PREDICTED: HrETR-1-like [Ciona intestinalis]

Sequence ID: [ref|XP\_002130974.2|](http://www.ncbi.nlm.nih.gov/protein/459176816?report=genbank&log$=protalign&blast_rank=1&RID=TMKUFB9D01R)Length: 539Number of Matches: 2

Related Information

[Gene](http://www.ncbi.nlm.nih.gov/gene?term=459176816%5bPUID%5d&RID=TMKUFB9D01R&log$=genealign&blast_rank=1)-associated gene details

Range 1: 79 to 256[GenPept](http://www.ncbi.nlm.nih.gov/protein/459176816?report=genbank&log$=protalign&blast_rank=1&RID=TMKUFB9D01R&from=79&to=256)[Graphics](http://www.ncbi.nlm.nih.gov/protein/459176816?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=71:264&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 354 bits(908) | 2e-117 | Compositional matrix adjust. | 165/178(93%) | 173/178(97%) | 1/178(0%) | +1 |

Query 1 IGQVPKNWDEKELRQIFAPFGEIFELSVLRDKYTGMHKGCAFLTYAHKTAAMNAQNSLHE 180

IGQVPKNW+EKELRQ+FAPFGEIFELSVLRDKYTGMHKGCAFLTY KT+AMNAQNSLHE

Sbjct 79 IGQVPKNWEEKELRQVFAPFGEIFELSVLRDKYTGMHKGCAFLTYTQKTSAMNAQNSLHE 138

Query 181 RKTPPGMNHPIQVKPADTVSKG-EDRKLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRT 357

RKT PGMNHPIQVKPADTVSKG EDRKLFVGMLGKRQNE+DVR+LFEPFGTIEECTILRT

Sbjct 139 RKTLPGMNHPIQVKPADTVSKGAEDRKLFVGMLGKRQNEDDVRILFEPFGTIEECTILRT 198

Query 358 PEGQSKGCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRRMQQM 531

PEGQSKGCAFVKL+CH EAK+AM+ALHGSQTMPGASSSLVVKFADTDKERAVRRMQQM

Sbjct 199 PEGQSKGCAFVKLSCHQEAKSAMEALHGSQTMPGASSSLVVKFADTDKERAVRRMQQM 256

Range 2: 61 to 164[GenPept](http://www.ncbi.nlm.nih.gov/protein/459176816?report=genbank&log$=protalign&blast_rank=1&RID=TMKUFB9D01R&from=61&to=164)[Graphics](http://www.ncbi.nlm.nih.gov/protein/459176816?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=56:169&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](http://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp459176816_1)

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| Alignment statistics for match #2 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 65.9 bits(159) | 8e-10 | Compositional matrix adjust. | 40/108(37%) | 62/108(57%) | 6/108(5%) | +1 |

Query 202 NHPIQVKPADTVSKGEDR-KLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRTP-EGQSK 375

+HP++ +T K +D KLF+G + K E+++R +F PFG I E ++LR G K

Sbjct 61 SHPLK----ETPEKDDDAVKLFIGQVPKNWEEKELRQVFAPFGEIFELSVLRDKYTGMHK 116

Query 376 GCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRR 519

GCAF+ + A A ++LH +T+PG + + VK ADT + A R

Sbjct 117 GCAFLTYTQKTSAMNAQNSLHERKTLPGMNHPIQVKPADTVSKGAEDR 164

[Download](http://blast.ncbi.nlm.nih.gov/Blast.cgi" \l "dlgDwnl_13537210" \o "Download information for dbj|BAB40781.1|) [GenPept](http://www.ncbi.nlm.nih.gov/protein/13537210?report=genbank&log$=protalign&blast_rank=2&RID=TMKUFB9D01R)[Graphics](http://www.ncbi.nlm.nih.gov/protein/13537210?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=96:291&appname=ncbiblast&link_loc=fromSubj)

Sort by:

Next Previous [Descriptions](http://blast.ncbi.nlm.nih.gov/Blast.cgi#dtr_13537210)

HrETR-1 [Halocynthia roretzi]

Sequence ID: [dbj|BAB40781.1|](http://www.ncbi.nlm.nih.gov/protein/13537210?report=genbank&log$=protalign&blast_rank=2&RID=TMKUFB9D01R)Length: 594Number of Matches: 2

Related Information

Range 1: 107 to 283[GenPept](http://www.ncbi.nlm.nih.gov/protein/13537210?report=genbank&log$=protalign&blast_rank=2&RID=TMKUFB9D01R&from=107&to=283)[Graphics](http://www.ncbi.nlm.nih.gov/protein/13537210?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=99:291&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 308 bits(789) | 6e-99 | Compositional matrix adjust. | 142/177(80%) | 158/177(89%) | 0/177(0%) | +1 |

Query 1 IGQVPKNWDEKELRQIFAPFGEIFELSVLRDKYTGMHKGCAFLTYAHKTAAMNAQNSLHE 180

IGQVPKNW E ELR IF P+GEI+ELSVL DKYTGMHKGCAFLTY KT A+NAQN LHE

Sbjct 107 IGQVPKNWTEHELRPIFEPYGEIYELSVLHDKYTGMHKGCAFLTYCKKTPAINAQNFLHE 166

Query 181 RKTPPGMNHPIQVKPADTVSKGEDRKLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRTP 360

+KT PGMNHP+QVKPADTV+KGEDRKLFVGMLGKRQ EED+R LFE FG IEECTILRTP

Sbjct 167 QKTLPGMNHPMQVKPADTVNKGEDRKLFVGMLGKRQTEEDIRQLFEKFGHIEECTILRTP 226

Query 361 EGQSKGCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRRMQQM 531

+GQSKGC+FVKL+ + A+ A+DALHGSQTMPGASSS+VVK ADTDKERA+R+MQQM

Sbjct 227 DGQSKGCSFVKLSTSTGARAAIDALHGSQTMPGASSSIVVKLADTDKERAIRKMQQM 283

Range 2: 104 to 193[GenPept](http://www.ncbi.nlm.nih.gov/protein/13537210?report=genbank&log$=protalign&blast_rank=2&RID=TMKUFB9D01R&from=104&to=193)[Graphics](http://www.ncbi.nlm.nih.gov/protein/13537210?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=100:197&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](http://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp13537210_1)

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| Alignment statistics for match #2 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 62.0 bits(149) | 2e-08 | Compositional matrix adjust. | 33/90(37%) | 51/90(56%) | 1/90(1%) | +1 |

Query 256 KLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRTP-EGQSKGCAFVKLACHSEAKTAMDA 432

KLF+G + K E ++R +FEP+G I E ++L G KGCAF+ + A A +

Sbjct 104 KLFIGQVPKNWTEHELRPIFEPYGEIYELSVLHDKYTGMHKGCAFLTYCKKTPAINAQNF 163

Query 433 LHGSQTMPGASSSLVVKFADTDKERAVRRM 522

LH +T+PG + + VK ADT + R++

Sbjct 164 LHEQKTLPGMNHPMQVKPADTVNKGEDRKL 193

[Download](http://blast.ncbi.nlm.nih.gov/Blast.cgi" \l "dlgDwnl_9246977" \o "Download information for gb|AAF86232.1|AF248650_1) [GenPept](http://www.ncbi.nlm.nih.gov/protein/9246977?report=genbank&log$=protalign&blast_rank=3&RID=TMKUFB9D01R)[Graphics](http://www.ncbi.nlm.nih.gov/protein/9246977?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=31:243&appname=ncbiblast&link_loc=fromSubj)

Sort by:

Next Previous [Descriptions](http://blast.ncbi.nlm.nih.gov/Blast.cgi#dtr_9246977)

RNA-binding protein BRUNOL4 [Homo sapiens]

Sequence ID: [gb|AAF86232.1|AF248650\_1](http://www.ncbi.nlm.nih.gov/protein/9246977?report=genbank&log$=protalign&blast_rank=3&RID=TMKUFB9D01R)Length: 294Number of Matches: 2

Related Information

[Gene](http://www.ncbi.nlm.nih.gov/gene?term=9246977%5bPUID%5d&RID=TMKUFB9D01R&log$=genealign&blast_rank=3)-associated gene details

[Map Viewer](http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?direct=on&gbgi=9246977&THE_BLAST_RID=TMKUFB9D01R&log$=mapalign&blast_rank=3)-aligned genomic context

Range 1: 58 to 234[GenPept](http://www.ncbi.nlm.nih.gov/protein/9246977?report=genbank&log$=protalign&blast_rank=3&RID=TMKUFB9D01R&from=58&to=234)[Graphics](http://www.ncbi.nlm.nih.gov/protein/9246977?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=50:242&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 280 bits(716) | 1e-91 | Compositional matrix adjust. | 127/177(72%) | 156/177(88%) | 0/177(0%) | +1 |

Query 1 IGQVPKNWDEKELRQIFAPFGEIFELSVLRDKYTGMHKGCAFLTYAHKTAAMNAQNSLHE 180

IGQ+P+N DEK+L+ +F FG+I+EL+VL+D++TGMHKGCAFLTY + +A+ AQ++LHE

Sbjct 58 IGQIPRNLDEKDLKPLFEEFGKIYELTVLKDRFTGMHKGCAFLTYCERESALKAQSALHE 117

Query 181 RKTPPGMNHPIQVKPADTVSKGEDRKLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRTP 360

+KT PGMN PIQVKPAD+ S+GEDRKLFVGML K+Q+E+DVR LFE FG IEECTILR P

Sbjct 118 QKTLPGMNRPIQVKPADSESRGEDRKLFVGMLNKQQSEDDVRRLFEAFGNIEECTILRGP 177

Query 361 EGQSKGCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRRMQQM 531

+G SKGCAFVK + H+EA+ A++ALHGSQTMPGASSSLVVKFADTDKER +RRMQQM

Sbjct 178 DGNSKGCAFVKYSSHAEAQAAINALHGSQTMPGASSSLVVKFADTDKERTMRRMQQM 234

Range 2: 40 to 144[GenPept](http://www.ncbi.nlm.nih.gov/protein/9246977?report=genbank&log$=protalign&blast_rank=3&RID=TMKUFB9D01R&from=40&to=144)[Graphics](http://www.ncbi.nlm.nih.gov/protein/9246977?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=35:149&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](http://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp9246977_1)

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| Alignment statistics for match #2 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 63.9 bits(154) | 1e-09 | Compositional matrix adjust. | 39/111(35%) | 59/111(53%) | 7/111(6%) | +1 |

Query 193 PGMNHPIQVKPADTVSKGEDRKLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRTP-EGQ 369

PG I +K D + KLF+G + + +E+D++ LFE FG I E T+L+ G

Sbjct 40 PGNPSTIPMKDHDAI------KLFIGQIPRNLDEKDLKPLFEEFGKIYELTVLKDRFTGM 93

Query 370 SKGCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRRM 522

KGCAF+ A A ALH +T+PG + + VK AD++ R++

Sbjct 94 HKGCAFLTYCERESALKAQSALHEQKTLPGMNRPIQVKPADSESRGEDRKL 144

[Download](http://blast.ncbi.nlm.nih.gov/Blast.cgi" \l "dlgDwnl_432858764" \o "Download information for ref|XP_004068927.1|) [GenPept](http://www.ncbi.nlm.nih.gov/protein/432858764?report=genbank&log$=protalign&blast_rank=4&RID=TMKUFB9D01R)[Graphics](http://www.ncbi.nlm.nih.gov/protein/432858764?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=18:241&appname=ncbiblast&link_loc=fromSubj)

Sort by:

Next Previous [Descriptions](http://blast.ncbi.nlm.nih.gov/Blast.cgi#dtr_432858764)

PREDICTED: CUGBP Elav-like family member 4-like [Oryzias latipes]

Sequence ID: [ref|XP\_004068927.1|](http://www.ncbi.nlm.nih.gov/protein/432858764?report=genbank&log$=protalign&blast_rank=4&RID=TMKUFB9D01R)Length: 505Number of Matches: 2

Related Information

[Gene](http://www.ncbi.nlm.nih.gov/gene?term=432858764%5bPUID%5d&RID=TMKUFB9D01R&log$=genealign&blast_rank=4)-associated gene details

[UniGene](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=protein&cmd=Display&dopt=protein_unigene&from_uid=432858764&RID=TMKUFB9D01R&log$=unigenealign&blast_rank=4)-clustered expressed sequence tags

Range 1: 55 to 231[GenPept](http://www.ncbi.nlm.nih.gov/protein/432858764?report=genbank&log$=protalign&blast_rank=4&RID=TMKUFB9D01R&from=55&to=231)[Graphics](http://www.ncbi.nlm.nih.gov/protein/432858764?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=47:239&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 282 bits(722) | 6e-90 | Compositional matrix adjust. | 129/177(73%) | 156/177(88%) | 0/177(0%) | +1 |

Query 1 IGQVPKNWDEKELRQIFAPFGEIFELSVLRDKYTGMHKGCAFLTYAHKTAAMNAQNSLHE 180

IGQ+P+N DEK+LR +F FG+I+EL+VL+D++TGMHKGCAFLTY + +A+ AQN+LHE

Sbjct 55 IGQIPRNLDEKDLRPLFEEFGKIYELTVLKDRFTGMHKGCAFLTYCARESALKAQNALHE 114

Query 181 RKTPPGMNHPIQVKPADTVSKGEDRKLFVGMLGKRQNEEDVRVLFEPFGTIEECTILRTP 360

+KT PGMN PIQVKPAD+ S+GEDRKLFVGML K+Q+E+DVR LFE FG+IEECTILR P

Sbjct 115 QKTLPGMNRPIQVKPADSESRGEDRKLFVGMLNKQQSEDDVRRLFESFGSIEECTILRGP 174

Query 361 EGQSKGCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRRMQQM 531

+G SKGCAFVK + H+EA+ A+ ALHGSQTMPGASSSLVVKFADTDKER +RRMQQM

Sbjct 175 DGNSKGCAFVKYSSHAEAQAAISALHGSQTMPGASSSLVVKFADTDKERTIRRMQQM 231

Range 2: 28 to 141[GenPept](http://www.ncbi.nlm.nih.gov/protein/432858764?report=genbank&log$=protalign&blast_rank=4&RID=TMKUFB9D01R&from=28&to=141)[Graphics](http://www.ncbi.nlm.nih.gov/protein/432858764?report=graph&rid=TMKUFB9D01R&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments%7CRefseq%20Alignments%7CGnomon%20Alignments%7CUnnamed,shown:false%5d&v=23:146&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](http://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp432858764_1)

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| Alignment statistics for match #2 | | | | | | |
| **Score** | **Expect** | **Method** | **Identities** | **Positives** | **Gaps** | **Frame** |
| 69.7 bits(169) | 4e-11 | Compositional matrix adjust. | 42/120(35%) | 63/120(52%) | 7/120(5%) | +1 |

Query 166 NSLHERKTPPGMNHPIQVKPADTVSKGEDRKLFVGMLGKRQNEEDVRVLFEPFGTIEECT 345

N L +P G I +K D + KLF+G + + +E+D+R LFE FG I E T

Sbjct 28 NGLSHSHSPAGCPATIPMKDHDAI------KLFIGQIPRNLDEKDLRPLFEEFGKIYELT 81

Query 346 ILRTP-EGQSKGCAFVKLACHSEAKTAMDALHGSQTMPGASSSLVVKFADTDKERAVRRM 522

+L+ G KGCAF+ A A +ALH +T+PG + + VK AD++ R++

Sbjct 82 VLKDRFTGMHKGCAFLTYCARESALKAQNALHEQKTLPGMNRPIQVKPADSESRGEDRKL 141