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20

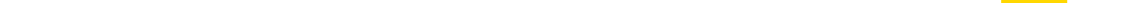
30

☐ **Disordered**

Transmembrane Heli

Signal Peptide



Cart 

Pred C C C C C C C C C C C C C C C C C C C C C C C C E E C C C C C C C

AA K A Y T W P I N K Q G G S A P G Q N K F G V D L G K Q Q D A D T A A W Y S P S M Y

10

20

30

40

Conf

Cart

Pred E E E E E E C C C C C C C C C C C H H H H H H H H H H C C C C C C C C H H

AA V H I V I K P D K E C V V N S G L G S V R G A R M A E M S Y S R A R S T Q L Q R I

60

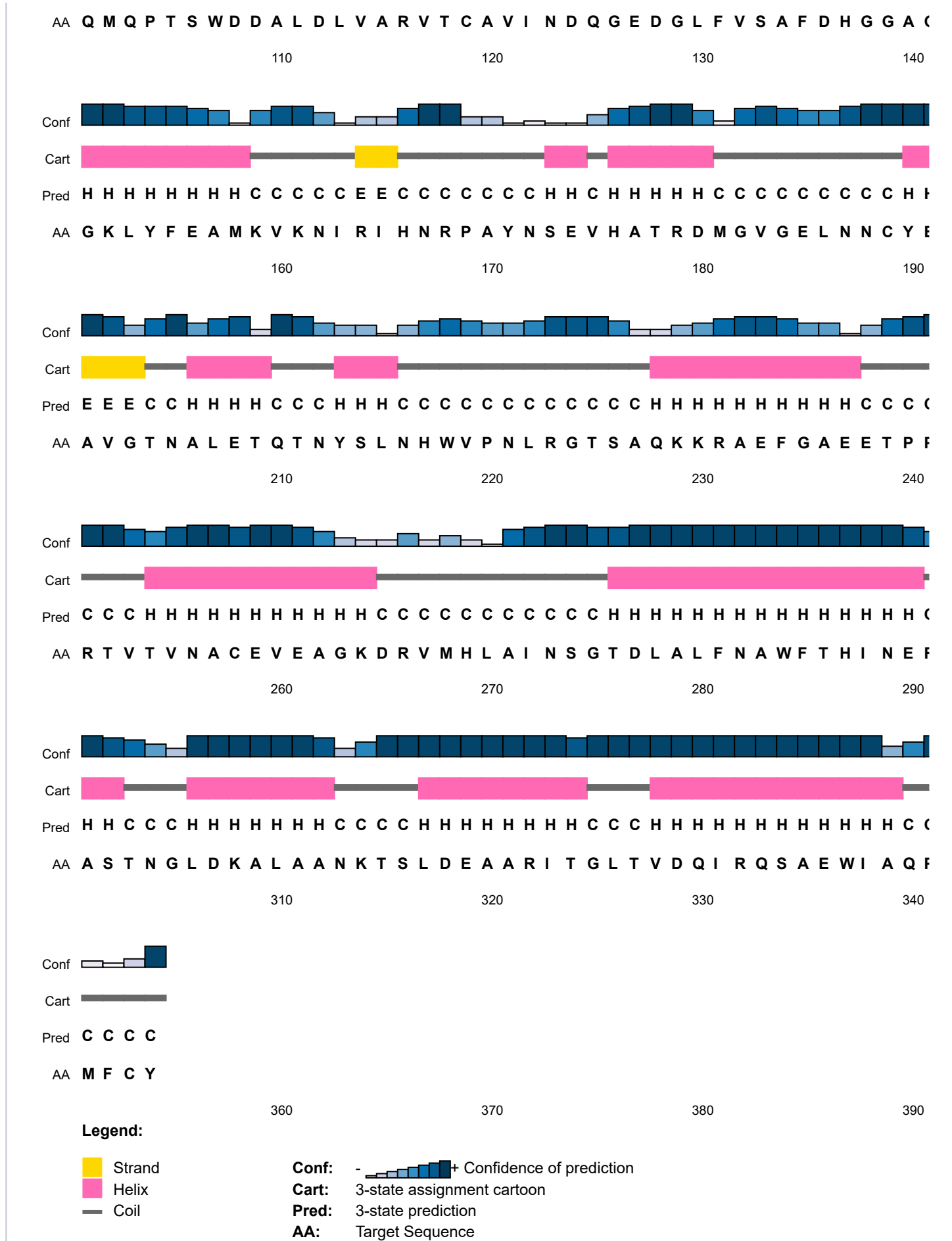
70

80

90

Cart 

Pred C E E E E C H H H H H H H H H H H H H H H H C C C E E E E E E C C C C C C



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Horiz Format Output (<http://bioinf.cs.ucl.ac.uk/psipred/api/submissions/6403bd2c-a036-11ea-bca0-00163e100d53.horiz>)
SS2 Format Output (<http://bioinf.cs.ucl.ac.uk/psipred/api/submissions/6403bd2c-a036-11ea-bca0-00163e100d53.ss2>)

Segment Resubmission





Name : Uncultured-2

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<http://bioinf.cs.ucl.ac.uk/psipred/>



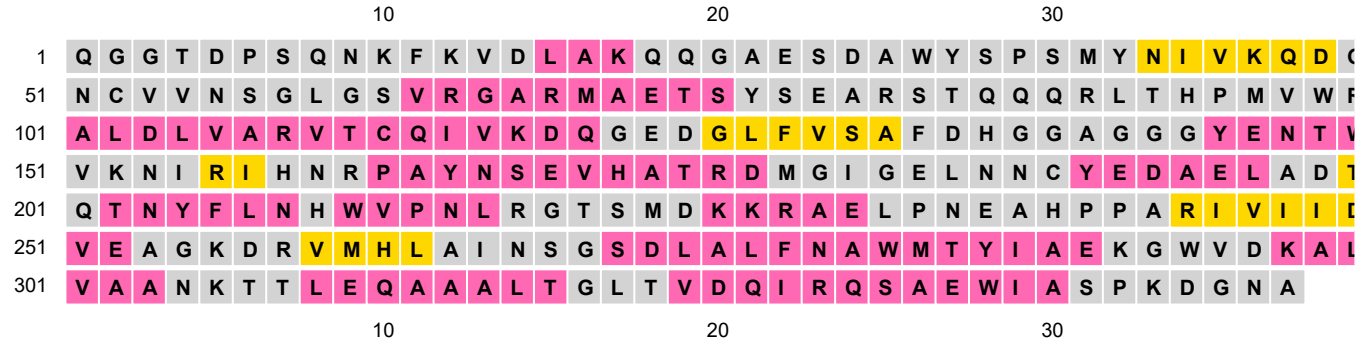
Sequence Plot

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Show psipred

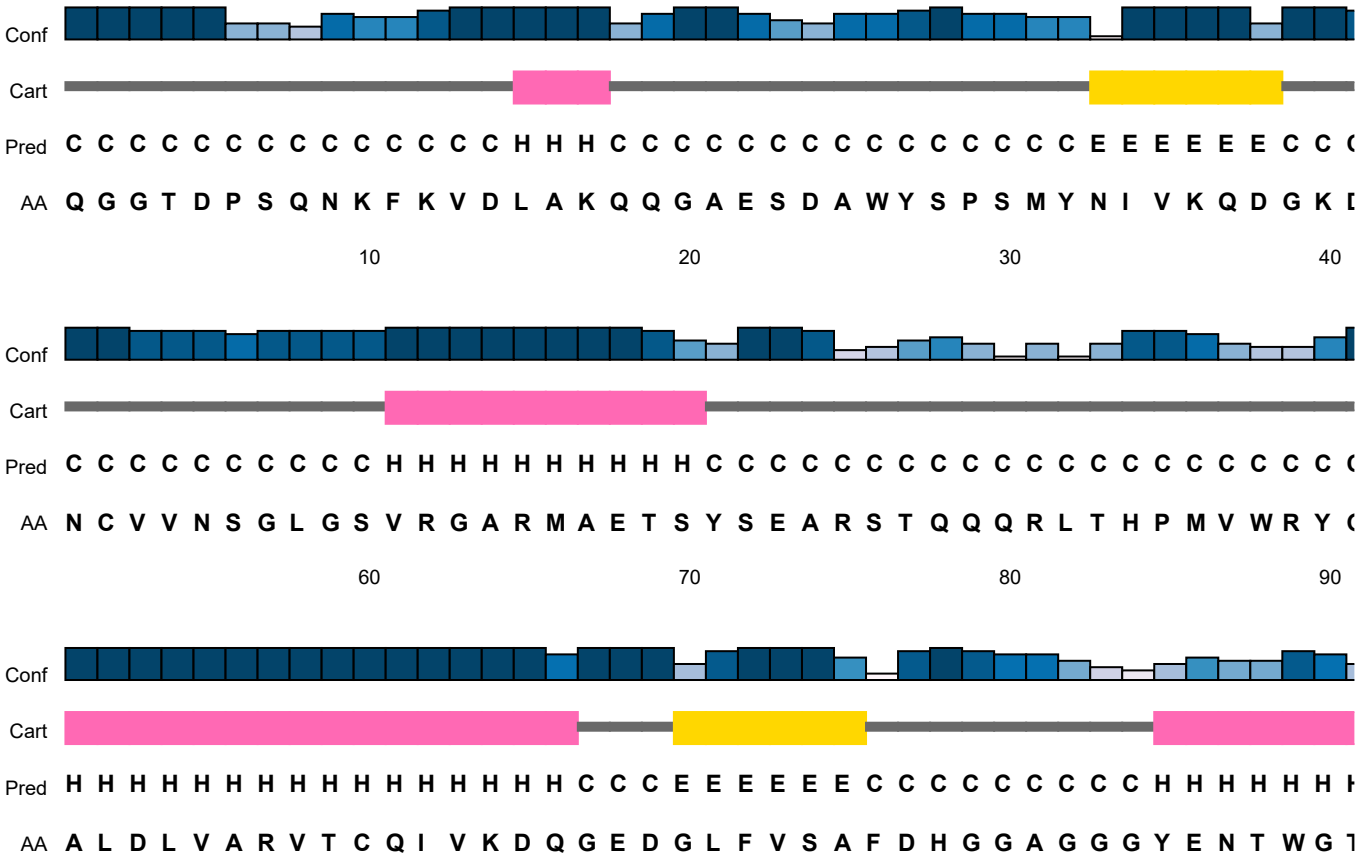
Show memsat

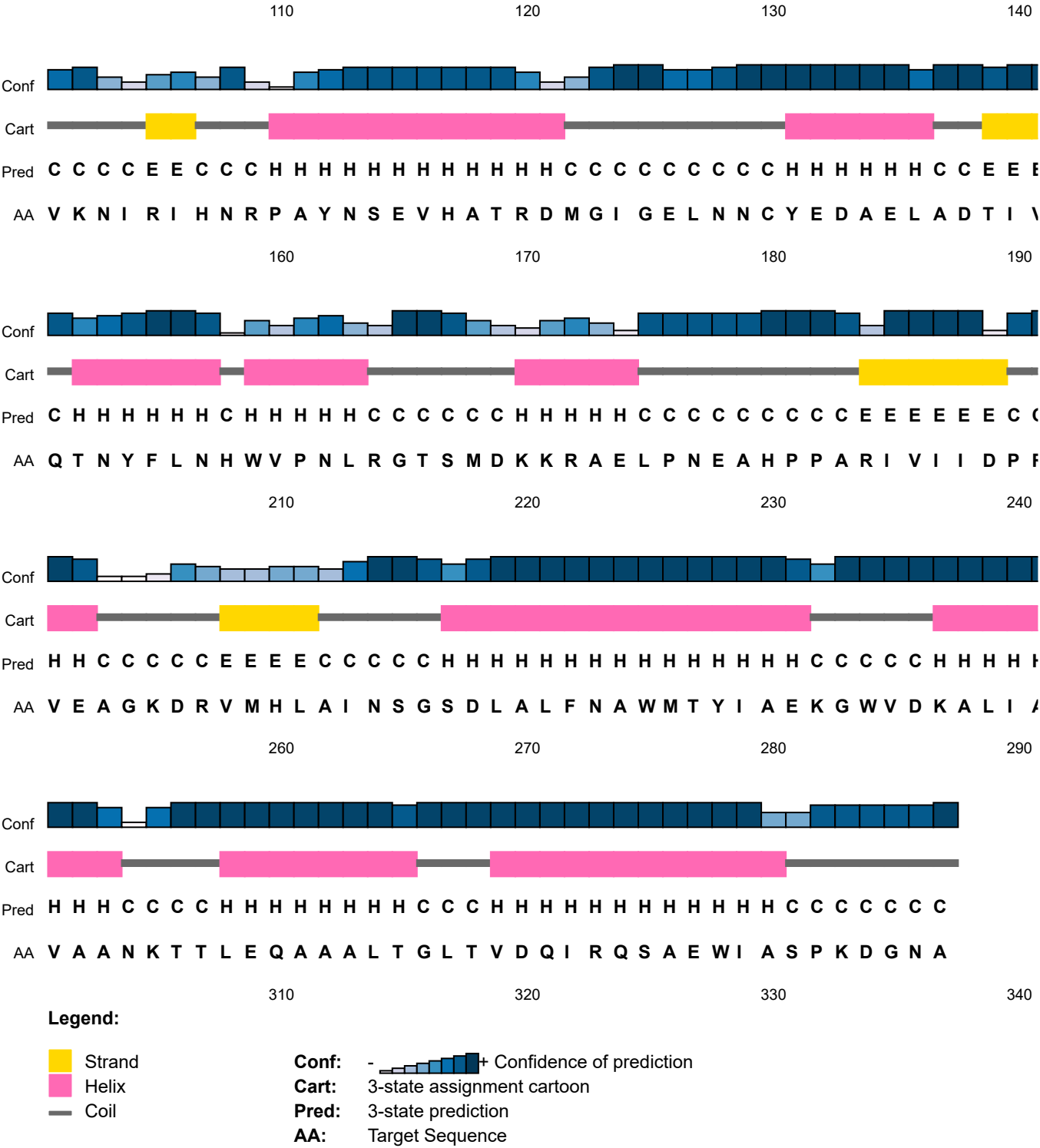
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PSIPRED Cartoon

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Horiz Format Output (<http://bioinf.cs.ucl.ac.uk/psipred/api/submissions/8d154dea-a039-11ea-b84e-00163e100d53.horiz>)
SS2 Format Output (<http://bioinf.cs.ucl.ac.uk/psipred/api/submissions/8d154dea-a039-11ea-b84e-00163e100d53.ss2>)

Segment Resubmission

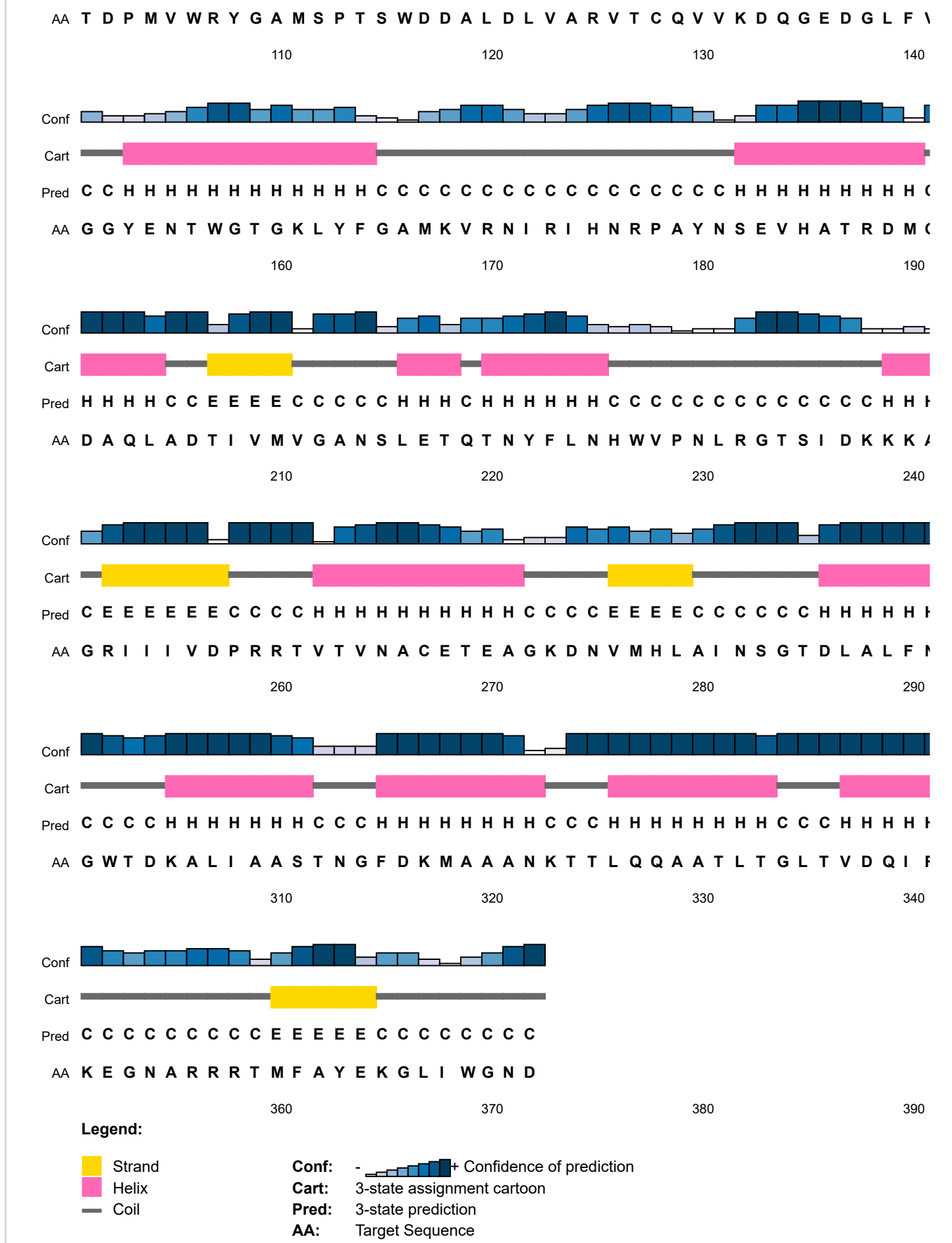




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Horiz Format Output (<http://bioinf.cs.ucl.ac.uk/psipred/api/submissions/bfd7de70-a041-11ea-bcdc-00163e100d53.horiz>)
SS2 Format Output (<http://bioinf.cs.ucl.ac.uk/psipred/api/submissions/bfd7de70-a041-11ea-bcdc-00163e100d53.ss2>)

Segment Resubmission



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<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>	<u>70</u>
KAYTWPINKQ	GGSA PGQNK F	GVDL GKQ QDA	DTAAWYSPSM	YNIVRQNGED	VHIVIKPDKE	CVVNSGLGSV
<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>	<u>130</u>	<u>140</u>
RGARMA EMSY	SRARSTQLQR	LTDPMVWRYG	QM QPTSWDDA	LDLVARVTCA	VINDQGEDGL	FVSAFDHGG A
<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>	<u>190</u>	<u>200</u>	<u>210</u>
GGGYENTWGT	GKLYFEAMKV	KNIRIHN RPA	YNSEVHATRD	MGVGELNNCY	EDAELADTIV	AVGTNALETQ
<u>220</u>	<u>230</u>	<u>240</u>	<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>
TNYSLNHWVP	NLRGTSAQKK	RAEFGAEETP	PARIIIIVDP R	RTVTVNACEV	EAGKDRVMHL	AINSGTDLAL
<u>290</u>	<u>300</u>	<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>
ENAWFTHINE	RGWTDKAFIG	ASTNGLDKAL	AANKTSLDEA	ARITGLTVDO	IROSAEWIAQ	PKAANARRRT

[illegible]

Query	351	MFCY	354
Helix	351		354
Sheet	351	EE	354
Turns	351		354
Struc	351	EECC	354

Total Residues:	H: 222	E: 203	T: 49
Percent:	H: 62.7	E: 57.3	T: 13.8

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Target Sequence:

10203040506070

QGGTDPSQNK FKVDLAKQQG AESDAWYSPS MYNIVKQDGK DVHVVIMPDK NCVVNSGLGS VRGARMAETS

8090100110120130140

YSEARSTQQQ RLTHPMVWRY GAMSPTSWDD ALDLVARVTC QIVKDQGEDG LFVSAFDHGG AGGGYENTWG

150160170180190200210

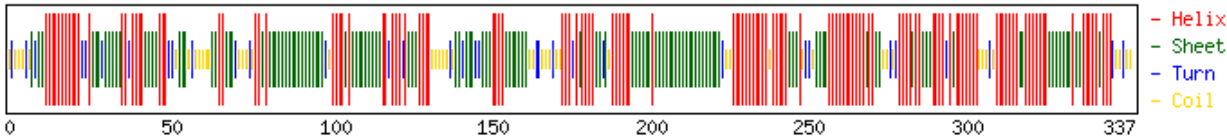
TGKLYFGAMK VKNIRIHNRP AYNSEVHATR DMGIGELNNC YEDAELADTI VVVGANPLET QTNFYLNHWV

220230240250260270280

PNLRGTSMDK KRAELPNEAH PPARIVIIDP RRTVTVNACE VEAGKDRVMH LAINSGSDLA LFNAWMTYIA

290300310320330

EKGWVDKALI AASTNGFDKM VAANKTTLEQ AAALTGLTVD QIRQSAEWIA SPKDGNA



Secondary Structure:

* * * * *

Query 1 QGGTDPSQNKFKVDLAKQQGAESDAWYSPSMYNIVKQDGKDVHVVIMPDKNCVVNSGLGSVRGARMAETS 70

Helix 1 HHHHHHHHHHHHHHHHH HHHHHHHHHHHHHHHHH HH 70

Sheet 1 EEEEEEEEEEE EEEEEEEEEEE EEEEE EEE EEEEEEE 70

Turns 1 T T T TT TT T T T TT T 70

Struc 1 CTCCCTCETEHHHHHHHHHTHEETEEEEHHTHHHEEEHHHTCEEECTCCCCCEEHHEETC 70

* * * * *

Query 71 YSEARSTQQQLRLTHPMVWRYGAMSPTSWDDALDLVARVTCQIVKDQGEDGLFVSAFDHGGAGGGYENTWG 140

Helix 71 HHHHHH HHHHHHHHHHHHHHHHHHHHHHHHHHHHH 140

Sheet 71 EEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEE EEEEE EEEEE 140

Turns 71 T TT T T T T T T 140

Struc 71 CCTCHHEHEEEEEEEEEEEEEETCHHHHEEEEEEEEEHHTHHHHEEEHHHHCCTCCTCEETEE 140

* * * * *

Query 141 TGKLYFGAMKVKNIRIHNRPAYNSEVHATRDMGIGELNNCYEDAELADTI VVVGANPLETQTNFYLNHWV 210

Helix 141 HHHHHHHHHHHH HHHHHHHHH HHHHHHHHHHHH HH 210

Sheet 141 EEEEEEEEEEEEEEEEE EEEEE EEEEE EEEEEEEEEEEEEEEEEEEEE 210

Turns 141 TT TT T T T T T 210

Struc 141 TTEEEHHHEEEEEECCTTCCCTCCHHHTHEHHHHEETECHHHHHHEEEEEHEEEEEEEEEEEEE 210

* * * * *

Query 211 PNLRGTSMDKKRAELPNEAHPPARIVIIDPRRTVTVNACEVEAGKDRVMHLAINSGSDLALFNAWMTYIA 280

Helix 211 HHHHHHHHHH HHHHHHHH HHHHHHHHHHHHHHHH HHHHHHHHHHHH 280

Sheet 211 EEEEE EEE EEEEE EEEEE EEEEEEEEEEE 280

Turns 211 T TT T TT TT TT T T 280

Struc 211 EEEETCCHHHHHHHHHHCHHHHEEHHCCTTCEEEHHHHHHHHHHHEHHEECCTCHHHHEHHEEH 280

* * * * *

Query 281 EKGWVDKALIAASTNGFDKMVAANKTTLEQAAALTGLTVDQIRQSAEWIASPKDGNA 337

Helix 281 HHHHHHHHHH HHHHHHHHHHHHHHHHHHHHHHHHHHHHH 337

Sheet 281 EEEEE EEEEEEEEEEEEEEEEEEEEEEEEEEE 337

Turns 281 T T T T T T T 337

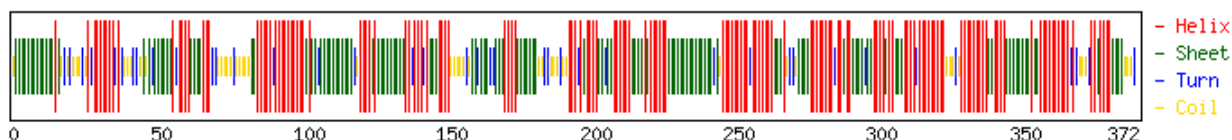
Struc 281 HTHHHHHHHHCCTCHHHHHHEHHHHHHHEEEEEHEHHHHHEHHHTCCTCC 337

Total Residues: H: 212 E: 202 T: 50

Percent: H: 62.9 E: 59.9 T: 14.8

Mail

<u>10</u>	<u>20</u>	<u>30</u>	<u>40</u>	<u>50</u>	<u>60</u>	<u>70</u>
HFCIVGCGYK	AYTWDINKQG	GADPSQNKFK	ADLSKQDGAN	SDAWYSPSMH	NIVKQGGKDV	HLVIMPDKGC
<u>80</u>	<u>90</u>	<u>100</u>	<u>110</u>	<u>120</u>	<u>130</u>	<u>140</u>
SVNSGLGSR	GARMAETSFS	EARSTQAQRL	TDPMVWRYGA	MSPTSWDDAL	DLVARVTCQV	VKDQGEDGLF
<u>150</u>	<u>160</u>	<u>170</u>	<u>180</u>	<u>190</u>	<u>200</u>	<u>210</u>
VSAFDHGGAG	GGYENTWGTG	KLYFGAMKVR	NIRIHNRPAY	NSEVHATRDM	GVGELNNCYE	DAQLADTIVM
<u>220</u>	<u>230</u>	<u>240</u>	<u>250</u>	<u>260</u>	<u>270</u>	<u>280</u>
VGANSLETQT	NYFLNHWVPN	LRGTSIDKKK	AELPNEPHAA	GRIIIVDPRR	TVTVNACETE	AGKDNVMHLA
<u>290</u>	<u>300</u>	<u>310</u>	<u>320</u>	<u>330</u>	<u>340</u>	<u>350</u>
INSGTDLALF	NAWMTYIAEK	GWTDKALIAA	STNGFDKMAA	ANKTTLQQAA	TLTGLTVDQI	RQSAEWIAMP
<u>360</u>	<u>370</u>					
KEGNARRRTM	FAYEKGITWG	ND				



			*	*	*	*	*	*	*	
Query	1	HFCIVGCGYKAYTWDINKQGGADPSQNKFKADLSKQDGSNDAWYSPSMHNIVKQGQKDVHLVIMPDKGC	70							
Helix	1	HH	HHHHHHHHHHHH	HHHHHHHHHHHHHHHHHHHHHH	70					
Sheet	1	EEEEEEEEEEEEEE	E	EEEEEEEEEE	EEEEEE	70				
Turns	1	T T T T T T T T T T	70							
Struc	1	CEEEEEEEEEEEHECTCTCCCTCHTHHHHHHHTHTCCCTTCECETEEEEEEEHTHHHHEEEHHHTTCC	70							
			*	*	*	*	*	*	*	
Query	71	SVNSGLGSGVRGARMAETSFSEARSTQAQRLTDPMVWRYGAMSPTSWDDALDLVARVTCQVVKDQGEDGLF	140							
Helix	71	HHHHHHHHHHHHHHHHHHHH	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	140						
Sheet	71	EEEEEEEE	EEEEEEEEEEEEEEEEEEEE	EEEEEEEEEEEEEEEEEE	EE	140				
Turns	71	T T T T T T T T T T	140							
Struc	71	CCCTCCCCCEEHHHHHTHHHHHHHHHHHEEETEEEEEEEEETCHHHHEHEEEEEEEHHHTHHHTHEE	140							
			*	*	*	*	*	*	*	
Query	141	VSAFDHGGAGGGYENTWGTGKLYFGAMKVRNIRIHNRPAYNSEVHATRDMGVGELNNCYEDAQLADTIVM	210							
Helix	141	HHHHH	HHHHHHHHHHHH	HHHHHHHHHH	HHHHHHHHHHH	210				
Sheet	141	EEE	EEEEEEEEEEEEEEEEEEEE	EEEEEEEEEEEEEEEEEEEE	EEEE	210				
Turns	141	T T TT TT T T T T	210							
Struc	141	EHHHHCCCCCTCEETEEETEEEEHHHEEEEEECCTTCCCTCCHHHTHEHHHHHEETEHHHHHHEEEEH	210							
			*	*	*	*	*	*	*	
Query	211	VGANSLETQTNFYFLNHWVPNLRGTSIDKKKAELPNEPHAAGRRIIVDPRTVTVNACETEAGKDNVMHLA	280							
Helix	211	HHHHHHH	HH	HHHHHHHHHHHHHHHHHHHHHH	HHHHHHHHHHHHHHHHHHHH	280				
Sheet	211	EEEEEEEEEEEEEEEEEEEEEEEE	EEE	EEEEEE	EEEEEE	280				
Turns	211	T T TT TT T TT TT	280							
Struc	211	EHHHHHHEEEEEEEEEEEEEETECHHHHHHHHHTHHHHHHHEEHCTTCEEEHHHHHHHHHTHHEHHEE	280							
			*	*	*	*	*	*	*	
Query	281	INSGTDLALFNAWMTYIAEKGWTDKALIAASTNGFDKMAAANKTTLQQAATLTGLTVDQIRQSAEWIAMP	350							
Helix	281	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	350						
Sheet	281	EEEEEEEEEEEEEEEEEE	EEEEEE	EEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	350					
Turns	281	T T TT T T TT	350							
Struc	281	EETEEHHHHEHHEEEHHHHTHHHHHHHHHCCTTCHHHHHHHHHEHHHHHEEEEEEHEEHHHHHHHHH	350							

```
Query 351 KEGNARRRTMFAYEKGLIWGND 372
Helix 351 HH      HHHHHHHHHHH 372
Sheet 351      EEEEEEEEEEE 372
Turns 351 T T    T      T      T 372
Struc 351 THTCCCTHHEHHHEEECCCT 372
```

```
Total Residues: H: 234   E: 218   T: 56
                Percent: H: 62.9  E: 58.6  T: 15.1
```

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