

BLAST参数

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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:Dnmdbp 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



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      KYRYHDEETPPLQHSPAHLPMHVSPAKPVLLPSGHAPYYATSMNGMDGD 148
•
•           \           \
•           |           |
•
•      STGKSAEMLHLGDSGHAPIDGIHAYT           TL
•
• 2371 194           QANPPPVLVNTDSLETPTY---VNGTDAD 219
•
• 2370 194           QANPPPVLVNTDSLETPTY---VNGTDAD 219
•
• 2367 107          EESPPSPSTPLSNPYQANPPPVVNTESLDSAPY---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---YRYQDETPPLEHSPAHL----- 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.AL.R.NV..---.....G.H-D..LPR-.----- 32
- 2374 5 .Y.AL.R.NV..---.....A.H-D..LPR-.----- 32
- 2375 5 .Y.AL.R.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---YRYQDEDTPPLEHSPAHL----- 29
- 2382 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAHL----- 29
- 2381 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAHL----- 29
- 2383 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAHL----- 29
- 2380 71 K---YRYHDEETPPLQHSPAHLSTGKSAEMLHLGDSGHAPIDGIHAY  
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 -----KYRYHDEETPPLQHSPAHLPMHVSPAKPVLLPSGHAPYYATSMNGMDGD 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---YRYQDEDTPPLEHSPAHL----- 29
- 2383 1 MDCLCIVTT--KK---YRYQDEDTPPLEHSPAHL----- 29
- 2380 71 -----K---YRYHDEETPPLQHSPAHLSTGKSAEMLHLGDSGHAPIDGIHAY 114
- 2371 -----
- 2370 -----
- 2367 107 -----EESPPSPSTPLSN----- 119
- 2372 180 -----PVPAESPVV-L----- 189
- 2373 61 ---LCLSTT--DSPHSYRYQDDSPPEHSFPR-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), ~&quot;Gapped BLAST and PSI-BLAST: a new generation of protein database search~programs&quot;, 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

- sequences 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