BLAST参数

Bian Yang

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-p Program Name [String]

- 选择程序
- blastn是用核酸序列搜索核酸序列数据库
- blastp是用蛋白序列搜索蛋白序列数据库
- blastx是将提交的核酸序列按照6个ORF翻译后搜索蛋白序列数据库
- tblastn是将提交的蛋白序列在核酸序列数据库中的核酸序列以6种ORF动态翻译后产生的蛋白序列中进行搜索
- tblastx是将提交的核酸序列按6种ORF翻译成蛋白后在核酸序列数据库中的核酸序列以6种ORF翻译后产生的蛋白序列中进行搜索。

- -i Query File [File In]
- default = stdin
- 待搜索的序列文件，默认为stdin
- -o Final output file name [File Out] Optional
- default = stdout
- 搜索结果输出文件，默认为 stdout

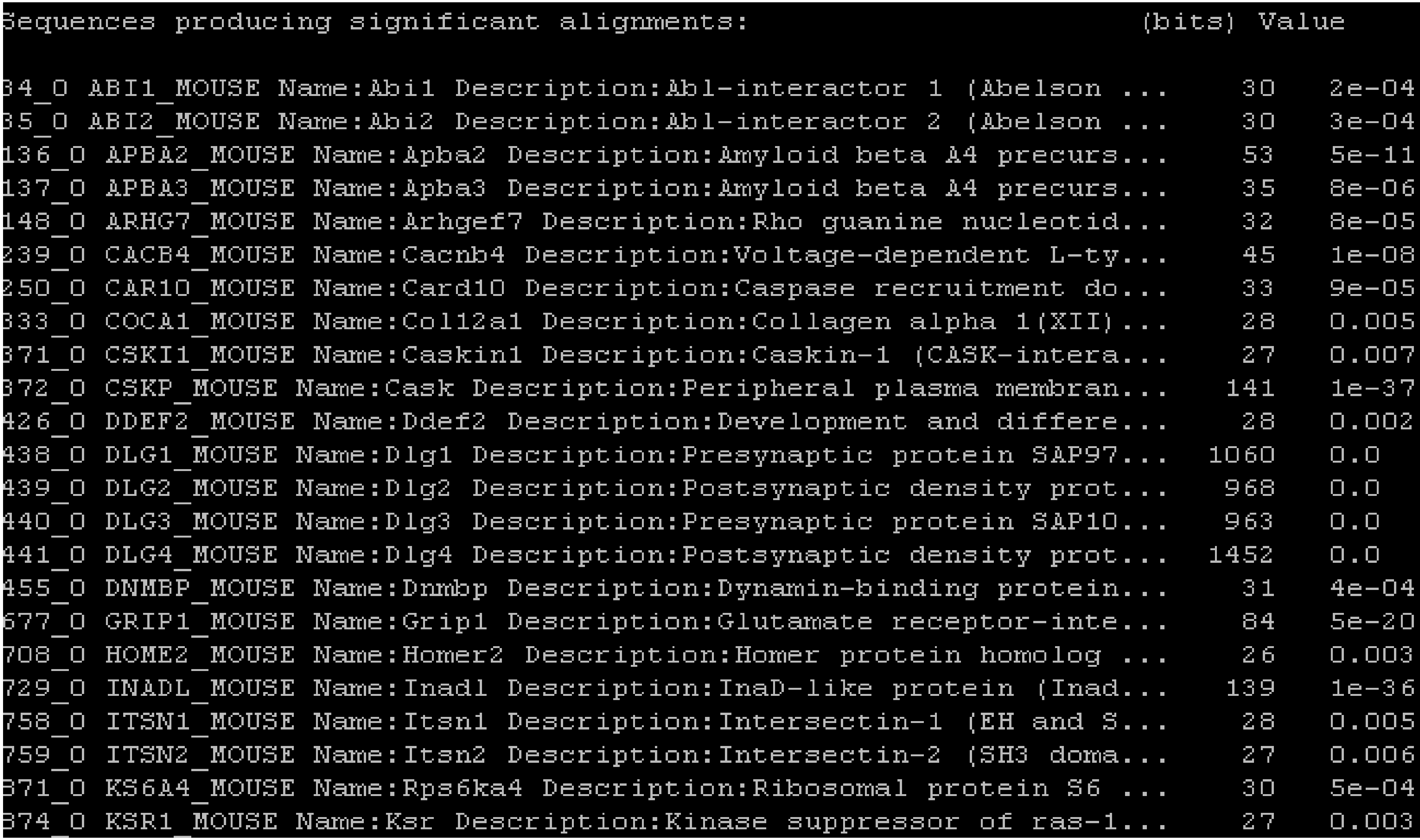
-d Database name (if not set, second sequence FASTA must be provided) [String] Optional

- 选择数据库 （如果没有设定就必须提供第二个FASTA序列文件）
- default = stdin

-j Subject File (for sequence sets comparison)

- 不用建好的数据库，而直接在含有多个序列的FASTA文件中进行blast
- 结果不按打分排序，而是按照FASTA文件中的顺序把每一条序列的bit score和e value都列举出来

-j结果不按打分和期望值排序, 而是按照FASTA文件中的原顺序排列



```
Sequences producing significant alignments:                          (bits) Value

34_0 ABI1_MOUSE Name:Abi1 Description:Abl-interactor 1 (Abelson ...    30   2e-04
35_0 ABI2_MOUSE Name:Abi2 Description:Abl-interactor 2 (Abelson ...    30   3e-04
136_0 APBA2_MOUSE Name:Apba2 Description:Amyloid beta A4 precurs...    53   5e-11
137_0 APBA3_MOUSE Name:Apba3 Description:Amyloid beta A4 precurs...    35   8e-06
148_0 ARHG7_MOUSE Name:Arhgef7 Description:Rho guanine nucleotid...    32   8e-05
239_0 CACB4_MOUSE Name:Cacnb4 Description:Voltage-dependent L-ty...    45   1e-08
250_0 CAR10_MOUSE Name:Card10 Description:Caspase recruitment do...    33   9e-05
333_0 COCA1_MOUSE Name:Col12a1 Description:Collagen alpha 1(XII)...    28   0.005
371_0 CSKI1_MOUSE Name:Caskin1 Description:Caskin-1 (CASK-intera...    27   0.007
372_0 CSKP_MOUSE Name:Cask Description:Peripheral plasma membran...   141   1e-37
426_0 DDEF2_MOUSE Name:Ddef2 Description:Development and differe...    28   0.002
438_0 DLG1_MOUSE Name:Dlg1 Description:Presynaptic protein SAP97...  1060   0.0
439_0 DLG2_MOUSE Name:Dlg2 Description:Postsynaptic density prot...   968   0.0
440_0 DLG3_MOUSE Name:Dlg3 Description:Presynaptic protein SAP10...   963   0.0
441_0 DLG4_MOUSE Name:Dlg4 Description:Postsynaptic density prot...  1452   0.0
455_0 DNMBP_MOUSE Name:Dnmbp Description:Dynamin-binding protein...    31   4e-04
677_0 GRIP1_MOUSE Name:Grip1 Description:Glutamate receptor-inte...    84   5e-20
708_0 HOME2_MOUSE Name:Homer2 Description:Homer protein homolog ...    26   0.003
729_0 INADL_MOUSE Name:Inadl Description:InaD-like protein (Inad...   139   1e-36
758_0 ITSN1_MOUSE Name:Itsn1 Description:Intersectin-1 (EH and S...    28   0.005
759_0 ITSN2_MOUSE Name:Itsn2 Description:Intersectin-2 (SH3 doma...    27   0.006
871_0 KS6A4_MOUSE Name:Rps6ka4 Description:Ribosomal protein S6 ...    30   5e-04
874_0 KSR1_MOUSE Name:Ksr Description:Kinase suppressor of ras-1...    27   0.003
```

-I Query location offsets; format: “start stop”

- Applies only if query file contains 1 sequence [String] Optional
- 用查询序列的某一部分来进行blast时用来指定查询部分的位置，当输入文件只有一条序列的时候适用;
- 格式是: “start stop”，例如 -I “1 200”
- -J Subject location offsets; format: "start stop";
- Applies only if subject file (-j) contains 1 sequence [String] Optional
- 用于指定用-j参数指定的subject file中序列界限; 只有subject file仅含一条序列时适用;格式为: "start stop"。

-e Expected value [Real]

- 期望值
- 描述搜索某一特定数据库时，随机出现的匹配序列数目
- default = 10.0 默认为10.0

修改-e的值，可以改变搜索到的序列条数

e value	10	1	1.00E-004	1.00E-020
seq num	216	173	104	32

- -F Filter query sequence
- 过滤查询序列，将那些影响比对结果的低复杂度区域过滤掉。
- (DUST with blastn, SEG with others) [String] 用blastn时用DUST程序过滤，其他的用SEG过滤 。
- default = T
- -C Mask lower case [T/F]
- 屏蔽掉小写字母 [T/F]默认为F
- default = F

- -G Gap open penalty (-1 means default: non-affine if greedy; 5 if dyn. prog.) [Integer]
- default = -1
- 起始空位罚分
- -E Gap extension penalty (-1 means default: non-affine if greedy; 2 otherwise) [Integer]
- default = -1
- 延伸空位罚分

- -Q Genetic code for translation of the query sequence [Integer]
- 翻译查询序列所用的遗传密码表，默认为0
- default = 0
- -D Genetic code for translation of the database [Integer]
- 数据库序列翻译所用的遗传密码表，默认为0
- default = 0

-m alignment view options 比对结果的输出选项

- 0 = pairwise, ,显示具体成对匹配信息，default = 0
- 1 = query-anchored showing identities,查询-比上区域，显示一致性
- 2 = query-anchored no identities,查询-比上区域,不显示一致性
- 3 = flat query-anchored, show identities,查询-比上区域的屏文形式，显示一致性
- 4 = flat query-anchored, no identities,查询-比上区域的屏文形式，不显示一致性
- 5 = query-anchored no identities and blunt ends,查询-比上区域，不显示一致性，无突然的结束

- 6 = flat query-anchored, no identities and blunt ends, 查询-比上区域的屏文形式，不显示一致性，无突然的结束
- 7 = XML Blast output,XML格式的输出
- 8 = tabular, TAB格式的输出
- 9 tabular with comment lines带注释行的TAB格式的输出
- 10 ASN, text本方式的ASN格式输出
- 11 ASN, binary [Integer]二进制方式的ASN格式输出

0 = pairwise, default

- Query= DLG4_MOUSE (Dlg4) Postsynaptic density protein 95 (PSD-95)
- (Synapse-associated protein 90) (SAP90) (Discs large homolog 4). (724
- aa) (Tax_id: 10090)   (724 letters)
- Score   E
- Sequences producing significant alignments: (bits) Value
- DLG4_MOUSE Name:Dlg4 Description:Postsynaptic density ...   1452   0.0
- DLG4_HUMAN Name:DLG4 Description:Postsynaptic density ... 1447   0.0
- ~~~~~~~
- >DLG4_MOUSE Name:Dlg4 Description:Postsynaptic density protein 95   (PSD-95) (Synapse-associated protein 90) (SAP90) (Discs large homolog 4). TaxID:10090   Length = 724
- Score = 1452 bits (3759), Expect = 0.0
- Identities = 724/724 (100%), Positives = 724/724 (100%)
- Query: 1   MDCLCIVTTKKYRYQDEDTPPLEHSPAHL 30
- MDCLCIVTTKKYRYQDEDTPPLEHSPAHL
- Sbjct: 1   MDCLCIVTTKKYRYQDEDTPPLEHSPAHL 30

1 = query-anchored showing identities,查询-比上区域，显示一致性（圆点表示相同的残基，短横线表示空位插入，反斜线下加一竖线下面的序列是插入到反斜线位置的）

```
1_0     1   MDCLCIVTTKKYRYQDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGE 60
2382    1   ............................................................ 60
2381    1   ............................................................ 60
2383    1   ............................................................ 60
2380    71            ....H..E....Q.......QMHV..AKP.LLPSGH..Y.ATSM..MD.D 148
                                          \                       \
                                          |                        |
                  STGKSAEMLHLGDSGHAPIDGIHAYT                      TL
2371    194                                ...P...L....S..T.T.---....DAD 219
2370    194                                ...P...L....S..T.T.---....DAD 219
2367    107                 .ES..SPST.LSN.Y...P...V...ES.DSAP.---.....AD 154
                                            \
                                            |
                                     PQSPVSV
```

2 = query-anchored no identities,查询比上区域，不显示一致性（相同残基不再用圆点表示）

- 1_0 1 MDCLCIVTTKKYRYQDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGE 60
- 2382 1 MDCLCIVTTKKYRYQDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGE 60
- 2381 1 MDCLCIVTTKKYRYQDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGE 60
- 2383 1 MDCLCIVTTKKYRYQDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGE 60
- 2380 71 KYRYHDEETPPLQHSPAHLPQMHVSPAKPVLLPSGHAPYYATSMNGMDGD 148
- \ \
- | |
- STGKSAEMLHLGDSGHAPIDGIHAYT TL
- 2371 194 QANPPPVLVNTDSLETPTY---VNGTDAD 219
- 2370 194 QANPPPVLVNTDSLETPTY---VNGTDAD 219
- 2367 107 EESPPSPSTPLSNPYQANPPPVVVNTESLDSAPY---VNGTEAD 154
- \
- |
- PQSPVSV

3 = flat query-anchored, show identities,,查询-比上区域的屏文形式，显示一致性（没有反斜线插入，而是用空位插入）

```
•  1_0   1     MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------- 29
•  2382  1     .........--..---.................-.------------------------- 29
•  2381  1     .........--..---.................-.------------------------- 29
•  2383  1     .........--..---.................-.------------------------- 29
•  2380  71                .---...H..E....Q.....-.STGKSAEMLHLGDSGHAPIDGIHAY 114
•  2367  107                        .ES..SPST.LS-N------------------------- 119
•  2372  180                           .VPAE..VV-.------------------------- 189
•  2373  61       ..LS..--DSPHS.....D.S..P...FPR-.------------------------- 89
•  2376  5      .Y.ALR.NV..---.......G.H-D..LPR-.------------------------- 32
•  2374  5      .Y.ALR.NV..---.......A.H-D..LPR-.------------------------- 32
•  2375  5      .Y.ALR.NV..---.......G.H-D..LPR-.------------------------- 32
•  2369  461                              Q.ATPM-V------------------------- 467
•  4656  1580                          .D..PI.S---------------------------- 1587
•  4655  1581                          .D..PI.S---------------------------- 1588
```

4 = flat query-anchored, no identities,查询-比上区域的屏文形式，不显示一致性

- 1_0 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------ 29
- 2382 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------ 29
- 2381 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------ 29
- 2383 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------ 29
- 2380 71 K---YRYHDEETPPLQHSPAH-LSTGKSAEMLHLGDSGHAPIDGIHAY 114
- 2367 107 EESPPSPSTPLS-N------------------------ 119
- 2372 180 PVPAESPVV-L------------------------ 189
- 2373 61 LCLSTT--DSPHSYRYQDDDSPPPEHSFPR-L------------------------ 89
- 2376 5 CYCALRTNVKK---YRYQDEDGPH-DHSLPR-L------------------------ 32
- 2374 5 CYCALRTNVKK---YRYQDEDAPH-DHSLPR-L------------------------ 32
- 2375 5 CYCALRTNVKK---YRYQDEDGPH-DHSLPR-L------------------------ 32
- 2369 461 QHATPM-V------------------------ 467
- 4656 1580 PDLEPIPS--------------------------- 1587
- 4655 1581 PDLEPIPS--------------------------- 1588

5 = query-anchored no identities and blunt ends,查询-比上区域，不显示一致性，无突然的结束（序列两端用空位（短横线）补齐）

```
2383  1     MDCLCIVTTKKYRYQDEDTPPLEHSPAHLPNQANSPPVIVNTDTLEAPGYELQVNGTEGE 60
2380  71    ----------KYRYHDEETPPLQHSPAHLPQMHVSPAKPVLLPSGHAPYYATSMNGMDGD 148
                                         \                       \
                                         |                       |
                STGKSAEMLHLGDSGHAPIDGIHAYT                      TL
2371  194   -------------------------------QANPPPVLVNTDSLETPTY---VNGTDAD 219
2370  194   -------------------------------QANPPPVLVNTDSLETPTY---VNGTDAD 219
2367  107   ----------------EESPPSPSTPLSNPYQANPPPVVVNTESLDSAPY---VNGTEAD 154
                                           \
                                           |
                                     PQSPVSV
2372  180   -------------------PVPAESPVVLPSQANPPPVLVNTDSLETPTY---VNGTDAD 219
                                           \
                                           |
                                          TP
```

6=flat query-anchored, no identities and blunt ends,查询-比上区域的屏文形式，不显示一致性，无突然的结束

```
•   2381   1     MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------- 29
•   2383   1     MDCLCIVTT--KK---YRYQDEDTPPLEHSPAH-L------------------------- 29
•   2380   71    ------------K---YRYHDEETPPLQHSPAH-LSTGKSAEMLHLGDSGHAPIDGIHAY 114
•   2371         ------------------------------------------------------------
•   2370         ------------------------------------------------------------
•   2367   107   ---------------------EESPPSPSTPLS-N------------------------- 119
•   2372   180   ------------------------PVPAESPVV-L------------------------- 189
•   2373   61    ---LCLSTT--DSPHSYRYQDDDSPPPEHSFPR-L------------------------- 89
•   2368         ------------------------------------------------------------
•   2376   5     --CYCALRTNVKK---YRYQDEDGPH-DHSLPR-L------------------------- 32
•   2374   5     --CYCALRTNVKK---YRYQDEDAPH-DHSLPR-L------------------------- 32
•   2375   5     --CYCALRTNVKK---YRYQDEDGPH-DHSLPR-L------------------------- 32
•   2379         ------------------------------------------------------------
```

7 = XML Blast output,XML格式的输出

- <?xml version="1.0"?>
- <!DOCTYPE BlastOutput PUBLIC "-//NCBI//NCBI BlastOutput/EN" "http://www.ncbi.nlm.nih.gov/dtd/NCBI_BlastOutput.dtd">
- <BlastOutput>
-   <BlastOutput_program>blastp</BlastOutput_program>
-   <BlastOutput_version>blastp 2.2.15 [Oct-15-2006]</BlastOutput_version>
-   <BlastOutput_reference>~Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, ~Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), ~"Gapped BLAST and PSI-BLAST: a new generation of protein database search~programs", Nucleic Acids Res. 25:3389-3402.</BlastOutput_reference>
-   <BlastOutput_db>syndb</BlastOutput_db>
-   <BlastOutput_query-ID>lcl|1_0</BlastOutput_query-ID>
-   <BlastOutput_query-def>DLG4_MOUSE (Dlg4) Postsynaptic density protein 95 (PSD-95) (Synapse-associated protein 90) (SAP90) (Discs large homolog 4). (724 aa) (Tax_id: 10090)</BlastOutput_query-def>

8 = tabular, TAB格式的输出

- DLG4_MOUSE DLG4_MOUSE 100.00 724 0 0 1 724 1 724 0.0 1452
- DLG4_MOUSE DLG4_HUMAN 99.59 724 3 0 1 724 1 724 0.0 1447
- DLG4_MOUSE DLG4_RAT 99.45 724 4 0 1 724 1 724 0.0 1446
- DLG4_MOUSE DLG4_BRARE 75.54 744 139 7 11 724 71 801 0.0 1089
- DLG4_MOUSE DLG1_MOUSE 73.51 721 154 4 32 724 194 905 0.0 1060
- DLG4_MOUSE DLG1_HUMAN 73.47 720 155 4 32 724 194 904 0.0 1057
- DLG4_MOUSE DLG1L_BRARE 71.15 728 183 4 17 724 107 827 0.0 1050
- DLG4_MOUSE DLG1_RAT 70.83 744 166 6 20 7 24 180 911 0.0 1040
- DLG4_MOUSE DLG2_BRARE 62.74 824 201 7 4 724 61 881 0.0 1000
- DLG4_MOUSE DLG1_BRARE 70.50 695 184 4 31 724 199 873 0.0 978

9 tabular with comment lines带注释行的TAB格式的输出

- # BLASTP 2.2.15 [Oct-15-2006]
- # Query: DLG4_MOUSE (Dlg4) Postsynaptic density protein 95 (PSD-95) (Synapse-associated protein 90) (SAP90) (Discs large homolog 4). (724 aa) (Tax_id: 10090)
- # Database: syndb
- # Fields: Query id, Subject id, % identity, alignment length, mismatches, gap openings, q. start, q. end, s. start, s. end, e-value, bit score
- DLG4_MOUSE DLG4_MOUSE 100.00 724 0 0 1 724 1 724 0.0 1452
- DLG4_MOUSE DLG4_HUMAN 99.59 724 3 0 1 724 1 724 0.0 1447
- DLG4_MOUSE DLG4_RAT 99.45 724 4 0 1 724 1 724 0.0 1446
- DLG4_MOUSE DLG4_BRARE 75.54 744 139 7 11 724 71 801 0.0 1089
- DLG4_MOUSE DLG1_MOUSE 73.51 721 154 4 32 724 194 905 0.0 1060

10 ASN, text本方式的ASN格式输出

```
•  data
•    align {
•     {
•      type partial ,
•      dim 2 ,
•      score {
•       {
•        id
•         str "score" ,
•        value
•         int 3759 } ,
•       {
•        id
•         str "e_value" ,
•        value
•         real { 0, 10, 0 } } ,
•       {
```

- -H Produce HTML output [T/F]
- default = F
- 以HTML格式输出 [T/F]默认为 F
- -M Matrix [String]
- default = BLOSUM62
- 计分矩阵，默认是BLOSUM62

-M BLOSUN62（红色部分与80矩阵不同）

- Sequences producing significant alignments: (bits) Value
- DLG4_MOUSE Name:Dlg4 Description:Postsynaptic density protein 95... 1452 0.0
- DLG4_HUMAN Name:DLG4 Description:Postsynaptic density protein 95... 1447 0.0
- DLG4_RAT Name:Dlg4 Description:Postsynaptic density protein 95 (... 1446 0.0
- DLG4_BRARE Name:dlg4 Description:Postsynaptic density protein 95... 1089 0.0
- DLG1_MOUSE Name:Dlg1 Description:Presynaptic protein SAP97 (Syna... 1060 0.0
- DLG1_HUMAN Name:DLG1 Description:Presynaptic protein SAP97 (Syna... 1057 0.0
- DLG1L_BRARE Name:dlg1l Description:Synapse-associated protein 97... 1050 0.0
- DLG1_RAT Name:Dlg1 Description:Presynaptic protein SAP97 (Synaps... 1040 0.0
- DLG2_BRARE Name:dlg2 Description:Postsynaptic density protein 93... 1000 0.0
- DLG1_BRARE Name:dlg1 Description:Synapse-associated protein 97A ... 978 0.0
- DLG2_RAT Name:Dlg2 Description:Postynaptic density protein PSD-9... 976 0.0
- DLG2_HUMAN Name:DLG2 Description:Postsynaptic density protein PS... 969 0.0
- DLG2_MOUSE Name:Dlg2 Description:Postsynaptic density protein PS... 968 0.0
- DLG3_RAT Name:Dlg3 Description:Presynaptic protein SAP102 (Synap... 963 0.0
- DLG3_MOUSE Name:Dlg3 Description:Presynaptic protein SAP102 (Syn... 963 0.0

- DLG3_HUMAN Name:DLG3 Description:Presynaptic protein SAP102 (Syn...   956   0.0
- DLG1_DROME Name:dlg1 Description:Discs large-1 tumor suppressor ...   756   0.0
- MPP5_MOUSE Name:Mpp5 Description:MAGUK p55 subfamily member 5 (P...   190   2e-48
- MPP5_HUMAN Name:MPP5 Description:MAGUK p55 subfamily member 5. T...   188   9e-48
- CSKP_HUMAN Name:CASK Description:Peripheral plasma membrane prot...   149   5e-36
- CSKP_RAT Name:Cask Description:Peripheral plasma membrane protei...   149   6e-36
- CSKP_MOUSE Name:Cask Description:Peripheral plasma membrane prot...   141   9e-34
- INADL_MOUSE Name:Inadl Description:InaD-like protein (Inadl prot...   139   5e-33
- MPP3_MOUSE Name:Mpp3 Description:MAGUK p55 subfamily member 3 (M...   137   2e-32
- MPDZ_RAT Name:Mpdz Description:Multiple PDZ domain protein (Mult...   136   3e-32
- CAKI_DROME Name:Caki Description:Calcium/calmodulin-dependent pr...   135   5e-32
- MPDZ_MOUSE Name:Mpdz Description:Multiple PDZ domain protein (Mu...   134   2e-31
- MPDZ_HUMAN Name:MPDZ Description:Multiple PDZ domain protein (Mu...   130   2e-30
- LAP4_DROME Name:scrib Description:LAP4 protein (Scribble protein...   125   5e-29
- MPP4_MOUSE Name:Mpp4 Description:MAGUK p55 subfamily member 4 (D...   116   4e-26
- PDZK1_PONPY Name:PDZK1 Description:PDZ domain containing protein...   99   7e-21
- PDZK1_HUMAN Name:PDZK1 Description:PDZ domain containing protein...   99   7e-21

-M BLOSUM80

- equences producing significant alignments: (bits) Value
- DLG4_MOUSE Name:Dlg4 Description:Postsynaptic density protein 95... 1860 0.0
- DLG4_HUMAN Name:DLG4 Description:Postsynaptic density protein 95... 1853 0.0
- DLG4_RAT Name:Dlg4 Description:Postsynaptic density protein 95 (... 1851 0.0
- DLG4_BRARE Name:dlg4 Description:Postsynaptic density protein 95... 1378 0.0
- DLG1_MOUSE Name:Dlg1 Description:Presynaptic protein SAP97 (Syna... 1330 0.0
- DLG1_HUMAN Name:DLG1 Description:Presynaptic protein SAP97 (Syna... 1323 0.0
- DLG1L_BRARE Name:dlg1l Description:Synapse-associated protein 97... 1310 0.0
- DLG1_RAT Name:Dlg1 Description:Presynaptic protein SAP97 (Synaps... 1303 0.0
- DLG2_BRARE Name:dlg2 Description:Postsynaptic density protein 93... 1248 0.0
- DLG1_BRARE Name:dlg1 Description:Synapse-associated protein 97A ... 1214 0.0
- DLG2_RAT Name:Dlg2 Description:Postynaptic density protein PSD-9... 1212 0.0
- DLG2_HUMAN Name:DLG2 Description:Postsynaptic density protein PS... 1203 0.0
- DLG3_RAT Name:Dlg3 Description:Presynaptic protein SAP102 (Synap... 1202 0.0
- DLG3_MOUSE Name:Dlg3 Description:Presynaptic protein SAP102 (Syn... 1202 0.0

- DLG2_MOUSE Name:Dlg2 Description:Postsynaptic density protein PS... 1202 0.0
- DLG3_HUMAN Name:DLG3 Description:Presynaptic protein SAP102 (Syn... 1191 0.0
- DLG1_DROME Name:dlg1 Description:Discs large-1 tumor suppressor ... 917 0.0
- MPP5_MOUSE Name:Mpp5 Description:MAGUK p55 subfamily member 5 (P... 198 9e-51
- MPP5_HUMAN Name:MPP5 Description:MAGUK p55 subfamily member 5. T... 197 2e-50
- INADL_MOUSE Name:Inadl Description:InaD-like protein (Inadl prot... 156 6e-38
- CSKP_HUMAN Name:CASK Description:Peripheral plasma membrane prot... 149 6e-36
- MPDZ_RAT Name:Mpdz Description:Multiple PDZ domain protein (Mult... 148 9e-36
- CAKI_DROME Name:Caki Description:Calcium/calmodulin-dependent pr... 146 6e-35
- MPDZ_MOUSE Name:Mpdz Description:Multiple PDZ domain protein (Mu... 145 8e-35
- CSKP_RAT Name:Cask Description:Peripheral plasma membrane protei... 144 1e-34
- LAP4_DROME Name:scrib Description:LAP4 protein (Scribble protein... 136 6e-32
- MPP4_MOUSE Name:Mpp4 Description:MAGUK p55 subfamily member 4 (D... 123 3e-28
- MPDZ_HUMAN Name:MPDZ Description:Multiple PDZ domain protein (Mu... 121 2e-27
- MPP3_MOUSE Name:Mpp3 Description:MAGUK p55 subfamily member 3 (M... 116 4e-26
- SYJ2B_RAT Name:Synj2bp Description:Synaptojanin 2 binding protei... 102 9e-22
- SYJ2B_HUMAN Name:SYNJ2BP Description:Synaptojanin 2 binding prot... 100 3e-21

- -q Penalty for a nucleotide mismatch (blastn only) [Integer]
- default = -3
- 核酸序列比对时的错配罚分 (仅用于blastn)默认是-3
- -r Reward for a nucleotide match (blastn only) [Integer]
- default = 1
- 核酸序列比对时每比对上一个碱基的得分(仅用于blastn)默认为1

- -k Pattern for PHI BLAST [String] Optional
- 做PHI BLAST（Patternn Hit Initiated BLAST）时，待搜索蛋白序列中含有的pattern [String] Optional
- PHI-BLAST can do a restricted protein pattern search.   Pattern-Hit Initiated (PHI)-BLAST is designed to search for proteins that contain a pattern specified by the user AND are similar to the query sequence in the vicinity of the pattern. This dual requirement is intended to reduce the number of database hits that contain the pattern, but are likely to have no true homology to the query.

- -W Word size, default if 0 (blastn 11, others 3) [Integer]
- Word size, 默认为0(blastn 核酸为11, 蛋白质为 3)
- default = 0
- -P Identity percentage cut-off [Real]
- default = 0
- 一致序列百分比的最低界限，默认为 0
- -u Do only ungapped alignment (always TRUE for tblastx) [T/F] default = F
- 仅做无空位插入的比对 (在进行tblastx时始终为真，其他默认为假)

-P 90

- # BLASTP 2.2.15 [Oct-15-2006]
- # Query: DLG4_MOUSE (Dlg4) Postsynaptic density protein 95 (PSD-95) (Synapse-associated protein 90) (SAP90) (Di
- scs large homolog 4). (724 aa) (Tax_id: 10090)
- # Database: syndb
- # Fields: Query id, Subject id, % identity, alignment length, mismatches, gap openings, q. start, q. end, s. st
- art, s. end, e-value, bit score
- DLG4_MOUSE DLG4_MOUSE 100.00 724 0 0 1 724 1 724 0.0 1452
- DLG4_MOUSE DLG4_HUMAN 99.59 724 3 0 1 724 1 724 0.0 1447
- DLG4_MOUSE DLG4_RAT 99.45 724 4 0 1 724 1 724 0.0 1446

- -b Number of database sequence to show alignments for (B) [Integer] default = 250
- 显示比对细节的序列条数。
- -a Number of threads to use in preliminary search stage [Integer] default = 1
- 初步搜索阶段的线程数，默认为1
- -n Show gis in sequence ids [T/F]
- 在序列ID中显示GI号
- default = F
- -N Show only accessions for sequence ids in tabular output [T/F] default = F
- 在列表输出时仅显示序列的ACCESSION号作为ID