

Search Panel

The screenshot displays a bioinformatics search interface. On the left, a 'Sequence' panel shows a peptide sequence: `>ce841567-f64e-4e8a-91d6-88155e2fc087 (sequence:MNA) 335 residues [Group1.25:352136-352297 + strand] [peptide]`. Below this, radio buttons allow selection of 'Peptide sequence' (selected), 'cDNA sequence', 'EST sequence', 'Genomic sequence', or 'Genomic sequence +/- 500 bases'. The main area shows a genomic track with multiple colored bars representing different annotations. On the right, a 'Hit protein' table lists search results. A callout box points to the 'Search' button in the top right. Another callout box points to the 'Save sequence' and 'Create annotation' buttons next to a selected hit. A third callout box points to a specific hit in the table.

Search directly from annotated sequence

Create Annotation from hit or download

Click and highlight region

	Start	End	Strand	Score	Significan	Identity	Action
Group 1.2	352,429	352,605	1	163	0	100	...
Group 1.2	356,713	356,940	1	161	0	100	...
Group 1.2	354,725	354,934	1	139	0	100	...
Group 1.2	383,547	383,720	1	135	0	100	...
Group 1.2	352,139	352,297	1	111	0	100	✓ Save sequence Create annotation
Group 1.2	329,433	329,453	1	12	536,000	85.71	...
Group 1.2	119,285	119,302	-1	12	536,000	100	...
Group 1.2	348,967	348,981	1	11	1,606,000	100	...
Group 1.2	88,885	88,709	1	11	2,000,000	87.5	...
Group 1.2	113,747	113,747	1	9	4,606,000	100	...
Group 1.2	9,872	9,872	1	9	4,606,000	100	...
Group 1.2	440,678	440,678	1	9	4,606,000	100	...
Group 1.2	417,548	417,548	1	9	4,606,000	100	...
Group 1.2	371,806	371,806	1	9	4,606,000	100	...
Group 1.2	352,072	352,072	1	9	4,606,000	100	...
Group 1.2	328,637	328,637	1	9	4,606,000	100	...
Group 1.2	126,053	126,067	-1	9	4,606,000	100	...
Group 1.2	186,233	186,247	-1	9	4,606,000	100	...
Group 1.2	293,497	293,511	-1	9	4,606,000	100	...
Group 1.2	380,318	380,332	-1	9	4,606,000	100	...
Group 1.2	271,818	271,832	1	8	10,000,000	100	...
Group 1.2	90,287	90,301	1	8	10,000,000	100	...
Group 1.2	338,373	338,386	1	8	14,000,000	100	...
Group 1.2	183,233	183,247	-1	8	14,000,000	100	...
Group 1.2	385,071	385,085	-1	8	14,000,000	100	...
Group 1.2	347,762	347,773	1	6	40,000,000	100	...

Gene Ontology (GO) Annotations

Edit GO Annotation for GB51596-RAa

Aspect: BP
Go Term: GO:0030318
Evidence Code: ECO:0000266

molonocyte differentiation (GO:0030318)
sequence orthology evidence used in manual assertion (SD) (ECO:0000266)

Relation between Gene Product and GO Term:
involved in
involved in

Wts:
Prefix: ID: + Add

RGD:735897

Reference:
PMID: 16790476

Meta: + Add

Save Cancel

- Typeahead lookups
- Utilize GO BioLink API
- Export GPAD2, GPI

<http://api.geneontology.org/api/>

Name	Seq	Type	Length	Updated
GB51596-RAa	Group1.37	gene	420	Jun 14, 2019
GB51596-RAa-00001		mRNA	419	Apr 26, 2019
35cdabb7-fba3-4cd8-8fb7-db4d4b750571		mRNA	420	Apr 26, 2019
Details GO				
Name	Evidence	Based On	Reference	
GO:0030318	ECO:00	RGD:735897	PMID:16790476	
GO:0051743	ECO:00	RGD:1624291	PMID:1713121	