

Additional Data

Figure S1

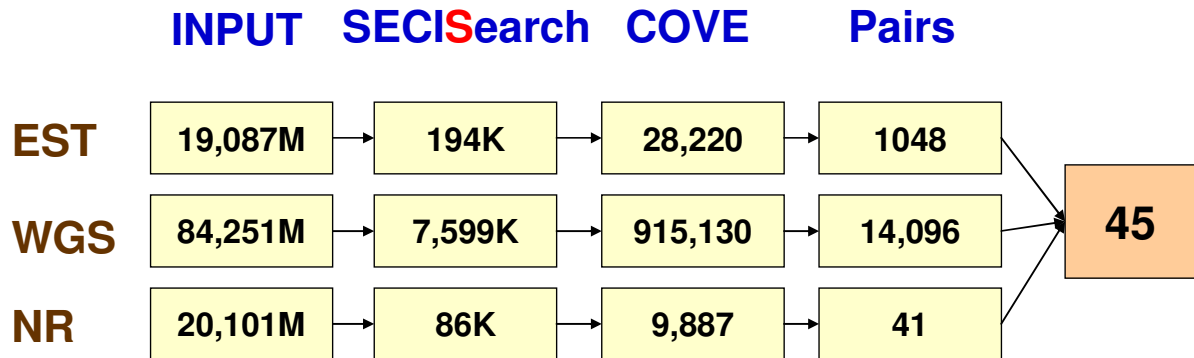


Figure S1. A search for sequences containing two SECIS elements specifically identifies Self sequences. Statistics of the searches of EST, WGS and NR databases for dual vicinal SECIS elements is shown. Query sequence size ("INPUT") and the number of SECIS candidates in each step ("SECISearch", "COVE", "Pairs") are shown in green boxes. A final number of identified sequences is shown in an orange box, including 43 Self sequences. Two false positives were also detected in the EST dataset (see text for details).

Figure S2

<i>D. rerio</i>	1	-----MWKALSLTLALCLLVGCSAESETEGARCKLPPEWKVGV-EPMKNAL
<i>C. carpio</i>	1	-----MWKALSLTLALCLLVGCSAESETDGARCKLPVVKIGEE-EPMKNAL
<i>I. punctatus</i>	1	-----MWRSLSLTLAALVVGCRGESETDGARCKPAAVWKIGDV-EPLKDSL
<i>T. nigroviridis</i>	1	-----MRACLGILLTLCLMLHGGGAESDGDGPRCOLPPTWKIGDL-EPMTGAM
<i>T. rubripes</i>	1	-----MRACLGILLALCLMLHGGGAESEGDGPRCOLPPVWKIGDL-EPMKIAM
<i>G. aculeatus</i>	1	-----MWAYLSLLVALCLLRGGGAESVGDGPHCOLPSPWRIGEV-EPMQGTM
<i>S. salar</i>	1	-----MKAGLSLLALCLLPGGGAESEGEGTRCKPPAGWSIGEV-EPMKGVM
<i>O. mykiss</i>	1	-----MQGLLTLLWLCAALPGLLCASPLLVEGDNDASKICKPAPHWEIKHGAPMKELL
<i>Haplochromis</i> sp.	1	-----MGSLLTLWLFAALPGLLWASHSTLIVEGDNDASRICKPAPQWDIKGY-APMQDLL
<i>O. latipes</i>	1	-----MLRLCSALPALLWASLSVLSLEGDSNASKICKPAPYWDIEGH-VPMQEHL
<i>F. heteroclitus</i>	1	-----MRSLLVLWLSAALPGLLVFHSAPPVEGDNDLSRICKPAPNWTIDGS-SPMEERK
<i>X. tropicalis_Cys</i>	1	-----MGLLGQVSS-----SEQTNSSICKPPPKWSIEGE-VPMAEAL
<i>X. tropicalis</i>	1	-----MWKGFALALALCLLPWGGGAESQGHRKRCKEPPWSIGDQ-NPMQNSA
<i>X. laevis</i>	1	-----MWKGFALALALCLLPWGGGAESQGHRSRCKOPPDWSIGDQ-NPMIQSA
<i>A. mexicanum</i>	1	-----MWGGGLGIALVLCLLPSSGGAESQGPRPHCKKPPDWSIGER-SPMLDSE
<i>H. sapiens</i>	1	-----MWRSLGLALALCLLPSSGGETESQDQSSICKOPPAWSIRDQ-DPMLNSN
<i>P. troglodytes</i>	1	-----MWRSLGLALALCLLPSSGGETESQDQSSICKOPPAWSIRDQ-DPMLNSS
<i>P. pygmaeus</i>	1	-----MWRSLGLALALCLLPSSGGETESQDQSSICKOPPAWSIRDQ-GPMLNSN
<i>M. mulatta</i>	1	-----MWRSLGLALALCLLPSSGGETESQDQSSFCOPPAWSIRDQ-DPMLDSN
<i>M. fascicularis</i>	1	-----MWRSLGLALALCLLPSSGGETESQDQSSFCOPPAWSIRDQ-DPMLDSN
<i>E. europaeus</i>	1	-----
<i>T. belangeri</i>	1	-----
<i>L. africana</i>	1	-----MWRSLGLALALCLLPWGGTESQVQSSFCOPPAWKIRE-EPMLNSI
<i>E. telfairi</i>	1	-----
<i>M. lucifugus</i>	1	-----
<i>C. familiaris</i>	1	-----MWRSLGLALALCLLPWGGGAESQGSFFCOPPAWSIRDQ-NPMLNSS
<i>S. araneus</i>	1	-----GNE-DPMLNSN
<i>S. lateralis</i>	1	-----MWR-----SQGENFTCKOPPDWSIRDQ-NPMQNSH
<i>S. tridecemlineatus</i>	1	-----MWRSLGLALALCLFLPYGGTESQGENFTCKOPPDWSIRDQ-NPMQNSH
<i>O. cuniculus</i>	1	-----MWKSLGLALALCLLPWGGTESHIPSSICKOPPSWSIAEQ-DPMLNSF
<i>O. aries</i>	1	-----MWRGLGLALALCLLLTGGETESQGQSSYCKOPPAWSIKDQ-DPMLNSY
<i>C. hircus</i>	1	-----MWRGLGLALALCLLLTGGETESQGQSSYCKOPPAWSIKDQ-DPMLNSY
<i>B. taurus</i>	1	-----MWRGLGLALALCLLLTGGETESQGQSSYCKOPPAWSIKDQ-DPMLNSY
<i>S. scrofa</i>	1	-----MWRGLGLALALCLLSWGGTESQGKSSFCQPPGWSIKDQ-DPMLNSY
<i>R. norvegicus</i>	1	-----MWRSLGLALALCLLPYGGGAESQGQSPACKQAPPWNIGDQ-NPMLNSE
<i>M. musculus</i>	1	-----MWRSLGLALALCLLPYGGGAESQGQSSACYKAPEWYIGDQ-NPMLNSE
<i>C. porcellus</i>	1	-----MWRSLGLALALCLLPGGGTQSQSKSSYCEQPPWSIGDQ-NPMQNTAT
<i>M. domestica</i>	1	-----MWRGLGLALALCLLPGGGAESQVQSTRCKDAPKWHIGDQ-DPMQDSL
<i>O. anatinus</i>	1	-----MWQGLGLALALCLLPGGGAESQSASSHCKEAPRWQIRDQ-DPMLNSL
<i>G. gallus</i>	1	-----MWAGLGLALVLCLLPGGGTESQR---COEPPHWHIGEE-SPMLNAR
<i>L. erinacea</i>	1	-----MQRCGLVALALCLLPVGVWAESQG---QCEKPKAWTIGEE-NPMEQSL
<i>S. acanthias</i>	1	-----MQKGLGVALTCLLLLGWAESQG---QCEKPKAWTIGEE-NPMEQSL
<i>B. floridae</i>	1	-----RLFLSAGRQSCGPCTTPPVQETTASPPTETPFCAHPPSWOLDGV-DHLEKSQ
<i>O. porcinus</i>	1	-----MVRVKIKVASIPLALVSLLLVSQPACGRPPICSQGDR---DLIEG
<i>B. microplus</i>	1	-----MAARLLVLLA---GCLQATAAARTPICGTPEAWTILGGQ-DPLAAHR
<i>C. gigas</i>	1	-----MRSPAGLWLVAWLTAAVLSSALGQTCORSTLPWRTADGTDPVKMA
<i>A. irradians</i>	1	TSPIKSAYKGGRTIKMRGLGPILLVWVLAAILVASAAGAQRCTRTPIWRTANGTSPMQETE

<i>D. rerio</i>	47	GQTVVAYLQASULFCL	EQASKLNDLLIKLENQ	-GYPNIAYMVVNREERS	QRLHHLLQE
<i>C. carpio</i>	47	GHVTVVAYLQASULFCL	EQASKLNDLLIKLENQ	-GYVNIINVMVNNRDER	QQLHHLLKE
<i>I. punctatus</i>	47	GRVTVVSFLQASUWFCL	SQATRLLEELRQKLEDA	-GFVNITYMVVNSQDENS	SLRVHSLKK
<i>T. nigroviridis</i>	47	GRVTVVALLDASULFCL	VQASRMDSLRQKLENQ	-GLRDVYVMVNVHQGAQ	ARGLHAMLAQ
<i>T. rubripes</i>	47	GRVTVVALLDSSULFCL	VQASRMDSLRQKLENQ	-GLRDVYVMVNVSHQGAH	APGLHAMLAQ
<i>G. aculeatus</i>	47	GRVTVVALLQASULFCL	VQASRMDSLRQKLESQ	-GLKDVAYMVVNQQGEQ	ARRLHPMLAQ
<i>S. salar</i>	47	GQTVVALLQASULFCL	VQASRLDELRIKLEGG	-GLDNVITYMVNVHQGDQ	AQHLHTLLSQ
<i>O. mykiss</i>	54	GNVVVIALLKASUHFCL	RQASKLGGLRDKLRS	-NLTDVSLTVNHEREAQ	SRAMYWELKR
<i>Haplochromis</i> sp.	55	GNVAVVALLKASUQFCL	RQASKIGGLRDLNRS	-NMTEVSFIIVNERDAH	SRAMYWELKR
<i>O. latipes</i>	50	GNVVVVALLKATUEFCL	TQASKIGNLRDKLNEN	-NITEVSFMITVNELEAL	SQTMHWKLLK
<i>F. heteroclitus</i>	55	GNVVVVALLKASUHFCL	SQASRIGRLRTKLTSR	-NITGVSVIVNDQDAVS	RSKYHKLKK
<i>X. tropicalis_Cys</i>	37	GKVTVVALLOASCGFCL	VQASRMGPLRYKLSLQ	-GMTDITKMIIVNDQSLH	SAHNPPELKR
<i>X. tropicalis</i>	47	GKVTVVALLOASUSLCL	LQASRLDLRIKLEKE	-KLVGISYVVNVHQGRQ	SRAKYDLLKS
<i>X. laevis</i>	47	GKVTVVALLOASUYLCL	LQASRLDLRIKLEKE	-KLVGISYVVNVHQGRH	SRAKYDLLKS
<i>A. mexicanum</i>	47	GQTVVALLDASUYVCL	LQASRLLEELRSKLEKD	-GLVNVSLTVNVHQKAS	QOQAYHLLKE
<i>H. sapiens</i>	47	GSVTVVALLQASUYLCL	IEASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SRLKYTHLKN
<i>P. troglodytes</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SRLKYTHLKN
<i>P. pygmaeus</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SRLKYTHLKN
<i>M. mulatta</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SRLKYTHLKN
<i>M. fascicularis</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SRLKYTHLKN
<i>E. europaeus</i>	1	-----	-----	-----	-----
<i>T. belangeri</i>	1	-----	-----	-----	-----
<i>L. africana</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQDLN	SRLKYIHLKN
<i>E. telfairi</i>	1	-----	RLNLRVKLEKE	-GYSNISYIVNVHQSLV	SOLKYTHLKD
<i>M. lucifugus</i>	1	-----	FVCIFFPKYFSLED	LRVKLEKEGFSNISY	IVNVHQGHPSRLRYNLLKN
<i>C. familiaris</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GFLNISYVVNVHQGLS	SOLKMYMLKN
<i>S. araneus</i>	11	GSVTVVALLQASUHLCL	IQASTLEDLRVKLEEE	-GYSNISYIVNVHQGFH	SOLRYRHLKN
<i>S. lateralis</i>	30	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SOLKYIHLKN
<i>S. tridecemlineatus</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGIS	SOLNYIHLKN
<i>O. cuniculus</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGID	SOLKYIHLKN
<i>O. aries</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYVVNVHQEIS	SRLKYAHLKN
<i>C. hircus</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYVVNVHQEIS	SRLKYVHLKN
<i>B. taurus</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYVVNVHQGIS	SRLKYVHLKN
<i>S. scrofa</i>	47	GSVTVVALLQASUYLCL	IQASKLEDLRVKLEKE	-GYSNISYIVNVHQGI	ASOLKYVYLKS
<i>R. norvegicus</i>	47	GTVTVVALLOASUYLCL	LQASRLDLRIKLENQ	-GYFNISYIVNVHQGPS	SOLKHAHLKK
<i>M. musculus</i>	47	GKVTVVALLOASUYLCL	LQASRLDLRIKLESQ	-GYFNISYIVNVHQGPS	SOLKHSHLKK
<i>C. porcellus</i>	47	GTVTVVALLDASUYVCL	IQASR-----	-----	-----
<i>M. domestica</i>	47	GRVTVVALLQASUYLCL	IQASRLDLRMKLEKE	-GFSNISYVVNVHQGN	ASRLNIKELQD
<i>O. anatinus</i>	47	GTVTVVALLOASUYLCL	IQASRLDLRVKLENE	-GYSNISYIVNVHQGM	PSOLNHKTLKE
<i>G. gallus</i>	43	GSVAVVALLQASUYLCL	LQASRLDLRVKLENE	-GLVNISYVVNVHQSP	HSQKKFHLLE
<i>L. erinacea</i>	44	GRVTVVSLLOASUHFCL	VQAASLKRLKHSLDHR	-GFVNISYIVNVHQAN	DSRRNYQQLKE
<i>S. acanthias</i>	44	GRVTVVSLLOASUHFCL	VQAASLMKLQ	-QKLDQAGLVNISFM	VNVHQKRSRGKYQLKS
<i>B. floridae</i>	53	GQAVLQFVFASURFCRS	QAERFESLRSTLVEG	--LTDISEGAVNGHLYN	APLEIGETEG
<i>O. porcinus</i>	44	GNVTIVALLSASURLC	WRQATGLESLLQDLRL	QHGMHKLQFVIVNSM	APNDTVNVQQLSS
<i>B. microplius</i>	35	GNVTIVALLKASUSLC	RQASGLEALLQRLRPN	--MTLQFLVVNDRKSAH	-----LRD
<i>C. gigas</i>	46	GNVTIVALLSASUPM	CQQQAEGLEKLMTSY	NI-GKRDISEFTIVNH	ARGEDSVN--ELTR
<i>A. irradians</i>	61	GKVRIVALLKASUGFC	VRVAMALERIRSSFER	-GLTGYKFMIVNMNL	ADAIANVKNLQD

<i>D. rerio</i>	106	RLLN-ITLYAQDL--SQPDVWQAVNAEKDDFLVYDR-CGRLTYHLSLPYITIL-----SH
<i>C. carpio</i>	106	RLMN-ITLYAQDL--SQPDVWQAVNVEKDDFLVYDR-CGRLTYHLSLPYITIL-----SH
<i>I. punctatus</i>	106	KLSDNITLYKONP--EEPNVWSMAKAEKDDFLIYDR-CGRLTHHLSMPYITIL-----SQ
<i>T. nigroviridis</i>	106	RLSEHISLHRODE--ALADVQWTLGGNKDDFLIYDR-CGRLTHRISLPYAVI-----GH
<i>T. rubripes</i>	106	KLTEHISLYKQDE--ALPDVWQTLGGNNDFLIYDR-CGRLTHRISLPYSITL-----GH
<i>G. aculeatus</i>	106	RLSVNIDLYKQDE--QQPDVWKTLLGGDKDDFLVYDR-CGRLTHHIALPYSITL-----GQ
<i>S. salar</i>	106	KLSENIILYKQEP--KQADVQWQALAGKKDDFLIYDR-CGRLTHHIFLPFSITL-----GT
<i>O. mykiss</i>	113	RAPPGIPVYQQAP--LQDDVWEALDGDKDDFLVYDR-CGRLTEHIVLPYSFSL-----HY
<i>Haplochromis</i> sp.	114	SAPTGVVPVQQQP--LQNDVWEALDGDKDDFLVYDR-CGRLTEHIVMPYSFSL-----HH
<i>O. latipes</i>	109	KAPTGVVPVYQSS--LQKDVWEILLDGDKDDFLIYDR-CGRLTEHIVLPNSFSL-----QN
<i>F. heteroclitus</i>	114	RAPERVPVYQSSA--NQSDVWELLLEGDKDDFLIYDW-CGRLTFHMLVPYITIL-----HN
<i>X. tropicalis_Cys</i>	96	WAFEGIPVYQTP--QDDVWELLDGNKDDFLIYDR-CGRLTEHIVRLPLSFL-----HF
<i>X. tropicalis</i>	106	KVSEHIPVYQQEE--YQPDVWSLLKGDKDDFLVYDR-CGRLVQHLELPYSITL-----HF
<i>X. laevis</i>	106	KVSEHIPVYQQEE--NQPDVWSLLKGDKDDFLIYDR-CGRLVQHLELPYSITL-----HF
<i>A. mexicanum</i>	106	KVSDHIPVYQQDE--GQPDVWNTLNATKSDFLIYDR-CGRLVSHLGLPYITFL-----SF
<i>H. sapiens</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGSKDDFLIYDR-CGRLVYHLGLPFSFSL-----TF
<i>P. troglodytes</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGSKDDFLIYDR-CGRLVYHLGLPFSFSL-----TF
<i>P. pygmaeus</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGSKDDFLIYDR-CGRLVYHLGLPFSFSL-----TF
<i>M. mulatta</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGSKDDFLIYDR-CGRLVYHLGLPFSFSL-----TL
<i>M. fascicularis</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGSKDDFLIYDR-CGRLVYHLGLPFSFSL-----TL
<i>E. europaeus</i>	1	-----R-CGRLVYHIGLPFSFSL-----SF
<i>T. belangeri</i>	1	-----LFSR-CGRLVSHLGLPFSFSL-----TF
<i>L. africana</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>E. telfairi</i>	39	QVSENIIVYQQEE--NQTDVWILLDGSKDDFLIYDR-CGRLVYHLGVPYSFSL-----TS
<i>M. lucifugus</i>	48	KVSEHIPVYQQEE--NQTDVWILLNGNKDDFLIYDR-CGRLVYHLGLPFSITL-----EF
<i>C. familiaris</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>S. araneus</i>	70	QVSEHIPVYQQEE--NQTDVWILLNGNKDDFLVYDRYCKYVCTVENNFKFI-----YE
<i>S. lateralis</i>	89	KVSDHIPVYQQEE--NQTDVWILLNGYKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>S. tridecemlineatus</i>	106	KVSDHIPVYQQEE--NQTDVWILLNGYKDDFLIYDRS-----
<i>O. cuniculus</i>	106	KVSHHILVYQQEE--NQTDVWILLKGSKDDFLIYDR-CGRLVYHLALPYSFSL-----TF
<i>O. aries</i>	106	KVSEHIPVYQQEE--DQPDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>C. hircus</i>	106	KVSEHIPVYQQED--DQPDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>B. taurus</i>	106	KVSEHIPVYQQEE--NQPDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>S. scrofa</i>	106	KVSEHIPVYQQEE--NQTDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>R. norvegicus</i>	106	QVSDHIAVYRODE--HQTDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>M. musculus</i>	106	QVSEHIAVYRQEE--DGDVWILLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----TF
<i>C. porcellus</i>	69	----ITLY-----LYPLL-----LFFFR-CGRLAYHLRMPYSFSL-----SF
<i>M. domestica</i>	106	QVSKNITVYQQEQ--NQKDVWITLLNGNKDDFLIYDR-CGRLVYHLGLPHITFL-----SF
<i>O. anatinus</i>	106	KVSEHIPVYQQDE--KQTDVWSTLKGKDDFLIYDR-CGRLVYHLSLPYITFL-----SF
<i>G. gallus</i>	102	SVSDHITVYQQDD--HQADVWITLLNGNKDDFLIYDR-CGRLVYHLGLPYSFSL-----SF
<i>L. erinacea</i>	103	KVEGQLPVYQQGT--DQPDVWNLRLRGEKDDFLIYDR-CGQQTETHLGLPFTITL-----SQ
<i>S. acanthias</i>	103	KVTEEIPVYQQDS--NKPQDVWELLQGDKDDFLIYDS-CGRLTHHLQLPFTITL-----TD
<i>B. floridae</i>	111	RVGFPPVYQDT----AEEEIWKLLDARKDDFLIYDR-CGRLVRHIRMPQANM-----DN
<i>O. porcinus</i>	104	RATFPVLQETAEK----PIWRELHGEKGDFLIYDR-CGRLVYFLPPLTKFPE---LMS
<i>B. microplus</i>	95	HLEQRVSFAVHQETA--EEPVWITMEGGKDDVFIFDR-CGRLAEYVPFPISLVLP---GHL
<i>C. gigas</i>	103	RVSFPPVYQDDNTS-----MTQQTLNASIDDLFIYDR-CGRLVYHLRKPESLV-----SH
<i>A. irradians</i>	120	VVK-----DDOLE-----IWRKLLGGDKDYLYFYDG-CGMFRILLTSDDILDREQNSINT

<i>D. rerio</i>	156	PHVEEAIKHTYCDRI CG-ECSESSAQLEECKKATEEVNKPVEEEPRQDHGHE-----
<i>C. carpio</i>	156	PHV-----
<i>I. punctatus</i>	157	PHVEEAI RNAYCAAVCG-ECERSDQLEE CNKTKEEKTETPKTEEDHHHHQ-----
<i>T. nigroviridis</i>	157	GHVEKAVKDTYCSSL CG-ECHEHTTETQECTPKTDTQPO-----EDTRHEC-----
<i>T. rubripes</i>	157	GHVERAVKDTYCNSL CG-ECHEHTTETLQECTPKTSALP NGVAPGAEE TGHEC-----
<i>G. aculeatus</i>	157	GHVESAIKDAYCKRT CG-DCVHESATTPEECVEKAVAQPADAPPVVEDNNGGG-----
<i>S. salar</i>	157	PYVENAIKETYCQSI CG-DCYESTEIPAECNRMVEVKPEGEEKP---VTGGDT-----
<i>O. mykiss</i>	164	PYVEAAVRATYHKDICG-NCTVDSTQPPQ-----
<i>Haplochromis</i> sp.	165	PHVEAAIRATYQKNIC--NCTHNSTSS-----
<i>O. latipes</i>	160	ADVENAITATYTQDIC--NCSGNST-----LSGGGNFTRNSSQSHSG---SPAGEEHQ
<i>F. heteroclitus</i>	165	THVENAISATYQGHLLQ-----LLHRDKPRRGYRTIVI-----GH
<i>X. tropicalis_Cys</i>	147	PYVEEAAILSTYNESFCG--NCSFTSNST-----L-----
<i>X. tropicalis</i>	157	PYVEEAI RIAYCEDKCG-ECCHKILDAD-VCKKPEEQQEOKPVEEKVERPRHHR-----
<i>X. laevis</i>	157	PYVEEAVRIAYCGDKCG-ECCHKIPDAD-VCKKPEEQQEOKPVEEKVERPRPHR-----
<i>A. mexicanum</i>	157	PYVGESIRSAYCENKCG-ICKNTIESVAEVCNASLKLPAEGVVEEQPEDTPKTHRHEPR
<i>H. sapiens</i>	157	PYVEEAIKIAYCEKKCG--NCSLTTLKDEDFCKRVSLATV DKTVETPSPHYHHEH-----
<i>P. troglodytes</i>	157	PYVEEAIKIAYCEKKCG--NCSLTTLKDEDFCKRVSLATV DKTVETPSPHYHHEH-----
<i>P. pygmaeus</i>	157	PYVEEAVKIAYCEKKCG--YCSLTTLKDEDFCKSVSLATV DKTVEAPSPHYHHEH-----
<i>M. mulatta</i>	157	PYVEEAIKIIVYCEKKCG--NCSLTTLKDEDFCKSVSLATV DETVEAPQPHYHHEH-----
<i>M. fascicularis</i>	157	PYVEEAIKIIVYCEKKCG--NCSLTTLKDEDFCKSVSLATV DETVEAPQPHYHHEH-----
<i>E. europaeus</i>	19	PYVEEAIKITIYCEKT CG--NCSHTTLLENGGFCKNISLATSENTTIA--PKHHHHD-----
<i>T. belangeri</i>	22	SYVEEAIKSAYCEEKCG--NCSLT-----
<i>L. africana</i>	157	PYVEEAIKIIVYCEEKCG--NCSLMTPEDEDFCKKVSSVNV EDTAEASKPHHHHSH-----
<i>E. telfairi</i>	90	PHVEEAIKTAYCEKKCG--NCSLMNLEDAVCKGIASASVQEATEAAKPHHHHHH-----
<i>M. lucifugus</i>	99	PYVEQAIKIAYCEEKCG--NCSLT-----
<i>C. familiaris</i>	157	PYVEEAIKRAYCEEKCG--NCSLTVLEDEEVCKMVSSGTV ESTEAPQPHPHDHH-----
<i>S. araneus</i>	121	R-LLYLLQTLKH EEFCK--NISLASAEKPTEAPHHFHQPH-----
<i>S. lateralis</i>	140	PYVEDAIKIAYCEDRCG--NCSFRTLENEDEFCRNVSFPTVEKT IEALQPHHHHN-----
<i>S. tridecemlineatus</i>	141	-----LQTLNEDELCRNVSLLTVEKTTEALQPHHHHN-----
<i>O. cuniculus</i>	157	PYVEEAIKIAYCEETCG--NCSLMTPEDESFCKRVSLATVEKVSEALRPHHHHTH-----
<i>O. aries</i>	157	TYVEDSIKTVYCEDKCG--NCSLKTQEDEDFCKNVSLATR RQQLRL-----
<i>C. hircus</i>	157	TYVEDSIKTVYCEDKCG--NCSLKTQEDEDFCKNVSLATKEK-----
<i>B. taurus</i>	157	TYVEDSIKTVYCEDKCG--NCSLSRPQDEDVCKNVFLATKEKTAEASQRHHHHPH-----
<i>S. scrofa</i>	157	PYVEEAIKTVYCENKCG--NCSLKTTLKDEDFCKNVYLATEEKTTEAPQPHHHHDH-----
<i>R. norvegicus</i>	157	PYVEEAIKIAYCEKRCG--NCSFTSLEDEAFCKNVSSATASKTTEPSEEHNHHKH-----
<i>M. musculus</i>	157	PYVEEAIKIAYCEERC CG--NCSLTSLDEDEDFCKTVTSATANKTAEPSEAHSHHKH-----
<i>C. porcellus</i>	100	PYVEQAIKIIVYCEVKCG--NCSLKNLEDDDFCKNVSLAAVTTEAPQKHHHRQIH-----
<i>M. domestica</i>	157	SYVEDAIKSAYCEKACG--NCSYTLDDDEGFCKNVSLVAEETITTSLHHHYHPP-----
<i>O. anatinus</i>	157	SYVEDSIKTTYCEQNCG--NCSYTMPEAEFFCTNTSSAAKEKATEAPLPHNDRPH-----
<i>G. gallus</i>	153	QYVEEAIKIAYCENNCG--NCSYTEPDIDNICENITLAGI EPEPEPSGQSHHHH-----
<i>L. erinacea</i>	154	VYVEEAI VQTYCHTMCT--NCSL--VEVPLE--CLAR-----
<i>S. acanthias</i>	154	LYVEYAIRQTYCQEICA--NCSL--VHDPPA--CSAR-----
<i>B. floridae</i>	159	SDVEDAIRAVYEE SP CG--PCITP-----
<i>O. porcinus</i>	155	SVTRKVLLETYYRSLCGNACPN-----
<i>B. microplus</i>	142	PHVEDSLRRAYDGEPCGLTCEEPTE-----
<i>C. gigas</i>	151	GTMQTNLLTTYLG NLCK--CEKFKS-----
<i>A. irradians</i>	168	RLIRRRRLRQVSRDR CARCRR-----

<i>D. rerio</i>	209	--HG-----	HHHQGEAERH-----	RHGHHHPHHHH-----
<i>C. carpio</i>	159	-----	-----	-----
<i>I. punctatus</i>	210	--HH-----	HHHGHEGHHH-----	RGHHHGHHPHDGVETRGGG
<i>T. nigroviridis</i>	203	--HHRHH-----	QGHQHHC DGHR-----	DHGDNQCTHTQGSGPGHGH
<i>T. rubripes</i>	210	--HH-----	HGRQHHC DGHR-----	DHGDSQCTHTRGSGRGHGH
<i>G. aculeatus</i>	210	--GH-----	HGHHHC GHG-----	HRGHHHGHHHG--HHHG
<i>S. salar</i>	207	--PHGG-----	RGHHHC NGHG-----	HHSKSHGHHGHE--SEVGR
<i>O. mykiss</i>	192	-----	-----	-----
<i>Haplochromis</i> sp.		-----	-----	-----
<i>O. latipes</i>	209	HQHPHHGHHGHNHGDNHGLHPR--	-----	GFGHGHDRHGHHR
<i>F. heteroclitus</i>	200	I-H-----	-----	-----
<i>X. tropicalis_Cys</i>	174	--IPMN-----	-----	-----
<i>X. tropicalis</i>	210	--NHHR-----	HHRPKHSC HR-----	HRHHHSEDGQVAELDVLR
<i>X. laevis</i>	210	--NHHR-----	HHRPKHSC HR-----	HRHHNNEGGQAAEVDAF--
<i>A. mexicanum</i>	188	-GHGHR--HHHHQQH--NHER-	DHLPEDPDSKP-----	HPHHNR-----
<i>H. sapiens</i>	210	--HHN-----	HGHQHLGSS-----	ELSENQQPGAPNAPT-HP
<i>P. troglodytes</i>	210	--HHN-----	HGHQHLGSS-----	ELSENQQPGAPNAPT-HP
<i>P. pygmaeus</i>	210	--HHN-----	HRHQHLGSS-----	ELSENQQPGAPDAPT-HP
<i>M. mulatta</i>	210	--HHN-----	QGHQHLGSS-----	ELSENQQPGAPDAPT-HP
<i>M. fascicularis</i>	210	--HHN-----	QGHQHLGSS-----	ELSENQQPGAPGAPT-HP
<i>E. europaeus</i>	70	--HHG-----	LGHQHAGNG-----	PLSENQQPGAQGAPE-HF
<i>T. belangeri</i>	44	-----	GISMIGEI-----	SFQENQQPGTHDDPL-HL
<i>L. africana</i>	210	--HHS-----	HGHQHLGNH-----	QHSNQQPGDPEAPQ-HS
<i>E. telfairi</i>	143	--HHH-----	HHHRPGHQH----	ENSQPSNQSPSEPDTIQ-HP
<i>M. lucifugus</i>	121	-----	-----	-----
<i>C. familiaris</i>	210	--LHH-----	HHHHHKKHWHRLMPHGND	ELSENQQPEEPDVSE-HP
<i>S. araneus</i>	159	--HHR-----	HGHQQLGHP-----	QFSEHQPEKTEASE-HP
<i>S. lateralis</i>	192	-----	HQHLGSS-----	ELSKNQPGAADTPS-NP
<i>S. tridecemlineatus</i>	173	-----	HQHLGSS-----	ELSENQQPGAADTPS-NP
<i>O. cuniculus</i>	210	--HHK-----	HGHQHLDSS-----	ELSEKHPTGPDAPL-HL
<i>O. aries</i>	201	-----	HSDITIT-----	WTPAGTGPEFPGRPT-RP
<i>C. hircus</i>	197	-----	-----	TAEAS-QR
<i>B. taurus</i>	210	--HSH-----	HGHQLHENA-----	HLSESPKPDTPDTPE-NP
<i>S. scrofa</i>	210	--HHHRHHH-----	HHHGHLGNG-----	HLSEHPKEAPDTPE-QP
<i>R. norvegicus</i>	210	--HDK-----	HGHEHLGSS-----	KPSENQQPGALDVET-SL
<i>M. musculus</i>	210	--HNK-----	HGQEHLCSS-----	KPSENQQGPS--ET-TL
<i>C. porcellus</i>	152	--PPK-----	RGHPLYCSR-----	EPEAPDNPVQS-----
<i>M. domestica</i>	210	--HRHG-----	HHPHHHGHHPPLG--	HPPSENDKPEGSEGAV-HS
<i>O. anatinus</i>	210	--HHH-----	HHHHHGHKHP-----	HPSGTEQAPADPDGPLRSP
<i>G. gallus</i>	206	--QLHR-----	HRHHHHHREG-----	GRHSKNQNHQAPSESQRRH
<i>L. erinacea</i>	185	-----	-----	-----
<i>S. acanthias</i>	185	-----	-----	-----
<i>B. floridae</i>	181	-----	-----	-----
<i>O. porcinus</i>	178	-----	-----	-----
<i>B. microplus</i>	175	-----	-----	-----
<i>C. gigas</i>	175	-----	-----	-----
<i>A. irradians</i>	190	-----	-----	-----

<i>D. rerio</i>	233	-----HHHRGQQQVDVDQQVLSQVDFGQVAVETPMMKRP--UAKHS--RUKVQYS--UQ
<i>C. carpio</i>	159	-----MLAQVDFGQAAIEPPVMKRP--UAKHT--RUKVQYS--UQ
<i>I. punctatus</i>	242	NQQHGHEGQVQVQRSQVDLGGQAHVGQIDLGQVGINQVMMRP--UAS--RUKFQFM--CQ
<i>T. nigroviridis</i>	238	GH-HGGQG--HQGHDAQGV--QRPDHLDELGQAQ--HDAAAAKP--UESK--RUKF--QFSUQ
<i>T. rubripes</i>	242	HHGHGGQQG--HEGRVHMGDIPQRPDHLDELGQAQ--HDAAAATP--UESK--RUKA--QFSUQ
<i>G. aculeatus</i>	238	DHGAGQQAVVHQEHERDGGASHGQHNSALDQMQAQAAPVRP--UVEENAKUKS--KHSUK
<i>S. salar</i>	240	DHGRGHGVEQQQHGHGAEGLHHGQAHGQLHVGQEEGHIMQRP--UVKGRARUKA--ELSH
<i>O. mykiss</i>	192	-----VEGGVUS
<i>Haplochromis</i> sp.		-----
<i>O. latipes</i>	246	HHHGRAETRLQEHQHHA--SSDQMQHAVQLEQIGQEVVGAPVRP--UQETARUKTK--FTUH
<i>F. heteroclitus</i>	202	-----GIGRRSVDTQQFSQEVLAFFVVRPUAADNVRLUKSK--FTUH
<i>X. tropicalis_Cys</i>	178	-----GTTVSP-----S
<i>X. tropicalis</i>	242	SSAQANNRAGSQNGQGSQVVPQSEVLF--VPQREADIPVLARQP--UKKA--KSUKK--QYLUQ
<i>X. laevis</i>	241	---QTNNRAGSHNGQGS--VVPQSEVVF--VPQREADIPVLALQP--UKKA--KSUKK--QYLUQ
<i>A. mexicanum</i>	210	--AMGPNRHGQRSG--QQVVDALPQPDVVGSPQREMKNRIR--QUNK--QSUNK--QFMUD
<i>H. sapiens</i>	239	APPGLHHHHK---HKGQHRQCHPENRDMPA--SED--LQDLQKKLCRK---RCIN--QLLCK
<i>P. troglodytes</i>	239	APPGLHHHHK---HKGQHRQCHPENQDMPG--SED--LQDLQKKLCRK---RCIN--QLLCK
<i>P. pygmaeus</i>	239	APPGLHHHHK---HKGQHRQCHPENRDMPG--SED--LQDLQKKLCRK---RCIN--QLLCK
<i>M. mulatta</i>	239	APPGLHHHHK---HKGQHRQCHPESUDMPG--SEG--LQHLQKKLURK---RCINP--QLLCK
<i>M. fascicularis</i>	239	APPGLHHHHK---HKGQHRQCHPESUDMPG--SEG--LQHLQKKLURK---RCIN--QLLCK
<i>E. europaeus</i>	99	APLGHRRHHR---HKGSHGEGHPEDUDMAG--SGRLHL--SLPQKRLURK---GCIN--QLLUQ
<i>T. belangeri</i>	69	PHTGLHHHHK---HKGHDROCHPESUDMP-----ELLQKKLURK---GCIN--QLLUQ
<i>L. africana</i>	239	PPPGLHHHHK---HKGPQRQCHPESUDMPG--SEGLQPSLPQKKLURK---GCIN--QLLUQ
<i>E. telfairi</i>	176	SPLDLHRHYK---HKGHESQCHPGNUDMPG--SESLLSLPRKQLURK---RCIN--QLLUQ
<i>M. lucifugus</i>	121	-----PLSSPQKKLUGK---RCIN--QLLUQ
<i>C. familiaris</i>	248	APQGLHRRHK---HKDHQROCHPDNUDMPAGSESLQLSVPQNQLURK---RCIN--QLLUQ
<i>S. araneus</i>	188	SLTHLHHHHK---HKGPPSQCHPENUDMPA--SGGSQSLPQKKLURK---RCIN--QLLUQ
<i>S. lateralis</i>	216	APLDLHHHHK---HKGQYRQCHNSESUQMAG--SEGLQLSLAQKKLCQK---GCIN--QLLUQ
<i>S. tridecemlineatus</i>	197	APLDLHHHHK---HKGQYRQCHNSESUQMAG--SEGLQLSLAQKKLCQK---GCIN--QLLUQ
<i>O. cuniculus</i>	239	PPSGLHHHHK---HRDQHRQCHNSESUDMPE--SESLLSLVRKKLURK---GCIN--QLLUQ
<i>O. aries</i>	225	-----HHHHHR---HKGHQROCHSDNCDTPVGSENQLSLPQKKLURK---RCIN--QLLUQ
<i>C. hircus</i>	204	-----HH-----
<i>B. taurus</i>	240	PTSGLHHHHHR---HKGPQRQCHSDNCDTPLGSESLQPSLPQKKLURK---RCIN--QLLUQ
<i>S. scrofa</i>	245	PPSGLHHHHG---HKGHQROCHSENUDMPAGESESLQLSLPQKKLURR---GCIN--QLLUQ
<i>R. norvegicus</i>	239	PPSGLHHHHHHHK---HKGQHRQCHLESUDMGA--SEGLQLSLAQKKLURR---GCIN--QLLUQ
<i>M. musculus</i>	237	PPSGLHHHHHR---HRGQHRQCHLESUDTTA--SEGLHLSLAQKKLURR---GCIN--QLLUQ
<i>C. porcellus</i>	175	LPLGLHNLHR---GQPRQVHSPSUDMVP--GEGFQPSQPKLURK---GCIN--QLLUQ
<i>M. domestica</i>	248	HPTQGLHHHHHEAAGPQHRHTDHPESQENPEISVS--ELSVPRKKLURKKGISGAN--QLLUQ
<i>O. anatinus</i>	242	APQGLHKKLR---PAGQPRQCHGGSREAAE--GRGEELPSPRKKLURKGNASCQN--QLLUQ
<i>G. gallus</i>	239	PHNGRRHRVFN---HNRHDQICSHQVETLPPGEGVENLPRVTKLUKKGKTKCN--QLLUQ
<i>L. erinacea</i>	185	-----NATQPKVVG--GHRGKHNP-----
<i>S. acanthias</i>	185	-----TEDIKT-----EEDDLHSHRNHN-----
<i>B. floridae</i>	181	-----
<i>O. porcinus</i>	178	-----
<i>B. microplus</i>	175	-----
<i>C. gigas</i>	175	-----KVSTKPTLYQ
<i>A. irradians</i>	190	-----YQSRLMSAADMDLMQGHQPNVVSMFVGQSSSSDDNRTFACMELHC

<i>D. rerio</i>	281	QGA--DSPVA---SUCUHUROLFGGEGNGRVAAGLUHCD-EPLPASUPUQGLKEQ--DNHIR
<i>C. carpio</i>	193	QGA--DASAT---SUCUHUROLFD-DSNGHVAAGLUHCE-GALPASURUQGLKE--DNHIR
<i>I. punctatus</i>	296	QGA--LSDPS---SUCUHUORRLIGLHLNERP--LUQCD-EPLAASCLUQGLLTD-QNNM-
<i>T. nigroviridis</i>	290	WTEASDPDASPASUCUHUORRLFGSVGSERPAGLURCS-EALPASUQUHGPMADRADA-R
<i>T. rubripes</i>	296	WAEASDTGAFPKASUCUHUORRLFGDVVGEEPVGLUHCS-EALPASUQURGPTGDVAVNAV-R
<i>G. aculeatus</i>	295	LTAGSDNEASLKLSSUCCHURRLFGFVGSEQPLGLUHCD-EALPASUQUHGLTIDGVPNNVR
<i>S. salar</i>	297	LKEGSDISPSKVSUCUHUORRLFGNGVSNEPIGLUHCD-EALPASUQUQGLMCDSTNHIR
<i>O. mykiss</i>	199	KS---LFQ----ASUCUHUORRLFGDGVSNPIGLUHCD-EALPASUQUQGLIG-----LR
<i>Haplochromis</i> sp.		-----
<i>O. latipes</i>	303	MVAGSENE---ASUCUHUORRLFGHAGSEQPLGLUHCC-EELPASUQCRGLTGELANTVI
<i>F. heteroclitus</i>	240	GAAGSDNEAAPKAGUCUHUORRMFGAADEQALGLUHCE-GALPASUQUQGLTSEAAAAVK
<i>X. tropicalis_Cys</i>	185	GD---DSSSP-----LQNKDEPVNK-EPS-PTLEKHNDQRKLDSELR--LH
<i>X. tropicalis</i>	299	WR---EEGKAFNSUCUHUORLSFEVTENEVA--UHQ-EALPSSCSUQELLS---DSLIP
<i>X. laevis</i>	294	WR---EDAGKAFNSUCUHUORLSFEIAQNEVA--URCQ-EALPASUQUQELLS---DSLIS
<i>A. mexicanum</i>	264	QQ---DVSGSASSSUCUHUORLSLSESPKAVT--UQCN-SVLPSSCKUQEQLS---EGAS
<i>H. sapiens</i>	289	LP---TDSELAPRSUCCHCRHLIFEKTGSAIT--UQCK-ENLPSSLCSUQGLRAE--ENIT
<i>P. troglodytes</i>	289	LP---KDSELAPRSCCCCHCRHLIFEKTGSAIT--UQCK-ENLPSSLCSUQGLRAE--ENIT
<i>P. pygmaeus</i>	289	LP---KDSELAPRSCCCCHCRHLIFEKTGSAIT--UQCK-ENLPSSLCSUQGLRAE--ENIT
<i>M. mulatta</i>	290	LP---KDSELAPRSUCCHCRHLIFEKTGSAIT--UQCK-ENLPSSLCSUQGLLAE--ENIT
<i>M. fascicularis</i>	289	LP---KDSELAPRSUCCHCRHLIFEKTGSAIT--UQCK-ENLPSSLCSUQGLLAE--ENIT
<i>E. europaeus</i>	151	LP---KESELAPSNUCUHCRLVFEKTGSVIT--UQCS-ENLPSSLCSUQGLWAA--ENVI
<i>T. belangeri</i>	114	LP---RDSELAPRSUCUHCRLIFEKTGAIT--UQCT-ENLPSSLCSUQGLRAE--ENVI
<i>L. africana</i>	291	LP---KDSELAPSSUCCHCRHLIFEKTGPAIT--UQCR-ENLPSSLCSUQGLLAE--ENVI
<i>E. telfairi</i>	228	LS---RGSELCSRSUCUHCRLIFEKAGSAIT--UQCE-EHLPTLCSUQGLWAE--ENVI
<i>M. lucifugus</i>	142	LP---RESESAASSUCUHCRLVFEHTGSAIT--URCR-EALPSSLCSULGLWAE--ENVI
<i>C. familiaris</i>	301	LP---RDSGLAPSSUCUHUORHLIFEKTGSAIT--UQCK-ETLPSSLCSUQGLWAE--ENVI
<i>S. araneus</i>	240	LP---KDSELAPSSUCUHCRLVFEKTGSAIT--UQCN-ENLPSSLCSUQGLWAE--ENVI
<i>S. lateralis</i>	268	LF---KDPQAASSSCCCCHCRHLIFEKRESAIT--UQCA-ENLPSSLCSUQGLRAE--ENVI
<i>S. tridecemlineatus</i>	249	LF---KDPQAASSSCCCCHCRHLIFEKRESAIT--UQCA-ENLPSSLCSUQGLRAE--ENVI
<i>O. cuniculus</i>	291	ML---KKSELAPSSCCCCHCRHLIFEKTGSAIT--URCR-ENLPSSLCSUQGLLAE--ENVI
<i>O. aries</i>	274	FP---KDSELALSSCCCCHCRHLVFEKTGSAIT--UQCT-ENLPSSLCSUQGLLAE--ENVI
<i>C. hircus</i>		-----
<i>B. taurus</i>	294	FP---KYSSESALSSCCCCHCRHLVFEKTGSAIT--UQCT-EKLPSSLCSUQGLLAE--ENVI
<i>S. scrofa</i>	298	FP---KNSESALRSUCUHCRLIFEKTESAVT--UQCG-ENLPSSLCSUQGLLAE--ENVI
<i>R. norvegicus</i>	294	LS---EESGAATSSCCCCHCRHLIFEKSGSAIT--UQCA-ENLPSSLCSUQGLFAE--EKVI
<i>M. musculus</i>	289	LS---KESEAPSSCCCCHCRHLIFEKSGSAIT--UQCA-ENLPSSLCSUQGLFAE--EKVT
<i>C. porcellus</i>	225	PP---KNHSAPSSCCCCHCRHLVFEQPGSSVT--CQCA-ENLPSSLCSCEGLFGE--EKVI
<i>M. domestica</i>	306	LS---QSSGSAPRSUCUHCRLIFEKRLGNVIT--UHKGTLPSSCSUQGLQRAE--ENIT
<i>O. anatinus</i>	297	WH---KRSGPAPSSUCUHCRLIFGSKATATAL--UQCR-DALPALCSUQGLRQSG--EDVI
<i>G. gallus</i>	296	WQ---TASDSTSSUCCHCRHLIFEELGNSIT--UQCR-GALPNSCRUHGQLLA--EDIT
<i>L. erinacea</i>	204	-----GHCHES-----P-----
<i>S. acanthias</i>		-----
<i>B. floridae</i>	181	-----PVPQETTPAPVITTAAPPTDTPVCAHPPSWQLDGVVDHL
<i>O. porcinus</i>	178	-----ATEACRSTETSSANGTAAAPQVREG
<i>B. microplus</i>	175	RNPRNTDNPARRNSLGRRIIHMFLGGEQDDESHENRKHQSOMRVCHHPN--SHTES--
<i>C. gigas</i>	185	LQ---RQAVSSLSSIIRRRRHVFNFHGTSLVSTNNVPSRNDRPSDU-----PN
<i>A. irradians</i>	235	ER---NTPQSRHRMIHRLURHMRRRGFLGCSHSHVCP-RNFRDVCSCTRYRQSRK---K

<i>D. rerio</i>	334	ETUQURPAPPAAEU-----ELSQPTUVUPAGDATUGURKK-----
<i>C. carpio</i>	244	ETUQURPAPPAAEU-----ELSQKTUUAUPAGDASUVUKEK-----
<i>I. punctatus</i>	346	ETUQURPAHLGDU-----QPAQPIUAUPAGISQUEUQVI-----
<i>T. nigroviridis</i>	348	ETUQURS-PLAVU-----QQPQAPUAUPQGAN-UGUEQV-----
<i>T. rubripes</i>	355	ETUQURS-PLAVU-----QQPQAPUAUPQGVN-UGUEQV-----
<i>G. aculeatus</i>	354	ETUQCRS-PPAAU-----QQPEPAPUAUAAGVS-UGUEQL-----
<i>S. salar</i>	356	ETUQURS-PPADU-----QQPPVPMUAUPLVES-UGUGQL-----
<i>O. mykiss</i>	246	ETUQURS-SLADU-----QQPQFVMAUPLGVESUGUGLL-----
<i>Haplochromis</i> sp.		-----
<i>O. latipes</i>	358	ESUQURS-PPAAU-----QQPQAPUAUAAPGAASUAUEQL-----
<i>F. heteroclitus</i>	299	ETUQURM-PPAAU-----QQPQAPUAUPPGVGSUAUEQL-----
<i>X. tropicalis_Cys</i>	224	DHSQ-HHPINSHKRQENQNNHPRNLKNGKQN-----
<i>X. tropicalis</i>	350	ESUQURL-SAAAUHSESTG--LPETKLESEPNAPUAUPQEAENUQUKELURFLM
<i>X. laevis</i>	345	ESUQURL-SAAAUHSHSTG--LPELDTSETNAPUAUPQEAENUQUKELURFLM
<i>A. mexicanum</i>	315	ESUQURV-SPAUPS LAVDQLHEQLPSESDPNVAUQUPKATGTUQUQVLTN---
<i>H. sapiens</i>	341	ESCQURL-PPAAU-----QISQQLIPTEASASURUKNOAKKUEUPSN----
<i>P. troglodytes</i>	341	ESCQURL-PPAAU-----QISQQLIPTEASTSUCUKNOAKKUEUPSN----
<i>P. pygmaeus</i>	341	ESCQURL-PPAAU-----QISQQLIPTEASTSUKNOAKKUEUPSN----
<i>M. mulatta</i>	342	ESCQURL-PPAAU-----QISQQLVPTVSTNURUKSKAKKUEUSSN----
<i>M. fascicularis</i>	341	ESCQURL-PPAAU-----QISQQLVPTVSTNURUKSKAKKUEUSSN----
<i>E. europaeus</i>	203	ESUQURL-PPAAU-----Q-SRQQLSPPTASATUSUNDKAGMUEUPSH----
<i>T. belangeri</i>	166	ESCQURL-PPAAU-----QT-SQQLSPTEVSTNOKUNKKAEUKULSN----
<i>L. africana</i>	343	ESCQURL-PPAAU-----QASQQLKPTGASTNUSUKNKAEMUKUPSN----
<i>E. telfairi</i>	280	ESUQURL-PLPAU-----QRS-QQFQPTASTSUSUKNTAEKUKUPSN----
<i>M. lucifugus</i>	194	ESUQURL-PPAAU-----QAGQLEPTASTTUSUKTEAEMUQUPSN----
<i>C. familiaris</i>	353	ESUQURW-PPAAU-----QASQQLRPTASTNUSUKYKTKMUKULTY----
<i>S. araneus</i>	292	ESUQURL-PPAAU-----QSGQQPKPTVDNTKUSUKNOAEMUKUPAN----
<i>S. lateralis</i>	320	ESCQURM-PPAAU-----QRSQQLDPTVGTNUSUKNKAKKUKUHSN----
<i>S. tridecemlineatus</i>	301	ESCQURM-PPAAU-----QRSQQLDPTVGTNUSUKNKAKKUKUHSN----
<i>O. cuniculus</i>	343	ESCQURL-PPAAU-----QTSQQLKPTASTNUSUNNLAKKUKUPSN----
<i>O. aries</i>	326	ESUQURL-PPAAU-----QAAGQQLNPTEASTKUSUKNKAKMUKUPSN----
<i>C. hircus</i>		-----
<i>B. taurus</i>	346	ESUQURL-PPAAU-----QAAGQQLNPTEASTKUSUKNKAKMUKUPSN----
<i>S. scrofa</i>	350	ESUQURL-PPAAU-----QAS-QQLNPTEASTKUSUKNKAGRUKUPSN----
<i>R. norvegicus</i>	346	ESCQCRS-PPAAU-----HSQHVSPTASPNUUNNKTKKUKUNLN----
<i>M. musculus</i>	341	ESCQCRS-PPAAU-----QNQPMNPMANPNUSUDNQTRKUKUHSN----
<i>C. porcellus</i>	277	ESCQURL-PLPAU-----QVSPQKPTETNPNUKNNMAQKUKUPSN----
<i>M. domestica</i>	359	ESUQURS-PPAAU-----HPGQLEPTETRNAUKKNNAGRUKUSTN----
<i>O. anatinus</i>	350	ESUQURS-PLPAU-----PPAAQLSPSPPTDPNAAUKUENTAGMUKUPTR----
<i>G. gallus</i>	348	ESUQURL-LTAAU-----ESAAGGGSETSDTUQUQERAGNUAKTN----
<i>L. erinacea</i>		-----
<i>S. acanthias</i>		-----
<i>B. floridae</i>	219	EKSQGGQ-----
<i>O. porcinus</i>	203	ESPEPRHNGV-----
<i>B. microplus</i>	215	PYCR---QAPSC-----EELGAACGSU-UQ-----
<i>C. gigas</i>	230	SRURQLSNIVCTQKSVPS-----
<i>A. irradians</i>	288	RFCACSEI-----

Figure S2. Multiple sequence alignment of Selenoprotein P sequences. Cysteine residues are highlighted in blue, and selenocysteine residues in red. Sequences with the following accession numbers were used generate the alignment:

H. sapiens (NP_001087195.1), *P. pygmaeus* (CAH91791.1), *D. rerio* (AAG53688.1), *B. taurus* (BAA84781.1), *R. norvegicus* (NP_062065.2), *M. musculus* (NP_033181.3), *C. familiaris* (XM_862927.1), *G. gallus* (NP_001026780.2), *M. domestica* (AAFR03031319.1), *P. troglodytes* (XM_530812.2), *S. scrofa* (AJ945481.1, DB795066.1), *M. mulatta* (XM_001087397.1), *M. fascicularis* (AB169844.1), *O. aries* (CO202513.1, CN823413.1), *O. cuniculus* (DN889827.1, EC620121.1), *C. hircus* (AAF67201.1), *O. anatinus* (XR_036552.1, XM_001519849.1), *X. tropicalis* (BC084988.1), *X. tropicalis* Cys homolog

(NM_001006907.1), *X. laevis* (BC128687.1), *S. lateralis* (CO739434.1), *S. tridecemlineatus* (ES429752.1, ES430681.1), *T. nigroviridis* (CR655078.2), *G. aculeatus* (BT027180.1), *S. salar* (DW536174.1, CA045197.1), *B. microplus* (CV452517.1), *A. mexicanum* (CN034653.1, CO790560.1), *O. latipes* (BJ910837.1, BJ734131.1), *O. mykiss* (CX255200.1, CA375171.1), *C. carpio* (CA966337.2, CF662894.2), *T. belangeri* (AAPY01533128.1, AAPY01533129.1), *E. europaeus* (AANN01197889.1), *M. lucifugus* (AAPE01210967.1, AAPE01518317.1), *E. telfairi* (AAIY01264272.1, AAIY01707893.1), *L. africana* (AAGU01358562.1, AAGU01358563.1), *C. porcellus* (AAKN01329275.1, AAKN01257578.1, AAKN01257577.1), *S. araneus* (AALT01420282.1, AALT01420283.1), *F. heteroclitus* (CN981462.1, CN980688.1), *L. erinacea* (CO051159.1), *O. porcinus porcinus* (CB722105.1), *T. rubripes* (CAAB01001108.1), *I. punctatus* (EE993430.2, CK420078.1), *A. irradians* (CK484474.1), *C. gigas* (AJ565579.1), *B. floridae* (BI386612.1).

Figure S3

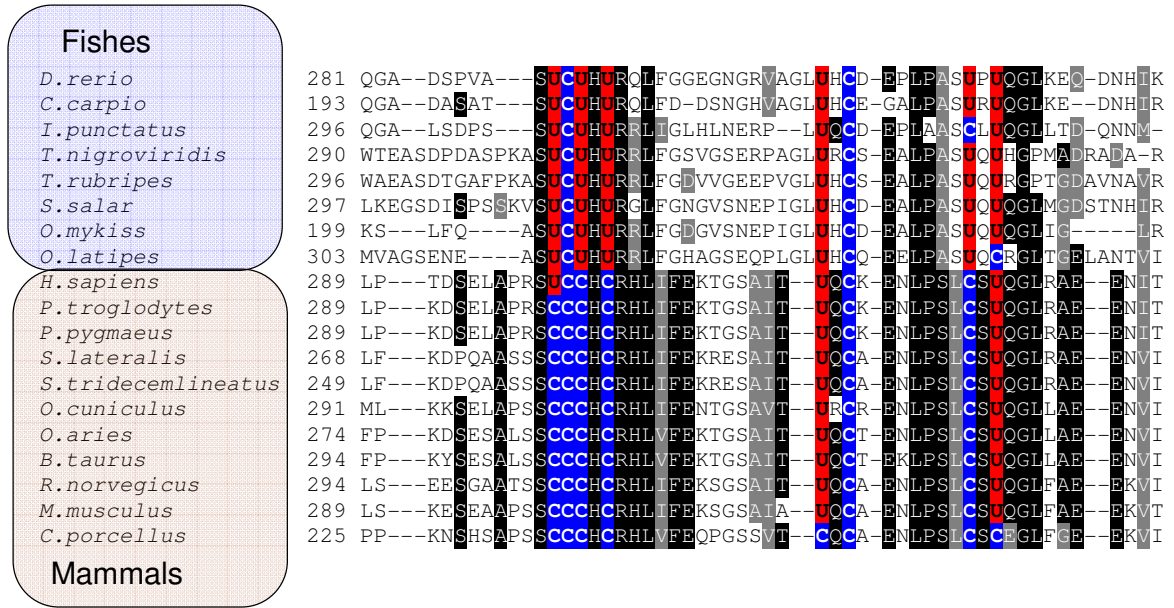


Figure S3. Partial alignment of fish and mammalian Selp sequences. Sec residues are highlighted in red and Cys residues in blue. Loss of Sec is shown by a box.

Figure S4

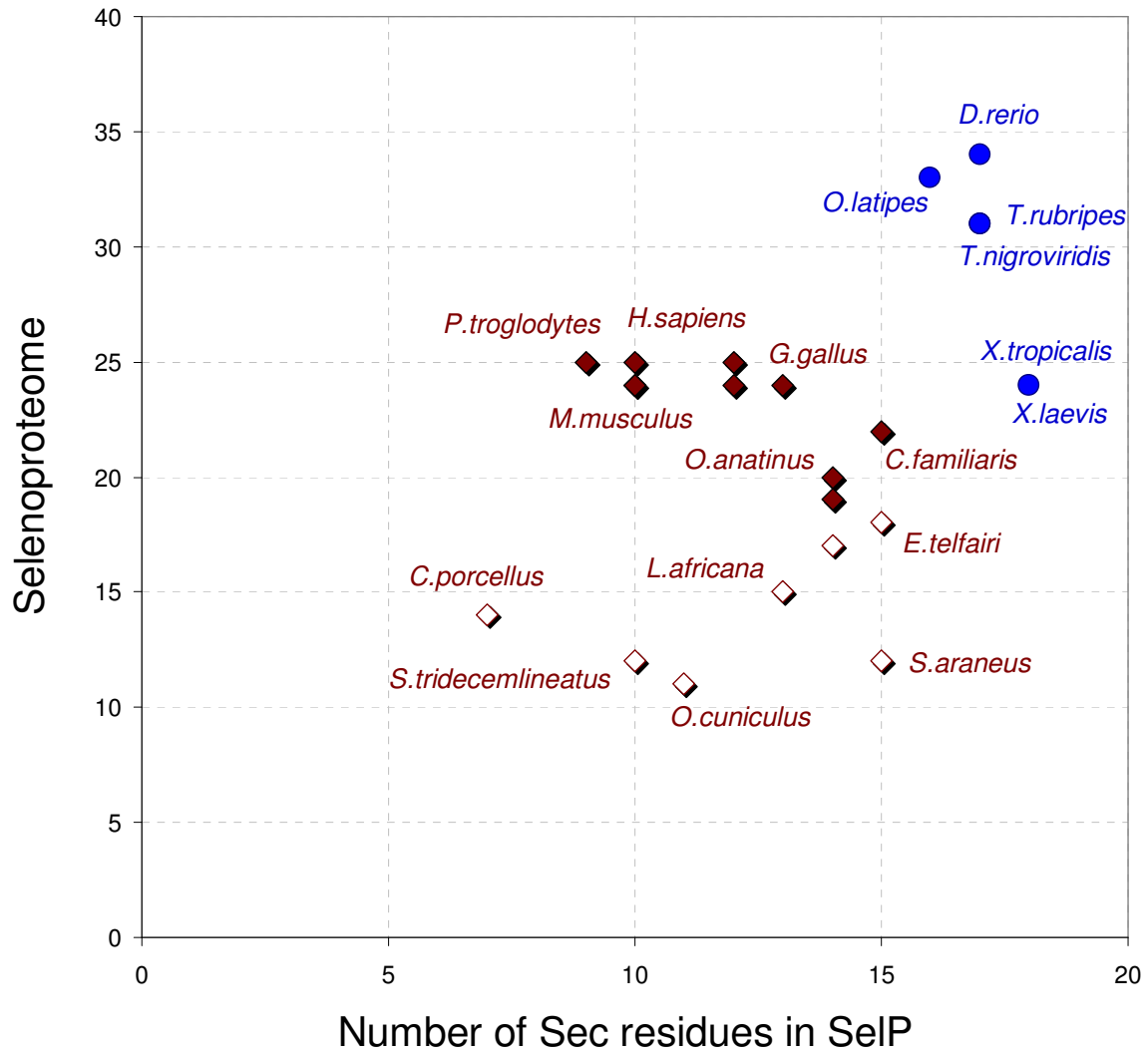


Figure S4. A plot of selenoproteome size versus Sec content of SelPs. A 2D-representation of the relationship between the number of Sec residues in SelPs and selenoproteome size in vertebrates is shown. The data for aquatic vertebrates (including fish and amphibians) are shown in blue, and terrestrial (mammals and birds) in brown. Open squares and circles correspond to genomes with 1.7x-2.3x coverage, and filled to genomes with 5x-9x coverage.

Figure S5

A. Selenocysteine loss in primates

<i>H. sapiens</i>	289	LPTDSELAPRS	U	C	C	H	CRHLIFE	310
<i>M. mulatta</i>	289	LPTDSELAPRS	U	C	C	H	CRHLIFE	310
<i>P. troglodytes</i>	289	LPTDSELAPRS	C	C	C	H	CRHLIFE	310
<i>P. pygmaeus</i>	290	LPTDSELAPRS	C	C	C	H	CRHLIFE	311



B. Selenocysteine loss in fish

<i>T. rubripes</i>	334	EALPAS	U	U	RGPTGDAVNAVR	354
<i>S. salar</i>	335	EALPAS	U	U	QGLMGDSTNHIR	356
<i>O. mykiss</i>	230	EALPAS	U	U	QGLIG-----LR	245
<i>O. latipes</i>	337	EELPAS	U	C	RGLTGELANTVI	357



C. Selenocysteine switch in *Xenopus*

<i>X. tropicalis</i>	325	ENEVA	U	H	U	QEALPSS	C	S	U	QELL	346
<i>X. laevis</i>	318	QNEVA	R	C	E	QEALPAS	U	U	Q	QELL	339

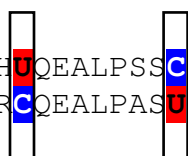


Figure S5. Recent Sec/Cys conversions in closely related species. A. Sec loss in primates. Partial amino acid sequence alignment is shown, with Sec residues highlighted in red and Cys residues in blue. Loss of Sec is indicated by a box. **B. Selenocysteine loss in fish.** Partial amino acid sequence alignment is shown. Sec and Cys residues are highlighted in red and blue, respectively. Box indicates the loss of Sec. **C. Sec switch in *Xenopus*.** Partial amino acid sequence alignment is shown, with Sec highlighted in red and Cys in blue. The number of Sec and Cys residues is the same in Selps from both *Xenopus* species, but the locations of the two indicated Sec residues are different, as shown by boxes.

Figure S6

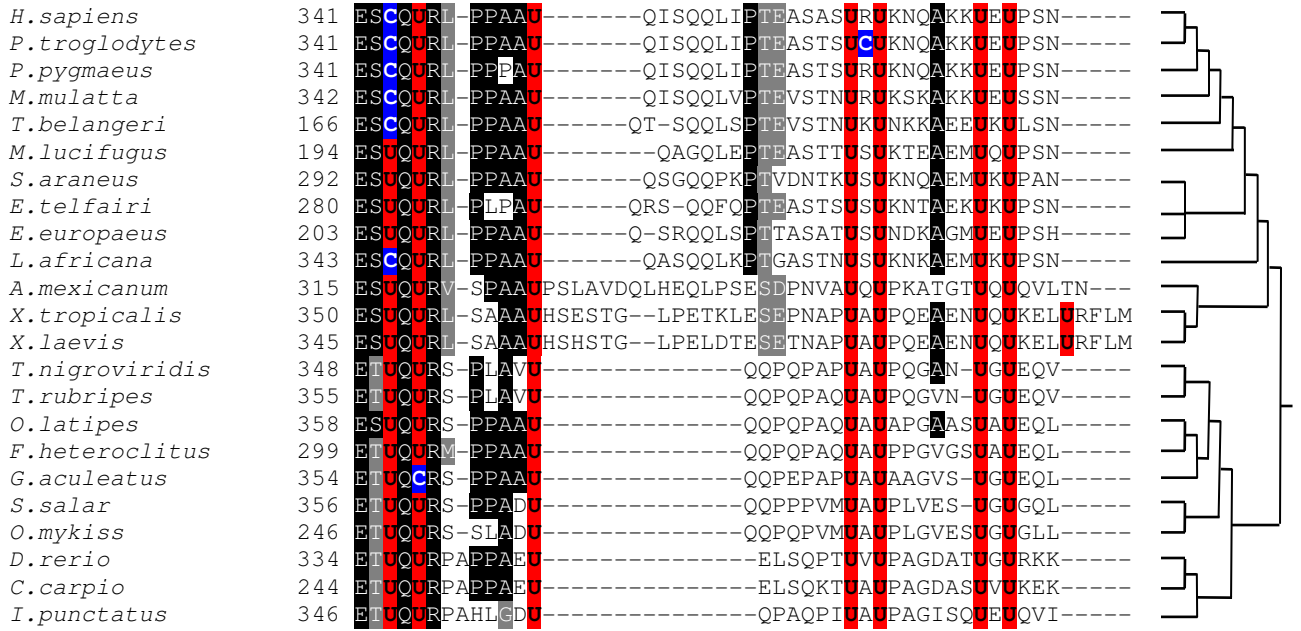


Figure S6. Evolution of new Sec residues by C-terminal extension. *Xenopus* SelP is extended at the C-terminus as shown here by partial alignment of C-terminal sequences of SelPs from indicated organisms. Sec residues are highlighted in red, and Cys residues in blue. The new Sec in *Xenopus* SelP corresponds to stop codons in most other vertebrate SelPs.

Figure S7

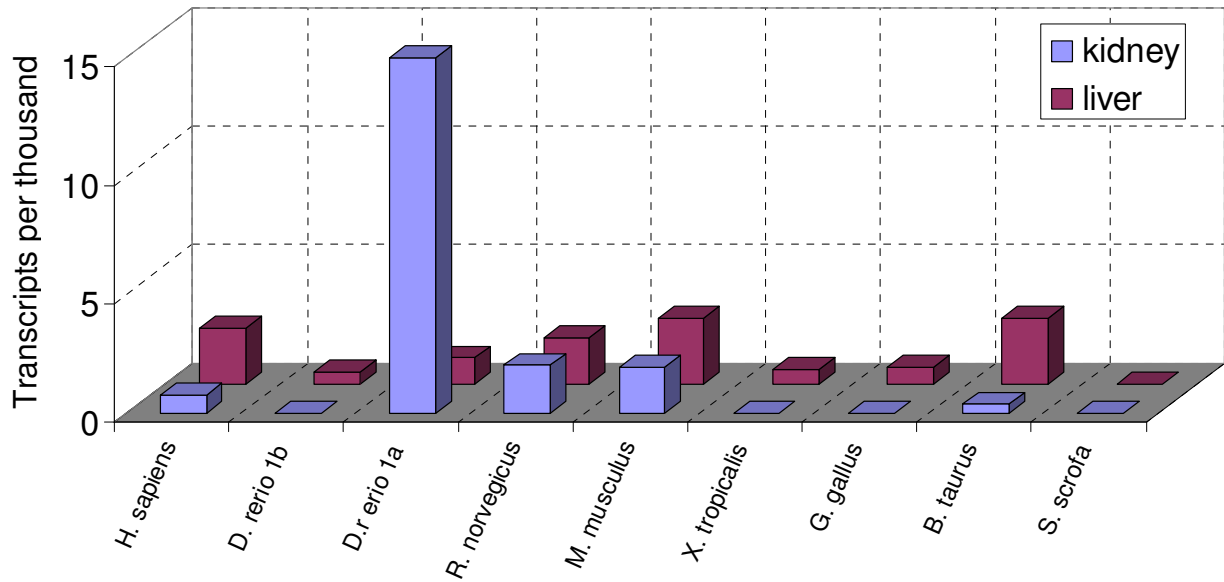


Figure S7. *In silico* expression profile of SelP based on abundance of SelP ESTs. Expression levels in kidney and liver for SelPs from different organisms are shown in transcripts per million. UniGene's EST ProfileViewer was used in this analysis.

Figure S8

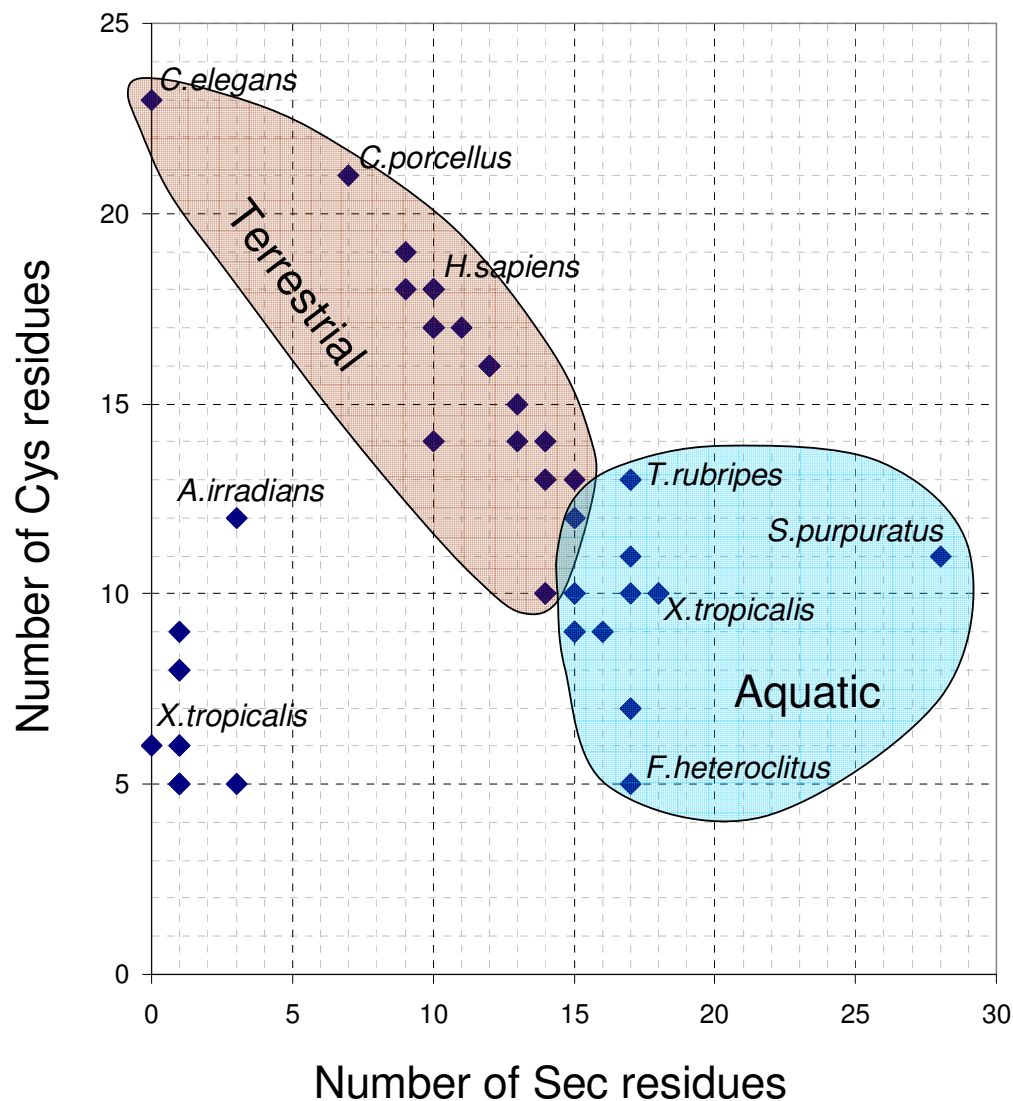


Figure S8. Correlation between Cys and Sec content of SelPs. A 2D-representation of Cys and Sec distribution in SelPs from different organisms is shown. Star symbols indicate that sequences used in analysis are incomplete, and the real number of Sec or Cys residues most likely is higher. Blue area highlights aquatic organisms and brown terrestrial SelP sequences containing a C-terminal Se transport domain. The data points outside of these areas show single-Sec SelPbs that lack the C-terminal Se transport domain.