**Bio Informatics Computing**

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\* Date: 18 Feb 2015. Author : Mukhasir Shah Syed

\* Using the below code we will calculat ooptimum local alignment score by implementing

Smith-Waterman algorithm using affine gap scoring tehnique.

\* Protein data is being used for this segment of code implementation.

\* In this code we will read one query file (EColi-query1.fa) which contains protein data for

one sequence .

\* We will also read database file (swissprot.fa) which contains multiple protein sequences.

\* Once reading from the query file is completed we implement the algorithm for getting

\* optimum local alignment score using Smith-Waterman Affine gap scoring algorithm.

\* We take 2 rows in this implementation where the first row will be defaulted to zero and in

the second row we we check the score and place it based on alignment.

\* Here as we are dealing with protein data we will consider GAP\_OPEN as 11 and GAP\_EXTEND as 1.

\* To calculate score we will run loop for database field data and check it with Single protein

\* query sequence, where SmithWatermanScore\_Affine() method will be called.

\* We will used BLOSUM62 matrix(for protein) and Affine gap opening and extension penality

which are from NCBI BLASTp implementation.

\* Input : We will provide protein query sequence (EColi-query1.fa) and database fasta file

(swissprot.fa). Note: swissprot.fa is relatively small protein sequence database which

contains about 460,670 known protein sequences.

\* Output: We will list file showing optimum local alignment score (Smith-Waterman score) for

each of the reference protein sequence.

\* Output would be displayed as mentioned below:

\* --- query len = 378

>gi|1684788|gb|AAB36530.1| 4-phosphoerythronate dehydrogenase [Escherichia coli str. K-12 substr. W3110]

MKILVDENMPYARDLFSRLGEVTAVPGRPIPVAQLADADALMVRSVTKVNESLLAGKPIKFVGTATAGTDHVDEAWLKQAGIGFSAAPGCNAIAVVEYVFSSLL

MLAERDGFSLYDRTVGIVGVGNVGRRLQARLEALGIKTLLCDPPRADRGDEGDFRSLDELVQRADILTFHTPLFKDGPYKTLHLADEKLIRSLKPGAILINACR

GAVVDNTALLTCLNEGQKLSVVLDVWEGEPELNVELLKKVDIGTSHIAGYTLEGKARGTTQVFEAYSKFIGHEQHVALDTLLPAPEFGRITLHGPLDQPTLKRL

VHLVYDVRRDDAPLRKVAGIPGEFDKLRKNYLERREWSSLYVICDDASAASLLCKLGFNAVHHPAR

>gi|745997998|sp|P0DKH9.1|AREP1\_ARATH RecName: Ful (len=40)

-- SW\_score = 20(Query Index = 47, Database Index = 13)

>gi|745997997|sp|P0DKH8.1|AMP2\_FAGES RecName: Full (len=40)

-- SW\_score = 17(Query Index = 88, Database Index = 13)....and so on.

\* To complie/run the code we have to create a Console Application using Visual Studio 2013

and compile/build this application which will create an executable file then run the

".exe" application to execute the code.

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using System;

using System.Collections.Generic;

using System.IO;

using System.Linq;

using System.Text;

using System.Threading.Tasks;

namespace SWScore\_Affine

{

class Program

{

/// <summary>

/// This is the method that gets hit first when this application is run.

/// In this Main() method we will read single protein sequence from EColi-query1.fa file

/// We will loop through the database data and place them in key value pair.

/// We will initialize BLOSUM62 scoring matrix and then loop through the database Key-Value pairs

/// We will call SmithWatermanScore\_Affine() method to get the optimum local alignment score

/// and store output in a file.

/// </summary>

/// <param name="args"></param>

static void Main(string[] args)

{

//Variables used to store label and data of query protein sequence

string querylabel = string.Empty;

string querydata= string.Empty;

//Read label and data from Protein sequence file and store in above mentioned variables respectiely.

foreach(string lines in File.ReadAllLines(@"E:\Bio Informatics\Assignment 3\EColi-query1.fa"))

{

if(lines.Contains(">"))

{

querylabel = lines;//stores label name

}

else

{

querydata += lines;//stores data/bases of protein.

}

}

//Variables used to store label and data of database file.

string Database\_label = string.Empty;

string Database\_Seq = string.Empty;

//Initialize KeyValuePair List for storing database sequences.

List<KeyValuePair<string, string>> Database\_Data = new List<KeyValuePair<string, string>>();

//Loop throug database file to store the label and bases respectivel in key-value pair format.

foreach (string Database in File.ReadLines(@"E:\Bio Informatics\Assignment 3\swissprot.fa"))

{

if (Database.Contains(">"))

{

if (Database\_Seq != string.Empty)

{

Database\_Data.Add(new KeyValuePair<string, string>(Database\_label, Database\_Seq));

Database\_Seq = string.Empty;

}

Database\_label = Database;

}

else

{

Database\_Seq += Database;

}

}

Database\_Data.Add(new KeyValuePair<string, string>(Database\_label, Database\_Seq));

//Initializing and declaration of ScoreMatrix (BLOSUM62)

int[,] ScoreMatrix = new int[25, 25]{

{ 4, -1, -2, -2, 0, -1, -1, 0, -2, -1, -1, -1, -1, -2, -1, 1, 0, -3, -2, 0, -2, -1, -1, -1, -4},

{-1, 5, 0, -2, -3, 1, 0, -2, 0, -3, -2, 2, -1, -3, -2, -1, -1, -3, -2, -3, -1, -2, 0, -1, -4},

{-2, 0, 6, 1, -3, 0, 0, 0, 1, -3, -3, 0, -2, -3, -2, 1, 0, -4, -2, -3, 4, -3, 0, -1, -4},

{-2, -2, 1, 6, -3, 0, 2, -1, -1, -3, -4, -1, -3, -3, -1, 0, -1, -4, -3, -3, 4, -3, 1, -1, -4},

{ 0, -3, -3, -3, 9, -3, -4, -3, -3, -1, -1, -3, -1, -2, -3, -1, -1, -2, -2, -1, -3, -1, -3, -1, -4},

{-1, 1, 0, 0, -3, 5, 2, -2, 0, -3, -2, 1, 0, -3, -1, 0, -1, -2, -1, -2, 0, -2, 4, -1, -4},

{-1, 0, 0, 2, -4, 2, 5, -2, 0, -3, -3, 1, -2, -3, -1, 0, -1, -3, -2, -2, 1, -3, 4, -1, -4},

{ 0, -2, 0, -1, -3, -2, -2, 6, -2, -4, -4, -2, -3, -3, -2, 0, -2, -2, -3, -3, -1, -4, -2, -1, -4},

{-2, 0, 1, -1, -3, 0, 0, -2, 8, -3, -3, -1, -2, -1, -2, -1, -2, -2, 2, -3, 0, -3, 0, -1, -4},

{-1, -3, -3, -3, -1, -3, -3, -4, -3, 4, 2, -3, 1, 0, -3, -2, -1, -3, -1, 3, -3, 3, -3, -1, -4},

{-1, -2, -3, -4, -1, -2, -3, -4, -3, 2, 4, -2, 2, 0, -3, -2, -1, -2, -1, 1, -4, 3, -3, -1, -4},

{-1, 2, 0, -1, -3, 1, 1, -2, -1, -3, -2, 5, -1, -3, -1, 0, -1, -3, -2, -2, 0, -3, 1, -1, -4},

{-1, -1, -2, -3, -1, 0, -2, -3, -2, 1, 2, -1, 5, 0, -2, -1, -1, -1, -1, 1, -3, 2, -1, -1, -4},

{-2, -3, -3, -3, -2, -3, -3, -3, -1, 0, 0, -3, 0, 6, -4, -2, -2, 1, 3, -1, -3, 0, -3, -1, -4},

{-1, -2, -2, -1, -3, -1, -1, -2, -2, -3, -3, -1, -2, -4, 7, -1, -1, -4, -3, -2, -2, -3, -1, -1, -4},

{ 1, -1, 1, 0, -1, 0, 0, 0, -1, -2, -2, 0, -1, -2, -1, 4, 1, -3, -2, -2, 0, -2, 0, -1, -4},

{ 0, -1, 0, -1, -1, -1, -1, -2, -2, -1, -1, -1, -1, -2, -1, 1, 5, -2, -2, 0, -1, -1, -1, -1, -4},

{-3, -3, -4, -4, -2, -2, -3, -2, -2, -3, -2, -3, -1, 1, -4, -3, -2, 11, 2, -3, -4, -2, -2, -1, -4},

{-2, -2, -2, -3, -2, -1, -2, -3, 2, -1, -1, -2, -1, 3, -3, -2, -2, 2, 7, -1, -3, -1, -2, -1, -4},

{ 0, -3, -3, -3, -1, -2, -2, -3, -3, 3, 1, -2, 1, -1, -2, -2, 0, -3, -1, 4, -3, 2, -2, -1, -4},

{-2, -1, 4, 4, -3, 0, 1, -1, 0, -3, -4, 0, -3, -3, -2, 0, -1, -4, -3, -3, 4, -3, 0, -1, -4},

{-1, -2, -3, -3, -1, -2, -3, -4, -3, 3, 3, -3, 2, 0, -3, -2, -1, -2, -1, 2, -3, 3, -3, -1, -4},

{-1, 0, 0, 1, -3, 4, 4, -2, 0, -3, -3, 1, -1, -3, -1, 0, -1, -2, -2, -2, 0, -3, 4, -1, -4},

{-1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -1, -4},

{-4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, -4, 1}

};

//Store the output format text into variable.

string FinalText = "--- query len = " + querydata.Length +" \n" + querylabel + "\n" + querydata + "\n\n";

//Loop through key-value pair of database sequence and then call SmithWatermanScore\_Affine() to get the score and indexes

//of database and query.

foreach (KeyValuePair<string, string> DatabaseValue in Database\_Data)

{

//As we are processing protein data the value for gao opening is '11' and gap extension is '1'

int gap\_open = 11;

int gap\_ext = 1;

//Forming string to show the output in required format.

//Store the database label and bases length into string for displaying it in output.

string header = DatabaseValue.Key.Substring(0, 50) + "\t" + "(len=" + DatabaseValue.Value.Length + ")\n";

//Call SmithWatermanScore\_Affine() method to get the score and indexes

string vallue = SmithWatermanScore\_Affine(DatabaseValue.Value, DatabaseValue.Value.Length, querydata, querydata.Length, gap\_open, gap\_ext, ScoreMatrix);

string ScoreText = "-- SW\_score = " + vallue;

FinalText += header + ScoreText;

}

//Store the output/complete result for sequences into Result.txt file.

File.WriteAllText(@"E:\Bio Informatics\Assignment 3\Result.txt", FinalText);

}

/// <summary>

/// We pass database sequence, query sequence, lengths of database sequence and query sequence, gap open, gap extend

/// and score matrix values.

/// In this we will initialize two seperate 1D arrays. Where first will be set value as 'zero'.

/// and set would be set -(gap\_open) as value in it.

/// Loop through the query sequence character and database characters and calculate optimum local alignment score

/// using Smith-Waterman affine scoring algorithm.

/// </summary>

/// <param name="dbSeq"></param>

/// <param name="dbSeq\_len"></param>

/// <param name="querySeq"></param>

/// <param name="querySeq\_len"></param>

/// <param name="gap\_open"></param>

/// <param name="gap\_ext"></param>

/// <param name="ScoreMatrix"></param>

/// <returns></returns>

public static string SmithWatermanScore\_Affine(string dbSeq, int dbSeq\_len,string querySeq, int querySeq\_len, int gap\_open, int gap\_ext, int[,] ScoreMatrix)

{

//intialize two 1 dimensional arrays of size each database sequence+ 1 that is passed.

int[] nogap = new int[dbSeq.Length + 1];

int[] b\_gap = new int[dbSeq.Length + 1];

//Variables used in the code.

int i =0 , j=0;

int last\_nogap, prev\_nogap;

int score = 0;

int GlobalScore = 0;

int queryIndex = 0;

int dbIndex = 0;

//loop through b\_gap array and set the value as -(gap\_open)

for (int counter = 0; counter <= dbSeq.Length; counter++)

{

b\_gap[counter] = -(gap\_open);

}

//loop through length of query sequence

for(i=0;i<querySeq\_len;++i)

{

//declare value for last\_nogap, prev\_nogap as 0

int a\_gap;

last\_nogap = prev\_nogap = 0;

a\_gap = -(gap\_open);

//loop through length of database sequence

for(j=0;j<dbSeq\_len;++j)

{

//Smith-Waterman Affine Scoring algorithm

a\_gap = Math.Max((last\_nogap-gap\_open-gap\_ext),(a\_gap-gap\_ext));

b\_gap[j] = Math.Max((nogap[j]-gap\_open-gap\_ext),(b\_gap[j]-gap\_ext));

//We will call BLOSUM62Value() method to get the gap penality value from scorematrix.

last\_nogap = Math.Max((prev\_nogap + BLOSUM62Value(ScoreMatrix,dbSeq[j],querySeq[i])), 0);

last\_nogap = Math.Max(last\_nogap,a\_gap);

last\_nogap = Math.Max(last\_nogap,b\_gap[j]);

prev\_nogap = nogap[j];

nogap[j] = last\_nogap;

score = Math.Max(score,last\_nogap);

//Check if the new score is greater than or equal to older one then place it in GlobalScore and store the indexes.

if (score >= GlobalScore)

{

GlobalScore = score;

queryIndex = i;

dbIndex = j;

}

}

}

//Send bacl score , query index and database index.

string ScoreTextValue = GlobalScore.ToString() + "(Query Index = " + queryIndex + ", Database Index = " + dbIndex + ")\n";

return ScoreTextValue;

}

/// <summary>

/// This method takes scorematrix, database sequence character and query sequence character

/// and get penality value and return it for optimum local alignment score calculation.

/// </summary>

/// <param name="ScoreMatrix"></param>

/// <param name="dbSeqChar"></param>

/// <param name="queryChar"></param>

/// <returns></returns>

public static int BLOSUM62Value(int[,] ScoreMatrix, char dbSeqChar, char queryChar)

{

int BLOSUMscore = 0;

//Intialize and declare the character set for protein sequences.(BLOSUM62)

char[] Alphabet = new char[25] { 'A', 'R','N', 'D', 'C', 'Q', 'E', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V', 'B', 'J', 'Z', 'X', '\*'};

int dbIndex =- 1 , queryIndex = -1;

//Loop through the array and get the index of character in DB and query

for (int k = 0; k < Alphabet.Length; k++)

{

if (Alphabet[k] == dbSeqChar)

{

dbIndex = k;

}

if (Alphabet[k] == queryChar)

{

queryIndex = k;

}

}

//Check if the character is not presnt in Alphabet array then assigh index= length - 1

if (dbIndex == -1)

{

dbIndex = Alphabet.Length - 1;

}

if (queryIndex==-1)

{

queryIndex = Alphabet.Length - 1;

}

//Get the penality value.

BLOSUMscore = ScoreMatrix[dbIndex, queryIndex];

//Return the penality score

return BLOSUMscore;

}

}

}

***Output:***

--- query len = 378

>gi|1684788|gb|AAB36530.1| 4-phosphoerythronate dehydrogenase [Escherichia coli str. K-12 substr. W3110]

MKILVDENMPYARDLFSRLGEVTAVPGRPIPVAQLADADALMVRSVTKVNESLLAGKPIKFVGTATAGTDHVDEAWLKQAGIGFSAAPGCNAIAVVEYVFSSLLMLAERDGFSLYDRTVGIVGVGNVGRRLQARLEALGIKTLLCDPPRADRGDEGDFRSLDELVQRADILTFHTPLFKDGPYKTLHLADEKLIRSLKPGAILINACRGAVVDNTALLTCLNEGQKLSVVLDVWEGEPELNVELLKKVDIGTSHIAGYTLEGKARGTTQVFEAYSKFIGHEQHVALDTLLPAPEFGRITLHGPLDQPTLKRLVHLVYDVRRDDAPLRKVAGIPGEFDKLRKNYLERREWSSLYVICDDASAASLLCKLGFNAVHHPAR

>gi|745997998|sp|P0DKH9.1|AREP1\_ARATH RecName: Ful (len=40)

-- SW\_score = 20(Query Index = 377, Database Index = 39)

>gi|745997997|sp|P0DKH8.1|AMP2\_FAGES RecName: Full (len=40)

-- SW\_score = 17(Query Index = 377, Database Index = 39)

>gi|745997996|sp|P0DKH7.1|AMP1\_FAGES RecName: Full (len=40)

-- SW\_score = 17(Query Index = 377, Database Index = 39)

>gi|745755594|sp|Q29243.2|DAG1\_PIG RecName: Full=D (len=877)

-- SW\_score = 29(Query Index = 377, Database Index = 876)

>gi|745755649|sp|P9WGI9.2|GLYA1\_MYCTU RecName: Ful (len=438)

-- SW\_score = 36(Query Index = 377, Database Index = 437)

>gi|745755659|sp|Q5PR66.2|IFT56\_DANRE RecName: Ful (len=557)

-- SW\_score = 32(Query Index = 377, Database Index = 556)

>gi|728048777|sp|I1JLC8.1|SLE2\_SOYBN RecName: Full (len=105)

-- SW\_score = 26(Query Index = 377, Database Index = 104)

>gi|728048695|sp|P0CT50.1|SDC\_TRIMF RecName: Full= (len=350)

-- SW\_score = 30(Query Index = 377, Database Index = 349)

>gi|728048694|sp|P0DKH6.1|RPS6R\_ARATH RecName: Ful (len=1127)

-- SW\_score = 37(Query Index = 377, Database Index = 1126)

>gi|728048647|sp|F1QEG2.1|KL41B\_DANRE RecName: Ful (len=605)

-- SW\_score = 35(Query Index = 377, Database Index = 604)

>gi|728048573|sp|C0HJB3.1|MANA\_CANEN RecName: Full (len=981)

-- SW\_score = 48(Query Index = 377, Database Index = 980)

>gi|728048514|sp|S4R3Y5.1|HMN11\_HUMAN RecName: Ful (len=24)

-- SW\_score = 20(Query Index = 377, Database Index = 23)

>gi|727863585|sp|Q6ZM89.3|RH42A\_DANRE RecName: Ful (len=805)

-- SW\_score = 33(Query Index = 377, Database Index = 804)

>gi|727863581|sp|Q6ZP82.2|CC141\_HUMAN RecName: Ful (len=1450)

-- SW\_score = 36(Query Index = 377, Database Index = 1449)

>gi|728047640|sp|D6REC4.1|CFA99\_HUMAN RecName: Ful (len=459)

-- SW\_score = 33(Query Index = 377, Database Index = 458)

>gi|728047699|sp|P0DMQ6.1|DHSO\_CHICK RecName: Full (len=355)

-- SW\_score = 30(Query Index = 377, Database Index = 354)

>gi|704045459|sp|G0SC29.2|NLE1\_CHATD RecName: Full (len=517)

-- SW\_score = 29(Query Index = 377, Database Index = 516)

>gi|704045435|sp|Q9SX54.2|SCRK8\_ARATH RecName: Ful (len=210)

-- SW\_score = 28(Query Index = 377, Database Index = 209)

>gi|704044129|sp|P0DMQ3.1|TO1D\_HADMO RecName: Full (len=84)

-- SW\_score = 24(Query Index = 377, Database Index = 83)

>gi|704044123|sp|P0DMQ2.1|TO1C\_HADMO RecName: Full (len=84)

-- SW\_score = 25(Query Index = 377, Database Index = 83)

>gi|704044116|sp|P0DMQ1.1|TO1B\_HADMO RecName: Full (len=84)

-- SW\_score = 25(Query Index = 377, Database Index = 83)

>gi|704044110|sp|P0DMQ0.1|TO1A\_HADMO RecName: Full (len=84)

-- SW\_score = 24(Query Index = 377, Database Index = 83)

>gi|704044094|sp|P0DMQ4.1|TK1A\_HADMO RecName: Full (len=73)

-- SW\_score = 23(Query Index = 377, Database Index = 72)

>gi|704043461|sp|C0HJD7.1|NXL4\_DENPO RecName: Full (len=72)

-- SW\_score = 21(Query Index = 377, Database Index = 71)

>gi|704045556|sp|Q9SUC3.2|MS5\_ARATH RecName: Full= (len=434)

-- SW\_score = 34(Query Index = 377, Database Index = 433)

>gi|704044187|sp|C0HJM7.1|TXL1\_PHOPT RecName: Full (len=10)

-- SW\_score = 15(Query Index = 377, Database Index = 9)

>gi|704000372|sp|E2RE76.2|APOA4\_CANFA RecName: Ful (len=378)

-- SW\_score = 38(Query Index = 377, Database Index = 377)

>gi|704000369|sp|C9JSJ3.2|BHMG1\_HUMAN RecName: Ful (len=638)

-- SW\_score = 36(Query Index = 377, Database Index = 637)

>gi|704000365|sp|B2NI93.2|GEDH\_CARLC RecName: Full (len=378)

-- SW\_score = 35(Query Index = 377, Database Index = 377)

>gi|704000364|sp|K7N5M5.2|HBA1\_ELEMC RecName: Full (len=142)

-- SW\_score = 30(Query Index = 377, Database Index = 141)

>gi|704000363|sp|G0S616.2|MRT4\_CHATD RecName: Full (len=270)

-- SW\_score = 31(Query Index = 377, Database Index = 269)

>gi|704000358|sp|C0HJM8.1|LEC\_ALLCE RecName: Full= (len=10)

-- SW\_score = 19(Query Index = 377, Database Index = 9)

>gi|704000357|sp|C0HJN0.1|KAX6V\_HETLA RecName: Ful (len=34)

-- SW\_score = 23(Query Index = 377, Database Index = 33)

>gi|704000346|sp|F1QDF8.1|FXJ1A\_DANRE RecName: Ful (len=458)

-- SW\_score = 28(Query Index = 377, Database Index = 457)

>gi|704000341|sp|P0DKH4.1|F26G\_SOLTO RecName: Full (len=61)

-- SW\_score = 27(Query Index = 377, Database Index = 60)

>gi|704000316|sp|W5EP13.1|CA1P\_WHEAT RecName: Full (len=495)

-- SW\_score = 32(Query Index = 377, Database Index = 494)

>gi|746590800|sp|P0CT51.1|BLP1\_CANAL RecName: Full (len=77)

-- SW\_score = 29(Query Index = 377, Database Index = 76)

>gi|704000362|sp|Q59PD6.2|MAD1\_CANAL RecName: Full (len=696)

-- SW\_score = 35(Query Index = 377, Database Index = 695)

>gi|703556459|sp|A2BD09.3|OLM2A\_PIG RecName: Full= (len=650)

-- SW\_score = 30(Query Index = 377, Database Index = 649)

>gi|703556455|sp|O55007.2|RGPA1\_RAT RecName: Full= (len=2035)

-- SW\_score = 38(Query Index = 377, Database Index = 2034)

>gi|703556453|sp|P84718.2|PSBO\_PINST RecName: Full (len=116)

-- SW\_score = 30(Query Index = 377, Database Index = 115)

>gi|703556448|sp|P81018.2|LADD\_ONCMY RecName: Full (len=190)

-- SW\_score = 29(Query Index = 377, Database Index = 189)

>gi|728048788|sp|C9J7I0.1|UMAD1\_HUMAN RecName: Ful (len=102)

-- SW\_score = 27(Query Index = 377, Database Index = 101)

>gi|694016595|sp|Q5TYJ0.4|OBP71\_ANOGA RecName: Ful (len=228)

-- SW\_score = 26(Query Index = 377, Database Index = 227)

>gi|694016591|sp|U3KRG0.2|LECB1\_CRATA RecName: Ful (len=165)

-- SW\_score = 38(Query Index = 377, Database Index = 164)

>gi|694016588|sp|C0HJA4.1|LECB2\_CRATA RecName: Ful (len=165)

-- SW\_score = 38(Query Index = 377, Database Index = 164)

>gi|694016584|sp|C0HJL9.1|TAN\_BACIU RecName: Full= (len=15)

-- SW\_score = 15(Query Index = 377, Database Index = 14)

>gi|694016581|sp|P0DKH2.1|RI2BC\_ARATH RecName: Ful (len=158)

-- SW\_score = 25(Query Index = 377, Database Index = 157)

>gi|694016580|sp|C0HJM0.1|PPO3\_SARAR RecName: Full (len=71)

-- SW\_score = 29(Query Index = 377, Database Index = 70)

>gi|694016558|sp|D4A693.2|AZIN2\_RAT RecName: Full= (len=457)

-- SW\_score = 36(Query Index = 377, Database Index = 456)

>gi|694016556|sp|F4I9R6.2|JA15S\_ARATH RecName: Ful (len=131)

-- SW\_score = 37(Query Index = 377, Database Index = 130)

>gi|694016548|sp|S4R3P1.1|HMN13\_HUMAN RecName: Ful (len=24)

-- SW\_score = 24(Query Index = 377, Database Index = 23)

>gi|694016547|sp|P0DMP1.1|HMN12\_HUMAN RecName: Ful (len=27)

-- SW\_score = 19(Query Index = 377, Database Index = 26)

>gi|694016530|sp|C0HJM6.1|CHIT\_TRISX RecName: Full (len=11)

-- SW\_score = 15(Query Index = 377, Database Index = 10)

>gi|694016529|sp|P86977.1|CHIT\_STRVO RecName: Full (len=10)

-- SW\_score = 19(Query Index = 377, Database Index = 9)

>gi|693586058|sp|Q6ZMS4.4|ZN852\_HUMAN RecName: Ful (len=543)

-- SW\_score = 32(Query Index = 377, Database Index = 542)

>gi|694016571|sp|P0DL37.1|KAX6L\_UROYA RecName: Ful (len=62)

-- SW\_score = 22(Query Index = 377, Database Index = 61)

>gi|75523137|sp|Q7M181.1|ACLR\_ACHOB RecName: Full= (len=436)

-- SW\_score = 35(Query Index = 377, Database Index = 435)

>gi|678021173|sp|Q9C918.2|UBC38\_ARATH RecName: Ful (len=326)

-- SW\_score = 29(Query Index = 377, Database Index = 325)

>gi|678019224|sp|C0HJK0.1|VP\_DINQU RecName: Full=V (len=20)

-- SW\_score = 20(Query Index = 377, Database Index = 19)

>gi|678019209|sp|C0HJK2.1|VP987\_DINQU RecName: Ful (len=9)

-- SW\_score = 19(Query Index = 377, Database Index = 8)

>gi|678019205|sp|C0HJK4.1|VP88\_DINQU RecName: Full (len=11)

-- SW\_score = 14(Query Index = 377, Database Index = 10)

>gi|678019201|sp|C0HJK3.1|VP32\_DINQU RecName: Full (len=9)

-- SW\_score = 14(Query Index = 377, Database Index = 8)

>gi|678019198|sp|C0HJK1.1|VP30\_DINQU RecName: Full (len=9)

-- SW\_score = 16(Query Index = 377, Database Index = 8)

>gi|678019123|sp|C0HJK5.1|TXHM3\_HERML RecName: Ful (len=35)

-- SW\_score = 18(Query Index = 377, Database Index = 34)

>gi|678019117|sp|C0HJH6.1|TX62\_DINQU RecName: Full (len=28)

-- SW\_score = 26(Query Index = 377, Database Index = 27)

>gi|678019113|sp|C0HJH7.1|TX04\_DINQU RecName: Full (len=28)

-- SW\_score = 24(Query Index = 377, Database Index = 27)

>gi|678000802|sp|I1N462.3|SBT1\_SOYBN RecName: Full (len=789)

-- SW\_score = 43(Query Index = 377, Database Index = 788)

>gi|678000774|sp|Q0J0A4.3|LPAAT\_ORYSJ RecName: Ful (len=414)

-- SW\_score = 27(Query Index = 377, Database Index = 413)

>gi|678000753|sp|Q7XMI0.3|KCY2\_ORYSJ RecName: Full (len=243)

-- SW\_score = 29(Query Index = 377, Database Index = 242)

>gi|678000260|sp|Q9SGX9.2|ESFL1\_ARATH RecName: Ful (len=80)

-- SW\_score = 27(Query Index = 377, Database Index = 79)

>gi|678000242|sp|A8MQP7.2|ESFL7\_ARATH RecName: Ful (len=88)

-- SW\_score = 23(Query Index = 377, Database Index = 87)

>gi|678000229|sp|O82377.2|ESFL6\_ARATH RecName: Ful (len=77)

-- SW\_score = 22(Query Index = 377, Database Index = 76)

>gi|678000206|sp|Q0J6P7.2|KAD5\_ORYSJ RecName: Full (len=608)

-- SW\_score = 31(Query Index = 377, Database Index = 607)

>gi|678000108|sp|A2ZU80.2|NRT24\_ORYSJ RecName: Ful (len=485)

-- SW\_score = 35(Query Index = 377, Database Index = 484)

>gi|678000080|sp|K7LFJ0.2|PP890\_SOYBN RecName: Ful (len=52)

-- SW\_score = 23(Query Index = 377, Database Index = 51)

>gi|677999394|sp|Q10RP4.2|SE14\_ORYSJ RecName: Full (len=1487)

-- SW\_score = 34(Query Index = 377, Database Index = 1486)

>gi|677995804|sp|P0DMM5.1|MCSB\_GEOSE RecName: Full (len=363)

-- SW\_score = 35(Query Index = 377, Database Index = 362)

>gi|677995449|sp|P86907.1|PA2A\_BOTAM RecName: Full (len=122)

-- SW\_score = 24(Query Index = 377, Database Index = 121)

>gi|677992918|sp|P0DMM7.1|SLB\_TROWA RecName: Full= (len=10)

-- SW\_score = 17(Query Index = 377, Database Index = 9)

>gi|677992907|sp|P0DMM6.1|SLA\_TROWA RecName: Full= (len=9)

-- SW\_score = 17(Query Index = 377, Database Index = 8)

>gi|677991645|sp|C0HJF7.1|ITR1\_JATCU RecName: Full (len=27)

-- SW\_score = 21(Query Index = 377, Database Index = 26)

>gi|677991295|sp|P0DKH1.1|ESFL2\_ARATH RecName: Ful (len=86)

-- SW\_score = 25(Query Index = 377, Database Index = 85)

>gi|677286758|sp|Q8NCS7.4|CTL5\_HUMAN RecName: Full (len=719)

-- SW\_score = 30(Query Index = 377, Database Index = 718)

>gi|677286751|sp|Q8IVT5.3|KSR1\_HUMAN RecName: Full (len=923)

-- SW\_score = 42(Query Index = 377, Database Index = 922)

>gi|677286748|sp|P0CF96.3|MZT1\_SCHPO RecName: Full (len=64)

-- SW\_score = 30(Query Index = 377, Database Index = 63)

>gi|677286739|sp|A1UI62.2|RSMH\_MYCSK RecName: Full (len=370)

-- SW\_score = 40(Query Index = 377, Database Index = 369)

>gi|677286738|sp|A3Q1M6.2|RSMH\_MYCSJ RecName: Full (len=370)

-- SW\_score = 40(Query Index = 377, Database Index = 369)

>gi|677286737|sp|A0R024.2|RSMH\_MYCS2 RecName: Full (len=373)

-- SW\_score = 38(Query Index = 377, Database Index = 372)

>gi|677286735|sp|B2HGS5.2|RSMH\_MYCMM RecName: Full (len=395)

-- SW\_score = 34(Query Index = 377, Database Index = 394)

>gi|677286732|sp|B1MP29.2|RSMH\_MYCA9 RecName: Full (len=384)

-- SW\_score = 34(Query Index = 377, Database Index = 383)

>gi|677286731|sp|A0QF44.2|RSMH\_MYCA1 RecName: Full (len=386)

-- SW\_score = 32(Query Index = 377, Database Index = 385)

>gi|677286728|sp|Q8NH95.2|O13C6\_HUMAN RecName: Ful (len=151)

-- SW\_score = 23(Query Index = 377, Database Index = 150)

>gi|677286723|sp|P20303.2|GTR1\_PIG RecName: Full=S (len=492)

-- SW\_score = 26(Query Index = 377, Database Index = 491)

>gi|677286761|sp|Q96JK9.4|MAML3\_HUMAN RecName: Ful (len=1138)

-- SW\_score = 39(Query Index = 377, Database Index = 1137)

>gi|694016578|sp|C0HJE6.1|PORA\_CORAY RecName: Full (len=386)

-- SW\_score = 29(Query Index = 377, Database Index = 385)

>gi|667467199|sp|B3EWZ2.1|USOM8\_ACRMI RecName: Ful (len=214)

-- SW\_score = 34(Query Index = 377, Database Index = 213)

>gi|667467198|sp|B8WI85.1|USOM7\_ACRMI RecName: Ful (len=422)

-- SW\_score = 36(Query Index = 377, Database Index = 421)

>gi|667467197|sp|B8VIX3.1|USOM6\_ACRMI RecName: Ful (len=436)

-- SW\_score = 30(Query Index = 377, Database Index = 435)

>gi|667467196|sp|B8VIU6.1|USOM5\_ACRMI RecName: Ful (len=256)

-- SW\_score = 35(Query Index = 377, Database Index = 255)

>gi|667467195|sp|B8UU74.1|USOM4\_ACRMI RecName: Ful (len=204)

-- SW\_score = 31(Query Index = 377, Database Index = 203)

>gi|667467194|sp|B8RJM0.1|USOM3\_ACRMI RecName: Ful (len=433)

-- SW\_score = 32(Query Index = 377, Database Index = 432)

>gi|667467193|sp|B7WFQ1.1|USOM2\_ACRMI RecName: Ful (len=505)

-- SW\_score = 26(Query Index = 377, Database Index = 504)

>gi|667467192|sp|B3EX00.1|USOM1\_ACRMI RecName: Ful (len=448)

-- SW\_score = 30(Query Index = 377, Database Index = 447)

>gi|667467190|sp|B3EWZ7.1|TRP\_ACRMI RecName: Full= (len=288)

-- SW\_score = 36(Query Index = 377, Database Index = 287)

>gi|667467184|sp|B3EWZ4.1|SAP2\_ACRMI RecName: Full (len=165)

-- SW\_score = 28(Query Index = 377, Database Index = 164)

>gi|667467183|sp|B3EWZ1.1|SAP1B\_ACRMI RecName: Ful (len=142)

-- SW\_score = 35(Query Index = 377, Database Index = 141)

>gi|667467182|sp|B3EWZ0.1|SAP1A\_ACRMI RecName: Ful (len=168)

-- SW\_score = 28(Query Index = 377, Database Index = 167)

>gi|667467181|sp|B3EWY8.1|SAAR2\_ACRMI RecName: Ful (len=390)

-- SW\_score = 34(Query Index = 377, Database Index = 389)

>gi|667467180|sp|B3EWY6.1|SAAR1\_ACRMI RecName: Ful (len=386)

-- SW\_score = 33(Query Index = 377, Database Index = 385)

>gi|667467176|sp|A8W7I5.3|INUE\_PICGM RecName: Full (len=514)

-- SW\_score = 30(Query Index = 377, Database Index = 513)

>gi|667467171|sp|A2EF58.2|PFP3\_TRIVA RecName: Full (len=387)

-- SW\_score = 37(Query Index = 377, Database Index = 386)

>gi|667467170|sp|Q5JN42.2|PSD2\_ORYSJ RecName: Full (len=593)

-- SW\_score = 43(Query Index = 377, Database Index = 592)

>gi|667467169|sp|Q5N8Q3.2|PSS3\_ORYSJ RecName: Full (len=419)

-- SW\_score = 29(Query Index = 377, Database Index = 418)

>gi|667467167|sp|Q0JR55.2|PSS1\_ORYSJ RecName: Full (len=425)

-- SW\_score = 40(Query Index = 377, Database Index = 424)

>gi|667467152|sp|B8UU59.1|PK1L\_ACRMI RecName: Full (len=3029)

-- SW\_score = 36(Query Index = 377, Database Index = 3028)

>gi|667467110|sp|B3EWZ9.1|HEPHL\_ACRMI RecName: Ful (len=1114)

-- SW\_score = 33(Query Index = 377, Database Index = 1113)

>gi|667467108|sp|B8UU51.1|GXN2\_ACRMI RecName: Full (len=275)

-- SW\_score = 33(Query Index = 377, Database Index = 274)

>gi|667467107|sp|B8VIW9.1|FP\_ACRMI RecName: Full=F (len=1280)

-- SW\_score = 47(Query Index = 377, Database Index = 1279)

>gi|667467105|sp|B8UU78.1|ELP\_ACRMI RecName: Full= (len=1124)

-- SW\_score = 35(Query Index = 377, Database Index = 1123)

>gi|667467104|sp|B3EWZ8.1|ECT\_ACRMI RecName: Full= (len=400)

-- SW\_score = 34(Query Index = 377, Database Index = 399)

>gi|667467102|sp|B8V7Q1.1|PCDL\_ACRMI RecName: Full (len=4467)

-- SW\_score = 46(Query Index = 377, Database Index = 4466)

>gi|667467099|sp|C0HJC1.1|PA2\_BOTLA RecName: Full= (len=122)

-- SW\_score = 23(Query Index = 377, Database Index = 121)