Q1.

I, Megan Chu, have read the Academic Integrity Policy, Grading Policy, and Syllabus for BENG/BIMM/CSE 182 and agree to them.

Q2. Program Output:

Hello Bioinformatics

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Q3. Program Output:
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>qi|6978799|ref|NP 036683.1| early growth response 1; nerve growth
factor-induced gene [Rattus norvegicus]
>qi|45768856|qb|AAH67618.1| Serum/qlucocorticoid regulated kinase
[Danio rerio]
>qi|45768786|qb|AAH68134.1| Unknown (protein for MGC:95907) [Mus
musculusl
423
>qi|27923854|sp|P59241|STK6 RAT Serine/threonine kinase 6 (Aurora-A)
(ratAurA)
397
>qi|45768720|qb|AAH67812.1| Cyclin L1 [Homo sapiens]
>gi|45768758|gb|AAH68160.1| Cdk7 protein [Mus musculus]
346
>qi|45219906|qb|AAH66834.1| Mastl protein [Mus musculus]
>qi|18202599|sp|Q63796|M3KC RAT Mitogen-activated protein kinase
kinase kinase 12 (MAPK-upstream kinase) (MUK)
>qi|4835224|emb|CAB42902.1| protein kinase ATN1 like protein
[Arabidopsis thaliana]
370
>qi|40787731|qb|AAH64804.1| SLK protein [Homo sapiens]
617
>gi|18202068|sp|055173|PDPK RAT 3-phosphoinositide dependent protein
kinase-1 (Protein kinase B kinase) (PkB kinase)
>qi|34191428|qb|AAH36504.2| C9orf96 protein [Homo sapiens]
700
>qi|29747774|qb|AAH50806.1| Gene model 711, (NCBI) [Mus musculus]
>qi|28856169|qb|AAH48033.1| Serine/threonine kinase 3 (STE20 homolog,
yeast) [Danio rerio]
>qi|20071571|qb|AAH26466.1| Unknown (protein for IMAGE:4485517) [Mus
musculus]
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202 >gi|45709347|gb|AAH67695.1| Unknown (protein for MGC:85918) [Danio rerio] 320

Q4. Program Output:

Creating filteredDatabase.txt with mouse and rat sequences... Contents of filteredDatabase:

 $>gi|6978799|ref|NP_036683.1|$ early growth response 1; nerve growth factor-induced gene [Rattus norvegicus]

MDNYPKLEEMMLLSNGAPQFLGAAGTPEGSGGNNSSSSSSSGGGGGGGGSNSGSSAFNP QGEPSEQPYEHLTTESFSDIALNNEKALVETSYPSQTTRLPPITYTGRFSLEPAPNSGNT LWPEPLFSLVSGLVSMTNPPTSSSSAPSPAASSSSSASQSPPLSCAVPSNDSSPIYSAAP TFPTPNTDIFPEPQSQAFPGSAGTALQYPPPAYPATKGGFQVPMIPDYLFPQQQGDLSLG TPDQKPFQGLENRTQQPSLTPLSTIKAFATQSGSQDLKALNNTYQSQLIKPSRMRKYPNR PSKTPPHERPYACPVESCDRRFSRSDELTRHIRIHTGQKPFQCRICMRNFSRSDHLTTHI RTHTGEKPFACDICGRKFARSDERKRHTKIHLRQKDKKADKSVVASSAASSLSSYPSPVA TSYPSPATTSFPSPVPTSYSSPGSSTYPSPAHSGFPSPSVATTYASVPPAFPAQVSTFQS AGVSNSFSTSTGLSDMTATFSPRTIEIC

>gi|45768786|gb|AAH68134.1| Unknown (protein for MGC:95907) [Mus musculus]

MSTRNCQGTDSVIKHLDTIPEDKKVRVQRTQSTFDPFEKPANQVKRVHSENNACINFKSS SAGKESPKVRRHSSPSSPTSPKFGKADSYEKLEKLGEGSYATVYKGKSKVNGKLVALKVI RLQEEEGTPFTAIREASLLKGLKHANIVLLHDIIHTKETLTLVFEYVHTDLCQYMDKHPG GLHPDNVKLFLFQLLRGLSYIHQRYILHRDLKPQNLLISDTGELKLADFGLARAKSVPSH TYSNEVVTLWYRPPDVLLGSTEYSTCLDMWGVGCIFVEMIQGVAAFPGMKDIQDQLERIF LVLGTPNEDTWPGVHSLPHFKPERFTVYSSKSLRQAWNKLSYVNHAEDLASKLLQCSPKN RLSAQAALSHEYFSDLPPRLWELTDMSSIFTVPNVRLQPEAGESMRAFGKNNSYGKSLSN SKH

>gi|27923854|sp|P59241|STK6_RAT Serine/threonine kinase 6 (Aurora-A)
(ratAurA)

MDRCKENCVSRPVKSTVPFGPKRVLVTEQIPSQHPGSASSGQAQRVLCPSNSQRVPPQAQ KPVAGQKPVLKQLPAASGPRPASRLSNPQKSEQPQPAASGNNSEKEQTSIQKTEDSKKRQ WTLEDFDIGRPLGKGKFGNVYLAREKQSKFILALKVLFKVQLEKAGVEHQLRREVEIQSH LRHPNILRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITELANALSYC HSKRVIHRDIKPENLLLGSNGELKIADFGWSVHAPSSRRTTLCGTLDYQPPEMIEGRMHD EKVDLWSLGVLCYEFLVGMPPFEAHTYQETYRRISRVEFTFPDFVTEGARDLISRLLKHN SSORLTLAEVLEHPWIKANSSKPPTGHNSKEATSKSS

>gi|45768758|gb|AAH68160.1| Cdk7 protein [Mus musculus]
MAVDVKSRAKRYEKLDFLGEGQFATVYKARDKNTNQIVAIKKIKLGHRSEAKDGINRTAL
REIKLLQELSHPNIIGLLDAFGHKSNISLVFDFMETDLEVIIKDNSLVLTPSHIKAYMLM
TLQGLEYLHQHWILHRDLKPNNLLLDENGVLKLADFGLAKSFGSPNRAYTHQVVTRWYRA
PELLFGARMYGVGVDMWAVGCILAELLLRVPFLPGDSDLDQLTRIFETLGTPTEEQWPDM
CSLPDYVTFKSFPGVPLQHIFIAAGDDLLELIQGLFLFNPCTRTTASQALKTKYFSNRPG
PTPGCQLPRPNCPVEALKEPANPTVATKRKRAEALEQGILPKKLIF

>gi|45219906|gb|AAH66834.1| Mastl protein [Mus musculus] SMSKPKQDYSRTPGQVLSLISSLGFFTPVGEKDQDSANMFSAPKSAAQLSRGFICPMSVD QKEPTSYSSKLLKSCFETLSSNPEIPVKCLTSNLLQCRKRLGTSSTSSQSHTFVSSVESE CHSNPKWERDCQSTESSGCAMSWNAVEMLYAKSTSAIKTKTELELALSPIHDSSAIPAAG SNQVTLPRKCFREISWEARDPDNENMTIDKGQSGFCQSSQRSVNSSATSEEHLGKRNYKR NFHLVDSSPCQEIMQSKKNCTEYEANKERQGCRANQSTGLTTEVQNLKLSGCESQQLDYA

NKENIVTYLTDRQTPEKLHIPTIAKNLMSELDEDRELSSKKDCLSSNSVCSDEDRALKTT CVDSDSSFPGVSMMESSLEIQALEPDKSIRDYSFEEPNTEDLFVLPKCQENSLPQDDCHA CIQDSSQVSAHPSKAPKALTSKINVVAFRSFNSHINASTNSEPSKISITSLDAMDISYDY SGSYPMAVSPTEKGRHYTSHQTPNQVKLGTSYRTPKSVRRGAAPVDDGRILGTPDYLAPE LLLGTAHGPAVDWWALGVCLFEFLTGIPPFNDETPQQVFQNILKRDIPWPEGEEKLSDNA QSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFVPQPDDETDTSYFEARNN AQHLTISGFSL

>qi|18202599|sp|Q63796|M3KC RAT Mitogen-activated protein kinase kinase kinase 12 (MAPK-upstream kinase) (MUK) MACLHETRTPSPSFGGFVSTLSEASMRKLDPDTSDCTPEKDLTPTQCVLRDVVPLGGQGG GGPSPSPGGEPPPEPFANSVLQLHEQDTGGPGGATGSPESRASRVRADEVRLQCQSGSGF LEGLFGCLRPVWTMIGKAYSTEHKQQQEDLWEVPFEEILDLQWVGSGAQGAVFLGRFHGE EVAVKKVRDLKETDIKHLRKLKHPNIITFKGVCTQAPCYCILMEFCAQGQLYEVLRAGRP VTPSLLVDWSMGIAGGMNYLHLHKIIHRDLKSPNMLITYDDVVKISDFGTSKELSDKSTK MSFAGTVAWMAPEVIRNEPVSEKVDIWSFGVVLWELLTGEIPYKDVDSSAIIWGVGSNSL HLPVPSSCPDGFKILLRQCWNRKPRNRPSFRQILLHLDIASADVLSTPQETYFKSQAEWR EEVKLHFEKIKSEGTCLHRLEEELVMRRREELRHALDIREHYERKLERANNLYMELNALM LQLELKERELLRREQALERRCPGLLKSHTSRSLLHGNTMEKLIKKRNVPQKLSPHSKRPD ILKTESLLPKLDAALSGVGLPGCPKAPPSPGRSRRGKTRHRKASAKGSCGDLPGLRAALP PHEPGGLGSPGGLGVGPTAWDASPPALRGLHHDLLLRKMSSSSPDLLSAALGARGRGATG GARDPGSPPPPOGDTPPSEGSAPGSTSPDSPGGAKGEPPPPVGPGEGVGLLGTGREGTTG RGGSRAGYQHLTPAALLYRAAVTRSQKRGISSEEEEGEVDSEVELPPSQRWPQGPNMRQS LSTFSSENPSDVEEGTASEPSPSGTPEVGSTNTDERPDERSDDMCSQGSEIPLDLPTSEV VPERETSSLPMOHODDOGPNPEDSDCDSTELDNSNSIDALPPPASLPP

>gi|18202068|sp|055173|PDPK_RAT 3-phosphoinositide dependent protein kinase-1 (Protein kinase B kinase) (PkB kinase)
MARTTSQLYDAVPIQSSVVLCSCPSPSMVRSQTEPSSSPGIPSGVSRQGSTMDGTTAEAR
PSTNPLOOHPAOLPPOPRKKRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRH

PSTNPLQQHPAQLPPQPRKKRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRH IIKENKVPYVTRERDVMSRLDHPFFVKLYFTFQDDEKLYFGLSYAKNGELLKYIRKIGSF DETCTRFYTAEIVSALEYLHGKGIIHRDLKPENILLNEDMHIQITDFGTAKVLSPDSKQA RANSFVGTAQYVSPELLTEKSACKSSDLWALGCIIYQLVAGLPPFRAGNEYLIFQKIIKL EYDFPEKFFPKARDLVEKLLVLDATKRLGCEEMEGYGPLKAHPFFESITWENLHQQTPPK LTAYLPAMSEDDEDCYGNYDNLLSQFGCMQVSSSSSSHSLCAVDASLPQRSGSNIEQYIH DLDTNSFELDLQFSEDEKRLLLEKQAGGNPWHQFVENNLILKMGPVDKRKGLFARRRQLL LTEGPHLYYVDPVNKVLKGEIPWSQELRPEAKNFKTFFVHTPNRTYYLMDPSGNAHKWCR KIQEVWRQQYQSSPDAAVQ

>gi|29747774|gb|AAH50806.1| Gene model 711, (NCBI) [Mus musculus]
MDYYSQGTFQNIMENKRKLKAVVDTEWMHTMLSQVLDAIEYLHKLNIVHRNLKPSNIVLV
NSGYCKLQDMSSQALMTHEAKWNVRAEEDPCQKSWMAPEALKFSFSTKSDIWSLGCIILD
MATCSFLNDTEAMQLRKAIRHHPGSLKPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRL
AIKDVMQVTFMSNSFKSSSVALNMQRQKVPIFITDVLLEGNMANILDVMQNFSSRPEVQL
RAINKLLTMPEDQLGLPWPTELLEEVISIIKQHGRILDILLSTCSLLLRVLGQALAKDPE
AEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEELEEEGLFQLAQENL
EHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHPEDVEIAEAGCAVL
WLLSLLGCIKESQFEQVVVLLLRSIQLCPGRVLLVNNAFRGLASLAKVSELVAFRIVVLE
EGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGGIKDLVQVIRGRFT
SSLELISYADEILQVLEANAQPGLQEDQLEPPAGQEAPLQGEPLFRP

>gi|20071571|gb|AAH26466.1| Unknown (protein for IMAGE:4485517) [Mus musculus]

PTRPTRLIVSNFSQAKQKSHLVDPQILRDQSRLAPEIITATQYKKCDEFQTGILIYEMLH LPNPFDENPELKEKEYTRTDLPRIPLRSPYSWGLQQLASCLLNPNPSERILISDAKGILQ CLLWGPREDLFQIFTTSATLAQKNALLQNWLDIKRTLLMIKFAEKSLDREGGISLEDWLC

Q5. Program Output:

Creating data.seg...

Contents of data.seq:

MDNYPKLEEMMLLSNGAPQFLGAAGTPEGSGGNNSSSSSSSSGGGGGGGSNSGSSAFNPQGEPSEQPYE HLTTESFSDIALNNEKALVETSYPSOTTRLPPITYTGRFSLEPAPNSGNTLWPEPLFSLVSGLVSMTNPP TSSSSAPSPAASSSSSASQSPPLSCAVPSNDSSPIYSAAPTFPTPNTDIFPEPQSQAFPGSAGTALQYPP PAYPATKGGFOVPMIPDYLFPQQGDLSLGTPDQKPFQGLENRTQQPSLTPLSTIKAFATQSGSQDLKAL NNTYQSQLIKPSRMRKYPNRPSKTPPHERPYACPVESCDRRFSRSDELTRHIRIHTGQKPFQCRICMRNF SRSDHLTTHIRTHTGEKPFACDICGRKFARSDERKRHTKIHLRQKDKKADKSVVASSAASSLSSYPSPVA TSYPSPATTSFPSPVPTSYSSPGSSTYPSPAHSGFPSPSVATTYASVPPAFPAOVSTFOSAGVSNSFSTS TGLSDMTATFSPRTIEIC@MTIOTETSVSAPDLTYSKTRGLVANLSAFMKORKMGLNDFIOKLSANSYAC KHPEVQSILNLTPPQDVELMNSNPSPPPSPSQQINLGPSSNPTAKPSDFDFLKVIGKGSFGKVLLARHRS DEKFYAVKVLOKKAILKKKEEKHIMSERNVLLKNVKHPFLVGLHYSFOTTDKLYFVLDYINGGELFYHLO RERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSOGHIILTDFGLCKENIEPNGTTSTFCG TPEYLAPEVLHKOPYDRTVDWWCLGAVLYEMLYGLPPFYSRNTAEMYDNILNKPLOLKPNISNAARHLLE GLLQKDRTKRLGFTDDFTEIKNHMFFSPINWDDLNAKKLTPPFNPNVTGPNDLRHFDPEFTDEPVPNSIG CSPDSALVTSSITEATEAFLGFSYAPAMDSYL@MSTRNCQGTDSVIKHLDTIPEDKKVRVQRTQSTFDPF EKPANQVKRVHSENNACINFKSSSAGKESPKVRRHSSPSSPTSPKFGKADSYEKLEKLGEGSYATVYKGK SKVNGKLVALKVIRLQEEEGTPFTAIREASLLKGLKHANIVLLHDIIHTKETLTLVFEYVHTDLCQYMDK HPGGLHPDNVKLFLFQLLRGLSYIHQRYILHRDLKPQNLLISDTGELKLADFGLARAKSVPSHTYSNEVV TLWYRPPDVLLGSTEYSTCLDMWGVGCIFVEMIOGVAAFPGMKDIODOLERIFLVLGTPNEDTWPGVHSL PHFKPERFTVYSSKSLROAWNKLSYVNHAEDLASKLLOCSPKNRLSAOAALSHEYFSDLPPRLWELTDMS SIFTVPNVRLQPEAGESMRAFGKNNSYGKSLSNSKH@MDRCKENCVSRPVKSTVPFGPKRVLVTEQIPSQ HPGSASSGQAQRVLCPSNSQRVPPQAQKPVAGQKPVLKQLPAASGPRPASRLSNPQKSEQPQPAASGNNS EKEQTSIQKTEDSKKRQWTLEDFDIGRPLGKGKFGNVYLAREKQSKFILALKVLFKVQLEKAGVEHQLRR EVEIQSHLRHPNILRLYGYFHDATRVYLILEYAPLGTVYRELOKLSKFDEQRTATYITELANALSYCHSK RVIHRDIKPENLLLGSNGELKIADFGWSVHAPSSRRTTLCGTLDYQPPEMIEGRMHDEKVDLWSLGVLCY EFLVGMPPFEAHTYQETYRRISRVEFTFPDFVTEGARDLISRLLKHNSSQRLTLAEVLEHPWIKANSSKP PTGHNSKEATSKSS@MASGPHSTATAAAAASSAAPSAGGSSSGTTTTTTTTTGGILIGDRLYSEVSLTID HSLIPEERLSPTPSMQDGLDLPSETDLRILGCELIQAAGILLRLPQVAMATGQVLFHRFFYSKSFVKHSF EIVAMACINLASKIEEAPRRIRDLINVFHHLRQLRGKRTPSPLILDQNYINTKNQVIKAERRVLKELGFC VHVKHPHKIIVMYLOVLECERNOTLVOTAWNYMNDSLRTNVFVRFOPETIACACIYLAARALOIPLPTRP HWFLLFGTTEEEIOEICIETLRLYTRKKPNYELLEKEVEKRKVALOEAKLKAKGLNPDGTPALSTLGGFS PASKPSSPREVKAEEKSPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRSRSRSRSRS HTPRRHYNNRRSRSGTYSSRSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSO SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSGHGRHRR@MAVDVKSRAKRYEKLDFL GEGQFATVYKARDKNTNQIVAIKKIKLGHRSEAKDGINRTALREIKLLQELSHPNIIGLLDAFGHKSNIS LVFDFMETDLEVIIKDNSLVLTPSHIKAYMLMTLQGLEYLHQHWILHRDLKPNNLLLDENGVLKLADFGL AKSFGSPNRAYTHQVVTRWYRAPELLFGARMYGVGVDMWAVGCILAELLLRVPFLPGDSDLDQLTRIFET LGTPTEEOWPDMCSLPDYVTFKSFPGVPLOHIFIAAGDDLLELIOGLFLFNPCTRTTASOALKTKYFSNR PGPTPGCQLPRPNCPVEALKEPANPTVATKRKRAEALEQGILPKKLIF@SMSKPKQDYSRTPGQVLSLIS SLGFFTPVGEKDQDSANMFSAPKSAAQLSRGFICPMSVDQKEPTSYSSKLLKSCFETLSSNPEIPVKCLT SNLLOCRKRLGTSSTSSOSHTFVSSVESECHSNPKWERDCOSTESSGCAMSWNAVEMLYAKSTSAIKTKT ELELALSPIHDSSAIPAAGSNOVTLPRKCFREISWEARDPDNENMTIDKGOSGFCOSSORSVNSSATSEE HLGKRNYKRNFHLVDSSPCQEIMQSKKNCTEYEANKERQGCRANQSTGLTTEVQNLKLSGCESQQLDYAN KENIVTYLTDRQTPEKLHIPTIAKNLMSELDEDRELSSKKDCLSSNSVCSDEDRALKTTCVDSDSSFPGV SMMESSLEIQALEPDKSIRDYSFEEPNTEDLFVLPKCQENSLPQDDCHACIQDSSQVSAHPSKAPKALTS KINVVAFRSFNSHINASTNSEPSKISITSLDAMDISYDYSGSYPMAVSPTEKGRHYTSHOTPNOVKLGTS YRTPKSVRRGAAPVDDGRILGTPDYLAPELLLGTAHGPAVDWWALGVCLFEFLTGIPPFNDETPQQVFQN

ILKRDIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMPFVPQPDDETD TSYFEARNNAOHLTISGFSL@MACLHETRTPSPSFGGFVSTLSEASMRKLDPDTSDCTPEKDLTPTOCVL RDVVPLGGQGGGPSPSPGGEPPPEPFANSVLQLHEQDTGGPGGATGSPESRASRVRADEVRLQCQSGSG FLEGLFGCLRPVWTMIGKAYSTEHKQQQEDLWEVPFEEILDLQWVGSGAQGAVFLGRFHGEEVAVKKVRD LKETDIKHLRKLKHPNIITFKGVCTQAPCYCILMEFCAQGQLYEVLRAGRPVTPSLLVDWSMGIAGGMNY LHLHKIIHRDLKSPNMLITYDDVVKISDFGTSKELSDKSTKMSFAGTVAWMAPEVIRNEPVSEKVDIWSF GVVLWELLTGEIPYKDVDSSAIIWGVGSNSLHLPVPSSCPDGFKILLRQCWNRKPRNRPSFRQILLHLDI ASADVLSTPOETYFKSOAEWREEVKLHFEKIKSEGTCLHRLEEELVMRRREELRHALDIREHYERKLERA NNLYMELNALMLOLELKERELLRREOALERRCPGLLKSHTSRSLLHGNTMEKLIKKRNVPOKLSPHSKRP DILKTESLLPKLDAALSGVGLPGCPKAPPSPGRSRRGKTRHRKASAKGSCGDLPGLRAALPPHEPGGLGS PGGLGVGPTAWDASPPALRGLHHDLLLRKMSSSSPDLLSAALGARGRGATGGARDPGSPPPPQGDTPPSE GSAPGSTSPDSPGGAKGEPPPPVGPGEGVGLLGTGREGTTGRGGSRAGYQHLTPAALLYRAAVTRSQKRG ISSEEEEGEVDSEVELPPSORWPOGPNMROSLSTFSSENPSDVEEGTASEPSPSGTPEVGSTNTDERPDE RSDDMCSOGSEIPLDLPTSEVVPERETSSLPMOHODDOGPNPEDSDCDSTELDNSNSIDALPPPASLPP@ MISRMIFRNYPSHNESDDEPFHFSISRELLLDRNDVVVGEMIGEGAYSIVYKGLLRNQFPVAVKIMDPST TSAVTKAHKKTFOKEVLLLSKMKHDNIVKFVGACIEPOLIIVTELVEGGTLORFMHSRPGPLDLKMSLSF ALDISRAMEFVHSNGIIHRDLNPRNLLVTGDLKHVKLADFGIAREETRGGMTCEAGTSKWMAPEVYSPEP LRVGEKKEYDHKADIYSFAIVLWQLVTNEEPFPDVPNSLFVPYLVSQGRRPILTKTPDVFVPIVESCWAQ DPDARPEFKEISVMLTNLLRRMSSDSSIGTTLPDGEAYEGEMEESENSPLLQEHFCKVKKPKEKKKKKKL VKMRFPFFKKFKVWLYNYKP@MSFFNFRKIFKLGSEKKKKQYEHVKRDLNPEDFWEIIGELGDGAFGKVY KAONKETSVLAAAKVIDTKSEEELEDYMVEIDILASCDHPNIVKLLDAFYYENNLWILIEFCAGGAVDAV MLELERPLTESQIQVVCKQTLDALNYLHDNKIIHRDLKAGNILFTLDGDIKLADFGVSAKNTRTIQRRDS FIGTPYWMAPEVVMCETSKDRPYDYKADVWSLGITLIEMAEIEPPHHELNPMRVLLKIAKSEPPTLAQPS RWSSNFKDFLKKCLEKNVDARWTTSOLLOHPFVTVDSNKPIRELIAEAKAEVTEEVEDGKEEDEEEETEN SLPIPASKRASSDLSIASSEEDKLSONACILESVSEKTERSNSEDKLNSKILNEKPTTDEPEKAVEDINE HITDAQLEAMTELHDRTAVIKENEREKRPKLENLPDTEDQETVDINSVSEGKENNIMITLETNIEHNLKS EEEKDQEKQQMFENKLIKSEEIKDTILQTVDLVSQETGEKEANIQAVDSEVGLTKEDTQEKLGEDDKTQK DVISNTSDVIGTCEAADVAQKVDEDSAEDTQSNDGKEVVEVGQKLINKPMVGPEAGGTKEVPIKEIVEMN EIEEKKKK@MARTTSQLYDAVPIQSSVVLCSCPSPSMVRSQTEPSSSPGIPSGVSRQGSTMDGTTAEARP STNPLQQHPAQLPPQPRKKRPEDFKFGKILGEGSFSTVVLARELATSREYAIKILEKRHIIKENKVPYVT RERDVMSRLDHPFFVKLYFTFQDDEKLYFGLSYAKNGELLKYIRKIGSFDETCTRFYTAEIVSALEYLHG KGIIHRDLKPENILLNEDMHIOITDFGTAKVLSPDSKOARANSFVGTAOYVSPELLTEKSACKSSDLWAL GCIIYQLVAGLPPFRAGNEYLIFQKIIKLEYDFPEKFFPKARDLVEKLLVLDATKRLGCEEMEGYGPLKA HPFFESITWENLHQQTPPKLTAYLPAMSEDDEDCYGNYDNLLSQFGCMQVSSSSSSHSLCAVDASLPQRS GSNIEOYIHDLDTNSFELDLOFSEDEKRLLLEKOAGGNPWHOFVENNLILKMGPVDKRKGLFARRROLLL TEGPHLYYVDPVNKVLKGEIPWSQELRPEAKNFKTFFVHTPNRTYYLMDPSGNAHKWCRKIQEVWRQQYQ SSPDAAVQ@LTHAGWGQGWTLARTRSLLIMLGPGSNRRRPTQGERGPGSPGEPMEKYQVLYQLNPGALGV NLVVEEMETKVKHVIKQVECMDDHYASQALEELMPLLKLRHAHISVYQELFITWNGEISSLYLCLVMEFN ELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALEYLHHLDIIHRNLKPSNIILISSDHCKLQDLSSNVL MTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIILDMTSCSFMDGTEAMHLRKSLRQSPGS LKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKDVVHITFLRGSFKSSCVSLTLHRQMVPASITD MLLEGNVASILEVMQKFSGWPEVQLRAMKRLLKMPADQLGLPWPPELVEVVVTTMELHDRVLDVQLCACS LLLHLLGOALVHHPEAKAPCNOAITSTLLSALOSHPEEEPLLVMVYSLLAITTTOESESLSEELONAGLL EHILEHLNSSLESRDVCASGLGLLWALLLDGIIVNKAPLEKVPDLISQVLATYPADGEMAEASCGVFWLL SLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKVSELAAFKVVVQEEGGSGLSLIKETY QLHRDDPEVVENVGMLLVHLASYEEILPELVSSSMKALLQEIKERFTSSLVSDSSAFSKPGLPPGGSPQL GCTTSGGLE@MDYYSQGTFQNIMENKRKLKAVVDTEWMHTMLSQVLDAIEYLHKLNIVHRNLKPSNIVLV NSGYCKLQDMSSQALMTHEAKWNVRAEEDPCQKSWMAPEALKFSFSTKSDIWSLGCIILDMATCSFLNDT EAMQLRKAIRHHPGSLKPILKTMEEKQIPGTDVYYLLLPFMLHINPSDRLAIKDVMQVTFMSNSFKSSSV ALNMQRQKVPIFITDVLLEGNMANILDVMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEEVISII KOHGRILDILLSTCSLLLRVLGOALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSO GOISEELEEEGLFOLAOENLEHFOEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHPEDV

EIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLRSIQLCPGRVLLVNNAFRGLASLAKVSELVAFRIVVLE EGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGGIKDLVQVIRGRFTSSLELISYAD EILQVLEANAQPGLQEDQLEPPAGQEAPLQGEPLFRP@MEHSVPKNKLKKLSEDSLTKQPEEVFDVLEKL GEGSYGSVFKAIHKESGQVVAIKQVPVESDLQEIIKEISIMQQCDSPYVVKYYGSYFKNTDLWIVMEYCG AGSVSDIIRLRNKTLTEDEIATVLKSTLKGLEYLHFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTD TMAKRNTVIGTPFWMAPEVIQEIGYNCVADIWSLGITSIEMAEGKPPYADIHPMRAIFMIPTNPPPTFRK PEHWSDDFTDFVKKCLVKNPEQRATATQLLQHPFIVGAKPVSILRDLITEAMDMKAKRQQEQQRELEEDD ENSEEEVEVDSHTMVKSGSESAGTMRATGTMSDGAQTMIEHGSTMLESNLGTMVINSDDEEEEEDLGSMR RNPTSOOIORPSFMDYFDKODSNKAOEGFNHNOODPCLISKTAFPDNWKVPODGDFDFLKNLDFEELOMR LTALDPMMEREIEELRORYTAKROPILDAMDAKKRROONF@PTRPTRLIVSNFSOAKOKSHLVDPOILRD QSRLAPEIITATQYKKCDEFQTGILIYEMLHLPNPFDENPELKEKEYTRTDLPRIPLRSPYSWGLQQLAS CLLNPNPSERILISDAKGILQCLLWGPREDLFQIFTTSATLAQKNALLQNWLDIKRTLLMIKFAEKSLDR EGGISLEDWLCAQYLAFATTDSLSYIVKILQYR@MONKENREPRVQQTPSAGVGPLRVEMNPDTHAVSGP GRVPVKSNSKVLSIDDFDIGRPLGKGKFGNVYLARERKLKVVIALKVLFKSOMVKEGVEHOLRREIEIOS HLRHPNILRFYNYFHDDTRVFLILEYAPRGEMYKELQRYGRFDDQRTATYMEEVSDALQYCHEKKVIHRD IKPENLLLGYRGELKIADFGWSVHAPSLRRRTMCGTLDYLPPEMIEGHSHDEKVDLWSIGVLCYECLVGN PPFETASHAETYKRITKVDLOFPKLVSEGARDLISKLLRHSPSMRLPLRSVMEHPWVKANSRRVLPPVCS SEPH

Q6. Program Output:

Getting contents of Q6query.txt...
Query is: MHIQITDFGTAKVLSPDS
gi # of database sequence containing query is: 18202068

07.

I spent around 12 hours total setting up python, learning basic python for the assignment, and doing the problems. The actual assignment took around 5 hours to code and package for submission. I posted on piazza for clarification about the Q3 header, but did not ask anyone else for help.