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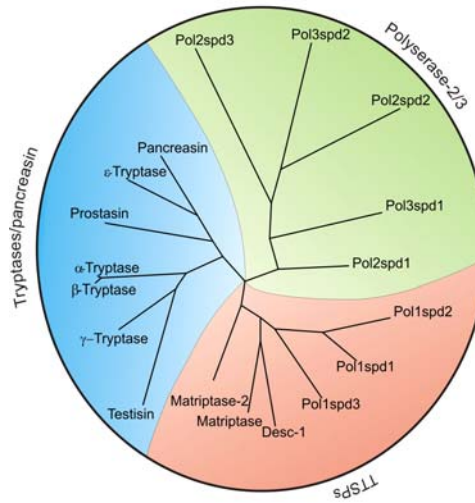
Pol3spd1 : ---KPQEGNTVPGEWPMQASVRRQG---AHICSGSLVADTWLTAAHCFEKAATELNS---WSVVLGSLQREGLS-PGAEEVGVAAQLP-RAYNHYSQGS*DLAL : 95
Pol3spd2 : SLRTAGPQAGAPSPWPWEARLMHQGQLA---CGGALVSEEA*VLTAAHCF-----IGRQAP-----EESVGLGTRPEEWGLKQLILH-GAYTHPEGGYDMAL : 88
Pol2spd1 : ---IVGGGNAQPGTWPMQVSLHH-GG--GHICGGSLIAPS*WVLSAAHCFMTNGT--LEPAAEWSVLLGVHSQDG-PLDGAHTRAVAAI*VVP-ANYSQVELGADLAL : 96
Pol2spd2 : -----KAPRPGAWPWEAQVMVPGSRP---CHGALVSES*WVLAAPASCF-----LDPNSSDSPPRDLDAWRVLLPSRPAERVARLVQH-ENASWDNAS-DLAL : 87
Pol2spd3 : ---LRLEAAPVGVLPWLA*EVHVAG---DRVCTGILLAPGWVLAATHCV-----LRPGSTTVPYIEVYLGRAGASSLPQGHQVSRLVISIRLPQHLGLRPP*LAL : 93
Pol1spd1 : ---IVGGMEASPGEFPMQASLRE-NK--EHFCGAAIINARWL*VSAAHCFNE-----FQDPTKWVAYVGATYLSGSEASTVRAQ-VVQIVKH-PLYNADTADF*DAV : 93
Pol1spd2 : ---VVGFGGAASGEVPMQVSLKE-GS--RHFCGATVVGDRWL*L*SAAHCFNH-----TKVEQVR-AHLGTASLLGLGGSPVKIG-LRRVVLH-PLYNPGILD*DLAV : 92
Pol1spd3 : ---IVGGSAAGRG*EWPMQVSLWLR--EHRCGAVLVAERWL*L*SAAHCFDV-----YGDPKQWAAFLG---TPFLSGAEGQLERVAR*IYKH-PFYNLYTLDY*DVAL : 92
Matriptase : ---VVG*GTDADEGEWPMQVSLHALGQ--GHICGASLISPNWL*VSAAHCIYDDRGRFYS*DPTQTAWTAFGLGLHDQSQRSAPGVQERRLKRIISH-PFFNDFTFDY*DIAL : 100
β-Tryptase : ---IVGGQAPRSKWPMQVSLRVHGPYWMHFCGGSLIHPQWLTA*AHC-----VGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVH-PQFYTAQIGADIAL : 94

Pol3spd1 : LQLAHPTTHT---PLCLPQPAHRFPFGASCWATGWDQ---DTSAPGTLRNLRLRLISRPT*CNCIYNQLHQRHLSNP-ARPGMLCGGPQP*GVQGP*CQ*GD*SGGPV : 192
Pol3spd2 : LLLAQPVTLGASLRPLCLPYPDHHLPDGERGWLGRARPG-----AGISSLQTVPTLLGPAC*SRLHA-APGGD*GSP-I-LPGMVC-TSAV*GELPSC*EGLSGAPL : 185
Pol2spd1 : LRLASPASLGPAVWPVCLPRASHRFVHGTA*WATGWDVQ*EADPLLPWVLQVEVLRLLGEATCQCLYSQPGPFNLTLQIL-PGMLCAGYPEGRRDTCQ*GD*SGGPL : 201
Pol2spd2 : LQLRTPVNL*SAASRPVCLPHPEHYFLPGSRCLARWGRGE---PALGPGALLEAELLGGWCHCLYGRQGA*AVPLPGDPPHALCPAYQEKEE*VGSCW*ND*SRWSL : 188
Pol2spd3 : LELSSRVEPSPSALPICLHPAG--IPPGASCWVLGWKEPQDRVPVAAA-----VSILTQRI*CDCLY-----QGILPPGTLCVLYAE*GQENRC*EMTSAPPL : 181
Pol1spd1 : LELTSPLPFGRHIQPVCLPAATHIFPPSKCLISGWGYLKE-DFLVKPEVLQKATVELLDQALCASLYG-----HSLT-DRMVCAGYLDGKVDSCQ*GD*SGGPL : 189
Pol1spd2 : LELASPLAFNKYIQPVCLPAIKQFVGRKCMISGWGNTQE-GNATKPELLQKASVGII*DQKTC*SVLYN-----FSLT-DRMVCAGYLDGKVDSCQ*GD*SGGPL : 188
Pol1spd3 : LELAGPVRRSRLYRPICLPEAPRPPDGT*RCVITGWGSVRE-G-GSMARQLQKA*AVRLLSEQT*CRRFYP-----VQIS-SRMLCAGFPQGGVDS*CSGDA*GGPL : 187
Matriptase : LELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQY-G-GTGALILQKGEIRVINQTT*CENLLP-----QQIT-PRMCMCVGLSGGVDSCQ*GD*SGGPL : 195
β-Tryptase : LELEEPVNVSSHVHTVTPPASETFPPGMP*QWVTGWGDV*DN*DERLPPFPFLKQYKVPIMENHICDAKYHLGAYTGDDVIRVDDMLCAG--NTRRDS*CQ*GD*SGGPL : 198

Pol3spd1 : LCLEPDGHWQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGA*AF----- : 242
Pol3spd2 : VH-EVRGTWFLAGLHSFGDA*CGPARPAVFTALPAYEDWSSLDWQVYFAEEPEPEAEPG*CLANISQPTSC----- : 256
Pol2spd1 : VCEE-GRWFQAGITSFGFGCGRRNRPGVFTAVATYEAMIREQVMGSEPGAF*P----- : 254
Pol2spd2 : LC-QEEGTWFLAGIRD*FPSG---LRPRAFFLQTHGPNISHVTRGAYLEDQLA----- : 238
Pol2spd3 : LCQMTGSGWILVGM-----AVQGSRELFAAIGPEEAMISQTVGEANFLPPSGSPHWPTGGSNLCPPELAKASGSPHAYVFLLLTLTIQS : 266
Pol1spd1 : VCEEPSGRFFLAGIVSWGIGCAEARRPGVYARVTRLRDWILE----- : 231
Pol1spd2 : ACEEAPGVFYLAGIVSWGIGCAQVKKPGVYTRITRLKGWILE----- : 230
Pol1spd3 : ACREPSGRWLTGVTSWGYGCGRPHFPGVYTRVAARVGIQ*GHQIE----- : 233
Matriptase : SSVEADGRIFQAGVSWGIGCAQRNKP*GVYTRLPLFRD*WIKENTGV----- : 241
β-Tryptase : VC-KVNGTWLQAGVSWGEGCAQNP*RPGIYTRVYYLDWIHHYVPKKP----- : 245

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