

A0A0R4IE04	A0A0R4IE04_DANRE	291	PPFQRTVCTTLLCPVDGGWTEWAKWSACGTECTHWSRSECQAPPPRNGGRHRCSGSMMESKN	350
B3DJL0	B3DJL0_DANRE	291	PPFQRTVCTTLLCPVDGGWTEWAKWSACGTECTHWSRSECQAPPPRNGGRHRCSGSMMESKN	350
B3DJ16	B3DJ16_DANRE	291	PPFQRTVCTTLLCPVDGGWTEWAKWSACGTECTHWSRSECQAPPPRNGGRHRCSGSMMESKN	350

A9JR35	M3ZT70_DANRE	324	PBQVRVTCITTLCPVDGGWTEWAKWSACGTECTHWSRRECQAPPPINGGKHCSCSGMMESKN	329
A0A096MDU2	A0A096MDU2_POEFO	295	PQVQRITCITTLCPVDGGWTEWAKWSACGTECTHWSRRECQAPPPINGGKHCSCSGMMESKN	354
A0A087YEW7	A0A087YEW7_POEFO	288	PQVQRITCITTLCPVDGGWTEWAKWSACGTECTHWSRRECQAPPPINGGKHCSCSGMMESKN	347
H2TSK8	H2TSK8_TAKRU	291	PPFQVRTCTTLCPVDGGWTEWAKWSACGTECTHWSRRECQAPPPINGGKHCSCSGMMESKN	350
A0A1A8AQH6	A0A1A8AQH6_NOTFU	293	PPVQRVTCITTLCPVDGGWTEWAKWSACGTECTHWSRRECQAPPPINGGKHCSCSGMMESKN	352
Q4RQ36	Q4RQ36_TETNG	294	PPFQVRTCTTLCPVDGGWTEWAKWSACGTECTHWSRRECQAPPSPRNGGKHCSCSGMMESKN *:*****:****:*****	353
A0A0R4IE04	A0A0R4IE04_DANRE	351	CTEGLCARNNKKVSVEHTSHPLGSGTGVAUYAGLVGALLLCVLVLCVGILVYRRSCRHLH	410
B3DJL0	B3DJL0_DANRE	351	CTEGLCARNNKKVSVEHTSHPLGSGTGVAUYAGLVGALLLCVLVLCVGILVYRRSCRHLH	410
B3DJ16	B3DJ16_DANRE	351	CTEGLCARNNKKVSVEHTSHPLGSGTGVAUYAGLVGALLLCVLVLCVGILVYRRSCRHLH	410
A9JR35	A9JR35_DANRE	351	CTEGLCARNNKKVSVEHTSHPLGSGTGVAUYAGLVGALLLCVLVLCVGILVYRRSCRHLH	410
M3ZTY0	M3ZTY0_XIPMA	384	CTEGLCARNNKKVSEIHASHPLSPMGMAVYTGLVALLTVVMALGVGVLAYRRRCRLH	414
A0A096MDU2	A0A096MDU2_POEFO	355	CTEGLCARNNKKVSEIHASHPLSPMGMAVYTGLVALLTVVMALGVGVLAYRRRCRLH	443
A0A087YEW7	A0A087YEW7_POEFO	348	CTEGLCARNNKKVSEIHASHPLSPMGMAVYTGLVALLTVVMALGVGVLAYRRRCRLH	407
H2TSK8	H2TSK8_TAKRU	351	CTEGLCAR-----SLADPTGVAVYAGLVGALLLCVLVLCVGILVYRRRCRLH	399
A0A1A8AQH6	A0A1A8AQH6_NOTFU	353	CTEGLCARNNKSIVEHASHPLPMGMVAVYTGLVALLSVMALGVGVLAYRRRCRLH	414
Q4RQ36	Q4RQ36_TETNG	354	CTEGLCARYKKVSEIHASHPLADPTGVAVYAGLVGALLLCVLVLCVGILVYRRRCRLH *****:*****:****:*****	413
A0A0R4IE04	A0A0R4IE04_DANRE	411	GEITDSSSALTAAFHGPNGYKPPRDNPHELLHTAPPDLTASAGTFRGPLFSLOQATLDHS	470
B3DJL0	B3DJL0_DANRE	411	GEITDSSSALTAAFHGPNGYKPPRDNPHELLHTAPPDLTASAGTFRGPLFSLOQATLDHS	470
B3DJ16	B3DJ16_DANRE	411	GEITDSSSALTAAFHGPNGYKPPRDNPHELLHTAPPDLTASAGTFRGPLFSLOQATLDHS	470
A9JR35	A9JR35_DANRE	411	GEITDSSSALTAAFHGPNGYKPPRDNPHELLHTAPPDLTASAGTFRGPLFSLOQATLDHS	470
M3ZTY0	M3ZTY0_XIPMA	444	GIDTDSSSALTAAFHGPNGYKAPRDN--PLHPSAPPDLTATAGAFRGPLFSLPQGINDSP	501
A0A096MDU2	A0A096MDU2_POEFO	415	GIDTDSSSALTAAFHGPNGYKPPRDN--PLHPSAPPDLTATAGAFRGPLFSLPQGINDSP	472
A0A087YEW7	A0A087YEW7_POEFO	408	GIDTDSSSALTAAFHGPNGYKPPRDN--PLHPSAPPDLTATAGAFRGPLFSLPQGINDSP	465
H2TSK8	H2TSK8_TAKRU	400	GIDTDSSSALTAAFHGPNGYKPSRDNPMLHPSAPPDLTATAGTFRGPLFSLOQGVNDSP	459
A0A1A8AQH6	A0A1A8AQH6_NOTFU	413	GIDTDSSSALTAAFHGPNGYKPPRDN--PLHPSAPPDLTATAGTFRGPLFSLPQGINDSP	470
Q4RQ36	Q4RQ36_TETNG	414	GIDTDSSSALTAAFHGPNGYKPSRDNPMLHPSAPPDLTATAGTFRGPLFSLPQGINDSP *:*****:*****:****:*****	473
A0A0R4IE04	A0A0R4IE04_DANRE	471	HKIPMTTSPLLDPLPSLKIKVYNSSSTMSSLELPTGLGSVDGIMSLKTVGSG--PKDHHG	528
B3DJL0	B3DJL0_DANRE	471	HKIPMTTSPLLDPLPSLKIKVYNSSSTMSSLELPTGLGSVDGIMSLKTVGSG--PKDHHG	528
B3DJ16	B3DJ16_DANRE	471	HKIPMTTSPLLDPLPSLKIKVYNSSSTMSSLELPTGLGSVDGIMSLKTVGSG--PKDHHG	528
A9JR35	A9JR35_DANRE	471	HKIPMTTSPLLDPLPSLKIKVYNSSSTMSSLELPTGLGSVDGIMSLKTVGSG--PKDHHG	528
M3ZTY0	M3ZTY0_XIPMA	502	HKIPMTTSPLLDPLPSLKIKVYNSSLSSELPAADMVGVDGEILSKSVGTVGGEREFHS	561
A0A096MDU2	A0A096MDU2_POEFO	473	HKIPMTTSPLLDPLPSLKIKVYNSSLSSELPAADMVGVDGEILSKSVGTVGGEREFHS	532
A0A087YEW7	A0A087YEW7_POEFO	466	HKIPMTTSPLLDPLPSLKIKVYNSSLSSELPAADMVGVDGEILSKSVGTVGGEREFHS	525
H2TSK8	H2TSK8_TAKRU	460	HKIPMTTSPLLDPLPSLKIKVYNSSLSSELPAADV-SDGEILTSLNSVTVGREDYYS	518
A0A1A8AQH6	A0A1A8AQH6_NOTFU	471	HKIPMTTSPLLDPLPSLKIKVYNSSLSSELPAADMSLSDGEILTSLKSVGTVGREDYYS	530
Q4RQ36	Q4RQ36_TETNG	474	HKIPMTTSPLLDPLPSLKIKVYNSSLSSELPAADVC-SDGEILTSLKSVGTVGREDCYG *****:*****:****:*****	532
A0A0R4IE04	A0A0R4IE04_DANRE	529	HTLPREPSSHASATLGLSGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWEKTTLPS	588
B3DJL0	B3DJL0_DANRE	529	HTLPREPSSHASATLGLSGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWEKTTLPS	588
B3DJ16	B3DJ16_DANRE	529	HTLPREPSSHASATLGLSGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWEKTTLPS	588
A9JR35	A9JR35_DANRE	529	HTLPREPSSHASATLGLSGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWEKTTLPS	588
M3ZTY0	M3ZTY0_XIPMA	562	HTLSREPLGSTSATLGHGGRLLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWDKTTLPS	621
A0A096MDU2	A0A096MDU2_POEFO	533	HTLSREPLGSTSATLGHGGRLLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWDKTTLPS	592
A0A087YEW7	A0A087YEW7_POEFO	526	HTLSREPLGSTSATLGHGGRLLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWDKTTLPS	585
H2TSK8	H2TSK8_TAKRU	519	HTLSREPLGSTSATLGNLGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWDKTTLPS	578
A0A1A8AQH6	A0A1A8AQH6_NOTFU	531	HTMSRESGLSTSATLGNLGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWEKTTLPS	590
Q4RQ36	Q4RQ36_TETNG	533	HTLSREPLGSTSATLGNLGGRLTIPTNTGVSLLVPPGTIPQKGFYEMYLIINKWDKTTLPS *:*****:*****:****:*****	592
A0A0R4IE04	A0A0R4IE04_DANRE	589	DGSQTIVLSPVVSCGPSMGLLRPVVLTLPHCAQLEP-PDWTLTLKMQNHOGAWEVLTIV	646
B3DJL0	B3DJL0_DANRE	589	DGSQTIVLSPVVSCGPSMGLLRPVVLTLPHCAQLEP-PDWTLTLKMQNHOGAWEVLTIV	646
B3DJ16	B3DJ16_DANRE	589	DGSQTIVLSPVVSCGPSMGLLRPVVLTLPHCAQLEP-PDWTLTLKMQNHOGAWEVLTIV	646
A9JR35	A9JR35_DANRE	589	DGSQTIVLSPVVSCGPSMGLLRPVVLTLPHCAQLEP-PDWTLTLKMQNHOGAWEVLTIV	646

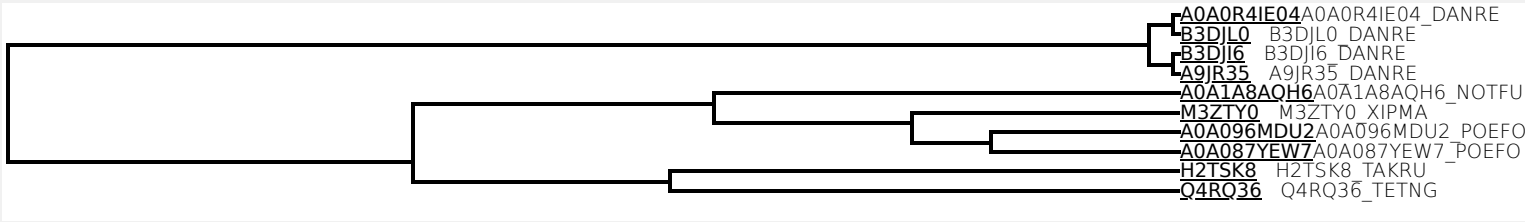
<u>A0A0R4IE04</u>	A0A0R4IE04_DANRE	827	-----TLPPHSPLPAGGSCLPSSQVGPYAFRLPVSIRQK	860
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<u>B3DJ16</u>	B3DJ16_DANRE	827	-----TLPPHSPLPAGGSCLPSSQVGPYAFRLPVSIRQK	860
<u>A9JR35</u>	A9JR35_DANRE	827	-----TLPPHSPLPAGGSCLPSSQVGPYAFRLPVSIRQK	860
<u>M3ZTY0</u>	M3ZTY0_XIPMA	862	-----TLPPHSPLPSGSTCLPSSQVGPYAFRLPDSIRQK	895
<u>A0A096MDU2</u>	A0A096MDU2_POEFO	833	-----TLPPHSPLPSGSTCLPSSQVGPYAFRLPDSIRQK	866
<u>A0A087YEW7</u>	A0A087YEW7_POEFO	826	-----TLPPHSPLPSGSTCLPSSQVGPYAFRLPDSIRQK	859
<u>H2TSK8</u>	H2TSK8_TAKRU	819	-----TLPPHSPLPSGGSCPPSSQVGPYAFRLPDSIRQK	852
<u>A0A1A8AQH6</u>	A0A1A8AQH6_NOTFU	831	-----TLPPHSPLPSGGSPCLPSSQVGPYAFRLPDSIRQK	864
<u>Q4RQ36</u>	Q4RQ36_TETNG	833	VTPAPDSAALNPSRPPKRPVSFQTLPPHSPLPSGGSCCLPSSQVGPYAFRLPDSIRQK	892
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<u>A0A0R4IE04</u>	A0A0R4IE04_DANRE	861	ICASLDAPSARGCDWRMLARSLAFDRYLNYPATKPSPTGVLLDLWEACHQGDADLVSLAT	920
<u>B3DJL0</u>	B3DJL0_DANRE	861	ICASLDAPSARGCDWRMLARSLAFDRYLNYPATKPSPTGVLLDLWEACHQGDADLVSLAT	920
<u>B3DJ16</u>	B3DJ16_DANRE	861	ICASLDAPSARGCDWRMLARSLAFDRYLNYPATKPSPTGVLLDLWEACHQGDADLVSLAT	920
<u>A9JR35</u>	A9JR35_DANRE	861	ICASLDAPSARGCDWRMLARSLAFDRYLNYPATKPSPTGVLLDLWEACHQGDADLVSLAT	920
<u>M3ZTY0</u>	M3ZTY0_XIPMA	896	ICASLDAPSARGCDWRLLARSLGFDRLNYFATKPSPTGVLLDLWEACHQGDADLVSLAT	955
<u>A0A096MDU2</u>	A0A096MDU2_POEFO	867	ICASLDAPSARGCDWRLLARSLGFDRLNYFATKPSPTGVLLDLWEACHQGDADLVSLAT	926
<u>A0A087YEW7</u>	A0A087YEW7_POEFO	860	ICASLDAPSARGCDWRLLARSLGFDRLNYFATKPSPTGVLLDLWEACHQGDADLVSLAT	919
<u>H2TSK8</u>	H2TSK8_TAKRU	853	ICASLDVPSARGCDWRLLARSLGFDRLNYFATKPSPTGVLLDLWEACHQADADLVSLAT	912
<u>A0A1A8AQH6</u>	A0A1A8AQH6_NOTFU	865	ICASLDAPSARGCDWRLLARSLGFDRLNYFATKPSPTGVLLDLWEACHQGDADLVSLAT	924
<u>Q4RQ36</u>	Q4RQ36_TETNG	893	ICASLDAPSARGCDWRLLARSLGFDRLNYFATKPSPTGVLLDLWEACHQGDADLVSLAT	952
*****.*****.*****.*****.*****.*****.*****				

<u>A0A0R4IE04</u>	A0A0R4IE04_DANRE	921	ALEEMGKSEVLVVMTTDGDG	940
<u>B3DJL0</u>	B3DJL0_DANRE	921	ALEEMGKSEVLVVMTTDGDG	940
<u>B3DJ16</u>	B3DJ16_DANRE	921	ALEEMGKSEVLVVMTTDGDG	940
<u>A9JR35</u>	A9JR35_DANRE	921	ALEEMGKSEVLVVMTTDGDG	940
<u>M3ZTY0</u>	M3ZTY0_XIPMA	956	ALEEMGKSEVLVVMTTDGDG	975
<u>A0A096MDU2</u>	A0A096MDU2_POEFO	927	ALEEMGKSEVLVVMTTDGDG	946
<u>A0A087YEW7</u>	A0A087YEW7_POEFO	920	ALEEMGKSEVLVVMTTDGDG	939
<u>H2TSK8</u>	H2TSK8_TAKRU	913	ALEDMGKSEVLVVMTTDGDG	932
<u>A0A1A8AQH6</u>	A0A1A8AQH6_NOTFU	925	ALEEMGKSEVLVVMTTDGDG	944
<u>Q4RQ36</u>	Q4RQ36_TETNG	953	ALEEMGKSEVLVVMTTDGDG	972
.**				

You may add additional sequences to this alignment (in FASTA format)

Tree



☐ Highlight Taxonomy

Result information

Query sequences

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Date of job execution	Mar 16, 2018
Job identifier	A20180316AAF7E4D2F1D05654627429E83DA5CCEF3ED1ED (jobs are stored for 7 days)
Running time	26.1 seconds
Identical positions	755
Identity	72.596%
Similar positions	90
Program	clustalo
Default parameters	Default parameters: The default transition matrix is Gonnet, gap opening penalty is 6 bits, gap extension is 1 bit. Clustal-Omega uses the HHalign algorithm and its default settings as its core alignment engine. The algorithm is described in Söding, J. (2005) 'Protein homology detection by HMM-HMM comparison'. Bioinformatics 21, 951-960.

	Entry	Entry name	Protein names	Organism	Gene name
A0A0R4IE04	A0A0R4IE04_DANRE	Unc-5 netrin receptor B	Danio rerio (Zebrafish) (Brachydanio rerio).	unc5b	
B3DJL0	B3DJL0_DANRE	Unc-5 homolog B (C. elegans)	Danio rerio (Zebrafish) (Brachydanio rerio).	unc5b	
B3DJI6	B3DJI6_DANRE	Unc-5 homolog B (C. elegans)	Danio rerio (Zebrafish) (Brachydanio rerio).	unc5b	
A9JR35	A9JR35_DANRE	Unc5B	Danio rerio (Zebrafish) (Brachydanio rerio).	unc5b	
M3ZTY0	M3ZTY0_XIPMA	Unc-5 netrin receptor B	Xiphophorus maculatus (Southern platyfish) (Platypoecilus maculatus).		
A0A096MDU2	A0A096MDU2_POEFO	Unc-5 netrin receptor B	Poecilia formosa (Amazon molly) (Limia formosa).		
A0A087YEW7	A0A087YEW7_POEFO	Unc-5 netrin receptor B	Poecilia formosa (Amazon molly) (Limia formosa).		
H2TSK8	H2TSK8_TAKRU	Unc-5 netrin receptor B	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes).	unc5b	
A0A1A8AQH6	A0A1A8AQH6_NOTFU	Unc-5 homolog B	Nothobranchius furzeri (Turquoise killifish) .	UNC5B	
Q4RQ36	Q4RQ36_TETNG	Chromosome 17 SCAF15006, whole geno...	Tetraodon nigroviridis (Spotted green pufferfish) (Chelonodon nigroviridis).	GSTENG00030788001	

