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BLAST® >> **Global Alignment** >> results for RID-PKDR1EU6114

Job Title	SEQ_ID_NO12 ...
RID	PKDR1EU6114 Search expires on 11-09 08:54 am
Program	Needleman-Wunsch alignment of two sequences
Query ID	lcl Query_48635 (dna)
Query Descr	SEQ_ID_NO12 ...
Query Length	10794

Subject ID

lcl|Query_48637 (dna)

Subject Descr

[SEQ_ID_NO72 ...](#)

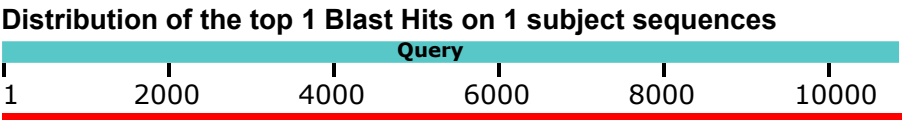
Subject Length

10773

Descriptions

Description	Score	Percent Ident	Accession
SEQ_ID_NO72	15498	89.00%	Query_48637

Graphic Summary



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SEQ_ID_NO72
Sequence ID: Query_48637 Length: 10773 Number of Matches: 1
Range 1: 1 to 10773

NW Score	Identities	Gaps	Strand	Frame
15498	9584/10810(89%)	53/10810(0%)	Plus/Plus	
Query 1	AGTTGTTGATCTGTGTGAGTCAGACTGCGACAGTTCGAGTCTGAAGCGAGAGCTAACAAC			60
Sbjct 1		CAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAAC		40
Query 61	AGTATCAACAGGTTTAAATTT -GGATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCCA			119
Sbjct 41	AGTATCAACAGGTTTATTTTGGATTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAA			100
Query 120	AAGAAGAAATCCGGAGGAT -CCGGATTGTCAATATGCTAAACGCGGAGTAGCCCGTGTA			178
Sbjct 101	AA -AAGAAATCCGGAGGATTCGGATTGTCAATATGCTAAACGCGGAGTAGCCCGTGTG			159
Query 179	AACCCCTTGGGAGGTTTGAAGAGGTTGCCAGCCGGACTTCTGCTGGGTCTGGACCCATC			238
Sbjct 160	AGCCCTTGGGGGCTTGAAGAGGCTGCCAGCCGGACTTCTGCTGGGTCTGGGCCATC			219
Query 239	AGAATGGTTTTGGCGATACTAGCCTTTTTGAGATTTACAGCAATCAAGCCATCACTGGGC			298
Sbjct 220	AGGATGGTCTTGGCGATTCTAGCCTTTTTGAGATTCACGGCAATCAAGCCATCACTGGGT			279
Query 299	CTTATCAACAGATGGGGTTCCGTGGGGAAAAAAGAGGCTATGGAAATAATAAAGAAGTTC			358
Sbjct 280	CTCATCAATAGATGGGGTTCAGTGGGGAAAAAAGAGGCTATGGAAATAATAAAGAAGTTC			339
Query 359	AAGAAAGATCTTGCTGCCATGTTGAGAATAATCAATGCTAGGAAAGAGAGGAAGAGACGT			418
Sbjct 340	AAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGACGA			399
Query 419	GGCGCAGACACCAGCATCGGAATCATTGGCCTCCTGCTGACTACAGCCATGGCAGCAGAG			478
Sbjct 400	GGCGCAGATACTAGTGTGGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAG			459
Query 479	ATCACTAGACGCGGGAGTGCATACTACATGTACTTGGATAGGAGCGATGCCGGGAAGGCC			538
Sbjct 460	GTCATACTAGAGTGGGAGTGCATACTATATGTACTTGGACAGAAACGACGCTGGGGAGGCC			519
Query 539	ATTTTCGTTTGCTACCACATTGGGAGTGAACAAGTGCCACGTACAGATCATGGACCTCGGG			598
Sbjct 520	ATATCTTTTCCAACCACATTGGGGATGAATAAGTGTTATATACAGATCATGGATCTTGGA			579
Query 599	CACATGTGTGACGCCACCATGAGTTATGAGTGCCCTATGCTGGATGAGGGAGTGGAACCA			658
Sbjct 580	CACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGTTGGAACCA			639
Query 659	GATGATGTCGATTGCTGGTGCAACACGACATCAACTTGGGTTGTGTACGGAACCTGTCAT			718

Sbjct	640	GATGACGTCGATTGTTGGTGAACACGACGTCACCTTGGGTTGTGTACGGAACCTGCCAT	699
Query	719	CACAAAAAAGGTGAGGCACGGCGATCTAGAAGAGCCGTGACGCTCCCTTCTACTCTACA	778
Sbjct	700	CACAAAAAAGGTGAAGCACGGAGATCTAGAAGAGCTGTGACGCTCCCTCCCATTCCACT	759
Query	779	AGGAAGTTGCAAACGCGGTGCGAGACCTGGTTAGAATCAAGAGAATACACGAAGCACTTG	838
Sbjct	760	AGGAAGCTGCAAACGCGGTGCGAAACCTGGTTGGAATCAAGAGAATACACAAAGCACTTG	819
Query	839	ATCAAGGTTGAAAACCTGGATATTCAGGAACCCCGGTTTGCCTAGTGGCCGTTGCCATT	898
Sbjct	820	ATTAGAGTCGAAAATTGGATATTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATC	879
Query	899	GCCTGGCTTTTGGGAAGCTCGACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTG	958
Sbjct	880	GCTTGGCTTTTGGGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTG	939
Query	959	ATTGCCCCGGCATAACAGTATCAGGTGCATTGGAGTCAGCAATAGAGACTTCGTGGAGGGC	1018
Sbjct	940	ATTGCCCCGGCATAACAGCATCAGGTGCATAGGAGTCAGCAATAGGGACTTTGTGGAAGGT	999
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Sbjct	1000	ATGTCAGGTGGGACTTGGGTTGATGTTGCTTGGAAACATGGAGGTTGTGTACCGTAATG	1059
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Sbjct	1060	GCACAGGACAAACCGACTGTCGCATAGAGCTGGTTACAACAACAGTCAGCAACATGGCG	1119
Query	1139	GAGGTAAGATCCTATTGCTACGAGGCATCGATATCGGACATGGCTTCGGACAGTCGTTGC	1198
Sbjct	1120	GAGGTAAGATCCTACTGCTATGAGGCATCAATATCGGACATGGCTTCGGACAGCCGCTGC	1179
Query	1199	CCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAAGA	1258
Sbjct	1180	CCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAAGA	1239
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Query	1319	ACATGTGCCAAGTTTACGTGTTCTAAGAAGATGACCGGGAAGAGCATTCAACCGGAAAAT	1378
Sbjct	1300	ACATGCGCTAAGTTTGCATGCTCAAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAAT	1359
Query	1379	CTGGAGTATCGGATAATGCTATCAGTGCATGGCTCCCAGCATAGCGGGATGATTG-----	1433
Sbjct	1360	CTGGAGTACCGGATAATGCTGTCAGTTCATGGCTCCCAGCACAGTGGGATGATCGTTAAT	1419
Query	1434	-----GATATGAACTGACGAAGATAGAGCGAAAGTCGAGGTTACGCCAATTACCA	1486
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Sbjct	1540	GGCCTTGACTTTTTCAGATTTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTCAC	1599
Query	1607	AAAGAGTGGTTTCATGACATCCCATTGCCTTGGCATGCTGGGGCAGACACCGGAATCCA	1666
Sbjct	1600	AAGGAGTGGTTCACGACATTCCATTACCTTGGCACGCTGGGGCAGACACCGGAATCCA	1659
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Sbjct	1660	CACTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAAACCT	1719
Query	1727	GTCGTCTGTTCTGGGGAGCCAGGAAGGAGCCGTTACACGCGCTCTCGCTGGAGCTCTAGAG	1786
Sbjct	1720	GTCGTGTTCTAGGGAGTCAAGAAAGGAGCAGTTACACGCGCCTTGCTGGAGCTCTGGAG	1779
Query	1787	GCTGAGATGGATGGTGCAAAGGGAAGGCTGTTCTCTGGCCATTTGAAATGCCGCTAAAA	1846
Sbjct	1780	GCTGAGATGGATGGTGCAAAGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAA	1839
Query	1847	ATGGACAAGCTTAGATTGAAGGGCGTGCATATTCCTTGTGCACTGCGGCATTACATTTC	1906
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Sbjct	1900	ACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGG	1959
Query	1967	ACAGATGGACCCTGCAAGATCCCAGTCCAGATGGCGGTGGACATGCAGACCCTGACCCCA	2026
Sbjct	1960	ACAGATGGACCCTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCCA	2019
Query	2027	GTTGGAAGGCTGATAACCGCCAACCCCGTGATTACTGAAAGCACTGAGAACTCAAAGATG	2086

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Sbjct  2020  GTTGGGAGGTTGATAACCGCTAACCCCGTAATCACTGAAAGCACTGAGAACTCTAAGATG 2079
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Sbjct  2080  ATGCTGGAACCTGATCCACCATTGTTGGGACTCTTACATTGTCATAGGAGTCGGGGAGAAG 2139
Query   2147  AAAATCACCCACCCTGGCATAGGAGTGGTAGCACCATCGGAAAGGCATTTGAGGCCACT 2206
Sbjct  2140  AAGATCACCCACCCTGGCACAGGAGTGGCAGCACCATTGGAAAAGCATTGAAGCCACT 2199
Query   2207  GTGAGAGGCGCCAAGAGAATGGCAGTCTTGGGGGATACAGCCTGGGACTTCGGATCAGTC 2266
Sbjct  2200  GTGAGAGGTGCCAAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTT 2259
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Sbjct  2260  GGAAGGCGCTCTCAACTCATTTGGGCAAGGGCATCCATCAAAATTTTGGAGCAGCTTCAAA 2319
Query   2327  TCACTGTTTGGAGGAATGTCTGGTTCTCACAGATCCTCATAGGCACGCTGCTAGTGTGG 2386
Sbjct  2320  TCATTGTTTGGAGGAATGTCTGGTTCTCAAAAATCTCATTGGAACGTTGCTGATGTGG 2379
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Sbjct  2380  TTGGGTCTGAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTG 2439
Query   2447  ATGATCTTCTCTCCACGGCTGTTTCTGCTGACGTGGGGTGCTCAGTGGACTTCTCAAAA 2506
Sbjct  2440  TTGATCTTCTTATCCACAGCTGTCTCTGCTGATGTGGGGTGCTCGGTGGACTTCTCAAAG 2499
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Sbjct  2500  AAGGAGACGAGATGCGGTACAGGGGTGTTCTGTCTATAACGACGTTGAAGCCTGGAGGGAC 2559
Query   2567  CGGTACAAGTACCATCCTGACTCCCCCGCAGATTGGCAGCAGCAGTCAAGCAGGCCTGG 2626
Sbjct  2560  AGGTACAAGTACCATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGG 2619
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Sbjct  2620  GAAGATGGTATCTGTGGGATCTCCTCTGTTTCAAGAATGGAAGAACATCATGTGGAATCA 2679
Query   2687  GTAGAAGGGGAGCTCAATGCTATCTAGAGGAGAATGGAGTTCAACTGACAGTTGTTGTG 2746
Sbjct  2680  GTAGAAGGGGAGCTCAACGCAATCCTGGAAGAGAATGGAGTTCAACTGACGGTCGTTGTG 2739
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Sbjct  2860  AACAGCTTTGTGCTGGATGGTGACACACTGAAGGAATGCCCACTCAAACATAGAGCATGG 2919
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Sbjct  2980  GTTAGAGAAGATTATTCATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGA 3039
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Query   3107  AGGCTGAAGAGGGCCACCTGATTGAGATGAAAACATGTGAATGGCCAAAGTCTCACACA 3166
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Sbjct  3220  CTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGT 3279
Query   3287  GAAGAGCTTGAAATCCGGTTTGGAGGAATGTCCAGGCACCAAGGTTTACGTGGAGGAGACA 3346
Sbjct  3280  GAAGAGCTTGAAATCCGGTTTGGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACA 3339
Query   3347  TCGGGAAGTCTAGAGGACCATCTCTGAGATCAACTACTGCAAGTGGAAGGGTCATTGAGGAA 3406
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Sbjct	3460	TATGGAATGGAGATAAGGCCAGGAAAGAACAGAAAGTAAGTTAGTAAGGTCAATGGTG	3519
Query	3527	ACAGCGGGGTCAACCGATCATATGGACCACTTCTCTTGGAGTGCTTGTGATTCTACTC	3586
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Sbjct	3580	ATGGTGCAGGAAGGGCTGAAGAAGAGAATGACCACAAAGATCATCATGAGCACATCGATG	3639
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Sbjct	3760	CTGATAGCGGCATTTAAAGTCAGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAAT	3819
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Sbjct	3820	TGGACACCCCGTGAAAGCATGCTGCTGGCCTTGGCCTCGTGCTTTTGCAAACTGCGATC	3879
Query	3887	TCTGCTCTTGAAGGTGACTTGATGGTCTCATTAAATGGATTTGCTTTGGCCTGGTTGGCA	3946
Sbjct	3880	TCCGCCCTTGAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCA	3939
Query	3947	ATTCGAGCAATGGCCGTGCCACGCACTGACAACATCGCTCTACCAATCTTGGCTGCTCTA	4006
Sbjct	3940	ATACGAGCGATGGTTGTTCCACGCACTGATAACATCACCTTGCAATCCTGGCTGCTCTG	3999
Query	4007	ACACCACTAGCTCGAGGCACACTGCTCGTGGCATGGAGAGCGGGCCTGGCTACTTGTGGA	4066
Sbjct	4000	ACACCACTGGCCCGGGGCACACTGCTTGTGGCGTGGAGAGCAGGCCTTGCTACTTGCGGG	4059
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Sbjct	4180	TTGCTCACAAGGAGTGGGAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGC	4239
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Sbjct	4300	GCCGCGGTGCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTAC	4359
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Query	4427	CGGCTTGACGTGGCACTGGATGAGAGTGGTGACTTCTCCTTGGTAGAGGAAGATGGTCCA	4486
Sbjct	4420	CGGCTCGATGTGGCGCTAGATGAGAGTGGTGATTCTCCCTGGTGGAGGATGACGGTCCC	4479
Query	4487	CCCATGAGAGAGATCATACTCAAGGTGGTCTGATGGCCATCTGTGGCATGAACCCAATA	4546
Sbjct	4480	CCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTGGCATGAACCCAATA	4539
Query	4547	GCTATACCTTTTGTGTCAGGAGCGTGGTATGTGTATGTGAAGACTGGGAAAAGGAGTGGC	4606
Sbjct	4540	GCCATACCTTTTGCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGT	4599
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Sbjct	4600	GCTCTATGGGATGTGCCTGCTCCCAAGGAAGTAAAAAGGGGAGACCACAGATGGAGTG	4659
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Query	4727	GAGGGAGTCTTCCACACCATGTGGCACGTTACAAAAGGAGCCGCACTGAGGAGCGGTGAG	4786
Sbjct	4720	GAGGGGCTCTTCCACACTATGTGGCACGTCACAAAAGGAGCCGCGCTGAGAAGCGGTGAA	4779

Query	4787	GGAAGACTTGATCCATACTGGGGGATGTCAAGCAGGACTTGGTGTCACTACTGTGGGCCT	4846
Sbjct	4780	GGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCACTACTGTGGTCCA	4839
Query	4847	TGGAAGTTGGATGCAGCTTGGGATGGACTCAGCGAGGTACAGCTTTTGGCCGTACCTCCC	4906
Sbjct	4840	TGGAAGCTAGATGCCGCCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCC	4899
Query	4907	GGAGAGAGGGCCAGAAACATTTCAGACCTGCCTGGAATATTCAAGACAAAGGACGGGGAC	4966
Sbjct	4900	GGAGAGAGAGCGAGGAACATCCAGACTCTGCCCGGAATATTTAAGACAAAGGATGGGGAC	4959
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Sbjct	5200	AGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTAAGTGATCTTA	5259
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Sbjct	5320	TATATGACAACAGCAGTCAATGTACCCACTCTGGAACAGAAATCGTCGACTTAATGTGC	5379
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Sbjct	5380	CATGCCACCTTCACTTCACGCTTACTACAGCCAATCAGAGTCCCCAATAATCTGTAT	5439
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Query	5507	ACAAGGGTTGAAATGGGCGAGGCGGCTGCCATTTTTATGACTGCCACACCACCAGGAACC	5566
Sbjct	5500	ACAAGGGTTGAGATGGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACCAGGAACC	5559
Query	5567	CGTGATGCGTTTCTGACTCTAACTACCAATCATGGACACAGAAGTGGAAGTCCCAGAG	5626
Sbjct	5560	CGTGACGCATTTCCGGACTCCAATCACCATTATGGACACCGAAGTGGAAGTCCCAGAG	5619
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Sbjct	5620	AGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGGAAAAACAGTTTGGTTT	5679
Query	5687	GTTCCAAGCGTGAGAAACGAAATGAAATCGCAGCCTGTCTGACAAAGGCTGGAAAGCGG	5746
Sbjct	5680	GTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAACGG	5739
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Sbjct	5740	GTCATACAGCTCAGCAGAAAGACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAG	5799
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Sbjct	5800	TGGGACTTTGTCTGACAACCTGACATTTAGAGATGGGCGCCAACCTTAAAGCTGACCGT	5859
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Sbjct	5980	AATCCCAACAAACCTGGAGATGAGTATCTGTATGGAGGTGGGTGCGCAGAGACTGACGAA	6039
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Sbjct 6820 CAAAGATCTCCCCAGGACAACCAATGGCAATCATCATCATGGTAGCAGTAGGTCTTCTG 6879

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Taxonomy

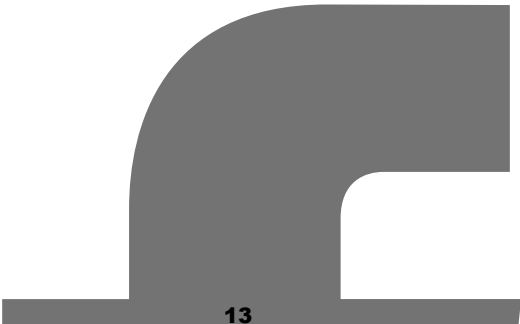
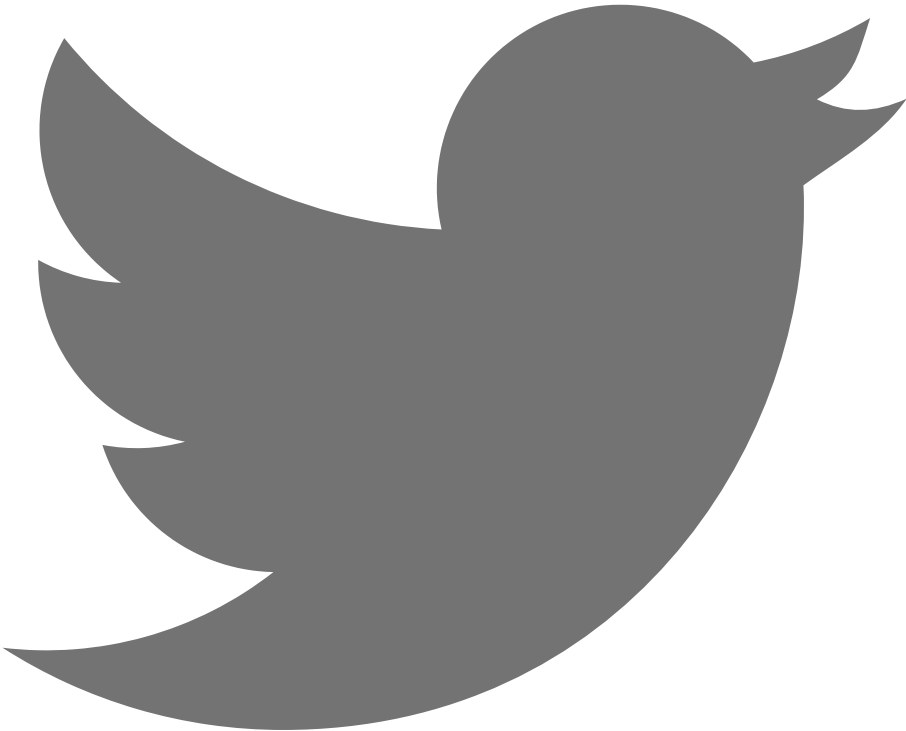
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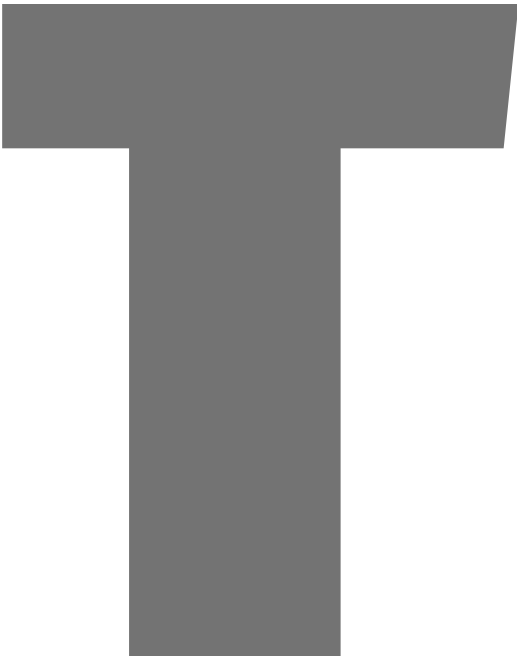
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Dot Plot

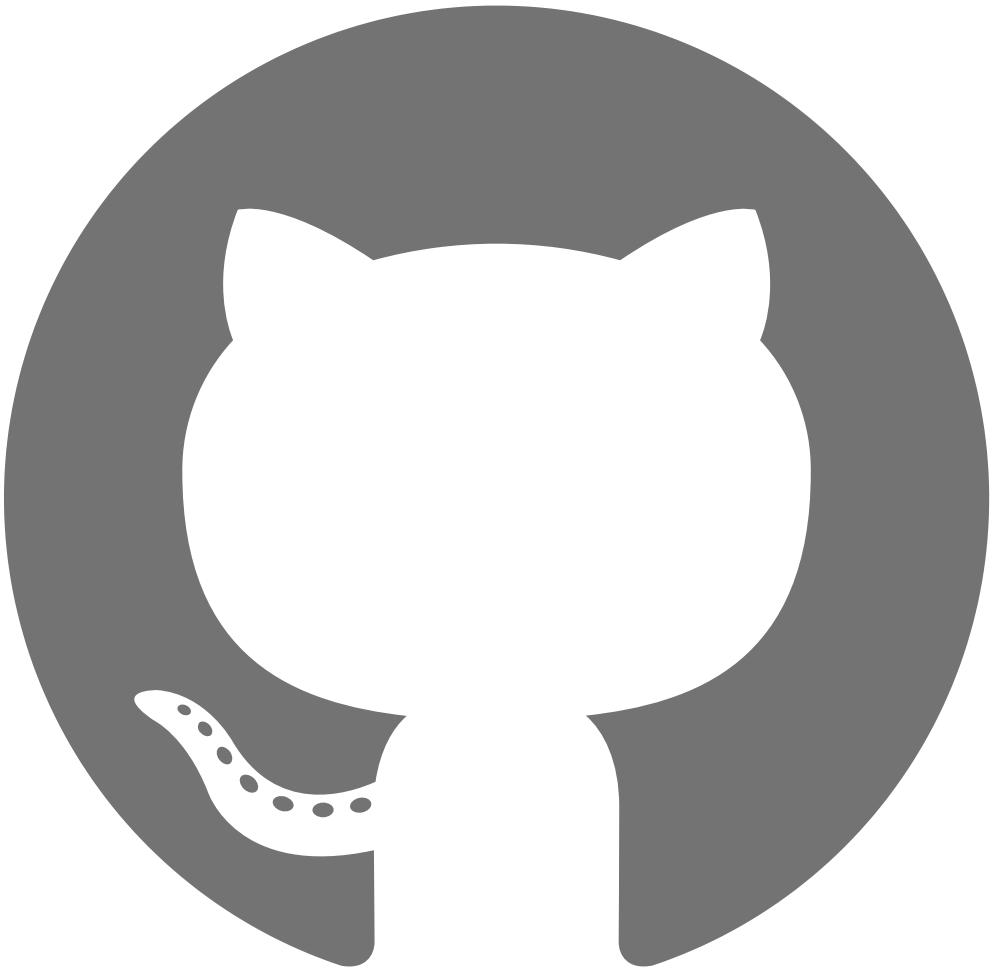
Plot of lcl|Query_48635 vs lcl|Query_48637

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