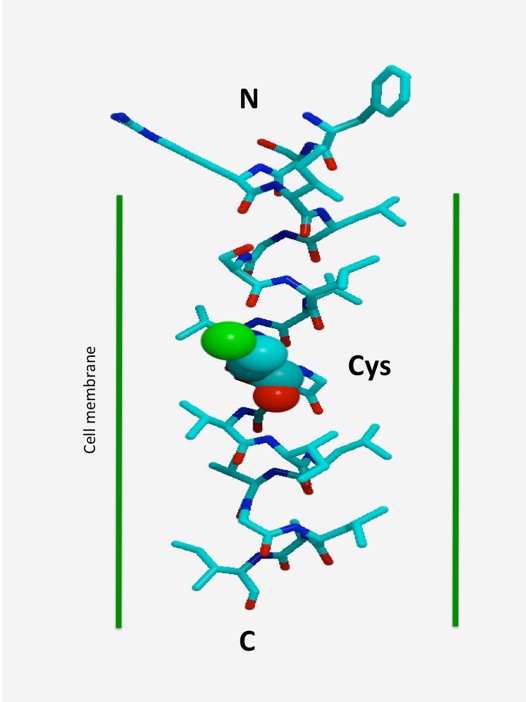


**Figure S1.** Complete sequence of *Trematomus bernacchii* polymeric Ig receptor (*pIgR)* gene. The deduced amino acid sequence is reported in one-letter code. The sequence comprises a promoter region, including the leader peptide (in cyan), a region encoding the D1 domain (in green), the D2 domain (in yellow), the extracellular membrane proximal domain (EMPD, in magenta), the transmembrane domain (TM, in dark green), the cytoplasmic tail (in blue), and the terminal sequence (in dark yellow). The stop codon is in white and underlined, polyadenylation signals are indicated in yellow. The intron sequences are shaded in grey; the donor and acceptor sites are depicted in red. The region containing the CpG island (CGI), located upstream of the 5’ end of *pIgR* gene, is highlighted in purple.



**Figure S2.** 3D molecular model of the transmembrane helix of *T. bernacchii* pIgR built with the Phyre2 tool (<http://www.sbg.bio.ic.ac.uk/phyre/html/>). The cysteine residue, located in the middle of the sequence with its side chain pointing out of the transmembrane helix, is shown. The N- and C-termini are indicated at the top and bottom, respectively.

**Signal peptide**

*Trematomus bernacchii* MLKPFLLTLSLLPWIPV

*Trematomus loennbergii* V

*Dissostichus eleginoides* PWIPA

*Dissostichus mawsoni*

*Notothenia coriiceps* LPWIPV

*Harpagifer antarticus* V

*Gymnodraco acuticeps* MLKPFLLTLSLLPWIPV

*Pseudochaennichthys georgianus* MLKPFLLTLSLLPWIPV

*Chionodraco myersi* V

*Chaenocephalus aceratus* V

*Chionodraco hamatus* SLLPWIPV

*Cottoperca gobio* MLQPFILALSLLPWIPA

*Sander lucioperca* MLQPFIITLSLLPWFPA

*Perca fluviatilis* MLQPFLIVLSLLPWFPA

*Perca flavescens* MLQPFIITLSLLPWFPA

*Etheostoma spectabile* MLPPFIIALSLFPFFPA

*Etheostoma cragini* MLQPFTITLSLLPFFPA

*Epinephelus coioides*  MRRLFILTLSLLPWIPA

*Epinephelus lanceolatus* MRRLFILTLSLLPWIPA

*Plectropomus leopardus*

*Sebastes umbrosus* MLQPFILALILLPWIPA

*Pungitius pungitius* MRKLFTLALTLFPWISG

*Anarrhichthys ocellatus* MQQPFILALSLLSWIPA

*Cyclopterus lumpus* MLRPFLLALSLLPWIPA

*Liparis tanakae*

*Gasterosteus aculeatus* MRKLFTLALTLLSWIPG

**/D1 L S S**

*Trematomus bernacchii* FLCGT-TTEEELSIMEGQSLTVPCHYEPQYASYVKYWCRGTMREFCSSLA

*Trematomus loennbergii* FLCGT-TTEEELSIMEGQSLTVPCHYEPQYASYVKYWCRGTMREFCSSLA

*Dissostichus eleginoides* FLCGT-PTEGELSVMEGQSLTVPCHYEPQYASYVKYWCRGKMREFCSSLA

*Dissostichus mawsoni* FLCGT-TTEEELSVMEGESLTVPCHYEPQYASYIKYWCRGKMREFCSSLG

*Notothenia coriiceps* FLCGT-TTEEELSVMEGQSLTVPCHYEPQYASYVKYWCRGTMREFCSSLA

*Harpagifer antarcticus* FLCGT-TTEEELSVMEGQSLTIPCHYEPQYASYIKYWCRGKMREFCSSLA

*Gymnodraco acuticeps* FLCGT-TTEEELSVMEGQSLTVPCHYEPQYASYIKYWCRGKMREFCSSLA

*Pseudochaennichthys georgianus* FLCGT-TTEEELSVMEGESLTVPCHYEPQYASYIKYWCRGKMREFCSSLA

*Chionodraco myersi* FLCGT-TTEEELSVMEGESLTVPCHYEPQYASYIKYWCRGKMREFCSSLA

*Chaenocephalus aceratus* FLCGT-TTEEELSVMEGESLTVPCHYEPQYASYIKYWCRGKTREFCSSLA

*Chionodraco hamatus* FLCGT-TTEEELSVMEGESLTVPCHYEPQYASYIKYWCRGKMREFCSSLA

*Cottoperca gobio* LLCST---EGELSVLEGQSLTVPCHYEPQYASYVKYWCRGKTKEFCSSLA

*Sander lucioperca* FLCRV-TTEGEHAVMEGQPLTVPCHYGPQYAGYVKYWCRGKMREFCTSLA

*Perca fluviatilis* FLCRV-TTEGEHAVMEGQPLTVPCHYGPQYAGYVKYWCQGKMREFCTSLA

*Perca flavescens* FLCRV-TTEGEHAVMEGQPLTVPCHYGPQYAGYVKYGCRGKMREFCTSLA

*Etheostoma spectabile* FHCGV-TTEGEHTVMEGQHLTVPCHYGPQYAGYVKYWCRGKMREFCSSLA

*Etheostoma cragini* FLCGV-TTEGEHAVMEGQHLTVPCHYGPQYAGYVKYWCRGKMREFCTSLA

*Epinephelus coioides* VLCKV-TTEGELSIMEGQSLTIPCHYEPQYASYVKYWCQGKTREFCTSLA

*Epinephelus lanceolatus* VICKV-TTEGELSIMEGQSLTIPCHYEPQYASYVKYWCQGKTREFCTSLA

*Plectropomus leopardus* FLCGT-TTEEELSIMEGQSLTVPCHYEPQYASYVKYWCRGKMKEFCTSLA

*Sebastes umbrosus* FHCRV-TTEGDIAVMEGQSLTVPCIYEPQHASYVKYWCRGKMKAFCTTLA

*Pungitius pungitius* FLCQPAFTGGELSVMEGQSLTVPCHYESQYAGHVKYWCRGKVRGFCTSLA

*Anarrhichthys ocellatus* FLCRV-TTEGELTVMEGQSLIVPCHYDPQYAGYVKYWCRGNTREFCTSLA

*Cyclopterus lumpus* FLCRV-TTEGELAVMEGQSLTVPCHYDPQYAGYVKYWCRGKMREFCTSLA

*Liparis tanakae* MDPRV-TTDAELAVMEGRSLTVPCHYDPQYAGYLKYWCRGKMREFCTSLA

*Gasterosteus aculeatus* FL-----SEAELSVMEGQSLTVPCHYEPQYAGYVKYWCRGKMRGFCTSLA

L

*Trematomus bernacchii* RTDESHSTNPSE-KKVRLFDDPVQQVFTVAMSNLREEDSGWYMCGVEIGG

*Trematomus loennbergii* RTDESHSA**NLS**E-KKVRLFDDPVQQVFTVAMSNLREEDSGWYMCGVEIGG

*Dissostichus eleginoides* RTDESHSA**NLS**E-KKVRLFDDPVQQVFTVAMSNLREEDSGWYMCGVEIGG

*Dissostichus mawsoni* RTDESHSA**NLS**E-KKVRLFDDPVQQVFTVAMSNLREEDSGWYMCGVEIGG

*Notothenia coriiceps* QTDESHSANPSE-KKVRLFDDPVQQVFTVAMSNLGEEDSGWYMCGVEIGG

*Harpagifer antarcticus* RTDESHSANPSE-KKVRLFDDPVQQLFTVAMSNLREEDSGWYMCGVEIGG

*Gymnodraco acuticeps*  RTDESHSANPSE-KKVRLFDDPVQQVFTVAISNLMEEDSGWYMCGVEIGG

*Pseudochaennichthys georgianus* RTDESHSVNPSE-KKVRLFDDPVQQVFTVAMSNLREEDSGWYICGVEIGG

*Chionodraco myersi* RTDESHSVNPSE-KKVRLFDDPVQHVFTVAMSNLREEDSGWYMCGVEIGG

*Chaenocephalus aceratus* RTDESHSVNPSE-KKVRLFDDPVQQVFTVAMNNLREEDSGWYMCGVEIGG

*Chionodraco hamatus* RTDESHSVNPSE-KKVRLFDDPVQQVFTVAMSNLREEDSGWYMCGVEIGG

*Cottoperca gobio* RTDVTRSANTAE-EKVGIFDDPVQLVFTVTMSNLREEDSGWYMCGVEIGG

*Sander lucioperca* RTDEPRSANQAE-EKVSIFDDPVQLVFAVTMSNLKEGDSGWYMCGVEIGG

*Perca fluviatilis* RTDEPRSANPAE-EKVSIFDDPVQLVFTVTMSNLKEGDSGWYMCGVEIGG

*Perca flavescens* RTDEPRSANPAE-EKVSIFDDPVQLVFTVTMSNLKEGDSGWYMCGVEIGG

*Etheostoma spectabile* RTDEPRSANPAE-EEVSIFDDPVQLVFTVTMSNLKEGDSGWYMCGVEIGG

*Etheostoma cragini* RTDEPHSANSAE-EKVSIFDDPVQLVFTVTMSNLKEGDSGWYMCAVEIGG

*Epinephelus coioides* RTDEPRSADPAE-KKVSIFDDQVQLVFTVTMNNLKEGDSGWYMCGVEIGG

*Epinephelus lanceolatus* RTDEPRSADPAE-KKVSVFDDQVQLVFTVTMNNLKEGDSGWYMCGVEIGG

*Plectropomus leopardus* RTDEPPSADSAK-KKVSIFDDQVQLVFTVTMNDLKEGDSGWYMCGVEIGG

*Sebastes umbrosus* RTDETRSADPAEEKKVSIFDDPVQLVFTVTMNNLKEDDSGWYMCGVEIEG

*Pungitius pungitius* RTDP----AIAAAGKVSISDDRVQLVFTVTMSDLKEGDSGWYLCGVEIGG

*Anarrhichthys ocellatus* RTDS----ANPAAGKVSIFDDPVQQVFTLTMSDLKEGDSGWYMCGVEIGG

*Cyclopterus lumpus* RTDP----AHPAARKVSIFDDPVQQVFTVTMGDLKETDSGWYMCGVEVGG

*Liparis tanakae* RTDP----ATPAVKTVSLLDDPVQQVFTVTMDDLKEADSGWYICGVEVGG

*Gasterosteus aculeatus* RTDT----ANPAAGKVSMSDDPVQLVSTVTMSDLKEGDSGWYICGVELGG

**/ /D2 L**

*Trematomus bernacchii* LWSADVVTHKNINVIHGMTVEDRRLSGEEGSSVTVECQYSERYRESEKKW

*Trematomus loennbergii* LWSADVVTHKNINVIHG KKW

*Dissostichus eleginoides* VWSADVVTYKNINVIHGMTVENSRLSGEEGSSITVECQYSERYRESEKKW

*Dissostichus mawsoni* LWSADVVTHKNINVIHGMTVENSRLSGEEGSSVTVECQYSERYRESEKKW

*Notothenia coriiceps* LWSADVVTHKNIKVIHGMTVENSRLSGEEGSSVTVECQYSERYRESEKKW

*Harpagifer antarcticus* LWSADVVIYKHIKVIHG KKW

*Gymnodraco acuticeps* LWSADVVTHKNIKVIHGMTVENSRLNEEEGSSVTVECQYSERYRESEKKW

*Pseudochaennichthys georgianus* LWSADVVTYKNIKVIHGMTVENSRLSGEEGGSVTVECQYSERYRESEKKW

*Chionodraco myersi* LWSADVVTYKNIKVIHG KKW

*Chaenocephalus aceratus* LWSADVVTYKNIKVIHG KKW

*Chionodraco hamatus* LWSADVVTYKNIKVIHGMTVENSRLSGEEGSSVTVECQYSERYRESEKKW

*Cottoperca gobio* VWSADVVTYTNIRVIHGLTVVNSRLSGGEGSSVTVECHYSERFRESEKKW

*Sander lucioperca* AWSADDVAYTNIKVIHGMSVVNSRLIGEEGSSITVECHYSERYRESEKKW

*Perca fluviatilis* AWSADDVAYTNIKVIHGMSVVNSRLIGEEGSSITVECHYSERYRESEKKW

*Perca flavescens* AWSADDVAYTNIKVIHGMSVVNSRLIGEEGSSITVECQYSERYRESEKKW

*Etheostoma spectabile* MWTADDVAYTNIKVIHGMSVVNSFLIGEEGSSITVECHYSERCRESEKRW

*Etheostoma cragini* IWSADDVAYTYIKVIHGMSVVNSFLIGEEGSSLTVECHYSERCRESEKRW

*Epinephelus coioides* VWSADDVAFTNIKVIHGMSVVNSRVSGEEGSSLTVECHYSERYRESEKKW

*Epinephelus lanceolatus* VWSADDVAFTNIKVIHGMSVVNSRVSGEEGSSLTVECHYSERYRESEKKW

*Plectropomus leopardus* VWHSDDVAFTNIKVIHG KKW

*Sebastes umbrosus* VWHSDDVAFTYISVIHGMSVVNSRLSGEEGSSVTVEC**NYS**ERYRESEKKW

*Pungitius pungitius* AWTADVVTQTYINVIHGMSVVNSRLSGEEGSSVTVECHYSEKYRDSEKKW

*Anarrhichthys ocellatus* VWTRDVVASTYIKVIHGMSVVNSRLSGEEGSSVTVECRYSERYRDSEKKW

*Cyclopterus lumpus* VWTADVVAYTYIKVVHGMSVVNSRLSGEEGSSVTVECHYSERYRDSEKKW

*Liparis tanakae* GWTPDVVAHTYIKVVH

*Gasterosteus aculeatus* AWTADAVTETYIQVIHGMSVVNSRLSGEEGSSVTVECHYSERYRDSQKKW

**S S L**

*Trematomus\_bernacchii* CRSGDSSSCLLAGSEGSNG**NSS**VDIKDDRSGSFTITFKKLQMRDTGWYWC

*Trematomus loennbergii*  CRSGDSSSCLLAGSEGSNE**NSS**VDIKDDRSGSFTITFKKLQMRDTGWYWC

*Dissostichus eleginoides* CRSGDWSSCLLAGSEGSNEDSSVDIKDDRSGSFTITFKKLQMRDTGWYWC

*Dissostichus mawsoni* CRSGDWSSCLLAGSEESNEDSSVDIEDDRSGSFTITFKKLQMRDTGWYWC

*Notothenia coriiceps* CRSGNWSSCLLAGSEGS**N-DS**SVDIKDDRSGSFTITFKKLQMRDTGWYWC

*Harpagifer antarcticus* CRSGDWSSCLLAGSEGS**N-DS**SVYIKDDRSGSFTITLKKLQMRDTGWYWC

*Gymnodraco acuticeps* CRSGDWSSCLLAGSEGS**N-DS**SVYIKDDRSGSFTITFKKLQMRDTGWYWC

*Pseudochaennichthys georgianus* CRSGDWSSCLLAGSEGS**N-DS**SVYIKDDRSGSFTITFKKLQMRDTGWYWC

*Chionodraco myersi* CRSGDWSSCLLAGSEGS**N-DS**SVYIKDDRSGSFTITFKKLQMRDTGWYWC

*Chaenocephalus aceratus* CRSGDSSSCLLAGSEGSNG**NSS**VDIKDDRSGSFTITFKKLQMRDTGWYWC

*Chionodraco hamatus* CRSGDWSSCLLAGSEGS**N-DS**SVYIKDDRSGSFTITFKKLQMRDTGWYWC

*Cottoperca gobio* CRSGDWSSCLSTGSEGSYDDTSVAISDDRTRTFTVTLKKLQMRNTGWYWC

*Sander lucioperca* CRSGDWSSCLLTGSDGSYEDTSVAISDDRTRTLTITLKKLQMRDTGWYWC

*Perca fluviatilis* CRSGDWSSCLLTGSDGSYEDTSVAISDDRTRTFTITLKKLQMRDTGWYWC

*Perca flavescens* CRSGDWSSCLLTGSDRSYEDTSVAISDDRTRTFTITLKKLKMRDTGWYWC

*Etheostoma spectabile* CRSGDWSSCLLTDSDGRYEDTSVAISDDRTRTLTITLKKLQMRDTGWYLC

*Etheostoma cragini* CRSGDWSSCLPTGSDGRYEDTSVAISDDRTRTLTITLKKLQMRDTGWYLC

*Epinephelus coioides* CRSGDWSSCLLTGSEGSYEDTSVAISDDRTRTFTITLKKLQMRDAGWYWC

*Epinephelus lanceolatus* CRSGDWSSCLLTGSEGNYEDTSVAISDDRTRTFTITLKKLQMRDTGWYWC

*Plectropomus leopardus* CRSGDWSSCLLIDSEGSYEDTSVAISDDRTRTFTVTLKKLQMRDTGWYWC

*Sebastes umbrosus* CRSGDWSSCLLTGSEGSYEDTSVAIRDDRTRTFTITLKKLQMRDNGWYWC

*Pungitius pungitius* CRIGDWSSCLLTGSEGSYDDTSVAIRDDRTRTFTVTLKKLQMKDTGWYWC

*Anarrhichthys ocellatus* CRSGDWSSCLLTGSEGSYEDTSVAISDDRTRAFTVTLKKLQMSDSGWYWC

*Cyclopterus lumpus* CRSGDWSSCLLTGSEGSYEDTSVALRDDRTRTFTITLKKLRMRDSGWHWC

*Liparis tanakae*

*Gasterosteus aculeatus* CRTGDWSSCLLTGSEGSY**NDT**SVAIRDDGSRTFTVTLKNLQMKDTGWYWC

**/EMPD**

*Trematomus bernacchii* SAGLQKMPVHVQVVPRPMTT-VS---VTTQPQTVANPLPPKPITKESWNG

*Trematomus loennbergii* SAGLQKMPVHVQVVPRPM

*Dissostichus eleginoides* SAGLQKMPVHVQVKPRPMTTAVS---VTSQPQT-ANPLPPKPITKESWSG

*Dissostichus mawsoni* SAGIQKMPVHVQYILLS---------VCDIPTSDCKSSSPKPITKESWSG

*Notothenia coriiceps* SAGLQKMPVHVQVKPRPMTT-VS---VTSQPQTV PKPITKESWSG

*Harpagifer antarcticus* SAGLQKMPVHVQVKPRPM

*Gymnodraco acuticeps* SAGLQKMPVHVQVKPRPMTMS-----VTSQPQTVANPPPPKPITKESWSG

*Pseudochaennichthys georgianus* SAGLQKMPVHVQVKPRPMTT-VS---VTSQPQTVANPLPPKPITKESWSG

*Chionodraco myersi* SAGLQKMPVHVQVKPRPM

*Chaenocephalus aceratus* SAGLQKMPVHVQVKPRPM

*Chionodraco hamatus* SAGLQKMPVHVQVKPRPMTT-VS---VTSQPQTVANPLPPKPITKESWSG

*Cottoperca gobio* SAGQQKMPVHVQVTPRP-TTTVS---VTSPPQSIAYLPPPKPITKESGNN

*Sander lucioperca* SAGQQQIAVHVLVTPRP-TTAVSVTSTPTTSQSVAYLPPPKPITKESWNS

*Perca fluviatilis* SAGQQQIAVHVLVTPRPTTAAVSVTSTPKTSQSVAYLPPPKPITKESWNS

*Perca flavescens* SAGQQQIAVHVLVTSRPTT--VSVTSTPTTSQSVAYLPPPKPITKESWNS

*Etheostoma spectabile* FAGRQQKDVHVLVTPRP-TTIASVTSTPTASQSVAYLPAPKPISKESWKS

*Etheostoma cragini* FAGRQKKDVHVLVTPRP-TTIASVTSTPTTSQSVAHLPAPKPISKESWNR

*Epinephelus coioides* SAGQQQMAVHVLVTRRATTTVVSVTSPPTRLHSAAYLPPPKPITKESWNS

*Epinephelus lanceolatus* SAGQQQMPVHVLVTRRATTT-VSVTSPLTHLHSAAYLPPPKPITKESWNS

*Plectropomus leopardus* SAGQQQMAVHVLVTPRP R

*Sebastes umbrosus* SAGQQQVSVHVQVTPRPTTT-VS---VTSPPTRSRVLAYLPPPKPITKES

*Pungitius pungitius*  CAGQHQMHVHVIVTPRLWTTAVTATSPPTQSQALAHLPPSEPITKDSWRS

*Anarrhichthys ocellatus* SAGQHQKLVYVLVTPTPTTTAVTATSPLTPSQSAAYLPPPKPITKESWNS

*Cyclopterus lumpus* SVGAQADAACMCWSPPRPTT-----SRLTPSRSVALLAAPEPITEESRKQ

*Liparis tanakae*

*Gasterosteus aculeatus* CAGQHKEHVHVIVTPRPSTTAVTVTSRPTASLSLAYLPPPKPITKESCNS

**/ Transmembrane /Cyt**

*Trematomus bernacchii* H**NFS**RILGSLLVCGSVIL-VGLAILARKWWKRH-------MQDPMLRQLNG

*Tremantomus loennbergii* SFSHILGSLLVCGSVIL-VGLAIVARKWWKRH QDPVLRQLNG

*Dissostichus eleginoides* H**NFS**HVLGSLLVCGSVIL-VGLAIVARKWWRHS-PEYPFLEQDPVLRQLDG

*Dissostichus mawsoni* HN--HVLGSLLVCGSVIL-VGLAIVARKWWKRHNPEYPFLEQDPVLRQLNG

*Notothenia coriiceps* H**NFS**HVLGSLLVCGSVIL-VGLA ARKWWKRH--------KDPVLRQLNG

*Harpagifer antarcticus* SFSHVLGSLLVCGSVIL-VGLAIVARKWWKRH------LE-DPVLRQLNG

*Gymnodraco acuticeps* H**NFS**HVLGSLLVCGSVIL-VGLAIVARKWWKRQ--------KDPVLRQLNG

*Pseudochaennichthys georgianus* H**NFS**HVLGSLLVCGSVIL-VGLAIVARKWWKRH--------KDPVLRQLNG

*Chionodraco myersi* SFSHVLGSLLVCGSVIL-VGLAIVARKWWKRH LE-DPVLRQLNG

*Chaenocephalus aceratus* FSHVLGSLLVCGSVIL-VGLAIVVRKWWKRH LE-DPVLRQLNG

*Chionodraco hamatus* H**NFS**HVLGSLLVCGSVIL-VGLAIVARKWWKRH------- KDPVLRQLNG

*Cottoperca gobio* HS--HILWSLLVCASVMLLLGLAILARKLWKKHK-------QDPVLRQLKE

*Sander lucioperca* HS--HILESLLVCASIMLLVGMAILARKLWKQHK-------QDPVLRQVKE

*Perca fluviatilis* HS--HILESLLVCASIMLLVGLVILARKLWKQHK-------QDPVLRQVKE

*Perca flavescens* HS--HILESLVVCASIMLLVGLLILARKLWKQHK-------QDPVLRQVKE

*Etheostoma spectabile* HS--HILESMLVCASIMILVGLAILARKLWIQQIH-----EQDPVLRPVKE

*Etheostoma cragini* HN--HILESMLVCATVMLLVGLAILARKLWIQQIQ-----EQDPVLRPVKE

*Epinephelus coioides* HS--HILESLLVCASIMLLVGLAILARKLWKQHK-------QDPLQRQLKA

*Epinephelus lanceolatus* HS--HILESLLVCASIMLLVGLAILARKLWKQHK-------QDPLQRQVKA

*Plectropomus leopardus* FS--HILESLLVCASIMLLVGLAILVRKLWKQH

*Sebastes umbrosus* S-HSLILESLLVCASVMLLVGLAILARKWWKQHK-------RDPVLRQVKA

*Pungitius pungitius* HR--HIMESFLVCASFLFLVGLAILVRKLWKRHR-------QDPLLRQVQM

*Anarrhichthys ocellatus* HS--HILETLLVCAFIMFIVGLAIWVRKLWRRHG-------QDPVLRQVNM

*Cyclopterus lumpus* H----ILESLLVCASIMFLVGMAILARKLWKQHRR-------DPVLRQVNR

*Liparis tanakae*

*Gasterosteus aculeatus* HS--HIMESFLVCASFLILLGLAILVRKLWKRHR-------QDPMLRQVKM

*Trematomus bernacchii* MNARRNEYS-DVGCDLQ**NAT**VVFVNKDSQDVHMY

*Trematomus loennbergii* MNARRNEYS-NVGCDLQNAAVVFVNKDSQDVHMY

*Dissostichus eleginoides* MNARRNQYS-DVGCDEQNAAVVFLNKDSQDVHMY

*Dissostichus mawsoni* MNARRNEYS-DVGCDLQNAAVVFLNKDSQDVHMY

*Notothenia coriiceps* MNARRNEYS-DVGCDLQ**NAT**VVFLNKDFQDVHMC

*Harpagifer antarcticus* MNARRNEYS-DVGCDLQ**NAT**VVFRNKDSQHVHM

*Gymnodraco acuticeps* MNARRNEYS-DVGCDLQ**NAT**VVFLNKDSQDVHMC

*Pseudochaennichthys georgianus* MNARRNEYS-DVSCDLQ**NAT**VVFLNKDSQDVHMC

*Chionodraco myersi* MNARRNEYS-DVSCDLQ**NAT**VVFLNKDSQDVHMC

*Chaenocephalus aceratus* MNARRNEYS-DVSCDLQ**NAT**VVFLNKDSQHVHM

*Chionodraco hamatus* MNARRNEYS-DVSCDLQ**NAT**VVFLNKDSQDVHMC

*Cottoperca gobio* IKARHNEYSGDVG-DQQSTAVIFLNRDSQDIHMY

*Sander lucioperca* IQARHNEYSG----DLQNSAVVFLNRDSQDVQMY

*Perca fluviatilis* IQARHNEYSG----DLQNSAVVFLNRDSQDVRIY

*Perca flavescens* IQARHNEYSG----DLQNSAVVFLNRDSQDVHMY

*Etheostema spectabile* I

*Etheostema cragini* I

*Epinephelus coioides* IKARHNEYSGDVG-DLQNAAVVFLNRDSQDVHMY

*Epinephelus lanceolatus* IKARHNEYSGDVG-DLQNTAVVFLNRDSQDVHMY

*Plectropomus leopardus*

*Sebastes umbrosus* IKAKHNEYSGDSD-DPQNAAVVFLKRDSQGVYIH

*Pungitius pungitius* IKARHNEYSGDVG-DPQSAAVVFLNRDCEDAHMH

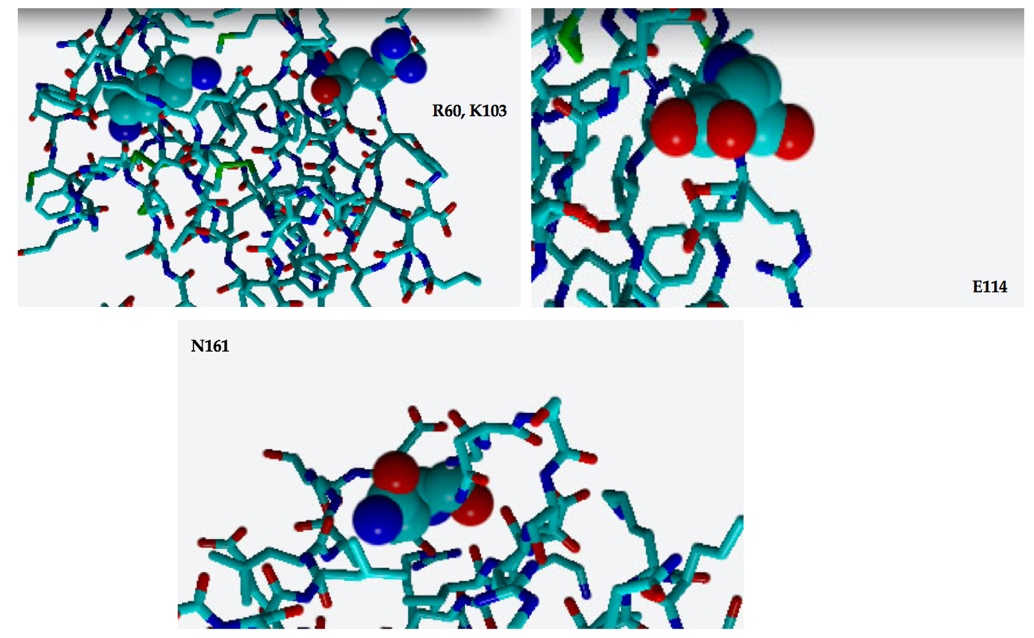
*Anarrhichthys ocellatus* IKARHNGYSGDVG-DPQSAAVVSQEY

*Cyclopterus lumpus* IKARHNEFSGDVD-DPQSTGVVFLNVDSQDVHMY

*Liparis tanakae*

*Gasterosteus aculeatus* IKARHNEGSGDVG-DPQSAAVVFLNRDCQEAYMH

**Figure S3.** Multiple alignment of the deduced amino acid sequences ofpIgRs available from Notothenioidei (Antarctic species in blue; non-Antarctic species in light blue) and from representative species of the perciform suborders Percoidei (in brown), Serranoidei (in red), Scorpaenoidei (in purple), and Cottoidei (in green). Notothenioid specific residues are highlighted in magenta. Putative N-glycosylation sites are reported in bold and underlined. Gaps are indicated by dashes.



**Figure S4.** Detail of R60, K103, E114, and N161 residues in the 3D molecular model built for the secretory componentof *T. bernacchii* pIgR. For each residue, the side chain exposed to solvent is shown.

**Table S1.** Predicted transcription factor-binding sites in the 5’-flanking region, and in the second and third introns of *T. bernacchii* polymeric Ig receptor (*pIgR)* gene.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| *pIgR* genomic region | Site | | Length | Position (nt) | Score (Gaps) | Occurrence | E-value |
| 5’-flanking region | | IFN-A2-B  IFN-A4-B  IL10-CEBP2’  Elf-1-IL-2R | 12  12  14  12 | 340  340  410  744 | 9 (0)  9 (0)  11 (0)  9 (0) | 1  1  1  1 | 4.78e-03  4.78e-03  3.47e-03  4.78e-03 |
| 2nd intron | | IRF-3 CS  IFN-A11-A  IFN-A2-A  TCR-Vbeta | 12  10  10  12 | 227  521  521  541 | 11 (0)  10 (0)  10 (0)  12 (0) | 1  1  1  1 | 3.48e-03  1.74e-03  1.74e-03  1.04e-04 |
| 3rd intron | | NF-IL6-erk1  NF-IL6-vimentin  NF-IL2-A-RS’  IFN-A11-A  IFN-A2-A | 9  10  10  10  10 | 8  109  198  430  430 | 9 (0)  10 (0)  10 (0)  10 (0)  10 (0) | 1  1  1  1  1 | 4.11e-03  1.03e-03  1.03e-03  1.03e-03  1.03e-03 |

**Table S2**. Amino acid composition of *T. bernacchii* pIgR and the respective regions SC (Secretory Component), EMPD (Extracellular Membrane Proximal Domain), TM (Transmembrane domain), Cyt (Cytoplasmic tail).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | pIgR | SC | | EMPD | TM | | Cyt |
| **Percentage of amino acid residues** | Ala (A): 3.8%  Arg (R): 5.6%  Asn (N): 4.1%  Asp (D): 4.7%  Cys (C): 3.3%  Gln (Q): 4.1%  Glu (E): 6.2%  Gly (G): 6.8%  His (H): 2.4%  Ile (I): 3.3%  **Leu (L): 8.3%**  Lys (K): 4.7%  Met (M): 3.8%  Phe (F): 2.7%  Pro (P): 4.7%  **Ser (S):10.7%**  Thr (T): 5.9%  Trp (W): 3.0%  Tyr (Y): 3.0%  **Val (V): 8.9%** | Ala (A): 3.7%  Arg (R): 5.7%  Asn (N): 3.7%  Asp (D): 4.5%  Cys (C): 3.3%  Gln (Q): 4.1%  **Glu (E): 8.2%**  Gly (G): 6.9%  His (H): 2.4%  Ile (I): 2.9%  Leu (L): 4.9%  Lys (K): 4.9%  Met (M): 3.3%  Phe (F): 2.4%  Pro (P): 4.9%  **Ser (S):12.7%**  Thr (T): 6.9%  Trp (W): 2.9%  Tyr (Y): 3.3%  **Val (V): 8.6%** | | Ala (A): 5.1%  Arg (R): 5.1%  Asn (N): 7.7%  Asp (D): 0.0%  Cys (C): 0.0%  Gln (Q): 5.1%  Glu (E): 2.6%  Gly (G): 2.6%  His (H): 2.6%  Ile (I): 2.6%  Leu (L): 2.6%  Lys (K): 5.1%  Met (M): 2.6%  Phe (F): 2.6%  **Pro (P):17.9%**  **Ser (S):10.3%**  **Thr (T):12.8%**  Trp (W): 2.6%  Tyr (Y): 0.0%  **Val (V):10.3%** | | **Ala (A):10.0%**  Arg (R): 0.0%  Asn (N): 0.0%  Asp (D): 0.0%  Cys (C): 5.0%  Gln (Q): 0.0%  Glu (E): 0.0%  **Gly (G):15.0%**  His (H): 0.0%  **Ile (I):15.0%**  **Leu (L):30.0%**  Lys (K): 0.0%  Met (M): 0.0%  Phe (F): 0.0%  Pro (P): 0.0%  **Ser (S):10.0%**  Thr (T): 0.0%  Trp (W): 0.0%  Tyr (Y): 0.0%  **Val (V):15.0%** | Ala (A): 3.9%  **Arg (R): 9.8%**  **Asn (N): 9.8%**  **Asp (D): 9.8%**  Cys (C): 2.0%  Gln (Q): 7.8%  Glu (E): 2.0%  Gly (G): 3.9%  His (H): 3.9%  Ile (I): 0.0%  Leu (L): 5.9%  Lys (K): 5.9%  Met (M): 7.8%  Phe (F): 2.0%  Pro (P): 2.0%  Ser (S): 3.9%  Thr (T): 2.0%  Trp (W): 3.9%  Tyr (Y): 3.9%  **Val (V): 9.8%** |
| **Theoretical pI** | **6.46** | **5.73** | **11.0** | | **5.52** | | **9.04** |

**Table S3.**  Splice-site prediction for the region encompassing the 3’ end of the fourth intron and the 5’ end of the EMPD exon of *T. bernacchii* *pIgR*.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Position (bp) | Putative splice site | Sequence | Score | Intron GC | Alternative/Cryptic | | Constitutive | | Confidence |
| 70  73  76 | **Constitutive acceptor**  Alt. isoform/cryptic acceptor  Alt. isoform/cryptic acceptor | ctttctttagCAGCAGTGTC  tctttagcagCAGTGTCTGT  ttagcagcagTGTCTGTGAC | 8.677  9.865  5.559 | 0.357  0.371  0.371 | 0.355  0.619  0.886 | 0.631  0.373  0.108 | | 0.437  0.398  0.878 | |

**Table S4**. List of primers used in PCR experiments.

|  |  |  |
| --- | --- | --- |
| Primer name | Sequence | pIgR domain |
| pIGR1Fwd forward | 5’- TTACGAGCCTCAGTATGCCAGC -3’ | *E. coioides* D1 |
| pIGR1Rev reverse | 5’- TGCAGAACACCAGTACCAGCC -3’ | *E. coioides* D2 |
| pIGRII forward | 5’- AGGGGGATTCTGGGTGGTA -3’ | *E. coioides* D1 |
| pIGRIIr reverse | 5’- CTTAGTGATGGGTTTGGGTGG -3’ | *E. coioides* EMPD |
| AAP1 | 5’- GGCCACGCGTCGACTAGTACGGGGGGGGGG -3’ |  |
| AP1 | 5’- GGCCACGCGTCGACTAGTACTTTTTTTTTTTTTTTTT -3’ |  |
| AUAP1 | 5’- GGCCACGCGTCGACTAGTAC -3’ |  |
| TbrtpIgRFwd forward | 5’- AAGAAGTGGTGTCGGAGTGG -3’ | *T. bernacchii* D1 |
| TbrtpIgRRev reverse | 5’- ACCAGCCTGTATCCCTCATC -3’ | *T. bernacchii* D1 |
| TbBACTfw2 | 5’- CCCAGATCATGTTCGAGACC -3’ |  |
| TbBACTrev2 | 5’- CATAGATGGGCACTGTGTGG -3’ |  |

1AAP, AP and AUAP are the Adaptor Primers used in 5’ and 3’ RACE.

2TbBACTfw and TbBACTrev are the primers designed on *-actin* gene, used as housekeeping gene in qPCR.

**Table S5.** List of perciform suborders and respective species investigated for the *pIgR* genomic and transcript sequences available.

|  |  |  |  |
| --- | --- | --- | --- |
| **Suborder** | **Species** | **Transcript accession number** | **Genomic scaffold accession number** |
| Notothenioidei | *Trematomus bernacchii*  *Trematomus loennbergii*  *Dissostichus eleginoides*  *Dissostichus mawsoni*  *Notothenia coriiceps*  *Harpagifer antarcticus*  *Gymnodraco acuticeps*  *Pseudochaenichthys georgianus*  *Chionodraco myersi*  *Chaenocephalus aceratus*  *Chionodraco hamatus*  *Cottopercagobio* | MZ540772; XM\_034138155.1; XM\_034138156.1  JAAOOA010000028.1  GHKE01202443  JAAKFY010000004  XM\_010780285.1  CADEHL010001073.1  XM\_034231973.1XM\_034231974.1; XM\_034231975.1  XM\_034104980.1; XM\_034104981.1  RQJG01055183.1  OMOC01081144.1  GFMN01023039.1  XM\_029454169.1 | NW\_022987689.1  N/A  N/A  N/A  N/A  N/A  NW\_022990743.1  NC\_047519.1  N/A  N/A  N/A  NC\_041371.1 |
| Percoidei | *Sander lucioperca*  *Perca fluviatilis* | XM\_036004850.1  XM\_039816568.1 | NC\_050181.1  NC\_053122.1 |
| *Perca flavescens*  *Etheostoma spectabile*  *Etheostoma cragini* | XM\_028593228.1  XM\_032532220.1  XM\_034887523.1 | NC\_041342.1  NC\_045744.1  NC\_048418.1 |
| Serranoidei | *Epinephelus coioides* | FJ803367.1 | N/A |
| *Epinephelus lanceolatus* | XM\_033651131.1 | NC\_047009.1 |
| *Plectropomus leopardus* | XM\_042597661.1 | NC\_056474.1 |
| Scorpaenoidei | *Sebastes umbrosus* | XM\_037788606.1 | NC\_051280.1 |
| Cottoidei | *Pingitius pungitius*  *Anarrhichthys ocellatus* | XM\_037459474.1  XM\_031855165.1 | NW\_023616457.1  NW\_022280045.1 |
| *Cyclopterus lumpus*  *Liparis tanakae*  *Gasterosteus aculeatus* | XM\_034544233.1  SRLO01000113.1  XM\_040171583.1 | N/A  N/A  NC\_053214.1 |

**Table S6**. Specific primers used for RT-PCR and sense and anti-sense probes.

|  |  |
| --- | --- |
| ISH | Sequences |
| RT-PCR forward | 5’ - GTCACAGTTGAACGCCAAT - 3’ |
| RT-PCR reverse | 5’ - ACAAGGATTACAGAACCAC - 3’ |
| Sense probe forward | 5’ - TAATACGACTCACTATAGGG - 3’ |
| Sense probe reverse | 5’ - ACAAGGATTACAGAACCAC - 3’ |
| Anti-sense probe forward | 5’ - GTCACAGTTGAACGCCAAT - 3’ |
| Anti-sense probe reverse | 5’ - GCATTTAGGTGACACTATAGAATAG - 3’ |