Multiple sequence alignment (two blocks, residues ~1–240), with secondary structure annotations (α-helices, η, β-strand) above the sequences.

Secondary structure track (top block): α1, α2, α3, η1, α4, α5, α6, η2, α7, η3, α8

Row identifiers (top block):

Label
seed_A0A225E1Q/1-871
seed_P36000/1-270
seed_P32074/1-292
UniRef50_A0A1N6/1-787
UniRef50_A3ZWK1/1-787
UniRef50_B4DAV1/1-787
UniRef50_E8QX92/1-785
UniRef50_A0A3C1/1-785
sp|O43079|AP1B1/1-270
sp|P63009|AP2B1/1-270
sp|Q9SUS3|APBLB/1-270
sp|Q54X82|AP1B_/1-270
sp|O43005|AP2B_/1-270
sp|Q0WW26|COPG_/1-284
sp|Q9QXK3|COPG2/1-284
sp|P87140|COPG_/1-284
sp|Q54HL0|COPG_/1-284
sp|Q8H852|COPG1/1-284
consensus>50

Secondary structure track (bottom block): η4, α9, α10, η5, α11, α12, η6, η7, α13, α14, α15, β1

Row identifiers (bottom block):

Label
seed_A0A225E1Q/1-871
seed_P36000/1-270
seed_P32074/1-292
UniRef50_A0A1N6/1-787
UniRef50_A3ZWK1/1-787
UniRef50_B4DAV1/1-787
UniRef50_E8QX92/1-785
UniRef50_A0A3C1/1-785
sp|O43079|AP1B1/1-270
sp|P63009|AP2B1/1-270
sp|Q9SUS3|APBLB/1-270
sp|Q54X82|AP1B_/1-270
sp|O43005|AP2B_/1-270
sp|Q0WW26|COPG_/1-284
sp|Q9QXK3|COPG2/1-284
sp|P87140|COPG_/1-284
sp|Q54HL0|COPG_/1-284
sp|Q8H852|COPG1/1-284
consensus>50

Sequence alignment (rotated figure). Row identifiers (left labels), repeated for both blocks:

```
_seed_A0A225E1Q/1-871
_seed_P36000/1-270
_seed_P32074/1-292
UniRef50_A0A1N6/1-787
UniRef50_A3ZWK1/1-787
UniRef50_B4DAV1/1-787
UniRef50_E8QX92/1-785
UniRef50_A0A3C1/1-785
sp|O43079|AP1B1/1-270
sp|P63009|AP2B1/1-270
sp|Q9SUS3|APBLB/1-270
sp|Q54X82|AP1B/1-270
sp|O43005|AP2B_/1-270
sp|Q0WW26|COPG_/1-284
sp|Q9QXK3|COPG2/1-284
sp|P87140|COPG_/1-284
sp|Q54HL0|COPG_/1-284
sp|Q8H852|COPG1/1-284
consensus>50
```

First block secondary-structure annotations (top): η8, α16, β2, α17, η9, α18, α19, η10, α20, α21
Position markers: 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360

Second block secondary-structure annotations (top): α22, α23, η11, α24, α25, α26, η12, α27, α28, η13, α29
Position markers: 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480

```
                        η14  α30          α31           α32           α33                β3      β4      β5   β6   β7   β8    η15
                        TT              TT                                                          TT    TT  TT
                        490       500       510       520       530       540       550       560       570       580       590       600

seed_A0A225E1Q/1-871    TPDIRAFDAYLEGLGSKNATVRDECRKAVTAIRVAALPKIDTRLDQTPPLSQAVVGELQRVYSTAAPIRSWRVLGAFTREAKPPFDPTTPTLDAEYKDANGKPVRWKATRTDAGGKVNLLR
seed_P36000/1-270       ...........................................................................................................................
seed_P32074/1-292       ...........................................................................................................................
UniRef50_A0A1N6/1-787   MPDLLALQVYLAGLTDKSLEIRKVSADALGRISIDAAPVLD.RLSARHELPPTLLPELRKIYTA....LTDWHLVGPFKIDAPMSERP.......VDLQARFVGAQGEPRLDL.H
UniRef50_A32WK1/1-787   VPDRRALPQYLRAVTSANQELRKATMNALLALRELVRDIV.ALNQSGELSNRARGPLQSVFET...PQQWQLIGPFPPKVGDPPFDF.......APNAEQLIHVGSRSRVSP.A
UniRef50_B4DAV1/1-787   LGGEQVMPVLITMLGDKNIRVRQEAAKALRKYRDKAWPIIE.QKFLTNELPPEYEPELRSLFES...GVKWKMIGPFENVWEPPTDA.......PDLAKKYTNAEGKELVDL.G
UniRef50_E8QX92/1-785   IPDLAALPIYLDALGGKNADLRRAAAQALGMIRDQAAPVLD.QLASRRELPARLLPELRDIYRT...RRSWKVIGPFREEVAFFPADG....IDFEMKVPGRSGREEINL.G
UniRef50_A0A3C1/1-785   IADHRAIDVYLQMLVDRSPELRQDTATALAGLKDSIVDDLR.RRSDDGALTSAMRVELSALFAR....PRRWMILGAWSQELGVPIDP.......PLDFDAPVRIGDRERFSP.A
sp|O43079|AP1B1/1-270   ...........................................................................................................................
sp|P63009|AP2B1/1-270   ...........................................................................................................................
sp|Q9SUS3|APBLB/1-270   ...........................................................................................................................
sp|Q54X82|AP1B/1-270    ...........................................................................................................................
sp|O43005|AP2B/1-270    ...........................................................................................................................
sp|Q0WW26|COPG/1-284    ...........................................................................................................................
sp|Q9QXK3|COPG2/1-284   ...........................................................................................................................
sp|P87140|COPG/1-284    ...........................................................................................................................
sp|Q54HL0|COPG/1-284    ...........................................................................................................................
sp|Q8H852|COPG1/1-284   ...........................................................................................................................
consensus>50            ...........................................................................................................................


                        α           β9        β10         β11      β12        β13      β14         β15          α34        α35
                                                                 TT       TT                TT
                        610       620       630       640       650       660       670       680       690       700       710       720       730

seed_A0A225E1Q/1-871    QGFSLTGDASAYAYAEIDSKTARAVEMIAGSDDGLTVWVNGKQVFEVKGDRGYNADAFHIKANLTAGRNVILAKITQGGPWEFSIAVPEAGTGRLFETTAHKLDPAEFATFATKTTGNPA
seed_P36000/1-270       ...........................................................................................................................
seed_P32074/1-292       ...........................................................................................................................
UniRef50_A0A1N6/1-787   KLYSNLEDLAVFGAAEFQSNAKWSAEMAVGSDDTLTVWLNGKQVYD..GRDGFRHDRNRVNVLLEGTNRILVKCGNRGGPWQFAVALATPADYAFLKVPAVGYKPEQFRAFAMEGRGKAE
UniRef50_A32WK1/1-787   NFLQGSRQVWCYAYTPVVRDSAGSATLQVGSDDQLIVWVNGMQVYE.RNSGWSKDRDSFSVDLNAGVNHVWLRCGNDGGPWDFSLATSQDPQLAFLYQDPEKLDIAAFRSFAGSHSGEAA
UniRef50_B4DAV1/1-787   QVFHTNGMVCAYAYAEIDSPEEADGKLLAGSDDQLAVWLNGKKVHD..GSRGFEPDQDQVDLHFKAGKNQLLLKIGNVSGTWQFAARLPGDGTKYVQSKETPEEKQRAYALATKPHAGDPK
UniRef50_E8QX92/1-785   RLYGEEAADHSAFAVSEIVSDRDRPTELAVGSDDTLTIWLNGQKVFE..GNRSFAHAQNTFTAPLRAGTNQVVVHCGNRGGGWQPQYAFLNESSAAFDPDRYRDVALKTPGDPA
UniRef50_A0A3C1/1-785   QTFDETSNVWALAVAIIDRQQAGKVRWQLGSDDQAVVSINGRVVYE..GDRGWGADQGSGEAELIEGRNVILFRTGNSSGPWEFGMAIGGDPQFAFLEVDSSIVGLAAYRERGLTGDGDVS
sp|O43079|AP1B1/1-270   ...........................................................................................................................
sp|P63009|AP2B1/1-270   ...........................................................................................................................
sp|Q9SUS3|APBLB/1-270   ...........................................................................................................................
sp|Q54X82|AP1B/1-270    ...........................................................................................................................
sp|O43005|AP2B/1-270    ...........................................................................................................................
sp|Q0WW26|COPG/1-284    ...........................................................................................................................
sp|Q9QXK3|COPG2/1-284   ...........................................................................................................................
sp|P87140|COPG/1-284    ...........................................................................................................................
sp|Q54HL0|COPG/1-284    ...........................................................................................................................
sp|Q8H852|COPG1/1-284   ...........................................................................................................................
consensus>50            ...........................................................................................................................
```

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                α36      TT   η16    TT     α37        α38      TT        β16    TT      β17         β18    TT      β19  η17    β20
              ooooooo   TT   ooo   TT    oooo    oooooooooo    TT       oooo   TT                            TT       ooo ooo
               730       740       750       760       770       780       790       800       810       820       830       840

_seed_A0A225E1Q/1-871   HGKVLYADLKGLACIKCHVAGPPGSPGGDVGPSLAGIGVKYNRLQLIESVLYPSKQILDGYQQTRVATLDGRVIVGVVRGETPDDVTILDAEARKIVIKKADIEERKVLDKSVMPEGLQAG
_seed_P36000/1-270      ....................................................................................................................
_seed_P32074/1-292      ....................................................................................................................
UniRef50_A0A1N6/1-787   RGRSLFQDLKGLACIRCHAVGKEG..........VGPELSSIGAKYPRHELIQSVLYPSAQIASGYEPVVVATGDGRVLTGIIKSDTPEALEIEDADAKRVRIPRDQIDDRKRSDVSLMPTGLAEG
UniRef50_A32WK1/1-787   RGKKFFENTQGAAACIKCHSVSGIG.........VGPDLVGIGTKYPREELIRSILEPSLRIANGYDTGVVMTVDGNVLTGVLKLESPEAVELVTAEGKTVRIADADIDDFKRSPLSSMPNGIQEG
UniRef50_B4DAV1/1-787   KGEKVFRDPTGGICATCHTVKGQG.........VGPDLSAIAANYKRADLITSILEPSKTIALGFEQVMIETTGGDTFFGALRVQTDDSLTIVGADAVKHVVKKADVKNRTDMKTSLMPQGLTLA
UniRef50_E8QX92/1-785   ...................................VGPDLTDVGAKYPKEELITAILQPSAKISSGYESVVVLTLDGAVINGILKAETDALVELEDGEGRRLTIKKEEIELVQRSEVSLMPSGLADG
UniRef50_A0A3C1/1-785   KGAELFFAAEGIGCAKCHAVGKQG.........IGPNLLGVGAKYPRDELIRSILEPSNRIFSGYEMTVVETDSGETIQGVVRSETAESLVIGDAKGELITIPIESIVARERSEQSAMPSGLEKG
sp|O43079|AP1B1/1-270   ....................................................................................................................
sp|P63009|AP2B1/1-270   ....................................................................................................................
sp|Q9SUS3|APBLB/1-270   ....................................................................................................................
sp|Q54X82|AP1B_/1-270   ....................................................................................................................
sp|O43005|AP2B_/1-270   ....................................................................................................................
sp|Q0WW26|COPG_/1-284   ....................................................................................................................
sp|Q9QXK3|COPG2/1-284   ....................................................................................................................
sp|P87140|COPG_/1-284   ....................................................................................................................
sp|Q54HL0|COPG_/1-284   ....................................................................................................................
sp|Q8H852|COPG1/1-284   ....................................................................................................................
consensus>50            ....................................................................................................................


                            α39
                        oooooooooooooooo
                         850       860       870

_seed_A0A225E1Q/1-871   LTPQDFADLIAFLESLKEKPPEKK
_seed_P36000/1-270      ........................
_seed_P32074/1-292      ........................
UniRef50_A0A1N6/1-787   LSQQDFADLIAYLETLKET......
UniRef50_A32WK1/1-787   MQLQDFADIVAYLESLKIA......
UniRef50_B4DAV1/1-787   LKLDDFVNLVSFLETLKGK......
UniRef50_E8QX92/1-785   LTPRDFADLIEYLSGLRGH......
UniRef50_A0A3C1/1-785   MTPDDFADLIAYLESLKQD......
sp|O43079|AP1B1/1-270   ........................
sp|P63009|AP2B1/1-270   ........................
sp|Q9SUS3|APBLB/1-270   ........................
sp|Q54X82|AP1B_/1-270   ........................
sp|O43005|AP2B_/1-270   ........................
sp|Q0WW26|COPG_/1-284   ........................
sp|Q9QXK3|COPG2/1-284   ........................
sp|P87140|COPG_/1-284   ........................
sp|Q54HL0|COPG_/1-284   ........................
sp|Q8H852|COPG1/1-284   ........................
consensus>50            ........................
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