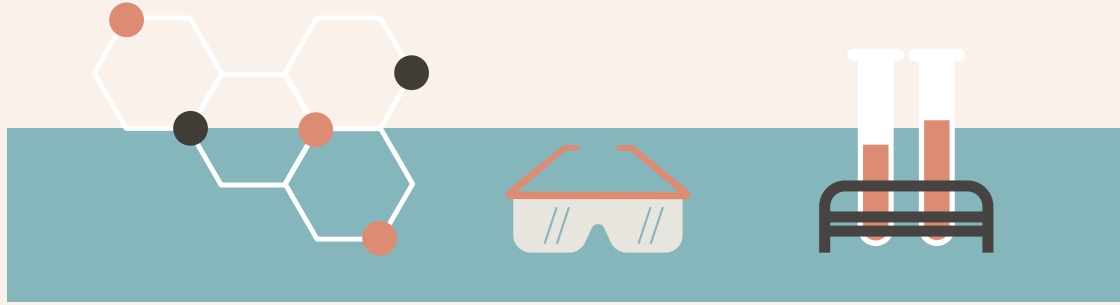


# Protein Sequence



Bruno Álvarez  
Jan Izquierdo  
Jaume Jurado  
Marc Trujillo



# Hmm in PFAM



cdt18182	<b>ATP synthase</b> F <sub>0</sub> complex subunit C3 (ATP5G3) and similar proteins	CDD	ATP5G3 (also called <b>ATP synthase</b> lipid-binding protein, <b>ATP synthase</b> proteolipid P3, <b>ATP synthase</b> proton-transporting mitochondrial F <sub>0</sub> complex subunit C3, ATPase protein 9, or ATPase subunit c) tran...
cd00310	<b>ATP synthase</b> Fo complex, subunit 6 (eukaryotes) and subunit a (prokaryotes)	CDD	Bacterial forms are designated as <b>ATP synthase</b> . Fo complex, subunit a; eukaryotic (chloroplast and mitochondrial) forms are designated as <b>ATP synthase</b> . Fo complex, subunit 6. The F <b>ATP synthase</b> (also...
TIGR01131	FOF1 <b>ATP synthase</b> subunit A	NCBIFAM	Bacterial forms should be designated <b>ATP synthase</b> . F <sub>0</sub> subunit A; eukaryotic (chloroplast and mitochondrial) forms should be designated <b>ATP synthase</b> . F <sub>0</sub> subunit 6. The F <sub>1</sub> /F <sub>0</sub> <b>ATP synthase</b> is a multisub...
IPR032238	Putative ATP-synthase-associated protein	INTERPRO	This is a family of short highly conserved plant proteins that might be associated with ATP-synthase atp operon.
PF04627	Mitochondrial <b>ATP synthase</b> epsilon chain	PFAM	This family constitutes the mitochondrial <b>ATP synthase</b> epsilon subunit. This is not to be confused with the bacterial epsilon subunit, which is homologous to the mitochondrial delta subunit (Pfam:PF0...
PF00231	<b>ATP synthase</b>	PFAM	
TIGR01146	<b>ATP synthase</b> F <sub>1</sub> subunit gamma	NCBIFAM	This model describes the <b>ATP synthase</b> gamma subunit in bacteria and its equivalents in organelles, namely, mitochondria and chloroplast. F <sub>1</sub> /F <sub>0</sub> <b>ATP synthase</b> is a multisubunit, membrane associated enzym...

[Browse](#) / [By Entry](#) / [Pfam](#) / [PF00231](#) / [Overview](#)

## Pfam PF00231 ATP synthase

[Pfam entry](#)

<b>Overview</b>	<b>Member database</b> <a href="#">Pfam</a>
Proteins 50k	<b>Pfam type</b> domain
Domain Architectures 113	<b>Short name</b> ATP-synt
Taxonomy 44k	<b>Description</b> <a href="#">Imported from IPR000131</a>
Proteomes 11k	The ATPase F <sub>1</sub> complex gamma subunit forms the central shaft that connects the F <sub>0</sub> rotary motor to the F <sub>1</sub> catalytic core. The gamma subunit functions as a rotary motor inside the cylinder formed by the $\alpha(3)\beta(3)$ subunits in the F <sub>1</sub> complex [1]. The most conserved region of the gamma subunit is its C terminus, which seems to be essential for assembly and catalysis.
Structures 314	
Signature	
AlphaFold 41k	

We used interprot to search for ATP synthase in PFAM database.

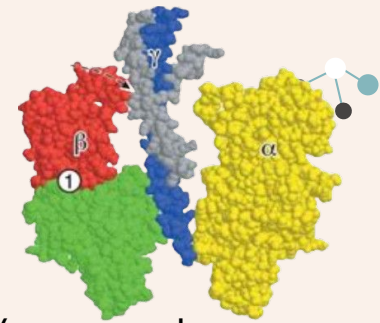
We found an entry, so a HMM is available.

```
$hmmfetch ~/Documents/databases/PFAM/Pfam-A.hmm ATP-synt_ab > alpha.hmm
```

We used the hmmfetch command and the short name to get the hmm file



# Family Protein Set



Now we need to try to find a model for our protein seq (example done with F1 alpha)

```
$hmmsearch ~/Documents/databases/PFAM/Pfam-A.hmm target_alpha.fa > alpha_HMM.out
```

Model: ATP-synt\_ab



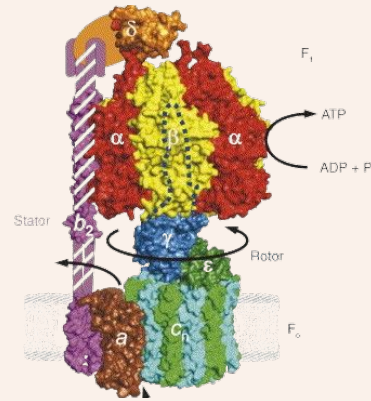
Markov model creation

```
$hmmfetch ~/Documents/databases/PFAM/Pfam-A.hmm ATP-synt_ab > alpha.hmm
```

Then we look for similar proteins to create a set of protein family

```
$hmmsearch alpha.hmm ~/Documents/databases/UniProt/uniprot_sprot.fasta > prot_fam_ids.out
```

Results: Q8TWL6, A3CS71, A8AUJ7, C6A5E8, A7IAU8, O29101, Q0W363



Despite getting the results, we will discard them because they form part of subunit F0 a, which we are not investigating. We will look exclusively for proteins that are F1 alpha

Final Results (alpha): Q8TWL6, A3CS71, A8AUJ7, C6A5E8, A7IAU8, O29101, Q0W363

We follow the same procedure for subunit F1 beta

Final Results (beta): B7IQV8, B7HFK1, Q814W2, A9VSA3, A0RL95, C1F0M8, C3LFH9, C3P1F4



# Why Uniprot?



**PDB**  
PROTEIN DATA BANK

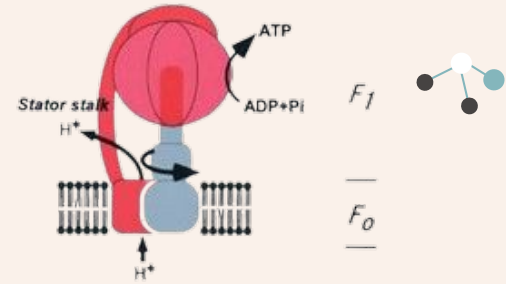
Biased and  
redundant



Unbiased and  
Non-redundant



# Sequence alignment



To align subunit F1, chain alpha we did the following

```
$cat seq* >> sequences.fa
```

Align the sequences against the model we created using PFAM

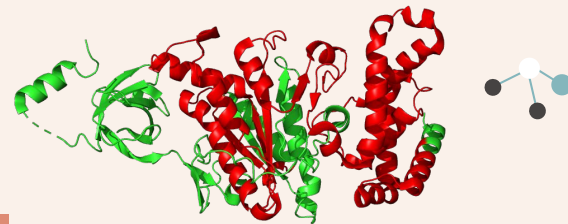
```
$hmmalign alpha.hmm sequences_F1_chain_alpha.fa > MSA_F1_alpha.sto
```

This gives us the alignment in Stockholm format, we use perl to transform it into an alignment file

```
$perl ~/Documents/perl_scripts/convertMod2.pl -in h -out c  
<MSA_F1_alpha.sto > aln_F1_alpha.aln
```

We used this steps for both subunit F1 alpha and beta

# Alignment (alpha)



In red the region that better fits the model

```

3 sp|Q8TWL6|VATA_METKA  -msnvkgeivkiagpvveavgcgagkyevfrvdegllgeviniesdrattiqvyeeet
4 sp|A3CS71|VATA_METMJ  ----mdkgkenragvklrisgppvtavgladahydvvkvgneelngevikiggenitlqv
5 sp|A8AUJ7|VATA_STRGC  ----msqgkllkvsplvasgmqeanlqdicrvdglglgetlenrrrdqasivyeets
6 sp|C6A5E8|VATA_THESM  -----ngkivrvrtgplvademrsmryevrvvgelglgetirlegdkavivgyeeta
7 sp|A7IAU8|VATA_METB6  mevkanaqektkgvlkriagppvtavnldahmydvrvvgnealngeviklqgdnlvlqv
8 sp|Q29101|VATA_ARCFU  ----mevkeagyvgytirsgplvvaeglkarnydlckvgeeglngevvglvvgkvlqv
9 sp|Q0W363|VATA_METAR  -----msqggtirvragppvtavglarnydvvkvgneelngeviniesdrattiqvy
10
11 sp|Q8TWL6|VATA_METKA  glqpgepvkgtgellsvlpgglltqifdgirqlpeirkevsgdfergillvsaldrkkk
12 sp|A3CS71|VATA_METMJ  yedtaglrpgesvngtgsisvelpgglltsydgirqlpevlvdkmgnflergvsapgl
13 sp|A8AUJ7|VATA_STRGC  glqpgepvltgspisvelpggllsqmfdgirqrplerfqtitesdfivrvglpnldret
14 sp|C6A5E8|VATA_THESM  gikpgepvmtgaisvelpgglltsydgirqlpeirlesqgdfigraltapalsrdkk
15 sp|A7IAU8|VATA_METB6  yedttglkpgpevsntglsisvelpgglltsydgirqlpevlvdkmgnflergvsapgl
16 sp|Q29101|VATA_ARCFU  edtegvkpgdkventgmplsvlpggllrinydgvarplvlkevsgdfirgieapgl
17 sp|Q0W363|VATA_METAR  edtsgvrpgpeventgmplsvlpgglltsydgirqlpevlvdkmgnflergvsapgl
18
19 sp|Q8TWL6|VATA_METKA  weftpkvkegekeevdgdlgtvpteflehtknvppvgsgveitlaadgsvyvedtlavi
20 sp|A3CS71|VATA_METMJ  shekkwefvptvkkgedvkgadllgtvqgetnlvhknvppkagkgkllkksigsftvdet
21 sp|A8AUJ7|VATA_STRGC  kmwfpvslsvdaveagdtlgtvqetnlvehimvpgvsgrlanisagstfveetvyei
22 sp|C6A5E8|VATA_THESM  whftpkvkgdkgvvgdtlgtvqetnlvehimvpgvsgrlanisagstfveetvyei
23 sp|A7IAU8|VATA_METB6  shekkwfkpvkagdkvepgalgtvqetnlvhknvppkagkgkllkksigsftvdet
24 sp|Q29101|VATA_ARCFU  rkakwefkplvkgekvkpgeltlgtvqetnvveqklvppnvkagvtaeyegsftvdet
25 sp|Q0W363|VATA_METAR  rtkkwkfvppvkgdkvgkgilgtvqetnlvhknvppnvgettllkidegeftvded
26
27 sp|Q8TWL6|VATA_METKA  edeegeehvmtmqewpvrkprpykrkldepeeliltQQRVIDTFPPVAKGTAAPGPGF
28 sp|A3CS71|VATA_METMJ  vcvgldgetelanlqrwpvrprvprptqklndpiltlQQRILDLGLFPFARGGTAAPGPGF
29 sp|A8AUJ7|VATA_STRGC  egaegsifkgtlnqkwpvrprprfaqlipveplvtQQRVIDTFPPVAKGTAAPGPGF
30 sp|C6A5E8|VATA_THESM  kapngelkevrnyqrwpvrprprpykqklpveplvtQQRVIDTFPPVAKGTAAPGPGF
31 sp|A7IAU8|VATA_METB6  ftvledgreypnqrwpvrprprpykqkntpliltQQRILDLGLFPFARGGTAAPGPGF
32 sp|Q29101|VATA_ARCFU  tvalvedgtelklyhkwpvrprprpykqklpvepliltQQRILDLTFPPVAKGTAAPGPGF
33 sp|Q0W363|VATA_METAR  tghlengtelnlkhkwpvrprprpykqklpvepliltQQRILDLFPFARGGTAAPGPGF
34
35 sp|Q8TWL6|VATA_METKA  SGKTVTQ00LAKWDAQIVVYIGCGERGNEMTVELDFpeledprTGRPLMERTVLANT
36 sp|A3CS71|VATA_METMJ  SGKTVTQ00LAKWSDAEIVVYIGCGERGNEMTVELTFpeledpdkTKPLMERTVLANT
37 sp|A8AUJ7|VATA_STRGC  AGKTVQHQVQAKFANVDIVYIGCGERGNEMTDVLNEFpelldpsTGQSIHQRTVLANT
38 sp|C6A5E8|VATA_THESM  SGKTVTQ00LAKWSDAEIVVYIGCGERGNEMTDVLNEFpelldpdkTKPLMERTVLANT
39 sp|A7IAU8|VATA_METB6  SGKTVTQ00LAKWSDAKIVVYIGCGERGNEMTVELTFpeledpdkTKPLMERTVLANT
40 sp|Q29101|VATA_ARCFU  SGKTVTQ00LAKWSDAEIVVYIGCGERGNEMTVELTFpeledpdkTKPLMERTVLANT
41 sp|Q0W363|VATA_METAR  SGKTVTQ00LAKWSDAEIVVYIGCGERGNEMTVELFephtldpdkTKPLMERTVLANT

```

```

43 sp|Q8TWL6|VATA_METKA  SNMPVAAREACIVTITMAEYVRDMGYDVALMDSTSRWAEALREISGRLEEMPGEEGYP
44 sp|A3CS71|VATA_METMJ  SNMPVAAREASVVTGIIAEYFRDMGYDVALMDSTSRWAEALREISGRLEEMPGEEGYP
45 sp|A8AUJ7|VATA_STRGC  SNMPVAAREASVVTGIIAEYFRDMGYDVALMDSTSRWAEALREISGRLEEMPGEEGYP
46 sp|C6A5E8|VATA_THESM  SNMPVAAREASVVTGIIAEYFRDMGYDVALMDSTSRWAEALREISGRLEEMPGEEGYP
47 sp|A7IAU8|VATA_METB6  SNMPVAAREASVVTGIIAEYFRDMGYDVALMDSTSRWAEALREISGRLEEMPGEEGYP
48 sp|Q29101|VATA_ARCFU  SNMPVAAREASVVTGIIAEYFRDMGYDVAIQADSTSRWAEALREISGRLEEMPGEEGYP
49 sp|Q0W363|VATA_METAR  SNMPVAAREASVVTGIIAEYVRDMGYDVALMDSTSRWAEALREISGRLEEMPGEEGYP
50
51 sp|Q8TWL6|VATA_METKA  AYLASRLAEFYERAGRvvcLGSDDRVGSVTVGVGAVSPGGDFSEPVQTNTLRIVKVFNAL
52 sp|A3CS71|VATA_METMJ  AYLAARLSEFYERAGRv--lSLNGEGGSVTVGVGAVSPGGDFSEPVQTNTLRIVKVFNAL
53 sp|A8AUJ7|VATA_STRGC  AYLGSRIAEYERAGRvktLGSTAREGSIITAIGAVSPGGDISPEVQTNTLRIVKVFNL
54 sp|C6A5E8|VATA_THESM  AYLASRLAEFYERAGRvvtLGSDDRVGSVTVGVGAVSPGGDISPEVQTNTLRIVKVFNAL
55 sp|A7IAU8|VATA_METB6  AYLAARLSEFYERAGLV--eTLNHQSGSVTVGVGAVSPGGDISPEVQTNTLRIVKVFNAL
56 sp|Q29101|VATA_ARCFU  AYLASRLAEFYERAGRv--KTLANGTGSVTVGVGAVSPGGDFSEPVQTNTLRIVKVFNAL
57 sp|Q0W363|VATA_METAR  AYLAARLSEFYERAGRv--LTIPIKGESVTVGVGAVSPGGDISPEVQTNTLRIVKVFNAL
58
59 sp|Q8TWL6|VATA_METKA  DSKLARRRHFPAINNLQSVSLylddvkwmheelggdwireldaeanelqresleelvg
60 sp|A3CS71|VATA_METMJ  DAKLSRRRHFPAINNLQSVSLyldalnewdykvepsvgnlrawngvlkqaeelqelvg
61 sp|A8AUJ7|VATA_STRGC  DAQLARRRHFPAINNLQSVSLyldvgyiddehklawaekvtkanilqkeselqelvg
62 sp|C6A5E8|VATA_THESM  DADLARRRHFPAINNLQSVSLyldgskdwgnvndkwaekvtkanilqkeselqelvg
63 sp|A7IAU8|VATA_METB6  DAKLSRRRHFPAINNLQSVSLyldalhdwydkvnsdpdnklrswangvlkqaeelqelvg
64 sp|Q29101|VATA_ARCFU  DAKLARRRHFPAINNLQSVSLyldtdkdwfaenveeennlrawngvlkqaeelqelvg
65 sp|Q0W363|VATA_METAR  DAKLARRRHFPAINNLQSVSLyldgskdwgydnkspewnqkaesnellqresleelvg
66
67 sp|Q8TWL6|VATA_METKA  lvgsdpalpeserillevarniredflqgnafhevdtcypckeyemltklhfkeraaea
68 sp|A3CS71|VATA_METMJ  lvgsdpalpeeqvilevarniredflqgnafhevdtcypckeyemltklhfkeraaea
69 sp|A8AUJ7|VATA_STRGC  lvgsdpalpeeqvilevarniredflqgnafhevdtcypckeyemltklhfkeraaea
70 sp|C6A5E8|VATA_THESM  lvgsdpalpeeqvilevarniredflqgnafhevdtcypckeyemltklhfkeraaea
71 sp|A7IAU8|VATA_METB6  lvgsdpalpeeqvilevarniredflqgnafhevdtcypckeyemltklhfkeraaea
72 sp|Q29101|VATA_ARCFU  lvgsdpalpeserillevarniredflqgnafhevdtcypckeyemltklhfkeraaea
73 sp|Q0W363|VATA_METAR  lvgsdpalpedqlltlearnirelflqgnafhevdtcysldkqlmksinqfgyayarta
74
75 sp|Q8TWL6|VATA_METKA  vdkgvdpdeilkldvddiarmkvipneakekigqirkkideqfeelteas-----
76 sp|A3CS71|VATA_METMJ  qtggatpqvgilrskneLpqikfirdyepelakinkmdaeafdmanrav-----
77 sp|A8AUJ7|VATA_STRGC  lelqagfreimegtvldrarskfvhedqleklqalsqteetlhlqllaqgldnerh
78 sp|C6A5E8|VATA_THESM  idaglpveetiaklpvreegrmknypnteiaevlnektkeqfeelfkkyge-----
79 sp|A7IAU8|VATA_METB6  qaagvspaqitttkakneLpqikfirkdkypakalekmdnfaelnsraa-----
80 sp|Q29101|VATA_ARCFU  leagktideagvegleefarakfeedykpamaalekirknfl-----
81 sp|Q0W363|VATA_METAR  lasgvpskiLnskdnlakvfkfeandyailtkvndmkkefkfslsea-----

```

Region better fit to the model (position): 223 - 500



# Alignment (beta)



In red the region that better fits the model

```

31 sp|B7IQV8|ATPB_BACC2 -mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengsmnltfevalhlgddtvtv
32 sp|B7HFK1|ATPB_BACC4 -mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengsmnltfevalhlgddtvtv
33 sp|Q814W2|ATPB_BACCR -mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengsmnltfevalhlgddtvtv
34 sp|A9VSA3|ATPB_BACMK mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengasnlntfevalhlgddtvtv
35 sp|A0RL95|ATPB_BACAH mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengtsnlntfevalhlgddtvtv
36 sp|C1F0M8|ATPB_BACC3 mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengtsnlntfevalhlgddtvtv
37 sp|C3LFH9|ATPB_BACAC mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengtsnlntfevalhlgddtvtv
38 sp|C3P1F4|ATPB_BACAA mnkgrvtqimgpvvdvkfdggklpeinalntvkqsnengtsnlntfevalhlgddtvtv
39
40 sp|B7IQV8|ATPB_BACC2 amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
41 sp|B7HFK1|ATPB_BACC4 amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
42 sp|Q814W2|ATPB_BACCR amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
43 sp|A9VSA3|ATPB_BACMK amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
44 sp|A0RL95|ATPB_BACAH amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
45 sp|C1F0M8|ATPB_BACC3 amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
46 sp|C3LFH9|ATPB_BACAC amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
47 sp|C3P1F4|ATPB_BACAA amsstdglvrgtevedtgkalsvpvgdatlgrvfnlvgdaiddgelpadvhrdpirhqa
48
49 sp|B7IQV8|ATPB_BACC2 pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
50 sp|B7HFK1|ATPB_BACC4 pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
51 sp|Q814W2|ATPB_BACCR pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
52 sp|A9VSA3|ATPB_BACMK pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
53 sp|A0RL95|ATPB_BACAH pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
54 sp|C1F0M8|ATPB_BACC3 pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
55 sp|C3LFH9|ATPB_BACAC pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
56 sp|C3P1F4|ATPB_BACAA pafeelstkvlelTGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELININIAQEHGgl
57
58 sp|B7IQV8|ATPB_BACC2 svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
59 sp|B7HFK1|ATPB_BACC4 svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
60 sp|Q814W2|ATPB_BACCR svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
61 sp|A9VSA3|ATPB_BACMK svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
62 sp|A0RL95|ATPB_BACAH svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
63 sp|C1F0M8|ATPB_BACC3 svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
64 sp|C3LFH9|ATPB_BACAC svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe
65 sp|C3P1F4|ATPB_BACAA svFAGVGERTREGNDLYHMSDSGVIKKTAMVFGQMNPEPPGARQORVALTGLTMAEHFRDe

```

```

39 sp|B7IQV8|ATPB_BACC2 QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
40 sp|B7HFK1|ATPB_BACC4 QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
41 sp|Q814W2|ATPB_BACCR QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
42 sp|A9VSA3|ATPB_BACMK QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
43 sp|A0RL95|ATPB_BACAH QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
44 sp|C1F0M8|ATPB_BACC3 QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
45 sp|C3LFH9|ATPB_BACAC QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
46 sp|C3P1F4|ATPB_BACAA QGQDVLFFIDNIFRFTQAGSEVSALLGRMPsAVGYQPTLATEmGQLQERITST---NKG
47
48 sp|B7IQV8|ATPB_BACC2 SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
49 sp|B7HFK1|ATPB_BACC4 SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
50 sp|Q814W2|ATPB_BACCR SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
51 sp|A9VSA3|ATPB_BACMK SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
52 sp|A0RL95|ATPB_BACAH SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
53 sp|C1F0M8|ATPB_BACC3 SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
54 sp|C3LFH9|ATPB_BACAC SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
55 sp|C3P1F4|ATPB_BACAA SITSIQAVYVPADDYTDPApATTfAHLdATTNLERRLTQMGIYpAVDPLASTsralSpeI
56
57 sp|B7IQV8|ATPB_BACC2 vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
58 sp|B7HFK1|ATPB_BACC4 vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
59 sp|Q814W2|ATPB_BACCR vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
60 sp|A9VSA3|ATPB_BACMK vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
61 sp|A0RL95|ATPB_BACAH vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
62 sp|C1F0M8|ATPB_BACC3 vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
63 sp|C3LFH9|ATPB_BACAC vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
64 sp|C3P1F4|ATPB_BACAA vgeehyevArvqqtlqrykelqdtIaIlgmDelseedklvvhrrarIqfflsqnfHvae
65
66 sp|B7IQV8|ATPB_BACC2 qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
67 sp|B7HFK1|ATPB_BACC4 qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
68 sp|Q814W2|ATPB_BACCR qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
69 sp|A9VSA3|ATPB_BACMK qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
70 sp|A0RL95|ATPB_BACAH qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
71 sp|C1F0M8|ATPB_BACC3 qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
72 sp|C3LFH9|ATPB_BACAC qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma
73 sp|C3P1F4|ATPB_BACAA qftgqkgsyvpkntvsgfkellegkyddlpedafrlvvggieevenakkmma

```

Region better fit to the model (position): 144 - 383





# Alpha and beta



Hypothesis of conservation:

- Active site (F1 alpha and beta are in charge of ATP synthesis)
- Vital zone for protein-protein interaction



In red the region that better fits the model