

S.salm1 MQRVNHNFHPESEVNINKLVNIKLTASYTYLSLGMFYFDRDDVALRSFSSFFLERSVKERE 60
O.nilh1 MQAVKQNFHAETEGDVNKLINLKLNASYTYLALGMFYFDRDDVALPNFSSFFLERSAKERE 60
D.rerM1 MSLIKQNLHSNNEANINKLINLKLNASYTYLSLGMFYFDRDDVALPNFSSFFLERSHKERD 60
D.rerM2 MEQIRQNYVRDSEAAINKMINLELYAGYTYTSMAHYFKRDDVALPGFAKFFKKNSEEEERE 60
D.rerM3 MEQIRQNYARDSEAAINKMINLELYAGYTYTSMAHYFKRDDVALPGFAKFFKKNSEEEERE 60
D.rerM4 MEQVRQNYARDSEAAINKMINLELYAGYTYTSMAHYFKRDDVALPGFAKFFKKNSEEEERE 60
D.rerM5 MEQIRQNYDRDCEAAINKMINLELYAGYTYTSMAHYFKRDDVALPGFAKFFKKNSEEEERE 60
D.rerM6 MEQIRQNYDRDCEAAINKMINLELYAGYTYTSMAHYFKRDDVALPGFAKFFKKNSEEEERE 60
D.rerM7 MEQIRQNYDSDCEASINKMISLELYAGYTYTSMAHYFKRDDVALNGFAKFFKKNSEEEERE 60
D.rerM8 MEQIRQNYDSDCEASINKMINLELYAGYTYTSMAHYFKRDDVALNGFAKFFKKNSEEEERE 60
DrerM9 MEQIRQNYDSDCEALINKMINLELYAGYTYTSMAHYFKRDDVALPGFAKFFKKNSEEEERE 60
D.rerH1 MDQVRQNYDRDCEALINKMINLELYAGYTYTSMAFYFDRDDVALPGFAKFFKKNSEEEERE 60
I.punM1 MEQIRQNYHRDCEAAINKMINMELYASYTYTSMAYYFTRDDVALEGFHFFKENSHEERE 60
I.punM2 MEQIRQNYHRDCEAAINKMINMELYASYTYTSMAYYFTRDDVALEGFHFFKENSHEERE 60
O.nilM1 MEQVRQNYHRDCEAAINRMVNMELFASYTYTSMAFYFDRDDVALPGFSSHFFKENSHEERE 60
O.nilM2 MEQVRQNYHRDCEAAINRMVNMELFASYTYTSMAFYFDRDDVALPGFSSHFFKENSHEERE 60
E.bruM1 MEQVRQNYHRDCEAAVNRMVNMELFASYTYTSMAFYFSRDDVALKGFSSHFFKENSDEERE 60
T.berM1 MDQVRQNYHRDCEAAVNRMINMELFASYSYTSMAFYFSRDDVALPGFAHFFKENSDEERE 60
T.berM2 MDQVRQNYHRDCEAAVNRMINMELFASYSYTSMAFYFSRDDVALPGFAHFFKENSDEERE 60
C.rasM1 MDQVRQSYHRDCEAAVNRMLNTELFASYSYTSMAFYFSRDDVALPGFAHFFKESSEEEERE 60
S.salm2 MEQIRQNYHHDCEAAINRMINMEMFASYTYTSMAFYFSRDDVALPGFAHFFKENSSEEEERE 60
D.rerH2 MSQVRQNFHQECEAAINRQIYLELYASYVYLSMGYFDRDDKSLPNFAKFFRDQSKEERE 60
S.salH1 MTQVRQNFHQECEAAINRQINLELYASYVYLSMGYFDRDDKSLPNFSKFFLTQPKEEKE 60
T.berH1 MSQVRQNFHQDCEAAINRQINLELYASYVYMSMGYFDRDDQALNNSKFFRQOSEEEERE 60
C.rasH1 MSQVRQNFHQDCEAAVNRQINLELYASYVYMSMGYFDRDDQALNNSKFFRQOSEEEERE 60
E.bruH1 MSQVRQNYHQDCEAAINRQINLELYASYVYLSMGYFDRDDQALHNFKFFRQOSHEERE 60
O.nilH3 MSQVRQNFHQDCEAAVNRQINLELYASYVYLSMSYFDRDDQALHNFKFFRQOSHEERE 60
I.punH1 MSQVRQNFHQDCEAAINRQINLELYASYVYLSMSYFDRDDQALHNFKFFRQOSHEERE 60
I.punH2 MSQVRQNFHQDCEAAINRQINLELYASYVYLSMSYFDRDDQALHNFKFFRQOSHEERE 60
S.salH2 MTQVRQNFHQDCEAAINRQINLELYASYVYLSMAYYFDRDDQALHNFKFFKQOSHEERE 60
S.salH3 MTQVRQNFHQDCEAAINRQINLELYASYVYLSMAYYFDRDDQALHNFKFFKQOSHEERE 60
D.rerH3 MSQVRQNFEEACEAAVNRQINMELYASYVYLSMSYFDRDDQALHNFKFFRQOSHEERE 60
O.nilH2 MTQIRQNFHHDCEAAINRQINLELYASYVYLSMAYYFERDDKCLPNFAKFFRQOSKEEVV 60
D.rerM10 SSQVKQNFPRVVEESLCGVSTLLLEVSYKLEALGRIFEQSNLALPRVAAYFHQESVKEQE 60

S.salm1 QAEKLLLEYQNMRRGGRVLLQPIAKPSREDWRGGLDAITFSLEFQKTLNNTSLEEVHRGANH 120
O.nilh1 QAEKLLLEYQNMRRGRILLQNIKSPSKEDWKGLDAMTFSLEYQKTLNTRTLVDVHRRAGSH 120
D.rerM1 HAEDLLEYQNTTRGGRILLQTVAKPSRDDWKGGLDALAFSLEHQKSNRSLLEVHRVAGEH 120
D.rerM2 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerM3 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerM4 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerM5 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerM6 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerM7 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerM8 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
DrerM9 HAEKFMFQNKRGGRIVLQDIKKPDRDVWGNLIAMQCALQLEKNVNQALLDLHKLATEM 120
D.rerH1 HAEKFMFQNKRGGRIVLQDIKKPERDEWDNGLTAMQCALQLEKNVNQALLDLHKLATEM 120
I.punM1 HAEKFMFQNKRGGRIFLQDVKKPERDEWGSGLAMQCALQLEKTVNQALLDLHKLASDK 120
I.punM2 HAEKFMFQNKRGGRIFLQDVKKPKRDEWGSGLAMQCALQLEKTVNQALLDLHKLASDK 120
O.nilM1 HADKLLSFQNKRGGRILLQDIKKPERDEWGSGLAMQCALELEKNVNQALLDLHKLASQH 120
O.nilM2 HADKLLSFQNKRGGRILLQDIKKPERDEWGSGLAMQCALQLEKNVNQALLDLHKLASQH 120
E.bruM1 HAEKLLSFQNKRGGRIFLQDVKKPDRDEWGSGLAMQCALQLEKNVNQALLDLHKLASDH 120
T.berM1 HADKLLTFQNSRGGRIFLQDIKKPERDEWGSGLDALQSSQLEKNVNQALLDLHKLASDH 120
T.berM2 HADKLLTFQNSRGGRIFLQDIKKPERDEWGNVDVMQCALQLEKNVNQALLDLHKLASDH 120
C.rasM1 HAHKLLTFQNSRGGRIFLQDIKKPERDEWGSGLAMQALQLEKNVNQALLDLHKLASVH 120
S.salm2 HADKLLSFQNKRGGRILLQDIKKPERDEWGNGLAMQCALQLEKNVNQALLDLHKLASDK 120
D.rerH2 HAEKLLSLQNRGGRIFLQDIKKPDRDEWGSGLAEALCALALEKSVNLSLLELHKLAVATQH 120
S.salH1 HAEKLLSQNQNRGGRIFLQDIKKPDRDEWGSGLAEALCALALEKSVNLSLLELHKLVAAGQ 120
T.berH1 HAEKLLMQNQNRGGRIFLQDVKKPDRDEWGSGLAEALCALALEKSVNLSLLELHKLCSDH 120
C.rasH1 HAEKLLMLQNRGGRIFLQDVKKPDRDEWGSGLAEALCALALEKSVNLSLLELHKLCSDH 120
E.bruH1 HAEKLLMLQNRGGRIFLQDVKKPERDEWGSGLAEALCALALEKSVNLSLLELHKLCSSEH 120
O.nilH3 HAEKLLMLQNRGGRIFLQDIKKPDRDEWGSGLAEALCALALEKSVNLSLLELHKLCSSEH 120
I.punH1 HAEKLLMKVQNRGGRIFLQDIKKPERDEWGSGLAEALCALALEKSVNLSLLELHKLAVTDH 120
I.punH2 HAEKLLMKIQNRGGRIFLQDIKKPERDEWGSGLAEALCALALEKSVNLSLLELHKLAVSTDH 120
S.salH2 HAEKLLMKVQNRGGRIFLQDVKKPEKDEWGSGLAEALCALALEKSVNLSLLELHKLVCSEH 120
S.salH3 HAEKLLTVQNRGGRIFLQDVKKPEKDEWGSGLAEALCALALEKSVNLSLLELHKLVCSEH 120
D.rerH3 HAEKLLMKFQNRGGRIFLQDVKKPEKDEWGSGLAEALCALALEKSVNLSLLELHKLASQH 120
O.nilH2 HAEKLLMTFQNKRGGRIFLQDIKKPDRDEWGSGLAEALCALALEKSVNLSLLELQKIMATEH 120
D.rerM10 RAEVMLQYLSQRGGKYCNKNIQRPGTEQVCAVLPALIMLNQWKEEMSVMLEINHLAHEH 120

S.salM1	TDPHLCDFLEQHFLSDSHDTIKKLGDLGSLTRLTSSEGSMEYLFDKHTL	171
O.nilH1	TDPHLCDFLEQHFLVDSHDTIKKLGDIYIGSLTRITASEGAMGEYLFDKHTL	171
D.rerM1	SDPHLSDFLEGKFFTDSETIKKTLGDYLGSLSRITSSDGKMAEYLFDKHTL	171
D.rerM2	GDPHLCDFLETHYLNEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKQTL	171
D.rerM3	GDPHLCDFLETHYLDEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
D.rerM4	GDPHLCDFLETHYLNEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
D.rerM5	GDPHLCDFLESHYLNEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKQTL	171
D.rerM6	GDPHLCDFLESHYLNEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
D.rerM7	GDPHLCDFLETHYLDEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
D.rerM8	GDPHLCDFLETHYLDEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
DrerM9	GDPHLCDFLESHYLNEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
D.rerH1	GDPHLCDFLESHYLNEQVEAIKKLGDHITNLSKMDAGNNRMAEYLFDKHTL	171
I.punM1	ADPHLCDFLETHYLNEQVEAIKKLGDHISNLTKMDAANNRMAEYLFDKHTL	171
I.punM2	ADPHLCDFLETHYLNEQVEAIKKLGDHISNLTKMDAASNRMAYLFDKHTL	171
O.nilM1	NDPHLCDFLESHYLDEQVKSIIKKLGDHITNLTRMDAHKNKMAEYLFDKHTL	171
O.nilM2	NDPHLCDFLESHYLDEQVKSIIKKLGDHITNLTRMDAHNNKMAEYLFDKHTL	171
E.bruM1	VDPHLCDFLETHYLNEQVEAIKKLGDYITNLSRMDAHNNKMAEYLFDKHTL	171
T.berM1	TDPHMCDFLETHYLNEQVESIIKKLGDYITNLSRMDAVKNKMAEYLFDKHTM	171
T.berM2	VDPHMCDFLETHYLNEQVESIIKKLGDYITNLSRMDAVKNKMAEYLFDKHTM	171
C.rasM1	ADPHMCDFLETHYLNEQVESIIKKLGDYITNLSRMDAVKNKMAEYLFDKHTM	171
S.salM2	VDPHLCDFLETHYLNEQVEAIKKLGDHITNLTKMDAVKNKMAEYLFDKHTL	171
D.rerH2	NDPHVCDLETHYLDEQVKSIIKELSDWVGLRRMGAPQNNMAEYLFDRHTL	171
S.salH1	NDPHMCDFIETHYLDEQVKSIIKELSDWITNLRMGAPQNGMAEYLFDKHTL	171
T.berH1	NDPHMCDFIETHYLDEQVKSIIKELGDWVTNLRMGAPQNGLAEYLFDKHTL	171
C.rasH1	NDPHLCDFIETHYLDEQVKSIIKELGDWVTNLRMGAPQNGLAEYLFDKHTL	171
E.bruH1	NDPHLCDFIETHYLDEQVKSIIKELADWVTNLRMGAPQNGLAEYLFDKHTM	171
O.nilH3	NDPHMCDFIETHYLDEQVKSIIKELADWVTNLRMGAPQNGMAEYLFDKHTL	171
I.punH1	NDPHMCDFIEAHYLDEQVKSIIKELSDWVTNLRMGAPQNGMAEYLFDKHTL	171
I.punH2	NDPHMCDFIESRYLDEQVKSIIKELSDWVTNLRMGAPQNGMAEYLFDKHTL	171
S.salH2	NDPHMCDFIETHYLDEQVKSIIKELGDWVTNLRMGAPQNGMAEYLFDKHTL	171
S.salH3	NDPHLCDFIETHYLDEQVKSIIKELGDWVTNLRMGAPQNGMAEYLFDKHTL	171
D.rerH3	NDPHMCDFIETHYLDEQVKSIIKELGDHVTNLRMGAPQNGMAEYMFDKLTL	171
O.nilH2	NDPHMCDFIETHFLDEQVKSIIKQLADWSSNLRMGAPQSGMAEYLFDKHTM	171
D.rerM10	DDPHTASVIKSQFIEPLVQVKLVGDLLTNARRVGTDAFGFEFLIDQLQE	171

Supplementary Figure 1. Alignment of the 34 amino acid sequences of the fish ferritins used to infer the phylogenetic tree shown in Figure 5. The alignment was obtained using the program ClustalW v2.1.