

BLAST Results

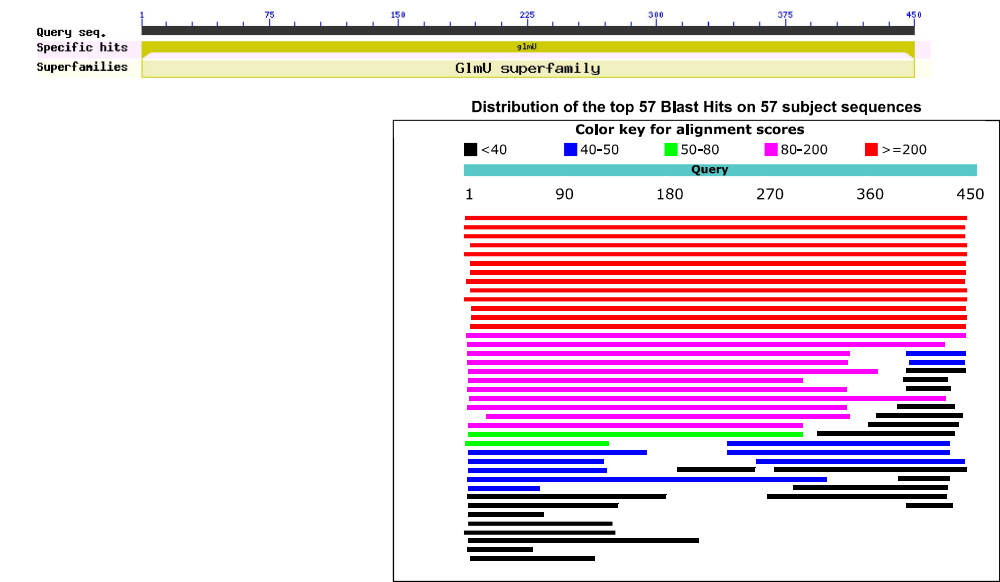
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Job title: BAB41687:gcaD [Staphylococcus aureus subsp....

RID	43NBX88F014 (Expires on 01-19 20:32 pm)	Database Name	SMARTBLAST/landmark
Query ID	BAB41687.1	Description	Landmark database for SmartBLAST
Description	gcaD [Staphylococcus aureus subsp. aureus N315]	Program	BLASTP 2.8.1+
Molecule type	amino acid		
Query Length	450		

Graphic Summary.

Putative conserved domains have been detected, click on the image below for detailed results.



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
bifunctional glucosamine-1-phosphate N-acetyltransferase/UDP-N-acetylglucosamine pyrophosphorylase [Bacillus subtilis subsp. subtilis str. 168]	528	528	99%	0.0	55%	NP_387931.1
bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Clostridioides difficile 630]	476	476	99%	5e-165	53%	YP_001090036.1
bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Streptococcus pneumoniae R6]	434	434	99%	3e-148	49%	NP_358485.1
bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Deinococcus radiodurans R1]	386	386	98%	2e-129	45%	NP_294532.1
bifunctional glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridylyltransferase [Pseudomonas aeruginosa PAO1]	369	369	100%	5e-123	44%	NP_254239.1
bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Streptomyces coelicolor A3(2)]	356	356	98%	9e-118	45%	NP_733593.1
Probable UDP-N-acetylglucosamine pyrophosphorylase glmU [Mycobacterium tuberculosis variant bovis AF2122/97]	355	355	98%	2e-117	41%	YP_009358380.1
bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Thermotoga maritima MSB8]	347	347	98%	1e-114	44%	NP_229429.1
fused N-acetylglucosamine-1-phosphate uridylyltransferase and glucosamine-1-phosphate acetyltransferase [Escherichia coli str. K-12 substr. MG1655]	342	342	98%	8e-113	44%	NP_418186.1
bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyl transferase GImU [Shewanella oneidensis MR-1]	342	342	100%	1e-112	42%	NP_720261.1
bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GImU [Microcystis aeruginosa]	342	342	98%	1e-112	42%	WP_014805027.1
MULTISPECIES: bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GImU [Synechocystis]	331	331	98%	2e-108	40%	WP_010874079.1
UDP-N-acetylglucosamine pyrophosphorylase [Neisseria meningitidis MC58]	328	328	98%	2e-107	43%	NP_273104.1
glucose-1-phosphate thymidyltransferase [Methanothermobacter thermautotrophicus]	145	145	99%	9e-38	28%	WP_010877197.1
nucleotidyltransferase [Sulfolobus acidocaldarius]	109	109	94%	7e-25	24%	WP_011277513.1
Glucose-1-phosphate adenyltransferase family protein [Arabidopsis thaliana]	101	101	75%	3e-22	28%	NP_181507.1
Glucose-1-phosphate adenyltransferase family protein [Arabidopsis thaliana]	100	100	75%	7e-22	28%	NP_191118.1
mannose-1-phosphate guanylyltransferase [Streptomyces coelicolor A3(2)]	102	102	81%	8e-22	26%	NP_625671.1
Mannose-1-phosphate guanylyltransferase beta [Caenorhabditis elegans]	96.7	96.7	66%	1e-20	27%	NP_502333.2
glucose-1-phosphate adenyltransferase family protein [Glycine max]	92.8	92.8	75%	3e-19	26%	NP_001242262.2
NDP-sugar synthase [Methanothermobacter thermautotrophicus]	90.1	90.1	94%	3e-18	24%	WP_010877361.1
mannose-1-phosphate guanylyltransferase 1-like [Glycine max]	89.0	89.0	75%	5e-18	25%	NP_001240188.1
Glucose-1-phosphate adenyltransferase family protein [Arabidopsis thaliana]	81.6	81.6	72%	9e-16	27%	NP_194786.1
MULTISPECIES: NDP-sugar synthase [Synechocystis]	80.9	80.9	66%	3e-15	27%	WP_010872999.1
MULTISPECIES: NDP-sugar synthase [Microcystis]	77.0	77.0	66%	6e-14	28%	WP_012267092.1
TIGR00454 family protein [Methanothermobacter thermautotrophicus]	59.7	59.7	28%	6e-09	28%	WP_010876776.1
hypothetical protein spr1145 [Streptococcus pneumoniae R6]	49.7	49.7	35%	2e-05	27%	NP_358738.1
CTP-phosphocholine cytidyltransferase [Clostridioides difficile 630]	47.8	47.8	26%	8e-05	31%	YP_001086679.1
mannose-1-phosphate guanylyltransferase [Microcystis aeruginosa]	47.8	47.8	27%	8e-05	28%	WP_012267855.1
uncharacterized protein Dmel_CG8207 [Drosophila melanogaster]	45.4	45.4	71%	0.001	23%	NP_611051.2
Trimeric LpxA-like enzymes superfamily protein [Arabidopsis thaliana]	44.3	44.3	44%	0.002	27%	NP_001328366.1
Trimeric LpxA-like enzymes superfamily protein [Arabidopsis thaliana]	44.3	44.3	44%	0.002	27%	NP_001328365.1
acetyltransferase [Thermotoga maritima MSB8]	42.0	42.0	41%	0.006	23%	NP_228568.1
maltose O-acetyltransferase [Clostridioides difficile 630]	40.4	40.4	11%	0.015	33%	YP_001087346.1
nucleotidyl transferase [Pseudomonas aeruginosa PAO1]	40.8	40.8	14%	0.015	38%	NP_249288.1
maltose O-acetyltransferase [Clostridioides difficile 630]	40.0	40.0	10%	0.017	40%	YP_001088169.1
mannose-1-phosphate guanylyltransferase [Deinococcus radiodurans R1]	39.3	39.3	39%	0.051	26%	NP_294433.1
galactoside O-acetyltransferase [Escherichia coli str. K-12 substr. MG1655]	38.9	38.9	38%	0.053	24%	NP_414876.1
acetyltransferase CysE/LacA/LpxA/NodL family [Shewanella oneidensis MR-1]	38.5	38.5	30%	0.078	27%	NP_718708.1
nucleotidyltransferase family protein [Shewanella oneidensis MR-1]	38.1	38.1	29%	0.10	26%	NP_719176.1
mannose-1-phosphate guanylyltransferase [Neisseria meningitidis MC58]	37.7	37.7	14%	0.15	35%	NP_274838.1
hypothetical protein DDB_G0291538 [Dictyostelium discoideum AX4]	36.6	36.6	11%	0.25	29%	XP_635301.1
hypothetical protein TM1393 [Thermotoga maritima MSB8]	36.6	36.6	28%	0.33	28%	NP_229194.1
acetyltransferase [Streptomyces coelicolor A3(2)]	35.8	35.8	8%	0.60	42%	NP_624622.1
translation initiation factor eIF-2B subunit gamma [Danio rerio]	36.2	36.2	29%	0.64	26%	NP_957368.1
glucose-1-phosphate adenyltransferase [Escherichia coli str. K-12 substr. MG1655]	35.8	35.8	45%	0.85	22%	NP_417888.1
hypothetical protein PA1090 [Pseudomonas aeruginosa PAO1]	35.0	35.0	12%	0.99	39%	NP_249781.1
maltose O-acetyltransferase [Escherichia coli str. K-12 substr. MG1655]	33.9	33.9	8%	2.0	39%	NP_414992.1
hypothetical protein CD630_02420 [Clostridioides difficile 630]	33.9	33.9	24%	2.4	26%	YP_001086710.1
sugar acetyltransferase [Streptomyces coelicolor A3(2)]	33.5	33.5	10%	2.6	33%	NP_631564.1
serine acetyltransferase [Thermotoga maritima MSB8]	33.5	33.5	16%	3.7	25%	NP_228475.1
UDP-N-acetylglucosamine acyltransferase [Neisseria meningitidis MC58]	33.1	33.1	35%	5.8	24%	NP_273236.1
acetyltransferase [Pseudomonas aeruginosa PAO1]	32.7	32.7	17%	6.0	29%	NP_250795.1
UDP-N-acetylglucosamine acyltransferase [Escherichia coli str. K-12 substr. MG1655]	32.7	32.7	26%	6.1	26%	NP_414723.1
acetyltransferase [Streptomyces coelicolor A3(2)]	32.7	32.7	9%	6.4	34%	NP_628278.1
maltose O-acetyltransferase [Bacillus subtilis subsp. subtilis str. 168]	32.3	32.3	8%	7.6	35%	NP_391965.1
peptidyl-prolyl cis-trans isomerase-like 2 isoform X3 [Homo sapiens]	32.7	32.7	15%	9.9	27%	XP_011526345.1

Alignments

bifunctional glucosamine-1-phosphate N-acetyltransferase/UDP-N-acetylglucosamine pyrophosphorylase [Bacillus subtilis subsp. subtilis str. 168]
Sequence ID: **NP_387931.1** Length: 456 Number of Matches: 1
Range 1: 3 to 451

Score	Expect	Method	Identities	Positives	Gaps	Frame								
528 bits(1360)	0.0()	Compositional matrix adjust.	249/449(55%)	334/449(74%)	0/449(0%)									
Features:														
Query	2	RRHAILAAGKGT	RMKSKKKYKVL	HEVAGKPM	VEHVLSEV	KGSGVDQVVTIVGHGAE	SVKG	61						
Sbjct	3	KRF	AVVLAAGGT	RMKSKKKYKVL	HVPCKGPM	VEHVDEALKLSKLVTIVGHGAE	VVK	62						
Query	62	HLGERSLYS	FOEKOLGTA	HAVQMAKSH	LEDKEGTTIV	CGDTP	PLITKETLET	IAHHEDA	121					
Sbjct	63	QLGDKSEYAL	QAKQLGTA	HAVKQAQPF	LAD	KEGVTIVICGDTPL	LTAETMEQMLKEHTQR		122					
Query	122	NAQATVLSAS	IQQPYGVGR	IVRNASGR	LERIVEEK	DATQAEKD	INEISSGTF	AFNKNKTLF	181					
Sbjct	123	EAKATILT	AVAE	DP	TGYGRIT	RSNGAVQK	IVENKQAS	EEERLVTETINTGYVCFDNEALF	182					
Query	182	EKL	TOVKNDNAO	GEYVLP	DVLSLILNDG	GIVEVYRT	NDVVEE	IMGVNDRV	VL	SOAEKAMQR	241			
Sbjct	183	RAID	OVSDNNAO	GEYVLP	DVIEILK	NEGETVA	AYQTGN	FQETL	GVNDRVL	SQAEQFMKE	242			
Query	242	RTNH	YHMLNG	VITIDP	DS	TFIG	PDVPTIE	PGVRI	NGRTEIG	EDVITGOYSE	INNS	301		
		R N	HM	NGVT	IDP	+T	I PD	IGSD	TVI	PG I G	+IGED	+IG	++EI	NS

Sbjct	243	RINKRHMQNGVTLLIDPMNTYISPDVIGSDTVIYPGTVIKGEVQIGEDITIGPHEIMNS	302
Query	302	TIENGACIQSVNDASVGNANTKVGPFQALRPGAQLGADVKGNFVEIKKADLKDGAKVS	361
Sbjct	303	ATGSRVTIKQSVNHSKVGNDVNIQGFARIKPDVIGNEVKGNFVEIKKTQFGDRSKAS	362
Query	362	HLISYIGDAVIGERTNIGCGTITVNYDGENKFKTIVGKDSFVGCNNVLVAPVTIGDDVLVA	421
Sbjct	363	HLISVVGDAEYGDVNLGCGSITVNYDGNKYLTKIEDGAFIGCNSNLVAPVTVGEYVVA	422
Query	422	AGSTIITDDVPNDSLAVARAROTTKEGYR	450
Sbjct	423	AGSTVTEDPGKALAIARARQVKNDDYVK	451

bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Clostridioides difficile 630]
Sequence ID: **YP_001090036.1** Length: 459 Number of Matches: 1
Range 1: 1 to 447

Score	Expect	Method	Identities	Positives	Gaps	Frame
476 bits(1224) 5e-165() Compositional matrix adjust. 239/448(53%) 318/448(70%) 1/448(0%)						
Features:						
Query	1	MRRHAIIILAAAGKTRMKS	KYKVLHEVAGKPMVEHVL	SVKSGSGVDQVVTIVGHGAESVK	60	
Sbjct	1	MNFKAIIILAAAGKTRMKS	KYKVLHEVAGKPMVEHVL	SVKSGSGVDQVVTIVGHGAESVK	60	
Query	61	GHLGERSLVSFOEKQLGTAH	AVQMAKSHLEDEKGTITV	CGDTPITKETLETLIAHED	120	
Sbjct	61	EKLAEIIIAHQTEQLGTGHA	VKMAKEYIND-EDITVVL	CGDTPLIKEITLKRLEFYHIE	119	
Query	121	ANAQATVLSASIQQPYGGR	IVRNASGRLERIVEEKDAT	QAEKDINEISSGIFAFNNKTL	180	
Sbjct	120	NKYHATVLTTRVGNTPYGR	IIRDKGDLKIVEQGDANS	EKMISETNSGIVGFGNKS	179	
Query	181	FEKLTQVKNDNAQGEYVL	PDVLSLINDGGIVEYR	TNDVEEIMGVNDRVMSQAEKAMQ	240	
Sbjct	180	REALDLNNSNGGEYVLT	DTAKIMRDKGLKVGA	FAGSITIEELMGVNSRVELSKAEIIMR	239	
Query	241	RRTNHYHMLNGVTIIDP	STFIIGPDDVTIGSDTV	IEPGRINGRTEIGEDVIGQYSEINN	300	
Sbjct	240	RRNHHMNGVTIIDTNT	SYIESDVMIGNDTIIP	VGMLQKTRIGSDCTIGMNSITN	299	
Query	301	STIENGACIQSVNDASV	GANTKVGPFQALRPGAQL	GADVKGNFVEIKKADLKDGAKV	360	
Sbjct	300	SEIGDGEIKNSTIIDS	KVGENSTVGPYALRP	KSDLGNNVKIGDFVEVKNAIEDGSKA	359	
Query	361	SHLSYIGDAVIGERTN	IGCGTITVNYDGENKFK	TIVGKDSFVGCNNVLVAPVTIGDDVLV	420	
Sbjct	360	SHLSYIGDAVIGKWN	IGCGVFNVDGKKNK	SVKDNVAFIGSNNLAPVVEEKGYI	419	
Query	421	AAGSTIITDDVPND	SLAVARAROTTKEGY	448		
Sbjct	420	ATGSTITHDVPDGA	LAIARERQVKEG	447		

bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Streptococcus pneumoniae R6]
Sequence ID: **NP_358485.1** Length: 479 Number of Matches: 1
Range 1: 21 to 468

Score	Expect	Method	Identities	Positives	Gaps	Frame
434 bits(1115) 3e-148() Compositional matrix adjust. 219/448(49%) 299/448(66%) 0/448(0%)						
Features:						
Query	1	MRRHAIIILAAAGKTRMKS	KYKVLHEVAGKPMVEHVL	SVKSGSGVDQVVTIVGHGAESVK	60	
Sbjct	21	MSNFAIIILAAAGKTRMKS	LDLPKVLHKGISMLHVF	RSVGAIQPKTIVTVGHKAELVE	80	
Query	61	GHLGERSLVSFOEKQLGTAH	AVQMAKSHLEDEKGTITV	CGDTPITKETLETLIAHED	120	
Sbjct	81	EVLAEQTEFVYQSEQLGT	GHAVMTEPILEGLSGHT	LVIAGDTPITGESLKNLIDOFHIN	140	
Query	121	ANAQATVLSASIQQPYGGR	IVRNASGRLERIVEEKDAT	QAEKDINEISSGIFAFNNKTL	180	
Sbjct	141	HKNVATILTAETDNP	FGYGRIVRNDAEVLRI	VEQKDATFEKQIKEINTGYVDFNERL	200	
Query	181	FEKLTQVKNDNAQGEYVL	PDVLSLINDGGIVEYR	TNDVEEIMGVNDRVMSQAEKAMQ	240	
Sbjct	201	FEAKNINTNNAQGEYV	ITDVIGIFRETGEKVG	AYTLKDFDES LGVNDRVALATAESVMR	260	
Query	241	RRTNHYHMLNGVTIIDP	STFIIGPDDVTIGSDTV	IEPGRINGRTEIGEDVIGQYSEINN	300	
Sbjct	261	RRINHKHMVNGVSV	FNPEATYIDIDVEI	APVQIEANVLKGQTKIGAEVTLTNGTVVD	320	
Query	301	STIENGACIQSVNDASV	GANTKVGPFQALRPGAQL	GADVKGNFVEIKKADLKDGAKV	360	
Sbjct	321	STIGAGAVITNSMIE	ESSVADGTVGPYAHIR	PNSLSGAQVHIGNFVEKSGSISGENTKA	380	
Query	361	SHLSYIGDAVIGERTN	IGCGTITVNYDGENKFK	TIVGKDSFVGCNNVLVAPVTIGDDVLV	420	
Sbjct	381	GHLTYIGNCEVGSNV	NFGAGTITVNYDGN	KNYKTVIGDNVFGVNSITIIAPVELGDNSLV	440	
Query	421	AAGSTIITDDVPND	SLAVARAROTTKEGY	448		
Sbjct	441	GAGSTITKDPADA	ITAGRQINKDEY	468		

bifunctional N-acetylglucosamine-1-phosphate uridylyltransferase/glucosamine-1-phosphate acetyltransferase [Deinococcus radiodurans R1]
Sequence ID: **NP_294532.1** Length: 487 Number of Matches: 1
Range 1: 14 to 459

Score	Expect	Method	Identities	Positives	Gaps	Frame
386 bits(991) 2e-129() Compositional matrix adjust. 202/447(45%) 274/447(61%) 3/447(0%)						
Features:						
Query	6	IILAAAGKTRMKS	KYKVLHEVAGKPMVEHVL	SVKSGSGVDQVVTIVGHGAESVK	65	
Sbjct	14	VILAAAGQTRMNSALPK	VLHPVAGRPMVAWAKA	ARDLGARKIVVTVGHGAEQVEAAVQQ	73	
Query	66	RSI-YSFQEKQLGTAH	AVQMAKSHLEDEKGTITV	CGDTPITKETLETLIAHEDANAQ	124	
Sbjct	74	PGVAFARQERQLGTG	DAFLSGASALTEGGAD	ILVLVGDTPLLRPDTLRELVASHREQGSA	133	
Query	125	ATVLSASIQQPYGGR	IVRNASGRLERIVEEKDAT	QAEKDINEISSGIFAFNNKTLFEKL	184	
Sbjct	134	MTVLGTGELPDATG	YGRIVRGGAVERIVE	QKSDAEKATGEFNSGVYVDERAP-ELA	192	
Query	185	TQVKNDNAQGEYVL	PDVLSLINDGGIVEYR	TNDVEEIMGVNDRVMSQAEKAMQRRTN	244	
Sbjct	193	RRIGNDNKAGEYVL	TDLLGLYRAGGATV	RAFRLSDPDEVLGANDRAGLTQLEATLQRRIN	252	
Query	245	HYHMLNGVTIIDP	STFIIGPDDVTIGSDTV	IEPGRINGRTEIGEDVIGQYSEINN	304	
Sbjct	253	EGHLKAGVSI	SLPGTGLIEDTVIEGR	DVIEPGALLRGQTRIAGGAVIGAVSVITDSVIH	312	
Query	305	NGACIQ-SVNDASV	GANTKVGPFQALRPGAQL	GADVKGNFVEIKKADLKDGAKVSHL	363	
Sbjct	313	ERAVIKAHVLSLE	QAEVAGSDVGPFA	RLRPGSVLGEVGHIGNFVETKNARLDAGVKAGHL	372	
Query	364	SYIGDAVIGERTN	IGCGTITVNYDGENKFK	TIVGKDSFVGCNNVLVAPVTIGDDVLVAAG	423	
Sbjct	373	AYLGDVEIGAE	TNAGTIVANFDGLN	HQSKVGAGVIGSNTTLIAPRVGDAAFIAGG	432	
Query	424	STIITDDVPND	SLAVARAROTTKEGYR	450		
Sbjct	433	SAIHDDVP	EGAMAVARGQRNIEG	WAR 459		

bifunctional glucosamine-1-phosphate acetyltransferase/N-acetylglucosamine-1-phosphate uridylyltransferase [Pseudomonas aeruginosa PAO1]
Sequence ID: **NP_254239.1** Length: 454 Number of Matches: 1
Range 1: 1 to 448

Score	Expect	Method	Identities	Positives	Gaps	Frame
369 bits(946) 5e-123() Compositional matrix adjust. 199/452(44%) 283/452(62%) 6/452(1%)						
Features:						
Query	1	MRRHAIIILAAAGKTRMKS	KYKVLHEVAGKPMVEHVL	SVKSGSGVDQVVTIVGHGAESVK	60	
Sbjct	1	MSLEIVILAAAGQTRM	RSALPKVLHPIAGKPM	LHIGDARQPERIHVIGHGADLVLR	60	
Query	61	GHLGERSLVSFOEKQLGTAH	AVQMAKSHLEDEKGTITV	CGDTPITKETLETLIAHHE	119	
Sbjct	61	ERMAADDLNFVLQAE	QLGTGHVAQALPFLSADQ	--VLILYGDVPLTLQDTLQRLLA--Q	116	
Query	120	DANAQATVLSASIQQPY	GGRIVRNASGRLERIVE	EKDATQAEKDINEISSGIFAFNNKT	179	

Sbjct 117 VTPDQLSLLTVDMLDPTGYGRIVRDDQGAVQAIVEHKDATPAQRQIGEINTGILAVPGKR 176
Query 180 LFEKLTQVKNDNAQGEYYLPDVLSLI.LNDGGIVEVVRTNDVVEEIMGVNDRVMLSQA EKAM 239
L + L ++ NDNAQGEYYL DV+++ + DG +V + D E+ GVNDR+ +0 E+
Sbjct 177 LADNLGRLSNDNAQGEYYLTDVTAMAVGDLVVASAQLDAMEVQGVNDRMQQAQLERHY 236
Query 240 QRRTNHYHMLNGVTIIPDPSFTIGPDVTIGSDTVIEPGVRINGRTEIGEDVVIGQYSEIN 299
OR M GVT++DP + ++++G D +i+ V + GR I +DV IG I
Sbjct 237 QRLRAEELMRQGVTL.LDPQRLDVRGEISVGRDVLIDNVVLEGRVVIEDDVRIGPNCVIR 296
Query 300 NSTIENGACIQ-QSVVNDASVGANTKVGPFQALRPGAQLGADVKVGNFVEIKKADLKDGA 358
+S + GA I+ S + A +G + GPFA+LRPG+ LGA VGNFVE+K A L +G+
Sbjct 297 DSVLRRGAVIKANSHLEGAELGEGSDAGPFARLRPGSVLGARAHVGNFVELKNARLGE GS 356
Query 359 KVSHLSYTGDAVIGERTNIGCGTITVNYDGENKFETIVGKDSFVGCNNVLVAPVTIGDDV 418
K HLSY+GDA +G NIG GTIT NYDG NKF+T +G D F+G N +LVAP+ IG D
Sbjct 357 KAGHLSYLGDAELGANCNIGAGTITCNVDGANKFRTELGDDVFIGSNNSLVAPLKIGDGA 416
Query 419 LVAAGSTIIDDPNDSLAVARARQTTKEGYRK 450
AAGSTIIT +VP +LA RARQ E +++
Sbjct 417 TTAAGSTITHEVPAKNLAFGRARQKNLENWKR 448

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