

表2 cDNA克隆有效序列比对结果

Table 2 Result of comparison of effective sequences of cDNA clones

克隆号 Clone	登录号 Locus	评分 Score	E 值 E-value	功能预测 Function predictions
Contig1	gb BT102973.1	252	2e-63	Picea glauca clone GQ0204_E15 mRNA sequence(blastn 结果)
Contig2	ref XP_002489002.1	78.6	3e-07	hypothetical protein SORBIDRAFT_0531s002010 [Sorghum bicolor]
S1	gb ACY06319.1	95.5	2e-18	class II chitinase 2-3 [Pseudotsuga menziesii]
S2				No hit found
S3	gb ACF06522.1	135	4e-30	60S ribosomal protein L44 [Elaeis guineensis]
S4	gb FJ071360.1	219	2e-53	Pinus taeda isolate 1658 anonymous locus 0_3696_01 genomic sequence
S5	ref NP_001168316.1	111	1e-22	hypothetical protein LOC100382082 [Zea mays]
S6	gb ADE77919.1	127	1e-27	unknown [Picea sitchensis]
S7	gb ADM78576.1	56.6	1e-06	glycosyl hydrolase-like protein [Picea sitchensis]
S8	gb BT122572.1	279	3e-72	Picea sitchensis clone WS0452_O03 unknown mRNA(blastn 结果)
S9				No hit found
S10	gb ADE76290.1	153	1e-35	unknown [Picea sitchensis]
S11				No hit found