

Figure S3

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>tr|Q7M0H5|Q7M0H5_CRIGR SubName: Full=Cre recombinase protein;
      Length = 350

Score = 144 bits (362), Expect = 2e-32, Method: Compositional matrix adjust.
Identities = 104/330 (31%), Positives = 174/330 (52%), Gaps = 23/330 (6%)

Socre: 58 EITQAKLKHFLDNGHRTRRA---NTWRALMSRWAKFESWCLTNNLTPLPATPEVVATFIE 114
      + T +++ L + R R+A +TW+ L+S + +WC NN PA PE V ++
Cre : 24 DATSDEVKRNLMDFRDRQAFSEHTWKMLLSVCRSAAWCKLNNRKFPAEPEDVRDYLL 83

Socre: 115 YYQAS--SYTTLsqYAWAINsfHVECGLLSPVSSKTVQDKQNEIRIVKLESGGLAQEQAT 172
      Y QA + T+ Q+ +N H GL P S V IR +++G A+ QA
Cre : 84 YLQARGLAVKTIQqHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGERAK-QAL 142

Socre: 173 PFRLHHLQMLIESYGESERLLDKRNLALLNIAYESLLRESELLRIKVGHLKSTFEGDYVL 232
      F + S+R D RNLA L IAY +LLR +E+ RI+V + T G ++
Cre : 143 AFERTDFDQVRSLMENSdRCQDIRNLAFLGIAYNTLLRIAETARIRVKDISRTDGGRLMI 202

Socre: 233 SVPYTKT--NDSGEEVVNITPLGF-KLIQRYIQGAGLTKE--DYLFQPIGRSNKVSVOA 287
      + TKT + +G E+ ++ LG KL++R+I +G+ + +YLF + R N V+ +
Cre : 203 HIGRTKTLVSTAGVEKALS---LGVTKLVERWISVSGVADDPNNYLFCRV-RKNGVAAPS 258

Socre: 288 KP--MSTRTVDRVF-----LWAFESLGIDRHSaWSGHSARIGAAQDLAAGYSIAQIQE 339
      +STR ++ +F ++ + R+ AWSGHSAR+GAA+D+ AG SI +I +
Cre : 259 ATSQLSTRALEGIFeATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQ 318

Socre: 340 NGRWKSpmMVLRYGKDIKAKESAMAKMLAE 369
      G W + +V+ Y +++ ++ AM ++L +
Cre : 319 AGGWTNVNIVMNYIRnLDSETGAMVRLLED 348
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