

The protein sequences were obtained by PCR amplification of cDNAs from *Loligo pealei* stellate ganglion RNA using degenerate primers, followed by comparison of obtained nucleotide sequences to the *Loligo pealei* transcriptome data base at <http://athyra.idyll.org/~t/blast/ceph/>

Phylogenetic relationships were determined using BLAST at <http://blast.ncbi.nlm.nih.gov/Blast.cgi>

lpNKX1-related protein 1

Predicted protein from *Loligo pealei* transcriptome

NNNNNNSSNQQAQQQRSQTTSFSVADILDPTKFTGTTSCIKTRVWHPWVDTSSSTDSTDLSEKASDT
AESKDESIFEDACDKDDASGILEPDDKDVDESGKQKIKSFSSSGSDSGKAGKPRRARTAFTEQLVAL
ENKFKTTRYLSVCERLNLALSINLTETQVKIWFQNRRTKWKQNPQMDVNSPTIPPSSGALSGFSSPY
SSTTPLYAQGLHPYLQNHNLYGALGLFRTHAASYGAQNHHIYYPYFSQTT

BLAST comparison of PCR amplified fragment

RecName: Full=NK1 transcription factor-related protein 1; AltName: Full=Homeobox protein 153; Short=HPX-153; AltName: Full=Homeobox protein SAX-2; AltName: Full=NKX-1.1
Sequence ID: [sp|Q15270.2|NKX11_HUMAN](http://www.ncbi.nlm.nih.gov/blast/blast.cgi?seqid=sp|Q15270.2|NKX11_HUMAN) Length: 411 Number of Matches: 1
Range 1: 250 to 324 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Method	Identities	Positives	Gaps
	144 bits(364)	4e-39	Compositional matrix adjust.	68/76(89%)	72/76(94%)	1/76(1%)
Query	111	SGSDSGKAGKPRRARTAFTEQLVALENKFKTTRYLSVCERLNLALSINLTETQVKIWFQ		170		
		+GSDS K+GKPRRARTAFTEQLVALENKFK TRYLSVCERLNLALS+LTETQVKIWFQ				
Sbjct	250	TGSDS-KSGKPRRARTAFTEQLVALENKFKATRYLSVCERLNLALSINLTETQVKIWFQ		308		
Query	171	NRRTKWKQNPQMDVN 186				
		NRRTKWKQNPQ D +				
Sbjct	309	NRRTKWKQNPQADTS 324				

BLAST comparison of predicted protein to closest homolog

PREDICTED: GATA zinc finger domain-containing protein 7-like [*Aplysia californica*]
Sequence ID: [ref|XP_005097511.1](http://www.ncbi.nlm.nih.gov/blast/blast.cgi?seqid=ref|XP_005097511.1) Length: 771 Number of Matches: 1
Range 1: 520 to 771 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Method	Identities	Positives	Gaps
	256 bits(655)	6e-76	Compositional matrix adjust.	142/254(56%)	160/254(62%)	23/254(9%)
Query	22	TFSVADILDPTKFTGTTSCIKTRVWHPWVDTSS-----TDSTDLSEKASDTAES		71		
		T+FVSADILDP+KFTG + VW PW S D T A+D +				
Sbjct	520	TAFVSADILDPSKFTGNGGGSRPVWSPWQSQHSPPGGPLAARADGTRSPGVAADARQG		579		
Query	72	K-----DESI-----FEDACDKDDAS-GILEPDDKDVDESGKQKIKSFSSSGSDSGKAGK		120		
		+ D SI F+ D D G D+D DE + + + SDS K GK				
Sbjct	580	QRHDDVSISSQENFDPEEDVDMCEDGKHHTGDEDSDEEKRNADDTGNGNISDSSKQGK		639		
Query	121	PRRARTAFTEQLVALENKFKTTRYLSVCERLNLALSINLTETQVKIWFQNRRTKWKQNP		180		
		PRRARTAFTEQLVALENKFKTTRYLSVCERLNLALSINLTETQVKIWFQNRRTKWKQNP				
Sbjct	640	PRRARTAFTEQLVALENKFKTTRYLSVCERLNLALSINLTETQVKIWFQNRRTKWKQNP		699		
Query	181	PGMDVNSPTIPPSSGALSGFSSPYSSSTTPLYAQGLHPYLQNHNLYGALGLFRTHAASYGA		240		
		PG+DVNSPTIPP+SG FSSPYSS LY Q +HPYL L L + R H +				

Sbjct 700 PGLDVNSPTIPPTSGGFGSFSSPYSSM--LYGQSIHPYLPASGLMSPLSILRAHGYSYSPG 757
 Query 241 QNHIIYYPYFSQTT 254
 QN +YYPYFSQTT
 Sbjct 758 QNPTVYYPYFSQTT 771

lpMSX2

Predicted protein from *Ioligo pealei* transcriptome

TAQKCTLRKHKTNRKPRTPFTTSQLLALERKFR TKQYLSIAERA EFSASLNL TETQVKIWFQNRRAKAKRLHEAE
 LEKLMKMAAKPMLPPALSITFPAAAALYGNQASRPQLIPHALLPPFGFYTTAPSTMIYHH

Msx protein, partial [Heterololigo bleekeri]

Sequence ID: [dbj|BAF91577.1](#)|Length: 114Number of Matches: 1

Range 1: 1 to 114[GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
228 bits(580)	3e-74	Compositional matrix adjust.	113/114(99%)	114/114(100%)	0/114(0%)
Query	21	TTSQLLALERKFR TKQYLSIAERA EFSASLNL TETQVKIWFQNRRAKAKRLHEAELEKLMKMAAKPMLPPALSITFPAAAALYGNQASRPQLIPHALLPPFGFYTTAPSTMIYHH	80		
Sbjct	1	TTSQLLALERKFR TKQYLSIAERA EFSASLNL TETQVKIWFQNRRAKAKRLHEAELEKLMKMAAKPMLPPALSITFPAAAALYGNQASRPQLIPHALLPPFGFYTTAPSTMIYHH	60		
Query	81	MAAKPMLPPALSITFPAAAALYGNQASRPQLIPHALLPPFGFYTTAPSTMIYHH	134		
Sbjct	61	MAAKPMLPPALSITFPAAAALYGSQASRPQLIPHALLPPFGFYTTAPSTMIYHH	114		

MSX2 protein [Homo sapiens]

Sequence ID: [dbj|BAA03611.1](#)|Length: 172Number of Matches: 1

Range 1: 39 to 170[GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
185 bits(470)	1e-58	Compositional matrix adjust.	99/134(74%)	106/134(79%)	7/134(5%)
Query	5	CTLRKHKTNRKPRTPFTTSQLLALERKFR TKQYLSIAERA EFSASLNL TETQVKIWFQNR	64		
Sbjct	39	CTLRKHKTNRKPRTPFTTSQLLALERKFR KQYLSIAERA EFS+SLNL TETQVKIWFQNR	98		
Query	65	RAKAKRLHEAELEKLMKMAAKPMLPPALSITFP-----AAAALYGNQASRPQLIPHALLPP	119		
Sbjct	99	RAKAKRLQEALEKLMKMAAKPMLPSSFSLPPISPLQAASIYG--ASYPFHRPVLPIPP	156		
Query	120	FGFYTTAPSTMIYH 133 G Y T +YH			
Sbjct	157	VGLYATPVGYGMYH 170			

lpZFHX4

Predicted protein from *Ioligo pealei* transcriptome

PPPPPPMPPHHPTSHGSSSSQCAPVSI P S S Q P S S S S S S S S S S H M S E K V L S G Q E M N L P Q N P L D F T Q M M P V F N M M H M
 P V P M N M N L A M G M H P P L M P M M M P P S I E S G F M P P M T M I D P N F L A A Q Q Q A Q H A Q N Q K R A R T R I N D E Q L K I L R A N F D I N
 N S P S E E Q I V Q M S E Q S G L P Q K V I K H W F R N T L F K E R Q R N K D S P Y N F S N P P Q T T I N L E E Y E K T G R I P S P S E Q D L D N E F
 K E E L K S R Y D D Q L D D C D L Q S R I D Q V S S E A D F P C T V T S V P M T F P P T L P I P S P L I N H M P Q T V P N H I T S T P V G H R H I P M
 E F Q E K N D Y F G N N S N N S N S S G S N N S Q G G S G K R A N R T R F T D Y Q I K V L Q E Y F E Q N A Y P K D D D L D H L S K L L N L S P R V I V
 V W F Q N A R Q K A R K I Y E N Q S P A D L K D D G S G N F S R S G P N Y Q Y Q C K K C H S I F P R Y Y D L M K H Q K R Q N C Q D G D K S G T S N M P
 N D E D S N S T V T S H E E T A H S E S G E I N A A E L P K P I S T I A N S N C N S L K E V T A T S T V M A I V P S G V A T T T S A P V A I S T T T S
 S V L S T P P T P T P I S C A G I S N N L P T S L T S G S A G S S S S S S K T E I H K C E K C N L M F P K F E Q W Q E H Q K V H S L N P N L F A N F P
 N D N T F G L L Q N I A P T P P Q Q Q P Q L P P Q H L Q N M L H D K V M T P I K R K A D E E E E E R D Q P R D K R L R T T I L P E Q L D Y L Y Q K Y Q
 I D C N P S R K Q L E T I A S E V G L K K R V V Q V W F Q N T R A R E R K G Q Y R A H Q Q L S H K R C P F C R A L F R A K S A L E S H L A T K H P E E
 M A K G E I N I D N I P D A T V D S T P P P P P P P P V S Q A P S S S S L T G N P D L S K L L S P T N M Q P F L P F M P Q G N M G M G F T G L S D P
 L Q T S M R Q F C E A S F K K F I N E L S A A S H G Q R P Q Q P N V E P P Q N K A A A S E P E K K P A R V I E N K N S E D N D A P L D L S K P I R V N
 T D C E K T S S D G P S T D V S E R S M D G Y L R R H S L D D S I S E T H S E S H E I E G C E D S S G M I D N S P S S P A N A T S S S S S S S H P H G
 K R Y R T Q M S S M Q V R V M K T L F A D Y K T P T M A E C E M L G R E I G L P K R V V Q V W F Q N A R A K E K K N L A Y S K T F G T D V D F S K P
 P E E C T L C N F K Y S H K Y T V Q D H I F T K K H I D N V R Q F I Q S Q S N A E R E L A D P S G M T K M L Q Q Q R E I E R M R K V W D E A S V A S S
 P H L A Q L Q A M R L N A L G L Q G T S S A F N T P F N A S S F F P D V K K E A L K A E G E K K E K E E T Q S R R D A A N F L S P Q L M A P F T G L G
 F E P S L L P N I Y T G F P N F F S G V N L P L F Q F G L M P G M E Q L L A Y D P V T F G T P L S L L Q I P E Q A R R H V S A K L L E P S S V V A Q Y
 T Q D C K T L A D L K S A V S D T D L K C V Q E S T V D V G Y I C K K C H I V Y P G K D G C E N H Q H L I C F P G G K V S D G I K P I L K L E Q V Q Y
 E C V V C Q E K F S T S Q E F I L H C S L E L H K N K S T R H L S K S E W R L A P S L T P A P S E N S A K E A K L P S V S M S T A L T K K Q S P G S D
 K I P L P S S D S M A S A A A T T T P T P T T T A A A A A T A L S S S V Q T Q N V L Q L A

PREDICTED: zinc finger homeobox protein 3-like [*Aplysia californica*]

Sequence ID: [ref|XP_005096810.1|](#) Length: 2638 Number of Matches: 8

Range 1: 1434 to 2515 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1						
Score	Expect	Method	Identities	Positives	Gaps	
849 bits(2193)	0.0	Compositional matrix adjust.	531/1147(46%)	685/1147(59%)	163/1147(14%)	
Query	329	GKRANRTRFTDYQIKVLQEYFEQNAYPKDDDLHLSKLLNLSPRVIVVWFQARQKARKI	388			
Sbjct	1434	GKRANRTRFTD+QIK LQEYFE+NAYPKDD+L+HLSK+L LS RVIVVWFQARQKARKI	1493			
Query	389	YENQSPADLKDDGSGNFSRSGPNYQYQCKKCHSIFPRYYDLMKHQKRONC--QDGDKSGT	446			
Sbjct	1494	YENQ ++ D + F R + P YQCKK+S+F RYY+L+KHQK +C + +	1551			
Query	447	SNMPNDEDSNSTVTSHEETAHSESSEGINAAELPKPISTIANSNCSNLKEVTATSTVMAIV	506			
Sbjct	1552	S+M D+ SN + S+E++ S+ + + + + T R H I P S S A T P ----	1583			
Query	507	PSGVATTTAPVAISTTTSSVLSPTPTPI SCAGISNNLPTSLTSGSAGSSSSSSKTEI	566			
Sbjct	1584	---VRERELMPRALAVETTSISTTPAKPV-LSASAVN---TSSSSPSTPSSSSSSSNPP	1635			
Query	567	HKCEKCNLMFPKFEQWQEHQKVHSLNPNLFANFPNDNTFGLLQNI-----	612			
Sbjct	1636	KC+KC L FP+F+ WQ+HQK HS+ P +F F + + FG+LQ +A FKCDKCTLTFFRDMWQDHQKAHSVAPAMFTPFSSSAFGMLQTLAQEDSKAVFAMAAM	1695			
Query	613	PTPPQQQPQL-----PPQH---LQNMLHDKVMT-----IKRKADEEEERDQPRDKRL	658			
Sbjct	1696	TP P + P H L VM+ KRK D E+E +QPRDKRL STPSSMHPTMVTTPIPA AHQPPAMTTLPTSVMSTSPSPATTKRKT DSEDESSEQPRDKRL	1755			
Query	659	RTTILPEQLDYLYQKYQIDCNPSRKQLETIASEVGLKRRVQVWFQNTARERKGYRAH	718			
Sbjct	1756	RTTILPEQLDYLYQ+YQIDCNPSRKQLE IAS V LKRRVQVWFQNTARERKGYRAH	1815			
Query	719	QQLSHKRCPCRALFRAKSALESHLATHKHP EEMAKGEINIDNIPDATVDSTPPPPPPPP	778			

Sbjct	1816	QQL +KRCPCRALFRAKSALESHLATAKHPEEMAKG+IN+D IPDA ++ PP QQLINKRCPCRALFRAKSALESHLATAKHPEEMAKGDINVDLIPDAMIE-----PPS	1867
Query	779	VSQAPS----SSSLTGN---PDLKLLSP---TNMQPFLPFM--PQGNMGMGFTGLSDPL S APS SS LT PD+SKLL P +M ++ FM G + + F + L	826
Sbjct	1868	SSHAPSLPASSSGLTSTHNTPDISKLLPPGAAASMPNYMSFMSAAAGGLSLPFPAPTADL	1927
Query	827	QTSMRQFCEASFKKFINELSAASHGQRPQQPNVEPPQ-----NAAAASEPEK-- S F + FKK+++EL A + RP+ +V PP + +A S P+	873
Sbjct	1928	-LSHPSFEDPFFKKYMSSEL-AGTMTSRPE--SVAPPLPHSMPRHSASPSISAHSTPKPSH	1983
Query	874	-----KPARVIENKNS-----EDNDAPLDLSKPIRVNTDCEKTSDDGPST +P + K S DAPLDLSKP+R + P +	913
Sbjct	1984	HSSPAPLNFATTSRPLDAHVKVKTSTPIPPASEDAPLDLSKPVSAHPEPSRTEQVPRS	2043
Query	914	-----DVSESRMD-GYLRR-HSLDDSIETHSESHEIEGCEDESSGMIDNSPSSPAN + S+RS++ YLRR +S+DDS SET SE+ + E + + + + PS +	962
Sbjct	2044	FALHHSSGQEQSDRSLELDYLRLNSMDDSFSETQSETADHEYLNE---VNNSPPSPNRS	2100
Query	963	ATSSSSSSSSHPHG-----KRYRTQMSSMQVRVMKTLFADYKTPMAECEMLGREIGLP ++SS+ +H G KRYRTQMS+ QV+VMK LF DYKTPMAECE+LG+EIGL	1015
Sbjct	2101	SSSSNPPQNHRSGNTPGSSTKRYRTQMSATQVKVMKHLFMDYKTPMAECELLGQEIGLA	2160
Query	1016	KRVVQVWFQNAARAKEKKNLAYSKTFGTVDVDFSKPPEECTLCNFKYSHKYTVQDHIPTTK KRVVQVWFQNAARAKEK KL+ K F ++DF K PEEC+LC +KY+HK TVQDHIPTTK	1075
Sbjct	2161	KRVVQVWFQNAARAKEKAKLSSGKPFNAELDFPKSPEECSLCGYKYTHKVTVDHIPTKA	2220
Query	1076	HIDNVRQFIQSQNAERELADPSGMTKMLQQREIERMRKVVDEASVASSPHLAQLQAMR HID V+ F+ ++ ER+L D SG + Q E ER RK+WDE S HLAQLQAM	1135
Sbjct	2221	HIDKVKNFL--SADGERDL-DLSSGSLPSQSSAETERARKMWDE----SGTHLAQLQAMG	2273
Query	1136	L--NALGLQGTSSAFNTPFNASSFFPDVKKKAEKKEKEEETQSRDAANFLSPQLM + +A+G S ++ + S P KK+ AE KE+ Q + A +S Q+M	1193
Sbjct	2274	ISPSAIGFPPLPSGESSKAHEKSESP--KKDKKPAEA-GSSKEQQQVAMEMA--MSAQMM	2328
Query	1194	APFTGL--GFEPSSLNIIYTGFPNFFSGVNLPLFQFGLMPGMEQLLAYDPVTFGTPLSL + G G +PS L +Y G P +F + +P+ Q GL+ G E ++ YDP+ +GTP+LL	1251
Sbjct	2329	SALGGYMPGLDPSYLSYMGGLPGYFPAMGVPVMVQPGLLSGAEHMMGYDPLAYGTPLALL	2388
Query	1252	QIPEQARRHVSAKLLEPSSVVAQYTDQCKTLADLKSASVSDTLKCVQESTVDVGYICKKC QIP A + VS KL E +V+A+YTQDC+ LADL S V+ DL E+T+DVGYICK C	1311
Sbjct	2389	QIPSAAIKSVSDKLSEAGAVLARYTQDCQALADLHVVTAADLTVAEATLDVGYICKTC	2448
Query	1312	HIVYPGKDGECENHQHLICFPG-GKVS DGIKPILKLEQVQYECVVCQEKFSTSQEFILHCS IVYP ++ C HQ +C G G +PI+KLEQVQYEC C ++FST EF HC	1370
Sbjct	2449	QIVYPARESCIAHQRTVCGTGQTRPKGFEPIMKLEQVQYECRACNDRFSTILEFKGHCQ	2508
Query	1371	LELHKNK 1377 E HK +	
Sbjct	2509	QEAHKTR 2515	

Zinc finger homeobox protein 4 [Homo sapiens]

Sequence ID: [dbj|BAD18546.1](#) | Length: 907 | Number of Matches: 5

Range 1: 2 to 392 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Method	Identities	Positives	Gaps	
	204 bits(518)	1e-52	Compositional matrix adjust.	154/406(38%)	197/406(48%)	83/406(20%)	
Query	413		QYQCKKCHSIFPRYYDLMKHQKRQNC---QDGDKSGTSNMPNDEDSNSTVTSHEETAHSE				469
Sbjct	2		QYQCKKC+ +FPR +DL+ HQK+Q C +D D S + D+ V T +				60
Query	470		-----SGEINAEL---PKP----ISTIANSNCSNLKEVTATSTVMAIVPS-				508

		SG + L PKP S K+ + P+	
Sbjct	61	TDAAKNAAAPAASSSGSGTSTPLIPSPKPEPEKTS PKPEYPAEKPKQSDPSPPSQGTKPAL	120
Query	509	GVATTTAPVAISTT-----TSSVLSTPP----TPTP-----ISCAGISNNLPTS	549
		+A+T+S P ST ++ PP TP P IS + N+LP	
Sbjct	121	PLASTSSDPPQASTAQFPQPQPQPPKQQLIGRPPSASQTPVPSSPLQISM TSLQNSLPPQ	180
Query	550	LTSGSAGSSSSSSKTEIHKCEKCNLMFPKFEQWQEHQKVHSL---NPNLFANF---PNDN	603
		L ++C++C + FP E WQEHQ VH L N L + F P D	
Sbjct	181	LLQ-----YQCDQCTVAFPTLELWQEHQHVHFLAAQNQFLHSPFLERPMDM	226
Query	604	TFGLLQNIAPTPPQQ-----QPQLPPQ--HLQNLHDKVMTPIKRKADEEEEE-----	649
		+ + P Q Q+PPQ V +KRK D++E+	
Sbjct	227	PYMI FDPNNPLMTGQLLGS SLTQMPPQASSSHTTAPTVAASLKRKLDDKEDNNCSEKEG	286
Query	650	----RDQPRDKRLRTTILPEQLDYLYQKYQIDCNPSRKQLETIASEVGLK KRVVQVWFQN	705
		DQ RDKRLRTTI PEQL+ LY+KY +D NP+RK L+ IA EVGLK KRVVQVWFQN	
Sbjct	287	GNSGEDQHRDKRLRTTITPEQLEILYEKYL LDSNPTRKMLDHIAREVGLK KRVVQVWFQN	346
Query	706	TRARERKGYRA-HQQLSHKRCPF CRALFRAKSALESHLATHKHP EE 750	
		TRARERKQ+RA SHKRCPF CRALF+AKSALESH+ ++H E	
Sbjct	347	TRARERKGFRAVGP AQSHKRCPF CRALFKAKSALESHIRSRHWNE 392	

lpGSC/lpArx

MKGGREGWLVASKRGKERQNEQIRMMEKQQDCSVSGNVSITENARGSIVCSSSKRPPPCAGTLAESPH
 LHSMQGSYSINGLLASHEGQTLGDNPSPRGTDGTGLTNGFNNSAKYLGYSQSPVATAAAAAALSSKENQ
 TSSTGNGEYQREPSSVGLNHYS DIPYGQQQVKKRQRRYRTTFTSYQLEELEKAFHKTHYPDVFCREEL
 ALRIDLTEARVQVWFQNRRAKWRKQQKQQGDASITQVLHSANAKCGVSGVGGQGPSVGTTL SGLS
 LPNIPPLPNMALPSMYFHSNMAAAAAGMDWPGPPIGGSLAPPQTSMASYMTTPGASAKCDNRL LHSSE
 MPTSIHGLKPVGLLNNQ

Aristaless-like homeobox protein, partial [Sepia officinalis]
 Sequence ID: [gb|AHY00644.1](#) | Length: 217 | Number of Matches: 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
381 bits(978)	4e-129	Compositional matrix adjust.	196/216(91%)	199/216(92%)	1/216(0%)
Query 2		KGREGWLVASKRGKERQNEQIRMMEKQQDCSVSGNVSITENARGSIVCSSSKRPPPCAG	61		
		+GG LV S ER NEQI MEKQ DCS+SGNVS I E+ARGSI CSSSKRPPPC G			
Sbjct 3		EGGEGRCLVVSNGRNERLNEQIGKMEKQ-DCSISGNVSI AEDARGSIACSSSKRPPPC TG	61		
Query 62		TLAESPHLHSMQGSYSINGLLASHEGQTLGDNPSPRGTDGTGLTNGFNNSAKYLGYSQSPV	121		
		TLAESPHLHSMQGSYSINGLLASHEGQTLGDNPSPRGTDGTGLTNGFNNSAKYLGYSQSPV			
Sbjct 62		TLAESPHLHSMQGSYSINGLLASHEGQTLGDNPSPRGTDGTGLTNGFNNSAKYLGYSQSPV	121		
Query 122		ATAAAAAALSSKENQTSSTGNGEYQREPSSVGLNHYS DIPYGQQQVKKRQRRYRTTFTSY	181		
		ATAAAAAALSSKENQTSSTGNGEYQRE SSVGLNHYS DIPYGQQQVKKRQRRYRTTFTSY			
Sbjct 122		ATAAAAAALSSKENQTSSTGNGEYQREQSSVGLNHYS DIPYGQQQVKKRQRRYRTTFTSY	181		
Query 182		QLEELEKAFHKTHYPDVFCREELALRIDLTEARVQV	217		
		QLEELEKAFHKTHYPDVFCREELALRIDLTEARVQV			
Sbjct 182		QLEELEKAFHKTHYPDVFCREELALRIDLTEARVQV	217		

homeobox protein ARX [Homo sapiens]
 Sequence ID: [ref|NP_620689.1](#) | Length: 562 | Number of Matches: 1

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps
135 bits(341)	3e-34	Compositional matrix adjust.	68/102(67%)	77/102(75%)	2/102(1%)
Query 130		LSSKENQTSSTGNGEYQREPSSVGLNHYS DIPYGQQQVKKRQRRYRTTFTSYQLEELEKA	189		
		LS KE + E + SV L+ SD G +KRKQRRYRTTFTSYQLEELE+A			
Sbjct 289		LSPKEELLLHPEDAEGKDGEDSVCL SAGSDSEGL--LKRKQRRYRTTFTSYQLEELERA	346		
Query 190		FHKTHYPDVFCREELALRIDLTEARVQVWFQNRRAKWRKQQK	231		
		F KTHYPDV F REELA+R+DLTEARVQVWFQNRRAKWRK++K			
Sbjct 347		FQKTHYPDVFTREELAMRLDLTEARVQVWFQNRRAKWRKREK	388		

lpPOU6-2

Predicted protein from *Loligo pealei* transcriptome

VLPPTTVSQQPTATRITVAAQSITSHTTTTSEGLPPNVSQLLPNTVSNSTESTTVDGINLDEIKEFAKQFKIRRLS
LGLTQTQVQALSATEGPAYSSAICRFEKLDITPKSAQKIKPVLERWMAEAEERYKNGVQNLTDFIGSEPSKKR
KRRTSFTTPQALEILNQHFENKTHPSGAELTELSENLSYDREVVVRVWFNCNRQALKNTIKLIRIF

PREDICTED: POU domain, class 6, transcription factor 1-like [*Aplysia californica*]

Sequence ID: [ref|XP_005107010.1|](#) Length: 432 Number of Matches: 1

Range 1: 240 to 428 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Method	Identities	Positives	Gaps	
	360 bits(923)	4e-120	Compositional matrix adjust.	169/189(89%)	182/189(96%)	1/189(0%)	
Query	25		SHTTTS-EGLPPNVSQLLPNTVSNSTESTTVDGINLDEIKEFAKQFKIRRLSLGLTQTQV				83
			SH ++S GLPPNVSQLLP+TV NSTESTTVDGINLDEIKEFA+QFKIRRLSLGLTQTQV				
Sbjct	240		SHISSSTNGLPPNVSQLLPHTVGNSTESTTVDGINLDEIKEFARQFKIRRLSLGLTQTQV				299
Query	84		GQALSATEGPAYSSAICRFEKLDITPKSAQKIKPVLERWMAEAEERYKNGVQNLTDFIG				143
			GQALSATEGPAYSSAICRFEKLDITPKSAQKIKPVLERWMAEAEERYKNGVQNLTDFIG				
Sbjct	300		GQALSATEGPAYSSAICRFEKLDITPKSAQKIKPVLERWMAEAEERYKNGVQNLTDFIG				359
Query	144		SEPSKKRKRRTSFTTPQALEILNQHFENKTHPSGAELTELSENLSYDREVVVRVWFNCNRQA				203
			SEPSKKRKRRTSFTTPQALE+LNQ+FE+NTHP+G E+TELSE L+YDREV+RVWFNCNRQA				
Sbjct	360		SEPSKKRKRRTSFTTPQALELLNQYFERNTHPTGTEMTELSERLNYDREVVIRVWFNCNRQA				419
Query	204		LKNTIKLIR 212				
			LKNTIK ++				
Sbjct	420		LKNTIKKLLK 428				

POU domain, class 6, transcription factor 2 [*Homo sapiens*]

Sequence ID: [gb|EAL23992.1|](#) Length: 647 Number of Matches: 1

Range 1: 453 to 626 [GenPeptGraphics](#) Next Match Previous Match

Alignment statistics for match #1

	Score	Expect	Method	Identities	Positives	Gaps	
	307 bits(787)	2e-99	Compositional matrix adjust.	144/177(81%)	161/177(90%)	3/177(1%)	
Query	36		NVSQLLPNTVSNSTESTTVDGINLDEIKEFAKQFKIRRLSLGLTQTQVQALSATEGPAY				95
			+V QL+ N + + E VDG+NL+EI+EFAK FKIRRLSLGLTQTQVQALSATEGPAY				
Sbjct	453		SVGQLVSNPQTAAGE---VDGVNLEEIREFAKAFKIRRLSLGLTQTQVQALSATEGPAY				509
Query	96		SQSAICRFEKLDITPKSAQKIKPVLERWMAEAEERYKNGVQNLTDFIGSEPSKKRKRRTS				155
			SQSAICRFEKLDITPKSAQKIKPVLERWMAEAE R++ G+QNL+FIGSEPSKKRKRRTS				
Sbjct	510		SQSAICRFEKLDITPKSAQKIKPVLERWMAEAEARHRAGMQLNTEFIGSEPSKKRKRRTS				569
Query	156		FTPQALEILNQHFENKTHPSGAELTELSENLSYDREVVVRVWFNCNRQALKNTIKLIR				212
			FTPQALEILN HFEKNTHPSG E+TE++E L+YDREVVVRVWFNCNRQALKNTIK ++				
Sbjct	570		FTPQALEILNAHFEKNTHPSGQEMTEIAEKLNLYDREVVVRVWFNCNRQALKNTIKRLK				626