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BLAST® >> **Global Alignment** >> results for RID-PKD84V7U114

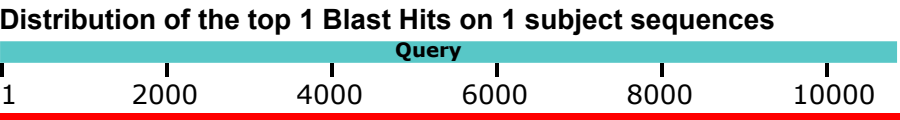
Job Title	SEQ_ID_NO3 ...
RID	PKD84V7U114 Search expires on 11-09 08:46 am
Program	Needleman-Wunsch alignment of two sequences
Query ID	lcl Query_38999 (dna)
Query Descr	SEQ_ID_NO3 ...
Query Length	10793

Subject ID lcl|Query_39001 (dna)
Subject Descr [SEQ_ID_NO72 ...](#)
Subject Length 10773

Descriptions

Description	Score	Percent Ident	Accession
SEQ_ID_NO72	21331	100.00%	Query_39001

Graphic Summary



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SEQ_ID_NO72
Sequence ID: Query_39001 Length: 10773 Number of Matches: 1
Range 1: 1 to 10773

NW Score	Identities	Gaps	Strand	Frame
21331	10740/10793(99%)	20/10793(0%)	Plus/Plus	
Query 1	CCAATCTGTGAATCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCA			60
Sbjct 1	C-----AGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCA			47
Query 61	ACAGGTTTTATTTTGGATTGGAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAA			120
Sbjct 48	ACAGGTTTTATTTTGGATTGGAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAA			107
Query 121	ATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGGAGTAGCCCGTGTGAGCCCCTT			180
Sbjct 108	ATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGGAGTAGCCCGTGTGAGCCCCTT			167
Query 181	TGGGGGCTTGAAGAGGCTGCCAGCCGGACTTCTGCTGGGTCATGGGCCCATCAGGATGGT			240
Sbjct 168	TGGGGGCTTGAAGAGGCTGCCAGCCGGACTTCTGCTGGGTCATGGGCCCATCAGGATGGT			227
Query 241	CTTGCGGATTCTAGCCTTTTTGAGATTACGGCAATCAAGCCATCACTGGGTCTCATCAA			300
Sbjct 228	CTTGCGGATTCTAGCCTTTTTGAGATTACGGCAATCAAGCCATCACTGGGTCTCATCAA			287
Query 301	TAGATGGGGTTCAGTGGGGAAAAAGAGGCTATGGAATAATAAAGAAGTTCAAGAAAGA			360
Sbjct 288	TAGATGGGGTTCAGTGGGGAAAAAGAGGCTATGGAATAATAAAGAAGTTCAAGAAAGA			347
Query 361	TCTGGCTGCCATGCTGAGAATAATCAATGCCAGGAAGGAGAAGAAGAGACGAGGCGCAGA			420
Sbjct 348	TCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGACGAGGCGCAGA			407
Query 421	TACTAGTGTGCGAATCGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAG			480
Sbjct 408	TACTAGTGTGCGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAG			467
Query 481	ACGTGGGAGTGCATACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTT			540
Sbjct 468	ACGTGGGAGTGCATACTATATGTACTTGGACAGAAACGACGCTGGGGAGGCCATATCTTT			527
Query 541	TCCAACCACATTGGGGATGAATAAGTGTTATATACAGATCATGGATCTTGGACACATGTG			600
Sbjct 528	TCCAACCACATTGGGGATGAATAAGTGTTATATACAGATCATGGATCTTGGACACATGTG			587
Query 601	TGATGCCACCATGAGCTATGAATGCCTATGCTGGATGAGGGGGTGAACACAGATGACGT			660
Sbjct 588	TGATGCCACCATGAGCTATGAATGCCTATGCTGGATGAGGGGGTGAACACAGATGACGT			647
Query 661	CGATTGTTGGTGCAACACGACGTCAACTGGGTTGTGTACGGAACCTGCCATCACAAAAA			720

Sbjct	648	CGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACTGCCATCACAAAAA	707
Query	721	AGGTGAAGCACGGAGATCTAGAAGAGCTGTGACGCTCCCCCTCCCATTCCTAGGAAGCT	780
Sbjct	708	AGGTGAAGCACGGAGATCTAGAAGAGCTGTGACGCTCCCCCTCCCATTCCTAGGAAGCT	767
Query	781	GCAAACGCGGTGCGAAACCTGGTTGGAATCAAGAGAATACACAAAGCACTTGATTAGAGT	840
Sbjct	768	GCAAACGCGGTGCGAAACCTGGTTGGAATCAAGAGAATACACAAAGCACTTGATTAGAGT	827
Query	841	CGAAAAATTGGATATTCAGGAACCTTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCT	900
Sbjct	828	CGAAAAATTGGATATTCAGGAACCTTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCT	887
Query	901	TTTGGGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCC	960
Sbjct	888	TTTGGGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCC	947
Query	961	GGCATAACGATCAGGTGCATAGGAGTCAGCAATAGGGACTTTGTGGAAGGTATGTCAGG	1020
Sbjct	948	GGCATAACGATCAGGTGCATAGGAGTCAGCAATAGGGACTTTGTGGAAGGTATGTCAGG	1007
Query	1021	TGGGACTTGGGTTGATGTTGTCTTGAACATGGGGGTTGTGTACCGTAATGGCACAGGA	1080
Sbjct	1008	TGGGACTTGGGTTGATGTTGTCTTGAACATGGAGGTTGTGTACCGTAATGGCACAGGA	1067
Query	1081	CAAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAG	1140
Sbjct	1068	CAAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAG	1127
Query	1141	ATCCTACTGCTATGAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACA	1200
Sbjct	1128	ATCCTACTGCTATGAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACA	1187
Query	1201	AGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAACGTTAGT	1260
Sbjct	1188	AGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAACGTTAGT	1247
Query	1261	GGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGAGCCTGGTGACATGCGC	1320
Sbjct	1248	GGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGAGCCTGGTGACATGCGC	1307
Query	1321	TAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTA	1380
Sbjct	1308	TAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTA	1367
Query	1381	CCGGATAATGCTGTGAGTTTATGGCTCCCAGCACAGTGGGATGATCGTTAATGACACAGG	1440
Sbjct	1368	CCGGATAATGCTGTGAGTTTATGGCTCCCAGCACAGTGGGATGATCGTTAATGACACAGG	1427
Query	1441	ACATGAAACTGATGAGAATAGAGCGAAGGTTGAGATAACGCCCAATTACCAAGAGCCGA	1500
Sbjct	1428	ACATGAAACTGATGAGAATAGAGCGAAGGTTGAGATAACGCCCAATTACCAAGAGCCGA	1487
Query	1501	AGCCACCCTGGGGGGTTTTGGAAGCTTAGGACTTGATTGTGAACCGAGGACAGGCCTTGA	1560
Sbjct	1488	AGCCACCCTGGGGGGTTTTGGAAGCTTAGGACTTGATTGTGAACCGAGGACAGGCCTTGA	1547
Query	1561	CTTTTCAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTCACAAGGAGTG	1620
Sbjct	1548	CTTTTCAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTCACAAGGAGTG	1607
Query	1621	GTTCCACGACATTCCATTACCTTGGCAGCTGGGGCAGACACCGGAATCCACACTGGAA	1680
Sbjct	1608	GTTCCACGACATTCCATTACCTTGGCAGCTGGGGCAGACACCGGAATCCACACTGGAA	1667
Query	1681	CAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAAACTGTCGTGGT	1740
Sbjct	1668	CAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAAACTGTCGTGGT	1727
Query	1741	TCTAGGGACTCAAGAAGGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGAT	1800
Sbjct	1728	TCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGAT	1787
Query	1801	GGATGGTGCAAAGGGAAGGCTGTCCTCTGGCCACTTGAAATGTCGCCTGAAAATGGATAA	1860
Sbjct	1788	GGATGGTGCAAAGGGAAGGCTGTCCTCTGGCCACTTGAAATGTCGCCTGAAAATGGATAA	1847
Query	1861	ACTTAGATTGAAGGGCGTGTCTACTCTTGTGTACCGCAGCGTTCACATTACCAAGAT	1920
Sbjct	1848	ACTTAGATTGAAGGGCGTGTCTACTCTTGTGTACCGCAGCGTTCACATTACCAAGAT	1907
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Sbjct	1908	CCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAGATGG	1967
Query	1981	ACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACCTCTGACCCAGTTGGGAG	2040
Sbjct	1968	ACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACCTCTGACCCAGTTGGGAG	2027
Query	2041	GTTGATAACCGCTAACCCCGTAATCACTGAAAGCACTGAAAGCACTTAAGATGATGCTGGA	2100

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Sbjct  2088  ACTTGATCCACCATTGGGGACTCTTACATTGTCATAGGAGTCGGGGAGAAGAAGATCAC 2147
Query   2161  CCACCACTGGCACAGGAGTGGCAGCACCATTGGAAGCACTTTGAAGCCACTGTGAGAGG 2220
Sbjct  2148  CCACCACTGGCACAGGAGTGGCAGCACCATTGGAAGCACTTTGAAGCCACTGTGAGAGG 2207
Query   2221  TGCCAAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGC 2280
Sbjct  2208  TGCCAAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGC 2267
Query   2281  TCTCAACTCATTGGGCAAGGGCATCCATCAAATTTTGGAGCAGCTTTCAAATCATTGTT 2340
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Query   2341  TGGAGGAATGTCCTGGTTCTCACAAATCTCATTGGAACGTTGCTGATGTGGTTGGGTCT 2400
Sbjct  2328  TGGAGGAATGTCCTGGTTCTCACAAATCTCATTGGAACGTTGCTGATGTGGTTGGGTCT 2387
Query   2401  GAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTT 2460
Sbjct  2388  GAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTT 2447
Query   2461  CTTATCCACAGCCGTCTCTGCTGATGTGGGGTGTCTCGGTGGACTTCTCAAAGAAGGAGAC 2520
Sbjct  2448  CTTATCCACAGCTGTCTCTGCTGATGTGGGGTGTCTCGGTGGACTTCTCAAAGAAGGAGAC 2507
Query   2521  GAGATGTGGTACAGGGGTGTTCTGCTATAACGACGTTGAAGCCTGGAGGGACAGGTACAA 2580
Sbjct  2508  GAGATGCGGTACAGGGGTGTTCTGCTATAACGACGTTGAAGCCTGGAGGGACAGGTACAA 2567
Query   2581  GTACCATCCTGACTCTCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATGG 2640
Sbjct  2568  GTACCATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATGG 2627
Query   2641  TATCTGCGGGATCTCCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGG 2700
Sbjct  2628  TATCTGTGGGATCTCCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGG 2687
Query   2701  GGAGCTTAACGCAATCCTGGAAGAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGT 2760
Sbjct  2688  GGAGCTCAACGCAATCCTGGAAGAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGT 2747
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Query   2821  CGGCTGGAAGGCTTGGGGGAAATCGTACTTCGTCAGAGCAGCAAAGACAAATAACAGCTT 2880
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Sbjct  2868  TGTCTGGGATGGTGACACACTGAAGGAATGCCCACTCAAACATAGAGCATGGAACAGCTT 2927
Query   2941  TCTTGTGGAGGATCATGGGTTGCGGGTATTTACACTAGTGTCTGGCTCAAGGTTAGAGA 3000
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Sbjct  2988  AGATTATTCATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGAAAGGAGGC 3047
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Sbjct  3048  TGTACACAGTGATCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAA 3107
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Sbjct  3108  GAGGGCCCATCTGATCGAGATGAAAACATGTGAATGGCCAAAGTCCCACACATTGTGGAC 3167
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Sbjct  3228  TCACAAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGAGCT 3287
Query   3301  TGAAATTCGGTTTGAGGAATGCCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAAC 3360
Sbjct  3288  TGAAATTCGGTTTGAGGAATGCCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAAC 3347
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Query	3481	GGAGATAAGGCCAGGAAAGAACAGAAAGCAACTTAGTAAGGTCAATGGTGAAGTGCAGG	3540
Sbjct	3468	GGAGATAAGGCCAGGAAAGAACAGAAAGTAACTTAGTAAGGTCAATGGTGAAGTGCAGG	3527
Query	3541	ATCAACTGATCACATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCA	3600
Sbjct	3528	ATCAACTGATCACATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCA	3587
Query	3601	GGAAGGGCTGAAGAAGAGAATGACCACAAAGATCATATAAGCACATCAATGGCAGTGCT	3660
Sbjct	3588	GGAAGGGCTGAAGAAGAGAATGACCACAAAGATCATATAAGCACATCGATGGCAGTGCT	3647
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Sbjct	3648	GGTAGCTATGATCCTGGGAGGATTTTCAATGAGTGACCTGGCTAAGCTTGCAATTTTGAT	3707
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Sbjct	3708	GGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGTGATAGC	3767
Query	3781	GGCATTCAAAGTCAGACCAGCGTTGCTGGTATCTTTTCATCTTCAGAGCTAATTGGACACC	3840
Sbjct	3768	GGCATTCAAAGTCAGACCAGCGTTGCTGGTATCTTTTCATCTTCAGAGCTAATTGGACACC	3827
Query	3841	CCGTGAAAGCATGCTGCTGGCCTTGGCCTCGTGTTTTTGCAAACTGCGATCTCCGCCTT	3900
Sbjct	3828	CCGTGAAAGCATGCTGCTGGCCTTGGCCTCGTGTTTTTGCAAACTGCGATCTCCGCCTT	3887
Query	3901	GGAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGC	3960
Sbjct	3888	GGAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGC	3947
Query	3961	GATGGTTGTTCCACGCACTGACAACATCACCTTGGCAATCCTGGCTGCTCTGACACCACT	4020
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Sbjct	4068	GCTCCTCTCTCTGAAGGGAAGGCAAGTGTGAAGAAGAACTTACCATTGTGATGGCCCT	4127
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Query	4261	CGCATTGGCTGGAGGGTTCGCCAAGGCAGATATAGAGATGGCTGGGCCCATGGCCGCGGT	4320
Sbjct	4248	CGCATTGGCTGGAGGGTTCGCCAAGGCAGATATAGAGATGGCTGGGCCCATGGCCGCGGT	4307
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Sbjct	4368	AGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGA	4427
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Sbjct	4428	TGTGGCGCTAGATGAGAGTGGTGATTCTCCCTGGTGGAGGATGACGGTCCCCCATGAG	4487
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Sbjct	4488	AGAGATCATACTCAAGGTGGTCTGATGACCATCTGTGGCATGAACCAATAGCCATACC	4547
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Sbjct	4548	CTTTGCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGTCTATG	4607
Query	4621	GGATGTGCCTGCTCCCAAGGAAGTAAAAAAGGGGGAGACCACAGATGGAGTGACAGAGT	4680
Sbjct	4608	GGATGTGCCTGCTCCCAAGGAAGTAAAAAAGGGGGAGACCACAGATGGAGTGACAGAGT	4667
Query	4681	AATGACTCGTAGACTGCTAGGTTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGT	4740
Sbjct	4668	AATGACTCGTAGACTGCTAGGTTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGT	4727
Query	4741	CTTTCACACTATGTGGCACGTCAAAAAGGATCCGCGCTGAGAAGCGGTGAAGGGAGACT	4800
Sbjct	4728	CTTTCACACTATGTGGCACGTCAAAAAGGATCCGCGCTGAGAAGCGGTGAAGGGAGACT	4787

Query	4801	TGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCT	4860
Sbjct	4788	TGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCT	4847
Query	4861	AGATGCCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAG	4920
Sbjct	4848	AGATGCCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAG	4907
Query	4921	AGCGAGGAACATCCAGACTCTGCCCCGAATATTTAAGACAAAGGATGGGGACATTGGAGC	4980
Sbjct	4908	AGCGAGGAACATCCAGACTCTGCCCCGAATATTTAAGACAAAGGATGGGGACATTGGAGC	4967
Query	4981	GGTTGCGCTGGATTACCCAGCAGGAACCTTCAAGATCTCCAATCCTAGACAAGTGTGGGAG	5040
Sbjct	4968	GGTTGCGCTGGATTACCCAGCAGGAACCTTCAAGATCTCCAATCCTAGACAAGTGTGGGAG	5027
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Sbjct	5028	AGTGATAGGACTTTATGGCAATGGGGTCGTGATCAAAAAATGGGAGTTATGTTAGTGCCAT	5087
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Sbjct	5088	CACCCAAGGGAGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAA	5147
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Sbjct	5148	GAAGAAGCAGCTAACTGTCTTAGACTTGCATCCTGGAGCTGGGAAAACAGGAGAGTTCT	5207
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Sbjct	5208	TCCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTACTGTGATCTTAGCTCCAAC	5267
Query	5281	CAGGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGTTATATGAC	5340
Sbjct	5268	CAGGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGTTATATGAC	5327
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Query	5461	TGAGGCCCACTTCACAGATCCCTCAAGCATAGCAGCAAGAGGATACATTTCAACAAGGGT	5520
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Sbjct	5508	TGAGATGGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACCAGGAACCCGTGACGC	5567
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Sbjct	5568	ATTTCCGGACTCCAACACCAATTATGGACACCGAAGTGGAGTCCCAGAGAGAGCCTG	5627
Query	5641	GAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGAAAAACAGTTTGGTTTGTTCGAAG	5700
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Query	5701	CGTGAGGAACGGCAATGAGATCGCAGCTTGCTGACAAAGGCTGGAAAAACGGGTCATACA	5760
Sbjct	5688	CGTGAGGAACGGCAATGAGATCGCAGCTTGCTGACAAAGGCTGGAAAAACGGGTCATACA	5747
Query	5761	GCTCAGCAGAAAGACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAGTGGGACTT	5820
Sbjct	5748	GCTCAGCAGAAAGACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAGTGGGACTT	5807
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Sbjct	5808	TGTCGTGACAACTGACATTTAGAGATGGGCGCCAACCTTTAAAGCTGACCGTGTATAGA	5867
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Sbjct	5868	TTCCAGGAGATGCCTAAAGCCGGTCATACCTGATGGCGAGAGAGTCATTCTGGCTGGACC	5927
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Sbjct	5928	CATGCCGTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAA	5987
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Sbjct	5988	CAAACCTGGAGATGAGTATCTGTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGC	6047
Query	6061	ACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTCCAAGATGGCCTCATAGC	6120
Sbjct	6048	ACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTCCAAGATGGCCTCATAGC	6107
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Taxonomy

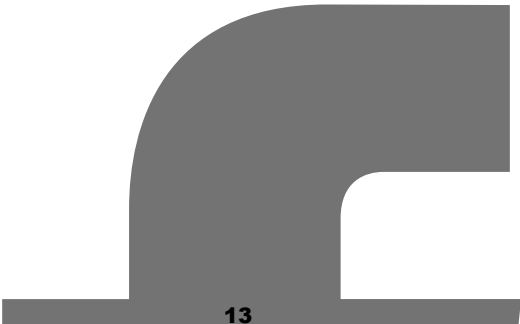
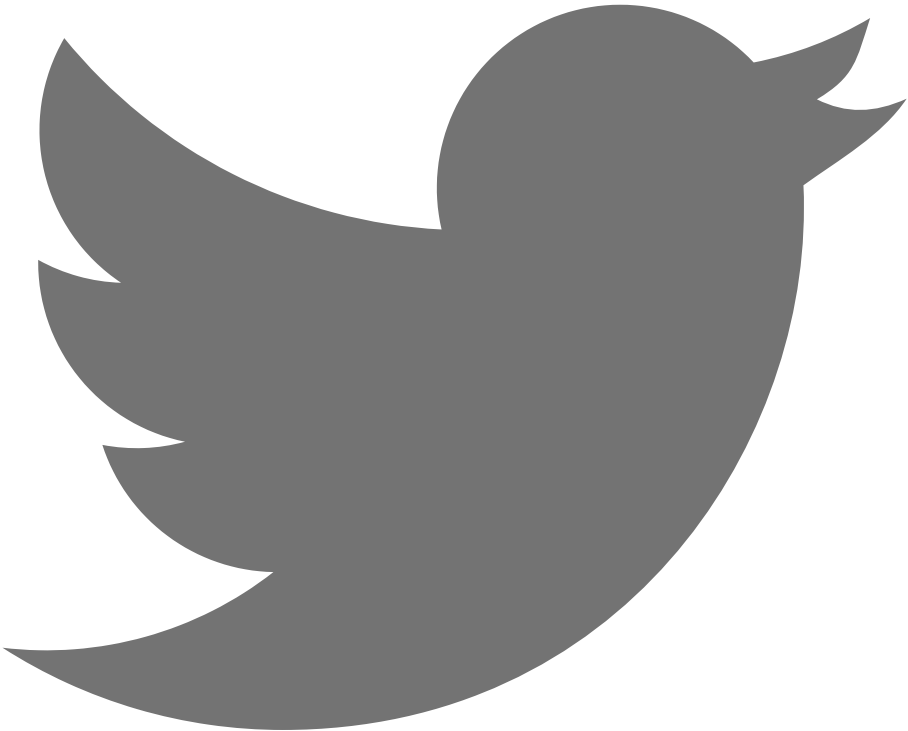
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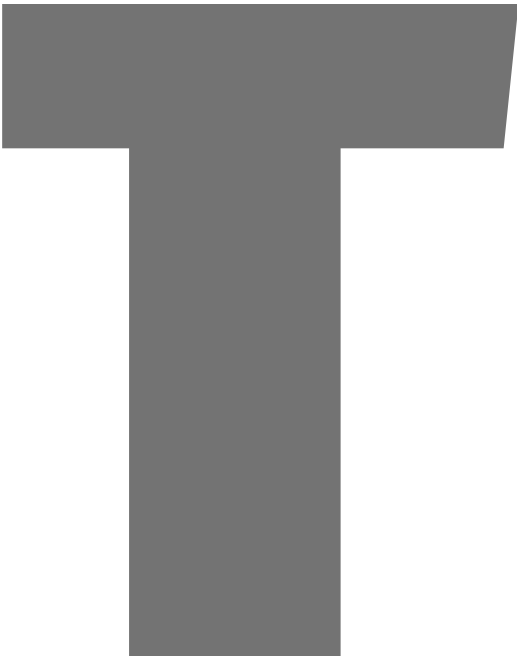
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- Taxonomy

Dot Plot

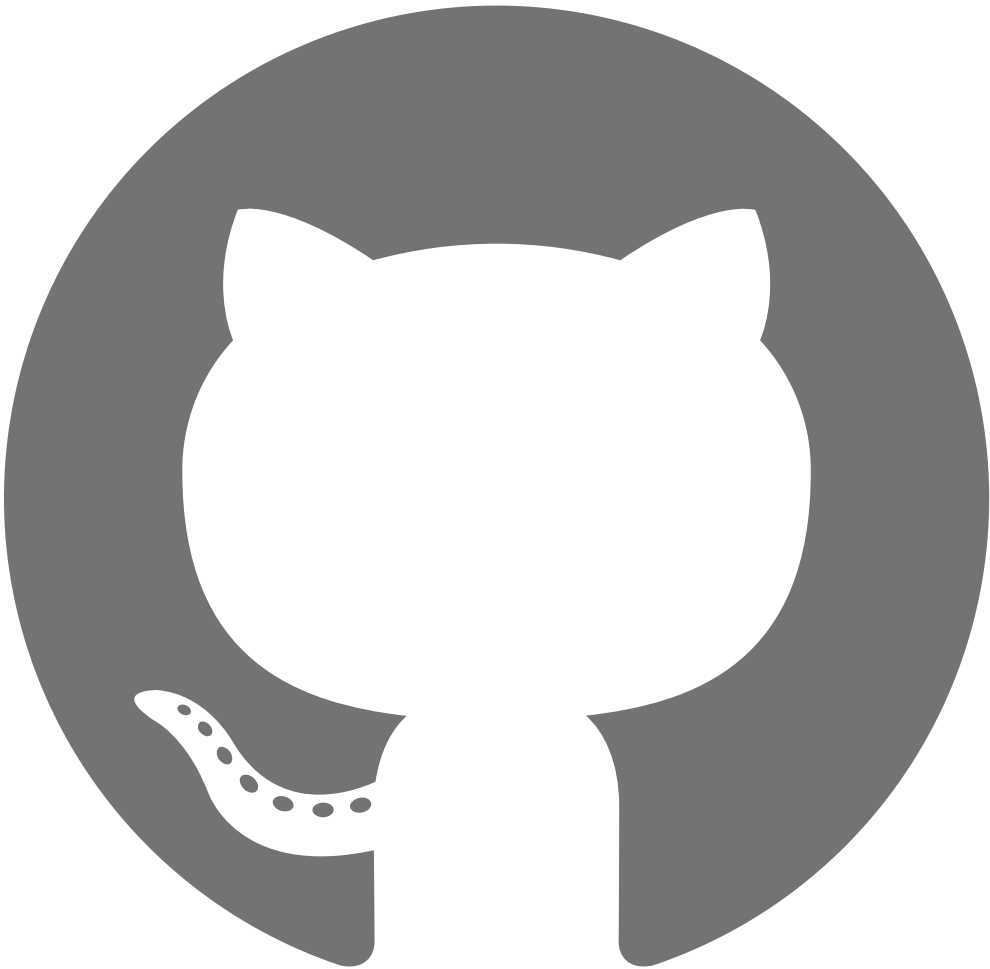
Plot of lcl|Query_38999 vs lcl|Query_39001

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