Figure 5. Multiple alignment of vitellogenin-like contigs

```
1      CQSGAQVQIQGQLEQTEGRREYLRRTPT GQQCAQQMQEGNKILPACRNVTARANFLNEG
2      ---------------------------- ------------------------------
4      --------------------QYMRDNDL YKQCESEMQRGQHFLNACRNFTVADNRLNEY
6      ---------------------------- ------------------------------
7      FENAAKVHFNANLKQSSERRQFLRNNAL YKQCESEMERGQYFLPACRNFTVADNRMNEY
8      ---------------------------- ------------------------------

1      SLTVKFSHVTDYMKNVSAR AYGLARYFGYHSAYENIVNPGNQKNGQIDFGYEISPDFQR
2      ------------------- ------------------------------------------
4      YYNFNFQNVPEYFKNYTYK AFSIARHLGYQYQSENFVNPHYKPN-EIEGVFKFSPSFRY
6      ------------------- ------------QSENFGNPNGQHN-KIDGYFKFSPKFDF
7      YYNFNFQNIPEYFKNYTYQ AFAFARHMGYQYQSENVVNPHYKPN-EIEGFFKFSPSFRY
8      ------------------- ------------------------------------------

1      LNVSMSAPGL DANITDLEIHPWARSIVAVDPVQSGARRFAREALAGQYNPTCVIDNNQA
2      ---------- ---------------------------------------RASCRKFGTKGTL
4      ANFSFYSPAF SAVFDNVPVNQYFSAIFAPHPTYSAFDFLMQETFRSRYQAACVADKGFA
6      AQFYFNAPSV AASFKNVPVHQYVADFFAPHPVYSGFDRLMQDTFQAKYQAACVADKMHA
7      ANFSFASPAL SAAFDNVPVNPYFAAIFAPHPTYTAFDFFMQETFRSKYQAACVADKGFA
8      ---------- ------------------------------------------------

1      S TFDNKTYPIELG-NCWHVVMTTIP-----------------DDEQNGDDE IPEDMRV
2      P XFDNKTYPLHMQQNNWYVLMTYVNRNNYYNNQYNSYFQGNNKNQYSYRDY NQKRFYT
4      T TFDNRTFPAHFQ-NNWYVLMAYVNRNNYYNNNFNGYFQ-QNKNQHSYRDY NEKRFYS
6      T TFDNKTYPLHMQQNNWYVLMTYVNRNNYYNNQYNSYFQGNNKNQYSYRDY NQKRFYT
7      T TFDNRTFPAHFQ-NNWYVLMAYMNRNNYYNNNFNQYLQ-QNKNQHSYRDY NEKRFYS
8      - ---------------------------------------------------- -------

1      SVVCRDINEHQRECRLVLGEAEIEM---------------YP NNDQAAIKVNGRAVQL
2      TVYARQNSNGQKELKIVLNNGEYEIFMQPASSQAGLHSSNSGK NNAAIKVFINKQEQQF
4      AVLARENSHGQKELKVVLNNGEYEFNFEPASQNAGFSNS-FSA SNPSAKIQFNKEYQHV
6      TVYARQNSNGQKELKIVLNNGEYEIFMQPASSQAGLHSSNSGK NNAAIKVFINKQEQQF
7      AVLARDNSHGQKELKVVLNNGEYEFNFEPASQNAGFSNS-FSA SNPAAKVQFNKEEQHV
8      ------------------------------------------- ----------------

1      SQEETYRYTSQNGEIQFEAYLKPSGVVYIHSEEY GVRALYDGERIKLILNNEYRDQIRG
2      NDKQFTDFHGHNGKIYAQFYALPDGAIRFFAPQS GLQAIYDGARIKIQAANQYRGAVRG
4      QYKYMNDFFDENGKIFAQFYALPDGAIRFFAPQA GLEFFYDGARVKFQAASQYRGAVRG
6      NDKQFTDFHGHNGKIYAQFYALPDGAIRFFAPQS GLQAIYDGARIKIQAANQYRGAVRG
7      QYKYMNDFFDKNGKIFAQFYALPDGTIRFFAPQA GLEFFYDGARVKFQAASQYRGAVRG
-------------------------------------- -------------ISTRPIRGAVRG
1      LCGTFNGEPATDFTAPQNCILKNPE HFAASYALTKDQCEGPAKENARRAQQAHCYREAV
2      MCGTYSNQYADDFTAPQNCVYKNPE DFAAVYAVIDSSSPSQVKSQKERAQQNFCAHKNN
4      ICGTYSNQYADDFTSPKNCIMSNPQ YFTAAYAFIDSSSPAELKSQRDHAEQGSCAYKTY
6      MCGTYSNQYADDFTAPQNCVYKNPE DFAAVYAVIDSSSPSQVKSQKERAQQNFCAHKNN
7      ICGTYSNQYADDFTSPKNCVMRNPE YFTAAYAFIDSSSPAQLKAQRDQAEQSSCAYKTY
8      MCGTYSNQYADDFTAPQNCVYKNPE DFAAVYAVIDSSSPSQVKSQKERAQQNFCAHKNN

1      LFGNVVSDQDAGR--- ------------------------------------------
2      QFGNYVSRSDAGYG-- -YKYNNNDKYYESAYKNTKYYDPS--NSQYNKYYKN-NKYAKD
4      LAGNYVSRNEGSNGYK YYKYNNSDKYYESAYKNSKYYDASRYNYQYNPYYQSQKKYARN
6      QFGNYVSRSDAGYG-- -YKYNNNDKYYESAYKNTKYYDPS--NSQYNKYYKN-NKYAKD
7      LAGNYVSRNEGQNGNK YYKYNNNDKYYESAYKNSKYYDAARYNHQYNPYYQN-KQYARN
8      QFGNYVSRSDAGYG-- -YKYNNNDKYYESAYKNTKYYDPS--NSQYNKYYKN-NKYAKD

1      ------- ------------------------SKNKDSKWE
2      QDSSYSS SSSSSSDSSSSSSSDSSSSSSSSSSSSSSSSSD
4      EDNSYSS SSSSS----------------SSSDSSSSSSSM
6      QDSSYSS SSSSSSDSSSSSSSDSSSSSSSSSSSSSSSSSD
7      EDASYSS SSSSS----------------SSSSDSSSSSSS
8      QDSSYSS SSSSSSDSSSSSSSDSSSSSSSSSSSSSSSSSD
```