

Salmo_salar	--MAEAFAGTWNLKDSKNFDEYMKALGVGFATRQVGMKPTTIIIEVAGD
Cryodraco_antarcticus	--MVDVFGTWNLKDSEKFDDEYMKKLGVGFATRQVGNVTKPTTIIISVEGD
Anguilla_japonica	MVIMEPFLGTWHLKTSNFDEYMKELGVGFATRKGNTTKPTLIIAADGD
Fundulus_heteroclitus	--MVEAFVGTWNLKESNFDDYMKELGVGFATRQVGNLTKPTTIIICVDGD
Tetraodon_nigroviridis	--MAEAFAGTWNLVKSEKFDDEYMKELGVGLAMRKMGNLAKPTLSITIEGD
Rattus_norvegicus	--MCDAFVGTWKLVSSENFDDYMKELGVGFATRQVGNLTKPTTIIISVEGD
Danio_rerio	--MVDKFGTWNKMTTSDNFDEYMKALGVGFATRQVGNRTKPNLVVCVDEQ
Echinococcus_granulosus	--MEAFVGTWNKMEKSEGFDKIMERLGVDFVTRKMGNLVKPNLIVTDLGG
Taenia_solium	--MEPFIGTWRMEKSEGFDKIMERLGVDFVTRKMGNLMPKSLIVSDLGD
Xenopus_laevis	--MVDQFVGSWKLTDQGFDEYMQSLGVGFATRQVGNLTKPTTIIISVNGD
	xx455354545555455524455455255525552555555555545555
Salmo_salar	-TVTLTKTQSTFKNTEISFKLGEEFDETTADDRKVKSLITIDGGKMHVQK
Cryodraco_antarcticus	-KVTCLKTQSAIKNTELSFKLGEEFDETTADDRKVKSFVTLDDGGKLVHTQK
Anguilla_japonica	-KFQVKTQSLKSTEINFKLGEFDETTADDRKVKSVVKLEDGKLVHLQK
Fundulus_heteroclitus	-KVTVKTQSTIKNTELSFKLGEEFDETTADDRKVKSLVTIEDGKLVHVQK
Tetraodon_nigroviridis	-KVTCLKNSSTFKNTEISFKLGEEFDETTADDRKVKSVVTVEDGKLVHVQK
Rattus_norvegicus	-LVVIRSESTFKNTEISFKLGVEFDEITPDDRKVKSIITLDGGVLVHVQK
Danio_rerio	GLICMKSQSTFKTTEIKFKLNEPFEETTADDRKTTTVMTIENGKLVQKQT
Echinococcus_granulosus	GKYKMRSESTFKTTECSFKLGKFKFVTPDSREVASLITVENGVMKHEQD
Taenia_solium	GKYSMRSESKFKTTEFTFKLGKFKFETTPDSREVTSLITVENGVMKQEQV
Xenopus_laevis	-EILLKTESSLKTTEVTFKLGQEFDEQTADNRKTKTIIITCDSGVNLQVQK
	x55255555535555555515555345554255155531545425455445
Salmo_salar	WDGKETTLVREVSGNALERT
Cryodraco_antarcticus	WDGKETSLVREVNGNSLTLT
Anguilla_japonica	WDSKETSLVRAVDGNKLTLT
Fundulus_heteroclitus	WDGKETTLVREVVDGNKLTLT
Tetraodon_nigroviridis	WDGKETSLVREVEGNLTLT
Rattus_norvegicus	WDGKSTTIKRRXDGDKLVE
Danio_rerio	WDGKESTIEREVSDGKLIK
Echinococcus_granulosus	DKTKVTYIERVVEGNELKAT
Taenia_solium	GKGKTTYIDRVIEGNELKTT
Xenopus_laevis	WDGKETTIQREIKNGHLVVT
	245555555525455555153

Figure A1
Multisequence alignment of the fatty acid binding protein family

Predicted RCRRs (red) and experimentally examined regions (green) are marked. The rare codon score S is displayed for each column.

Table A1
Organisms and GenBank identifiers of the fatty acid binding protein family

<i>Salmo salar</i>	GenBank: AAR91708
<i>Cryodraco antarcticus</i>	GenBank: AAC60357
<i>Anguilla japonica</i>	GenBank: BAA92355
<i>Fundulus heteroclitus</i>	GenBank: AAK61550
<i>Tetraodon nigroviridis</i>	GenBank: CAG10013
<i>Rattus norvegicus</i>	GenBank: NP_445817
<i>Danio rerio</i>	GenBank: NP_001004682
<i>Echinococcus granulosus</i>	GenBank: Q02970
<i>Taenia solium</i>	GenBank: ABB76135
<i>Xenopus laevis</i>	GenBank: AAH78499