGGCTCTATCGGGGCCTGGGCAAGTGAGGGAA**ATGCAT**CGGGTAACAAGCTGTTTAGACGGTTTCGGAAAATGAATGCCAGGCAGTCCAAGTGCTATGAGATGGAAGATGTCCTGAAACATCACTGGCTGTATACTTCAAAATACCTCCAGAAGTTTATGAATGCTCATAACGCGTTAAAAAGCTCTGGGTTTACCATGAACTCAAAGGAGACCTTAGGGGACCCTTTGGGCATTGAGGACTCTCTGGAAAGCCAAGATTCAATGGAGTTT**TAA**ATAGGATCTCC***GGATCC***TGAGAACTTCAGGGTGAGTCTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTTTCTATGGTTAAGTTCATGTCATAGGAAGGGGAGAAGTAACAGGGTACAGTTTAGAATGGGAAACAGACGAATGATTGCATCAGTGTGGAAGTCTCAGGATCGTTTTAGTTTCTTTTATTTGCTGTTCATAACAATTGTTTTCTTTTGTTTAATTCTTGCTTTCTTTTTTTTTCTTCTCCGCAATTTTTACTATTATACTTAATGCCTTAACATTGTGTATAACAAAAGGAAATATCTCTGAGATACATTAAGTAACTTAAAAAAAAACTTTACACAGTCTGCCTAGTACATTACTATTTGGAATATATGTGTGCTTATTTGCATATTCATAATCTCCCTACTTTATTTTCTTTTATTTTTAATTGATACATAATCATTATACATATTTATGGGTTAAAGTGTAATGTTTTAATATGTGTACACATATTGACCAAATCAGGGTAATTTTGCATTTGTAATTTTAAAAAATGCTTTCTTCTTTTAATATACTTTTTTGTTTATCTTATTTCTAATACTTTCCCTAATCTCTTTCTTTCAGGGCAATAATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAATAACAGTGATAATTTCTGGGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAACTGATGTAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTGCTTTTATTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCATGTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAA***GAATTC***ACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAATTTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAAGGGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACATTTATTTTCATTGCAATGATGTATTTAAATTATTTCTGAATATTTTACTAAAAAGGGAATGTGGGAGGTCAGTGCATTTAAAACATAAAGAAATGAAGAGCTAGTTCAAACCTTGGGAAAATACACTATATCTTAAACTCCATGAAAGAAGGTGAGGCTGCAAACAGCTAATGCACATTGGCAACAGCCCCTGATGCCTATGCCTTATTCATCCCTCAGAAAAGGATTCAAGTAGAGGCTTGATTTGGAGGTTAAAGTTTTGCTATGCTGTATTTTACATTACTTATTGTTTTAGCTGTCCTCATGAATGTCTTTTCACTACCCATTTGCTTATCCTGCATCTCTCAGCCTTGACTCCACTCAGTTCTCTTGCTTAGAGATACCACCTTTCCCCTGAAGTGTTCCTTCCATGTTTTACGGCGAGATGGTTTCTCCTCGCCTGGCCACTCAGCCTTAGTTGTCTCTGTTGTCTTATAGAGGTCTACTTGAAGAAGGAAAAACAGGGGGCATGGTTTGACTGTCCTGTGAGCCCTTCTTCCCTGCCTCCCCCACTCACAGTGACCCGGAATCTGCAG***GCATGC***AAGCTCAGATCCCCCCTCGAC***GGTACC***GTATCGC***GAGCTCGAATTC***TAAATACATTTTAGAAGTCGATAAACTTAAGTTTGGGGAAACTAGAACTACTCAAGCTAAAATTAAAAGGTTGAACTCAATAAGTTAAAAGAGGACCTCTCCAGTTTCGGCTGAATCCTCAACTTATTTTAGAAATGCAAATTACCCAGGTGGTGTTTTGCTCAGCCTGGACTTTCGGTTTGGTGGGGCTGGACAGAGTGTTTCAAAACCACTTCTTCAAACCACAGCTACAAGTTTACCTAGTGGTTTTATTTTCCCTTCCCCAAATAGCCTTGCCACATGACCTGCTTCCTGCCAGCTGCTGCAGGTGTTCTGGTTCTGATCGGCCATCTTGACTCCAACTCAACATTGCTCAATTCATTTAAAAATATTTTAAACTTAATTTATTATTGTTAAAAGTCAGTTCTGAATAGGGTATGAGAGAGCCTCACTCCCATTCCTCGGTTAAACTTTAAGTAATGTCAGTTCTACACAAACAAGACCTCAAATTGATTGACAAAAATTTTGGACATTTAAAAAAATGAGTACTTGAAAACCCTCTCACATTTTAAAGTCACAGTATTTAACTATTTTTCCTAGGAACCAACTTAAGAGTAAAAGCAACATCTTCTAATATTCCATACACATACTTCTGTGTTCCTTTGAAAGCTGGACTTTTGCAGGCTCCACCAGACCTCTCTAGACAGCAACTACCCTTTTGAGACCGAGGCTAGATGCCTTTCTCCCTTGACTCAATCACTAAGACAGCTCTCCTTCCAACAAATGAAGTTTTAAACAATCTAGTGTGGAACATTCCTCACAAATCTAAAGAAAGTGCCCCACTCCACTCTTTGTCCCTATGCATCGGATACTGTATAAATGCTGTCACAGAGGTGGTCCTGAAGTATATTCCGCAGCTAATACTTTTATTCTAAAAACTGAAAATCTCCAACTACAGCCCCAACTATCCCTCCAGCCATAGGATTGTTTTAGCATCTCCCTCAAATGAGCCTCCAAAGTCCCTATCCCATCATCCAGGGACTCCACCAACACCATCACACAGATTCTTAGTTTTTCAAAGATGTGGAGATAATCTGTCCTAAAGGCTCTGAGATCCCTAGACAGTTTATTTCCCAACTTCTCTCAGCCGGCTCCCTCAGGGACAAATATCCAAGATTAGTCTGCAATGCTCAGAAAACTCCATAACAAAGGTTAAAAATAAAGACCTGGAGAGGCCATTCTTACCT***GAGGAGACGGTGACTGAGGTTC***CTTGACCCCAGTAGTCCATAGCATAGTAATCACAATAGTGGATTTTTCCTCTATACCCGACAAAAACCCCAGAGTCTGACTAGAATCACCCCTGGGCAACTCAGACATTATGCCAATTCCTGGTGTCACACAAGAATCAACCATTCAAGTCATTGTTCCACATTCTGTTCCCTGCCTGTGCAGAAGCCCCCTGGACCCCTCTTAAGTCTTCAAGGTGACCTATATTCCAGCCTCACCTCAGAGAAACCAGACAGTCACTGACCCTGAAATTGTCACCATCAACTGTCAGCCCCTAATTCTCACAAGAGTCCGATAGACCCTGGACAAGATTCTGCCTCAGACTTCAAGCTCCC***GAATTCCTCGAG***GAGCTTGGCCCACAAGGAGTGGCAATGTTAGGAGTGTGACTGTGTTAGAGGAAGTGTGTCACTTTGAGGTTGGCCTTTGAGGTCTCCTATGCTCATGAGCTGCCCAGTGTGGAATGAAAGCCTCTTCCT***GGCTGCATTTGGATCAAGATG***TAGAAGTCTCCCCTTCTCCAGCACCATGTCTACCTGCACACTGGCATGCTTCCTGTCATGATGGACTAAATCCCTGAAACTGTAAGCCAGACCCTATTAAATGTCTCCCTTTAGAAGGAATGCCTTGGTCATGGTGTTTCTTCACAGCAACAAAACCAAAACTAACACACCCAGCACTTAGGATGCAAAGGCAGATGTATCTCTGTGAGTTCAAGGGCAGCCTGATCTACATAATGAATTACAGAATAGCCAGGGCTGTGCAGATAGACCTTGTCTAAACAAGCAAACAAACAAAACCCATAGTAAAATAAGAAGAAAAGTAATGGAGACAGATCCTTTGTGTAGCTGCCTAACCCCAACAGCATCCCTAGGTTGATCAGGAAGAAACCTAAGAGCATCAAGTCCCCATGGAAAATGCTCACAACATCTAATAAGAGGGGTTCAGGGAGACAGGGTCTGCTGAATCCTGGTGAGGCTGGGGGGCTGCTGTGGGGATCTGCATGGGGAGGTGACTGGAGTTCACACCTGTGGTCACACGCATTCATTGCTCTGTGTGATGAGTGACTCTCTTCAGGAGTCCCCACCCATCTATGCTCTTCTTTCCACTTCACTTCTGTGACTGATTTGAAAAGATCCACAGAATCATGAAATGGGTAAATTTAATCTTTCCCCACACTACTGATCAGGGATGAAACCTCACATCACAGTGTGTGCTCTCTGGCATGAGAATCATCTTTCTCCCAGTGTCCACACTGCACAGGCCTGAGGA**ACTCTGGGGCCAACTCAATTATCAGAACCCGTGTCCCACACAGCTGTGACATTCATGTCCCTCACCTCATCAGC**

Figure 2. Diagram of transgene construct



From: Pircher H, Mak TW, Lang R, Ballhausen W, Rüedi E, Hengartner H, Zinkernagel RM, Bürki K. EMBO J. 1989 Mar;8(3):719-27. (Construct B; dnRAG1 replaces TCRbeta sequence)

Figure 3. PCR to confirm tandem dnRAG1 transgene organization

A picture containing table

Description automatically generated

Figure 4. Sequence alignments

V(D)J recombination-activating protein 1 [Mus musculus]

Sequence ID: [NP\_033045.2](https://www.ncbi.nlm.nih.gov/protein/NP_033045.2?report=genbank&log$=protalign&blast_rank=1&RID=17UU0MJT016)Length: 1040 Number of Matches:

Range 1: 1 to 1040[GenPept](https://www.ncbi.nlm.nih.gov/protein/NP_033045.2?report=genbank&log$=protalign&blast_rank=1&RID=17UU0MJT016&from=1&to=1040)[Graphics](https://www.ncbi.nlm.nih.gov/projects/sviewer/?RID=17UU0MJT016&id=NP_033045.2&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=0:1091&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Alignment statistics for match #1 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 2136 bits(5535) | 0.0 | Compositional matrix adjust. | 1037/1040(99%) | 1037/1040(99%) | 0/1040(0%) | +3 |

Query 3 MAASLPSTLSFSSAPDEIQHPQIKFSEWKFKLFRVRSFEKAPEEAQKEKDSSEGKPYLEQ 182

MAASLPSTLSFSSAPDEIQHPQIKFSEWKFKLFRVRSFEKAPEEAQKEKDSSEGKPYLEQ

Sbjct 1 MAASLPSTLSFSSAPDEIQHPQIKFSEWKFKLFRVRSFEKAPEEAQKEKDSSEGKPYLEQ 60

Query 183 SPVVPEKPGGQNSILTQRALKLHPKFSKKFHADGKSSDKAVHQARLRHFCRICGNRFKSD 362

SPVVPEKPGGQNSILTQRALKLHPKFSKKFHADGKSSDKAVHQARLRHFCRICGNRFKSD

Sbjct 61 SPVVPEKPGGQNSILTQRALKLHPKFSKKFHADGKSSDKAVHQARLRHFCRICGNRFKSD 120

Query 363 GHSRRYPVHGPVDAKTQSLFRKKEKRVTSWPDLIARIFRIDVKADVDSIHPTEFCHDCWS 542

GHSRRYPVHGPVDAKTQSLFRKKEKRVTSWPDLIARIFRIDVKADVDSIHPTEFCHDCWS

Sbjct 121 GHSRRYPVHGPVDAKTQSLFRKKEKRVTSWPDLIARIFRIDVKADVDSIHPTEFCHDCWS 180

Query 543 IMHRKFSSSHSQVYFPRKVTVEWHPHTPSCDICFTAHRGLKRKRHQPNVQLSKKLKTVLN 722

IMHRKFSSSHSQVYFPRKVTVEWHPHTPSCDICFTAHRGLKRKRHQPNVQLSKKLKTVLN

Sbjct 181 IMHRKFSSSHSQVYFPRKVTVEWHPHTPSCDICFTAHRGLKRKRHQPNVQLSKKLKTVLN 240

Query 723 HArrdrrkrtqarVSSKEVLKKISNCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADP 902

HARRDRRKRTQARVSSKEVLKKISNCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADP

Sbjct 241 HARRDRRKRTQARVSSKEVLKKISNCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADP 300

Query 903 VETSCKHLFCRICILRCLKVMGSYCPSCRYPCFPTDLESPVKSFLNILNSLMVKCPAQDC 1082

VETSCKHLFCRICILRCLKVMGSYCPSCRYPCFPTDLESPVKSFLNILNSLMVKCPAQDC

Sbjct 301 VETSCKHLFCRICILRCLKVMGSYCPSCRYPCFPTDLESPVKSFLNILNSLMVKCPAQDC 360

Query 1083 NEEVSLEKYNHHVSSHKESKETLVHINKGGRPRQHLLSLTRRAQKHRLRELKIQVKEFAD 1262

NEEVSLEKYNHHVSSHKESKETLVHINKGGRPRQHLLSLTRRAQKHRLRELKIQVKEFAD

Sbjct 361 NEEVSLEKYNHHVSSHKESKETLVHINKGGRPRQHLLSLTRRAQKHRLRELKIQVKEFAD 420

Query 1263 KEEGGDVKAVCLTLFLLALRARNEHRQADELEAIMQGRGSGLQPAVCLAIRVNTFLSCSQ 1442

KEEGGDVKAVCLTLFLLALRARNEHRQADELEAIMQGRGSGLQPAVCLAIRVNTFLSCSQ

Sbjct 421 KEEGGDVKAVCLTLFLLALRARNEHRQADELEAIMQGRGSGLQPAVCLAIRVNTFLSCSQ 480

Query 1443 YHKMYRTVKAITGRQIFQPLHALRNAEKVLLPGYHPFEWQPPLKNVSSRTDVGIIDGLSG 1622

YHKMYRTVKAITGRQIFQPLHALRNAEKVLLPGYHPFEWQPPLKNVSSRTDVGIIDGLSG

Sbjct 481 YHKMYRTVKAITGRQIFQPLHALRNAEKVLLPGYHPFEWQPPLKNVSSRTDVGIIDGLSG 540

Query 1623 LASSVDEYPVDTIAKRFRYDSALVSALMDMEEDILEGMRSQDLDDYLNGPFTVVVKESC**A** 1802

LASSVDEYPVDTIAKRFRYDSALVSALMDMEEDILEGMRSQDLDDYLNGPFTVVVKESC

Sbjct 541 LASSVDEYPVDTIAKRFRYDSALVSALMDMEEDILEGMRSQDLDDYLNGPFTVVVKESC**D** 600

Query 1803 GMGDVSEKHGSGPAVPEKAVRFSFTVMRITIEHGSQNVKVFEEPKPNSELCCKPLCLMLA 1982

GMGDVSEKHGSGPAVPEKAVRFSFTVMRITIEHGSQNVKVFEEPKPNSELCCKPLCLMLA

Sbjct 601 GMGDVSEKHGSGPAVPEKAVRFSFTVMRITIEHGSQNVKVFEEPKPNSELCCKPLCLMLA 660

Query 1983 DESDHETLTAILSPLIAEREAMKSSELTLEMGGIPRTFKFIFRGTGY**A**EKLVREVEGLEA 2162

DESDHETLTAILSPLIAEREAMKSSELTLEMGGIPRTFKFIFRGTGY EKLVREVEGLEA

Sbjct 661 DESDHETLTAILSPLIAEREAMKSSELTLEMGGIPRTFKFIFRGTGY**D**EKLVREVEGLEA 720

Query 2163 SGSVYICTLCDTTRLEASQNLVFHSITRSHAENLQRYEVWRSNPYHESVEELRDRVKGVS 2342

SGSVYICTLCDTTRLEASQNLVFHSITRSHAENLQRYEVWRSNPYHESVEELRDRVKGVS

Sbjct 721 SGSVYICTLCDTTRLEASQNLVFHSITRSHAENLQRYEVWRSNPYHESVEELRDRVKGVS 780

Query 2343 AKPFIETVPSIDALHCDIGNAAEFYKIFQLEIGEVYKHPNASKEERKRWQATLDKHLRKR 2522

AKPFIETVPSIDALHCDIGNAAEFYKIFQLEIGEVYKHPNASKEERKRWQATLDKHLRKR

Sbjct 781 AKPFIETVPSIDALHCDIGNAAEFYKIFQLEIGEVYKHPNASKEERKRWQATLDKHLRKR 840

Query 2523 MNLKPIMRMNGNFARKLMTQETVDAVCELIPSEERHEALRELMDLYLKMKPVWRSSCPAK 2702

MNLKPIMRMNGNFARKLMTQETVDAVCELIPSEERHEALRELMDLYLKMKPVWRSSCPAK

Sbjct 841 MNLKPIMRMNGNFARKLMTQETVDAVCELIPSEERHEALRELMDLYLKMKPVWRSSCPAK 900

Query 2703 ECPESLCQYSFNSQRFAELLSTKFKYRYEGKITNYFHKTLAHVPEIIERDGSIGAWASEG 2882

ECPESLCQYSFNSQRFAELLSTKFKYRYEGKITNYFHKTLAHVPEIIERDGSIGAWASEG

Sbjct 901 ECPESLCQYSFNSQRFAELLSTKFKYRYEGKITNYFHKTLAHVPEIIERDGSIGAWASEG 960

Query 2883 N**A**SGNKLFRRFRKMNARQSKCYEMEDVLKHHWLYTSKYLQKFMNAHNALKSSGFTMNSKE 3062

N SGNKLFRRFRKMNARQSKCYEMEDVLKHHWLYTSKYLQKFMNAHNALKSSGFTMNSKE

Sbjct 961 N**E**SGNKLFRRFRKMNARQSKCYEMEDVLKHHWLYTSKYLQKFMNAHNALKSSGFTMNSKE 1020

Query 3063 TLGDPLGIEDSLESQDSMEF 3122

TLGDPLGIEDSLESQDSMEF

Sbjct 1021 TLGDPLGIEDSLESQDSMEF 1040

Human beta globin region on chromosome 11

Sequence ID: [U01317.1](https://www.ncbi.nlm.nih.gov/nucleotide/U01317.1?report=genbank&log$=nuclalign&blast_rank=1&RID=17VJ4VKY016)Length: 73308Number of Matches: 2

Range 1: 62613 to 64302[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/U01317.1?report=genbank&log$=nuclalign&blast_rank=1&RID=17VJ4VKY016&from=62613&to=64302)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/U01317.1?report=graph&rid=17VJ4VKY016%5bU01317.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=62529:64386&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| --- | --- | --- | --- | --- |
| Alignment statistics for match #1 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 3116 bits(1687) | 0.0 | 1690/1691(99%) | 1/1691(0%) | Plus/Plus |

Query 1 GGATCCTGAGAACTTCAGGGTGAGTCTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTT 60

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Sbjct 62613 GGATCCTGAGAACTTCAGGGTGAGTCTATGGGACCCTTGATGTTTTCTTTCCCCTTCTTT 62672

Query 61 TCTATGGTTAAGTTCATGTCATAGGAAGGGGAGAAGTAACAGGGTACAGTTTAGAATGGG 120

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Sbjct 62673 TCTATGGTTAAGTTCATGTCATAGGAAGGGGAGAAGTAACAGGGTACAGTTTAGAATGGG 62732

Query 121 AAACAGACGAATGATTGCATCAGTGTGGAAGTCTCAGGATCGttttagtttcttttattt 180

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Sbjct 62733 AAACAGACGAATGATTGCATCAGTGTGGAAGTCTCAGGATCGTTTTAGTTTCTTTTATTT 62792

Query 181 gctgttcataacaattgttttcttttgtttaattcttgctttctttttttttCTTCTCCG 240

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Query 301 AGATACATTAAGTAACTTaaaaaaaaaCTTTACACAGTCTGCCTAGTACATTACTATTTG 360

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Sbjct 63093 CACATATTGACCAAATCAGGGTAATTTTGCATTTGTAATTTTAAAAAATGCTTTCTTCTT 63152

Query 541 ttaatatacttttttgtttatcttatttctaatactttccctaatctctttctttcAGGG 600

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Sbjct 63153 TTAATATACTTTTTTGTTTATCTTATTTCTAATACTTTCCCTAATCTCTTTCTTTCAGGG 63212

Query 601 CAATAATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAATAACAGTGATAATT 660

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Sbjct 63213 CAATAATGATACAATGTATCATGCCTCTTTGCACCATTCTAAAGAATAACAGTGATAATT 63272

Query 661 TCTGGGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAAC 720

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Sbjct 63273 TCTGGGTTAAGGCAATAGCAATATTTCTGCATATAAATATTTCTGCATATAAATTGTAAC 63332

Query 721 TGATGTAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTGCTTTTA 780

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Sbjct 63333 TGATGTAAGAGGTTTCATATTGCTAATAGCAGCTACAATCCAGCTACCATTCTGCTTTTA 63392

Query 781 TTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCA 840

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Sbjct 63393 TTTTATGGTTGGGATAAGGCTGGATTATTCTGAGTCCAAGCTAGGCCCTTTTGCTAATCA 63452

Query 841 TGTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGG 900

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Sbjct 63453 TGTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCTGG 63512

Query 901 CCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGG 960

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Sbjct 63513 CCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGG 63572

Query 961 CTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAAT 1020

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Sbjct 63573 CTGGTGTGGCTAATGCCCTGGCCCACAAGTATCACTAAGCTCGCTTTCTTGCTGTCCAAT 63632

Query 1021 TTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAAG 1080

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Sbjct 63633 TTCTATTAAAGGTTCCTTTGTTCCCTAAGTCCAACTACTAAACTGGGGGATATTATGAAG 63692

Query 1081 GGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACATTTATTTTCATTGCAATGATGTAT 1140

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Sbjct 63693 GGCCTTGAGCATCTGGATTCTGCCTAATAAAAAACATTTATTTTCATTGCAATGATGTAT 63752

Query 1141 TTAAATTATTTCTGAATATTTTACTAAAAAGGGAATGTGGGAGGTCAGTGCATTTAAAAC 1200

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Sbjct 63753 TTAAATTATTTCTGAATATTTTACTAAAAAGGGAATGTGGGAGGTCAGTGCATTTAAAAC 63812

Query 1201 ATAAAGAAATGAAGAGCTAGTTCAAACCTTGGGAAAATACACTATATCTTAAACTCCATG 1260

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Sbjct 63813 ATAAAGAAATGAAGAGCTAGTTCAAACCTTGGGAAAATACACTATATCTTAAACTCCATG 63872

Query 1261 AAAGAAGGTGAGGCTGCAAACAGCTAATGCACATTGGCAACAGCCCCTGATGCCTATGCC 1320

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Sbjct 63873 AAAGAAGGTGAGGCTGCAAACAGCTAATGCACATTGGCAACAG-CCCTGATGCCTATGCC 63931

Query 1321 TTATTCATCCCTCAGAAAAGGATTCAAGTAGAGGCTTGATTTGGAGGTTAAAGTTTTGCT 1380

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Sbjct 63932 TTATTCATCCCTCAGAAAAGGATTCAAGTAGAGGCTTGATTTGGAGGTTAAAGTTTTGCT 63991

Query 1381 ATGCTGTATTTTACATTACTTATTGTTTTAGCTGTCCTCATGAATGTCTTTTCACTACCC 1440

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Sbjct 63992 ATGCTGTATTTTACATTACTTATTGTTTTAGCTGTCCTCATGAATGTCTTTTCACTACCC 64051

Query 1441 ATTTGCTTATCCTGCATCTCTCAGCCTTGACTCCACTCAGTTCTCTTGCTTAGAGATACC 1500

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Sbjct 64052 ATTTGCTTATCCTGCATCTCTCAGCCTTGACTCCACTCAGTTCTCTTGCTTAGAGATACC 64111

Query 1501 ACCTTTCCCCTGAAGTGTTCCTTCCATGTTTTACGGCGAGATGGTTTCTCCTCGCCTGGC 1560

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Sbjct 64112 ACCTTTCCCCTGAAGTGTTCCTTCCATGTTTTACGGCGAGATGGTTTCTCCTCGCCTGGC 64171

Query 1561 CACTCAGCCTTAGTTGTCTCTGTTGTCTTATAGAGGTCTACTTGAAGAAGGAAAAACAGG 1620

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Sbjct 64172 CACTCAGCCTTAGTTGTCTCTGTTGTCTTATAGAGGTCTACTTGAAGAAGGAAAAACAGG 64231

Query 1621 GGGCATGGTTTGACTGTCCTGTGAGCCCTTCTTCCCTGCCTCCCCCACTCACAGTGACCC 1680

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Sbjct 64232 GGGCATGGTTTGACTGTCCTGTGAGCCCTTCTTCCCTGCCTCCCCCACTCACAGTGACCC 64291

Query 1681 GGAATCTGCAG 1691

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Sbjct 64292 GGAATCTGCAG 64302

Mus musculus immunoglobulin heavy chain locus constant region and partial variable region, strain 129S1

Sequence ID: [AJ851868.3](https://www.ncbi.nlm.nih.gov/nucleotide/AJ851868.3?report=genbank&log$=nuclalign&blast_rank=1&RID=17V9YMCP016)Length: 1593281Number of Matches: 1

Range 1: 1415684 to 1417287[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AJ851868.3?report=genbank&log$=nuclalign&blast_rank=1&RID=17V9YMCP016&from=1415684&to=1417287)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AJ851868.3?report=graph&rid=17V9YMCP016%5bAJ851868.3%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=1415604:1417367&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 2963 bits(1604) | 0.0 | 1604/1604(100%) | 0/1604(0%) | Plus/Minus |

Query 1 GAATTCTAAATACATTTTAGAAGTCGATAAACTTAAGTTTGGGGAAACTAGAACTACTCA 60

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Sbjct 1417287 GAATTCTAAATACATTTTAGAAGTCGATAAACTTAAGTTTGGGGAAACTAGAACTACTCA 1417228

Query 61 AGCTAAAATTAAAAGGTTGAACTCAATAAGTTAAAAGAGGACCTCTCCAGTTTCGGCTGA 120

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Sbjct 1417227 AGCTAAAATTAAAAGGTTGAACTCAATAAGTTAAAAGAGGACCTCTCCAGTTTCGGCTGA 1417168

Query 121 ATCCTCAACTTATTTTAGAAATGCAAATTACCCAGGTGGTGTTTTGCTCAGCCTGGACTT 180

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Sbjct 1417167 ATCCTCAACTTATTTTAGAAATGCAAATTACCCAGGTGGTGTTTTGCTCAGCCTGGACTT 1417108

Query 181 TCGGTTTGGTGGGGCTGGACAGAGTGTTTCAAAACCACTTCTTCAAACCACAGCTACAAG 240

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Sbjct 1417107 TCGGTTTGGTGGGGCTGGACAGAGTGTTTCAAAACCACTTCTTCAAACCACAGCTACAAG 1417048

Query 241 TTTACCTAGTGGTTTTATTTTCCCTTCCCCAAATAGCCTTGCCACATGACCTGCTTCCTG 300

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Sbjct 1417047 TTTACCTAGTGGTTTTATTTTCCCTTCCCCAAATAGCCTTGCCACATGACCTGCTTCCTG 1416988

Query 301 CCAGCTGCTGCAGGTGTTCTGGTTCTGATCGGCCATCTTGACTCCAACTCAACATTGCTC 360

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Sbjct 1416987 CCAGCTGCTGCAGGTGTTCTGGTTCTGATCGGCCATCTTGACTCCAACTCAACATTGCTC 1416928

Query 361 AATTCATTTAAAAATATTTTAAACTTAATTTATTATTGTTAAAAGTCAGTTCTGAATAGG 420

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Sbjct 1416927 AATTCATTTAAAAATATTTTAAACTTAATTTATTATTGTTAAAAGTCAGTTCTGAATAGG 1416868

Query 421 GTATGAGAGAGCCTCACTCCCATTCCTCGGTTAAACTTTAAGTAATGTCAGTTCTACACA 480

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Sbjct 1416867 GTATGAGAGAGCCTCACTCCCATTCCTCGGTTAAACTTTAAGTAATGTCAGTTCTACACA 1416808

Query 481 AACAAGACCTCAAATTGATTGACAAAAATTTTGGACATTTaaaaaaaTGAGTACTTGAAA 540

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Sbjct 1416807 AACAAGACCTCAAATTGATTGACAAAAATTTTGGACATTTAAAAAAATGAGTACTTGAAA 1416748

Query 541 ACCCTCTCACATTTTAAAGTCACAGTATTTAACTATTTTTCCTAGGAACCAACTTAAGAG 600

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Sbjct 1416747 ACCCTCTCACATTTTAAAGTCACAGTATTTAACTATTTTTCCTAGGAACCAACTTAAGAG 1416688

Query 601 TAAAAGCAACATCTTCTAATATTCCATACACATACTTCTGTGTTCCTTTGAAAGCTGGAC 660

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Sbjct 1416687 TAAAAGCAACATCTTCTAATATTCCATACACATACTTCTGTGTTCCTTTGAAAGCTGGAC 1416628

Query 661 TTTTGCAGGCTCCACCAGACCTCTCTAGACAGCAACTACCCTTTTGAGACCGAGGCTAGA 720

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Sbjct 1416627 TTTTGCAGGCTCCACCAGACCTCTCTAGACAGCAACTACCCTTTTGAGACCGAGGCTAGA 1416568

Query 721 TGCCTTTCTCCCTTGACTCAATCACTAAGACAGCTCTCCTTCCAACAAATGAAGTTTTAA 780

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Sbjct 1416567 TGCCTTTCTCCCTTGACTCAATCACTAAGACAGCTCTCCTTCCAACAAATGAAGTTTTAA 1416508

Query 781 ACAATCTAGTGTGGAACATTCCTCACAAATCTAAAGAAAGTGCCCCACTCCACTCTTTGT 840

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Sbjct 1416507 ACAATCTAGTGTGGAACATTCCTCACAAATCTAAAGAAAGTGCCCCACTCCACTCTTTGT 1416448

Query 841 CCCTATGCATCGGATACTGTATAAATGCTGTCACAGAGGTGGTCCTGAAGTATATTCCGC 900

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Sbjct 1416447 CCCTATGCATCGGATACTGTATAAATGCTGTCACAGAGGTGGTCCTGAAGTATATTCCGC 1416388

Query 901 AGCTAATACTTTTATTCTAAAAACTGAAAATCTCCAACTACAGCCCCAACTATCCCTCCA 960

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Sbjct 1416387 AGCTAATACTTTTATTCTAAAAACTGAAAATCTCCAACTACAGCCCCAACTATCCCTCCA 1416328

Query 961 GCCATAGGATTGTTTTAGCATCTCCCTCAAATGAGCCTCCAAAGTCCCTATCCCATCATC 1020

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Sbjct 1416327 GCCATAGGATTGTTTTAGCATCTCCCTCAAATGAGCCTCCAAAGTCCCTATCCCATCATC 1416268

Query 1021 CAGGGACTCCACCAACACCATCACACAGATTCTTAGTTTTTCAAAGATGTGGAGATAATC 1080

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Sbjct 1416267 CAGGGACTCCACCAACACCATCACACAGATTCTTAGTTTTTCAAAGATGTGGAGATAATC 1416208

Query 1081 TGTCCTAAAGGCTCTGAGATCCCTAGACAGTTTATTTCCCAACTTCTCTCAGCCGGCTCC 1140

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Sbjct 1416207 TGTCCTAAAGGCTCTGAGATCCCTAGACAGTTTATTTCCCAACTTCTCTCAGCCGGCTCC 1416148

Query 1141 CTCAGGGACAAATATCCAAGATTAGTCTGCAATGCTCAGAAAACTCCATAACAAAGGTTA 1200

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Sbjct 1416147 CTCAGGGACAAATATCCAAGATTAGTCTGCAATGCTCAGAAAACTCCATAACAAAGGTTA 1416088

Query 1201 AAAATAAAGACCTGGAGAGGCCATTCTTACCTGAGGAGACGGTGACTGAGGTTCCTTGAC 1260

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Sbjct 1416087 AAAATAAAGACCTGGAGAGGCCATTCTTACCTGAGGAGACGGTGACTGAGGTTCCTTGAC 1416028

Query 1261 CCCAGTAGTCCATAGCATAGTAATCACAATAGTGGATTTTTCCTCTATACCCGACAAAAA 1320

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Sbjct 1416027 CCCAGTAGTCCATAGCATAGTAATCACAATAGTGGATTTTTCCTCTATACCCGACAAAAA 1415968

Query 1321 CCCCAGAGTCTGACTAGAATCACCCCTGGGCAACTCAGACATTATGCCAATTCCTGGTGT 1380

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Sbjct 1415967 CCCCAGAGTCTGACTAGAATCACCCCTGGGCAACTCAGACATTATGCCAATTCCTGGTGT 1415908

Query 1381 CACACAAGAATCAACCATTCAAGTCATTGTTCCACATTCTGTTCCCTGCCTGTGCAGAAG 1440

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Sbjct 1415907 CACACAAGAATCAACCATTCAAGTCATTGTTCCACATTCTGTTCCCTGCCTGTGCAGAAG 1415848

Query 1441 CCCCCTGGACCCCTCTTAAGTCTTCAAGGTGACCTATATTCCAGCCTCACCTCAGAGAAA 1500

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Sbjct 1415847 CCCCCTGGACCCCTCTTAAGTCTTCAAGGTGACCTATATTCCAGCCTCACCTCAGAGAAA 1415788

Query 1501 CCAGACAGTCACTGACCCTGAAATTGTCACCATCAACTGTCAGCCCCTAATTCTCACAAG 1560

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Sbjct 1415787 CCAGACAGTCACTGACCCTGAAATTGTCACCATCAACTGTCAGCCCCTAATTCTCACAAG 1415728

Query 1561 AGTCCGATAGACCCTGGACAAGATTCTGCCTCAGACTTCAAGCT 1604

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Sbjct 1415727 AGTCCGATAGACCCTGGACAAGATTCTGCCTCAGACTTCAAGCT 1415684

Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl transferase), ribosomal protein subunit S18 (RPS18), Sacm21 (Sacm21), H2K1(b) (H2-K1(b)), RING1 (RING1), KE6a (KE6a), KE4 (KE4), RXRbeta (RXRbeta), collagen alpha-2 (XI) (COLA11A2), H2-O alpha (H2-Oalpha), RING3 (RING3), H2-M alpha (H2-M alpha), H2-M beta 2 (H2-M beta2), and H2-M beta1 (H2-M beta1) genes, complete cds; and LMP 2 gene, partial cds

Sequence ID: [AF100956.1](https://www.ncbi.nlm.nih.gov/nucleotide/AF100956.1?report=genbank&log$=nuclalign&blast_rank=3&RID=17VZGT7B016)Length: 273800Number of Matches: 3

Range 1: 86930 to 88956[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AF100956.1?report=genbank&log$=nuclalign&blast_rank=3&RID=17VZGT7B016&from=86930&to=88956)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AF100956.1?report=graph&rid=17VZGT7B016%5bAF100956.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=86829:89057&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 3744 bits(2027) | 0.0 | 2027/2027(100%) | 0/2027(0%) | Plus/Minus |

Query 1 AGCTTGGCCCACAAGGAGTGGCAATGTTAGGAGTGTGACTGTGTTAGAGGAAGTGTGTCA 60

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Sbjct 88956 AGCTTGGCCCACAAGGAGTGGCAATGTTAGGAGTGTGACTGTGTTAGAGGAAGTGTGTCA 88897

Query 61 CTTTGAGGTTGGCCTTTGAGGTCTCCTATGCTCATGAGCTGCCCAGTGTGGAATGAAAGC 120

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Sbjct 88896 CTTTGAGGTTGGCCTTTGAGGTCTCCTATGCTCATGAGCTGCCCAGTGTGGAATGAAAGC 88837

Query 121 CTCTTCCTGGCTGCATTTGGATCAAGATGTAGAAGTCTCCCCTTCTCCAGCACCATGTCT 180

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Sbjct 88836 CTCTTCCTGGCTGCATTTGGATCAAGATGTAGAAGTCTCCCCTTCTCCAGCACCATGTCT 88777

Query 181 ACCTGCACACTGGCATGCTTCCTGTCATGATGGACTAAATCCCTGAAACTGTAAGCCAGA 240

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Sbjct 88776 ACCTGCACACTGGCATGCTTCCTGTCATGATGGACTAAATCCCTGAAACTGTAAGCCAGA 88717

Query 241 CCCTATTAAATGTCTCCCTTTAGAAGGAATGCCTTGGTCATGGTGTTTCTTCACAGCAAC 300

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Sbjct 88716 CCCTATTAAATGTCTCCCTTTAGAAGGAATGCCTTGGTCATGGTGTTTCTTCACAGCAAC 88657

Query 301 AAAACCAAAACTAACACACCCAGCACTTAGGATGCAAAGGCAGATGTATCTCTGTGAGTT 360

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Sbjct 88656 AAAACCAAAACTAACACACCCAGCACTTAGGATGCAAAGGCAGATGTATCTCTGTGAGTT 88597

Query 361 CAAGGGCAGCCTGATCTACATAATGAATTACAGAATAGCCAGGGCTGTGCAGATAGACCT 420

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Sbjct 88596 CAAGGGCAGCCTGATCTACATAATGAATTACAGAATAGCCAGGGCTGTGCAGATAGACCT 88537

Query 421 TGTCTAAACAAGCAAACAAACAAAACCCATAGTAAAATAAGAAGAAAAGTAATGGAGACA 480

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Sbjct 88536 TGTCTAAACAAGCAAACAAACAAAACCCATAGTAAAATAAGAAGAAAAGTAATGGAGACA 88477

Query 481 GATCCTTTGTGTAGCTGCCTAACCCCAACAGCATCCCTAGGTTGATCAGGAAGAAACCTA 540

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Sbjct 88476 GATCCTTTGTGTAGCTGCCTAACCCCAACAGCATCCCTAGGTTGATCAGGAAGAAACCTA 88417

Query 541 AGAGCATCAAGTCCCCATGGAAAATGCTCACAACATCTAATAAGAGGGGTTCAGGGAGAC 600

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Sbjct 88416 AGAGCATCAAGTCCCCATGGAAAATGCTCACAACATCTAATAAGAGGGGTTCAGGGAGAC 88357

Query 601 AGGGTCTGCTGAATCCTGGTGAGGCTGGGGGGCTGCTGTGGGGATCTGCATGGGGAGGTG 660

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Sbjct 88356 AGGGTCTGCTGAATCCTGGTGAGGCTGGGGGGCTGCTGTGGGGATCTGCATGGGGAGGTG 88297

Query 661 ACTGGAGTTCACACCTGTGGTCACACGCATTCATTGCTCTGTGTGATGAGTGACTCTCTT 720

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Sbjct 88296 ACTGGAGTTCACACCTGTGGTCACACGCATTCATTGCTCTGTGTGATGAGTGACTCTCTT 88237

Query 721 CAGGAGTCCCCACCCATCTATGCTCTTCTTTCCACTTCACTTCTGTGACTGATTTGAAAA 780

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Sbjct 88236 CAGGAGTCCCCACCCATCTATGCTCTTCTTTCCACTTCACTTCTGTGACTGATTTGAAAA 88177

Query 781 GATCCACAGAATCATGAAATGGGTAAATTTAATCTTTCCCCACACTACTGATCAGGGATG 840

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Sbjct 88176 GATCCACAGAATCATGAAATGGGTAAATTTAATCTTTCCCCACACTACTGATCAGGGATG 88117

Query 841 AAACCTCACATCACAGTGTGTGCTCTCTGGCATGAGAATCATCTTTCTCCCAGTGTCCAC 900

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Sbjct 88116 AAACCTCACATCACAGTGTGTGCTCTCTGGCATGAGAATCATCTTTCTCCCAGTGTCCAC 88057

Query 901 ACTGCACAGGCCTGAGGAACTCTGGGGCCAACTCAATTATCAGAACCCGTGTCCCACACA 960

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Sbjct 88056 ACTGCACAGGCCTGAGGAACTCTGGGGCCAACTCAATTATCAGAACCCGTGTCCCACACA 87997

Query 961 GCTGTGACATTCATGTCCCTCACCTCATCAGCTCAAAAGTGTGAGTGAAGGTCAGGGAGG 1020

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Sbjct 87996 GCTGTGACATTCATGTCCCTCACCTCATCAGCTCAAAAGTGTGAGTGAAGGTCAGGGAGG 87937

Query 1021 GAGGGAGAGGGTCAGAGATTACATAACTTCTACCACACTAGCATCCTTATTCTGTGTTAT 1080

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Sbjct 87936 GAGGGAGAGGGTCAGAGATTACATAACTTCTACCACACTAGCATCCTTATTCTGTGTTAT 87877

Query 1081 AGTTGGTGACAGCTCCTCTCCTACTGTGATTGAGTCACTAAAGCAACTGCACCATGGAAG 1140

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Sbjct 87876 AGTTGGTGACAGCTCCTCTCCTACTGTGATTGAGTCACTAAAGCAACTGCACCATGGAAG 87817

Query 1141 TGCAGACACAGAGAAGTCCAGTGGAGACAGGGATCAGTGCCCTGCTGTCTGTGGTCTGCA 1200

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Sbjct 87816 TGCAGACACAGAGAAGTCCAGTGGAGACAGGGATCAGTGCCCTGCTGTCTGTGGTCTGCA 87757

Query 1201 CGGGGTCTCTCTTCAGTGGACAAGGGGGTCTCCTGTGCTGAGACAATGTCCCAGATCCAC 1260

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Sbjct 87756 CGGGGTCTCTCTTCAGTGGACAAGGGGGTCTCCTGTGCTGAGACAATGTCCCAGATCCAC 87697

Query 1261 AGAGACAAACTCAGGACTCAGAATGAAGATCCTTGTTTCAAATacacacacacacacata 1320

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Sbjct 87696 AGAGACAAACTCAGGACTCAGAATGAAGATCCTTGTTTCAAATACACACACACACACATA 87637

Query 1321 cacacacacacacacacacacacacacacacacacacacCTGCAGCCACAGACTTTTCAT 1380

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Sbjct 87636 CACACACACACACACACACACACACACACACACACACACCTGCAGCCACAGACTTTTCAT 87577

Query 1381 CTAGGAATTAACACAAGGAATCTGTGTCTCAGCACAGGGCTGAGAAGACAGATCCTGAGG 1440

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Sbjct 87576 CTAGGAATTAACACAAGGAATCTGTGTCTCAGCACAGGGCTGAGAAGACAGATCCTGAGG 87517

Query 1441 GGAGAGGCAAAGTCTACACTTAACAGATGAGAGTCCTGCACTCAGGCTTGGCAGTGTGAG 1500

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Sbjct 87516 GGAGAGGCAAAGTCTACACTTAACAGATGAGAGTCCTGCACTCAGGCTTGGCAGTGTGAG 87457

Query 1501 CCGCCCATTGCAGGTGAACAGAGCCTGGTCTCTGTGGGGTCCCTGTGGGGCTTGCAGCCC 1560

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Sbjct 87456 CCGCCCATTGCAGGTGAACAGAGCCTGGTCTCTGTGGGGTCCCTGTGGGGCTTGCAGCCC 87397

Query 1561 AGCGCCTTGACTTTAAGGAAAAGCCTCTCTCTCCACTGCATCCCTAAGCGCTTGTGTCGC 1620

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Sbjct 87396 AGCGCCTTGACTTTAAGGAAAAGCCTCTCTCTCCACTGCATCCCTAAGCGCTTGTGTCGC 87337

Query 1621 CATTGTATTCCCGGAAGAGGCTTTTCTTCTAGAAGACTCCAGGGTCTGACTTCTgaagag 1680

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Sbjct 87336 CATTGTATTCCCGGAAGAGGCTTTTCTTCTAGAAGACTCCAGGGTCTGACTTCTGAAGAG 87277

Query 1681 aagaagaaagaggaagagtggaagagaggacacagagagTCTGGCCTGCGGGTCTCTCCT 1740

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Sbjct 87276 AAGAAGAAAGAGGAAGAGTGGAAGAGAGGACACAGAGAGTCTGGCCTGCGGGTCTCTCCT 87217

Query 1741 GGTGTTTTGAGAGTTTCTGGATCAGAACTCGGAGACGACAGCACAGGGTTCAGGCAAAGT 1800

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Sbjct 87216 GGTGTTTTGAGAGTTTCTGGATCAGAACTCGGAGACGACAGCACAGGGTTCAGGCAAAGT 87157

Query 1801 CTTAGTCGCCAGGCAGTGAGGTCAGGGGTGGGGAAGCCCAGGGCTGGGGATTCCCCATCT 1860

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Sbjct 87156 CTTAGTCGCCAGGCAGTGAGGTCAGGGGTGGGGAAGCCCAGGGCTGGGGATTCCCCATCT 87097

Query 1861 CCACAGTTTCACTTCTGCACCTAACCTGGGTCAGGTCCTTCTGTCCGGACACTGTTGACG 1920

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Sbjct 87096 CCACAGTTTCACTTCTGCACCTAACCTGGGTCAGGTCCTTCTGTCCGGACACTGTTGACG 87037

Query 1921 CGCAGTCAGCTCTTACCCCCATTGGGTGGCGCGATCACCAAGAACCAATCAGTGTCGCCG 1980

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Sbjct 87036 CGCAGTCAGCTCTTACCCCCATTGGGTGGCGCGATCACCAAGAACCAATCAGTGTCGCCG 86977

Query 1981 CGGACGCTGGATATAAAGTCCACGCAGCCCGCAGAACTCAGAAGTCG 2027

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Sbjct 86976 CGGACGCTGGATATAAAGTCCACGCAGCCCGCAGAACTCAGAAGTCG 86930