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BLAST[®] >> **Global Alignment** >> results for RID-PKEJEXRF114

Job Title	PRVABC59_AA ...
RID	PKEJEXRF114 Search expires on 11-09 09:09 am
Program	Needleman-Wunsch alignment of two sequences
Query ID	lcl Query_63959 (amino acid)
Query Descr	PRVABC59_AA ...
Query Length	3423

Subject ID

lcl|Query_63961 (amino acid)

Subject Descr

[SEQ_ID_NO40 ...](#)

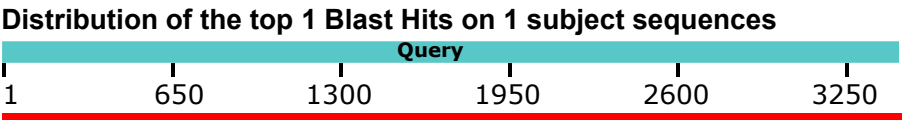
Subject Length

504

Descriptions

Description	Score	Percent Ident	Accession
SEQ_ID_NO40	-274.0	15.00%	Query_63961

Graphic Summary



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SEQ_ID_NO40
Sequence ID: Query_63961 Length: 504 Number of Matches: 1
Range 1: 1 to 504

NW Score	Identities	Positives	Gaps	Frame
-274	504/3423(15%)	504/3423(14%)	2919/3423(85%)	
Query 1	MKNPKKKSGGFRIVNMLKRGVARVSPFGGLKRLPAGLLLGHGPIRMVLAILAFLRFTA			60
Query 61	PSLGLINRWGSGVKKKEAMETIKKFKKDLAAMLRIINARKEKKRRGADTSVGIVGLLLTTA			120
Query 121	MAAEVTRRGSAYMYLDRNDAGEAISFPTTLGMNKCQIQIMDLGHMCDATMSYECPLDE			180
Query 181	GVEPDDVDCWCNTTSTWVVYGTCHHKKGAEARRSRAVTLPSHSTRKLQTRSQTWLESREY			240
Query 241	TKHLIRVENWIFRNPGFALAAAAIAWLLGSSTSQKVIYLMILLIAPAYSIRCIGVSNRD			300
Sbjct 1			IRCIGVSNRD	10
Query 301	FVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMAS			360
Sbjct 11	FVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMAS			70
Query 361	DSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSI			420
Sbjct 71	DSRCPTQGEAYLDKQSDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFACSKKMTGKSI			130
Query 421	QPENLEYRIMLSVHGSQHSGMIVNDTGHEVDENRAKVEITPNSPRAEATLGGFGSLGLDC			480
Sbjct 131	QPENLEYRIMLSVHGSQHSGMIVNDTGHEVDENRAKVEITPNSPRAEATLGGFGSLGLDC			190
Query 481	EPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNEALVEFKDAHA			540
Sbjct 191	EPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNEALVEFKDAHA			250
Query 541	KRQTVVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTA			600
Sbjct 251	KRQTVVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTA			310
Query 601	AFTFTKIPAEATLHGTVTVEVQYAGTDGPKKVPQAQMAVDMQTLTPVGRITANPVITESTE			660
Sbjct 311	AFTFTKIPAEATLHGTVTVEVQYAGTDGPKKVPQAQMAVDMQTLTPVGRITANPVITESTE			370
Query 661	NSKMMLELDPFGDSYIVIGVGEKKITHHWHRSRGSTIGKAFAEATVRGAKRMAVLGDTAWD			720
Sbjct 371	NSKMMLELDPFGDSYIVIGVGEKKITHHWHRSRGSTIGKAFAEATVRGAKRMAVLGDTAWD			430
Query 721	FGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLA			780

Sbjct	431	FGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLA	490
Query	781	LGGVLIFLSTAVSADVGCSDVFSKKETRCGTGVFVYNDVEAWRDYKYHPDSPRRLAHAV	840
Sbjct	491	LGGVLIFLSTAVSA	504
Query	841	KQAWEDGICGISSVSRMENIMWRSVEGELNAILEENGVQLTVVVGSVKNPMWRGPQRLPV	900
Query	901	PVNELPHGWKAWGKSYFVRAAKTNNSFVVDGDTLKECPLKHWANSFLVEDHGFVFHTS	960
Query	961	VWLKVREDYSLECDPAVIGTAVKGKEAVHSDLGWIESEKNDTWRLKRAHLIEMKTCEWP	1020
Query	1021	KSHTLWTDGIEESDLIIPKSLAGPLSHHNTREGYRTQMKGPWHSEEELEIRFEPCPGTKVH	1080
Query	1081	VEETCGTRGPSRLRSTTASGRVIEEWCCRECTMPPLSFRAKDGCWYGMEIRPRKEPESNLV	1140
Query	1141	RSMVTAGSTDHMDHFSGLGVLVILLMVQEGKKRMTTKIIISTMAVLVAMILGGFSMSDL	1200
Query	1201	AKLAILMGATFAEMNTGGDVAHLALIAAFKVRPALLVSFIFRANWTPRESMLLALASCLL	1260
Query	1261	QTAISALEGDLMLVINGFALAWLAIRAMVVPRTDNITLAILAALTPLARGTLLVAWRAGL	1320
Query	1321	ATCGGFMLLSLKKGKSVKKNLPFVMALGLTAVRLVDPINVVGLLLLTRSGKRSWPPSEVL	1380
Query	1381	TAVGLICALAGGFAKADIEMAGPMAAVGLLIVSYVVSFGKSDMYIERAGDITWEKDAEVT	1440
Query	1441	GNSPRLDVALDESGDFSLVEDDGPPMREIILKVVMTICGMNPIAIPFAAGAWYVYVKTG	1500
Query	1501	KRSGALWDVPAPKEVKKGETTDGVYRVMTRRLLGSTQVGVGMQEGVFHTMWHVTKGSAL	1560
Query	1561	RSGEGRDPYWGDKQDLVSYCGPWKLDAAWDGHSEVQLLAVPPGERARNIQTLPGIFKT	1620
Query	1621	KDGDIGAVALDYPAGTSGSPIIDKCGRVIGLYNGGVVKNKNGSYVSAITQGRREEETPVEC	1680
Query	1681	FEPSMLKKKQLTVLDLHPGAGKTRRVLPFIVREAIKTRLRTVILAPTRVVAEMEEALRG	1740
Query	1741	LPVRYMTTAVNVTHSGTEIVDLMCHATFTSRLLQPIRVPNYLYIMDEAHFTDPSSIAAR	1800
Query	1801	GYISTRVEMGEAAAIFMTATPPGTRDAFPDSNSPIMDTEVEVPERAWSSGFDWVDHSGK	1860
Query	1861	TWVFVPSVRNGNEIAACLTAKGKRVIQLSRKTFETEFQKTKHQEWDFFVTTDISEMGANF	1920
Query	1921	KADRVIDSRRLKPVILDGERVILAGPMPVTHASAAQRRGRIGRNPKNKPGDEYLYGGGCA	1980
Query	1981	ETDEDHAHWLEARMLLDNIYLQDGLIASLYRPEADKVAIEGEFKLRTEQRKTFVELMKR	2040
Query	2041	GDLPVWLAYQVASAGITYTDRRWCFDGTNTIMEDSVPAEVWTRHGEKRVLPKRWMDAR	2100
Query	2101	VCSHAALKSFKEFAAGKRGAAFGVMEALGTLPGHMTERFQEAIDNLAVLMRAETGSRPY	2160
Query	2161	KAAAAQLPETLETIMLLGLLGTVSLGIFVLMRNKGIGKMGFMVTLGASAWLMWLSEIE	2220
Query	2221	PARIACVLIVVFLLLVVLIPPEKQSRPQDNQMAIIMVAVGLLGLITANELGLWERTKS	2280
Query	2281	DLSHLMGRREEGATIGFSMDIDLRPASAWAIYAALTTFITPAVQHAVTTSYNNYSLMAMA	2340
Query	2341	TQAGVLFMGKGMFPYAWDFGVPLLMIGCYSQLTPLTLIVAIILLVAHYMYLIPGLQAAA	2400
Query	2401	ARAAQKRTAAGIMKNPVVDGIVVTDIDTMTIDPQVEKKMGQVLLIAVAVSSAILLSRTAWG	2460
Query	2461	WGEAGALITAATSTLWEGSPNKYWNSSSTATSLCNIFRGSYLAGASLIYTVTRNAGLVKRR	2520
Query	2521	GGGTGETLGEKWKARLNQMSALEFYYSKSGITEVCREEAARRALKDGVATGGHAVSRGSA	2580

Query 2581 KLRWLVERGYLPYGVKVIDLGCGRGGWSYYVATIRKVQEVKGYTKGGPGHEEPVLVQSYG 2640

Query 2641 WNIVRLKSGVDVFHMAAEPDITLLCDIGESSSSPEVEEARTLRVLSMVGDWLEKRPAGFC 2700

Query 2701 IKVLCPYTSTMMETLERLQRRYGGGLVRVPLSRNSTHEMYWVSGAKSNTIKSVSTTSQLL 2760

Query 2761 LGRMDGPRRPVKYEEDVNLGSGTRAVVSCAEAPNMKIIGNRIERIRSEHAETWFFDENHP 2820

Query 2821 YRTWAYHGSYEAPTQGSASSLINGVVRLLSKPWDVVTGVTGIAMTDTTPYGQQRVFKEKV 2880

Query 2881 DTRVPDPQEGTRQVMSMVSSWLWKELGKHKRPRVCTKEEFINKVRSNAALGAIFEEKEW 2940

Query 2941 KTAVEAVNDPRFWALVDKEREHLRGECQSCVYNNMGKREKKQGEFGKAKGSRAIWMWL 3000

Query 3001 GARFLEFEALGFLNEDHWMGRENSGGGVEGLGLQRLGYVLEEMSRIPGGGRMYADDTAGWD 3060

Query 3061 TRISRFDLENEALITNQMEKGHRALALAIKYTYQNKVVKLPAEKGKTVMDIISRQDQ 3120

Query 3121 RSGSQVVTYALNTFTNLVVQLIRNMEAEEVLEMQDLWLLRSEKVTNWLQSNQWDRKRM 3180

Query 3181 AVSGDDCVVKPIDDRFAHALRFLNDMGKVRKDTQEWKPSTGWDNWEEVPFCSHHFNKLHL 3240

Query 3241 KDGRSIVVPCRHQDELIGRARVSPGAGWSIRETACLAKSYAQMWQLLYFHRRDLRLMANA 3300

Query 3301 ICSSVPVDWVPTGRTTWSIHKGGEWMTTEDMLVVWNRVWIEENDHMDKTPVTKWTDIPY 3360

Query 3361 LGKREDLWCGSLIGHRPRTTWAENIKNTVMVRRRIIGDEEKYMDYLSTQVRYLGEEGSTP 3420

Query 3421 GVL 3423

Taxonomy

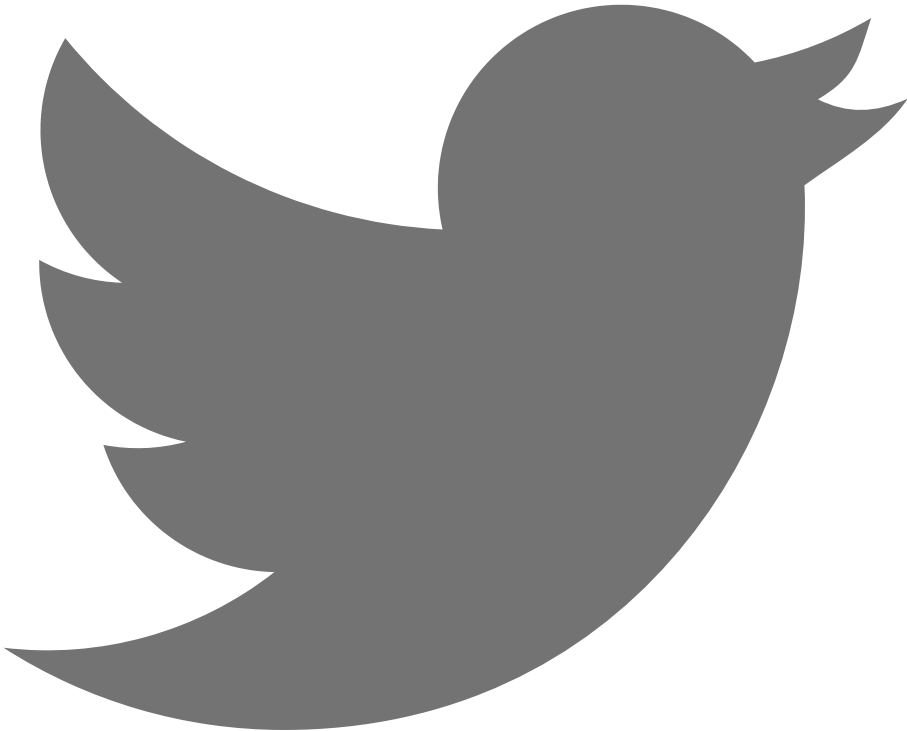
Reports

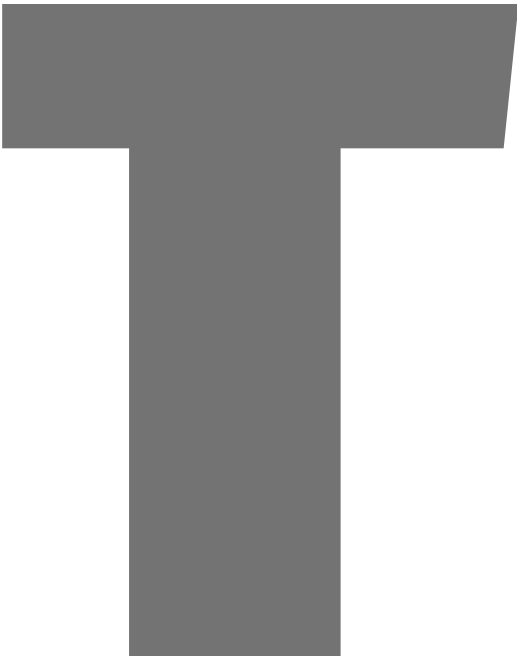
- Lineage
- Organism
- Taxonomy

Dot Plot

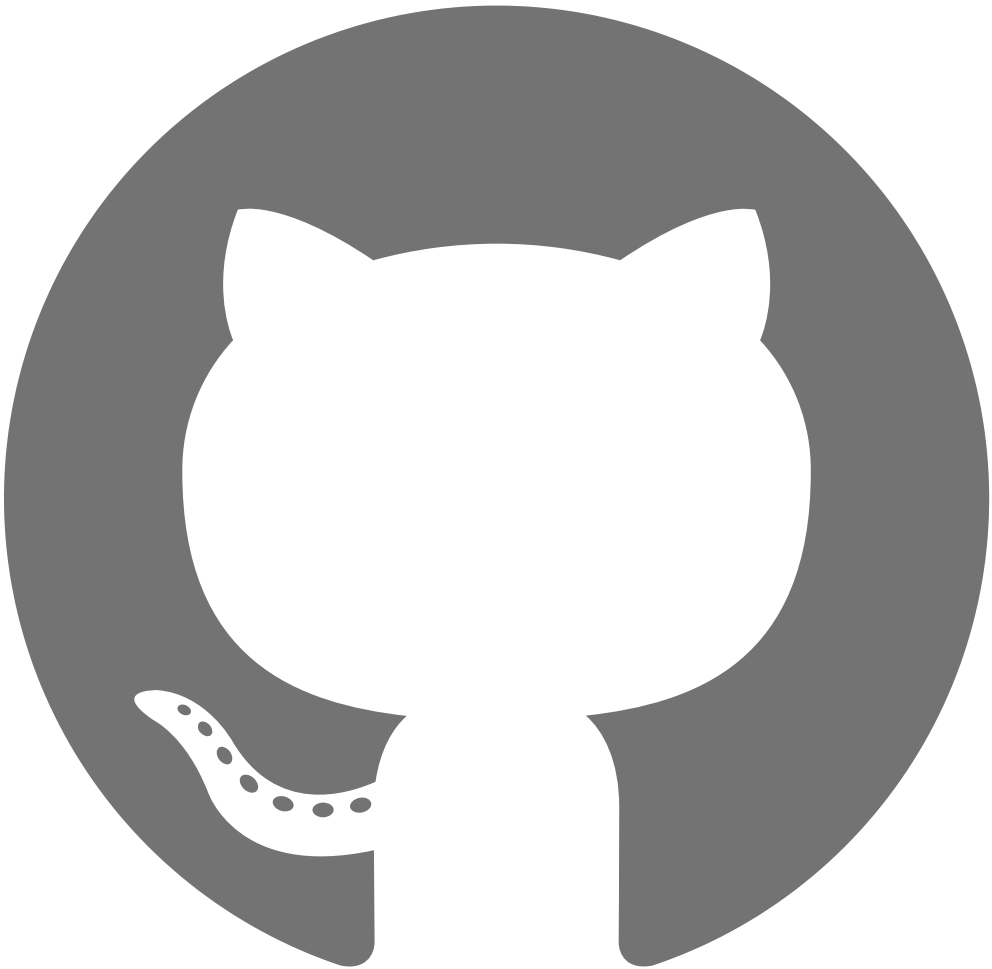
Plot of lcl|Query_63959 vs lcl|Query_63961

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