BLAST ® » blastp suite » RID-DBFJ4AW6015

BLAST Results

Questions/comments

Job title: 2 sequences (Sequentie 1)

RID DBFJ4AW6015 (Expires on 04-18 17:28 pm)

Query ID | |cl||Query_93343 Description | Sequentie 1

Molecule type amino acid Query Length 350 Database Name nr

Description All non-redundant GenBank CDS

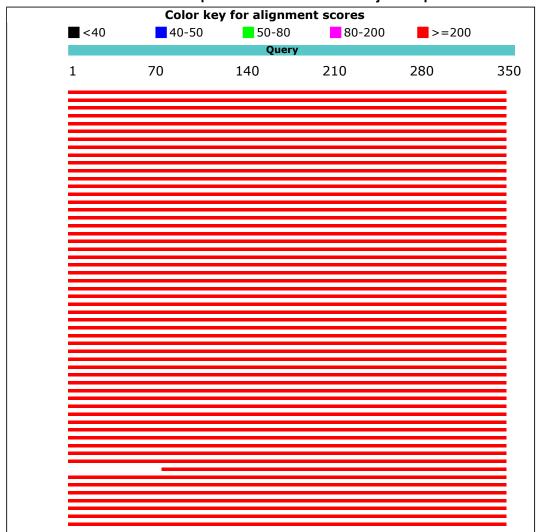
translations+PDB+SwissProt+PIR+PRF excluding environmental samples from

WGS projects

Program BLASTP 2.8.0+

Graphic Summary

Distribution of the top 100 Blast Hits on 100 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
acetateCoA ligase [Lactococcus lactis]	735	735	100%	0.0	100%	WP_058213135.1
acetateCoA ligase [Lactococcus lactis]	735	735	100%	0.0	100%	WP_058218837.1
long-chain acyl-CoA synthetase [Lactococcus lactis]	735	735	100%	0.0	100%	WP_010905493.1
acetateCoA ligase [Lactococcus lactis]	734	734	100%	0.0	100%	WP_081213417.1
long-chain acyl-CoA synthetase [Lactococcus lactis subsp. lactis]	734	734	100%	0.0	99%	PCS18680.1
acyl-coenzyme A synthetases/AMP- (fatty) acid ligases [Lactococcus lactis subsp. lactis]	733	733	100%	0.0	99%	GAM79651.1
acetateCoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	WP_033899641.1
long-chain-fatty-acidCoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	WP_023188928.1
AcetateCoA ligase [Lactococcus lactis subsp. lactis CNCM I-1631]	733	733	100%	0.0	99%	EHE94728.1
acetateCoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	WP_085624039.1
acetateCoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	WP_032398871.1
long-chain acyl-CoA synthetase [Lactococcus lactis]	733	733	100%	0.0	99%	WP_021723121.1
acetateCoA ligase [Lactococcus lactis]	732	732	100%	0.0	99%	WP_098394061.1
acetateCoA ligase [Lactococcus lactis]	732	732	100%	0.0	99%	WP_058211161.1
acetateCoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	WP_098407787.1
acetateCoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	WP_060416383.1
acetateCoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	WP_058225361.1
acetateCoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	WP_058203219.1
acetateCoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	WP_014570399.1
acetateCoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	WP_058217542.1
acetateCoA ligase [Lactococcus lactis]	730	730	100%	0.0	99%	WP_104143433.1
acetateCoA ligase [Lactococcus lactis]	730	730	100%	0.0	99%	WP_038599620.1
acetateCoA ligase [Lactococcus lactis]	730	730	100%	0.0	99%	WP_029344950.1
acetateCoA ligase [Lactococcus lactis]	728	728	100%	0.0	99%	WP_058205270.1
acetateCoA ligase [Lactococcus lactis]	728	728	100%	0.0	99%	WP_058218957.1

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Description	Max score	Total score	Query cover	E value	Ident	Accession
long-chain acyl-CoA synthetase [Lactococcus lactis subsp. lactis]	728	728	100%	0.0	99%	KRO23413.1
acetateCoA ligase [Lactococcus lactis]	727	727	100%	0.0	99%	WP_103054515.1
acetateCoA ligase [Lactococcus lactis]	727	727	100%	0.0	99%	WP_082272274.1
acetateCoA ligase [Lactococcus lactis]	727	727	100%	0.0	99%	WP_057720320.1
long-chain acyl-CoA synthetase [Lactococcus lactis subsp. hordniae]	723	723	100%	0.0	98%	PCS10929.1
acetateCoA ligase [Lactococcus lactis]	723	723	100%	0.0	98%	WP_058209009.1
long-chain acyl-CoA synthetase [Lactococcus lactis]	715	715	100%	0.0	97%	WP_015425959.1
acetateCoA ligase [Lactococcus lactis]	685	685	100%	0.0	92%	WP_061778018.1
Acs family protein [Lactococcus lactis]	685	685	100%	0.0	92%	WP_021211606.1
acetateCoA ligase [Lactococcus lactis]	685	685	100%	0.0	92%	WP_014573007.1
acetateCoA ligase [Lactococcus lactis subsp. cremoris TIFN3]	684	684	100%	0.0	92%	EQC94180.1
long-chain acyl-CoA synthetase [Lactococcus lactis]	684	684	100%	0.0	92%	WP_015082155.1
amino acid adenylation domain protein [Lactococcus lactis subsp. cremoris]	684	684	100%	0.0	92%	KKW73985.1
acetateCoA ligase [Lactococcus lactis]	683	683	100%	0.0	92%	WP_063281423.1
acetateCoA ligase [Lactococcus lactis]	683	683	100%	0.0	92%	WP_011675629.1
acetateCoA ligase [Lactococcus lactis]	683	683	100%	0.0	92%	WP_011834637.1
AMP-binding protein [Lactococcus lactis]	682	682	100%	0.0	92%	WP_021036845.1
acetateCoA ligase [Lactococcus lactis]	682	682	100%	0.0	92%	WP_081196842.1
acetateCoA ligase [Lactococcus lactis]	682	682	100%	0.0	92%	WP_101913658.1
acetateCoA ligase [Lactococcus lactis subsp. cremoris TIFN6]	681	681	100%	0.0	92%	EQC53627.1
Acs family protein [Lactococcus lactis]	680	680	100%	0.0	92%	WP_021166362.1
acetateCoA ligase [Lactococcus lactis]	680	680	100%	0.0	92%	WP_043736020.1
acetateCoA ligase [Lactococcus lactis]	679	679	100%	0.0	91%	WP_046124848.1
amino acid adenylation domain protein [Lactococcus lactis subsp. lactis]	576	576	78%	0.0	98%	KLK97297.1
Acs family protein [Lactococcus petauri]	576	576	100%	0.0	76%	WP_086582890.1
Acs family protein [Lactococcus garvieae]	574	574	100%	0.0	76%	WP_004256244.1
acetateCoA ligase [Lactococcus sp. DD01]	574	574	100%	0.0	76%	WP_061412802.1
acetateCoA ligase [Lactococcus garvieae]	574	574	100%	0.0	76%	WP_046400975.1

			NODI DIGOLE	0094011000 (009	juditud 1)		
	Description	Max score	Total score	Query cover	E value	Ident	Accession
	acetateCoA ligase [Lactococcus garvieae]	572	572	100%	0.0	76%	WP_096369325.1
	acetateCoA ligase [Lactococcus garvieae]	572	572	100%	0.0	76%	WP_019293837.1
	acetateCoA ligase [Lactococcus garvieae]	570	570	100%	0.0	75%	WP_081166459.1
	acetateCoA ligase [Lactococcus garvieae]	570	570	100%	0.0	76%	WP_017369201.1
	Acs family protein [Lactococcus garvieae]	570	570	100%	0.0	75%	WP_003135509.1
	acetateCoA ligase [Lactococcus garvieae]	568	568	100%	0.0	75%	WP_042219301.1
	acetateCoA ligase [Lactococcus garvieae]	568	568	100%	0.0	75%	WP_017371191.1
	acetateCoA ligase [Lactococcus garvieae TRF1]	568	568	100%	0.0	75%	ETD05431.1
	acetateCoA ligase [Lactococcus garvieae]	567	567	100%	0.0	75%	WP_074750230.1
	acetateCoA ligase [Lactococcus garvieae]	566	566	100%	0.0	75%	WP_014024564.1
	acetateCoA ligase [Enterococcus quebecensis]	446	446	100%	9e-152	59%	WP_069635203.1
	acetateCoA ligase [Carnobacterium gallinarum]	445	445	100%	1e-151	60%	WP_034561934.1
	acetateCoA ligase [Enterococcus aquimarinus]	444	444	100%	2e-151	61%	WP_071874412.1
	AMP-binding protein [Enterococcus haemoperoxidus]	443	443	100%	1e-150	59%	WP_010762120.1
	AMP-binding enzyme [Listeria grayi DSM 20601]	443	443	100%	1e-150	62%	EFI84138.1
	acetateCoA ligase [Listeria grayi]	442	442	100%	1e-150	62%	WP_040486682.1
	acetateCoA ligase [Enterococcus sp. TR]	442	442	100%	3e-150	59%	WP_025870565.1
	acetateCoA ligase [Enterococcus termitis]	442	442	100%	3e-150	59%	WP_086345729.1
	acetateCoA ligase [Listeria grayi]	441	441	100%	6e-150	62%	WP_036103250.1
	acetateCoA ligase [Enterococcus ureasiticus]	440	440	100%	1e-149	59%	WP_069647056.1
	acetateCoA ligase [Enterococcus sp. 9D6_DIV0238]	440	440	100%	1e-149	59%	WP_087641642.1
	AMP-binding protein [Enterococcus cecorum]	440	440	100%	2e-149	61%	WP_016250857.1
	AMP-binding protein [Enterococcus cecorum DSM 20682 = ATCC 43198]	440	440	100%	2e-149	61%	OJG33678.1
	AMP-binding protein [Enterococcus moraviensis]	439	439	100%	2e-149	59%	WP_010766613.1
	acetateCoA ligase [Enterococcus rotai]	438	438	100%	6e-149	59%	ALS36562.1
	acetateCoA ligase [Enterococcus sp. 7F3_DIV0205]	438	438	100%	7e-149	59%	WP_086314805.1
	acetateCoA ligase [Enterococcus cecorum]	438	438	100%	7e-149	61%	WP_087213839.1
	AMP-binding protein [Enterococcus faecalis]	438	438	100%	1e-148	58%	WP_016624877.1
- 1							

		NCDI Diast.2 sequences (Sequentie 1)				
Description	Max score	Total score	Query cover	E value	Ident	Accession
acetateCoA ligase [Enterococcus cecorum]	437	437	100%	3e-148	60%	WP_047341861.1
acetateCoA ligase [Enterococcus wangshanyuanii]	436	436	100%	4e-148	59%	WP_088270465.1
acetateCoA ligase [Enterococcus sp. 12C11_DIV0727]	436	436	100%	4e-148	59%	WP_086445388.1
MULTISPECIES: acetateCoA ligase [Enterococcus]	436	436	100%	4e-148	59%	WP_086277663.1
acetateCoA ligase [Enterococcus ureilyticus]	436	436	100%	5e-148	58%	WP_069640119.1
AMP-binding protein [Enterococcus caccae]	436	436	100%	6e-148	59%	WP_010770289.1
acetateCoA ligase [Enterococcus cecorum]	436	436	100%	8e-148	60%	WP_047242231.1
acetateCoA ligase [Enterococcus cecorum]	436	436	100%	8e-148	60%	WP_047340890.1
acetateCoA ligase [Enterococcus sp. 4G2_DIV0659]	435	435	100%	1e-147	58%	WP_086330426.1
acetateCoA ligase [Enterococcus rivorum]	434	434	100%	3e-147	57%	WP_069697264.1
AMP-binding protein [Enterococcus termitis]	434	434	100%	3e-147	58%	OJG99592.1
acetateCoA ligase [Enterococcus thailandicus]	434	434	100%	4e-147	59%	WP_067482067.1
acetateCoA ligase [Enterococcus cecorum]	434	434	100%	5e-147	60%	WP_087662663.1
acetateCoA ligase [Enterococcus termitis]	434	434	100%	5e-147	58%	WP_069663271.1
acetateCoA ligase [Enterococcus cecorum]	433	433	100%	6e-147	60%	WP_087402632.1
acetateCoA ligase [Enterococcus plantarum]	433	433	100%	8e-147	59%	WP_069653501.1
acetateCoA ligase [Enterococcus cecorum]	433	433	100%	9e-147	60%	WP_047334704.1
acetateCoA ligase [Enterococcus sp. 5B7_DIV0075]	433	433	100%	9e-147	59%	WP_086270931.1
acetateCoA ligase [Enterococcus silesiacus]	433	433	100%	1e-146	58%	WP_071878110.1

Alignments

acetate--CoA ligase [Lactococcus lactis]

Sequence ID: WP_058213135.1 Length: 507 Number of Matches: 1

See 1 more title(s) Range 1: 71 to 420

Score		Expect Method	Identities	Positives	Gaps	Frame
735 bits	s(1897) 0.0() Compositional matri	x adjust. 350/350(100%	5) 350/350(100%	6) 0/350(0%	6)
Feature	es:					
Query	1	IFKSSAFDTYLLAVAVSYLGAVF IFKSSAFDTYLLAVAVSYLGAVF				50
Sbjct	71	IFKSSAFDTYLLAVAVSYLGAVE				130
Query	61	KNLEDSKKLSVSKFALEKPTQIA KNLEDSKKLSVSKFALEKPTQIA	ADSQQLASDEIAYLTHTSG	TTGVPKLIAHSAN	ISMGWRW :	120
Sbjct	131	KNLEDSKKLSVSKFALEKPTQIA	NDSQQLASDEIAYLTHTSG NDSQQLASDEIAYLTHTSG	TTGVPKLIAHSAN	ISMGWRW :	190

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VLORTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGLMPLNDLSKDNLVNLFAKH
VLORTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGLMPLNDLSKDNLVNLFAKH
VLORTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGLMPLNDLSKDNLVNLFAKH
Query
                121
Sbjct
                191
                                                                                                                                                                                          250
                              QPYAFETHPNDFVRLANLAKQEPEIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ
QPYAFETHPNDFVRLANLAKQEPEIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ
QPYAFETHPNDFVRLANLAKQEPEIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ
Query
                 181
                                                                                                                                                                                          240
Sbjct
                251
                                                                                                                                                                                          310
Query
                 241
                              \label{thm:continuous} IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEDGNECPAGTPGRIHFLS\\ IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEDGNECPAGTPGRIHFLS\\ IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEDGNECPAGTPGRIHFLS\\ \\
                                                                                                                                                                                          300
Sbjct 311
                                                                                                                                                                                          370
                             KGRALTYYKEEERFNKEVYGDWWDTGDWGLMNEDGILFLHDRQVDLIDKI
KGRALTYYKEEERFNKEVYGDWWDTGDWGLMNEDGILFLHDRQVDLIDKI
KGRALTYYKEEERFNKEVYGDWWDTGDWGLMNEDGILFLHDRQVDLIDKI
Query
                 301
Sbjct 371
                                                                                                                                                                420
```

acetate--CoA ligase [Lactococcus lactis]

Sequence ID: WP_058218837.1 Length: 507 Number of Matches: 1

See 1 more title(s) Range 1: 71 to 420

Score		Expec	t Method		Identities	Positives	Gaps	Frame
735 bits	s(1897	") 0.0()	Composition	nal matrix adjus	t. 350/350(1009	%) 350/350(100	%) 0/350(0)%)
Feature	es:							
Query	1			/SYLGAVPAMISY				60
Sbjct	71			/SYLGAVPAMISY /SYLGAVPAMISY				130
Query	61	KNLED!	SKKLSVSKFAL	EKPTQIADSQQL EKPTQIADSQQL	ASDEIAYLTHTS	GTTGVPKLIAHS	ANSMGWRW	120
Sbjct	131	KNLED:	SKKLSVSKFAL	EKPTQIADSQQL	ASDETAYLTHTS	GTTGVPKLIAHS/	ANSMGWRW	190
Query	121	VLQRT\	VMDWMPDKEEI	LAFHISPVHSRF	NIGVSSAMTFGF	GLMPLNDLSKDNI	LVNLFAKH	180
Sbjct	191	VLQRT\	VMDWMPDKEEI	LAFHISPVHSRF	NIGVSSAMTFGF	GLMPLNDLSKDNI	LVNLFAKH	250
Query	181	QPYAFI	ETHPNDFVRLA	ANLAKQEPEIFAS ANLAKQEPEIFAS ANLAKQEPEIFAS	IRYLHSTFDAINI	KETMHTFLSASKO KETMHTELSASKO	OKDPVFLQ	240
Sbjct	251	QPYAF	ETHPNDFVRLA	NLAKQEPETFAS	İRYLHSTFDAİN	KETMHTFLSASK	ŽKDPVFLQ	310
Query	241			RLSTLADTNAREM RLSTLADTNAREM				300
Sbjct	311			RESTEADTNAREM				370
Query	301			(EVYGDWWDTGDW (EVYGDWWDTGDW			350	
Sbjct	371			(EVYGDWWDTGDW			120	

long-chain acyl-CoA synthetase [Lactococcus lactis]

Sequence ID: WP_010905493.1 Length: 507 Number of Matches: 1

See 39 more title(s)

Range 1: 71 to 420

Score		Expec	t Method	Identities	Positives	Gaps	Frame
735 bits	(1897	") 0.0()	Compositional matrix a	adjust. 350/350(1009	%) 350/350(100	%) 0/350(C)%)
Feature	es:						
Query	1		AFDTYLLAVAVSYLGAVPA AFDTYLLAVAVSYLGAVPA				60
Sbjct	71		AFDTYLLAVAVSYLGAVPAI AFDTYLLAVAVSYLGAVPAI				130
Query	61	KNLEDS	SKKLSVSKFALEKPTQIAD SKKLSVSKFALEKPTQIAD	SQQLASDEIAYLTHTS	GTTGVPKLIAHS/	ANSMGWRW	120
Sbjct	131	KNLED	SKKLSVSKFALEKPTQIAD:	SQQLASDEIAYLTHTS	GTTGVPKLIAHSA	ANSMGWRW	190
Query	121	VLQRT\	VMDWMPDKEEILAFHISPV VMDWMPDKEEILAFHISPV	HSRFNIGVSSAMTFGF	GLMPLNDLSKDNI	-VNLFAKH	180
Sbjct	191	VLQRT\	VMDWMPDKEEILAFHISPVI	HSRFNIGVSSAMTFGF	ĞLMPLNDLSKDNI	VNLFAKH	250
Query	181	QPYAFI	ETHPNDFVRLANLAKQEPE	IFASIRYLHSTFDAINI TEASTRYLHSTEDATNI	KETMHTFLSASK()KDPVFLQ	240
Sbjct	251	QPYAFI	ETHPNDFVRLANLAKÕEPE ETHPNDFVRLANLAKÕEPE	ĪFASĪRYLHSTFDAĪNI	KETMHTFLSASK	ĮKDPVFLQ	310
Query	241	IYGQSI	ECGPMIWKKHRLSTLADTN ECGPMIWKKHRLSTLADTN	AREMGIGMPGLSKARI	ADEDGNECPAGT	GRIHFLS	300
Sbjct	311		ECGPMIWKKHRLSTLADTN				370
Query	301	KGRAL	TYYKEEERFNKEVYGDWWD TYYKEEERFNKEVYGDWWD	TGDWGLMNEDGILFLHI		350	
Sbjct	371	KGRAL	TYYKEEERFNKEVYGDWWD	TGDWGLMNEDGILFLHI	ORQVDLIDKI 4	120	

acetate--CoA ligase [Lactococcus lactis]

Sequence ID: WP_081213417.1 Length: 507 Number of Matches: 1

See 1 more title(s) Range 1: 71 to 420

Score		Expect	Method		Identities	Positives	Gaps	Frame
734 bits	(1896	0.0()	Compositional matrix	adjust.	350/350(100%) 350/350(10	00%) 0/350(0)%)
Feature	s:							
Query	1		AFDTYLLAVAVSYLGAVPA AFDTYLLAVAVSYLGAVPA					60
Sbjct	71		FDTYLLAVAVSYLGAVPA FDTYLLAVAVSYLGAVPA					130
Query	61	KNLEDS	KKLSVSKFALEKPTQIAD KKLSVSKFALEKPTÕIAD	SQQLAS	SDEIAYLTHTSG	TTGVPKLIAH	SANSMGWRW	120
Sbjct	131		KKLSVSKFALEKPTQIAL					190
Query	121	VLQRTV	/MDWMPDKEEILAFHISP\ /MDWMPDKEEILAFHISP\	/HSRFN:	IGVSSAMTFGFG	LMPLNDLSKDI	NLVNLFAKH	180
Sbjct	191	VLQRTV	/MDWMPDKEEILAFHISP\	/HSRFN	İĞVSSAMTFĞFĞ	LMPLNDLSKDI	NLVNLFAKH	250
Query	181	OPYAFE OPYAFE	THPNDFVRLANLAKQEPE THPNDFVRLANLAKQEPE THPNDFVRLANLAKQEPE	IFASI	RYLHSTFDAINK	ETMHTFLSASI	KOKDPVFLO	240
Sbjct	251	QPYAFE	THPNDFVRLANLAKQEPE	ĪFĀŠĪ	RYLHSTFDAINK	ETMHTFLSASI	KQKDPVFLQ	310
Query	241		CGPMIWKKHRLSTLADTN CGPMIWKKHRLSTLADTN					300
Sbjct	311		CGPMIWKKHRLSTLADTI					370
Query	301		YYKEEERFNKEVYGDWWI YYKEEERFNKEVYGDWWI				350	
Sbjct	371		YYKEEERFNKEVYGDWWD				420	

long-chain acyl-CoA synthetase [Lactococcus lactis subsp. lactis]

Sequence ID: PCS18680.1 Length: 498 Number of Matches: 1

Range 1: 62 to 411

Score		Expect	Method		Identities	Positives	Gaps	Frame
734 bits	(1894	0.0()	Compositiona	al matrix adjust.	349/350(99%)	350/350(10	0%) 0/350(0	%)
Feature	s:							
Query	1			YLGAVPAMISYHI YLGAVPAMISYHI				60
Sbjct	62			YLGAVPAMISYHI YLGAVPAMISYHI				121
Query	61	KNLEDS	KKLSVSKFALE	KPTQIADSQQLAS KPTQIADSQQLAS	DETAYLTHTSG	TTGVPKLIAH	SANSMGWRW	120
Sbjct	122	KNLEDS	KKLSVSKFALE	KPTQIADSQQLAS	DETAYLTHISG	TTGVPKLIAH	SANSMGWRW	181
Query	121	VLORTV	MDWMPDKEEIL	AFHISPVHSRFN] AFHISPVHSRFN]	IGVSSAMTEGEG	LMPLNDLSKDI	NLVNLFAKH	180
Sbjct	182	VLQRTV	MDWMPDKEEIL	AFHISPVHSRFN	IGVSSAMTFGFG	LMPLNDLSKDI	NLVNLFAKH	241
Query	181	QPYAFE ODVAFE	THPNDFVRLAN	LAKQEPEIFASIF LAKQEPEIFASIF LAKQEPEIFASIF	RYLHSTFDAINK	ETMHTFLSASI	(OKTDVELO	240
Sbjct	242	QPYAFE	THPNDFVRLAN	LAKQEPETFAST	RYLHSTFDAINK	ETMHTFLSASI	K ČKEPVFLQ	301
Query	241	IYGQSE	CGPMIWKKHRL	STLADTNAREMGI STLADTNAREMGI	IGMPGLSKARIA	DEDGNECPAG	TPGRIHFLS	300
Sbjct	302			STLADTNAREMG				361
Query	301			VYGDWWDTGDWGI VYGDWWDTGDWGI			350	
Sbjct	362			VYGDWWDTGDWGI			411	

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