Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BGA695014

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Blast report description

Nucleotide Sequence (1189 letters)

RID <u>B8BGA695014</u> (Expires on 02-06 12:07 pm)

Query ID lcl|Query_351335

Description None

Molecule type nucleic acid

Query Length 1189

Database Name nr

Description All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

excluding environmental samples from

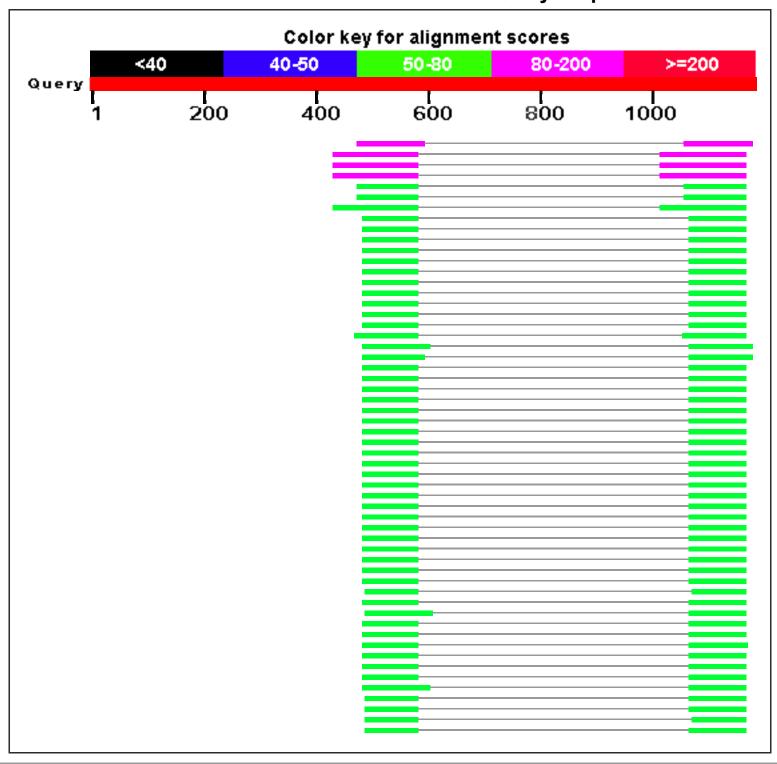
WGS projects

Program BLASTX 2.3.1+

□ Graphic Summary

No putative conserved domains have been detected

Distribution of 200 Blast Hits on the Query Sequence



$\begin{tabular}{ll} \hline \blacksquare \underline{Descriptions} \\ \hline \end{tabular}$

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
hypothetical protein FF38_00987 [Lucilia cuprina]	80.1	160	20%	3e-15	85%	KNC20993.1
PREDICTED: transcription factor Sp4 [Bactrocera cucurbitae]	82.8	164	25%	1e-13	73%	XP_011187312.1
PREDICTED: Krueppel-like factor 7 [Bactrocera dorsalis]	82.8	164	25%	1e-13	73%	XP_011205494.1
PREDICTED: transcription factor Sp4 [Ceratitis capitata]	82.8	164	25%	1e-13	73%	XP_004520626.1
PREDICTED: transcription factor Sp4 [Musca domestica]	79.7	159	18%	1e-12	92%	XP_011296126.1
PREDICTED: probable serine/threonine- protein kinase yakA [Stomoxys calcitrans]	79.7	159	18%	1e-12	92%	XP_013118858.1
PREDICTED: Krueppel-like factor 7 [Bactrocera oleae]	79.3	157	25%	2e-12	71%	XP_014087536.1
GD25946 [Drosophila simulans]	77.4	154	17%	7e-12	100%	XP_002080971.1
uncharacterized protein Dsimw501_GD25946 [Drosophila simulans]	77.4	154	17%	8e-12	100%	KMY92900.1
GM20477 [Drosophila sechellia]	77.4	154	17%	8e-12	100%	XP_002033321.1
luna, isoform B [Drosophila melanogaster]	77.4	154	17%	8e-12	100%	NP_995811.1
uncharacterized protein Dyak_GE13058, isoform A [Drosophila yakuba]	77.0	153	17%	9e-12	100%	XP_002090341.1
uncharacterized protein Dere_GG22702 [Drosophila erecta]	77.0	153	17%	9e-12	100%	XP_001976143.1
GL20646 [Drosophila persimilis]	74.7	149	17%	1e-11	97%	XP_002026405.1
uncharacterized protein Dpse_GA25126 [Drosophila pseudoobscura pseudoobscura]	75.5	150	17%	3e-11	97%	XP_002139002.2
uncharacterized protein Dvir_GJ18175, isoform C [Drosophila virilis]	74.3	148	17%	7e-11	94%	XP_002059288.2
GH20565 [Drosophila grimshawi]	71.6	143	17%	5e-10	91%	XP_001986367.1
uncharacterized protein Dana_GF12443, isoform C [Drosophila ananassae]	70.9	141	17%	9e-10	88%	XP_001958687.2
PREDICTED: Krueppel-like factor 6 [Octopus bimaculoides]	64.7	128	19%	4e-08	74%	XP_014770070.1
conserved hypothetical protein [Pediculus humanus corporis]	59.3	117	19%	1e-07	66%	XP_002430467.1
Krueppel-like factor 7 [Habropoda laboriosa]	59.7	119	19%	1e-07	68%	KOC67104.1
Krueppel-like factor 6 [Harpegnathos saltator]	58.5	116	17%	2e-07	74%	EFN86983.1
hypothetical protein LOTGIDRAFT_126955 [Lottia gigantea]	58.5	117	17%	2e-07	74%	XP_009061298.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Cimex lectularius]	58.9	117	17%	2e-06	74%	XP_014239878.1

PREDICTED: Krueppel-like factor 6 [Halyomorpha halys]	58.5	116	17%	2e-06	74%	XP_014290567.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Nasonia vitripennis]	59.3	118	17%	3e-06	74%	XP_008208238.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Polistes canadensis]	59.3	118	17%	4e-06	74%	XP_014605830.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Dinoponera quadriceps]	58.9	117	17%	4e-06	74%	XP_014480191.1
PREDICTED: Krueppel-like factor 7 [Ceratosolen solmsi marchali]	58.9	117	17%	4e-06	74%	XP_011499687.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Athalia rosae]	58.9	117	17%	4e-06	74%	XP_012264721.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Diachasma alloeum]	58.9	117	17%	4e-06	74%	XP_015127225.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Fopius arisanus]	58.9	117	17%	4e-06	74%	XP_011299771.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Diachasma alloeum]	58.9	117	17%	4e-06	74%	XP_015127226.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Cimex lectularius]	58.5	116	17%	4e-06	74%	XP_014239870.1
PREDICTED: Krueppel-like factor 6 [Orussus abietinus]	58.9	117	17%	4e-06	74%	XP_012279401.1
PREDICTED: LOW QUALITY PROTEIN: Krueppel-like factor 7 [Apis florea]	58.9	117	17%	4e-06	74%	XP_003693621.2
PREDICTED: Krueppel-like factor 6 [Microplitis demolitor]	58.9	117	17%	4e-06	74%	XP_008553910.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Megachile rotundata]	58.9	117	17%	5e-06	74%	XP_012146207.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Bombus terrestris]	58.9	117	17%	5e-06	74%	XP_003396776.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Harpegnathos saltator]	58.9	117	17%	5e-06	74%	XP_011135638.1
PREDICTED: Krueppel-like factor 6 [Lingula anatina]	58.2	115	17%	6e-06	68%	XP_013406198.1
PREDICTED: Krueppel-like factor 6 [Crassostrea gigas]	57.4	114	17%	1e-05	68%	XP_011451658.1
Krueppel-like factor 6 [Camponotus floridanus]	53.1	105	16%	1e-05	69%	EFN71037.1
hypothetical protein BRAFLDRAFT_124706 [Branchiostoma floridae]	55.5	110	17%	3e-05	71%	XP_002588272.1
Krueppel-like factor [Cerapachys biroi]	53.1	105	18%	3e-05	60%	EZA60583.1
PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]	55.8	111	17%	4e-05	65%	XP_013777058.1
PREDICTED: Krueppel-like factor 7 [Polistes dominula]	55.8	111	17%	4e-05	71%	XP_015182091.1
PREDICTED: zinc finger protein 1-like [Aplysia californica]	55.8	111	17%	5e-05	66%	XP_005099170.1
PREDICTED: Krueppel-like factor 6 [Biomphalaria glabrata]	54.3	108	17%	1e-04	65%	XP_013085087.1
PREDICTED: Krueppel-like factor 6 [Acyrthosiphon pisum]	53.9	107	17%	2e-04	65%	XP_003242773.1
PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]	53.9	107	17%	2e-04	68%	XP_013779231.1
hypothetical protein TcasGA2_TC003609 [Tribolium castaneum]	52.4	104	18%	2e-04	56%	EFA00728.1
PREDICTED: Krueppel-like factor 6						

isoform X1 [Wasmannia auropunctata]	53.5	106	16%	3e-04	69%	XP_011697933.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Cerapachys biroi]	53.5	106	16%	3e-04	69%	XP_011352442.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Pogonomyrmex barbatus]	53.1	106	16%	3e-04	69%	XP_011629870.1
PREDICTED: Krueppel-like factor 6 [Vollenhovia emeryi]	53.1	105	16%	3e-04	69%	XP_011872379.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Solenopsis invicta]	53.1	105	16%	3e-04	69%	XP_011168430.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Camponotus floridanus]	53.1	105	16%	3e-04	69%	XP_011252310.1
PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]	53.1	105	17%	3e-04	68%	XP_013780917.1
Uncharacterized protein OBRU01_08947 [Operophtera brumata]	49.7	99.4	17%	3e-04	59%	KOB74566.1
putative Kruppel-like factor 6 [Daphnia pulex]	53.1	105	17%	4e-04	65%	EFX88687.1
hypothetical protein KGM_08804 [Danaus plexippus]	49.3	98.6	20%	5e-04	50%	EHJ66609.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Tribolium castaneum]	52.0	103	17%	6e-04	65%	XP_008192084.1
zinc finger protein [Ciona intestinalis]	52.0	103	17%	6e-04	65%	NP_001071864.1
hypothetical protein RR46_12790 [Papilio xuthus]	47.4	94.0	17%	0.002	56%	KPI96760.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Acromyrmex echinatior]	50.4	100	16%	0.002	66%	XP_011062998.1
PREDICTED: Krueppel-like factor 7 [Amyelois transitella]	49.3	98.2	17%	0.002	56%	XP_013189432.1
PREDICTED: Krueppel-like factor 6-like isoform X1 [Saccoglossus kowalevskii]	49.7	98.6	17%	0.003	59%	XP_002736455.1
PREDICTED: Krueppel-like factor 7-like [Metaseiulus occidentalis]	49.7	99.0	17%	0.003	65%	XP_003748452.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Papilio xuthus]	48.1	95.9	17%	0.006	56%	XP_013179377.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Papilio xuthus]	48.1	95.5	17%	0.006	56%	XP_013179376.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Papilio machaon]	48.1	95.5	17%	0.006	56%	XP_014366548.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Papilio machaon]	48.1	95.5	17%	0.006	56%	XP_014366549.1
PREDICTED: Krueppel-like factor 6 [Papilio polytes]	48.1	95.5	17%	0.006	56%	XP_013147462.1
PREDICTED: Krueppel-like factor 6 [Bombyx mori]	48.5	96.3	17%	0.007	56%	XP_004932855.1
PREDICTED: Krueppel-like factor 6 [Plutella xylostella]	48.5	96.3	17%	0.007	56%	XP_011553149.1
unknown [Homo sapiens]	43.9	86.3	17%	0.024	53%	AAY15081.1
PREDICTED: Krueppel-like factor 7 [Callorhinchus milii]	46.6	92.4	17%	0.029	56%	XP_007898243.1
Kruppel-like factor 7 (ubiquitous) [Homo sapiens]	44.3	87.8	17%	0.029	53%	CC002792.1
hypothetical protein QR98_0081480 [Sarcoptes scabiei]	43.9	87.8	17%	0.033	54%	KPM09609.1
PREDICTED: Krueppel-like factor 6 [Thamnophis sirtalis]	44.3	88.2	17%	0.033	53%	XP_013913916.1
Kruppel-like factor 7 (ubiquitous) [Homo						

sapiens]	43.9	87.0	17%	0.051	53%	CCO02791.1
Bcd orf1 [Homo sapiens]	43.5	86.3	17%	0.057	53%	AAB94792.1
Kruppel-like factor 7 [Strongylocentrotus purpuratus]	45.8	90.9	17%	0.060	59%	NP_001189420.1
PREDICTED: Krueppel-like factor 6 [Clupea harengus]	44.7	89.0	17%	0.060	50%	XP_012695379.1
unnamed protein product [Oncorhynchus mykiss]	45.8	90.9	17%	0.061	56%	CDQ87105.1
PREDICTED: Krueppel-like factor 6 [Salmo salar]	45.4	90.5	17%	0.063	56%	XP_014012942.1
PREDICTED: Krueppel-like factor 7 [Notothenia coriiceps]	45.8	90.9	18%	0.069	47%	XP_010783713.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Latimeria chalumnae]	45.1	89.3	17%	0.10	53%	XP_005996009.1
Klf7l protein [Danio rerio]	43.9	87.4	17%	0.12	50%	AAI50424.1
PREDICTED: Krueppel-like factor 6 [Colius striatus]	44.3	88.2	16%	0.15	55%	XP_010194633.1
Krueppel-like factor 6 [Amazona aestiva]	44.7	88.6	26%	0.16	44%	KQK80056.1
Kruppel-like factor 6, isoform CRA_c [Homo sapiens]	43.5	86.6	17%	0.17	53%	EAW86478.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Anser cygnoides domesticus]	43.9	87.0	17%	0.17	53%	XP_013041223.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Melopsittacus undulatus]	43.9	87.0	17%	0.18	53%	XP_005153078.1
Krueppel-like factor 6-like isoform 1 [Camelus ferus]	43.5	86.3	17%	0.18	53%	EPY86871.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Nipponia nippon]	43.9	87.0	17%	0.19	53%	XP_009474236.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Egretta garzetta]	43.9	87.0	17%	0.19	53%	XP_009639640.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Ficedula albicollis]	43.9	87.0	17%	0.19	53%	XP_005040665.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Opisthocomus hoazin]	43.9	87.0	17%	0.19	53%	XP_009943445.1

□ <u>Alignments</u>

hypothetical protein FF38_00987 [Lucilia cuprina]

Sequence ID: **gb|KNC20993.1|** Length: 47 Number of Matches: 2 Range 1: 2 to 42

Score		Expect	Method	Identities	Positives	Gaps	Frame
80.1 bits	s(196)	3e-15()	Compositional matrix adjust.	35/41(85%)	38/41(92%)	0/41(0%)	+3
Features	s:						
Query	1059		OILPSGNIFSELERICTTGYYSS OILPSGNIFSELERICTTGY+SS		TR 1181		
Sbjct	2		ILPSGNIFSELERICTTGYFSS		•		

Score	Expect	Method	Identities	Positives	Gaps	Frame
80.1 bits(196)	4e-15()	Compositional matrix adjust.	35/41(85%)	38/41(92%)	0/41(0%)	+2

Features:

Query	476	DIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQKPTR	598
~ 1		D+ MDILPSGNIFSELERICTTGY+SSQPSIEDQWQQK +	
Sbict	2	DVNMDILPSGNIFSELERICTTGYFSSOPSIEDOWOOKTVK	42

PREDICTED: transcription factor Sp4 [Bactrocera cucurbitae]

Sequence ID: ref|XP_011187312.1| Length: 596 Number of Matches: 2

▶ See 1 more title(s)

Range 1: 1 to 48

Score		Expect	Method	Identities	Positives	Gaps	Frame
82.8 bits	s(203)	1e-13()	Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+3
Features	S:						
Query	1017	LKTDS +KT+S	LEFLRCEEEDIKMDILPSGNIFSE L+F D+ MDILPSGNIFSE				
Sbjct	1		LDFHSMDLNMDILPSGNIFSE				

Range 2: 1 to 48

Score		Expect Method	Identities	Positives	Gaps	Frame	
82.0 bits	s(201)	2e-13() Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+2	
Features	s:						
Query	434		KTDSLEFLRCEEEDIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ KT+SL+F D+ MDILPSGNIFSELE +CTTGY+SSQPSIEDQWQQ				
Sbjct	1	+KT+SL+F D+ MDILPSGNIFSE MKTESLDFHSMDLNMDILPSGNIFSE					

PREDICTED: Krueppel-like factor 7 [Bactrocera dorsalis]

Sequence ID: ref|XP_011205494.1| Length: 597 Number of Matches: 2

Range 1: 1 to 48

Score		Expect	Method	Identities	Positives	Gaps	Frame
82.8 bits	(203)	1e-13()	Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+3
Features	S :						
Query	1017	LKTDS +KT+S	LEFLRCEEEDIKMDILPSGNIFSI L+F D+ MDILPSGNIFSI				
Sbjct	1		LDFHSMDLNMDILPSGNIFS				

Range 2: 1 to 48

Score		Expect	Method	Identities	Positives	Gaps	Frame
82.0 bits	s(201)	2e-13()	Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+2
Feature	s:						
Query	434	LKTDSL +KT+SL	EFLRCEEEDIKMDILPSGNIFSE L+F D+ MDILPSGNIFSE				
Sbjct	1		DFHSMDLNMDILPSGNIFSE				

PREDICTED: transcription factor Sp4 [Ceratitis capitata]

Sequence ID: ref[XP_004520626.1] Length: 612 Number of Matches: 2

Range 1: 1 to 48

Score	Expect	Method	Identities	Positives	Gaps	Frame
82.8 bits(203)	1e-13()	Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+3
Features:						

Query 1017 LKTDSLEFLRCEEEDIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169

Range 2: 1 to 48

Score		Expect Method	Identities	Positives	Gaps	Frame
82.0 bits	(201)	2e-13() Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+2
Features	3 :					
Query	434	LKTDSLEFLRCEEEDIKMDILPSGNIFSEL +KT+SL+F D+ MDILPSGNIFSEL				
Sbjct	1	MKTESLDFHSMDLNMDILPSGNIFSEL				

PREDICTED: transcription factor Sp4 [Musca domestica]

Sequence ID: ref[XP_011296126.1] Length: 616 Number of Matches: 2

Range 1: 2 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
79.7 bits	s(195)	1e-12()	Compositional matrix adjust.	34/37(92%)	36/37(97%)	0/37(0%)	+3
Features	S :						
Query	1059		OILPSGNIFSELERICTTGYYSSQI OILPSGNIFSELERICTTGY+SSQI		1169		
Sbjct	2		OILPSGNIFSELERICTTGYFSSQI		38		

Range 2: 2 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
79.3 bits	(194)	2e-12()	Compositional matrix adjust.	34/37(92%)	36/37(97%)	0/37(0%)	+2
Features	S :						
Query	476		LPSGNIFSELERICTTGYYSSQPS LPSGNIFSELERICTTGY+SSQPS		86		
Sbjct	2		LPSGNIFSELERICTTGYFSSQP		88		

PREDICTED: probable serine/threonine-protein kinase yakA [Stomoxys calcitrans]

Sequence ID: ref|XP_013118858.1| Length: 620 Number of Matches: 2

Range 1: 2 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
79.7 bits	(195)	1e-12()	Compositional matrix adjust.	34/37(92%)	36/37(97%)	0/37(0%)	+3
Features	s:						
Query	1059		ILPSGNIFSELERICTTGYYSSQI ILPSGNIFSELERICTTGY+SSQI		1169		
Sbjct	2		ILPSGNIFSELERICTTGYFSSQF		38		

Range 2: 2 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
79.3 bits	s(194)	2e-12()	Compositional matrix adjust.	34/37(92%)	36/37(97%)	0/37(0%)	+2
Features	s:						
Query	476		DILPSGNIFSELERICTTGYYSSQPSIEDQWQQ DILPSGNIFSELERICTTGY+SSQPSIEDQWQQ		86		
Sbjct	2		LPSGNIFSELERICTTGYFSSQP:		88		

PREDICTED: Krueppel-like factor 7 [Bactrocera oleae]

Sequence ID: ref|XP_014087536.1| Length: 599 Number of Matches: 2

Range	1:	1	to	48
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Score		Expect	Method	Identities	Positives	Gaps	Frame
79.3 bits	(194)	2e-12()	Compositional matrix adjust.	36/51(71%)	42/51(82%)	3/51(5%)	+3
Features	S:						
Query	1017	LKTDS +KT+	LEFLRCEEEDIKMDILPSGNIFS: L+F D+ MDILPSGNIFS:				
Sbjct	1		LDFHGMDLNMDILPSGNIFS				

Range 2: 1 to 48

Score		Expect	Method	Identities	Positives	Gaps	Frame
78.6 bits	s(192)	3e-12()	Compositional matrix adjust.	36/51(71%)	42/51(82%)	3/51(5%)	+2
Features	S :						
Query	434	LKTDSL +KT+ L	EFLRCEEEDIKMDILPSGNIFSEI +F D+ MDILPSGNIFSEI				
Sbjct	1		DFHGMDLNMDILPSGNIFSEI				

GD25946 [Drosophila simulans]

Sequence ID: ref|XP_002080971.1| Length: 569 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
77.4 bits	s(189)	7e-12()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+3
Feature	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPS PSGNIFSELERICTTGYYSSQPS		69		
Shict	1		PSGNIFSELERICTTGYYSSOPS	~ ~~			

Range 2: 1 to 34

Score		Expect	Method	Identitie	S	Positives	Gaps	Frame
77.0 bits	(188)	1e-11()	Compositional matrix adjust.	34/34(1	00%)	34/34(100%)	0/34(0%)	+2
Features	S :							
Query	485		GGNIFSELERICTTGYYSSQPSIE GGNIFSELERICTTGYYSSQPSIE		586			
Sbjct	1		GGNIFSELERICTTGYYSSQPSII		34			

uncharacterized protein Dsimw501_GD25946 [Drosophila simulans]

Sequence ID: **gb|KMY92900.1|** Length: 568 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
77.4 bits	(189)	8e-12()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+3
Features	S:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIFSELERICTTGYYSSQPSI		69		
Sbjct	1		PSGNIFSELERICTTGYYSSQPSI				

Score	Expect	Method	Identities	Positives	Gaps	Frame
77.0 bits(188)	1e-11()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+2

Features:

Query 485 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Sbjct 1 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 34

GM20477 [Drosophila sechellia]

Sequence ID: ref|XP_002033321.1| Length: 570 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities		Positives	Gaps	Frame
77.4 bits	s(189)	8e-12()	Compositional matrix adjust.	34/34(100)%)	34/34(100%)	0/34(0%)	+3
Feature	s:							
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIFSELERICTTGYYSSQPSI		116	59		
Sbjct	1		PSGNIFSELERICTTGYYSSQPSI		34			

Range 2: 1 to 34

Score		Expect	Method	Identitie	S	Positives	Gaps	Frame
77.0 bits	s(188)	1e-11()	Compositional matrix adjust.	34/34(10	00%)	34/34(100%)	0/34(0%)	+2
Features	S :							
Query	485		SGNIFSELERICTTGYYSSQPSIE SGNIFSELERICTTGYYSSQPSIE		586			
Sbjct	1		SGNIFSELERICTTGYYSSQPSIE		34			

luna, isoform B [Drosophila melanogaster]

Sequence ID: ref|NP_995811.1| Length: 570 Number of Matches: 2

▶ See 8 more title(s) Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
77.4 bits	s(189)	8e-12()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIFSELERICTTGYYSSQPSI		69		
Sbjct	1		SGNIFSELERICTTGYYSSQPS1				

Range 2: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
77.0 bits	s(188)	1e-11()	Compositional matrix adjust.	34/34(10	00%)	34/34(100%)	0/34(0%)	+2
Features	S :							
Query	485		SGNIFSELERICTTGYYSSQPSIE SGNIFSELERICTTGYYSSQPSIE		586			
Sbjct	1		GGNIFSELERICTTGYYSSQPSIE		34			

uncharacterized protein Dyak_GE13058, isoform A [Drosophila yakuba] Sequence ID: ref[XP_002090341.1] Length: 576 Number of Matches: 2

See 3 more title(s)

Score	Expect Method	Identities	Positives	Gane	Frame
Score	Expect Method	เนยแนเยร	FUSILIVES	Gaps	i i aiiie

77.0 bits(188) 9e-12() Compositional matrix adjust. 34/34(100%) 34/34(100%) 0/34(0%) +3

Features:

MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 1068 1169 Sbjct 1 34

Range 2: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
76.6 bits	s(187)	1e-11()	Compositional matrix adjust.	34/34(1	00%)	34/34(100%)	0/34(0%)	+2
Features	S :							
Query	485		GGNIFSELERICTTGYYSSQPSIE GGNIFSELERICTTGYYSSQPSIE		586			
Sbjct	1		SGNIFSELERICTTGYYSSQPSIE		34			

uncharacterized protein Dere_GG22702 [Drosophila erecta]

Sequence ID: ref[XP_001976143.1] Length: 562 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
77.0 bits	s(188)	9e-12()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPS PSGNIFSELERICTTGYYSSQPS		69		
Sbjct	1		PSGNIFSELERICTTGYYSSQPS				

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
76.6 bits	s(187)	1e-11() Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+2
Features	s:					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSI MDILPSGNIFSELERICTTGYYSSQPSI				
Sbjct	1	MDILPSGNIFSELERICTTGYYSSQPSI				

GL20646 [Drosophila persimilis]

Sequence ID: ref[XP_002026405.1] Length: 255 Number of Matches: 2

▶ See 1 more title(s) kange 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
74.7 bit	s(182)	1e-11()	Compositional matrix adjust.	33/34(97%	34/34(100%)	0/34(0%)	+3
Feature	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPS1 PSGNIFSELERICTTGY+SSQPS1		169		
Sbjct	1		SGNIFSELERICTTGYFSSQPS1		4		

Score		Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	1e-11()	Compositional matrix adjust.	33/34(97%) 34/34(100%)	0/34(0%)	+2
Features:							
Query 4	485	MDILPS	GNIFSELERICTTGYYSSQPSIE	DQWQQ 58	6		

MDILPSGNIFSELERICTTGY+SSQPSIEDQWQQ Sbjct 1 MDILPSGNIFSELERICTTGYFSSQPSIEDQWQQ 34

uncharacterized protein Dpse_GA25126 [Drosophila pseudoobscura pseudoobscura]

Sequence ID: ref[XP_002139002.2] Length: 543 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
75.5 bits	s(184)	3e-11()	Compositional matrix adjust.	33/34(97%)	34/34(100%)	0/34(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIFSELERICTTGY+SSQPSI		69		
Shict	1		PSCNTFSELERTCTTGYFSSOPST				

Range 2: 1 to 34

Score		Expect	Method	Identiti	es	Positives	Gaps	Frame
75.1 bits	s(183)	4e-11()	Compositional matrix adjust.	33/34(9	97%)	34/34(100%)	0/34(0%)	+2
Features	3 :							
Query	485		GNIFSELERICTTGYYSSQPSIE GNIFSELERICTTGY+SSQPSIE		586			
Sbjct	1		GNIFSELERICTTGYFSSQPSIE		34			

uncharacterized protein Dvir_GJ18175, isoform C [Drosophila virilis] Sequence ID: **ref[XP_002059288.2**] Length: 558 Number of Matches: 2

See 3 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits	s(181)	7e-11()	Compositional matrix adjust.	32/34(94%)	34/34(100%)	0/34(0%)	+3
Features	S :						
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIF+ELERICTTGY+SSQPSI		69		
Sbjct	1		SGNIFNELERICTTGYFSSQPSI				

Range 2: 1 to 34

Score		Expect	Method	Identiti	es	Positives	Gaps	Frame
73.9 bits	(180)	9e-11()	Compositional matrix adjust.	32/34(9	94%)	34/34(100%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIE GNIF+ELERICTTGY+SSQPSIE		586			
Sbjct	1		GNIFNELERICTTGYFSSÕPSIE		34			

GH20565 [Drosophila grimshawi]

Sequence ID: ref|XP_001986367.1| Length: 595 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
71.6 bits(174)	5e-10()	Compositional matrix adjust.	31/34(91%)	33/34(97%)	0/34(0%)	+3

Features:

Query	1068	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ	1169
_		MDILPSG IF+ELERICTTGY+SSQPSIEDQWQQ	
Sbict	1	MDILPSGTIFNELERICTTGYFSSOPSIEDOWOO	34

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
71.6 bits	s(174)	6e-10()	Compositional matrix adjust.	31/34(91%)	33/34(97%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEDQWQQ		586			
Sbjct	1		G IF+ELERICTTGY+SSQPSIEI GTIFNELERICTTGYFSSQPSIEI		34			

uncharacterized protein Dana_GF12443, isoform C [Drosophila ananassae] Sequence ID: **ref|XP_001958687.2|** Length: 559 Number of Matches: 2

See 3 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
70.9 bits	s(172)	9e-10()	Compositional matrix adjust.	30/34(88%)	32/34(94%)	0/34(0%)	+3
Feature	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF+ELE IC TGY+SSQPSI		59		
Sbjct	1		SGNIFNELEHICNTGYFSSQPSI				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
70.5 bits	s(171)	1e-09()	Compositional matrix adjust.	30/34(88%)	32/34(94%)	0/34(0%)	+2
Features	s:							
Query	485		PSGNIFSELERICTTGYYSSQPSIEDQWQQ PSGNIF+ELE IC TGY+SSQPSIEDQWQQ		586			
Sbjct	1		GNIFNELEHICNTGYFSSÕPSIED GNIFNELEHICNTGYFSSÕPSIED		34			

PREDICTED: Krueppel-like factor 6 [Octopus bimaculoides]

Sequence ID: ref|XP_014770070.1| Length: 289 Number of Matches: 2

Range 1: 3 to 40

Score		Expect	Method	Identities	Positives	Gaps	Frame
64.7 bits	(156)	4e-08()	Compositional matrix adjust.	28/38(74%)	33/38(86%)	0/38(0%)	+3
Features	S :						
Query	1056		DILPSGNIFSELERICTTGYYSS DILPSGNIF EL+ + TGY+SS		1169		
Sbjct	3		DILPSGNIFRELQVVHETGYFSS		40		

Score		Expect Method	Identities	Positives	Gaps	Frame
63.9 bits	s(154)	6e-08() Compositional matrix adjust.	28/38(74%)	33/38(86%)	0/38(0%)	+2
Features	s:					
Query	473	EDIKMDILPSGNIFSELERICTTGYYSSQ EDI MDILPSGNIF EL+ + TGY+SSQ				
Sbjct	3	EDIAMDILPSGNIFRELQVVHETGYFSSQ		40		

conserved hypothetical protein [Pediculus humanus corporis]

Sequence ID: ref|XP_002430467.1| Length: 52 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 41

Score		Expect	Method	Identities	Positives	Gaps	Frame
59.3 bits	s(142)	1e-07()	Compositional matrix adjust.	27/41(66%)	31/41(75%)	0/41(0%)	+2
Feature	s:						
Query	485		GNIFSELERICTTGYYSSQPSIE		P 607		
Sbjct	1		GNIFRELQTIHDTGYFSSEPSLE		_		

Range 2: 1 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	2e-07()	Compositional matrix adjust.	26/38(68%)	30/38(78%)	0/38(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+SS+PS+		1181		
Sbjct	1		SGNIFRELQTIHDTGYFSSEPSL		38		

Krueppel-like factor 7 [Habropoda laboriosa]

Sequence ID: **gb|KOC67104.1|** Length: 82 Number of Matches: 2 Range 1: 1 to 38

Score		Expect Method	Identities	Positives	Gaps	Frame
59.7 bits	s(143)	1e-07() Compositional matrix adjust.	26/38(68%)	30/38(78%)	0/38(0%)	+3
Features	3:					
Query	1068	MDILPSGNIFSELERICTTGYYSSQPSI MDILPSGNIF EL+ I TGY+S+QPS+		1181		
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSI		38		

Range 2: 1 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
59.7 bits	s(143)	2e-07()	Compositional matrix adjust.	26/38(68%)	30/38(78%)	0/38(0%)	+2
Features	s:						
Query	485		GNIFSELERICTTGYYSSQPSIE		598		
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		38		

Krueppel-like factor 6, partial [Harpegnathos saltator]

Sequence ID: gb|EFN86983.1| Length: 34 Number of Matches: 2

Score		Expect	Method	Identities	Positives	Gaps	Frame	
58.5 bits	(140)	2e-07()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3	
Features	:							
Query	1068		SGNIFSELERICTTGYYSSQPSIE SGNIF EL+ I TGY+S+QPS+E		69			
Sbict.	1		SGNIFRELODIHDTGYFSAOPSLE	~~				

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
58.2 bits	(139)	2e-07()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		586			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI		34			

hypothetical protein LOTGIDRAFT_126955 [Lottia gigantea]

Sequence ID: ref|XP_009061298.1| Length: 50 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	2e-07()	Compositional matrix adjust.	25/34(74%)	30/34(88%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIF EL+ + TGY+SSQPS+		59		
Sbjct	1		SGNIFRELQVVHDTGYFSSQPSL				

Range 2: 1 to 34

Score		Expect	Method	Identi	ties	Positives	Gaps	Frame
58.5 bits	s(140)	2e-07()	Compositional matrix adjust.	25/34((74%)	30/34(88%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIE GNIF EL+ + TGY+SSQPS+E		586			
Sbjct	1		GNIF ELT TIGITSSOFSTE GNIFRELQVVHDTGYFSSQPSLE		34			

PREDICTED: Krueppel-like factor 7 isoform X2 [Cimex lectularius]

Sequence ID: ref|XP_014239878.1| Length: 233 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	2e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSII SGNIF EL+ I TGY+S+QPS+I		69		
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSLI				

Range 2: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
58.5 bits	(140)	2e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		586			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI		34			

PREDICTED: Krueppel-like factor 6 [Halyomorpha halys]

Sequence ID: ref|XP_014290567.1| Length: 252 Number of Matches: 2

Score	Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits(140)	2e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3

Features:

Query	1068	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ	1169
2 1		MDILPSGNIF EL+ I TGY+S+OPS+ED WOO	
		MDILESGNIE EL! I IGI'S'QES'ED WQQ	
Sbjct	1	MDILPSGNIFRELQDIHETGYFSAQPSLEDHWQQ	34

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
58.2 bits	(139)	3e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	S :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MDILPSGNIF EL+ I TGY+S+QPS+E				
Sbjct	1	MDILPSGNIFRELQDIHETGYFSAQPSLE				

PREDICTED: Krueppel-like factor 7 isoform X1 [Nasonia vitripennis]

Sequence ID: ref|XP_008208238.1| Length: 383 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
59.3 bits	s(142)	3e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Feature	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIF EL' I IGITS OFST SGNIFRELQDIHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect	Method	Identities		Positives	Gaps	Frame
58.9 bits	s(141)	4e-06()	Compositional matrix adjust.	25/34(74%	%)	29/34(85%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSOPSIE GNIF EL+ I TGY+S+OPS+E		36			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		1			

PREDICTED: Krueppel-like factor 6 isoform X1 [Polistes canadensis] Sequence ID: **ref|XP_014605830.1|** Length: 378 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
59.3 bits	s(142)	4e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features:							
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIF ELT 1 1G1151QF51				

Score		Expect Method	Identities	Positives	Gaps	Frame	
58.9 bits	s(141)	4e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2	
Feature	s:						
Query	485	MDILPSGNIFSELERICTTGYYSSQPSII MDILPSGNIF EL+ I TGY+S+QPS+1					
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSLI					

PREDICTED: Krueppel-like factor 6 isoform X1 [Dinoponera quadriceps] Sequence ID: ref|XP_014480191.1| Length: 320 Number of Matches: 2

Range 1: 1 to 34

Score	Expect Method	Identities	Positives	Gaps	Frame
58.9 bits(14°) 4e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features:					
Query 10	8 MDILPSGNIFSELERICTTGYYSSQPSI MDILPSGNIF EL+ I TGY+S+QPS+		59		
Sbjct 1	MDILPSGNIF ELV I IGITSTOFST MDILPSGNIFRELQDIHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
58.5 bits	(140)	5e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	s:					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MDILPSGNIF EL+ I TGY+S+QPS+E				
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSLE				

PREDICTED: Krueppel-like factor 7 [Ceratosolen solmsi marchali]

Sequence ID: ref|XP_011499687.1| Length: 382 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	4e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	5e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	S :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MDILPSGNIF EL+ I TGY+S+QPS+E				
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSLE				

PREDICTED: Krueppel-like factor 7 isoform X1 [Athalia rosae]

Sequence ID: **ref|XP_012264721.1|** Length: 378 Number of Matches: 2 Range 1: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	4e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	s:					
Query	1068	MDILPSGNIFSELERICTTGYYSSQPSI MDILPSGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSI				

Score	Expect Method	Identities	Positives	Gaps	Frame

58.5 bits(140) 5e-06() Compositional matrix adjust. 25/34(74%) 29/34(85%) 0/34(0%) +2

Features:

Query 485 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

PREDICTED: Krueppel-like factor 7 isoform X1 [Diachasma alloeum] Sequence ID: **ref[XP_015127225.1**] Length: 383 Number of Matches: 2

Range 1: 1 to 34

Score Expect Method Identities Positives Frame Gaps 25/34(74%) 29/34(85%) 0/34(0%) 58.9 bits(141) 4e-06() Compositional matrix adjust. +3 Features: 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 Query

MDILPSGNIF EL+ I TGY+S+QPS1EDQWQQ 1109 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

Range 2: 1 to 34

Score **Expect Method** Identities **Positives** Gaps Frame 5e-06() Compositional matrix adjust. 58.5 bits(140) 25/34(74%) 29/34(85%) 0/34(0%) +2Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 Query 485 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 34 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ

PREDICTED: Krueppel-like factor 7 isoform X1 [Fopius arisanus]

Sequence ID: ref|XP_011299771.1| Length: 383 Number of Matches: 2

Range 1: 1 to 34

Score **Expect Method** Identities **Positives** Gaps Frame 0/34(0%) 58.9 bits(141) 4e-06() Compositional matrix adjust. 25/34(74%) 29/34(85%) +3 Features: 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ

Range 2: 1 to 34

Score Identities **Expect Method Positives Frame** Gaps 58.5 bits(140) 6e-06() Compositional matrix adjust. 25/34(74%) 29/34(85%) 0/34(0%) +2 Features: Query MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 485 586 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ Sbjct 34

PREDICTED: Krueppel-like factor 6 isoform X2 [Diachasma alloeum]

Sequence ID: ref|XP 015127226.1| Length: 375 Number of Matches: 2

Range 1: 1 to 34

ScoreExpectMethodIdentitiesPositivesGapsFrame58.9 bits(141)4e-06()Compositional matrix adjust.25/34(74%)29/34(85%)0/34(0%)+3Features:

Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169

Score		Expect Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	6e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	s:					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MDILPSGNIF EL+ I TGY+S+QPS+E				
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSLE				

PREDICTED: Krueppel-like factor 6 isoform X1 [Cimex lectularius]
Sequence ID: **ref|XP_014239870.1**| Length: 296 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame	
58.5 bits	s(140)	4e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3	
Features	Features:							
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		69			
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSL					

Range 2: 1 to 34

Score		Expect	Method	Identities	6	Positives	Gaps	Frame
58.2 bits	s(139)	6e-06()	Compositional matrix adjust.	25/34(74	%)	29/34(85%)	0/34(0%)	+2
Features	s:							
Query	485		ILPSGNIFSELERICTTGYYSSQPSIEDQWQQ ILPSGNIF EL+ I TGY+S+QPS+ED WQQ		86			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		4			

PREDICTED: Krueppel-like factor 6 [Orussus abietinus]

Sequence ID: ref|XP_012279401.1| Length: 378 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	4e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	6e-06() Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	3 :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPS MDILPSGNIF EL+ I TGY+S+QPS-				
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSI				

PREDICTED: LOW QUALITY PROTEIN: Krueppel-like factor 7 [Apis florea] Sequence ID: **ref|XP_003693621.2|** Length: 374 Number of Matches: 2

Range 1: 1 to 34

Score		Expect N	Method	Identities	Positives	Gaps	Frame
58.9 bits	(141)	4e-06() C	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	:						
Query	1068		GNIFSELERICTTGYYSSQPSI GNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		GNIF ELT I IGITSTOFST. GNIFRELQDIHDTGYFSAQPSL:				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
58.5 bits	s(140)	6e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIED GNIF EL+ I TGY+S+QPS+ED		586			
Sbjct	1		SNIFRELQDIHDTGYFSAQPSLED		34			

PREDICTED: Krueppel-like factor 6 [Microplitis demolitor]

Sequence ID: ref|XP_008553910.1| Length: 378 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	4e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect	Method	Identiti	es	Positives	Gaps	Frame
58.5 bits	s(140)	6e-06()	Compositional matrix adjust.	25/34(7	'4%)	29/34(85%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIE GNIF EL+ I TGY+S+QPS+E		586			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X1 [Megachile rotundata]
Sequence ID: **ref|XP_012146207.1**| Length: 378 Number of Matches: 2
Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	5e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSL				

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits	(140)	6e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	:						
Query	485	MDILPS	GNIFSELERICTTGYYSSQPSIED	OQWQQ 586			

MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

PREDICTED: Krueppel-like factor 6 isoform X1 [Bombus terrestris]

Sequence ID: ref|XP_003396776.1| Length: 378 Number of Matches: 2

See 1 more title(s)

Range 1: 1 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits(141)	5e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3

Features:

Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
58.5 bits	s(140)	6e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIE GNIF EL+ I TGY+S+QPS+E		586			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X1 [Harpegnathos saltator] Sequence ID: **ref|XP_011135638.1**| Length: 377 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	5e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+QPS+		59		
Sbjct	1		SGNIFRELQDIHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
58.5 bits	(140)	6e-06()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+2
Features	3 :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		586			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI		34			

PREDICTED: Krueppel-like factor 6 [Lingula anatina]

Sequence ID: ref|XP_013406198.1| Length: 283 Number of Matches: 2

Score		Expect	Method	Identities	S	Positives	Gaps	Frame
58.2 bits((139)	6e-06()	Compositional matrix adjust.	23/34(68	8%)	30/34(88%)	0/34(0%)	+3
Features:								
Query	1068		SGNIFSELERICTTGYYSSQPSIE SGNIF EL+ + TGY+S+QPS+E		116	9		
Sbjct	1		SGNIFRELQVVHDTGYFSAQPSLE		34			

Score		Expect	Method	Identit	ties	Positives	Gaps	Frame
57.8 bits	s(138)	7e-06()	Compositional matrix adjust.	23/34(68%)	30/34(88%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ + TGY+S+QPS+EI		586			
Sbjct	1		GNIFRELQVVHDTGYFSAQPSLEI		34			

PREDICTED: Krueppel-like factor 6 [Crassostrea gigas]

Sequence ID: ref|XP_011451658.1| Length: 337 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
57.4 bits	s(137)	1e-05()	Compositional matrix adjust.	23/34(68%)	30/34(88%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ + TGY+S+QPS+		59		
Sbjct	1		SGNIFRELQVVHDTGYFSAQPSL				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
57.0 bits	s(136)	2e-05()	Compositional matrix adjust.	23/34(68%)	30/34(88%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIE GNIF EL+ + TGY+S+QPS+E		586			
Sbjct	1		GNIFRELQVVHDTGYFSAQPSLE		34			

Krueppel-like factor 6, partial [Camponotus floridanus]

Sequence ID: **gb|EFN71037.1**| Length: 32 Number of Matches: 2 Range 1: 1 to 32

Score		Expect	Method	Ident	tities	Positives	Gaps	Frame
53.1 bits	(126)	1e-05()	Compositional matrix adjust.	22/32	2(69%)	27/32(84%)	0/32(0%)	+3
Features	s:							
Query	1074		NIFSELERICTTGYYSSQPSIEDONIF EL+ I TGY+S+QPS+ED		1169			
Sbjct	1		NIFRELQDIHDTGYFSAQPSLED		32			

Range 2: 1 to 32

Score		Expect	Method	ldent	ities	Positives	Gaps	Frame
52.8 bits	s(125)	2e-05()	Compositional matrix adjust.	22/32	2(69%)	27/32(84%)	0/32(0%)	+2
Feature	s:							
Query	491		IFSELERICTTGYYSSQPSIEDQI IF EL+ I TGY+S+QPS+ED I		586			
Sbjct	1		IFRELQDIHDTGYFSAQPSLEDH		32			

hypothetical protein BRAFLDRAFT_124706 [Branchiostoma floridae] Sequence ID: ref|XP_002588272.1| Length: 267 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
55.5 bits	(132)	3e-05()	Compositional matrix adjust.	24/34(7	1%)	28/34(82%)	0/34(0%)	+3
Features	3 :							
Query	1068		SGNIFSELERICTTGYYSSQPS SG IFSEL+ I TGY+S QPS-		116	59		
Sbict	1		SGEIFSELT I IGITS QPS SGEIFSELOMIHDTGYFSCOPSI	~~	34			

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
55.1 bits	s(131)	5e-05()	Compositional matrix adjust.	24/34(71%)	28/34(82%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI G IFSEL+ I TGY+S QPS+EI		586			
Sbjct	1		GEIFSELQMIHDTGYFSCQPSLEI		34			

Krueppel-like factor [Cerapachys biroi]

Sequence ID: **gb|EZA60583.1|** Length: 92 Number of Matches: 2 Range 1: 4 to 40

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-05() Composition-based stats.	24/40(60%)	31/40(77%)	3/40(7%)	+2
Features	S :					
Query	491	ILPSGNIFSELERICTTGYYSSQPSIE +LPSGNIF EL+ I TGY+S+QPS+E				
Sbjct	4	LLPSGNIFRELQDIHDTGYFSAQPSLE				

Range 2: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
52.8 bits	s(125)	5e-05()	Compositional matrix adjust.	24/35(69%) 29/35(82%)	1/35(2%)	+3
Features	S :						
Query	1068		PSGNIFSELERICTTGYYSSQPS PSGNIF EL+ I TGY+S+QPS		1169		
Sbjct	1		PSGNIFRELQDIHDTGYFSAQPS		35		

PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]

Sequence ID: **ref|XP_013777058.1**| Length: 374 Number of Matches: 2 Range 1: 24 to 57

Score		Expect Method	Identities	Positives	Gaps	Frame
55.8 bits	s(133)	4e-05() Compositional matrix adju	ust. 22/34(65%)	29/34(85%)	0/34(0%)	+3
Feature	s:					
Query	1068	MDILPSGNIFSELERICTTGYYSS MD+LPSG IF EL+ + TGY+S+		59		
Sbjct	24	MDVLPSGGIFGELQVVHDTGYFSA				

Range 2: 24 to 57

Score	Expect Method	Identities	Positives	Gaps	Frame
55.5 bits(132)	5e-05() Compositional matrix adjust.	22/34(65%)	29/34(85%)	0/34(0%)	+2
Features:					
Query 485	MDILPSGNIFSELERICTTGYYSSQPSIE MD+LPSG IF EL+ + TGY+S+QPS+E				

Sbjct 24 MDVLPSGGIFGELQVVHDTGYFSAQPSLEDRWQQ 57

PREDICTED: Krueppel-like factor 7 [Polistes dominula]

Sequence ID: ref|XP_015182091.1| Length: 378 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
55.8 bits	s(133)	4e-05()	Compositional matrix adjust.	24/34(71%)	28/34(82%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+Q S+		59		
Sbjct	1		SGNIFRELQLIHDTGYFSAQASL				

Range 2: 1 to 34

Score		Expect N	Method	Identit	ies	Positives	Gaps	Frame
55.5 bits	s(132)	6e-05() C	Compositional matrix adjust.	24/34(71%)	28/34(82%)	0/34(0%)	+2
Features	s:							
Query	485		SGNIFSELERICTTGYYSSQPSIEDQWQQ SGNIF EL+ I TGY+S+Q S+ED WQQ		586			
Sbjct	1		NIF ELT I IGITSTO STED NIFRELQLIHDTGYFSAQASLED		34			

PREDICTED: zinc finger protein 1-like [Aplysia californica]

Sequence ID: ref|XP_005099170.1| Length: 513 Number of Matches: 2

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
55.8 bits	s(133)	5e-05()	Compositional matrix adjust.	23/35(66%)	29/35(82%)	0/35(0%)	+3
Features	S:						
Query	1068		SGNIFSELERICTTGYYSSQPSII S NIF EL+ + TGY+S+QPS+I		172		
Sbjct	1		SSNIFRELQVVHDTGYFSAQPSLI		5		

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
55.5 bits	s(132)	6e-05()	Compositional matrix adjust.	23/34(68%)	29/34(85%)	0/34(0%)	+2
Features	S :							
Query	485		OILPSGNIFSELERICTTGYYSSQPSIEDQW OILPS NIF EL+ + TGY+S+QPS+ED+W		586			
Sbjct	1		SNIFRELQVVHDTGYFSAQPSLE		34			

PREDICTED: Krueppel-like factor 6 [Biomphalaria glabrata]

Sequence ID: ref|XP_013085087.1| Length: 425 Number of Matches: 2

Score		Expect	Method	Identities	Positives	Gaps	Frame
54.3 bits	s(129)	1e-04()	Compositional matrix adjust.	22/34(65%)	29/34(85%)	0/34(0%)	+3
Features	S:						
Query	1068		SGNIFSELERICTTGYYSSOPSIE + NIF EL+ + TGY+S+OPS+E		59		
Sbjct	1		TSNIFRELQVVHETGYFSAQPSLE				

Score		Expect Method Identities Positives	Gaps	Frame
54.3 bits	(129)	e-04() Compositional matrix adjust. 22/34(65%) 29/34(85%) 0	0/34(0%)	+2
Features	s:			
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 MDILP+ NIF EL+ + TGY+S+QPS+ED+WQQ		
Sbjct	1	MDILPTSNIFRELQVVHETGYFSAQPSLEDRWQQ 34		

PREDICTED: Krueppel-like factor 6 [Acyrthosiphon pisum]

Sequence ID: ref|XP_003242773.1| Length: 350 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame	
53.9 bits	s(128)	2e-04()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+3	
Features:								
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ I TGY+S+ S+1		59			
Sbjct	1		SGNIFRELQDIHDTGYFSAHVSL					

Range 2: 1 to 34

Score		Expect Meth	hod	Identiti	ies	Positives	Gaps	Frame
53.5 bits	s(127)	2e-04() Com	npositional matrix adjust.	22/34(6	65%)	27/34(79%)	0/34(0%)	+2
Features	s:							
Query	485		MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MD+LPSGNIF EL+ I TGY+S+ S+ED WOO					
Sbjct	1		FRELQDIHDTGYFSAHVSLED	~~	34			

PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]

Sequence ID: ref|XP_013779231.1| Length: 334 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame	
53.9 bits	(128)	2e-04()	Compositional matrix adjust.	23/34(68%)	28/34(82%)	0/34(0%)	+3	
Features:								
Query	1068		GGNIFSELERICTTGYYSSQPSIEDQWQQ GGNIF EL+ + TG++SSQ S+ED WQQ GGNIFRELQTVHDTGFFSSQLSLEDMWQQ		69			
Sbjct	1							

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-04() Compositional matrix adjust.	23/34(68%)	28/34(82%)	0/34(0%)	+2
Features	S :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIEMDILPSGNIF EL+ + TG++SSQ S+EMDILPSGNIF EL+ + TG++SQ S+S-EMDILPSGNIF				
Sbjct	1	MDILPSGNIFRELQTVHDTGFFSSQLSLE				

hypothetical protein TcasGA2_TC003609 [Tribolium castaneum]
Sequence ID: **gb|EFA00728.1|** Length: 213 Number of Matches: 2

Score	Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits(124)	2e-04()	Compositional matrix adjust.	25/45(56%)	30/45(66%)	4/45(8%)	+2

Features:

Query	485	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQKPTRKRP	607
guor ₁	100	MDILPS IF EL+ I TGY+S+QPS++D WQQ P R P	00,
Sbjct	1	MDILPSVGIFRELQDIHDTGYFSAQPSLDDHWQQVIYGSPPRGAP	45

Range 2: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
52.4 bits	s(124)	2e-04()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+3
Features:							
Query	1068	MDILP MDILP	SGNIFSELERICTTGYYSSQPSII		59		
Sbjct	1		SVGIFRELQDIHDTGYFSAQPSLI				

PREDICTED: Krueppel-like factor 6 isoform X1 [Wasmannia auropunctata] Sequence ID: **ref|XP_011697933.1|** Length: 378 Number of Matches: 2

Range 1: 1 to 35

Score		Expect Method		Identities	Positives	Gaps	Frame
53.5 bits	s(127)	3e-04() Composit	tional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+3
Features	S:						
Query	1068		ELERICTTGYYSSQ EL+ I TGY+S+Q		169		
Sbict	1		ELODIHDTGYFSAÖ		5		

Range 2: 4 to 35

Score		Expect	Method	identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-04()	Compositional matrix adjust.	22/32(69%)	27/32(84%)	0/32(0%)	+2
Feature	s:						
Query	491		IFSELERICTTGYYSSQPSIEDQW IF EL+ I TGY+S+QPS+ED W				
Sbjct	4		IFRELQDIHDTGYFSAQPSLEDHV				

PREDICTED: Krueppel-like factor 6 isoform X1 [Cerapachys biroi]
Sequence ID: ref|XP_011352442.1| Length: 377 Number of Matches: 2

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.5 bits	s(127)	3e-04()	Compositional matrix adjust.	24/35(69%	(a) 29/35(82%)	1/35(2%)	+3
Features	S :						
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGNIF EL+ I TGY+S+QPS-		1169		
Sbjct	1		PSGNIFRELQDIHDTGYFSAQPSI		35		

Range 2: 4 to 35

Score		Expect	Method	Identi	ties	Positives	Gaps	Frame	
53.1 bit	s(126)	3e-04()	Compositional matrix adjust.	22/32((69%)	27/32(84%)	0/32(0%)	+2	
Feature	s:								
Query	491		IFSELERICTTGYYSSQPSIEDQW IF EL+ I TGY+S+QPS+ED W		86				
Sbjct	4		IFRELQDIHDTGYFSAQPSLEDHW		5				

PREDICTED: Krueppel-like factor 6 isoform X1 [Pogonomyrmex barbatus] Sequence ID: ref|XP_011629870.1| Length: 377 Number of Matches: 2

Range 1: 4 to 35

Score	Expect Method	Identities	Positives	Gaps	Frame
53.1 bits(126)	3e-04() Compositional matrix adjust.	22/32(69%)	27/32(84%)	0/32(0%)	+3
Features:					
Query 1074	ILPSGNIFSELERICTTGYYSSQPSIED +LPSGNIF EL+ I TGY+S+QPS+ED				
Sbjct 4	LLPSGNIFRELQDIHDTGYFSAQPSLED				

Range 2: 4 to 35

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-04() Compositional matrix adjust.	22/32(69%)	27/32(84%)	0/32(0%)	+2
Features	s:					
Query	491	ILPSGNIFSELERICTTGYYSSQPSIED +LPSGNIF EL+ I TGY+S+QPS+ED				
Sbjct	4	LLPSGNIFRELQDIHDTGYFSAQPSLED				

PREDICTED: Krueppel-like factor 6 [Vollenhovia emeryi]

Sequence ID: ref|XP_011872379.1| Length: 378 Number of Matches: 2

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-04()	Compositional matrix adjust.	24/35(69%	%) 29/35(82%)	1/35(2%)	+3
Features	3 :						
Query	1068		PSGNIFSELERICTTGYYSSQPS		1169		
Sbjct	1		PSGNIFRELQDIHDTGYFSAQPS		35		

Range 2: 4 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
52.8 bits	s(125)	4e-04()	Compositional matrix adjust.	22/32(69%)	27/32(84%)	0/32(0%)	+2
Features	S :						
Query	491		IFSELERICTTGYYSSQPSIEDQW IF EL+ I TGY+S+QPS+ED W				
Sbjct	4		IFRELQDIHDTGYFSAQPSLEDHV				

PREDICTED: Krueppel-like factor 7 isoform X1 [Solenopsis invicta] Sequence ID: ref|XP_011168430.1| Length: 378 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 35

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-04() Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+3
Features	S :					
Query	1068	MD-ILPSGNIFSELERICTTGYYSSQP MD +LPSGNIF EL+ I TGY+S+QP		L69		
Sbjct	1	MDTLLPSGNIFRELQDIHDTGYFSAQP		5		

Score		Expect	Method	lde	entities	Positives	Gaps	Frame
52.8 bits	s(125)	4e-04()	Compositional matrix adjust.	22/	32(69%)	27/32(84%)	0/32(0%)	+2
Features	s:							
Query	491		NIFSELERICTTGYYSSOPSIED NIF EL+ I TGY+S+OPS+ED		586			
Sbjct	4		NIFRELQDIHDTGYFSAQPSLED		35			

PREDICTED: Krueppel-like factor 6 isoform X1 [Camponotus floridanus] Sequence ID: **ref|XP_011252310.1**| Length: 377 Number of Matches: 2

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	3e-04()	Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPS PSGNIF EL+ I TGY+S+QPS		169		
Sbjct	1		PSGNIF EL' I IGITS OFS PSGNIFRELQDIHDTGYFSAQPS		5		

Range 2: 4 to 35

Score		Expect	Method	lde	ntities	Positives	Gaps	Frame
52.8 bits	s(125)	4e-04()	Compositional matrix adjust.	22/	32(69%)	27/32(84%)	0/32(0%)	+2
Features	s:							
Query	491		IFSELERICTTGYYSSQPSIEDQ IF EL+ I TGY+S+QPS+ED T		586			
Sbjct	4		IFRELQDIHDTGYFSAQPSLEDH		35			

PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]

Sequence ID: ref|XP_013780917.1| Length: 351 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits	(126)	3e-04()	Compositional matrix adjust.	23/34(68%)	28/34(82%)	0/34(0%)	+3
Features	3 :						
Query	1068		SGNIFSELERICTTGYYSSOPSI SG IF EL+ + TGY+SSO S+		59		
Sbjct	1		SGGIFRELQVVHDTGYFSSQLSL				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
52.8 bits	(125)	4e-04()	Compositional matrix adjust.	23/34(68%)	28/34(82%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSOPSIEI G IF EL+ + TGY+SSO S+EI		586			
Sbjct	1		GGIFRELQVVHDTGYFSSÕLSLEI		34			

Uncharacterized protein OBRU01_08947 [Operophtera brumata] Sequence ID: **gb|KOB74566.1|** Length: 72 Number of Matches: 2

Range 1: 1 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.7 bits(117)	3e-04()	Composition-based stats.	20/34(59%)	26/34(76%)	0/34(0%)	+3

Features:

Query	1068	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ	1169
		MD+LPSGN+F ELE + TGY+ + S+ED WQQ	
Sbjct	1	MDVLPSGNLFRELEHVTDTGYFEWKLSLEDYWQQ	34

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
49.7 bits	s(117)	4e-04() Composition-based stats.	20/34(59%)	26/34(76%)	0/34(0%)	+2
Features	s:					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSI		<u>, </u>		
Sbjct	1	MD+LPSGN+F ELE + TGY+ + S+ MDVLPSGNLFRELEHVTDTGYFEWKLSI				

putative Kruppel-like factor 6 [Daphnia pulex]

Sequence ID: **gb|EFX88687.1|** Length: 429 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame	
53.1 bits	s(126)	4e-04()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+3	
Features:								
Query	1068		SGNIFSELERICTTGYYSSQPSI SGNIF EL+ + TGY S+O S+		59			
Sbjct	1		SGNIFRELQVVHDTGYLSAQTSL					

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
52.4 bits	s(124)	5e-04() Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+2
Features	S :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSII MDILPSGNIF EL+ + TGY S+Q S+I				
Sbjct	1	MDILPSGNIFRELQVVHDTGYLSAQTSLI				

hypothetical protein KGM_08804 [Danaus plexippus]

Sequence ID: **gb|EHJ66609.1|** Length: 58 Number of Matches: 2 Range 1: 1 to 40

Score		Expect	Method	Identities	Positives	Gaps	Frame
49.3 bits	s(116)	5e-04()	Compositional matrix adjust.	20/40(50%)	28/40(70%)	0/40(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSII		R 1187		
Sbjct	1		SGNLFRELQDVTDTGYFEWKLSLI				

Score		Expect	Method	Identities	Positives	Gaps	Frame	
49.3 bits(1	116)	5e-04()	Compositional matrix adjust.	20/40(50%)	28/40(70%)	0/40(0%)	+2	•
Features:								
Query 4	485		GNIFSELERICTTGYYSSQPSIED GN+F EL+ + TGY+ + S+ED		604			
Sbjct 1	1		GNLFRELQDVTDTGYFEWKLSLED		40			

Sequence ID: ref|XP_008192084.1| Length: 304 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
52.0 bits	s(123)	6e-04()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+3
Features	S :						
Query	1068	MDILPS MDILPS	GNIFSELERICTTGYYSSQPSII G IF EL+ I TGY+S+QPS+-		59		
Sbjct	1		SVGIFRELQDIHDTGYFSAQPSLI				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
51.6 bits(1	122)	9e-04()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+2
Features:								
Query 4	485	MDILPS MDILPS	GNIFSELERICTTGYYSSQPSIEI IF EL+ I TGY+S+QPS++I		586			
Sbjct 1	1		VGIFRELQDIHDTGYFSAQPSLDI		34			

zinc finger protein [Ciona intestinalis]

Sequence ID: ref|NP_001071864.1| Length: 312 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame		
52.0 bits	s(123)	6e-04()	Compositional matrix adjust.	22/34(65%)	28/34(82%)	0/34(0%)	+3		
Features:									
Query	Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 MDILP GNIF+EL+ I TGY+S+ PS+E+ WQQ								
Sbjct	1		CGNIFNELQIIHDTGYFSALPSL						

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
51.2 bits	s(121)	0.001()	Compositional matrix adjust.	22/34(6	65%)	28/34(82%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GNIF+EL+ I TGY+S+ PS+E-		586			
Sbjct	1		GNIFNELQIIHDTGYFSALPSLE	~ ~	34			

hypothetical protein RR46_12790 [Papilio xuthus]

Sequence ID: **gb|KPI96760.1**| Length: 40 Number of Matches: 2

▶ See 1 more title(s) kange 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
47.4 bits	s(111)	0.002()	Composition-based stats.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Feature	s:						
Query	1068		SGNIFSELERICTTGYYSSOPS SGN+F EL+ + TGY+ + S		169		
Shict	1		SGNIFRELODVTDTGYFEWKI.		1		

Range 2: 1 to 34

Score Expect Method Identities Positives Gaps Frame

46.6 bits(109)	0.002()	Composition-based stats.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features:						

Query 485 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ 34

PREDICTED: Krueppel-like factor 6 isoform X1 [Acromyrmex echinatior] Sequence ID: **ref|XP_011062998.1**| Length: 378 Number of Matches: 2

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
50.4 bits	s(119)	0.002()	Compositional matrix adjust.	23/35(66%)	28/35(80%)	1/35(2%)	+3
Feature	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPS		169		
Sbjct	1		PSSNIFRELQDIHDTGYFSAQPS		5		

Range 2: 4 to 35

Score		Expect	Method	lde	ntities	Positives	Gaps	Frame
50.1 bits	s(118)	0.003()	Compositional matrix adjust.	21/3	32(66%)	26/32(81%)	0/32(0%)	+2
Features	S :							
Query	491		 IFSELERICTTGYYSSQPSIEDQ IF EL+ I TGY+S+QPS+ED		586			
Sbjct	4		IFRELQDIHDTGYFSAQPSLEDH		35			

PREDICTED: Krueppel-like factor 7 [Amyelois transitella]

Sequence ID: ref|XP_013189432.1| Length: 218 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
49.3 bits	s(116)	0.002()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGN+F EL+ + TGY+ + S+	~ ~~	59		
Sbjct	1		SGNLFRELQDVTDTGYFEYKVSL				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
48.9 bits	s(115)	0.003()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GN+F EL+ + TGY+ + S+EI		586			
Sbjct	1		GNLFRELQDVTDTGYFEYKVSLEI		34			

PREDICTED: Krueppel-like factor 6-like isoform X1 [Saccoglossus kowalevskii]

Sequence ID: ref|XP_002736455.1| Length: 283 Number of Matches: 2

Score	Expect	Method	Identities	Positives	Gaps	Frame
49.7 bits(117)	0.003()	Compositional matrix adjust.	20/34(59%)	27/34(79%)	0/34(0%)	+3
Features:						

Query	1068	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ	1169
		MDILPS IF+ELE + +TGY+S+ PS+E+ W Q	
Sbict	1	MDILPSSAIFNELEVVHSTGYFSALPSLEEHWHO	34

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
48.9 bits	s(115)	0.006()	Compositional matrix adjust.	20/34(59%)	27/34(79%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIE		586			
Sbjct	1		SAIFNELEVVHSTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 7-like [Metaseiulus occidentalis]

Sequence ID: **ref|XP_003748452.1|** Length: 284 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
49.7 bits	s(117)	0.003()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SG+IF+EL+ I TGY SOPS+:	EDQWQQ 116 E+ WOO	59		
Sbjct	1		SGSIFNELQAIHDTGYLPSQPSL				

Range 2: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
49.3 bits	s(116)	0.005()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+2
Features	s:						
Query	485		GNIFSELERICTTGYYSSQPSIE GG+IF+EL+ I TGY SQPS+E				
Sbjct	1		GSIFNELQAIHDTGYLPSQPSLE				

PREDICTED: Krueppel-like factor 7 isoform X2 [Papilio xuthus]

Sequence ID: **ref|XP_013179377.1**| Length: 211 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits	s(113)	0.006()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSII SGN+F EL+ + TGY+ + S+I		9		
Sbjct	1		SGNLFRELQDVTDTGYFEWKLSL				

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame	
47.8 bits(1	112)	0.008()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2	
Features:									
Query 4	485		GNIFSELERICTTGYYSSQPSIED GN+F EL+ + TGY+ + S+ED		586				
Sbjct 1	1		GNLFRELQDVTDTGYFEWKLSLED		34				

Sequence ID: ref|XP_013179376.1| Length: 212 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits	s(113)	0.006()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI PSGN+F EL+ + TGY+ + S+		59		
Sbjct	1		SGNLFRELQDVTDTGYFEWKLSI				

Range 2: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
47.4 bits	s(111)	0.009()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI GN+F EL+ + TGY+ + S+EI		586			
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLEI		34			

PREDICTED: Krueppel-like factor 7 isoform X1 [Papilio machaon]

Sequence ID: ref|XP_014366548.1| Length: 212 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits	s(113)	0.006()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI SGN+F EL+ + TGY+ + S+		59		
Sbjct	1		SGNLFRELQDVTDTGYFEWKLSL				

Range 2: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
47.4 bits	s(111)	0.010()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features	s:							
Query	485		GGNIFSELERICTTGYYSSQPSIE GGN+F EL+ + TGY+ + S+E		586			
Sbjct	1		GONLFRELQDVTDTGYFEWKLSLE		34			

PREDICTED: Krueppel-like factor 7 isoform X2 [Papilio machaon]

Sequence ID: ref|XP_014366549.1| Length: 211 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits	s(113)	0.006()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI		69		
Shict	1		SCNI.FREI.ODVTDTCVFFWKI.SI.				

Score	Expect	Method	Identities	Positives	Gaps	Frame
47.4 bits(111)	0.010()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features:						

MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 Query MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ 34

PREDICTED: Krueppel-like factor 6 [Papilio polytes]

Sequence ID: ref|XP_013147462.1| Length: 212 Number of Matches: 2

Range 1: 1 to 34

Score Identities Expect Method Positives Frame Gaps 19/34(56%) 26/34(76%) 0/34(0%) 48.1 bits(113) 0.006() Compositional matrix adjust. +3 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 1068 1169 MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ

Range 2: 1 to 34

Identities Score **Expect Method Positives** Gaps Frame 19/34(56%) 47.4 bits(111) 0.010() Compositional matrix adjust. 26/34(76%) 0/34(0%) +2 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 Query 485 MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ 34

PREDICTED: Krueppel-like factor 6 [Bombyx mori]

Sequence ID: ref|XP_004932855.1| Length: 272 Number of Matches: 2

Range 1: 1 to 34

Score Expect Method Identities **Positives** Gaps Frame 48.5 bits(114) 0.007() Compositional matrix adjust. 19/34(56%) 26/34(76%) 0/34(0%) +3 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 1068 MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ

Range 2: 1 to 34

Score **Expect Method** Identities **Positives Frame** Gaps 47.8 bits(112) 0.011() Compositional matrix adjust. 19/34(56%) 26/34(76%) 0/34(0%) +2 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MD+LPSGN+F EL+ + TGY+ + S+ED WQQ 586 Query 485 Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ 34

PREDICTED: Krueppel-like factor 6 [Plutella xylostella]

Sequence ID: ref|XP_011553149.1| Length: 250 Number of Matches: 2

Range 1: 1 to 34

Sbjct

1

Expect Method Score Identities Frame Positives Gaps 48.5 bits(114) 0.007() Compositional matrix adjust. 19/34(56%) 26/34(76%) 0/34(0%) +3 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MD+LPSGN+F EL+ + TGY+ + S+ED WQQ MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ Query 1068 1169

34

Score		Expect	Method	Identities	S	Positives	Gaps	Frame
47.8 bits	s(112)	0.010()	Compositional matrix adjust.	19/34(56	8%)	26/34(76%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIEI GN+F EL+ + TGY+ + S+EI		86			
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLEI		34			

unknown [Homo sapiens]

Sequence ID: **gb|AAY15081.1**| Length: 34 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.024()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Features	s:						
Query	485		GNIFSELERICTTGYYSSQPSIE + + + + + + + + + + + + + + + + + + +				
Sbjct	1		SYSIFQELQLVHDTGYFSALPSLE				

Range 2: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
42.4 bits	s(98) (0.079()	Composition-based stats.	18/34(53%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPS S +IF EL+ + TGY+S+ PS		169		
Sbjct	1		ASYSIFQELQLVHDTGYFSALPS		1		

PREDICTED: Krueppel-like factor 7 [Callorhinchus milii]

Sequence ID: **ref|XP_007898243.1|** Length: 272 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
46.6 bits	s(109)	0.029()	Compositional matrix adjust.	19/34(56%) 27/34(79%)	0/34(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSII + +IF EL+ + TGY+SSQPS+		169		
Sbjct	1		NYSIFQELQLVHDTGYFSSQPSL		4		

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
45.8 bits	s(107)	0.048() Compositional matrix adjust.	19/34(56%)	27/34(79%)	0/34(0%)	+2
Features	S :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MD+L + +IF EL+ + TGY+SSQPS+E				
Sbjct	1	MDVLANYSIFQELQLVHDTGYFSSQPSLE				

Kruppel-like factor 7 (ubiquitous) [Homo sapiens]

Sequence ID: emb|CCO02792.1| Length: 87 Number of Matches: 2

Score Expect Method	Identities	Positives	Gaps	Frame	
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44.3 bits(103) 0.029() Compositional matrix adjust. 18/34(53%) 26/34(76%) 0/34(0%) +3

Features:

Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 MD+L S +IF EL+ + TGY+S+ PS+E+ WQQ Sbjct 1 MDVLASYSIFQELQLVHDTGYFSALPSLEETWQQ 34

Range 2: 1 to 34

Score		Expect	Method	Identities	;	Positives	Gaps	Frame
43.5 bits	s(101)	0.049()	Composition-based stats.	18/34(53	%)	26/34(76%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSI +IF EL+ + TGY+S+ PS+		586			
Sbjct	1		YSIFQELQLVHDTGYFSALPSL		34			

hypothetical protein QR98_0081480 [Sarcoptes scabiei]

Sequence ID: gb|KPM09609.1| Length: 63 Number of Matches: 2

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.033()	Composition-based stats.	19/35(54%)	28/35(80%)	0/35(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPS SG+ F+EL+ I TGY+ + S-		172		
Sbjct	1		SGHFFNELQAIHDTGYFPANLS		5		

Range 2: 1 to 35

Score		Expect Method		Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.033() Compositi	on-based stats.	19/35(54%)	28/35(80%)	0/35(0%)	+2
Features	s:						
Query	485	MDILPSGNIFSELER MDILPSG+ F+EL+			9		
Sbjct	1	MDILPSGHFFNELQA			i		

PREDICTED: Krueppel-like factor 6 [Thamnophis sirtalis]

Sequence ID: ref|XP_013913916.1| Length: 115 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identitie	S	Positives	Gaps	Frame	
44.3 b	its(103)	0.033()	Compositional matrix adjust.	18/34(53	3%)	26/34(76%)	0/34(0%)	+3	
Featu	es:								
Query	1068		SGNIFSELERICTTGYYSSQPSIF +IF EL+ + TGY+S+ PS+F		116	9			
Sbjct	: 1		MCSIFQELQIVHDTGYFSALPSLE		34				

Score		Expect Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.050() Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Feature	s:					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MD+LP +IF EL+ + TGY+S+ PS+E				
Sbjct	1	MDVLPMCSIFQELQIVHDTGYFSALPSLE				

Kruppel-like factor 7 (ubiquitous) [Homo sapiens]

Sequence ID: emb|CCO02791.1| Length: 112 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.051()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+3
Features	S:						
Query	1068		SGNIFSELERICTTGYYSSQPSI S +IF EL+ + TGY+S+ PS+		59		
Sbjct	1		SYSIFQELQLVHDTGYFSALPSL				

Range 2: 1 to 34

Score		Expect	Method	Identiti	ies	Positives	Gaps	Frame
43.1 bits	s(100)	0.081()	Compositional matrix adjust.	18/34(5	53%)	26/34(76%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIEI HIF EL+ + TGY+S+ PS+E-		586			
Sbjct	1		SYSIFQELQLVHDTGYFSALPSLE		34			

Bcd orf1 [Homo sapiens]

Sequence ID: **gb|AAB94792.1|** Length: 79 Number of Matches: 2 Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits	s(101)	0.057()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		SGNIFSELERICTTGYYSSQPSI +IF EL+ + TGY+S+ PS+		59		
Sbjct	1		MCSIFQELQIVHETGYFSALPSL				

Range 2: 1 to 34

Score		Expect	Method	Identiti	ies	Positives	Gaps	Frame
42.7 bits	(99)	0.087()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Features	3 :							
Query	485		SGNIFSELERICTTGYYSSQPSIE +IF EL+ + TGY+S+ PS+E		586			
Sbjct	1		MCSIFQELQIVHETGYFSALPSLE		34			

Kruppel-like factor 7 [Strongylocentrotus purpuratus]

Sequence ID: ref|NP_001189420.1| Length: 291 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 34

Score		Expect	Method	Identities	<u> </u>	ositives	Gaps	Frame
45.8 bits	(107)	0.060()	Compositional matrix adjust.	20/34(599	%) 2	25/34(73%)	0/34(0%)	+3
Features	:							
Query	1068		SGNIFSELERICTTGYYSSQPSIE SG IF+ELE I TG +S+ PS+E		1169			
Sbjct	1		SGGIFNELEIIGETGCFSALPSVE		34			

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
45.1 bits	s(105)	0.094()	Compositional matrix adjust.	20/34(5	9%)	25/34(73%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIER G IF+ELE I TG +S+ PS+E-		586			
Sbjct	1		GGIFNELEIIGETGCFSALPSVE		34			

PREDICTED: Krueppel-like factor 6 [Clupea harengus]

Sequence ID: ref|XP_012695379.1| Length: 188 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.060()	Compositional matrix adjust.	17/34(50%)	27/34(79%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI P +IF+EL+ + TGY+S+ PS+		59		
Shict	1		PMCSTFNELOTVHDTGYFSALPST				

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	(103)	0.096() Compositional matrix adjust.	17/34(50%)	27/34(79%)	0/34(0%)	+2
Features	3 :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE				
Sbjct	1	MD++P +IF+EL+ + TGY+S+ PS+E MDVIPMCSIFNELQTVHDTGYFSALPSLE				

unnamed protein product [Oncorhynchus mykiss]

Sequence ID: emb|CDQ87105.1| Length: 286 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
45.8 bits	(107)	0.061()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3
Features	S :						
Query	1068		SGNIFSELERICTTGYYSSQPSII +IF EL+ + TGY+S+ PS+1		59		
Sbjct	1		MCSIFQELQIVHDTGYFSALPSLI				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
45.1 bits	(105)	0.096()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+EI		586			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 [Salmo salar]

Sequence ID: ref|XP_014012942.1| Length: 286 Number of Matches: 2

▶ See 1 more title(s) Range 1: 1 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
45.4 bits(106)	0.063()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+3

Features:

Query	1068	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ	1169
_		MD+LP +IF EL+ + TGY+S+ PS+ED WQQ	
Sbjct	1	MDVLPMCSIFQELQIVHDTGYFSALPSLEDYWQQ	34

Range 2: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
45.1 bits	s(105)	0.097() Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+2
Features	S :					
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIE MD+LP +IF EL+ + TGY+S+ PS+E				
Sbjct	1	MDVLPMCSIFQELQIVHDTGYFSALPSLE				

PREDICTED: Krueppel-like factor 7 [Notothenia coriiceps]

Sequence ID: ref[XP_010783713.1] Length: 331 Number of Matches: 2

Range 1: 25 to 60

Score		Expect	Method	Identities	Positives	Gaps	Frame
45.8 bits	s(107)	0.069()	Compositional matrix adjust.	17/36(47%)	27/36(75%)	0/36(0%)	+3
Feature	s:						
Query	1062		LPSGNIFSELERICTTGYYSSQP L + +IF EL+ + TGY+S+ P		.169		
Sbjct	25		LANHSIFQELQIVHDTGYFSAMP		50		

Range 2: 25 to 60

Score		Expect	Method	Identities	Positives	Gaps	Frame
45.1 bits	s(105)	0.12()	Compositional matrix adjust.	17/36(47%)	27/36(75%)	0/36(0%)	+2
Features	s:						
Query 479 IKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 + MD+L + +IF EL+ + TGY+S+ PS+E+ WOO							
Sbjct	25		ANHSIFQELQIVHDTGYFSAMPS	~~	0		

PREDICTED: Krueppel-like factor 7 isoform X2 [Latimeria chalumnae] Sequence ID: **ref|XP_005996009.1|** Length: 294 Number of Matches: 2 Range 1: 1 to 34

Score Expect Method Identities Positives Gaps Frame

45.1 bits(105) 0.10() Compositional matrix adjust. 18/34(53%) 26/34(76%) 0/34(0%) +3

Features:

Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169
MD+L S +IF EL+ + TGY+S+ PS+E+ WQQ
Sbjct 1 MDVLASYSIFQELQLVLDTGYFSALPSLEENWQQ 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame	
44.3 bits(103)	0.17()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2	-
Features:									
Query	485		GNIFSELERICTTGYYSSQPSIED +IF EL+ + TGY+S+ PS+E+		586				
Sbjct	1		YSIFQELQLVLDTGYFSALPSLEE		34				

Sequence ID: gb|AAI50424.1| Length: 195 Number of Matches: 2

Range 1: 1 to 34

Score **Expect Method Identities Positives Gaps** Frame Compositional matrix adjust. 43.9 bits(102) 0.12() 17/34(50%) 26/34(76%) 0/34(0%) +3 Features: Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MD+L + +IF EL+ + TGY+S+ PS+E+ WQQ Sbjct 1 MDVLANYSIFQELQLVHDTGYFSAMPSLEENWQQ 1169

34

Range 2: 1 to 34

Score		Expect	Method	Identitie	s	Positives	Gaps	Frame
43.5 bits	s(101)	0.18()	Compositional matrix adjust.	17/34(50	0%)	26/34(76%)	0/34(0%)	+2
Features	s:							
Query	485		GNIFSELERICTTGYYSSQPSIE + +IF EL+ + TGY+S+ PS+E		586			
Sbjct	1		YSIFQELQLVHDTGYFSAMPSLE:		34			

PREDICTED: Krueppel-like factor 6 [Colius striatus]

Sequence ID: ref[XP_010194633.1] Length: 283 Number of Matches: 2

Range 1: 1 to 33

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
44.3 bits	s(103)	0.15()	Compositional matrix adjust.	18/33(55%)	25/33(75%)	0/33(0%)	+3
Features	S :							
Query	1068		SGNIFSELERICTTGYYSSQPSI + HF EL+ + TGY+S+ PS+		1166	j		
Sbjct	1		MCSIFQELQIVHDTGYFSALPSL		33			

Range 2: 1 to 33

Score		Expect	Method	ldent	ities	Positives	Gaps	Frame
43.9 bits	s(102)	0.25()	Compositional matrix adjust.	18/33	3(55%)	25/33(75%)	0/33(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+EI		583			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		33			

Krueppel-like factor 6 [Amazona aestiva]

Sequence ID: gb|KQK80056.1| Length: 324 Number of Matches: 2

Range 1: 24 to 75

Score	Expec	t Method	Identities	Positives	Gaps	Frame
44.7 bits(104) 0.16()	Compositional matrix adjust.	24/55(44%)	35/55(63%)	5/55(9%)	+3
Features:						
Query :		TDSLEFLRCEEEDIKMDILPS T + E RC + MD+LP				1169
Sbjct 2		TPMIKSERQRCVRDMDVLPM			~~	75

Range 2: 24 to 75

Score	Expect Method	Identities	Positives	Gaps	Frame	
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43.9 bits(102) 0.23() Compositional matrix adjust. 24/55(44%) 35/55(63%) 5/55(9%) +2

Features:

Query 428 NGLKTDSL--EFLRCEEEDIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 586 NG+ T + E RC + MD+LP +IF EL+ + TGY+S+ PS+E+ WQQ Sbjct 24 NGISTPMIKSERQRCVRD---MDVLPMCSIFQELQIVHDTGYFSALPSLEEYWQQ 75

Kruppel-like factor 6, isoform CRA_c [Homo sapiens]

Sequence ID: gb|EAW86478.1| Length: 195 Number of Matches: 2

Range 1: 1 to 34

Score Identities Positives Frame Expect Method Gaps 43.5 bits(101) 0.17() Compositional matrix adjust. 18/34(53%) 26/34(76%) 0/34(0%) +3 Features: Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169 MD+LP +IF EL+ + TGY+S+ PS+E+ WQQ

34

Range 2: 1 to 34

1

Sbjct

Score		Expect	Method	Identiti	es	Positives	Gaps	Frame
43.1 bits	s(100)	0.25()	Compositional matrix adjust.	18/34(5	3%)	26/34(76%)	0/34(0%)	+2
Features	3 :							
Query	485		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E-		586			
Sbjct	1		CSIFQELQIVHETGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Anser cygnoides domesticus] Sequence ID: **ref|XP_013041223.1**| Length: 221 Number of Matches: 2

MDVLPMCSIFQELQIVHETGYFSALPSLEEYWQQ

Range 1: 1 to 34

Score Identities Positives Expect Method Gaps Frame 43.9 bits(102) 0.17() Compositional matrix adjust. 18/34(53%) 26/34(76%) 0/34(0%) +3 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1068 1169 MD+LP +IF EL+ + TGY+S+ PS+E+ WQQ Sbjct 1 MDVLPMCSIFQELQIVHDTGYFSALPSLEEYWQQ

Range 2: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
43.1 bits	s(100)	0.28()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Features	3 :							
Query	485		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E-		586			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Melopsittacus undulatus] Sequence ID: **ref|XP 005153078.1**] Length: 241 Number of Matches: 2

Range 1: 1 to 34

ScoreExpectMethodIdentitiesPositivesGapsFrame43.9 bits(102)0.18()Compositional matrix adjust.18/34(53%)26/34(76%)0/34(0%)+3Features:

Query 1068 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 1169

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
43.1 bits	s(100)	0.29()	Compositional matrix adjust.	18/34(5	3%)	26/34(76%)	0/34(0%)	+2
Features	S :							
Query	485		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E-		586			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

Krueppel-like factor 6-like isoform 1 [Camelus ferus]

Sequence ID: **gb|EPY86871.1|** Length: 200 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits	s(101)	0.18()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+3
Features	S :						
Query	1068		PSGNIFSELERICTTGYYSSQPSI P +IF EL+ + TGY+S+ PS+		59		
Sbjct	1		PMCSIFQELQIVHETGYFSALPSL				

Range 2: 1 to 34

Score		Expect	Method	ldentiti	ies	Positives	Gaps	Frame
42.7 bits	s(99)	0.29()	Compositional matrix adjust.	18/34(5	53%)	26/34(76%)	0/34(0%)	+2
Feature	s:							
Query	485		SGNIFSELERICTTGYYSSQPSIE +IF EL+ + TGY+S+ PS+E		586			
Sbjct	1		MCSIFQELQIVHETGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Nipponia nippon]

Sequence ID: ref|XP_009474236.1| Length: 241 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.19()	Compositional matrix adjust.	18/34(53%	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI P +IF EL+ + TGY+S+ PS+		.69		
Sbjct	1		PMCSIFQELQIVHDTGYFSALPSL		:		

Range 2: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
43.1 bits	s(100)	0.32()	Compositional matrix adjust.	18/34(5	3%)	26/34(76%)	0/34(0%)	+2
Features	3 :							
Query	485		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E+		586			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Egretta garzetta]
Sequence ID: ref|XP_009639640.1| Length: 241 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.19()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+3
Features	s:						
Query	1068		PSGNIFSELERICTTGYYSSQPSI P +IF EL+ + TGY+S+ PS+	~ ~~	69		
Sbjct	1		PMCSIFQELQIVHDTGYFSALPSL				

Range 2: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
43.1 bits	s(100)	0.30()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Features	s:							
Query	485	MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MD+LP +IF EL+ + TGY+S+ PS+E+ WQQ			586			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Ficedula albicollis]
Sequence ID: **ref|XP_005040665.1**| Length: 241 Number of Matches: 2

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.19()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+3
Features	S:						
Query	1068		SGNIFSELERICTTGYYSSQPSI + + + + + + + + + + + + + + + + + + +		59		
Sbjct	1		MCSIFQELQIVHDTGYFSALPSL				

Range 2: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
43.1 bits(100)		0.31()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Features	Features:							
Query	485		GNIFSELERICTTGYYSSQPSIE +IF EL+ + TGY+S+ PS+E		586			
Sbjct	1		MCSIFQELQIVHDTGYFSALPSLE:		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Opisthocomus hoazin]
Sequence ID: **ref|XP_009943445.1**| Length: 241 Number of Matches: 2
Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame		
43.9 bits	s(102)	0.19()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+3		
Features:									
Query	1068		SGNIFSELERICTTGYYSSQPSI + + + + + + + + + + + + + + + + + + +		69				
Sbjct	1		MCSIFQELQIVHDTGYFSALPSL						

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits	s(100)	0.32()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+2
Features	s:						
Query	485	MDILPS	GNIFSELERICTTGYYSSQPSIE	DQWQQ 586			