Basic Local Alignment Search Tool

NCBI/ BLAST/ blastx/ Formatting Results - B8BWHKTX014

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Blast report description

Nucleotide Sequence (641 letters)

RID <u>B8BWHKTX014</u> (Expires on 02-06 12:13 pm)

Query ID |cl|Query_175049

Description None

Molecule type nucleic acid

Query Length 641

Database Name nr

Description All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

excluding environmental samples from

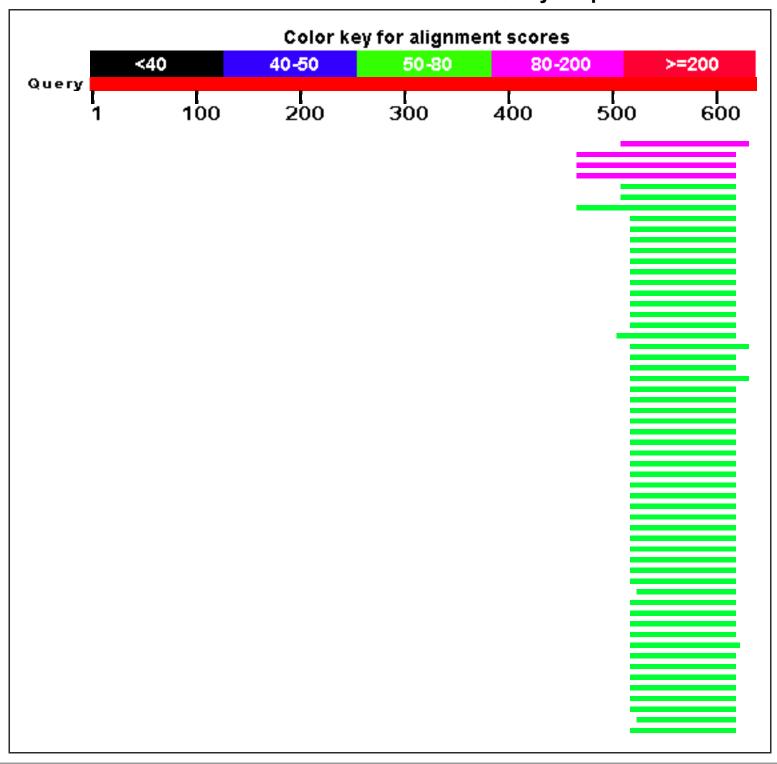
WGS projects

Program BLASTX 2.3.1+

□ Graphic Summary

No putative conserved domains have been detected

Distribution of 100 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	80.1	19%	4e-16	85%	KNC20993.1
PREDICTED: transcription factor Sp4 [Bactrocera cucurbitae]	82.8	82.8	23%	1e-14	73%	XP_011187312.1
PREDICTED: Krueppel-like factor 7 [Bactrocera dorsalis]	82.8	82.8	23%	1e-14	73%	XP_011205494.1
PREDICTED: transcription factor Sp4 [Ceratitis capitata]	82.8	82.8	23%	1e-14	73%	XP_004520626.1
PREDICTED: transcription factor Sp4 [Musca domestica]	79.7	79.7	17%	1e-13	92%	XP_011296126.1
PREDICTED: probable serine/threonine- protein kinase yakA [Stomoxys calcitrans]	79.7	79.7	17%	1e-13	92%	XP_013118858.1
PREDICTED: Krueppel-like factor 7 [Bactrocera oleae]	79.3	79.3	23%	2e-13	71%	XP_014087536.1
GD25946 [Drosophila simulans]	77.4	77.4	15%	7e-13	100%	XP_002080971.1
uncharacterized protein Dsimw501_GD25946 [Drosophila simulans]	77.4	77.4	15%	8e-13	100%	KMY92900.1
GM20477 [Drosophila sechellia]	77.4	77.4	15%	8e-13	100%	XP_002033321.1
luna, isoform B [Drosophila melanogaster]	77.4	77.4	15%	8e-13	100%	NP_995811.1
uncharacterized protein Dyak_GE13058, isoform A [Drosophila yakuba]	77.0	77.0	15%	9e-13	100%	XP_002090341.1
GL20646 [Drosophila persimilis]	74.7	74.7	15%	9e-13	97%	XP_002026405.1
uncharacterized protein Dere_GG22702 [Drosophila erecta]	77.0	77.0	15%	9e-13	100%	XP_001976143.1
uncharacterized protein Dpse_GA25126 [Drosophila pseudoobscura pseudoobscura]	75.5	75.5	15%	3e-12	97%	XP_002139002.2
uncharacterized protein Dvir_GJ18175, isoform C [Drosophila virilis]	74.3	74.3	15%	7e-12	94%	XP_002059288.2
GH20565 [Drosophila grimshawi]	71.6	71.6	15%	5e-11	91%	XP_001986367.1
uncharacterized protein Dana_GF12443, isoform C [Drosophila ananassae]	70.9	70.9	15%	1e-10	88%	XP_001958687.2
PREDICTED: Krueppel-like factor 6 [Octopus bimaculoides]	64.7	64.7	17%	5e-09	74%	XP_014770070.1
Krueppel-like factor 7 [Habropoda laboriosa]	59.7	59.7	17%	2e-08	68%	KOC67104.1
Krueppel-like factor 6 [Harpegnathos saltator]	58.5	58.5	15%	2e-08	74%	EFN86983.1
hypothetical protein LOTGIDRAFT_126955 [Lottia gigantea]	58.5	58.5	15%	2e-08	74%	XP_009061298.1
conserved hypothetical protein [Pediculus humanus corporis]	58.5	58.5	17%	3e-08	68%	XP_002430467.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Cimex lectularius]	58.9	58.9	15%	3e-07	74%	XP_014239878.1

	PREDICTED: Krueppel-like factor 6 [Halyomorpha halys]	58.5	58.5	15%	4e-07	74%	XP_014290567.1
	PREDICTED: Krueppel-like factor 7 soform X1 [Nasonia vitripennis]	59.3	59.3	15%	5e-07	74%	XP_008208238.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Polistes canadensis]	59.3	59.3	15%	5e-07	74%	XP_014605830.1
	PREDICTED: Krueppel-like factor 7 [Ceratosolen solmsi marchali]	58.9	58.9	15%	6e-07	74%	XP_011499687.1
	PREDICTED: Krueppel-like factor 7 soform X1 [Athalia rosae]	58.9	58.9	15%	6e-07	74%	XP_012264721.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Dinoponera quadriceps]	58.9	58.9	15%	6e-07	74%	XP_014480191.1
	PREDICTED: Krueppel-like factor 7 soform X1 [Diachasma alloeum]	58.9	58.9	15%	6e-07	74%	XP_015127225.1
	PREDICTED: Krueppel-like factor 7 soform X1 [Fopius arisanus]	58.9	58.9	15%	6e-07	74%	XP_011299771.1
	PREDICTED: Krueppel-like factor 6 soform X2 [Diachasma alloeum]	58.9	58.9	15%	6e-07	74%	XP_015127226.1
	PREDICTED: Krueppel-like factor 6 [Orussus abietinus]	58.9	58.9	15%	6e-07	74%	XP_012279401.1
	PREDICTED: LOW QUALITY PROTEIN: Krueppel-like factor 7 [Apis florea]	58.9	58.9	15%	6e-07	74%	XP_003693621.2
	PREDICTED: Krueppel-like factor 6 Microplitis demolitor]	58.9	58.9	15%	7e-07	74%	XP_008553910.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Megachile rotundata]	58.9	58.9	15%	7e-07	74%	XP_012146207.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Bombus terrestris]	58.9	58.9	15%	7e-07	74%	XP_003396776.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Harpegnathos saltator]	58.9	58.9	15%	7e-07	74%	XP_011135638.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Cimex lectularius]	58.5	58.5	15%	7e-07	74%	XP_014239870.1
	PREDICTED: Krueppel-like factor 6 [Lingula anatina]	58.2	58.2	15%	1e-06	68%	XP_013406198.1
	PREDICTED: Krueppel-like factor 6 Crassostrea gigas]	57.4	57.4	15%	2e-06	68%	XP_011451658.1
	Krueppel-like factor 6 [Camponotus loridanus]	53.1	53.1	14%	2e-06	69%	EFN71037.1
ı	nypothetical protein BRAFLDRAFT_124706 [Branchiostoma floridae]	55.5	55.5	15%	6e-06	71%	XP_002588272.1
	PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]	55.8	55.8	15%	6e-06	65%	XP_013777058.1
	PREDICTED: Krueppel-like factor 7 [Polistes dominula]	55.8	55.8	15%	7e-06	71%	XP_015182091.1
ı	Krueppel-like factor [Cerapachys biroi]	52.8	52.8	15%	7e-06	69%	EZA60583.1
	PREDICTED: zinc finger protein 1-like Aplysia californica]	55.8	55.8	16%	8e-06	66%	XP_005099170.1
	PREDICTED: Krueppel-like factor 6 Biomphalaria glabrata]	54.3	54.3	15%	2e-05	65%	XP_013085087.1
	PREDICTED: Krueppel-like factor 6 [Acyrthosiphon pisum]	53.9	53.9	15%	3e-05	65%	XP_003242773.1
	PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]	53.9	53.9	15%	3e-05	68%	XP_013779231.1
	PREDICTED: Krueppel-like factor 6 soform X1 [Wasmannia auropunctata]	53.5	53.5	15%	5e-05	69%	XP_011697933.1
	PREDICTED: Krueppel-like factor 6						

isoform X1 [Cerapachys biroi]	53.5	53.5	15%	5e-05	69%	XP_011352442.1
Uncharacterized protein OBRU01_08947 [Operophtera brumata]	50.1	50.1	15%	5e-05	59%	KOB74566.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Pogonomyrmex barbatus]	53.1	53.1	14%	5e-05	69%	XP_011629870.1
PREDICTED: Krueppel-like factor 6 [Vollenhovia emeryi]	53.1	53.1	15%	5e-05	69%	XP_011872379.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Solenopsis invicta]	53.1	53.1	15%	5e-05	69%	XP_011168430.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Camponotus floridanus]	53.1	53.1	15%	5e-05	69%	XP_011252310.1
PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]	53.1	53.1	15%	6e-05	68%	XP_013780917.1
putative Kruppel-like factor 6 [Daphnia pulex]	53.1	53.1	15%	6e-05	65%	EFX88687.1
hypothetical protein TcasGA2_TC003609 [Tribolium castaneum]	52.4	52.4	15%	7e-05	65%	EFA00728.1
hypothetical protein KGM_08804 [Danaus plexippus]	49.3	49.3	18%	9e-05	50%	EHJ66609.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Tribolium castaneum]	52.0	52.0	15%	1e-04	65%	XP_008192084.1
zinc finger protein [Ciona intestinalis]	52.0	52.0	15%	1e-04	65%	NP_001071864.1
hypothetical protein RR46_12790 [Papilio xuthus]	47.4	47.4	15%	3e-04	56%	KPI96760.1
PREDICTED: Krueppel-like factor 6 isoform X1 [Acromyrmex echinatior]	50.4	50.4	15%	5e-04	66%	XP_011062998.1
PREDICTED: Krueppel-like factor 7 [Amyelois transitella]	49.3	49.3	15%	7e-04	56%	XP_013189432.1
PREDICTED: Krueppel-like factor 6-like isoform X1 [Saccoglossus kowalevskii]	49.7	49.7	15%	8e-04	59%	XP_002736455.1
PREDICTED: Krueppel-like factor 7-like [Metaseiulus occidentalis]	49.7	49.7	15%	9e-04	65%	XP_003748452.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Papilio xuthus]	48.1	48.1	15%	0.002	56%	XP_013179377.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Papilio xuthus]	48.1	48.1	15%	0.002	56%	XP_013179376.1
PREDICTED: Krueppel-like factor 6 [Bombyx mori]	48.5	48.5	15%	0.002	56%	XP_004932855.1
PREDICTED: Krueppel-like factor 7 isoform X1 [Papilio machaon]	48.1	48.1	15%	0.002	56%	XP_014366548.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Papilio machaon]	48.1	48.1	15%	0.002	56%	XP_014366549.1
PREDICTED: Krueppel-like factor 6 [Plutella xylostella]	48.5	48.5	15%	0.002	56%	XP_011553149.1
PREDICTED: Krueppel-like factor 6 [Papilio polytes]	48.1	48.1	15%	0.002	56%	XP_013147462.1
Kruppel-like factor 7 (ubiquitous) [Homo sapiens]	44.3	44.3	15%	0.008	53%	CCO02792.1
PREDICTED: Krueppel-like factor 7 [Callorhinchus milii]	46.6	46.6	15%	0.009	56%	XP_007898243.1
hypothetical protein QR98_0081480 [Sarcoptes scabiei]	43.9	43.9	16%	0.009	54%	KPM09609.1
PREDICTED: Krueppel-like factor 6 [Thamnophis sirtalis]	44.3	44.3	15%	0.011	53%	XP_013913916.1
Bcd orf1 [Homo sapiens]	43.5	43.5	15%	0.016	53%	AAB94792.1
Kruppel-like factor 7 (ubiquitous) [Homo						

sapiens]	43.9	43.9	15%	0.017	53%	CCO02791.1
Kruppel-like factor 7 [Strongylocentrotus purpuratus]	45.8	45.8	15%	0.018	59%	NP_001189420.1
unnamed protein product [Oncorhynchus mykiss]	45.8	45.8	15%	0.018	56%	CDQ87105.1
PREDICTED: Krueppel-like factor 6 [Salmo salar]	45.4	45.4	15%	0.019	56%	XP_014012942.1
PREDICTED: Krueppel-like factor 7 [Notothenia coriiceps]	45.8	45.8	16%	0.020	47%	XP_010783713.1
unknown [Homo sapiens]	42.4	42.4	15%	0.022	53%	AAY15081.1
PREDICTED: Krueppel-like factor 6 [Clupea harengus]	44.7	44.7	15%	0.023	50%	XP_012695379.1
PREDICTED: Krueppel-like factor 7 isoform X2 [Latimeria chalumnae]	45.1	45.1	15%	0.031	53%	XP_005996009.1
Krueppel-like factor 6 [Amazona aestiva]	44.7	44.7	24%	0.048	44%	KQK80056.1
PREDICTED: Krueppel-like factor 6 [Colius striatus]	44.3	44.3	15%	0.049	55%	XP_010194633.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Anser cygnoides domesticus]	43.9	43.9	15%	0.063	53%	XP_013041223.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Melopsittacus undulatus]	43.9	43.9	15%	0.063	53%	XP_005153078.1
Kruppel-like factor 6, isoform CRA_c [Homo sapiens]	43.5	43.5	15%	0.064	53%	EAW86478.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Nipponia nippon]	43.9	43.9	15%	0.065	53%	XP_009474236.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Egretta garzetta]	43.9	43.9	15%	0.065	53%	XP_009639640.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Ficedula albicollis]	43.9	43.9	15%	0.065	53%	XP_005040665.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Opisthocomus hoazin]	43.9	43.9	15%	0.066	53%	XP_009943445.1
PREDICTED: zinc finger protein 396 isoform X2 [Acanthisitta chloris]	43.9	43.9	15%	0.066	53%	XP_009082634.1
PREDICTED: Krueppel-like factor 6 isoform X2 [Manacus vitellinus]	43.9	43.9	15%	0.067	53%	XP_008931128.1

■ <u>Alignments</u>

hypothetical protein FF38_00987 [Lucilia cuprina]

Sequence ID: gb|KNC20993.1| Length: 47 Number of Matches: 1

Range 1: 2 to 42

Score		Expect	Method	Identities	Positives	Gaps	Frame
80.1 bits	s(196)	4e-16()	Compositional matrix adjust.	35/41(85%)	38/41(92%)	0/41(0%)	+1
Features	3 :						
Query	511		LPSGNIFSELERICTTGYYSSQP; LPSGNIFSELERICTTGY+SSQP;		R 633		
Shict	2		LPSGNIFSELERICTTGYFSSOP	~ ~~	'к 42		

PREDICTED: transcription factor Sp4 [Bactrocera cucurbitae]

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

▶ See 1 more title(s) Range 1: 1 to 48

Score		Expect Method	Identities	Positives	Gaps	Frame	
82.8 bits	s(203)	1e-14() Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+1	
Features	s:						
Query	469		KTDSLEFLRCEEEDIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 62-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: 1

Range 1: 1 to 48

Score		Expect Method	Identities	Positives	Gaps	Frame
82.8 bits	(203)	1e-14() Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+1
Features	S :					
Query	469	LKTDSLEFLRCEEEDIKMDILPSGNIFSE +KT+SL+F D+ MDILPSGNIFSE				
Sbjct	1	MKTESLDFHSMDLNMDILPSGNIFSE				

PREDICTED: transcription factor Sp4 [Ceratitis capitata]

Sequence ID: ref|XP_004520626.1| Length: 612 Number of Matches: 1

Range 1: 1 to 48

Score		Expect	Method	Identities	Positives	Gaps	Frame
82.8 bits	s(203)	1e-14()	Compositional matrix adjust.	37/51(73%)	43/51(84%)	3/51(5%)	+1
Features	s:						
Query	469	LKTDSL +KT+SL	EFLRCEEEDIKMDILPSGNIFSE +F D+ MDILPSGNIFSE				
Sbjct	1		DFHSMDLNMDILPSGNIFSE				

PREDICTED: transcription factor Sp4 [Musca domestica]

Sequence ID: ref|XP_011296126.1| Length: 616 Number of Matches: 1

Range 1: 2 to 38

Score		Expect Method	Identities	Positives	Gaps	Frame
79.7 bits	s(195)	1e-13() Compositional mat	trix adjust. 34/37(92%	(a) 36/37(97%)	0/37(0%)	+1
Features	s:					
Query	511		MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIFSELERICTTGY+SSQPSIEDQWQQ			
Sbjct	2	DLNMDILPSGNIFSELERIC		38		

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

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

Score		Expect Method	Identities	Positives	Gaps	Frame
79.7 bits	s(195)	1e-13() Compositional matrix adjust.	34/37(92%)	36/37(97%)	0/37(0%)	+1
Feature	s:					
Query	511	DIKMDILPSGNIFSELERICTTGYYSSQPS D+ MDILPSGNIFSELERICTTGY+SSQPS		21		
Sbjct	2	DLNMDILPSGNIFSELERICTTGYFSSQPS		8		

PREDICTED: Krueppel-like factor 7 [Bactrocera oleae]

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

Range 1: 1 to 48

Gaps Score **Expect Method** Identities **Positives Frame** 79.3 bits(194) 2e-13() Compositional matrix adjust. 36/51(71%) 42/51(82%) 3/51(5%) +1 Features: LKTDSLEFLRCEEEDIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621 Query 469 D+ MDILPSGNIFSELE +CTTGY+SSQPSIEDQWQQ Sbjct 48 MKTELLDF---HGMDLNMDILPSGNIFSELEHVCTTGYFSSQPSIEDQWQQ

GD25946 [Drosophila simulans]

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

See 1 more title(s)

Range 1: 1 to 34

Expect Method Score Identities **Positives** Gaps **Frame** 34/34(100%) 34/34(100%) 0/34(0%) +1 77.4 bits(189) 7e-13() Compositional matrix adjust. Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 621 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Sbjct 1 34

uncharacterized protein Dsimw501_GD25946 [Drosophila simulans]

Sequence ID: gb|KMY92900.1| Length: 568 Number of Matches: 1

Range 1: 1 to 34

Identities Score **Expect Method Positives** Gaps Frame 77.4 bits(189) 8e-13() Compositional matrix adjust. 34/34(100%) 34/34(100%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 520 621 Sbjct 1 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 34

GM20477 [Drosophila sechellia]

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

See 1 more title(s)

Range 1: 1 to 34

Score Expect Method Identities **Positives** Gaps Frame 77.4 bits(189) 8e-13() Compositional matrix adjust. 34/34(100%) 34/34(100%) 0/34(0%) +1Features: Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Sbjct 1 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ

luna, isoform B [Drosophila melanogaster]

Sequence ID: ref[NP_995811.1] Length: 570 Number of Matches: 1

See 8 more title(s)

Range 1: 1 to 34

Score Expect Method Identities Positives Gaps Frame

77.4 bits(189) 8e-13() Compositional matrix adjust. 34/34(100%) 34/34(100%) 0/34(0%) +1

Features:

Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 34 Sbjct 1 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 34

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

See 3 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
77.0 bits	s(188)	9e-13()	Compositional matrix adjust.	34/34(100%	34/34(100%)	0/34(0%)	+1
Feature	s:						
Query	520		GGNIFSELERICTTGYYSSQPSII GGNIFSELERICTTGYYSSQPSII				
Sbjct	1		SGNIFSELERICTTGYYSSQPSI				

GL20646 [Drosophila persimilis]

Sequence ID: ref|XP_002026405.1| Length: 255 Number of Matches: 1

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identities	S	Positives	Gaps	Frame
74.7 bits	s(182)	9e-13()	Compositional matrix adjust.	33/34(97	'%)	34/34(100%)	0/34(0%)	+1
Features	s:							
Query	520		ILPSGNIFSELERICTTGYYSSQPSIEDQWQ ILPSGNIFSELERICTTGY+SSQPSIEDQWQ					
Sbjct	1		GNIFSELERICTTGYFSSQPSIE		34			

uncharacterized protein Dere_GG22702 [Drosophila erecta]

Sequence ID: ref|XP_001976143.1| Length: 562 Number of Matches: 1

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

Score		Expect Method	Identities	Positives	Gaps	Frame
77.0 bits((188)	9e-13() Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	+1
Features:	:					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSIE MDILPSGNIFSELERICTTGYYSSQPSIE				
Sbjct	1	MDILPSGNIFSELERICTTGYYSSQPSIE				

uncharacterized protein Dpse_GA25126 [Drosophila pseudoobscura pseudoobscura]

Sequence ID: ref|XP_002139002.2| Length: 543 Number of Matches: 1

See 1 more title(s)

Score		Expect	Method	Identities	Positives	Gaps	Frame
75.5 bits	s(184)	3e-12()	Compositional matrix adjust.	33/34(97%)	34/34(100%)	0/34(0%)	+1
Features	S :						
Query	520		GNIFSELERICTTGYYSSQPSIE GNIFSELERICTTGY+SSQPSIE				

Sbjct 1 MDILPSGNIFSELERICTTGYFSSQPSIEDQWQQ 34

uncharacterized protein Dvir_GJ18175, isoform C [Drosophila virilis]
Sequence ID: **ref[XP_002059288.2**] Length: 558 Number of Matches: 1

See 3 more title(s)

Range 1: 1 to 34

Score		Expect	Method	ldentiti	es	Positives	Gaps	Frame
74.3 bit	s(181)	7e-12()	Compositional matrix adjust.	32/34(9	94%)	34/34(100%)	0/34(0%)	+1
Feature	es:							
Query	520		GNIFSELERICTTGYYSSQPSIE GGNIF+ELERICTTGY+SSQPSIE		621			
Sbjct	1		GNIFNELERICTTGYFSSQPSIE		34			

GH20565 [Drosophila grimshawi]

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

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
71.6 bits	s(174)	5e-11() (Compositional matrix adjust.	31/34(91%)	33/34(97%)	0/34(0%)	+1
Feature	s:							
Query	520		SNIFSELERICTTGYYSSOPSIED G IF+ELERICTTGY+SSOPSIED		621			
Sbjct	1		TIFNELERICTTGYFSSQPSIED		34			

uncharacterized protein Dana_GF12443, isoform C [Drosophila ananassae] Sequence ID: **ref|XP_001958687.2|** Length: 559 Number of Matches: 1

See 3 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identiti	es	Positives	Gaps	Frame
70.9 bits	(172)	1e-10()	Compositional matrix adjust.	30/34(8	38%)	32/34(94%)	0/34(0%)	+1
Features	3 :							
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF+ELE IC TGY+SSQPSIEI		621			
Sbjct	1		GNIFNELEHICNTGYFSSÕPSIEI		34			

PREDICTED: Krueppel-like factor 6 [Octopus bimaculoides]

Sequence ID: ref[XP_014770070.1] Length: 289 Number of Matches: 1

Range 1: 3 to 40

Score		Expect	Method	Identities	Positives	Gaps	Frame
64.7 bits	s(156)	5e-09()	Compositional matrix adjust.	28/38(74%)	33/38(86%)	0/38(0%)	+1
Features	s:						
Query	Query 508 EDIKMDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ EDI MDILPSGNIF EL+ + TGY+SSQPS+ED+WQQ			621			
Sbjct	3	EDIAMDILPSGNIFRELQVVHETGYFSSQPSLEDRWQQ			40		

Krueppel-like factor 7 [Habropoda laboriosa]

Sequence ID: gb|KOC67104.1| Length: 82 Number of Matches: 1

Range 1: 1 to 38

Score		Expect Method	Identities	Positives	Gaps	Frame
59.7 bits	s(143)	2e-08() Compositional matrix adjust.	26/38(68%)	30/38(78%)	0/38(0%)	+1
Features	s:					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSII		633		
Sbjct	1	MDILPSGNIF EL+ I TGY+S+QPS+I MDILPSGNIFRELQDIHDTGYFSAQPSLI		38		

Krueppel-like factor 6, partial [Harpegnathos saltator]

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

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	2e-08()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+1
Feature	s:						
Query	520		GNIFSELERICTTGYYSSQPSIE				
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE				

hypothetical protein LOTGIDRAFT_126955 [Lottia gigantea]

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

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

Score		Expect Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	2e-08() Compositional matrix adjust.	25/34(74%)	30/34(88%)	0/34(0%)	+1
Feature	s:					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSIEMDILPSGNIF EL+ + TGY+SSQPS+EMDILPSGNIF EL+ + TGY+SQPS+EMDILPSGNIF EL- + TGY+SQPS-EMDILPSGNIF EL- +				
Sbjct	1	MDILPSGNIFRELQVVHDTGYFSSQPSLE				

conserved hypothetical protein [Pediculus humanus corporis]

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

See 1 more title(s)

Range 1: 1 to 38

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.5 bits	s(140)	3e-08()	Compositional matrix adjust.	26/38(68%)	30/38(78%)	0/38(0%)	+1
Features	S :						
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+SS+PS+EI		633		
Sbjct	1		GNIFRELQTIHDTGYFSSEPSLEI		38		

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

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

Score		Expect	Method		Identities	Positives	Gaps	Frame	
58.9 bits(141)	3e-07()	Compositional matrix adj	iust.	25/34(74%)	29/34(85%)	0/34(0%)	+1	
Features:									
Query	520		GNIFSELERICTTGYYSS(GNIF EL+ I TGY+S+(

Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 3

PREDICTED: Krueppel-like factor 6 [Halyomorpha halys]

Sequence ID: ref[XP_014290567.1] Length: 252 Number of Matches: 1

Range 1: 1 to 34

Score **Expect Method** Identities **Positives Frame** Gaps 58.5 bits(140) 4e-07() Compositional matrix adjust. 25/34(74%) 29/34(85%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Query 520 621 Sbjct MDILPSGNIFRELQDIHETGYFSAQPSLEDHWQQ 1

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

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

Range 1: 1 to 34

Identities Score **Expect Method Positives** Gaps Frame 59.3 bits(142) 5e-07() Compositional matrix adjust. 25/34(74%) 29/34(85%) 0/34(0%) Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ 621 Query 520 Sbjct MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34 1

PREDICTED: Krueppel-like factor 6 isoform X1 [Polistes canadensis]

Sequence ID: ref|XP_014605830.1| Length: 378 Number of Matches: 1

Range 1: 1 to 34

Score **Expect Method** Identities **Positives** Gaps Frame 59.3 bits(142) 5e-07() Compositional matrix adjust. 25/34(74%) 29/34(85%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 520 621 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

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

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

Range 1: 1 to 34

Score Expect Method Identities Positives Gaps Frame

58.9 bits(141) 6e-07() Compositional matrix adjust. 25/34(74%) 29/34(85%) 0/34(0%) +1

Features:

Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621
MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ
Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

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

Sequence ID: ref|XP_012264721.1| Length: 378 Number of Matches: 1

Range 1: 1 to 34

 Score
 Expect
 Method
 Identities
 Positives
 Gaps
 Frame

 58.9 bits(141)
 6e-07()
 Compositional matrix adjust.
 25/34(74%)
 29/34(85%)
 0/34(0%)
 +1

Features:

Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621 MDILPSGNIF EL+ I TGY+S+QPS+ED WQQ Sbjct 1 MDILPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 34

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

Range 1: 1 to 34

Score		Expect	Method	Identities	•	Positives	Gaps	Frame
58.9 bits	s(141)	6e-07()	Compositional matrix adjust.	25/34(74	%)	29/34(85%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIE GNIF EL+ I TGY+S+QPS+E		21			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		4			

PREDICTED: Krueppel-like factor 7 isoform X1 [Diachasma alloeum]

Sequence ID: ref|XP_015127225.1| Length: 383 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
58.9 bits	(141)	6e-07()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		621			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI		34			

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

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

Range 1: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
58.9 bits	(141)	6e-07() Compositional matrix adjust.	25/34(74%	(a) 29/34(85%)	0/34(0%)	+1
Features	S :					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSIE MDILPSGNIF EL+ I TGY+S+QPS+E		1		
Sbjct	1	MDILPSGNIFRELQDIHDTGYFSAQPSLE				

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

Sequence ID: ref[XP_015127226.1] Length: 375 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	6e-07()	Compositional matrix adjust.	25/34(74%) 29/34(85%)	0/34(0%)	+1
Feature	s:						
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		-		
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI				

PREDICTED: Krueppel-like factor 6 [Orussus abietinus]

Sequence ID: ref[XP_012279401.1] Length: 378 Number of Matches: 1

Score		Expect	Method	Identitie	s	Positives	Gaps	Frame
58.9 bits	s(141)	6e-07()	Compositional matrix adjust.	25/34(74	4%)	29/34(85%)	0/34(0%)	+1
Feature	s:							
Query	520		GNIFSELERICTTGYYSSQPSIE		621			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		34			

PREDICTED: LOW QUALITY PROTEIN: Krueppel-like factor 7 [Apis florea] Sequence ID: **ref|XP_003693621.2|** Length: 374 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
58.9 bits	s(141)	6e-07()	Compositional matrix adjust.	25/34(74%) 29/34(85%)	0/34(0%)	+1
Feature	s:						
Query	520		GNIFSELERICTTGYYSSQPSIE GNIF EL+ I TGY+S+QPS+E		-		
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE				

PREDICTED: Krueppel-like factor 6 [Microplitis demolitor]

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

Range 1: 1 to 34

Score	Expect Method Identities		Positives	Gaps	Frame			
58.9 bits(141)		7e-07()	Compositional matrix adjust.	25/34(74%)		29/34(85%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIE GNIF EL+ I TGY+S+QPS+E		621			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLE		34			

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

Range 1: 1 to 34

Score		Expect	Method	Identiti	ies	Positives	Gaps	Frame
58.9 bits	(141)	7e-07()	Compositional matrix adjust.	25/34(7	74%)	29/34(85%)	0/34(0%)	+1
Features	3 :							
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		621			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI		34			

PREDICTED: Krueppel-like factor 6 isoform X1 [Bombus terrestris]
Sequence ID: **ref|XP_003396776.1**| Length: 378 Number of Matches: 1

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

Score		Expect	Method	Identit	ies	Positives	Gaps	Fram
58.9 bits	(141)	7e-07()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIED GNIF EL+ I TGY+S+QPS+ED		621			
			GNIFRELODIHDTGYFSAÖPSLEI		34			

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

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
58.9 bits	s(141)	7e-07()	Compositional matrix adjust.	25/34(74%)	29/34(85%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+QPS+EI		621			
Sbjct	1		GNIFRELQDIHDTGYFSAQPSLEI		34			

PREDICTED: Krueppel-like factor 6 isoform X1 [Cimex lectularius]

Sequence ID: ref|XP_014239870.1| Length: 296 Number of Matches: 1

Range 1: 1 to 34

Score		Expect Method	I	Identitie	es	Positives	Gaps	Frame
58.5 bits(140)		7e-07() Compos	sitional matrix adjust.	25/34(7	4%)	29/34(85%)	0/34(0%)	+1
Feature	s:							
Query	520		LERICTTGYYSSQPSIEI L+ I TGY+S+QPS+EI		621			
Sbjct	1		LQDIHDTGYFSAQPSLEI		34			

PREDICTED: Krueppel-like factor 6 [Lingula anatina]

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

Range 1: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
58.2 bits(139)		1e-06()	Compositional matrix adjust.	23/34(68%)	30/34(88%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIE GNIF EL+ + TGY+S+QPS+E		621			
Sbjct	1		GNIFRELQVVHDTGYFSAQPSLE		34			

PREDICTED: Krueppel-like factor 6 [Crassostrea gigas]

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

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
57.4 bits(137)		2e-06()	Compositional matrix adjust.	23/34(68%)	30/34(88%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIE		621			
Sbjct	1		GNIFRELQVVHDTGYFSAQPSLE		34			

Krueppel-like factor 6, partial [Camponotus floridanus]

Sequence ID: gb|EFN71037.1| Length: 32 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	2e-06()	Compositional matrix adjust.	22/32(69%) 27/32(84%)	0/32(0%)	+1
Features	S :						
Query	526		IIFSELERICTTGYYSSQPSIED IIF EL+ I TGY+S+QPS+ED				

Sbjct 1 LLPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 32

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

See 1 more title(s)

Range 1: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
55.5 bits	s(132)	6e-06() Compositional matrix adjust.	24/34(71%	28/34(82%)	0/34(0%)	+1
Feature	s:					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSIE MD+LPSG IFSEL+ I TGY+S QPS+E				
Sbjct	1	MDLLPSGEIFSELQMIHDTGYFSCQPSLE				

PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]

Sequence ID: ref|XP_013777058.1| Length: 374 Number of Matches: 1

Range 1: 24 to 57

Score		Expect Method	Identities	Positives	Gaps	Frame
55.8 bits	s(133)	6e-06() Compositional matrix adjus	t. 22/34(65%)	29/34(85%)	0/34(0%)	+1
Feature	s:					
Query	520	MDILPSGNIFSELERICTTGYYSSQP: MD+LPSG IF EL+ + TGY+S+QP:				
Sbjct	24	MDVLPSGGIFGELQVVHDTGYFSAQP:				

PREDICTED: Krueppel-like factor 7 [Polistes dominula]

Sequence ID: ref[XP_015182091.1] Length: 378 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
55.8 bits	(133)	7e-06()	Compositional matrix adjust.	24/34(71%)	28/34(82%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI GNIF EL+ I TGY+S+Q S+EI		621			
Sbjct	1		GNIFRELQLIHDTGYFSAQASLEI		34			

Krueppel-like factor [Cerapachys biroi]

Sequence ID: gb|EZA60583.1| Length: 92 Number of Matches: 1

Range 1: 1 to 35

Score		Expect Method	Identities	Positives	Gaps	Frame	
52.8 bits	s(125)	7e-06() Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+1	
Feature	s:						
Query	520	MD-ILPSGNIFSELERICTTGYYSSQPSI MD +LPSGNIF EL+ I TGY+S+QPS+		1			
Sbjct	1	MDTLLPSGNIFRELQDIHDTGYFSAQPSL					

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

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

Range 1: 1 to 35

Score Expect Method Identities Positives Gaps Frame

55.8 bits(133) 8e-06() Compositional matrix adjust. 23/35(66%) 29/35(82%) 0/35(0%) +1

Features:

Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQK 624 MDILPS NIF EL+ + TGY+S+QPS+ED+WQQ Sbjct 1 MDILPSSNIFRELQVVHDTGYFSAQPSLEDRWQQN 35

PREDICTED: Krueppel-like factor 6 [Biomphalaria glabrata]

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

Range 1: 1 to 34

Score Expect Method Identities Positives Frame Gaps 22/34(65%) 29/34(85%) 0/34(0%) +1 54.3 bits(129) 2e-05() Compositional matrix adjust. Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILP+ NIF EL+ + TGY+S+QPS+ED+WQQ Query 520 621 MDILPTSNIFRELQVVHETGYFSAQPSLEDRWQQ Sbjct 1 34

PREDICTED: Krueppel-like factor 6 [Acyrthosiphon pisum]

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

Range 1: 1 to 34

Score Expect Method Identities **Positives** Gaps Frame 22/34(65%) 27/34(79%) 0/34(0%) 53.9 bits(128) 3e-05() Compositional matrix adjust. Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 520 621 MD+LPSGNIF EL+ I TGY+S+ S+ED WQQ Sbjct 1 MDVLPSGNIFRELQDIHDTGYFSAHVSLEDHWQQ

PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]

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

Range 1: 1 to 34

Score **Expect Method** Identities **Positives** Gaps **Frame** 53.9 bits(128) 3e-05() Compositional matrix adjust. 23/34(68%) 28/34(82%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPSGNIF EL+ + TG++SSQ S+ED WQQ 621 Query Sbjct 1 MDILPSGNIFRELQTVHDTGFFSSQLSLEDMWQQ

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

Range 1: 1 to 35

Score Expect Method Identities Positives Gaps Frame

53.5 bits(127) 5e-05() Compositional matrix adjust. 24/35(69%) 29/35(82%) 1/35(2%) +1

Features:

Query 520 MD-ILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621

Sbjct 1 MDTLLPSGNIF EL+ I TGY+S+QPS+ED WQQ
Sbjct 1 MDTLLPSGNIFRELQDIHDTGYFSAQPSLEDHWQQ 35

PREDICTED: Krueppel-like factor 6 isoform X1 [Cerapachys biroi]

Sequence ID: ref|XP_011352442.1| Length: 377 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.5 bits	(127)	5e-05()	Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+1
Features	s:						
Query	520		PSGNIFSELERICTTGYYSSQPSI PSGNIF EL+ I TGY+S+QPS+		l		
Sbjct	1		SGNIF ELT I IGITSTOFST SGNIFRELQDIHDTGYFSAQPSL				

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

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
50.1 bits	s(118)	5e-05()	Compositional matrix adjust.	20/34(59%)	26/34(76%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIEI GN+F ELE + TGY+ + S+EI		621			
Sbjct	1		GNLFRELEHVTDTGYFEWKLSLEI		34			

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

Range 1: 4 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	5e-05()	Compositional matrix adjust.	22/32(69%)	27/32(84%)	0/32(0%)	+1
Features	S :						
Query	526		IFSELERICTTGYYSSQPSIEDQWIF EL+ I TGY+S+QPS+ED W				
Sbjct	4		IFRELQDIHDTGYFSAQPSLEDHV				

PREDICTED: Krueppel-like factor 6 [Vollenhovia emeryi]

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

Range 1: 1 to 35

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bits	(126)	5e-05() Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+1
Features	S :					
Query	520	MD-ILPSGNIFSELERICTTGYYSSQPSI MD +LPSGNIF EL+ I TGY+S+QPS+		L		
Sbjct	1	MDTLLPSGNIFRELQDIHDTGYFSAQPSI				

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

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

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bit	s(126)	5e-05() Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+1
Feature	es:					
Query	520	MD-ILPSGNIFSELERICTTGYYSSQPSI MD +LPSGNIF EL+ I TGY+S+QPS+		L		
Sbjct	1	MDTLLPSGNIFRELQDIHDTGYFSAQPSL				

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

Range 1: 1 to 35

Score		Expect Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	5e-05() Compositional matrix adjust.	24/35(69%)	29/35(82%)	1/35(2%)	+1
Features	s:					
Query	520	MD-ILPSGNIFSELERICTTGYYSSOPSI		L		
Sbjct	1	MD +LPSGNIF EL+ I TGY+S+QPS+ MDTLLPSGNIFRELQDIHDTGYFSAQPSI				

PREDICTED: Krueppel-like factor 6 [Limulus polyphemus]

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

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
53.1 bits	(126)	6e-05()	Compositional matrix adjust.	23/34(6	68%)	28/34(82%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIEI G IF EL+ + TGY+SSQ S+EI		621			
Sbjct	1		GGIFRELQVVHDTGYFSSQLSLEI		34			

putative Kruppel-like factor 6 [Daphnia pulex]

Sequence ID: gb|EFX88687.1| Length: 429 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
53.1 bits	s(126)	6e-05()	Compositional matrix adjust.	22/34(65%) 27/34(79%)	0/34(0%)	+1
Features	s:						
Query	520		GNIFSELERICTTGYYSSQPSIE		1		
Sbjct	1		GNIFRELQVVHDTGYLSAQTSLE				

hypothetical protein TcasGA2_TC003609 [Tribolium castaneum]

Sequence ID: gb|EFA00728.1| Length: 213 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
52.4 bits	s(124)	7e-05()	Compositional matrix adjust.	22/34(65%)	27/34(79%)	0/34(0%)	+1
Features	s:							
Query	520	MDILPS MDILPS	GNIFSELERICTTGYYSSQPSIE IF EL+ I TGY+S+QPS++		621			
Sbjct	1		VGIFRELQDIHDTGYFSAQPSLD		34			

hypothetical protein KGM_08804 [Danaus plexippus]

Sequence ID: **gb|EHJ66609.1|** Length: 58 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
49.3 bits	(116)	9e-05()	Compositional matrix adjust.	20/40(50%)	28/40(70%)	0/40(0%)	+1
Features	:						
Query	520		GNIFSELERICTTGYYSSQPSIED GN+F EL+ + TGY+ + S+ED				
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLED				

PREDICTED: Krueppel-like factor 6 isoform X1 [Tribolium castaneum]

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

Range 1: 1 to 34

Score Expect Method Identities **Positives** Gaps Frame 52.0 bits(123) 1e-04() Compositional matrix adjust. 22/34(65%) 27/34(79%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDILPS IF EL+ I TGY+S+QPS++D WQQ MDILPSVGIFRELQDIHDTGYFSAQPSLDDHWQQ Query 520 621 Sbjct 1 34

zinc finger protein [Ciona intestinalis]

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

See 1 more title(s)

Range 1: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
52.0 bits	s(123)	1e-04() Compositional matrix adjust.	22/34(65%)	28/34(82%)	0/34(0%)	+1
Features	s:					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSIE MDILP GNIF+EL+ I TGY+S+ PS+E				
Sbjct	1	MDILPCGNIFNELQIIHDTGYFSALPSLE				

hypothetical protein RR46_12790 [Papilio xuthus]

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

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

Score		Expect	Method	Identities	Positives	Gaps	Frame
47.4 bits	s(111)	3e-04()	Composition-based stats.	19/34(56%)	26/34(76%)	0/34(0%)	+1
Features	S :						
Query	520		GNIFSELERICTTGYYSSQPSI GN+F EL+ + TGY+ + S+	~ ~~	-		
Sbjct	1		GNLFRELQDVTDTGYFEWKLSL	~~			

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

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
50.4 bits	(119)	5e-04()	Compositional matrix adjust.	23/35(66%)	28/35(80%)	1/35(2%)	+1
Features	s:						
Query	520		PSGNIFSELERICTTGYYSSQPSIPS NIF EL+ I TGY+S+QPS+		L		
Shict	1		PSSNIFRELODIHDTGYFSAÖPSL				

PREDICTED: Krueppel-like factor 7 [Amyelois transitella]

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

Range 1: 1 to 34

Score Expect Method Identities Positives Gaps Frame 49.3 bits(116) 7e-04() Compositional matrix adjust. 19/34(56%) 26/34(76%) 0/34(0%) +1

Features:

Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621 MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEYKVSLEDNWQQ 34

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

MDILPSSAIFNELEVVHSTGYFSALPSLEEHWHQ

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

Range 1: 1 to 34

Score Identities **Positives Expect Method** Gaps Frame 49.7 bits(117) 8e-04() Compositional matrix adjust. 20/34(59%) 27/34(79%) 0/34(0%) +1 Features: Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621 MDILPS IF+ELE + +TGY+S+ PS+E+ W Q

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

Sequence ID: ref|XP_003748452.1| Length: 284 Number of Matches: 1

Range 1: 1 to 34

Sbjct 1

Expect Method Score Identities **Positives** Frame Gaps 9e-04() Compositional matrix adjust. 22/34(65%) 27/34(79%) 49.7 bits(117) 0/34(0%) Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ MDIL SG+IF+EL+ I TGY SQPS+E+ WQQ Query 520 621 MDILASGSIFNELQAIHDTGYLPSQPSLEETWQQ Sbjct 1 34

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

Sequence ID: ref|XP_013179377.1| Length: 211 Number of Matches: 1

Range 1: 1 to 34

Score Identities **Positives** Expect Method Gaps Frame 48.1 bits(113) 0.002() Compositional matrix adjust. 19/34(56%) 26/34(76%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 520 621 Query MD+LPSGN+F EL+ + TGY+ + S+ED WQQ Sbjct 1 MDVLPSGNLFRELQDVTDTGYFEWKLSLEDYWQQ 34

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

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

Range 1: 1 to 34

Identities **Positives** Score **Expect Method** Gaps Frame 48.1 bits(113) 0.002() Compositional matrix adjust. 19/34(56%) 26/34(76%) 0/34(0%) +1 Features: MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ Query 520 621 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: 1

Range 1: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
48.5 bits	s(114)	0.002()	Compositional matrix adjust.	19/34(5	6%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIE		621			
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLE		34			

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

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

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits	s(113)	0.002()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+1
Feature	s:						
Query	520		GNIFSELERICTTGYYSSQPSIE GN+F EL+ + TGY+ + S+E				
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLE:				

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

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

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
48.1 bits	s(113)	0.002()	Compositional matrix adjust.	19/34(56%	o) 26/34(76%)	0/34(0%)	+1
Features	s:						
Query	520		GNIFSELERICTTGYYSSQPSIEI GN+F EL+ + TGY+ + S+EI		1		
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLEI				

PREDICTED: Krueppel-like factor 6 [Plutella xylostella]

Sequence ID: **ref|XP_011553149.1**| Length: 250 Number of Matches: 1 Range 1: 1 to 34

Score		Expect	Method	Identities	s	Positives	Gaps	Frame
48.5 bits	s(114)	0.002()	Compositional matrix adjust.	19/34(56	8%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI GN+F EL+ + TGY+ + S+EI		21			
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLEI		34			

PREDICTED: Krueppel-like factor 6 [Papilio polytes]

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

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
48.1 bits	s(113)	0.002()	Compositional matrix adjust.	19/34(5	6%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI GN+F EL+ + TGY+ + S+EI		621			
Sbjct	1		GNLFRELQDVTDTGYFEWKLSLEI		34			

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

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

Range 1: 1 to 34

Score		Expect	Method	Identiti	ies	Positives	Gaps	Frame
44.3 bits	s(103)	0.008()	Compositional matrix adjust.	18/34(5	53%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEL +IF EL+ + TGY+S+ PS+E+		621			
Sbjct	1		YSIFQELQLVHDTGYFSALPSLEE		34			

PREDICTED: Krueppel-like factor 7 [Callorhinchus milii]

Sequence ID: ref|XP_007898243.1| Length: 272 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
46.6 bits	46.6 bits(109)		Compositional matrix adjust.	19/34(56%)		27/34(79%)	0/34(0%)	+1
Feature	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI + +IF EL+ + TGY+SSQPS+E+		621			
Sbjct	1		YSIFQELQLVHDTGYFSSQPSLE		34			

hypothetical protein QR98_0081480 [Sarcoptes scabiei]

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

Range 1: 1 to 35

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.009()	Composition-based stats.	19/35(54%)	28/35(80%)	0/35(0%)	+1
Features	3 :						
Query	520		GNIFSELERICTTGYYSSQPSIE G+ F+EL+ I TGY+ + S+E		4		
Sbjct	1		GHFFNELQAIHDTGYFPANLSLE				

PREDICTED: Krueppel-like factor 6 [Thamnophis sirtalis]

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

Range 1: 1 to 34

Score		Expect	Method	Identities		Positives	Gaps	Frame
44.3 bits	s(103)	0.011()	Compositional matrix adjust.	ıst. 18/34(53%)		26/34(76%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIE +IF EL+ + TGY+S+ PS+E-		621			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

Bcd orf1 [Homo sapiens]

Sequence ID: gb|AAB94792.1| Length: 79 Number of Matches: 1

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits	s(101)	0.016()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+1
Feature	s:						
Query	520		GNIFSELERICTTGYYSSQPSII				

Sbjct 1 MDVLPMCSIFQELQIVHETGYFSALPSLEEYWQQ 34

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

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

Range 1: 1 to 34

Score Expect Method Identities Positives Gaps Frame

43.9 bits(102) 0.017() Compositional matrix adjust. 18/34(53%) 26/34(76%) 0/34(0%) +1

Features:

Query 520 MDILPSGNIFSELERICTTGYYSSQPSIEDQWQQ 621
MD+L S +IF EL+ + TGY+S+ PS+E+ WQQ
Sbjct 1 MDVLASYSIFQELQLVHDTGYFSALPSLEETWQQ 34

Kruppel-like factor 7 [Strongylocentrotus purpuratus]

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

See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
45.8 bits(107)		0.018()	Compositional matrix adjust.	20/34(5	9%)	25/34(73%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIER G IF+ELE I TG +S+ PS+E-		621			
Sbjct	1		GGIFNELEIIGETGCFSALPSVE		34			

unnamed protein product [Oncorhynchus mykiss]

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

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
45.8 bits	(107)	0.018()	Compositional matrix adjust.	19/34(56%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+EI		621			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLEI		34			

PREDICTED: Krueppel-like factor 6 [Salmo salar]

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

▶ See 1 more title(s)

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
45.4 bits(106)		0.019()	Compositional matrix adjust.	19/34(56%)		26/34(76%)	0/34(0%)	+1
Feature	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+EI		621			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLEI		34			

PREDICTED: Krueppel-like factor 7 [Notothenia coriiceps]

Sequence ID: ref|XP_010783713.1| Length: 331 Number of Matches: 1

Range 1: 25 to 60

Score		Expect	Method	Identities	Positives	Gaps	Frame
45.8 bits	s(107)	0.020()	Compositional matrix adjust.	17/36(47%) 27/36(75%)	0/36(0%)	+1
Feature	s:						
Query	514		PSGNIFSELERICTTGYYSSQPS + +IF EL+ + TGY+S+ PS		521		
Sbjct	25		ANHSIFQELQIVHDTGYFSAMPS	~~	50		

unknown [Homo sapiens]

Sequence ID: gb|AAY15081.1| Length: 34 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
42.4 bits	s(98)	0.022()	Composition-based stats.	18/34(53%)	26/34(76%)	0/34(0%)	+1
Features	s:						
Query	520		SGNIFSELERICTTGYYSSQPS S +IF EL+ + TGY+S+ PS-		1		
Sbjct	1		SYSIFQELQLVHDTGYFSALPSI				

PREDICTED: Krueppel-like factor 6 [Clupea harengus]

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

Range 1: 1 to 34

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
44.7 bits(104)		0.023()	Compositional matrix adjust.	17/34(50%)		27/34(79%)	0/34(0%)	+1
Feature	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF+EL+ + TGY+S+ PS+E-		621			
Sbjct	1		CSIFNELQTVHDTGYFSALPSLEI		34			

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

Range 1: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
45.1 bits	(105)	0.031()	Compositional matrix adjust.	18/34(53%)		26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E+		621			
Sbjct	1		YSIFQELQLVLDTGYFSALPSLE		34			

Krueppel-like factor 6 [Amazona aestiva]

Sequence ID: **gb|KQK80056.1|** Length: 324 Number of Matches: 1 Range 1: 24 to 75

Score		Expect Method	Identities	Positives	Gaps	Frame
44.7 bits	s(104)	0.048() Compositional matrix adjust.	24/55(44%)	35/55(63%)	5/55(9%)	+1
Features	S :					
Query	463	NGLKTDSLEFLRCEEEDIKMDILPSGNII NG+ T + E RC + MD+LP +II				21
Sbjct	24	NGISTPMIKSERQRCVRDMDVLPMCSI				5

PREDICTED: Krueppel-like factor 6 [Colius striatus]

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

Range 1: 1 to 33

Score		Expect Method	Identities	Positives	Gaps	Frame
44.3 bits	s(103)	0.049() Compositional matrix adjust.	18/33(55%) 25/33(75%)	0/33(0%)	+1
Features	s:					
Query	520	MDILPSGNIFSELERICTTGYYSSQPSI MD+LP +IF EL+ + TGY+S+ PS+				
Sbjct	1	MDVLPMCSIFQELQIVHDTGYFSALPSL				

PREDICTED: Krueppel-like factor 6 isoform X2 [Anser cygnoides domesticus]

Sequence ID: ref|XP_013041223.1| Length: 221 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identities	Po	sitives	Gaps	Frame
43.9 bits	s(102)	0.063()	Compositional matrix adjust.	18/34(53%	(a) 26/	/34(76%)	0/34(0%)	+1
Features	S :							
Query	520		GNIFSELERICTTGYYSSQPSIED +IF EL+ + TGY+S+ PS+E+		1			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLEE					

PREDICTED: Krueppel-like factor 6 isoform X2 [Melopsittacus undulatus] Sequence ID: **ref|XP_005153078.1**| Length: 241 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.063()	Compositional matrix adjust.	18/34(53%) 26/34(76%)	0/34(0%)	+1
Feature	s:						
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E-		I		
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE				

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

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

Range 1: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
43.5 bits	s(101)	0.064() Compositional mat	rix adjust. 18/34(53%	6) 26/34(76%)	0/34(0%)	+1
Features	s:					
Query	520	MDILPSGNIFSELERICTTG MD+LP +IF EL+ + TG		1		
Sbjct	1	MDVLPMCSIFQELQIVHETG				

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

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

Score		Expect	Method	Identit	ies	Positives	Gaps	Frame
43.9 bits	s(102)	0.065()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E+		621			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Egretta garzetta]

Sequence ID: ref|XP_009639640.1| Length: 241 Number of Matches: 1

Range 1: 1 to 34

Score	Expect Method	Identities	Positives	Gaps	Frame
43.9 bits(102) 0.065() Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+1
Features:					
Query 52	MDILPSGNIFSELERICTTGYYSSQPSIE MD+LP +IF EL+ + TGY+S+ PS+E				
Sbjct 1	MDVLPMCSIFQELQIVHDTGYFSALPSLE				

PREDICTED: Krueppel-like factor 6 isoform X2 [Ficedula albicollis]

Sequence ID: ref|XP_005040665.1| Length: 241 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	Identitie	es	Positives	Gaps	Frame
43.9 bits	s(102)	0.065()	Compositional matrix adjust.	18/34(5	3%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E-		621			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Opisthocomus hoazin]

Sequence ID: ref[XP_009943445.1] Length: 241 Number of Matches: 1

Range 1: 1 to 34

Score		Expect Method	Identities	Positives	Gaps	Frame
43.9 bits	s(102)	0.066() Compositional mat	rix adjust. 18/34(53%)	26/34(76%)	0/34(0%)	+1
Features	S :					
Query	520	MDILPSGNIFSELERICTTG	~ ~~~			
Sbjct	1	MD+LP +IF EL+ + TG MDVLPMCSIFQELQIVHDTG				

PREDICTED: zinc finger protein 396 isoform X2 [Acanthisitta chloris]

Sequence ID: ref|XP_009082634.1| Length: 241 Number of Matches: 1

Range 1: 1 to 34

Score		Expect	Method	ldentit	ies	Positives	Gaps	Frame
43.9 bits	s(102)	0.066()	Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+1
Features	s:							
Query	520		GNIFSELERICTTGYYSSQPSIEI +IF EL+ + TGY+S+ PS+E-		621			
Sbjct	1		CSIFQELQIVHDTGYFSALPSLE		34			

PREDICTED: Krueppel-like factor 6 isoform X2 [Manacus vitellinus]

Sequence ID: ref|XP_008931128.1| Length: 241 Number of Matches: 1

Score	Expect Method	Identities	Positives	Gaps	Frame
43.9 bits(102)	0.067() Compositional matrix adjust.	18/34(53%)	26/34(76%)	0/34(0%)	+1
Features:					
Query 520	MDILPSGNIFSELERICTTGYYSSQPSIE MD+LP +IF EL+ + TGY+S+ PS+E				