

Species	Hit	Description	BLAST E-value	% Length
<b>C. briggsae</b>	BP:CBP11354	gene CBG20056	3.4e-136	93.2%
<b>C. remanei</b>	cr01.sctg327.wum.5.1 <i>Note: C. remanei predictions are based on an early assembly of the genome. Predictions subject to possibly dramatic revision pending final assembly. Sequences available at <a href="ftp://dev.wormbase.org/">ftp://dev.wormbase.org/</a>.</i>		2e-82	40.2%
<b>D. pseudoobscura</b>	TR:Q299A5	GA21945-PA (Fragment).	3.4e-53	47.3%
<b>B. rerio</b>	SW:Q91428	Transcription factor GATA-3 (GATA-binding factor 3).	6.1e-53	60.2%
<b>D. melanogaster</b>	FLYBASE:CG9656-PA	Flybase gene name is gm-PA	2.1e-51	33.8%
<b>H. sapiens</b>	ENSEMBL:ENSP00000218266	isoform 1 of Erythroid transcription factor	8.2e-49	43.2%
<b>C. elegans</b>	WP:CE31430	zinc finger protein (GATA type)	1.3e-16	12.1%
<b>S. cerevisiae</b>	SGD:YFL021W	Transcriptional activator of genes involved in nitrogen catabolite repression, member of the GATA family of DNA binding proteins; activity and localization regulated by nitrogen limitation and Ure2p	2.3e-12	30.1%

Supplemental Figure 5 – A summary of the best BLASTP alignment with *C. remanei* is located on the *C. elegans* Gene page in the Similarities sections (red arrow).