```
logo
```

```
NTDB id 122181 B6116 RS01385 WP 011799029.1  MLYPEKMSGMAGRHPYGVRSGLRRNGLKLWDIHFRMTRFIVARCGLLFATLKGKTMKKMFVLFCMLFSCAFSLAAVNINA   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                                                         **!*!**  ***!***!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

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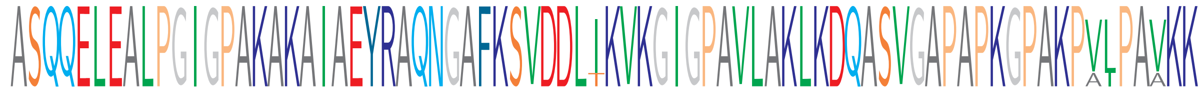
logo
```


```
NTDB id 122181 B6116 RS01385 WP 011799029.1  ASQQELEALPGIGPAKAKAIAEYRAQNGAFKSVDDLTKVKGIGPAVLAKLKDQASVGAPAPKGPAKPAIPAAKK   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 $\geq 50\%$ conserved