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BLAST[®] >> **Global Alignment** >> results for RID-PKDHCCCHB114

Job Title	SEQ_ID_NO9 ...
RID	PKDHCCCHB114 Search expires on 11-09 08:51 am
Program	Needleman-Wunsch alignment of two sequences
Query ID	lcl Query_46391 (dna)
Query Descr	SEQ_ID_NO9 ...
Query Length	10648

Subject ID

lcl|Query_46393 (dna)

Subject Descr

[SEQ_ID_NO72 ...](#)

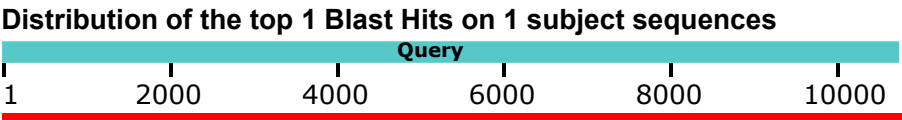
Subject Length

10773

Descriptions

Description	Score	Percent Ident	Accession
SEQ_ID_NO72	20901	99.00%	Query_46393

Graphic Summary



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

SEQ_ID_NO72
Sequence ID: Query_46393 Length: 10773 Number of Matches: 1
Range 1: 1 to 10773

NW Score	Identities	Gaps	Strand	Frame
20901	10622/10773(99%)	1/10773(0%)	Plus/Plus	
Query 1	GACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTT			52
Sbjct 1	CAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTT			60
Query 53	-GGATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAAGAAATCCGGAGGATTC			111
Sbjct 61	TGGATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAAGAAATCCGGAGGATTC			120
Query 112	CGGATTGTCAATATGCTAAACGCGGAGTAGCCCGTGTGAGCCCTTTGGGGGCTTGAAG			171
Sbjct 121	CGGATTGTCAATATGCTAAACGCGGAGTAGCCCGTGTGAGCCCTTTGGGGGCTTGAAG			180
Query 172	AGGCTGCCAGCCGGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTTGGCGATTCTA			231
Sbjct 181	AGGCTGCCAGCCGGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTTGGCGATTCTA			240
Query 232	GCCTTTTGGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCA			291
Sbjct 241	GCCTTTTGGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCA			300
Query 292	GTGGGGAAAAAAGAGGCTATGGAAATAATAAGAAGTTCAAGAAAGATCTGGCTGCCATG			351
Sbjct 301	GTGGGGAAAAAAGAGGCTATGGAAATAATAAGAAGTTCAAGAAAGATCTGGCTGCCATG			360
Query 352	CTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGACGAGGCGCAGATACTAGTGTGCGGA			411
Sbjct 361	CTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGACGAGGCGCAGATACTAGTGTGCGGA			420
Query 412	ATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGTGCA			471
Sbjct 421	ATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGTGCA			480
Query 472	TACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTTCCAACCACATTG			531
Sbjct 481	TACTATATGTACTTGGACAGAAACGACGCTGGGGAGGCCATATCTTTTCCAACCACATTG			540
Query 532	GGGATGAATAAGTGTTATATACAGATCATGGATCTTGGACACATGTGTGATGCCACCATG			591
Sbjct 541	GGGATGAATAAGTGTTATATACAGATCATGGATCTTGGACACATGTGTGATGCCACCATG			600
Query 592	AGCTATGAATGCCCTATGCTGGATGAGGGGGTGGAACCAGATGACGTCGATTGTTGGTGC			651
Sbjct 601	AGCTATGAATGCCCTATGCTGGATGAGGGGGTGGAACCAGATGACGTCGATTGTTGGTGC			660
Query 652	AACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAAGGTGAAGCACGG			711

Sbjct	661	AACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGG	720
Query	712	AGATCTAGAAGAGCTGTGACGCTCCCTCCCATTCCTAGGAAGCTGCAAACGCGGTCTG	771
Sbjct	721	AGATCTAGAAGAGCTGTGACGCTCCCTCCCATTCCTAGGAAGCTGCAAACGCGGTCTG	780
Query	772	CAAACTGGTTGGAATCAAGAGAATACACAAAGCACTTGATTAGAGTCGAAAATTGGATA	831
Sbjct	781	CAAACTGGTTGGAATCAAGAGAATACACAAAGCACTTGATTAGAGTCGAAAATTGGATA	840
Query	832	TTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTGGGAAGCTCA	891
Sbjct	841	TTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTGGGAAGCTCA	900
Query	892	ACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATC	951
Sbjct	901	ACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATC	960
Query	952	AGGTGCATAGGAGTCAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACCTGGGTT	1011
Sbjct	961	AGGTGCATAGGAGTCAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTT	1020
Query	1012	GATGTTGTCTTGGAACATGGAGGTTGTGTACCGTAATGGCACAGGACAAACCGACTGTC	1071
Sbjct	1021	GATGTTGTCTTGGAACATGGAGGTTGTGTACCGTAATGGCACAGGACAAACCGACTGTC	1080
Query	1072	GACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCTAT	1131
Sbjct	1081	GACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCTAT	1140
Query	1132	GAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTAC	1191
Sbjct	1141	GAGGCATCAATATCGGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTAC	1200
Query	1192	CTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGG	1251
Sbjct	1201	CTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGG	1260
Query	1252	GGAAATGGATGTGGACTTTTTGGCAAAGGGAGCCTGGTGACATGCGCTAAGTTTGCATGC	1311
Sbjct	1261	GGAAATGGATGTGGACTTTTTGGCAAAGGGAGCCTGGTGACATGCGCTAAGTTTGCATGC	1320
Query	1312	TCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTG	1371
Sbjct	1321	TCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTG	1380
Query	1372	TCAGTTCATGGCTCCCAGCACAGTGGGATGATTGTTAATGACACAGGACATGAACTGAT	1431
Sbjct	1381	TCAGTTCATGGCTCCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAACTGAT	1440
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Sbjct	1501	GGTTTTGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTTTTCAGATTTG	1560
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Sbjct	1681	CTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAAACTGTCGTGGTTCTAGGGAGTCAA	1740
Query	1732	GAAGGAGCAGTTACACACGGCCCTTGTGAGCTCTGGAGGCTGAGATGGATGGTGCAAAG	1791
Sbjct	1741	GAAGGAGCAGTTACACACGGCCCTTGTGAGCTCTGGAGGCTGAGATGGATGGTGCAAAG	1800
Query	1792	GGAAAGGCTGTCCTCTGGCCACTTGAAATGTCGCCTGAAAATGGATAAACTTAGATTGAAG	1851
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Query	1972	CCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCT	2031
Sbjct	1981	CCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCT	2040
Query	2032	AAACCCGTAATCACTGAAAGCACTGAGAAGCTCTAAGATGATGCTGGAAGTTGATCCACCA	2091

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Query   2152  AGGAGTGGCAGCACCATTGAAAAAGCATTGTAAGCCACTGTGAGAGGTGCCAAGAGAATG 2211
Sbjct  2161  AGGAGTGGCAGCACCATTGAAAAAGCATTGTAAGCCACTGTGAGAGGTGCCAAGAGAATG 2220
Query   2212  GCAGTCTTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTG 2271
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Query   2392  GGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTTGATCTTCTTATCCACAGCC 2451
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Query   2452  GTCTCTGCTGATGTGGGGTCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACA 2511
Sbjct  2461  GTCTCTGCTGATGTGGGGTCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACA 2520
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Query   2632  TCCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCA 2691
Sbjct  2641  TCCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCA 2700
Query   2692  ATCTTGGAAGAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTAAAAAACCCTATG 2751
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Query   2752  TGGAGAGGTCCACAGAGATTGCCCGTGCCTGTGAACGAGCTGCCCCACGGCTGGAAGGCT 2811
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Sbjct  2941  CATGGGTTTCGGGGTATTTCACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTCATTA 3000
Query   2992  GAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGAAAGGAGGCTGTACACAGTGAT 3051
Sbjct  3001  GAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGAAAGGAGGCTGTACACAGTGAT 3060
Query   3052  CTAGGCTACTGGATTGAGAGTGAGAAAGATGACACATGGAGGCTGAAGAGGGCCCATCTG 3111
Sbjct  3061  CTAGGCTACTGGATTGAGAGTGAGAAAGATGACACATGGAGGCTGAAGAGGGCCCATCTG 3120
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Query	3532	ATGGACCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAG	3591
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Query	3592	AAGAGAATGACCACAAAGATCATCATAAGCACATCAATGGCAGTGCTGGTAGCTATGATC	3651
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Sbjct	3661	CTGGGAGGATTTTCAATGAGTGACCTGGCTAAGCTTGCAATTTTGATGGGTGCCACCTTC	3720
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Query	3772	AGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAAGCATG	3831
Sbjct	3781	AGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAAGCATG	3840
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Sbjct	3841	CTGCTGGCCTTGGCCTCGTGTCTTTTGCAAACCTGCGATCTCCGCCCTTGAAGGCGACCTG	3900
Query	3892	ATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGCGATGGTTGTTCCA	3951
Sbjct	3901	ATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGCGATGGTTGTTCCA	3960
Query	3952	CGCACTGATAACATCACCTTGGAATCCTGGCTGCTCTGACACCACTGGCCCGGGGCACA	4011
Sbjct	3961	CGCACTGATAACATCACCTTGGAATCCTGGCTGCTCTGACACCACTGGCCCGGGGCACA	4020
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Sbjct	4021	CTGCTTGTGGCGTGGAGAGCAGGCCCTTGCTACTTGCGGGGGGTTTATGCTCCTCTCTCTG	4080
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Sbjct	4141	GTGAGGCTGGTTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAGTGGGAAG	4200
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Sbjct	4321	GTCAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTACATTGAAAGAGCAGGTGACATC	4380
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Sbjct	4381	ACATGGGAAAAAGATGCGGAAGTCACTGGAACAGTCCCCGGCTCGATGTGGCGCTAGAT	4440
Query	4432	GAGAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTC	4491
Sbjct	4441	GAGAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTC	4500
Query	4492	AAGGTGGTCTGATGACCATCTGTGGCATGAACCCAATAGCCATACCCTTTGCAGCTGGA	4551
Sbjct	4501	AAGGTGGTCTGATGACCATCTGTGGCATGAACCCAATAGCCATACCCTTTGCAGCTGGA	4560
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Sbjct	4621	CCCAAGGAAGTAAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGA	4680
Query	4672	CTGCTAGGTTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATG	4731
Sbjct	4681	CTGCTAGGTTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATG	4740
Query	4732	TGGCACGTCAAAAAGGATCCGCGCTGAGAAGCGGTGAAGGGAGACTTGATCCATACTGG	4791
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Sbjct 4801 GGAGATGTCAAGCAGGATCTGGTGTCACTGTGGTCCATGGAAGCTAGATGCCGCCTGG 4860

Query 4852 GACGGGCACAGCGAGGTGCAGCTCTTGCCCGTGCCCCCGGAGAGAGCGAGGAACATC 4911
Sbjct 4861 GACGGGCACAGCGAGGTGCAGCTCTTGCCCGTGCCCCCGGAGAGAGCGAGGAACATC 4920

Query 4912 CAGACTCTGCCCGGAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGAT 4971
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Sbjct 5581 AACTCACCAATTATGGACACCGAAGTGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTT 5640

Query 5632 GATTGGGTGACGGATCATTCTGGAAAAACAGTTTGGTTTGTCCAAGCGTGAGGAACGGC 5691
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Sbjct 5701 AATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTACATACAGCTCAGCAGAAAG 5760

Query 5752 ACTTTTGAGACAGAGTTCCAGAAAACAAAACATCAAGAGTGGGACTTTGTCGTGACAACT 5811
Sbjct 5761 ACTTTTGAGACAGAGTTCCAGAAAACAAAACATCAAGAGTGGGACTTTGTCGTGACAACT 5820

Query 5812 GACATTTTACAGATGGGCGCCAACTTTAAAGCTGACCGTGTCATAGATTCCAGGAGATGC 5871
Sbjct 5821 GACATTTTACAGATGGGCGCCAACTTTAAAGCTGACCGTGTCATAGATTCCAGGAGATGC 5880

Query 5872 CTAAGCCGGTCATACTTGATGGCGAGAGAGTCATTCTGGCTGGACCCATGCCTGTCACA 5931
Sbjct 5881 CTAAGCCGGTCATACTTGATGGCGAGAGAGTCATTCTGGCTGGACCCATGCCTGTCACA 5940

Query 5932 CATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGAT 5991
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Query 6052 GCAAGAATGCTCCTTGACAATATTTACCTCCAAGATGGCCTCATAGCCTCGCTCTATCGA 6111
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Query 6112 CCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGAGCAAAGG 6171
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Taxonomy

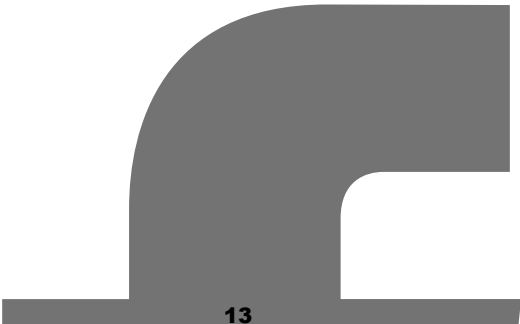
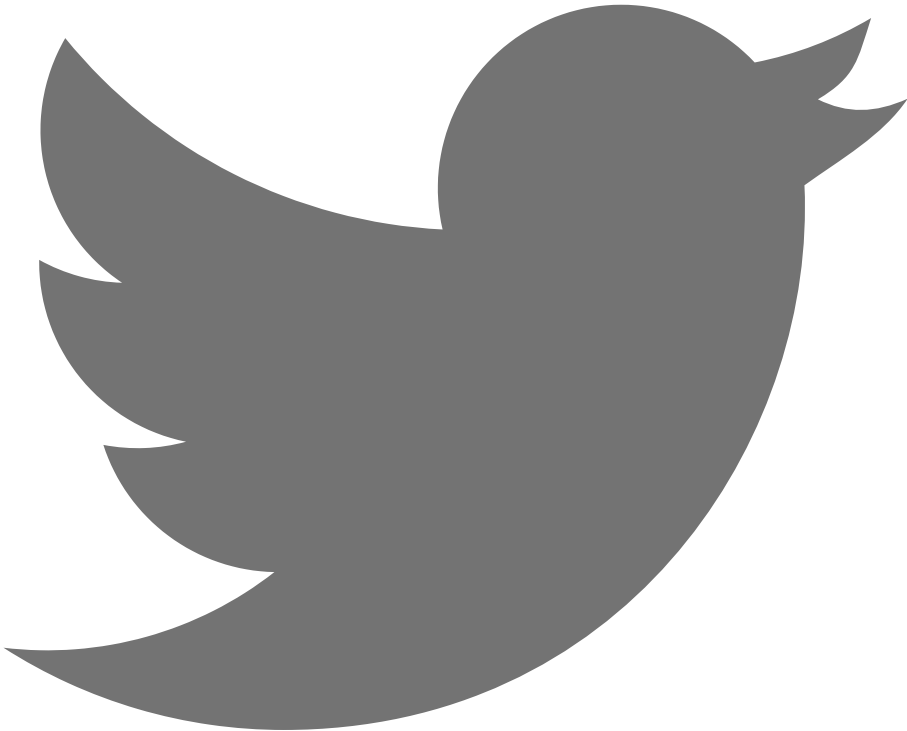
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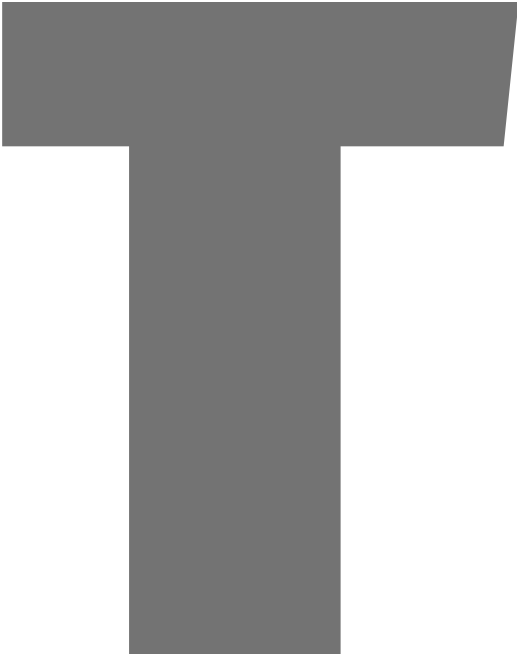
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- Taxonomy

Dot Plot

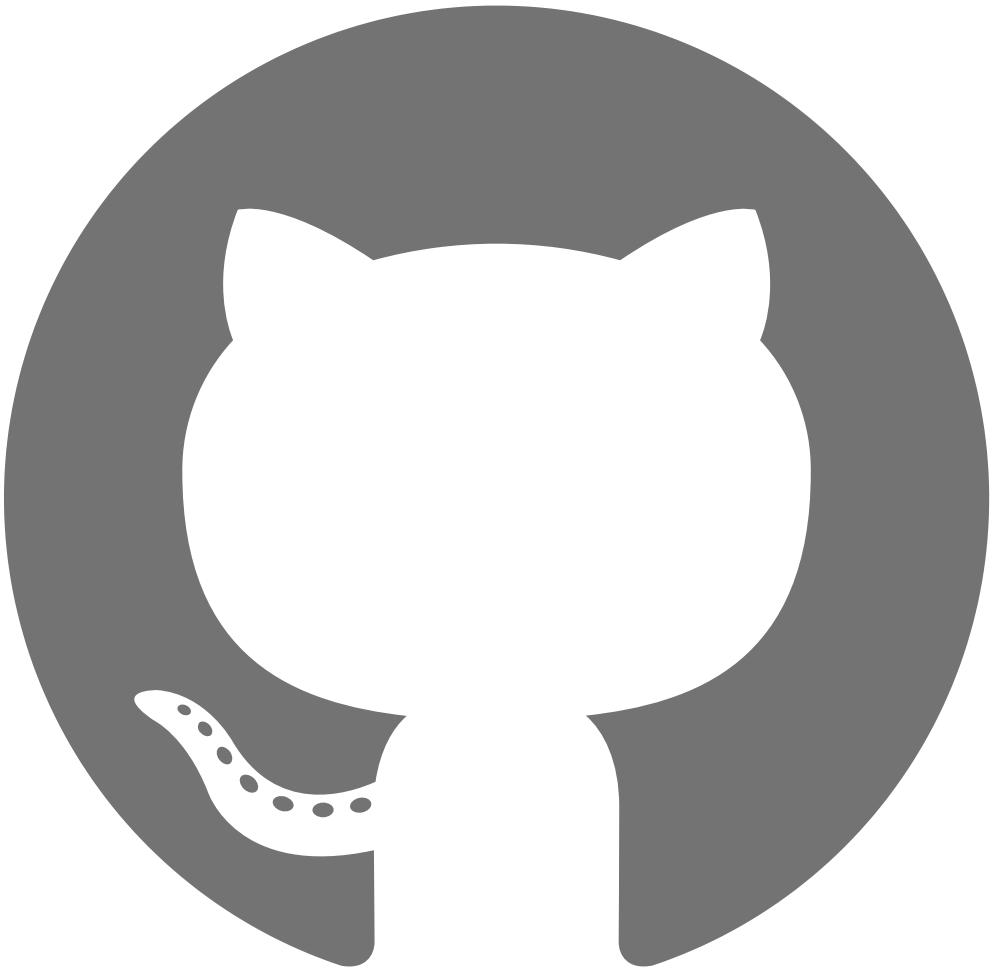
Plot of lcl|Query_46391 vs lcl|Query_46393

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