alignment of Prs proteins

```
AER083Cp       M----------RKCKVFMGTSHPELGKLVCEKLGIEPAPCTLKKFANGETSVQIGVSVRDEDVYVIQSGSST--INDHIMELLILVSACK 78
AGR371Cp       MSS--------NSIKLLAGNSHPDLAEKVSVRLGVPLSKIGVYHYSNKETSVTIGESIRDEDVYIIQTGTGEQEINDFLMELLIMIHACR 82
AGL080Cp       MAT--------NAIKLLAPDIHRGLAELVAKRLGLRLTDCKLKRDCNGEATFSIGESVRDQDIYIII-TQVGSGDVNDRVLELLIMINASK 81
ADR314Cp       MN----------NIIVFAGSSHPSLVNKICENLSIRPAEVKLGKFSNGETSINIGESVREKDVYVIQSGCG--HVNDNFMELLILINACK 78
Sc_Prs1        M----------RKCKIFVGNSHPELGNMVCQRLGIEPAPCTLKKFANGETSVQIGVSVRDEDVYVIQSGSPS--INDDIMELLILVSACR 78
Sc_Prs2        MST--------NSIKLLAGNSHPGLAELISQRLGVPLSKVGVYQYSNKETSVTIGESIRDEDVYIIQTGYGEHEINDFLMELLILIHACK 82
Sc_Prs3        MPT--------NSIKLLAPDVHRGLAELVAKRLGLQLTSSKLKRDPTGEVSFSIGESVRDQDIFII-TQIGSGVVNDRVLELLIMINASK 81
Sc_Prs4        MNSESREDMAINSIKLLAGNSHPDLAEQISKKLGIPLSKVGVYQYSNKETSVTIGESLRDEDVYIIQTGIGEQEINDFLMELLILIHACQ 90
Sc_Prs5        MS---------MSNIVVFGGDSHPELVTKICENLDIHPSKVELGKFSNGETNIALRESVREKDVYIIQSGCG--QVNDTFMQLLILISACK 80
B. subtilis_prs MSNQYGD----KNLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQS--TSDPVNEHIMELLIMVDALK 84

AER083Cp       GGSARKVTAVIPQFPYSKQ-----------CKMKKH------------------------------------------------ 103
AGR371Cp       SASARKITAVIPNFPYARQDK----------KDK------------------------------------------------------ 106
AGL080Cp       TASARRITAVIPNFPYARQDR----------KDK------------------------------------------------------ 105
ADR314Cp       TSSASRVTAVMPYFKCYSRQPDIPYTAKGAPLISKARKA---GEKGAEAVESVLTTQKPVSQSARKSIELAIENSISTLQLGESAPVRAKL 165
Sc_Prs1        GGSARKITAVIPQFPYSKQ-----------CKMKRH------------------------------------------------ 103
Sc_Prs2        TASVRRITAVIPNFPYARQDK----------KDK------------------------------------------------------ 106
Sc_Prs3        TASARRITAIIPNFPYARQDR----------KDK------------------------------------------------------ 105
Sc_Prs4        IASARKITTVIPNFPYARQDK----------KDK------------------------------------------------------ 114
Sc_Prs5        SASASRVTAVMPYLCYSRQPDIPYTAKGAPIISKPKENYTFESHPGTPVSSSLMTQRPGAESSLKSLDSAIRSTIN---LENPQPIRTPN 167
B. subtilis_prs RASAKTINIVIPYYGYARQDR----------KAR------------------------------------------------------ 108

AER083Cp       ------------------RGAI--------------------------------TARMLANLLIIAGADHVVSMDLHASQMQGFFTKPVD 143
AGR371Cp       ------------------SRAPI--------------------------------TAKLVAKMLETAGCNHVITMDLHASQIQGFFHIPVD 147
AGL080Cp       ------------------SRAPI--------------------------------TAKLMADMLTTAGCDHVITMDLHASQIQGFFDVPVD 146
ADR314Cp       EHSGSN-----------SRIPVIQ--KHEEASSSEAAGTAFNSNNSSYKLWVAQSGTLVANLLTTAGADHVITMDLHDPQFQGFFSIGVD 242
Sc_Prs1        ------------------RGAI--------------------------------TARMLANLLVMAGADHVVSMDLHASQMQGFFTKPVD 143
Sc_Prs2        ------------------SRAPI--------------------------------TAKLIANLLETAGCDHVITMDLHASQIQGFFHIPVD 147
Sc_Prs3        ------------------SRAPI--------------------------------TAKLMADMLTTAGCDHVITMDLHASQIQGFFDVPVD 146
Sc_Prs4        ------------------SRAPI--------------------------------TAKLVANLLQTAGADHVITMDLHASQIQGFFHIPVD 155
Sc_Prs5        SSATANNNFDIKKTLSFSRIPMIPGGKLQNTSNSTDAGELFNAQNAGYKLWVVQAGTLIAHLLSAAGADHVITMDLHDPQFPGFFDIPVD 257
B. subtilis_prs ------------------SREPI--------------------------------TAKLFANLLETAGATRVIALDLHAPQIQGFFDIPID 149

AER083Cp       NLYGGPSLAKWIRENVEDYQHAVVVSKNPGGTKRVTALADSLKINFAMIHTDRRRSKDLYSQTKDMKQLRMRKQSMLRKNRPIVRPGAAE 233
AGR371Cp       NLYAEPNILHYIQ-HNVDFQNSMLVAPDAGSAKRTSTLSDKLNLNFALIHKER---------------------------------- 199
AGL080Cp       NLYAEPSVVKYIKEH-IPHDDAIIISPDAGGAKRASLLSDRLNLNFALIHKER---------------------------------- 198
ADR314Cp       NLYCKPLIQAYIQHRIPEYKDAVIVSPDSGGVKRSSKVADALGLPFALIHKER-------------------SQILKGPP--------- 304
Sc_Prs1        NLYGGPSLAKWIRENVEDYEDAVVVSKNPGGTKRVTALADSLKINFAMIHTDRRRSKDLYSQNKDLQQLKLRKQSMLRKNRPIIRQGDHP 233
Sc_Prs2        NLYGEPSVLNYIRT-KTDFNNAILVSPDAGGAKRVASLADKLDMNFALIHKER---------------------------------- 199
Sc_Prs3        NLYAEPSVVRYIKEN-VNYMDSIIISPDAGGAKRAATLADRLDLNFALIHKER---------------------------------- 198
Sc_Prs4        NLYAEPSVLNYIRARKTDFDNAILVSPDAGGAKRVAALADKLDLNFALIHKER---------------------------------- 208
Sc_Prs5        NLYCKPIAQNYIQHRIPDYQDAVIVSPDAGGAKRATAIADALELSFALIHKER-------------------SQLLKGPP--------- 319
B. subtilis_prs HLMGVPILGEYFEGK--NLEDIVIVSPDHGGVTRARKLADRLKAPIAIIDKRR------------------------------------ 200

AER083Cp       DEEENIILTNGIQTARIINGHVIDDDVDDAYHSDVVVSDQE--GSLASDSYPIGGSYEAAADSEDEEAPQEKQEKLITLVGNVNGRSAII 321
AGR371Cp       ------------------------------------------------------------------QKANEVSRMV-LVGDVADKSCII 221
AGL080Cp       ------------------------------------------------------------------AKANEVSRMV-LVGDVTDKVCII 220
ADR314Cp       ----DATLASG-GGMPLSPKPLISNLNSTDVKSSL--------G-------------------------SSKYVQTTM-LVGQVRDKVCIL 356
Sc_Prs1        NEEENIILSNGIQTARIRNGHVIGDDEADDDEDAILESDSELHSIDGLDSHGLGGTYDAVDSEDEEEIPVLYREQLITLVGNVRGRSAII 323
Sc_Prs2        ------------------------------------------------------------------QKANEVSRML-LVGDVAGKSCLL 221
Sc_Prs3        ------------------------------------------------------------------ARANEVSRMV-LVGDVTDKICII 220
Sc_Prs4        ------------------------------------------------------------------QKANEVSKMV-LVGDVTNKSCLL 230
Sc_Prs5        ----DATLTSG-GSLPVSPRPLVTTLVSSQNTTSS--------GATGVAALEMKKTTSTSSTSSQSSNSSKFVQTTM-LVGDVRNKVCII 395
B. subtilis_prs ------------------PRPNVAEV-------------------------------------------------MN-IVGNIEGKTAIL 222

AER083Cp       LDDMIDRPGSFISAAEHMVKNCGAKRVYVVATHGIFTGDCLEQLEQSDAVYQVIVTNTYPINRD-RMKRSQKLVVIDTSSIFAECIRRDH 410
AGR371Cp       VDDMADTCGTLVKATDTLIEN-GAKEVIAIVTHGIFSGGAREKLRNSK-LARIVSTNTVPVDLNLDIY--HQ---IDISAILAEAIRRLH 304
AGL080Cp       VDDMADTCGTLAKAAEVLLEH-NARSVIAIVTHGILSGKAIENINNSK-LDRVVCTNTVPFEEKMKLC--PKLDVIDISAVLAESIRRLH 306
ADR314Cp       LDDLVDTSYTITRAATLLKEQ-GATKVYAVVTHGVFSGDALNRVAQSA-IDKIIITNTVPQEETVRILGKDRVDIIDVSRVFGEAIRRIH 444
Sc_Prs1        LDDMIDRPGSFISAAEHLVQNCGAKKVYVVATHGIFTGDCLEELEKSDAIDTIVVTNTYPISGE-RIAGSKKLVTIDVSPIFAECIRRDH 412
Sc_Prs2        IDDMADTCGTLVKACDTLMDH-GAKEVIAIVTHGIFSGSAREKLINSR-LSRIVCTNTVPVDLDLDIV--DQ---VDISPTIAEAIRRLH 304
Sc_Prs3        VDDMADTCGTLAKAAEILLEN-RAKSVIAIVTHGVLSGRAIENINNSK-LDRVVCTNTVPFEEKIKKC--PKLAVIDISSVLAESIRRLH 306
Sc_Prs4        VDDMADTCGTLVKACDTLMEH-GAKEVIAIVTHGIFSGSAREKLRNSR-LSRIVCTNTVPVDLDLPIA--DQ---IDISPTFAEAIRRLH 313
Sc_Prs5        VDDLVDTSYTITRAAKLLKDQ-GSTKVYALITHGVFSGDALERIGQSS-IDKLIISNTVPQDRTLQYLGKDRVDVIDVSCIIGEAIRRIH 483
B. subtilis_prs IDDIIDTAGTITLAANALVEN-GAKEVYACCTHPVLSGPAVERINNST-IKELVVTNSIKLPEEKKI---ERFKQLSVGPLLAEAIRVH 307

AER083Cp       YGESISVLFDSLASL 425
AGR371Cp       NGESVSYLFNN-AVM 318
AGL080Cp       NGESISYLFKN-NPL 320
ADR314Cp       NGESISMLFEY-V-T 457
Sc_Prs1        YGESISVLFDSLAAL 427
Sc_Prs2        NGESVSYLFTH-APV 318
Sc_Prs3        NGESISYLFKN-YPL 320
Sc_Prs4        NGESVSYLFTH-APV 327
Sc_Prs5        NGESISMLFEH-G-W 496
B. subtilis_prs EQQSVSYLFS     317
```

alignment of Prs3 proteins

```
AGL080Cp MATNAIKLLAPDIHRGLAELVAKRLGLRLTDCKLKRDCNGEATFSIGESVRDQDIYIITQVGSGDVNDRVLELLIMINASKTASARRITA 90
Sc_PRS3  MPTNSIKLLAPDVHRGLAELVAKRLGLQLTSSKLKRDPTGEVSFSIGESVRDQDIFIITQIGSGVVNDRVLELLIMINASKTASARRITA 90

AGL080Cp VIPNFPYARQDRKDKSRAPITAKLMADMLTTAGCDHVITMDLHASQIQGFFDVPVDNLYAEPSVVKYIKEHIPHDDAIIISPDAGGAKRA 180
Sc_PRS3  IIPNFPYARQDRKDKSRAPITAKLMADMLTTAGCDHVITMDLHASQIQGFFDVPVDNLYAEPSVVRYIKENVNYMDSIIISPDAGGAKRA 180

AGL080Cp SLLSDRLNLNFALIHKERAKANEVSRMVLVGDVTDKVCIIVDDMADTCGTLAKAAEVLLEHNARSVIAIVTHGILSGKAIENINNSKLDR 270
Sc_PRS3  ATLADRLDLNFALIHKERARANEVSRMVLVGDVTDKICIIVDDMADTCGTLAKAAEILLENRAKSVIAIVTHGVLSGRAIENINNSKLDR 270

AGL080Cp VVCTNTVPFEEKMKLCPKLDVIDISAVLAESIRRLHNGESISYLFKNNPL 320
Sc_PRS3  VVCTNTVPFEEKIKKCPKLAVIDISSVLAESIRRLHNGESISYLFKNYPL 320
```

alignment of Prs2 and Prs4 proteins

```
AGR371Cp MSS--------NSIKLLAGNSHPDLAEKVSVRLGVPLSKIGVYHYSNKETSVTIGESIRDEDVYIIQTGTGEQEINDFLMELLIMIHACR 82
Sc_Prs2  MST--------NSIKLLAGNSHPGLAELISQRLGVPLSKVGVYQYSNKETSVTIGESIRDEDVYIIQTGYGEHEINDFLMELLILIHACK 82
Sc_Prs4  MNSESREDMAINSIKLLAGNSHPDLAEQISKKLGIPLSKVGVYQYSNKETSVTIGESLRDEDVYIIQTGIGEQEINDFLMELLILIHACQ 90

AGR371Cp SASARKITAVIPNFPYARQDKKDKSRAPITAKLVAKMLETAGCNHVITMDLHASQIQGFFHIPVDNLYAEPNILHYIQ-HNVDFQNSMLV 171
Sc_Prs2  TASVRRITAVIPNFPYARQDKKDKSRAPITAKLIANLLETAGCDHVITMDLHASQIQGFFHIPVDNLYGEPSVLNYIRT-KTDFNNAILV 171
Sc_Prs4  IASARKITTVIPNFPYARQDKKDKSRAPITAKLVANLLQTAGADHVITMDLHASQIQGFFHIPVDNLYAEPSVLNYIRARKTDFDNAILV 180

AGR371Cp APDAGSAKRTSTLSDKLNLNFALIHKERQKANEVSRMVLVGDVADKSCIIVDDMADTCGTLVKATDTLIENGAKEVIAIVTHGIFSGGAR 261
Sc_Prs2  SPDAGGAKRVASLADKLDMNFALIHKERQKANEVSRMLLVGDVAGKSCLLIDDMADTCGTLVKACDTLMDHGAKEVIAIVTHGIFSGSAR 261
Sc_Prs4  SPDAGGAKRVAALADKLDLNFALIHKERQKANEVSKMVLVGDVTNKSCLLVDDMADTCGTLVKACDTLMEHGAKEVIAIVTHGIFSGSAR 270

AGR371Cp EKLRNSKLARIVSTNTVPVDLNLDIYHQIDISAILAEAIRRLHNGESVSYLFNNAVM 318
Sc_Prs2  EKLINSRLSRIVCTNTVPVDLDLDIVDQVDISPTIAEAIRRLHNGESVSYLFTHAPV 318
Sc_Prs4  EKLRNSRLSRIVCTNTVPVDLDLPIADQIDISPTFAEAIRRLHNGESVSYLFTHAPV 327
```