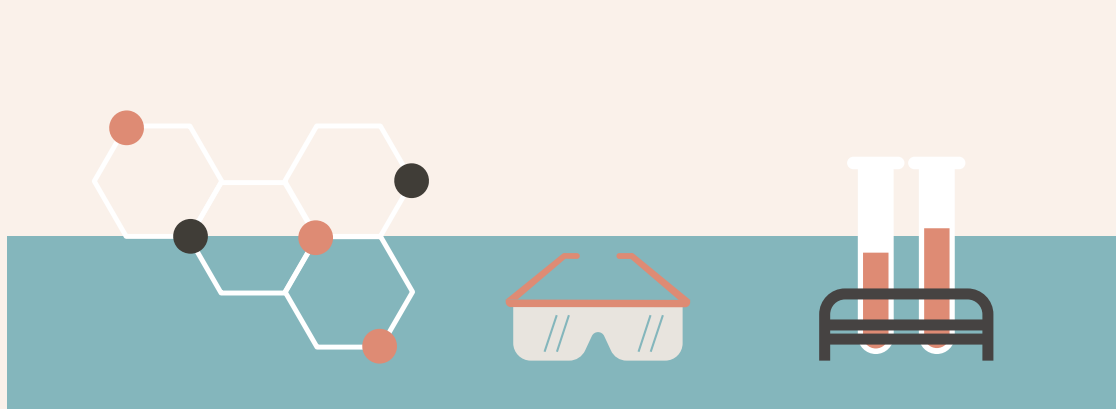


Protein Structure



Bruno Álvarez
Jan Izquierdo
Jaume Jurado
Marc Trujillo



PDB structures

We used psiblast to create a pssm of a protein of the family based on uniprot, and used the pssm to get a list of sequence structures from the pdb_seq database.

Subunit F1 alpha

		Score (Bits)	E Value
37	Sequences producing significant alignments:		
38			
39			
40	1vdz_A mol:protein length:588 A-type ATPase subunit A	837	0.0
41	2qe7_F mol:protein length:462 ATP synthase subunit beta	777	0.0
42	2qe7_E mol:protein length:462 ATP synthase subunit beta	777	0.0
43	2qe7_D mol:protein length:462 ATP synthase subunit beta	777	0.0
44	1kmh_B mol:protein length:498 ATPase beta subunit	760	0.0
45	1fx0_B mol:protein length:498 ATP SYNTHASE BETA CHAIN	760	0.0
46	1sky_E mol:protein length:473 F1-ATPASE	759	0.0
47	2f43_B mol:protein length:479 ATP synthase beta chain, mitochon...	746	0.0
48	1nab_B mol:protein length:479 PROTEIN (F1-ATPASE BETA CHAIN)	746	0.0
49	2v7q_F mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
50	2v7q_E mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
51	2v7q_D mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
52	2jj2_M mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
53	2jj2_L mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
54	2jj2_K mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
55	2jj2_F mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	744	0.0
56			
57	2obm_A mol:protein length:347 EscN	192	1e-55
58	2obl_A mol:protein length:347 EscN	192	1e-55
59	2dpy_B mol:protein length:438 Flagellum-specific ATP synthase	178	2e-49
60	2dpy_A mol:protein length:438 Flagellum-specific ATP synthase	178	2e-49
61	3b2q_B mol:protein length:469 V-type ATP synthase beta chain	132	9e-33
62	3b2q_A mol:protein length:469 V-type ATP synthase beta chain	132	9e-33
63	2rkw_B mol:protein length:469 V-type ATP synthase beta chain	132	9e-33
64	2rkw_A mol:protein length:469 V-type ATP synthase beta chain	132	9e-33
65	2c61_B mol:protein length:469 A-TYPE ATP SYNTHASE NON-CATALYTIC...	131	1e-32
66	2c61_A mol:protein length:469 A-TYPE ATP SYNTHASE NON-CATALYTIC...	131	1e-32
67	1kmh_A mol:protein length:507 ATPase alpha subunit	123	1e-29
68	1fx0_A mol:protein length:507 ATP SYNTHASE ALPHA CHAIN	123	1e-29
69	1sky_B mol:protein length:502 F1-ATPASE	120	1e-28
70	2v7q_C mol:protein length:510 ATP SYNTHASE SUBUNIT ALPHA HEART ...	115	1e-26
71	2v7q_B mol:protein length:510 ATP SYNTHASE SUBUNIT ALPHA HEART ...	115	1e-26
72	2v7q_A mol:protein length:510 ATP SYNTHASE SUBUNIT ALPHA HEART ...	115	1e-26
73	2jj2_J mol:protein length:510 ATP SYNTHASE SUBUNIT ALPHA HEART ...	115	1e-26

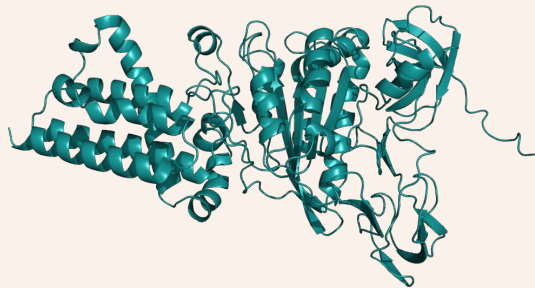
Subunit F1 beta

		Score (Bits)	E Value
37	Sequences producing significant alignments:		
38			
39			
40	2qe7_F mol:protein length:462 ATP synthase subunit beta	833	0.0
41	2qe7_E mol:protein length:462 ATP synthase subunit beta	833	0.0
42	2qe7_D mol:protein length:462 ATP synthase subunit beta	833	0.0
43	1sky_E mol:protein length:473 F1-ATPASE	818	0.0
44	2v7q_F mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
45	2v7q_E mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
46	2v7q_D mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
47	2jj2_M mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
48	2jj2_L mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
49	2jj2_K mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
50	2jj2_F mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
51	2jj2_E mol:protein length:482 ATP SYNTHASE SUBUNIT BETA	795	0.0
52	3b2q_B mol:protein length:469 V-type ATP synthase beta chain	405	6e-138
53	3b2q_A mol:protein length:469 V-type ATP synthase beta chain	405	6e-138
54	2rkw_B mol:protein length:469 V-type ATP synthase beta chain	405	6e-138
55	2rkw_A mol:protein length:469 V-type ATP synthase beta chain	405	6e-138
56	2c61_B mol:protein length:469 A-TYPE ATP SYNTHASE NON-CATALYTIC...	404	3e-137
57	2c61_A mol:protein length:469 A-TYPE ATP SYNTHASE NON-CATALYTIC...	404	3e-137
58	2dpy_B mol:protein length:438 Flagellum-specific ATP synthase	341	3e-113
59	2dpy_A mol:protein length:438 Flagellum-specific ATP synthase	341	3e-113
60	2obm_A mol:protein length:347 EscN	312	3e-103
61	2obl_A mol:protein length:347 EscN	312	3e-103
62	2qe7_C mol:protein length:502 ATP synthase subunit alpha	218	6e-65
63	2qe7_B mol:protein length:502 ATP synthase subunit alpha	218	6e-65
64	2qe7_A mol:protein length:502 ATP synthase subunit alpha	218	6e-65
65	1sky_B mol:protein length:502 F1-ATPASE	212	1e-62
66	2r9v_A mol:protein length:515 ATP synthase subunit alpha	212	2e-62
67	1kmh_A mol:protein length:507 ATPase alpha subunit	208	3e-61

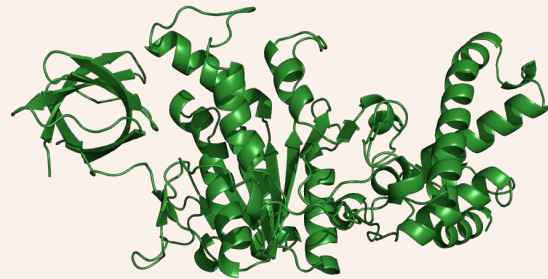
Structure superimposition

We superimpose the structures against the protein used as psiblast query and measure the RMSD

We used A3CS71 as a query and as the alignment base for F1 alpha subunit



We used A0RL95 as a query and as the alignment base for F1 beta subunit

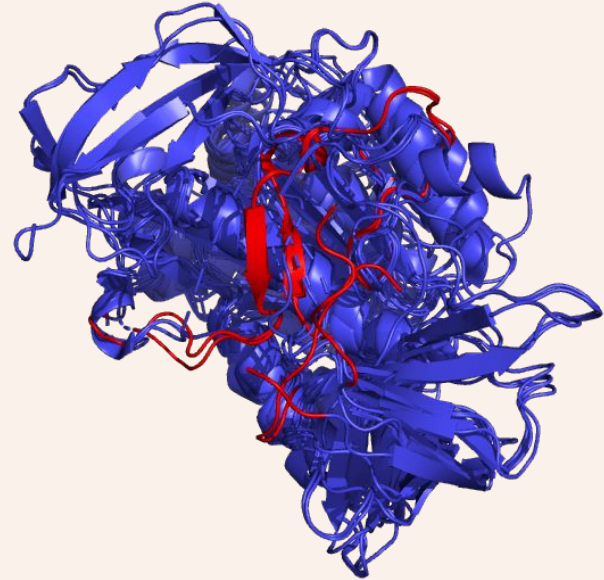


High variability region

Using Pymol and the superimposition alignment we identify that:

Subunit F1 alpha presents high variability at the beginning of the sequence

```
/1 6 11 16 21 26 31 36 41 46 51 56 61 66
MVAKGRIIRVTGPLVWADGMKGAKMYEVVRVGELGLIGEIRLEGDKAVIQVYEETAGVRPGEPVVG TG---
/1 6 11 16
MRINPTTSDPGVSTLEKK-----NL
/1 6 11 16
MRINPTTSDPGVSTLEKK-----NL
/100 106 111 116 121 126 131 136 141 146
GSHKIRVGDALLGRLIDGIGRPMESNIVAPYLPFERSLYAEPPDLL-----
/100 106 111 116 121 126 131 136 141 146
GSHKIRVGDALLGRLIDGIGRPMESNIVAPYLPFERSLYAEPPDLL-----
/19 26
MALLPAV-----RRY
```



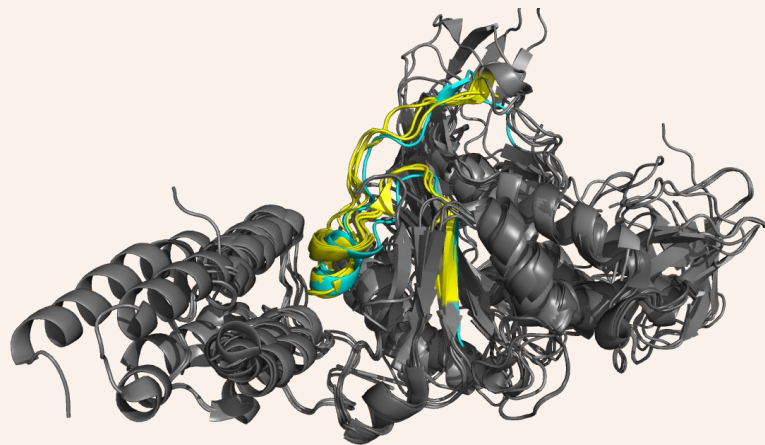
Superimposed structure (in red the most variable part)

Region conservation

We identify conserved regions in subunit F1 alpha using Pymol and the alignment, it can be seen that it presents 2 conserved regions, here is the first one

This is the first conserved region the blue region is from 1vdz_A and the yellow is from the other structures.

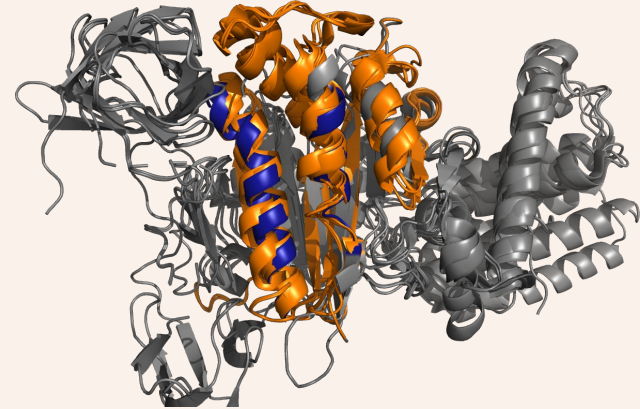
```
196      201      206      211      216      221      226      231      236
RVK-----RKYKE-K-LP-PEVPLITGQRVIDTFFPQAKGGTAIPGPFSGSK-----
1  136      141      146      151      156      161      166      171
HRSAPFT-----Q-L-DTK-LSIFETGIKVVNLLAPYRRGGKIGL-----FGGA
1  136      141      146      151      156      161      166      171
HRSAPFT-----Q-L-DTK-LSIFETGIKVVNLLAPYRRGGKIGL-----FGGA
                        151      156      161      166      171
-----RQV-IDQPFILGVRAIDGLLTCGIGQRIGI-----FA-
                        151      156      161      166      171
-----RQV-IDQPFILGVRAIDGLLTCGIGQRIGI-----FA-
1   146      151      156      161      166      171      176      181
-ITPPFNPL-----QR-TP-IEHVLDTGVRRAINALLTVGRGQRMGL-----FA-
```



Region conservation

Here we can see the alignment of the second conserved region of F1 alpha, the grey overlapping zone belongs to the non-matching aligned region of 1vdz_A depicted in the sequence alignment

This is the second conserved region the blue region belongs to 1vdz_A and the orange belongs to the other structures.



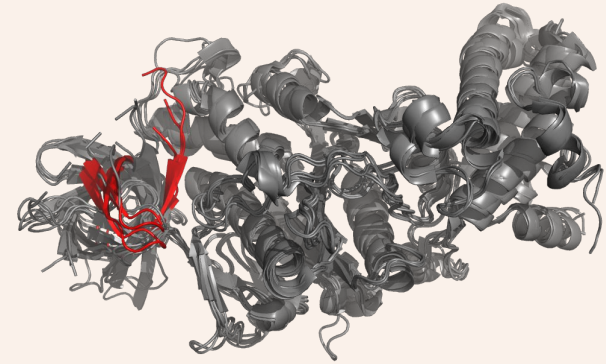
```

      291 296      301 306 311 316      321 326 331 336 341 346 351 356      361 366 371
-----MERTVLIRHT--SN--MPVARGESITYTITITIEYFR--TMGYDVALMADSTSRWAEALREISGRLEEMPGEEGYP-----A-YL-A--SKLAEFYERAG--
1 226 231      236      241 246 251 256 261      266 271 276 281 286      291 296      301 306 311
NEQNI AESK---VALVYGQM--NE-PPGARMRVGLTALTMAEYFR-----DVN-EQDVLLFIDNIFRFVQAGSEVSAL-LG-RMPSAVGYQP-TL-S--TEMGSLQERIT--
1 226 231      236      241 246 251 256 261      266 271 276 281 286      291 296      301 306 311
NEQNI AESK---VALVYGQM--NE-PPGARMRVGLTALTMAEYFR-----DVN-EQDVLLFIDNIFRFVQAGSEVSAL-LG-RMPSAVGYQP-TL-S--TEMGSLQERIT--
226 231      236 241 246 251 256      261 266 271 276 281 286 291      296 301 306
-----LSKCVLVVTTSS--DR-PALERMKAAFTATTIAEYFR--D-----QGKNVLLMMSVTRYARAARDVGLA-S-GEPDVRGGFPSPS--V--FSSLPKLLERAG--
226 231      236 241 246 251 256      261 266 271 276 281 286 291      296 301 306
-----LSKCVLVVTTSS--DR-PALERMKAAFTATTIAEYFRDQ-----GKNVLLMMSVTRYARAARDVGLAS--GEPDVRGGFPSPS--V-F--SSLPKLLERAGPAH
231 236      241 246 251 256 261      266 271 276 281 286      291 296      301 306 311
-----GRARSVVIAPFA--DV-SPLLAMQGAAYATRIAEDFR--D-----RGQHVLLIMDSLTRYAMAQREIALA-IG-EPPATKGYP--SV-F--AKLPALVERAG--

```

High variability region

Subunit F1 beta we can observe high variability at the beginning of the sequence



Superimposed structure (in red the most variable part)

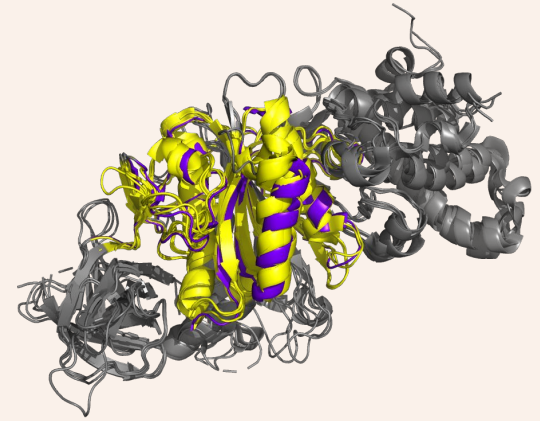
```

K-----6 11
-----GRIIQVMGP
6 11
-----TRGRVIQVMGP
/-3 1 6 11 16 21 26 31 36 41
AAQASPSPKAGA-----TTGRIVAVIGA
-4 1 6 11 16 21 26 31 36 41
HHHHHHPMVKEYKTITQIAGPLIFVEKTEPVGYNEIVNIKMGDGTVRRGQ-----
-4 1 6 11 16
HHHHHHPMVKEYKTITQIAGPLIF-----
-4 1 6 11 16 21 26 31 36 41
HHHHHHPMVKEYKTITQIAGPLIFVEKTEPVGYNEIVNIKMGDGTVRRGQ-----
```

Region conservation

Using Pymol and the alignment it can be seen that subunit F1 beta presents 2 conserved regions, here is the first one.

The first conserved region, 2jj2_E is represented in purple as the position of its conserved region differs slightly from the others, colored in yellow.

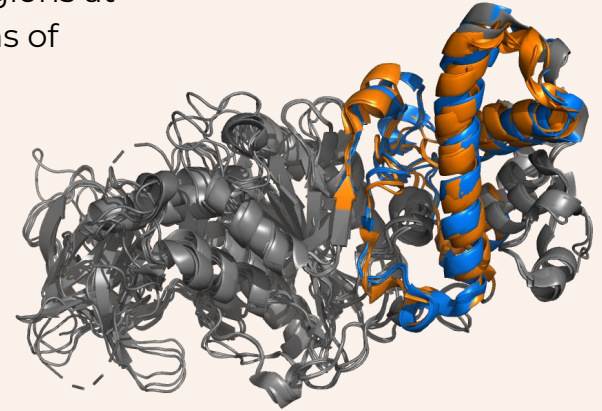


```
81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256 261 266
PVGKATLGRVFNVLGEPTDEQGEVNAEERHPHAPAFEEELSTADEILGTGIKVIDLLAPYAKGGKIGLFGGAGVGKTVLIQELINNVAQEHGGLSVFAGVGERTREGNDLYHEMKDSGVISKTSMVVFGQMNEPPGARLRVALTGLTMAEYFRDREGQDVLLFIDNIFRFTQAGSEVSALLGRMPSAVGN
81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256 261 266
GAPISVPVGQVTLGRVFNVLGEPTDEQGEVNAEERHPHAPAFEEELSTADEILGTGIKVIDLLAPYAKGGKIGLFGGAGVGKTVLIQELINNVAQEHGGLSVFAGVGERTREGNDLYHEMKDSGVISKTSMVVFGQMNEPPGARLRVALTGLTMAEYFRDREGQDVLLFIDNIFRFTQAGSEVSALLGR
6 71 76 81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256
EGLVRGQKVLDSGAPIRIPVGPETLGRIMNVIGEPIDERGPIKTQFAIHAEAPFEFVEMSVGEIILVTGIKVIDLLAPYAKGGKIGLFGGAGVGKTVLIQELINNVAQEHGGLSVFAGVGERTREGNDLYHEMKDSGVISKTSMVVFGQMNEPPGARLRVALTGLTMAEYFRDREGQDVLLFIDN
71 76 81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256
FTGETLKLPAVDLLGRILSGSGEPRDGGPRIVPDQLLDINGARMNPYARLPKDFIQTGISTIDGTNTLVRGQKLPIFSASGLPHNEIALQIARQASVPGSESAFAVVFARMGITNEEAQYFMSDFEKTGALERAVVFLNLADDAVERIVTPRMALTAEYFRDREGQDVLLFIDN
71 76 81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256
FTGETLKLPAVDLLGRILSGSGEPRDGGPRIVPDQLLDINGARMNPYARLPKDFIQTGISTIDGTNTLVRGQKLPIFSASGLPHNEIALQIARQASVPGSESAFAVVFARMGITNEEAQYFMSDFEKTGALERAVVFLNLADDAVERIVTPRMALTAEYFRDREGQDVLLFIDN
71 76 81 86 91 96 101 106 111 116 121 126 131 136 141 146 151 156 161 166 171 176 181 186 191 196 201 206 211 216 221 226 231 236 241 246 251 256
FTGETLKLPAVDLLGRILSGSGEPRDGGPRIVPDQLLDINGARMNPYARLPKDFIQTGISTIDGTNTLVRGQKLPIFSASGLPHNEIALQIARQASVPGSESAFAVVFARMGITNEEAQYFMSDFEKTGALERAVVFLNLADDAVERIVTPRMALTAEYFRDREGQDVLLFIDN
```


Region conservation

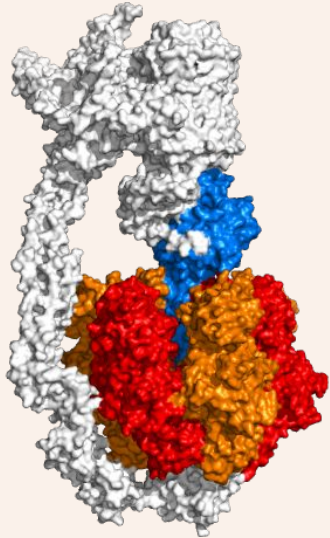
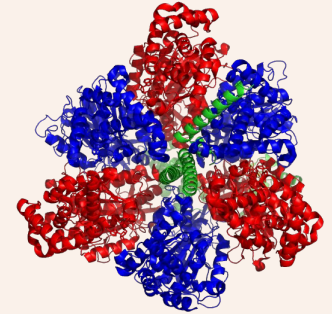
This is the second conserved region of F1 beta, the grey-colored regions at the end of the longer helix belong to non-matching aligned regions of structures 3b2q_B, 2rkw_B and 2c6l_A

In this structure we can observe the blue region, that belongs to 1sky_E and 2jj2_E, which have slightly different positions of conserved regions that the other structures, represented in orange.



```
321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446 451 456 461
PATNLERKLAEMGIYPVDPLASTSRILSPAVVGEEHYRVARGVQVQLQRYNDLQDIIAILGMDELSDDEKLIVARARKIQRFSLQPPFHVAEQFTGMPGKYVPVKETVRGFK
321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446 451 456 461
ITTFSHLDATTNLERKLAEMGIYPVDPLVSTSRALAPEIVGEEHYQVARKVQQTLERYKELQDIIAILGMDELSDDEKLIVHRRARIQFSLQNFHVAEQFTGQPGSYVPVKETVRG
06 311 316 321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446 451
VQAIYVPADDLTDPAPATTFAHLDATTVLSRAIAELGIYPVDPLDSTSRIMDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTVSRARKIQRFSLQPPFQV
311 316 321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446 451 456
THPIPDLSGYITEGQIVVARELHRKGIYPPINVLPSLSRLMNSGIGAGKTRDHKAVSDQMYAGYAEGRDLRGLVAIVGKEALSERDTKFLFADLFEDKFVRQGMNENRTIEDTLEI
311 316 321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446 451 456
THPIPDLSGYITEGQIVVARELHRKGIYPPINVLPSLSRLMNSGIGAGKTRDHKAVSDQMYAGYAEGRDLRGLVAIVGKEALSERDTKFLFADLFEDKFVRQGMNENRTIEDTLEI
311 316 321 326 331 336 341 346 351 356 361 366 371 376 381 386 391 396 401 406 411 416 421 426 431 436 441 446 451 456
THPIPDLSGYITEGQIVVARELHRKGIYPPINVLPSLSRLMNSGIGAGKTRDHKAVSDQMYAGYAEGRDLRGLVAIVGKEALSERDTKFLFADLFEDKFVRQGMNENRTIEDTLEI
```

Regions for protein function



Gamma
Alpha
Beta

Alpha Beta complex has 3 states

Open:
Lets ATP out

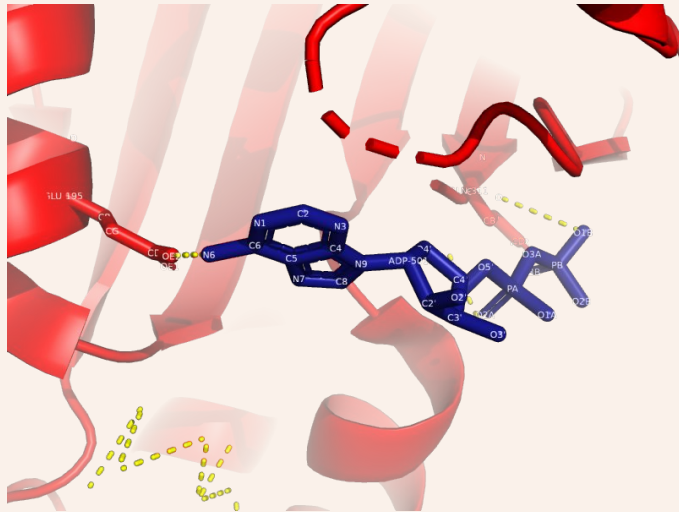
Loose:
Lets ADP in and
prepares

Tight:
Synthesis

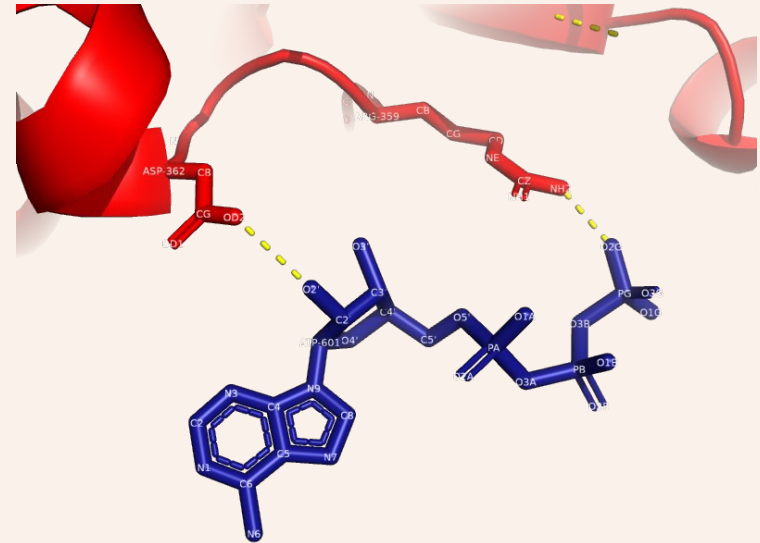
The cycle perpetuates because of Gamma protein
spinnings produced by proton gradient

We will analyze Alpha and Beta interactions
with Gamma among other interactions

ATP binding and synthesis



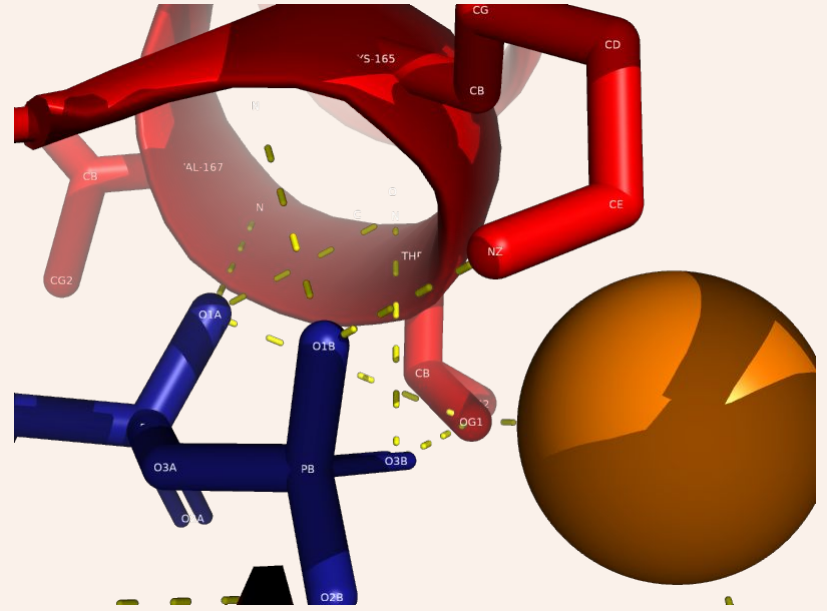
- Open state
- Binds to GLU-195



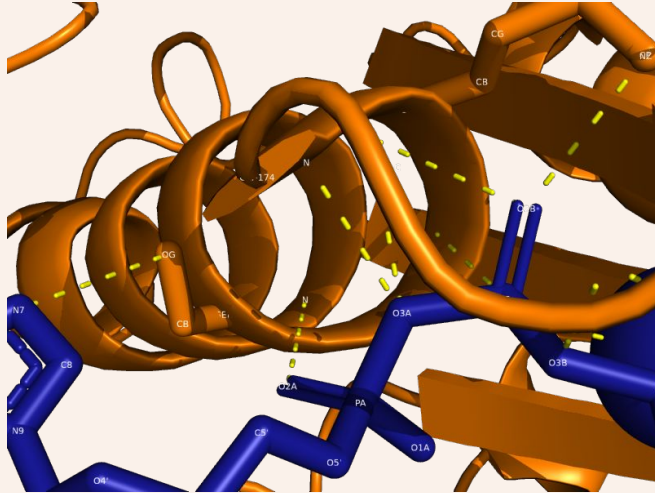
- Loose state
- ARG-359: retains the ATP
- ASP-362: retains ATP

ADP catalytic site (α DP)

- Mg: stabilizes protein during reaction
- LYS-165: stabilizes protein to catalyze reaction
- THR-166: stabilizes protein to catalyze reaction

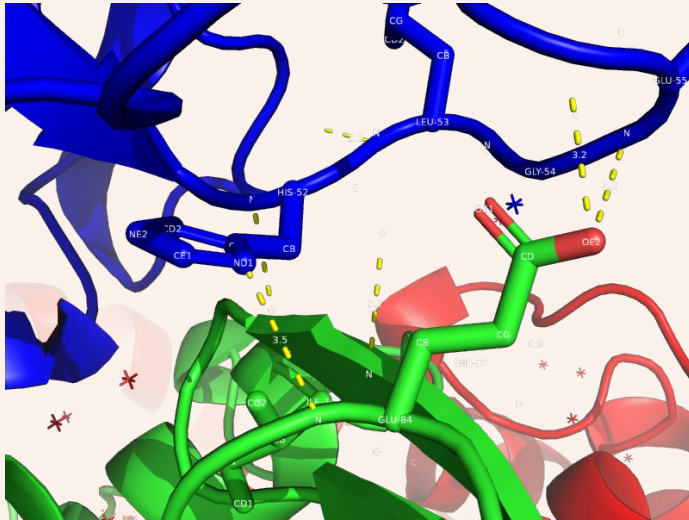


Interaction: beta chain -ATP

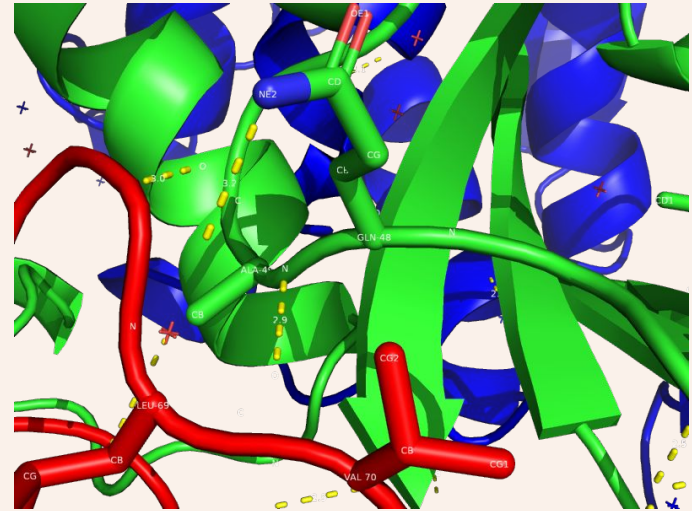


LYS-175 binds through N
GLY-174 and SER-177 and Mg stabilize the
reaction and proteins

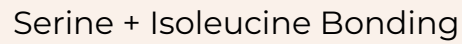
Interaction: alpha + beta



Glutamic acid of Alpha chain binds to Histidine with N and also interacts with the Beta chain



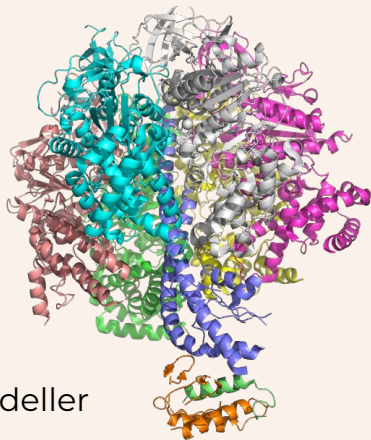
In this other case we observe a Leucine, Alanine and a Glutamine bond.



Modeling the protein

Mutation: var_088542; position 207 (R>H)

We used blast to find a template, we will use 2jdi



We separate the chains into different fasta files to use only chain A to align it with our mutation, we obtain a good alignment quality.

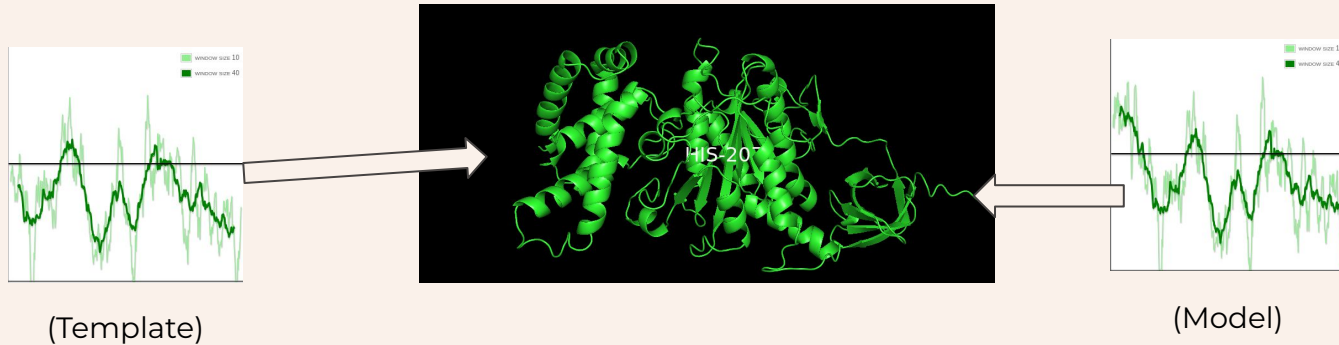
Then we model our structure with modeller

```
automodel(env,  
  alnfile = 'mutation_template.pir', # alignment filename  
  knowns  = ('TemplateA'),          # codes of the templates  
  sequence = 'P25705')               # code of the target
```

```
CLUSTAL 2.1 Multiple Sequence Alignments  
  
Sequence format is Pearson  
Sequence 1: P25705      553 aa  
Sequence 2: TemplateA  487 aa  
Start of Pairwise alignments  
Aligning...  
  
Sequences (1:2) Aligned. Score: 98  
Guide tree file created: [mutation_template.dnd]  
  
There are 1 groups  
Start of Multiple Alignment  
  
Aligning...  
Group 1: Sequences: 2      Score:10394  
Alignment Score 2849
```

Model Analysis: Models in pymol

After putting our models in pymol we quickly realize what is that part that we have that gave us a peak when putting the model in prosa

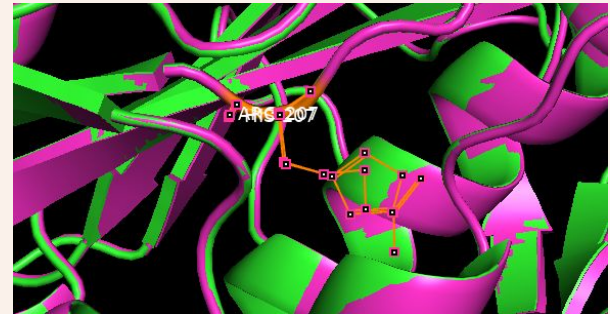


Model Analysis: Models in Pymol

To check for the differences between both models, we performed a superimposition to check if we can see the differences between the models



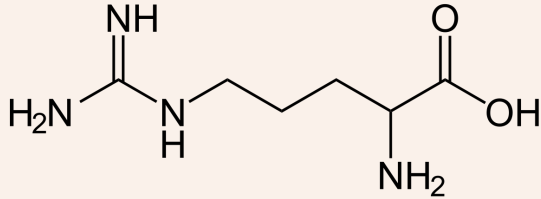
Superimposition: pink(mutation),
green(template)



(Mutation)

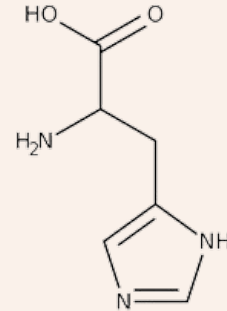
Model Analysis: Hypothesis

This mutation changes arginine (R) to histidine (H), both positively charged. However, histidine's ring structure suggests potential issues with DNA binding to the alpha helix, potentially affecting protein folding.



Arginine

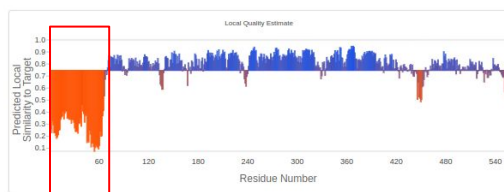
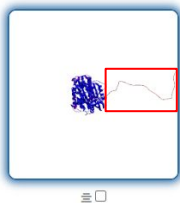
Histidine



Energy profile: mutant model

Quality for P25705.B99990001.pdb

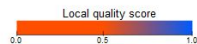
Downloads



QMEANDisCo Global: **0.75** ± 0.05

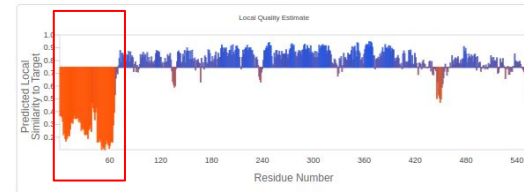
Sequence colored by local quality:

A: **MLSVRVAAAVRALPRRAGLVSRNALGSSFIAARNFHASNTHLQKTGTAEMSSILEERILGADTSV** 100
A: **GLKGMSLNLEPDNVGVVFGNDKLIKEDIVKRTGALVDVPPYGEELLGRVVDALGNAIDGKPIGSKTRRRVGLKAPGIIPRISVREPMQTGIKAVDSL** 200
A: **PIGRGQRELIIGDRQTGKTSIAIDTIINQKRENDGSEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYITVVSATASDAAPLQYLAPYSGCSMGYEY** 300
A: **RDNGKHALIIYDLSKQAVAYRQMSLLRRPPGREAYPGDVFLHSRLLEAAKMNDAPGGSLTALPVIETQAGDVSAYIPTNVISITDGGIFLETELR** 400
A: **YKGIKPAINVLVSVRVGSAAQTRAMKQVAGTMKLELAQYREVAFAQFGSDLDAAATQQLSRGVRLTELLKQGQSPMAIEEQVAVIYAGVRGYLDKLE** 500
A: **PSKITKFENAFLSHVVSQHALLGTIRADGKISEQSDAKLKEIVTNFLAGFEA** 553



Quality for P25705.B99990002.pdb

Downloads



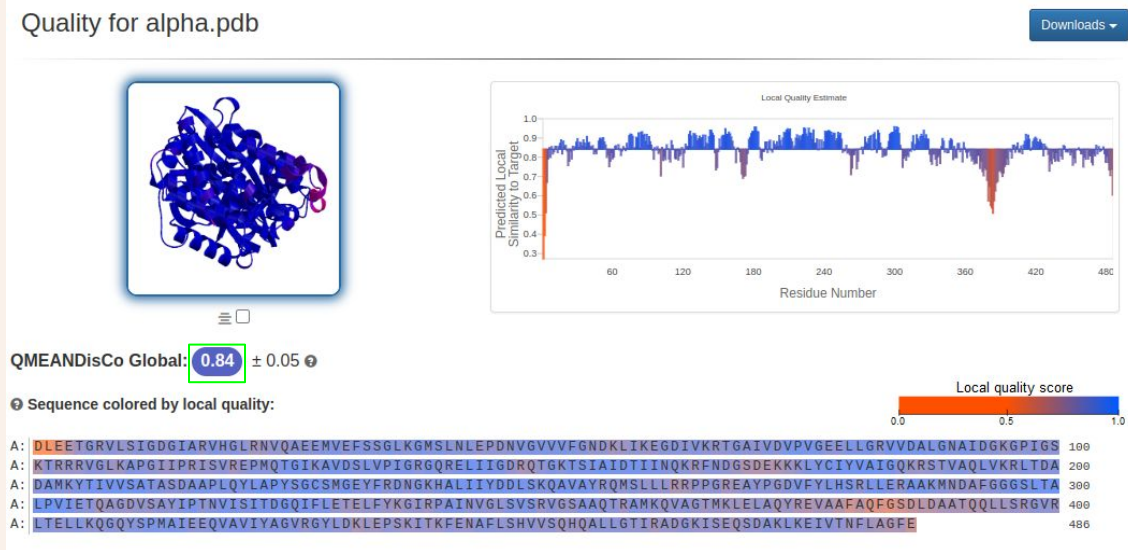
QMEANDisCo Global: **0.75** ± 0.05

Sequence colored by local quality:

A: **MLSVRVAAAVRALPRRAGLVSRNALGSSFIAARNFHASNTHLQKTGTAEMSSILEERILGADTSV** 100
A: **GLKGMSLNLEPDNVGVVFGNDKLIKEDIVKRTGALVDVPPYGEELLGRVVDALGNAIDGKPIGSKTRRRVGLKAPGIIPRISVREPMQTGIKAVDSL** 200
A: **PIGRGQRELIIGDRQTGKTSIAIDTIINQKRENDGSEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYITVVSATASDAAPLQYLAPYSGCSMGYEY** 300
A: **RDNGKHALIIYDLSKQAVAYRQMSLLRRPPGREAYPGDVFLHSRLLEAAKMNDAPGGSLTALPVIETQAGDVSAYIPTNVISITDGGIFLETELR** 400
A: **YKGIKPAINVLVSVRVGSAAQTRAMKQVAGTMKLELAQYREVAFAQFGSDLDAAATQQLSRGVRLTELLKQGQSPMAIEEQVAVIYAGVRGYLDKLE** 500
A: **PSKITKFENAFLSHVVSQHALLGTIRADGKISEQSDAKLKEIVTNFLAGFEA** 553



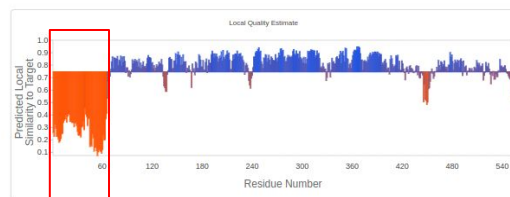
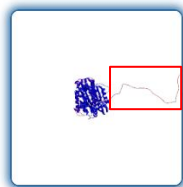
Energy profile: wild



Energy profile wild model

Quality for P25705.B99990001.pdb

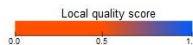
Downloads



QMEANDisCo Global: **0.75** ± 0.05

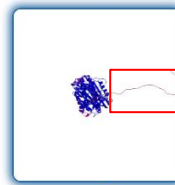
Sequence colored by local quality:

A: **MLSVRVAAVVRALPRRAGLVSRNALGSSFIAARNFHASNTHLQKTGTAEMSSILEERILGADTSV**LEETGRVLSIGDGIARVHGLRNVQAEEMVEFSS 100
A: **SLKGNLSNLEPDNVGVVFGNDKLIKEDIVKRTGAIYDVPVGEELGVRVVALGNALDGKPIGSKTRRRVGLKAPGIIPRISVREPMQTGIKAVDSLV** 200
A: **PIGRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGSEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIIVSATASDAAPLQYLAPYSGCSMGVEYF** 300
A: **RONGKHALIYDDLKQAVAYRQMSLLRRPPGREAYPGDVFYLHSRL LERAAKMNDAFGGGSLTALPVIETQAGDVSAIPTNVISITDGIQIFLETLE** 400
A: **YKGI RPAINVGLSVSRVGSAAQTRAMKQVAGTMKLELAQYREVAFAQFGSDLDAATQQLSRGVRLTELLKQGQYSPMAIEEQVAVIYAGVRGLDKLE** 500
A: **PSKITKFENAFLSHVVSQHALLGTIRADGKISEQSDAKLKEIVTNFLAGFEA** 553

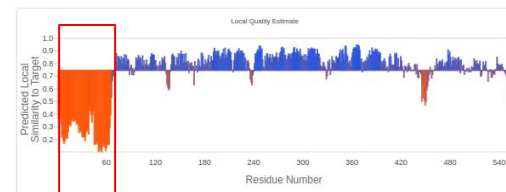


Quality for P25705.B99990002.pdb

Downloads



Compare



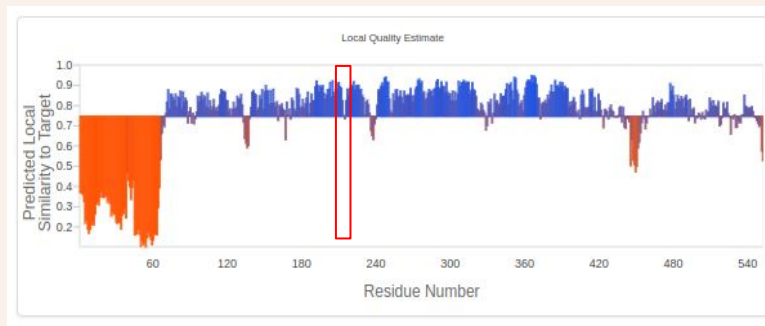
QMEANDisCo Global: **0.75** ± 0.05

Sequence colored by local quality:

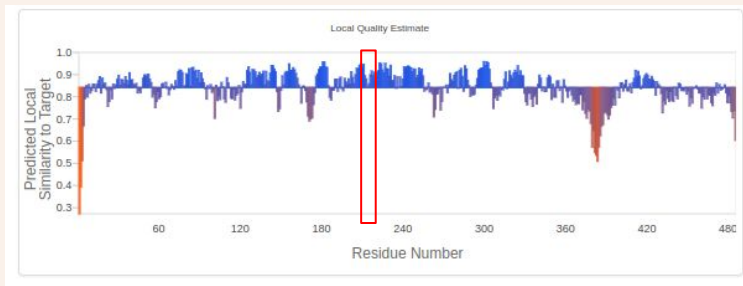
A: **MLSVRVAAVVRALPRRAGLVSRNALGSSFIAARNFHASNTHLQKTGTAEMSSILEERILGADTSV**LEETGRVLSIGDGIARVHGLRNVQAEEMVEFSS 100
A: **SLKGNLSNLEPDNVGVVFGNDKLIKEDIVKRTGAIYDVPVGEELGVRVVALGNALDGKPIGSKTRRRVGLKAPGIIPRISVREPMQTGIKAVDSLV** 200
A: **PIGRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGSEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIIVSATASDAAPLQYLAPYSGCSMGVEYF** 300
A: **RONGKHALIYDDLKQAVAYRQMSLLRRPPGREAYPGDVFYLHSRL LERAAKMNDAFGGGSLTALPVIETQAGDVSAIPTNVISITDGIQIFLETLE** 400
A: **YKGI RPAINVGLSVSRVGSAAQTRAMKQVAGTMKLELAQYREVAFAQFGSDLDAATQQLSRGVRLTELLKQGQYSPMAIEEQVAVIYAGVRGLDKLE** 500
A: **PSKITKFENAFLSHVVSQHALLGTIRADGKISEQSDAKLKEIVTNFLAGFEA** 553



Comparison of profiles



Mutant model



Wild



Wild model 1