```
NTDB id 190904 A6L26 RS00825 WP 164715743.1  MLCPEKMSGMAGRHPYGVRSGLRRNGLKLWDIHFRMTRFIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINA  80
NTDB id 1127 NGFG RS10560 WP 003703428.1     ......................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINA  57
NTDB id 1126 NGFG RS09375 WP 003703428.1     ......................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINA  57
NTDB id 1125 NGFG RS07215 WP 003703428.1     ......................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINA  57
NTDB id 1108 NGFG RS06525 WP 003703428.1     ......................MSRGGAT..PYRFLLIRHIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINA  57
consensus                                    ......................**!*!**  ***!***!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
NTDB id 190904 A6L26 RS00825 WP 164715743.1  ASQQELEALPGIGPAKAKAIAEYRAQNGAFKSVDDLTKVKGIGPAVLAKLKDQASVGAPAPKGPAKPALPADKK  154
NTDB id 1127 NGFG RS10560 WP 003703428.1     ASQQELEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
NTDB id 1126 NGFG RS09375 WP 003703428.1     ASQQELEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
NTDB id 1125 NGFG RS07215 WP 003703428.1     ASQQELEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
NTDB id 1108 NGFG RS06525 WP 003703428.1     ASQQELEALPGIGPAKAKAIAEYRAQNGAFKSVDDLIKVKGIGPAVLAKLKDQASVGAPAPKGPAKPVLPAVKK  131
consensus                                    !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*!!!*!!
```

X non conserved
X similar
X ≥ 50% conserved