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BLAST[®] >> **Global Alignment** >> results for RID-PKDUZMG3114

Job Title	SEQ_ID_NO11 ...
RID	PKDUZMG3114 Search expires on 11-09 08:56 am
Program	Needleman-Wunsch alignment of two sequences
Query ID	lcl Query_63257 (dna)
Query Descr	SEQ_ID_NO11 ...
Query Length	10807

Subject ID

lcl|Query_63259 (dna)

Subject Descr

[SEQ_ID_NO12 ...](#)

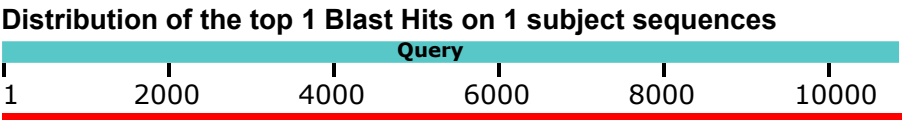
Subject Length

10794

Descriptions

Description	Score	Percent Ident	Accession
SEQ_ID_NO12	21440	100.00%	Query_63259

Graphic Summary



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SEQ_ID_NO12
Sequence ID: Query_63259 Length: 10794 Number of Matches: 1
Range 1: 1 to 10794

NW Score	Identities	Gaps	Strand	Frame
21440	10776/10809(99%)	17/10809(0%)	Plus/Plus	
Query 1	AGTTGTTGATCTGTGTGAGTCAGACTGCGACAGTTCGAGTCTGAAGCGAGAGCTAACAAC			60
Sbjct 1	AGTTGTTGATCTGTGTGAGTCAGACTGCGACAGTTCGAGTCTGAAGCGAGAGCTAACAAC			60
Query 61	AGTATCAACAGGTTTAATTTGGATTTGGAACGAGAGTTTCTGGTCATGAAAAACCC-AA			119
Sbjct 61	AGTATCAACAGGTTTAATTTGGATTTGGAACGAGAGTTTCTGGTCATGAAAAACCCCAA			120
Query 120	AGAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAACGCGGAGTAGCCCGTGTA			179
Sbjct 121	AGAAGAAATCCGGAGGAT-CCGGATTGTCAATATGCTAAAACGCGGAGTAGCCCGTGTA			179
Query 180	ACCCCTTGGGAGGTTTGAAGAGGTTGCCAGCCGGACTTCTGCTGGGTATGGACCCATCA			239
Sbjct 180	ACCCCTTGGGAGGTTTGAAGAGGTTGCCAGCCGGACTTCTGCTGGGTATGGACCCATCA			239
Query 240	GAATGGTTTTGGCGATACTAGCCTTTTTGAGATTTACAGCAATCAAGCCATCACTGGGCC			299
Sbjct 240	GAATGGTTTTGGCGATACTAGCCTTTTTGAGATTTACAGCAATCAAGCCATCACTGGGCC			299
Query 300	TTATCAACAGATGGGGTTCGTGGGGAAAAAGAGGCTATGGAAATAATAAGAAAGTTCA			359
Sbjct 300	TTATCAACAGATGGGGTTCGTGGGGAAAAAGAGGCTATGGAAATAATAAGAAAGTTCA			359
Query 360	AGAAAGATCTTGCTGCCATGTTGAGAATAATCAATGCTAGGAAAGAGAGGAAGAGACGTG			419
Sbjct 360	AGAAAGATCTTGCTGCCATGTTGAGAATAATCAATGCTAGGAAAGAGAGGAAGAGACGTG			419
Query 420	GCGCAGACACCAGCATCGGAATCATTGGCCTCCTGCTGACTACAGCCATGGCAGCAGAGA			479
Sbjct 420	GCGCAGACACCAGCATCGGAATCATTGGCCTCCTGCTGACTACAGCCATGGCAGCAGAGA			479
Query 480	TCTAGACGCGGGAGTGCATACTACATGTACTTGGATAGGAGCGATGCCGGGAAGGCCA			539
Sbjct 480	TCTAGACGCGGGAGTGCATACTACATGTACTTGGATAGGAGCGATGCCGGGAAGGCCA			539
Query 540	TTTCGTTTGCTACACATTGGGAGTGAACAAGTGCCACGTACAGATCATGGACCTCGGGC			599
Sbjct 540	TTTCGTTTGCTACACATTGGGAGTGAACAAGTGCCACGTACAGATCATGGACCTCGGGC			599
Query 600	ACATGTGTGACGCCACCATGAGTTATGAGTGCCCTATGCTGGATGAGGGAGTGAACCAG			659
Sbjct 600	ACATGTGTGACGCCACCATGAGTTATGAGTGCCCTATGCTGGATGAGGGAGTGAACCAG			659
Query 660	ATGATGTCGATTGCTGGTGAACACGACATCAACTTGGGTTGTGTACGGAACCTGTCATC			719

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Sbjct 660 ATGATGTCGATTGCTGGTGCAACACGACATCAACTTGGGTTGTGTACGGAACCTGTCATC 719
Query 720 ACAAAAAAGGTGAGGCACGGCGATCTAGAAGAGCCGTGACGCTCCCTTCTCACTCTACAA 779
Sbjct 720 ACAAAAAAGGTGAGGCACGGCGATCTAGAAGAGCCGTGACGCTCCCTTCTCACTCTACAA 779
Query 780 GGAAGTTGCAAACGCGGTCGACAGCTGTTAGAATCAAGAGAATACACGAAGCACTTGA 839
Sbjct 780 GGAAGTTGCAAACGCGGTCGACAGCTGTTAGAATCAAGAGAATACACGAAGCACTTGA 839
Query 840 TCAAGGTTGAAAACGGATATTCAGGAACCCCGGGTTTGCCTAGTGGCCGTTGCCATTG 899
Sbjct 840 TCAAGGTTGAAAACGGATATTCAGGAACCCCGGGTTTGCCTAGTGGCCGTTGCCATTG 899
Query 900 CCTGGCTTTTGGGAAGCTCGACGAGCCAAAAGTCATATACTTGGTCATGATACTGCTGA 959
Sbjct 900 CCTGGCTTTTGGGAAGCTCGACGAGCCAAAAGTCATATACTTGGTCATGATACTGCTGA 959
Query 960 TTGCCCCGGCATAAGTATCAGGTGCATTGGAGTCAGCAATAGAGACTTCGTGGAGGGCA 1019
Sbjct 960 TTGCCCCGGCATAAGTATCAGGTGCATTGGAGTCAGCAATAGAGACTTCGTGGAGGGCA 1019
Query 1020 TGTCAAGTGGGACCTGGGTTGATGTTGTCTTGAACATGGAGGCTGCGTTACCGTGATGG 1079
Sbjct 1020 TGTCAAGTGGGACCTGGGTTGATGTTGTCTTGAACATGGAGGCTGCGTTACCGTGATGG 1079
Query 1080 CACAGGACAAGCCAACAGTTGACATAGAGTTGGTCACGACGACGGTTAGTAACATGGCCG 1139
Sbjct 1080 CACAGGACAAGCCAACAGTCGACATAGAGTTGGTCACGACGACGGTTAGTAACATGGCCG 1139
Query 1140 AGGTAAGATCCTATTGCTACGAGGCATCGATATCGGACATGGCTTCGGACAGTCGTTGCC 1199
Sbjct 1140 AGGTAAGATCCTATTGCTACGAGGCATCGATATCGGACATGGCTTCGGACAGTCGTTGCC 1199
Query 1200 CAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAA 1259
Sbjct 1200 CAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAA 1259
Query 1260 CATTAGTGGACAGAGGTTGGGGAACCGTTGTGGACTTTTGGCAAAGGGAGCTTGGTGA 1319
Sbjct 1260 CATTAGTGGACAGAGGTTGGGGAACCGTTGTGGACTTTTGGCAAAGGGAGCTTGGTGA 1319
Query 1320 CATGTGCCAAGTTTACGTGTTCTAAGAAGATGACCGGAAGAGCATTCAACCGGAAAATC 1379
Sbjct 1320 CATGTGCCAAGTTTACGTGTTCTAAGAAGATGACCGGAAGAGCATTCAACCGGAAAATC 1379
Query 1380 TGGAGTATCGGATAATGCTATCAGTGCATGGCTCCCAGCATAGCGGGATGACTGTCAATG 1439
Sbjct 1380 TGGAGTATCGGATAATGCTATCAGTGCATGGCTCCCAGCATAGCGGGATGATTG----- 1433
Query 1440 ATATAGGATATGAAACTGACGAAAATAGAGCGAAAGTCGAGGTTACGCCTAATTCACCAA 1499
Sbjct 1434 -----GATATGAAACTGACGAAGATAGAGCGAAAGTCGAGGTTACGCCTAATTCACCAA 1487
Query 1500 GAGCGGAAGCAACCTTGGGAGGCTTTGGAAGCTTAGGACTTGACTGTGAACCAAGGACAG 1559
Sbjct 1488 GAGCGGAAGCAACCTTGGGAGGCTTTGGAAGCTTAGGACTTGACTGTGAACCAAGGACAG 1547
Query 1560 GCCTTGACTTTTTCAGATCTGTATTACCTGACCATGAACAATAAGCATTGGTTGGTGCACA 1619
Sbjct 1548 GCCTTGACTTTTTCAGATCTGTATTACCTGACCATGAACAATAAGCATTGGTTGGTGCACA 1607
Query 1620 AAGAGTGGTTTCATGACATCCCATGCTTGGCATGCTGGGGCAGACACTGGAATCCAC 1679
Sbjct 1608 AAGAGTGGTTTCATGACATCCCATGCTTGGCATGCTGGGGCAGACACCGGAATCCAC 1667
Query 1680 ACTGGAACAACAAAGAGGCATTGGTAGAATTCAGGATGCCACGCCAAGAGGCAAAACCG 1739
Sbjct 1668 ACTGGAACAACAAAGAGGCATTGGTAGAATTCAGGATGCCACGCCAAGAGGCAAAACCG 1727
Query 1740 TCGTCGTTCTGGGGAGCCAGGAAGGAGCCGTTACACGGCTCTCGCTGGAGCTCTAGAGG 1799
Sbjct 1728 TCGTCGTTCTGGGGAGCCAGGAAGGAGCCGTTACACGGCTCTCGCTGGAGCTCTAGAGG 1787
Query 1800 CTGAGATGGATGGTGCAAAGGGAAGCTGTTCTCTGGCCATTTGAAATGCCGCCTAAAAA 1859
Sbjct 1788 CTGAGATGGATGGTGCAAAGGGAAGCTGTTCTCTGGCCATTTGAAATGCCGCCTAAAAA 1847
Query 1860 TGGACAAGCTTAGATTGAAGGGCGTGTCTATTCCTTGTGCACTGCGGCATTACATTCA 1919
Sbjct 1848 TGGACAAGCTTAGATTGAAGGGCGTGTCTATTCCTTGTGCACTGCGGCATTACATTCA 1907
Query 1920 CCAAGGTCCAGCTGAAACACTGCATGGAACAGTCACAGTGGAGGTGCAGTATGCAGGGA 1979
Sbjct 1908 CCAAGGTCCAGCTGAAACACTGCATGGAACAGTCACAGTGGAGGTGCAGTATGCAGGGA 1967
Query 1980 CAGATGGACCTTGCAAGATCCAGTCCAGATGGCGGTGGACATGCAGACCCTGACCCAG 2039
Sbjct 1968 CAGATGGACCTTGCAAGATCCAGTCCAGATGGCGGTGGACATGCAGACCCTGACCCAG 2027
Query 2040 TTGGAAGGCTGATAACCGCCAACCCCGTGATTACTGAAAGCACTGAGAAGCTCAAGATGA 2099
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Sbjct	2028	TTGGAAGGCTGATAACCGCCAACCCCGTGATTACTGAAAGCACTGAGAACTCAAAGATGA	2087
Query	2100	TGTTGGAGCTTGACCCACCATTTGGGGATTCTTACATTGTCATAGGAGTTGGGGACAAGA	2159
Sbjct	2088	TGTTGGAGCTTGACCCACCATTTGGGGATTCTTACATTGTCATAGGAGTTGGGGACAAGA	2147
Query	2160	AAATCACCACCACTGGCATAGGAGTGGTAGCACCATCGGAAAGGCATTTGAGGCCACTG	2219
Sbjct	2148	AAATCACCACCACTGGCATAGGAGTGGTAGCACCATCGGAAAGGCATTTGAGGCCACTG	2207
Query	2220	TGAGAGGCGCCAAGAGAATGGCAGTCCTGGGGGATACAGCCTGGGACTTCGGATCAGTCG	2279
Sbjct	2208	TGAGAGGCGCCAAGAGAATGGCAGTCCTGGGGGATACAGCCTGGGACTTCGGATCAGTCG	2267
Query	2280	GGGGTGTGTTCAACTCACTGGGTAAGGGCATTACCAGATTTTGGAGCAGCCTTCAAAT	2339
Sbjct	2268	GGGGTGTGTTCAACTCACTGGGTAAGGGCATTACCAGATTTTGGAGCAGCCTTCAAAT	2327
Query	2340	CACTGTTTGGAGGAATGTCCTGGTTCTCACAGATCCTCATAGGCACGCTGCTAGTGTGGT	2399
Sbjct	2328	CACTGTTTGGAGGAATGTCCTGGTTCTCACAGATCCTCATAGGCACGCTGCTAGTGTGGT	2387
Query	2400	TAGGTTTGAACACAAAGAATGGATCTATCTCCCTCACATGCTTGGCCCTGGGGGGAGTGA	2459
Sbjct	2388	TAGGTTTGAACACAAAGAATGGATCTATCTCCCTCACATGCTTGGCCCTGGGGGGAGTGA	2447
Query	2460	TGATCTTCCTCTCCACGGCTGTTTCTGCTGACGTGGGGTGCTCAGTGGACTTCTCAAAAA	2519
Sbjct	2448	TGATCTTCCTCTCCACGGCTGTTTCTGCTGACGTGGGGTGCTCAGTGGACTTCTCAAAAA	2507
Query	2520	AGGAAACGAGATGTGGCACGGGGTATTCATCTATAATGATGTTGAAGCCTGGAGGGACC	2579
Sbjct	2508	AGGAAACGAGATGTGGCACGGGGTATTCATCTATAATGATGTTGAAGCCTGGAGGGACC	2567
Query	2580	GGTACAAGTACCATCCTGACTCCCCCGCAGATTGGCAGCAGCAGTCAAGCAGGCCTGGG	2639
Sbjct	2568	GGTACAAGTACCATCCTGACTCCCCCGCAGATTGGCAGCAGCAGTCAAGCAGGCCTGGG	2627
Query	2640	AAGAGGGGATCTGTGGGATCTCATCCGTTTCAAGAATGGAAAACATCATGTGGAAATCAG	2699
Sbjct	2628	AAGAGGGGATCTGTGGGATCTCATCCGTTTCAAGAATGGAAAACATCATGTGGAAATCAG	2687
Query	2700	TAGAAGGGGAGCTCAATGCTATCCTAGAGGAGAATGGAGTTCAACTGACAGTTGTTGTGG	2759
Sbjct	2688	TAGAAGGGGAGCTCAATGCTATCCTAGAGGAGAATGGAGTTCAACTGACAGTTGTTGTGG	2747
Query	2760	GATCTGTAAAAAACCCCATGTGGAGAGGTCCACAAAGATTGCCAGTGCCTGTGAATGAGC	2819
Sbjct	2748	GATCTGTAAAAAACCCCATGTGGAGAGGTCCACAAAGATTGCCAGTGCCTGTGAATGAGC	2807
Query	2820	TGCCCCATGGCTGGAAAGCCTGGGGGAAATCGTATTTTGTAGGGCGGCAAAGACCAACA	2879
Sbjct	2808	TGCCCCATGGCTGGAAAGCCTGGGGGAAATCGTATTTTGTAGGGCGGCAAAGACCAACA	2867
Query	2880	ACAGTTTTGTTGTCGACGGTGACACACTGAAGGAATGTCCGCTTGAGCACAGAGCATGGA	2939
Sbjct	2868	ACAGTTTTGTTGTCGACGGTGACACACTGAAGGAATGTCCGCTTGAGCACAGAGCATGGA	2927
Query	2940	ATAGTTTTCTTGTGGAGGATCACGGGTTTGGAGTCTTCCACACCAAGTGTCTGGCTTAAGG	2999
Sbjct	2928	ATAGTTTTCTTGTGGAGGATCACGGGTTTGGAGTCTTCCACACCAAGTGTCTGGCTTAAGG	2987
Query	3000	TCAGAGAAGATTACTATTAGAATGTGACCCAGCCGTATAGGAACAGCTGTTAAGGGAA	3059
Sbjct	2988	TCAGAGAAGATTACTATTAGAATGTGACCCAGCCGTATAGGAACAGCTGTTAAGGGAA	3047
Query	3060	GGGAGGCCGCGCACAGTGATCTGGGCTATTGGATTGAAAGTGAAAAGAATGACACATGGA	3119
Sbjct	3048	GGGAGGCCGCGCACAGTGATCTGGGCTATTGGATTGAAAGTGAAAAGAATGACACATGGA	3107
Query	3120	GGCTGAAGAGGGCCACCTGATTGAGATGAAAACATGTGAATGGCCAAAGTCTCACACAT	3179
Sbjct	3108	GGCTGAAGAGGGCCACCTGATTGAGATGAAAACATGTGAATGGCCAAAGTCTCACACAT	3167
Query	3180	TGTGGACAGATGGAGTAGAAGAAAGTGATCTTATCATACCCAAGTCTTTAGCTGGTCCAC	3239
Sbjct	3168	TGTGGACAGATGGAGTAGAAGAAAGTGATCTTATCATACCCAAGTCTTTAGCTGGTCCAC	3227
Query	3240	TCAGCCACCACAACACCAGAGAGGGTTACAGAACCCAAGTGAAAGGGCCATGGCACAGTG	3299
Sbjct	3228	TCAGCCACCACAACACCAGAGAGGGTTACAGAACCCAAGTGAAAGGGCCATGGCACAGTG	3287
Query	3300	AAGAGCTTGAAATCCGGTTTGAGGAATGTCCAGGCACCAAGGTTTACGTGGAGGAGACAT	3359
Sbjct	3288	AAGAGCTTGAAATCCGGTTTGAGGAATGTCCAGGCACCAAGGTTTACGTGGAGGAGACAT	3347
Query	3360	GCGGAACCTAGAGGACCATCTCTGAGATCAACTACTGCAAGTGGAAGGGTCATTGAGGAAT	3419
Sbjct	3348	GCGGAACCTAGAGGACCATCTCTGAGATCAACTACTGCAAGTGGAAGGGTCATTGAGGAAT	3407

Query	3420	GGTGCTGTAGGGAATGCACAATGCCCCACTATCGTTTCGAGCAAAAGACGGCTGCTGGT	3479
Sbjct	3408	GGTGCTGTAGGGAATGCACAATGCCCCACTATCGTTTCGAGCAAAAGACGGCTGCTGGT	3467
Query	3480	ATGGAATGGAGATAAGGCCAGGAAAGAACAGAGAGCAACTTAGTGAGGTCAATGGTGA	3539
Sbjct	3468	ATGGAATGGAGATAAGGCCAGGAAAGAACAGAGAGCAACTTAGTGAGGTCAATGGTGA	3527
Query	3540	CAGCGGGGTCAACCGATCATATGGACCACCTTCTCTCTGGAGTGCTTGTGATTCTACTCA	3599
Sbjct	3528	CAGCGGGGTCAACCGATCATATGGACCACCTTCTCTCTGGAGTGCTTGTGATTCTACTCA	3587
Query	3600	TGGTGCAGGAGGGGTTGAAGAAGAGAATGACCACAAAGATCATCATGAGCACATCAATGG	3659
Sbjct	3588	TGGTGCAGGAGGGGTTGAAGAAGAGAATGACCACAAAGATCATCATGAGCACATCAATGG	3647
Query	3660	CAGTGCTGGTAGTCATGATCTTGGGAGGATTTTCAATGAGTGACCTGGCCAAGCTTGTGA	3719
Sbjct	3648	CAGTGCTGGTAGTCATGATCTTGGGAGGATTTTCAATGAGTGACCTGGCCAAGCTTGTGA	3707
Query	3720	TCCTGATGGGTGCTACTTTTCGAGAAATGAACACTGGAGGAGATGTAGCTCACTTGGCAT	3779
Sbjct	3708	TCCTGATGGGTGCTACTTTTCGAGAAATGAACACTGGAGGAGATGTAGCTCACTTGGCAT	3767
Query	3780	TGGTAGCGGCATTTAAAGTCAGACCAGCCTTGCTGGTCTCCTTCATTTTCAGAGCCAATT	3839
Sbjct	3768	TGGTAGCGGCATTTAAAGTCAGACCAGCCTTGCTGGTCTCCTTCATTTTCAGAGCCAATT	3827
Query	3840	GGACACCCCGTGAGAGCATGCTGCTAGCCCTGGCTTCGTGTCTTCTGCAAACTGCGATCT	3899
Sbjct	3828	GGACACCCCGTGAGAGCATGCTGCTAGCCCTGGCTTCGTGTCTTCTGCAAACTGCGATCT	3887
Query	3900	CTGCTCTTGAAGGTGACTTGATGGTCCTCATTAAATGGATTTGCTTTGGCCTGGTTGGCAA	3959
Sbjct	3888	CTGCTCTTGAAGGTGACTTGATGGTCCTCATTAAATGGATTTGCTTTGGCCTGGTTGGCAA	3947
Query	3960	TTTGAGCAATGGCCGTGCCACGCACTGACAACATCGCTCTACCAATCTTGGCTGCTCTAA	4019
Sbjct	3948	TTTGAGCAATGGCCGTGCCACGCACTGACAACATCGCTCTACCAATCTTGGCTGCTCTAA	4007
Query	4020	CACCACTAGCTCGAGGCACACTGCTCGTGGCATGGAGAGCGGGCCTGGCTACTTGTGGAG	4079
Sbjct	4008	CACCACTAGCTCGAGGCACACTGCTCGTGGCATGGAGAGCGGGCCTGGCTACTTGTGGAG	4067
Query	4080	GGATCATGCTCCTCTCCCTGAAAGGGAAAGGTAGTGTGAAGAAGAACCTGCCATTTGTCA	4139
Sbjct	4068	GGATCATGCTCCTCTCCCTGAAAGGGAAAGGTAGTGTGAAGAAGAACCTGCCATTTGTCA	4127
Query	4140	TGGCCCTGGGATTGACAGCTGTGAGGGTAGTAGACCTATTAATGTGGTAGGACTACTGT	4199
Sbjct	4128	TGGCCCTGGGATTGACAGCTGTGAGGGTAGTAGACCTATTAATGTGGTAGGACTACTGT	4187
Query	4200	TACTCACAAGGAGTGGGAAGCGGAGCTGGCCCCCTAGTGAAGTTCTCACAGCCGTTGGCC	4259
Sbjct	4188	TACTCACAAGGAGTGGGAAGCGGAGCTGGCCCCCTAGTGAAGTTCTCACAGCCGTTGGCC	4247
Query	4260	TGATATGTGCACTGGCCGGAGGGTTTGCCAAGGCAGACATTGAGATGGCTGGACCCATGG	4319
Sbjct	4248	TGATATGTGCACTGGCCGGAGGGTTTGCCAAGGCAGACATTGAGATGGCTGGACCCATGG	4307
Query	4320	CTGCAGTAGGCTTGCTAATTGTCAGCTATGTGGTCTCGGGAAAGAGTGTGGACATGTACA	4379
Sbjct	4308	CTGCAGTAGGCTTGCTAATTGTCAGCTATGTGGTCTCGGGAAAGAGTGTGGACATGTACA	4367
Query	4380	TTGAAAGAGCAGGTGACATCACATGGGAAAAGGACGCGGAAGTCACTGGAAACAGTCCTC	4439
Sbjct	4368	TTGAAAGAGCAGGTGACATCACATGGGAAAAGGACGCGGAAGTCACTGGAAACAGTCCTC	4427
Query	4440	GGCTTGACGTGGCACTGGATGAGAGTGGTGATTTCTCCTTGGTAGAGGAAGATGGTCCAC	4499
Sbjct	4428	GGCTTGACGTGGCACTGGATGAGAGTGGTGATTTCTCCTTGGTAGAGGAAGATGGTCCAC	4487
Query	4500	CCATGAGAGAGATCATACTTAAGGTGGTCCTGATGGCCATCTGTGGCATGAACCCAATAG	4559
Sbjct	4488	CCATGAGAGAGATCATACTCAAGGTGGTCCTGATGGCCATCTGTGGCATGAACCCAATAG	4547
Query	4560	CTATACCTTTTGTGTCAGGAGCGTGGTATGTGTATGTGAAGACTGGGAAAAGGAGTGGCG	4619
Sbjct	4548	CTATACCTTTTGTGTCAGGAGCGTGGTATGTGTATGTGAAGACTGGGAAAAGGAGTGGCG	4607
Query	4620	CCCTCTGGGACGTGCCTGCTCCCAAAGAAGTGAAGAAAGGAGAGACCACAGATGGAGTGT	4679
Sbjct	4608	CCCTCTGGGACGTGCCTGCTCCCAAAGAAGTGAAGAAAGGAGAGACCACAGATGGAGTGT	4667
Query	4680	ACAGAGTGATGACTCGCAGACTGCTAGGTTCAACACAGGTTGGAGTGGGAGTCATGCAAG	4739
Sbjct	4668	ACAGAGTGATGACTCGCAGACTGCTAGGTTCAACACAGGTTGGAGTGGGAGTCATGCAAG	4727
Query	4740	AGGGAGTCTTCCACACCATGTGGCACGTTACAAAAGGAGCCGCACTGAGGAGCGGTGAGG	4799
Sbjct	4728	AGGGAGTCTTCCACACCATGTGGCACGTTACAAAAGGAGCCGCACTGAGGAGCGGTGAGG	4787

Query	4800	GAAGACTTGATCCATACTGGGGGGATGTCAAGCAGGACTTGGTGTCTACTGTGGGCCTT	4859
Sbjct	4788	GAAGACTTGATCCATACTGGGGGGATGTCAAGCAGGACTTGGTGTCTACTGTGGGCCTT	4847
Query	4860	GGAAGTTGGATGCAGCTTGGGATGGACTCAGCGAGGTACAGCTTTTGGCCGTACCTCCCG	4919
Sbjct	4848	GGAAGTTGGATGCAGCTTGGGATGGACTCAGCGAGGTACAGCTTTTGGCCGTACCTCCCG	4907
Query	4920	GAGAGAGGGCCAGAAACATTAGACCTGCCTGGAATATTCAAGACAAAGGACGGGGACA	4979
Sbjct	4908	GAGAGAGGGCCAGAAACATTAGACCTGCCTGGAATATTCAAGACAAAGGACGGGGACA	4967
Query	4980	TCGGAGCAGTTGCTCTGGACTACCCTGCAGGGACCTCAGGATCTCCGATCCTAGACAAAT	5039
Sbjct	4968	TCGGAGCAGTTGCTCTGGACTACCCTGCAGGGACCTCAGGATCTCCGATCCTAGACAAAT	5027
Query	5040	GTGGAAGAGTGATAGGACTCTATGGCAATGGGGTTGTGATCAAGAATGGAAGCTATGTTA	5099
Sbjct	5028	GTGGAAGAGTGATAGGACTCTATGGCAATGGGGTTGTGATCAAGAATGGAAGCTATGTTA	5087
Query	5100	GTGCTATAACCCAGGGAAAGAGGGAGGAGGAGACTCCGGTTGAATGTTTCGAACCTCGA	5159
Sbjct	5088	GTGCTATAACCCAGGGAAAGAGGGAGGAGGAGACTCCGGTTGAATGTTTCGAACCTCGA	5147
Query	5160	TGCTGAAGAAGAAGCAGCTAACTGTCTTGGATCTGCATCCAGGAGCCGAAAAACAGGA	5219
Sbjct	5148	TGCTGAAGAAGAAGCAGCTAACTGTCTTGGATCTGCATCCAGGAGCCGAAAAACAGGA	5207
Query	5220	GAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAAGAGACTCCGGACAGTGATCTTGG	5279
Sbjct	5208	GAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAAGAGACTCCGGACAGTGATCTTGG	5267
Query	5280	CACCAACTAGGGTTGTGCTGCTGAGATGGAGGAGGCCTTGAGAGGACTTCCGGTGCGTT	5339
Sbjct	5268	CACCAACTAGGGTTGTGCTGCTGAGATGGAGGAGGCCTTGAGAGGACTTCCGGTGCGTT	5327
Query	5340	ACATGACAACAGCAGTCAACGTCACCCATTCTGGGACAGAAATCGTTGATTTGATGTGCC	5399
Sbjct	5328	ACATGACAACAGCAGTCAACGTCACCCATTCTGGGACAGAAATCGTTGATTTGATGTGCC	5387
Query	5400	ATGCCACTTTCACCTTACGCTTACTACAACCCATCAGAGTCCCTAATTACAATCTCTACA	5459
Sbjct	5388	ATGCCACTTTCACCTTACGCTTACTACAACCCATCAGAGTCCCTAATTACAATCTCAACA	5447
Query	5460	TCATGGATGAAGCCCACTTACAGACCCCTCAAGTATAGCTGCAAGAGGATATATATCAA	5519
Sbjct	5448	TCATGGATGAAGCCCACTTACAGACCCCTCAAGTATAGCTGCAAGAGGATACATATCAA	5507
Query	5520	CAAGGGTTGAAATGGGCGAGGCGGCTGCCATTTTTATGACTGCCACACCACAGGAACCC	5579
Sbjct	5508	CAAGGGTTGAAATGGGCGAGGCGGCTGCCATTTTTATGACTGCCACACCACAGGAACCC	5567
Query	5580	GTGATGCGTTTCTGACTCTAACTACCAATCATGGACACAGAAGTGAAGTCCCAGAGA	5639
Sbjct	5568	GTGATGCGTTTCTGACTCTAACTACCAATCATGGACACAGAAGTGAAGTCCCAGAGA	5627
Query	5640	GAGCCTGGAGCTCAGGCTTTGATTGGGTGACAGACCATTCTGGGAAAACAGTTTGGTTCTG	5699
Sbjct	5628	GAGCCTGGAGCTCAGGCTTTGATTGGGTGACAGACCATTCTGGGAAAACAGTTTGGTTCTG	5687
Query	5700	TTCCAAGCGTGAGAAACGGAATGAAATCGCAGCCTGTCTGACAAAGGCTGGAAGCGGG	5759
Sbjct	5688	TTCCAAGCGTGAGAAACGGAATGAAATCGCAGCCTGTCTGACAAAGGCTGGAAGCGGG	5747
Query	5760	TCATACAGCTCAGCAGGAAGACTTTTGGAGACAGAATTCAGAAAAACAAAAATCAAGAGT	5819
Sbjct	5748	TCATACAGCTCAGCAGGAAGACTTTTGGAGACAGAATTCAGAAAAACAAAAATCAAGAGT	5807
Query	5820	GGGACTTTGTCTAACAACCTGACATCTCAGAGATGGGCGCCAATTCAAGGCTGACCGGG	5879
Sbjct	5808	GGGACTTTGTCTAACAACCTGACATCTCAGAGATGGGCGCCAATTCAAGGCTGACCGGG	5867
Query	5880	TCATAGACTCTAGGAGATGCCTAAAACAGTCATACTTGATGGTGAGAGAGTCATCTTGG	5939
Sbjct	5868	TCATAGACTCTAGGAGATGCCTAAAACAGTCATACTTGATGGTGAGAGAGTCATCTTGG	5927
Query	5940	CTGGGCCCATGCCTGTACGCGATGCTAGTGCTGCTCAGAGGAGAGGACGTATAGGCAGGA	5999
Sbjct	5928	CTGGGCCCATGCCTGTACGCGATGCTAGTGCTGCTCAGAGGAGAGGACGTATAGGCAGGA	5987
Query	6000	ACCCTAACAAACCTGGAGATGAGTACATGTATGGAGGTGGGTGTGCAGAGACTGATGAAG	6059
Sbjct	5988	ACCCTAACAAACCTGGAGATGAGTACATGTATGGAGGTGGGTGTGCAGAGACTGATGAAG	6047
Query	6060	GCCATGCACACTGGCTTGAAGCAAGAATGCTTCTTGACAACATCTACCTCCAGGATGGCC	6119
Sbjct	6048	GCCATGCACACTGGCTTGAAGCAAGAATGCTTCTTGACAACATCTACCTCCAGGATGGCC	6107
Query	6120	TCATAGCCTCGCTCTATCGGCCTGAGGCCGATAAGGTAGCCGCCATTGAGGGAGAGTTTA	6179

Sbjct	6108	TCATAGCCCTCGCTCTATCGGCCCTGAGGCCGATAAGGTAGCCGCCATTGAGGGAGAGTTTA	6167
Query	6180	AGCTGAGGACAGAGCAAAGGAAGACCTTCGTGGAACATCATGAAGAGAGGAGACCTTCCCG	6239
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Query	6240	TCTGGCTAGCCTATCAGGTTGCATCTGCCGGAATAACTTACACAGACAGAAGATGGTGCT	6299
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Query	6300	TTGATGGCACAACCAACAACACCATAATGGAAGACAGCGTACCAGCAGAGGTGTGGACAA	6359
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Query	6360	AGTATGGAGAGAAGAGAGTCTCAAACCGAGATGGATGGATGCTAGGGTCTGTTCAGACC	6419
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Query	6420	ATGCGGCCCTGAAGTCGTTCAAAGAATTGCGCGCTGGAAAAAGAGGAGCGGCTTTGGGAG	6479
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Query	6540	ACAACCTCGCCGTGCTCATGCGAGCAGAGACTGGAAGCAGGCCTTATAAGGCAGCGGCAG	6599
Sbjct	6528	ACAACCTCGCCGTGCTCATGCGAGCAGAGACTGGAAGCAGGCCTTATAAGGCAGCGGCAG	6587
Query	6600	CCCAACTGCCGGAGACCCTAGAGACCATTATGCTCTTAGGTTTGCTGGGAACAGTTTCAC	6659
Sbjct	6588	CCCAACTGCCGGAGACCCTAGAGACCATTATGCTCTTAGGTTTGCTGGGAACAGTTTCAC	6647
Query	6660	TGGGGATCTTCTTCGTCTTGATGCGGAATAAGGGCATCGGGAAGATGGGCTTTGGAATGG	6719
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Query	6720	TAACCCCTTGGGGCCAGTGCATGGCTCATGTGGCTTTCGGAATTGAACCAGCCAGAATTG	6779
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Query	9599	GTGACCAGATGGTTGCAGAGCAATGGATGGGATAGACTCAAACGAATGGCGGTCAGTGGA	9658
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Query	10019	GTGCCAGTTGACTGGGTACCAACTGGGAGAACCACCTGGTCAATCCATGGAAAGGGAGAA	10078
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Taxonomy

Reports

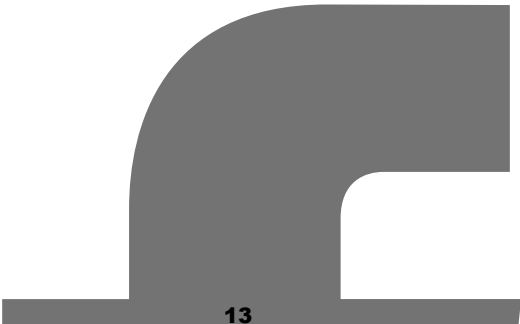
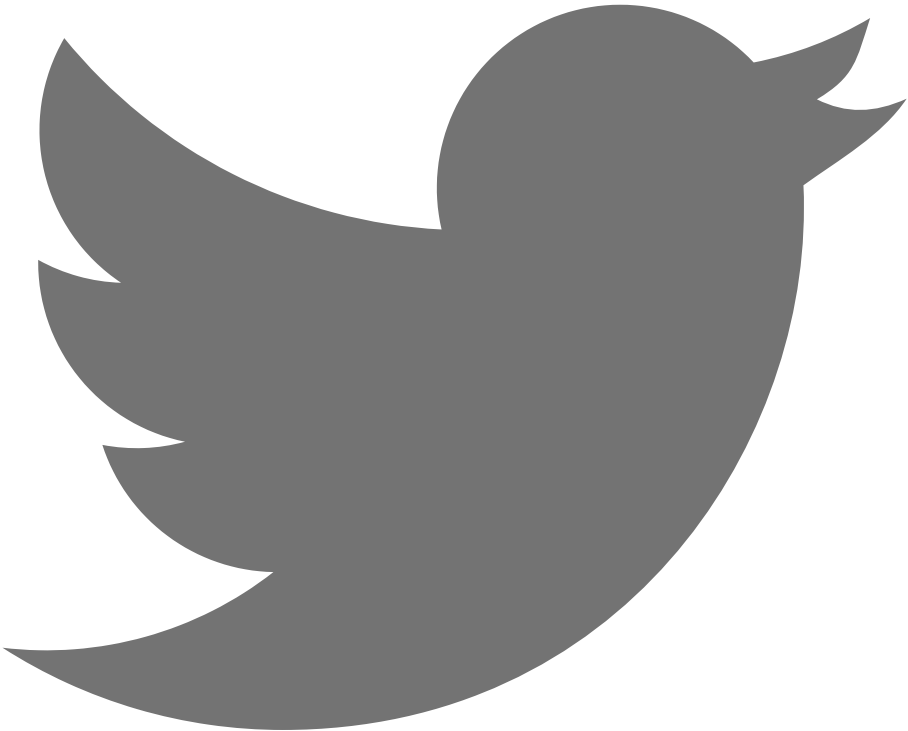
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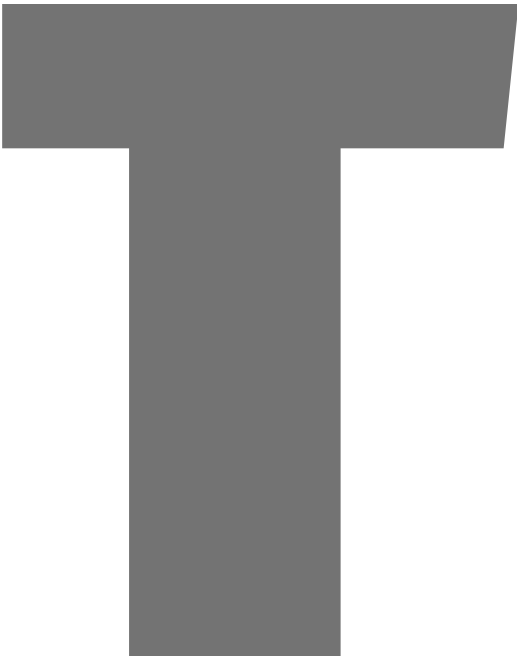
Dot Plot

Plot of lcl|Query_63257 vs lcl|Query_63259

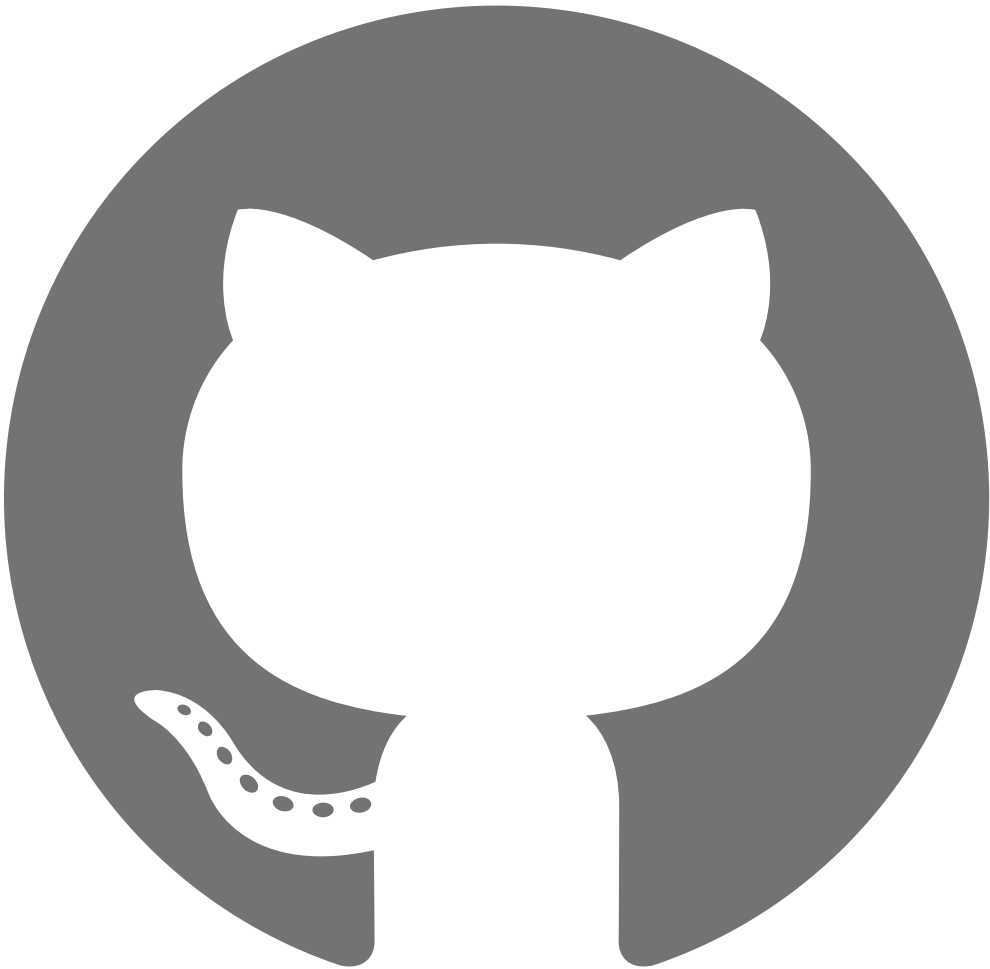
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