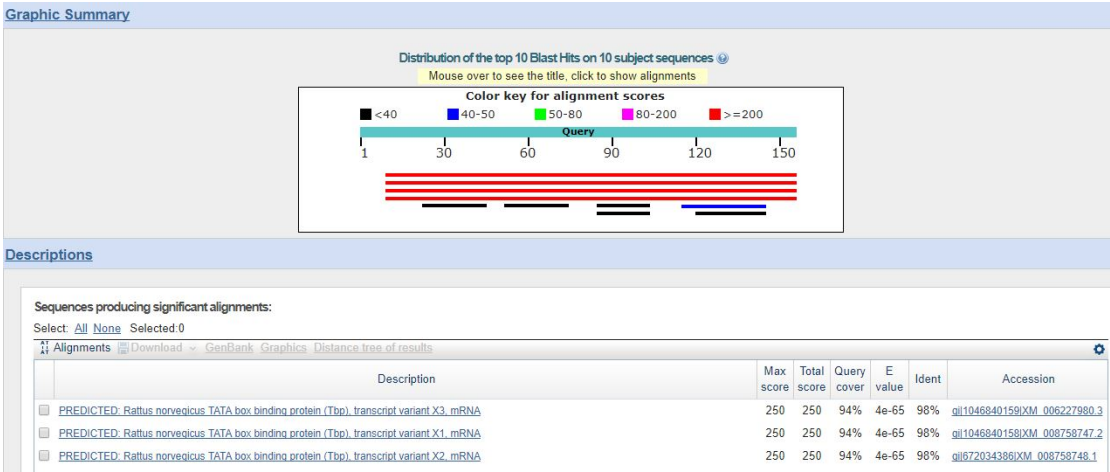
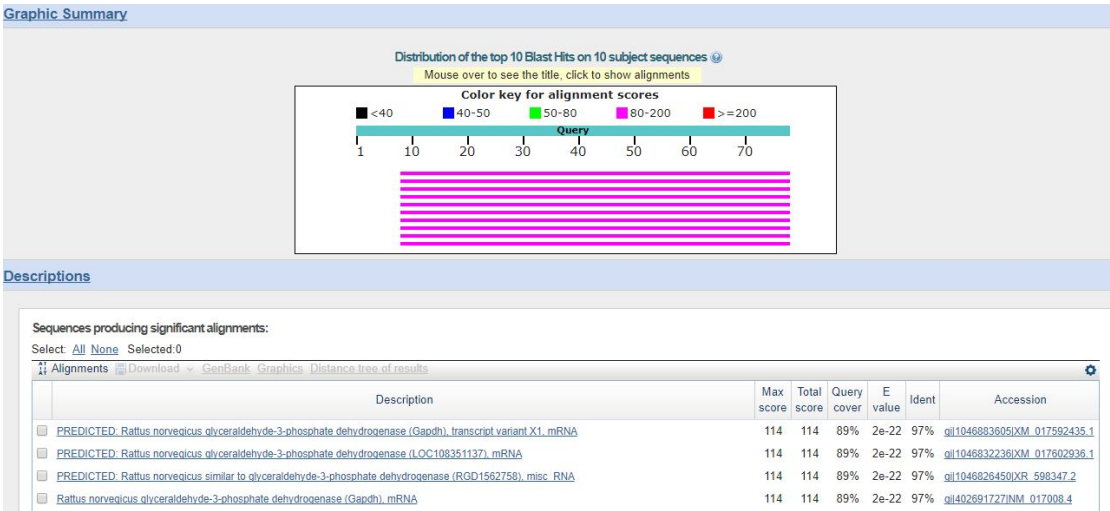


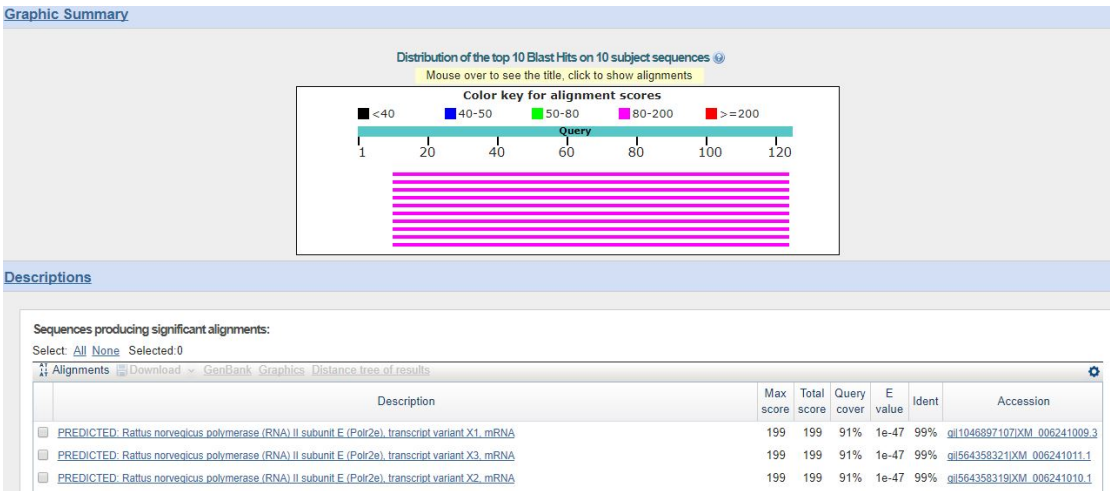
Additional file 2. RT-qPCR validation data.



Tbp

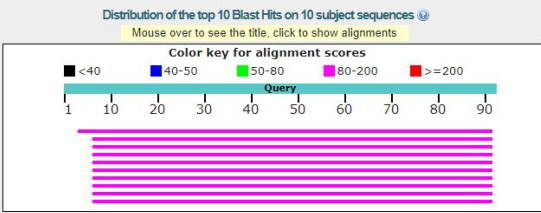


Gapdh



Polr2e

Graphic Summary



Descriptions

Sequences producing significant alignments:

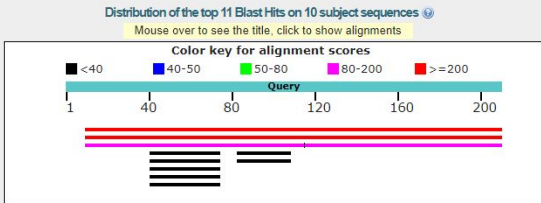
Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Rattus norvegicus TL0ADA46YP06 mRNA sequence	145	145	95%	1e-31	98%	gi 298881191 FQ229722.1
☐	Rattus norvegicus ribosomal protein lateral stalk subunit P0 (Rplp0), mRNA	143	143	92%	4e-31	98%	gi 310616731 NM_022402.2
☐	Rattus norvegicus TL0ABA29YC07 mRNA sequence	143	143	92%	4e-31	98%	gi 298916695 FQ210412.1
☐	Rattus norvegicus TL0ACA39YL23 mRNA sequence	143	143	92%	4e-31	98%	gi 298916498 FQ216913.1

Rplp0

Graphic Summary



Descriptions

Sequences producing significant alignments:

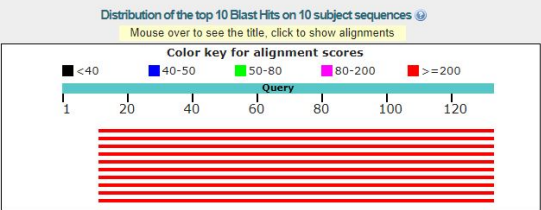
Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Rattus norvegicus succinate dehydrogenase complex subunit A (SDHA) mRNA, partial cds	352	352	95%	6e-96	99%	gi 89574166 DQ402976.1
☐	Rattus norvegicus succinate dehydrogenase complex flavoprotein subunit A (Sdha), mRNA	352	352	95%	6e-96	99%	gi 18426857 NM_130428.1
☐	Rattus norvegicus CH230-2P9 (Children's Hospital Oakland Research Institute Rat (BN/SsNHsd/MCW) BAC library) complete sequence	181	357	95%	2e-44	98%	gi 226514538 AC094217.7

Sdha

Graphic Summary



Descriptions

Sequences producing significant alignments:

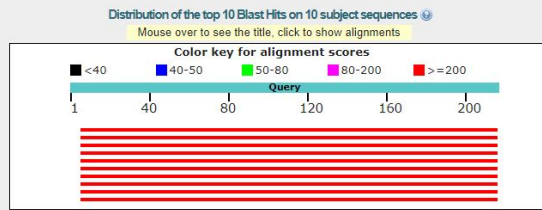
Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: Rattus norvegicus ribosomal protein L13A (Rpl13a), transcript variant X1, mRNA	219	219	91%	1e-53	100%	gi 1046842905 XM_017589309.1
☐	Rattus norvegicus TL0ADA19YK18 mRNA sequence	219	219	91%	1e-53	100%	gi 298915883 FQ222814.1
☐	Rattus norvegicus TL0ADA47YG07 mRNA sequence	219	219	91%	1e-53	100%	gi 298914584 FQ229596.1
☐	Rattus norvegicus TL0ADA47YK12 mRNA sequence	219	219	91%	1e-53	100%	gi 298914501 FQ229513.1
☐	Rattus norvegicus TL0ADA47Y1.04 mRNA sequence	219	219	91%	1e-53	100%	gi 298914487 FQ229499.1

Rpl13a

Graphic Summary



Descriptions

Sequences producing significant alignments:

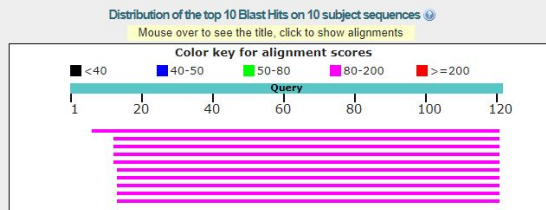
Select: [All](#) [None](#) Selected: 0

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Rattus norvegicus actin, beta (Actb), mRNA	363	363	97%	8e-97	99%	gi 492744873 NM_031144.3
☐	Rattus norvegicus TL0AE64YM19 mRNA sequence	363	363	97%	8e-97	99%	gi 298914700 FQ232682.1
☐	Rattus norvegicus TL0AD48YH01 mRNA sequence	363	363	97%	8e-97	99%	gi 298911322 FQ229293.1
☐	Rattus norvegicus TL0AE64YO15 mRNA sequence	363	363	97%	8e-97	99%	gi 298911110 FQ232650.1
☐	Rattus norvegicus TL0AE67YC11 mRNA sequence	363	363	97%	8e-97	99%	gi 298907175 FQ232063.1

Actb

Graphic Summary



Descriptions

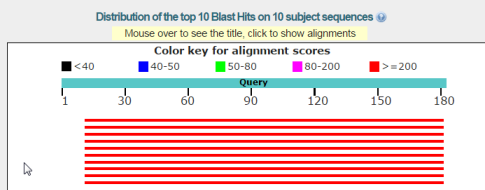
Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Schistocophalus solidus genome assembly S. solidus_NST_G2_scaffold0003238	196	196	94%	1e-46	98%	gi 689428055 LL903470.1
☐	Plagiostomum stellatum 28S ribosomal RNA gene, partial sequence	196	196	89%	1e-46	100%	gi 588313914 KC869872.1
☐	Plagiostomum whitmani 28S ribosomal RNA gene, partial sequence	196	196	89%	1e-46	100%	gi 588313913 KC869871.1
☐	Amastigomonas bermudensis 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	196	196	89%	1e-46	100%	gi 300078505 GU001167.1

Rna28s4



Descriptions

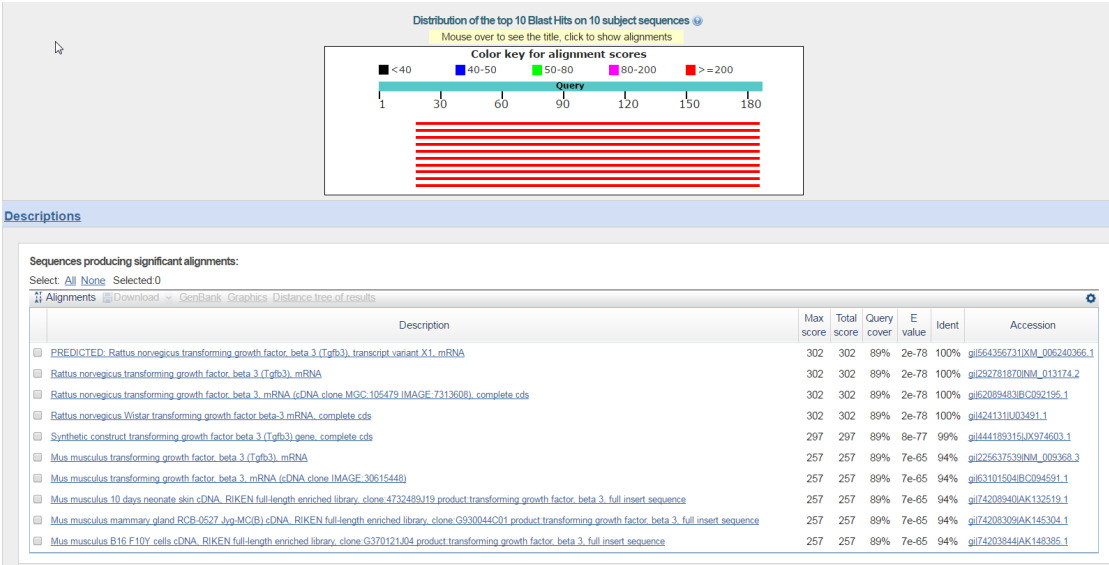
Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

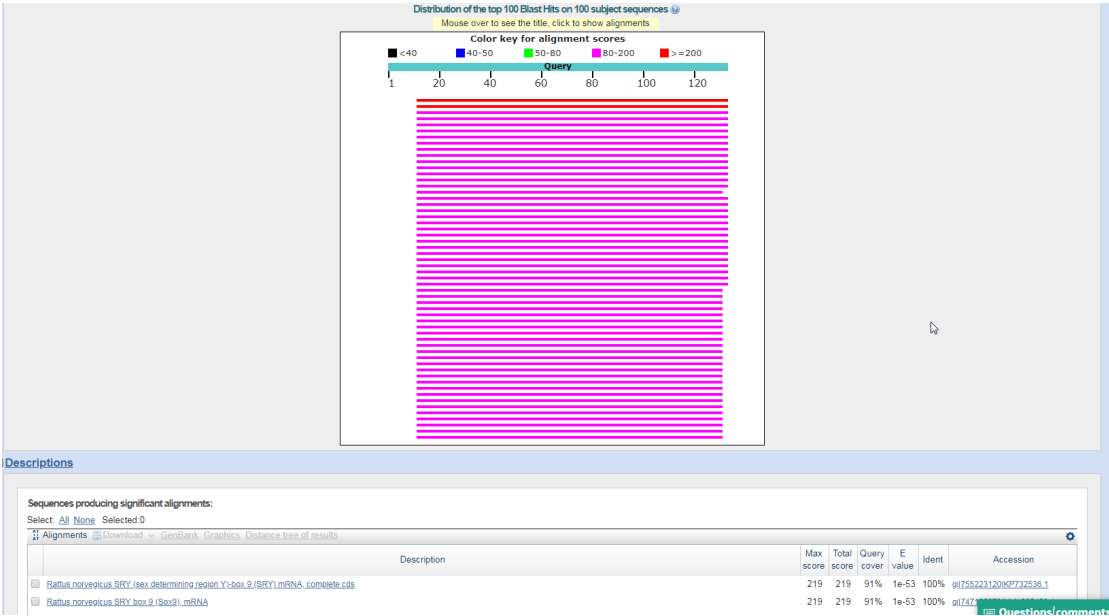
[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Rattus norvegicus transforming growth factor, beta 1 (Tgfb1), mRNA	298	298	93%	2e-77	99%	gi 148747597 NM_021578.2
☐	Rattus norvegicus TGF beta 1 mRNA, complete cds	298	298	93%	2e-77	99%	gi 452390494 AY550025.1
☐	Rat mRNA for transforming growth factor-beta 1	298	298	93%	2e-77	99%	gi 573411X S2498.1
☐	PREDICTED: Mus caroli transforming growth factor beta 1 (Tgfb1), mRNA	277	277	93%	8e-71	96%	gi 1195729563 XM_021167684.1
☐	PREDICTED: Mus pahari transforming growth factor beta 1 (Tgfb1), transcript variant X2, mRNA	277	277	93%	8e-71	96%	gi 1195523161 XM_021219156.1
☐	PREDICTED: Mus pahari transforming growth factor beta 1 (Tgfb1), transcript variant X1, mRNA	277	277	93%	8e-71	96%	gi 1195523159 XM_021219155.1
☐	Mus musculus transforming growth factor, beta 1 (Tgfb1), mRNA	277	277	93%	8e-71	96%	gi 930697458 NM_011577.2
☐	Mus musculus transforming growth factor, beta 1, mRNA (cDNA clone MGC:5747 IMAGE:3586216), complete cds	277	277	93%	8e-71	96%	gi 15489274 BC013738.1
☐	Mus musculus B cells CRL-1702 WEHI 231 cDNA, RIKEN full-length enriched library, clone:G430055L01 product:transforming growth factor, beta 1, full insert sequence	277	277	93%	8e-71	96%	gi 74184430 AK144163.1
☐	Mus musculus mRNA for transforming growth factor-beta 1	277	277	93%	8e-71	96%	gi 3688423 J002862.1

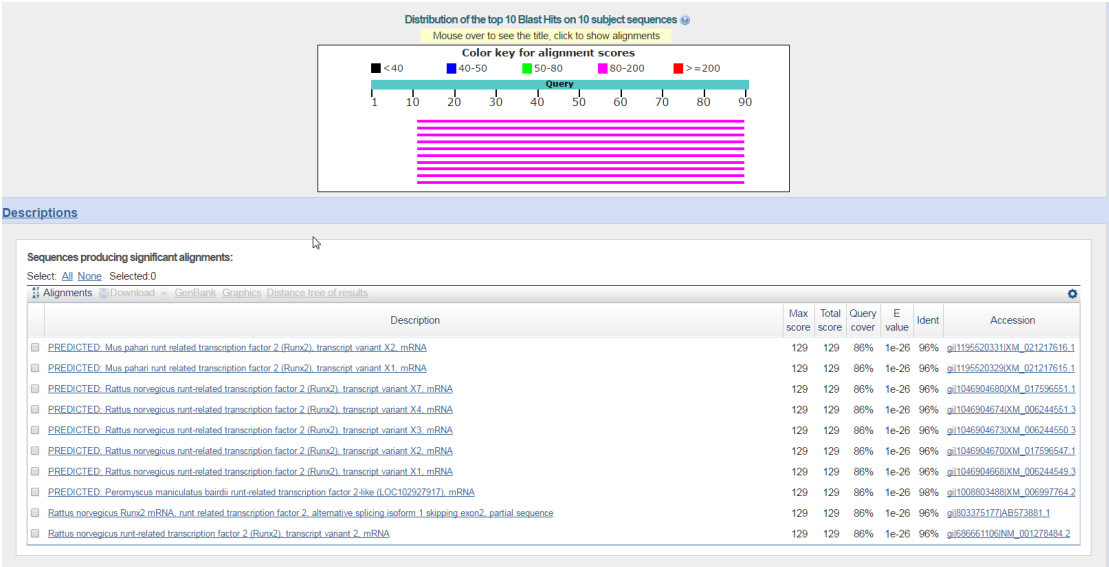
Tgf- β ₁



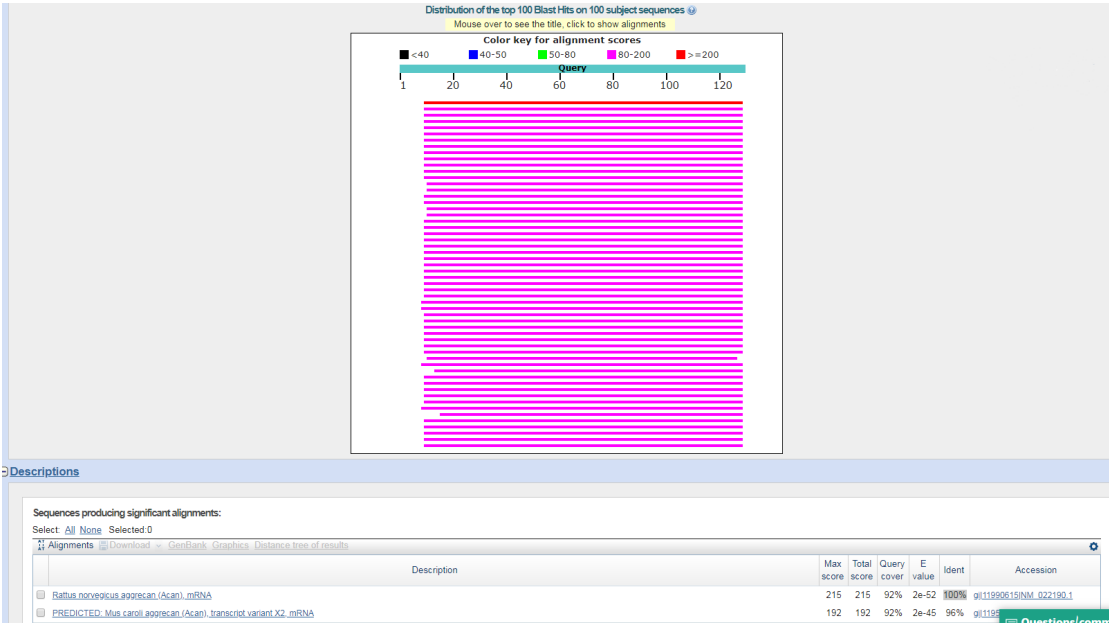
Tgf-β₃



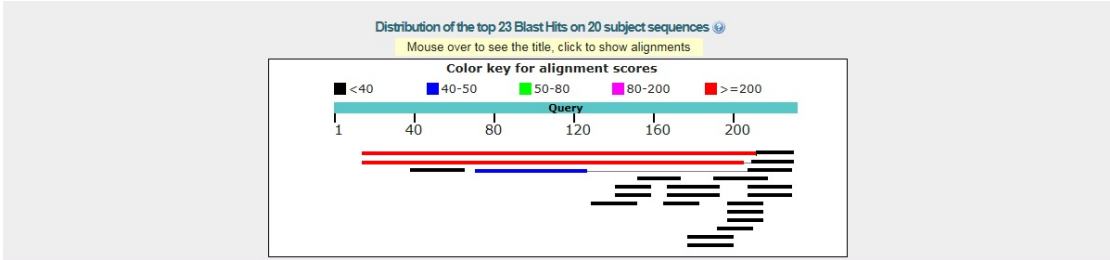
Sox9



Runx2



Acan



Descriptions

Sequences producing significant alignments:

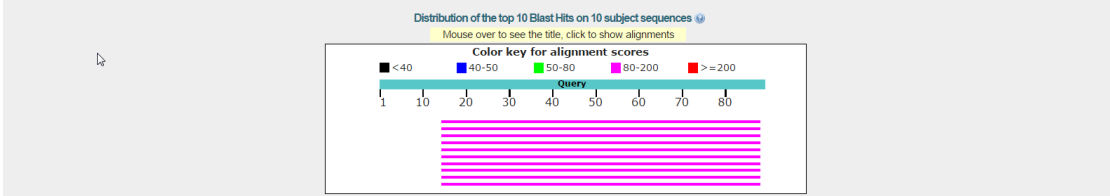
Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	Rattus norvegicus bone morphogenetic protein 6 (Bmp6), mRNA	298	337	93%	1e-79	95%	gi 29789037 INM_013107.1
☐	Rattus norvegicus bone morphogenetic protein-6 (BMP-6), mRNA, partial cds	288	327	91%	2e-76	95%	gi 1854674 U66298.1
☐	Rattus norvegicus bone morphogenetic protein 5 (Bmp5), mRNA	42.8	78.3	33%	0.015	77%	gi 157823366 INM_001108168.1

Bmp-6

Graphic Summary



Descriptions

Sequences producing significant alignments:

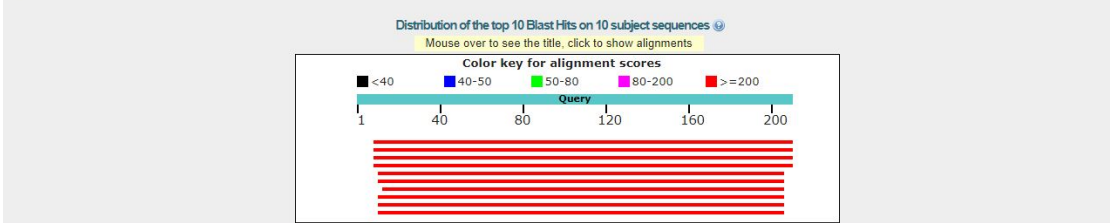
Select: [All](#) [None](#) Selected: 0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: Rattus norvegicus bone morphogenetic protein 2 (Bmp2), transcript variant X1, mRNA	127	127	82%	3e-26	99%	gi 104687854 XM_008762246.2
☐	Rattus norvegicus bone morphogenetic protein 2 (Bmp2), mRNA	127	127	82%	3e-26	99%	gi 8352898 NM_017178.1
☐	Rat bone morphogenetic protein 2 related mRNA sequence	127	127	82%	3e-26	99%	gi 3101758 L20678.1
☐	PREDICTED: Mus pahari bone morphogenetic protein 2 (Bmp2), mRNA	114	114	82%	2e-22	95%	gi 119553758 XM_021193195.1
☐	PREDICTED: Mesocricetus auratus bone morphogenetic protein 2 (Bmp2), transcript variant X2, mRNA	109	109	82%	9e-21	93%	gi 1196035704 XM_021226375.1
☐	PREDICTED: Mesocricetus auratus bone morphogenetic protein 2 (Bmp2), transcript variant X1, mRNA	109	109	82%	9e-21	93%	gi 1196035703 XM_005068676.3
☐	PREDICTED: Cricetus griseus bone morphogenetic protein 2 (Bmp2), transcript variant X2, mRNA	109	109	82%	9e-21	93%	gi 1032963906 XM_007638750.2
☐	PREDICTED: Cricetus griseus bone morphogenetic protein 2 (Bmp2), transcript variant X1, mRNA	109	109	82%	9e-21	93%	gi 1032829534 XM_003495268.3
☐	PREDICTED: Mus musculus bone morphogenetic protein 2 (Bmp2), transcript variant X1, mRNA	109	109	82%	9e-21	93%	gi 568915158 XM_006498619.1

Bmp-2

Graphic Summary



Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected: 0

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	Description	Max score	Total score	Query cover	E value	Ident	Accession
☐	PREDICTED: Rattus norvegicus bone gamma-carboxylglutamate protein (Bglap), transcript variant X1, mRNA	351	351	96%	5e-93	99%	gi 1046871701 XM_006232594.3
☐	Rattus norvegicus bone gamma-carboxylglutamate protein (Bglap), mRNA	351	351	96%	5e-93	99%	gi 11761542 NM_013414.1
☐	Rat mRNA for bone gla protein (BGP)	351	351	96%	5e-93	99%	gi 55826 X04141.1
☐	Rat BGP mRNA encoding gamma-carboxylglutamic acid (Gla) protein, complete cds	351	351	96%	5e-93	99%	gi 203147 M11777.1

Ocn