



Quickfinder

CS-BLAST	HHblits	HHpred	HHsenser	HMMER3	PatternSearch	ProtBLAST	ProtBLAST+	PSI-BLAST	PSI-BLAST+	SimShiftDB
New job	Resubmit	Resubmit_HMM	Resubmit/HHsenser	Realign	Log	Input-params	Delete			

Help

Create model Merge Q/T alignments Forward to PCoils Forward MSA Save Export

View Alignment

72 712

100 200 300 400 500 600 700






Resubmit section

No	Hit	Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1	4xmm_B Nucleoporin NUP145; str	100.0	7E-159	2E-163	1371.3	43.9	641	72-712	12-652 (652)
2	3bgi_B Nucleoporin NUP145; NPC	100.0	1E-104	3E-109	884.3	40.9	427	126-552	15-441 (442)
3	5a9q_5 Nuclear pore complex pr	100.0	2E-104	4E-109	946.2	37.0	538	154-703	299-935 (937)
4	4jro_A Fusion protein of prote	100.0	2.4E-83	6.7E-88	755.9	31.9	449	107-555	305-753 (753)
5	4ycz_A Fusion protein of SEC13	100.0	2.8E-84	7.7E-89	778.9	16.5	484	152-701	356-871 (876)
6	5a9q_8 Nuclear pore complex pr	98.2	1.8E-05	4.9E-10	93.0	16.2	311	234-572	145-503 (656)
7	33f3_C Nucleoporin NUP85; stru	100.0	0.00021	5.7E-09	82.7	20.5	312	230-570	177-570 (570)
8	4xmm_D Nucleoporin NUP85; stru	98.0	0.00012	3.3E-09	86.7	18.7	341	230-601	148-568 (715)
9	3jrp_A Fusion protein of prote	97.5	2.8E-05	7.6E-10	84.1	1.0	58	122-179	322-379 (379)
10	3iko_C Nucleoporin NUP84; NPC,	96.2	0.05	1.4E-06	61.3	14.1	267	231-513	71-451 (460)
11	2pm7_A Protein WEB1, protein t	96.2	0.066	1.8E-06	59.3	14.7	219	289-518	144-382 (399)
12	4ycz_B NUP85; structural prote	96.1	0.019	5.3E-07	69.3	10.4	276	289-572	221-650 (933)
13	3mzk_B Protein transport prote	95.7	0.029	8.1E-07	62.9	9.2	112	292-411	154-288 (441)
14	4bzbj_A Protein transport prote	95.6	0.067	1.7E-06	68.0	12.5	215	288-514	507-742 (1273)
15	5a9q_4 Nuclear pore complex pr	94.7	0.61	1.8E-05	56.7	17.1	268	292-574	347-714 (925)
16	5cqr_A Elongator complex prote	84.4	7.1	0.0002	45.7	12.3	102	473-581	277-395 (622)
17	5cqs_A Elongator complex prote	76.9	8	0.00022	43.2	9.0	109	473-581	109-225 (435)
18	2qx5_A Nucleoporin NIC96; mRNA	70.7	1.1E+02	0.0029	36.2	16.7	271	295-578	159-485 (661)
19	1o3u_A Conserved hypothetical	37.9	2.8E+02	0.0076	25.5	10.8	93	475-572	19-125 (135)
20	2pm7_A Protein WEB1, protein t	35.4	3E+02	0.0084	30.1	11.9	166	140-346	7-231 (399)
21	3mkq_B Coatomer subunit alpha;	29.4	4.4E+02	0.012	25.2	11.0	96	476-574	10-114 (177)
22	4bzbj_A Protein transport prote	27.7	5.9E+02	0.016	32.2	14.2	173	479-658	527-744 (1273)
23	3mkq_B Coatomer subunit alpha;	22.8	2.5E+02	0.007	22.0	7.6	61	279-339	80-140 (177)



PROTEIN DATA BANK


























[illegible]

T ss_pred	CCCCHHHHhhccCCCCCccCHHHHHHHCCccccccCcccccCccccHHhhccccchHHHHccccccccCccccc	
Q ss_pred	hhccCCEeecccccccccccccceccccccccchHHHHHHHHHHHHhhCeeccCCCCCeeCCCCHHHHHHccccchHH	
Q Fri_Mar_04_23:	152 AKFSTGSMLLTKDIVGKSGVSIKRLPTLQKKFLFDVYLDKEIEKVTIEARKSNPYQISSESLFLKDALDYMEKTTSSD	231 (712)
Q Consensus	152 ~f~ll~l~s~i~ng~P~l~f~d~e	231 (712)
T Consensus	92 ~f~ll~l~s~i~ng~P~l~f~d~e	171 (652)
T 4xmm_B	92 AKFSTGSMLLTKDIVGKSGVSIKRLPTLQKKFLFDVYLDKEIEKVTIEARKSNPYQISSESLFLKDALDYMEKTTSSD	171 (652)
T ss_dssp	EEECSSSEEEECSSSSSEEECCCCCSCGGGSHHHHHHHHTTEEEECSSSSSEEEECSCGGGGGSGCTTSHH	
T ss_pred	ccccCCEeeccccccCceccccchhhHHHHHHHHHHhhCeeccCCCCCeeCCCCHHHHHHccccchHH	
Q ss_pred	hHHHHHHHHhCCccccccCChHHHHHHHHHHHHHHHHHHHHHHHHHHHHhCCCHHHHHHHhCCCHHHHHHH	
Q Fri_Mar_04_23:	232 YNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCLRTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLNDVVRASKLA	311 (712)
Q Consensus	232 ~vW~L~saLfd~R~Ls~WL~v~l~e~if~L~g~I~A~A	311 (712)
T Consensus	172 ~vW~L~saLfd~R~Ls~WL~v~l~e~if~L~I~eA~A	251 (652)
T 4xmm_B	172 YNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCLRTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLNDVVRASKLA	251 (652)
T ss_dssp	HHHHHHHHHHSCCCCCCSCSSHH	
T ss_pred	hHHHHHHHHhCCccccccCchHHHHHHHHHHHHHHHHHHHHHHHHHHHHhCCCHHHHHHHhCCCHHHHHHH	
Q ss_pred	HHCCCCcHHHHHHHHhCCChHHHHHHHHHHHHHHHHHHHHHHHHHHHHhCCCHHHHHHHhCCccccccccchhccCCCCHHHHHHHH	
Q Fri_Mar_04_23:	312 IESKNGHLSVLISYLGSDNPRIKRLAEQLQKWSGTGGCSIDKNISKIYKLLSGSPFEGFLSLKLESEFSLWCLLNLTL	391 (712)
Q Consensus	312 i~gn~rLA~Llsq~gs~r~QL~W~I~kIY~LLAG~e~i~e~ldW~ralgl~LW	391 (712)
T Consensus	252 i~gd~rLA~Llsq~gs~r~QL~W~I~kIY~LLAG~e~i~e~ldW~ralgl~LW	331 (652)
T 4xmm_B	252 IESKNGHLSVLISYLGSDNPRIKRLAEQLQKWSGTGGCSIDKNISKIYKLLSGSPFEGFLSLKLESEFSLWCLLNLTL	331 (652)
T ss_dssp	HHHTCHHHHHHHHTTSCCHHH	
T ss_pred	HHCCCCcHHHHHHHHhCCChHHHHHHHHHHHHHHHHHHHHHHHHHHHHhCCCHHHHHHHhCCccccccccchhccCCCCHHHHHHHH	
Q ss_pred	cCCCCCCHHHHHHHHHHHhCCcCcCHHHHHHHHHhCCCHHHHHhCcccCCCCccccchHHHHHHHHhCccccCchhh	
Q Fri_Mar_04_23:	392 YGQIDEYSLLESVLQSHLDKFSLPYDDPIGVIFQLYAANENTKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETS	471 (712)
Q Consensus	392 Yg~sl~av~y~P~D~LLkLya~le~vL~p~s~t~lD~rLsW~L~vL~a~g~s~	471 (712)
T Consensus	332 Y~sl~av~y~P~D~LLkLya~le~vL~p~s~t~lD~rLsW~L~vL~a~g~s~	411 (652)
T 4xmm_B	332 YGQIDEYSLLESVLQSHLDKFSLPYDDPIGVIFQLYAANENTKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETS	411 (652)
T ss_dssp	STTTTTSCCHHHHHHHHHHTTCCCTTCHHHHHHHHHHHGGGHHHHHHHHHHHSCSSCHHHHHHHHHHHHTSSCCCCHHHH	
T ss_pred	cCCCCCCHHHHHHHHHHHhCCcCcCHHHHHHHHHhCCCHHHHHhCcccCCCCccccchHHHHHHHHhCccccCchhh	
Q ss_pred	HHHHHHHHHHHHCCCCCHHHHHHHHHhCCCHHHHHHHHHHHhccccchHHHHHHHHhCcCHHHHHHHHHHHhCCC	
Q Fri_Mar_04_23:	472 DEATFAFAAQLEFAQLHGHSFLVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRLKIPSQILFNAQALDRYEGN	551 (712)
Q Consensus	472 d~Lt~sfA~QLe~Glw~AvFVlHl~d~R~aIr~lL~R~L~e~L~IP~WI~eAkAl~ar~gd	551 (712)
T Consensus	412 d~l~fa~QLe~Glw~aIFVlHl~d~R~aIr~lL~R~L~e~L~IP~WI~eAkAl~a~ar~gd	491 (652)
T 4xmm_B	412 DEATFAFAAQLEFAQLHGHSFLVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRLKIPSQILFNAQALDRYEGN	491 (652)
T ss_dssp	HHHHHHHHHHHHHTTCHHHHHHHHHHTTCSCHHH	
T ss_pred	HHHHHHHHHHHHCCCCCHHHHHHHHHhCCCHHHHHHHHHHHhccccchHHHHHHHHhCcCHHHHHHHHHHHhCCC	
Q ss_pred	HHHHHHHHHHhCcCHHHHHHHHHHHhHHHHHHHHhccccCccccCHHHHHHHHHhCccccCChhhcchHHHHHHHHhCCcCcH	
Q Fri_Mar_04_23:	552 YLSEVQNLLLGSSYDLAEMAIVTSLGPRLLSNPNVQNNELKTLREILNEFPDSERDKWSVSNVFEVYLKLVLDNVETQ	631 (712)
Q Consensus	552 ~e~Ll~A~eAh~v~v~laP~II~d~L~Ll~fp~I~W~Gg~Vy~dyl~l~	631 (712)
T Consensus	492 ~e~Ll~A~eAh~v~v~vaP~II~d~L~Ll~fp~I~W~Gg~vy~dyl~l~	571 (652)
T 4xmm_B	492 YLSEVQNLLLGSSYDLAEMAIVTSLGPRLLSNPNVQNNELKTLREILNEFPDSERDKWSVSNVFEVYLKLVLDNVETQ	571 (652)
T ss_dssp	---CHHHHHH---CHHHHHHHHHH---CHHHHHHHHHHHH---CHHHHHHHHHHHH---CHHHHHHHHHHHH---C	
T ss_pred	HHHHHHHHHHhCcCHHHHHHHHHHHhHHHHHHHHhccccCccccCHHHHHHHHHhCccccCChhhcchHHHHHHHHhCCcCcH	
Q ss_pred	HHHHHHHHHHHHhCcCHHHHHHHHHHHHHHHHHHHHHhccccchHHHHHHhCCCCCHHHHHHHHHHHhccccCccc	
Q Fri_Mar_04_23:	632 ETIDSLISGKIFYDQYKHCREVAACCNVMSQEIIVSKILEKNPNISIGDSKAKLLEPLGQPEKAYLRGEFAQDLMKCTYK	711 (712)
Q Consensus	632 ~l~L~L~l~va~ems~v~l~il~LPL~ed~Y~l~	711 (712)
T Consensus	572 ~l~L~L~l~r~va~ema~v~l~il~LPL~ed~y~l~	651 (652)
T 4xmm_B	572 ETIDSLISGKIFYDQYKHCREVAACCNVMSQEIIVSKILEKNPNISIGDSKAKLLEPLGQPEKAYLRGEFAQDLMKCTYK	651 (652)
T ss_dssp	HHHHHHHHHHHHH---CHHHHHHHHHHHHHHHHHHHHHH---CHHHHHHTTC---CHHHHHHHHHH	
T ss_pred	HHHHHHHHHHHHhCcCHHHHHHHHHHHHHHHHHHHHHhccccccccchHHHHHHhCCCCCHHHHHHHHHHHhccccCccc	
Q ss_pred	C	
Q Fri_Mar_04_23:	712 I 712 (712)	
Q Consensus	712 ~ 712 (712)	
T Consensus	652 ~ 652 (652)	
T 4xmm_B	652 I 652 (652)	
T ss_dssp	C	
T ss_pred	C	
No 2		
   		
3bg1_B Nucleoporin NUP145; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore complex, nucleus, phosphoprotein; 3.00A {Saccharomyces cerevisiae} PDB: 3bgo_B 3iko_B		
Probab=100.00 E-value=9.7e-105 Score=884.32 Aligned_cols=427 Identities=100% Similarity=1.448 Sum_probs=0.0		
Q ss_pred	ccccchHHHHhhccccccccCccchhhccCccceccccccccccccccccchHHHHHHHHHHhCeeccccc	
Q Fri_Mar_04_23:	126 FSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTLQKKFLFDVYLDKEIEKVTIEARKS	205 (712)

No 3     

☐ >5a9q_5 Nuclear pore complex protein NUP96; transport protein; 23.00A {Homo sapiens}
Probab=100.00 E-value=1.6e-104 Score=946.21 Aligned_cols=538 Identities=18% Similarity=0.296 Sum_probs=0.0

☐ **>3jro_A** Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic vesicle, endoplasmic reticulum, transport, membrane, mRNA transport; 4.00A [Saccharomyces cerevisiae]
 Probab=100.0 E-value=2.4e-83 Score=755.86 Aligned cols=449 Identities=100% Similarity=1.435 Sum_probs=0.0

No 5                          

No 8

PDB PROTEIN DATA BANK NCBI PubMed

>4xmn_D Nucleoporin NUP85; structural protein, immune system, transport protein-immune complex; 7.38Å {Saccharomyces cerevisiae S288C} PDB: 4xmn_D
Probab=98.04 E-value=0.00012 Score=86.74 Aligned_cols=341 Identities=13% Similarity=0.079 Sum_probs=0.0

Q ss_pred HHHHHHHHCCCCccccCCCHHHHHHHHH-----HHHHHHhhc---c---CCHH----

Q Fri_Mar_04_23: 230 SDYLNKWLKSILFPVSPYPKYTDNQVKMALLKKERHC--RLTSWIVSQ--TGPETEEKLRN--S--SNEL----- 292 (%)

Q Consensus 230 -e-vw-L-saLfD--Rr---Ls-WL- v-v-l --S-SNEL----- 292 (%)

T Consensus|+||.+|=+.+.+. . |-. |+|.+. . ..+..+.. . .|. |.

T 4xmn_D 148 Iw-Le-f-g-----l-Ll-Wln-p-e-ll~----p-h-F 216 (%)

T T ss_dssp ESILTVLNCIRLMYPLDGQVEEN--RSEPTESLLNWLNRSDEPDEEYIEQVFSSVDSTAGKVFEQYF 216 (%)

T ss_pred HHHHHHHHHHSSSTTCSCGGC-----HHHHHHHHHHCCCCSHHHHHHTTC-----CSSSSCSHHH

H HHcccccccccHCCCCCCCCCcHccccCCCCCCCchhh

Q ss_pred -----HHHHHHHHCCCCCCCCCCCCHHCC-----CCcHHHHHH--HHcCCCCHHHHHHHHHHHHHH-----CCC-

Q Fri_Mar_04_23: 293 EQIFLYLLNDVVRRASKLAIESK-----NGHLSSLVIS--YLGSNDPRIRDLAEQLQKWST-----GGC- 349 (%)

Q Consensus 293 -e-if~L-g-I-A-Ai-g-----n-rLA-Lls-q-gs r-QI-W----- 349 (%)

.|+.+.+.|++||+.+.+. +.+.+. ++.+. +....|+. . +.

T Consensus 217 W-V-lvLrG-A-IL-----l-Ll-v L-P-----w-W-----l----- 293 (%)

T 4xmn_D 217 WKLLNLGVLRGLLSQAIGCTIERSDLLPYLSYDTCAVSFDAVDSITELLKQVPK--DSSSTRFRWKLVKLQSQAFGSSAT 293 (%)

T ss_dssp HHHHHHHHTTCCHHHHHHTTTTCCCCCHHTCHHHHHHHHHHHHHHTTCCS--SCHHHHHHHHHHHHHHHHTTSCC

T ss_pred HHHHHHHHHcCHHHHHHHHHccccchhhhChHHHHHHHHHHHHHHHHHHCHH---HHHHHHHHHHHHHHHHHHhhcccc

Q ss_pred cCC-----HHHHHHHHHHCCCCccccccccchhhcc-CCHHHHHHHHHHHCCCCCCCCHHHHHHHHHHHHCCCCcCHHHHHHH

Q Fri_Mar_04_23: 350 SID-----KNISKIKYLGSGSPFEGFLFSKELES-EPSFLCNLLNTLCYGIDEPYSLESLIQVSHLDKFSLPYDDPIGWIFQ 424 (%)

Q Consensus 350 I-----KIY-LLAG-----i-e-Dlw-raIgL-LWyg-sl-av-y-----P-D-----LLk 424 (%)

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      .++   +.+.+|++|+.   ..|++ .+=|..+++---|-.|...+.+.+---.+.+|+...+.+.+
T Consensus 294 ~~~~i~~~L~~~l~~~l~~~Gd~~~~~I~~~s~~~WyE~~~va~~~ly~~~Pt~~~l~~~y~~~d~~~e~~~ 365 (715)
T 4xmm_D 294 DISGELELDYIEDFLVIGGNQ-----RKILQYSRTWYSEFCGLFYIIPSLLSAEYLQMSLEAN-VVDITNDWEQPC 365 (715)
T ss_dssp CSCHHHHHHHHHHHHHHHCH-----HHHHHTCSSHHHHHHHHCCCCCCCCGGGHHHHHHHHHHHS-CCCTSSSSHHH
T ss_pred cCchHHHHHHHHHHhCCH-----HHHHHHhhHHHHHHHHhheCCCCchHHHHHHHHhC-CCCCCCHHHHH

```

Q ss_pred HhCCCCCHHHhhCccccCCCCccccchHHHHHHHHhCcc-----ccc-----CchHHHHHHHHH

Q Fri_Mar_04_23: 425 LYAANENTKLYKEVQRQTNALDVQPCWYLQTLRFNGT-----RVF-----SKETSDEATFAFA 479 (712)

Q Consensus 425 Lya~~~le~vL~p~s~t~~~lD~rLsW~L~vL~a~g~~~~~RVF~~~~~s~~~~d~L~t~sFA 479 (712)

+.+.+.+.+|+.+.+.+|+---++=|+.+.+|. .+. .+.+.+.+|+.+.+.+|

T Consensus 366 ~i~egd~~~vL~~~l~~~ld~w~aAhladL~~~g~L~~~~~dl~s~~~lre~~~Ll~YA 441 (715)

T 4xmm_D 366 VDIISGKIHSILPVMES-----LDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLDLFSYRNGMASYMLNSFA 441 (715)

T ss_dssp HHHHTTCCSCSHHHHHH-----CHHHHHHHHHHHHTSSCCCCC-----CCSSSSSSCHHHHHHHHH

T ss_pred HHHhCCHHHHHHHh-----cCHHHHHHHHHhCccccccccccccccccchhhhhcccCchHHHHHHHHH

Q ss_pred HHHH---HCCCCCHHHHHHHhC---CHHHHHHHHHHHhhccccchh-HH---HHHHhCcc---HHHHHHHHHHhC

Q Fri_Mar_04_23: 480 AQLE---FAQLHGHSFLVSCFLN---DDKAAEDTIKRLVMREITLLRAST-ND---HILNRLKIP--FQLIFNAQALKDRYE 549 (712)

Q Consensus 480 -QLe---Glw---AvFVllHl---d---R---aIr~lL~R~~~~~L~e~L~IP~~~~~WI~eAkAl~ar~~~ 549 (712)

..|-. .+.+|+|+=|.+.+ +.---+.+.+.+|.+.+| ++.++++ ++ -+.+.+|. .+=|+.+.+.+.

T Consensus 442 ~l~l~~~lW~vai~yL~~~c~~~g~~~r~~~i~eL~r~Pl~t~~~~~k~l~iC~~~L~~~a~~~l~~~g~~~~~ 520 (715)

T 4xmm_D 442 FELCSLGDKELWPVAIGLIALSATGTRSARKMVIaELLPH-YPFVTNDIDWMLSCIVEWRLPEIAKEIYTTLGNQMLSA 520 (715)

T ss_dssp HHHHTSCCTTTHHHHHHHHHCSSSCHHHHHHHHHHGGG-CCCCCHHHHHHHHHHHHTCHHHHHHHHHHHC-----

T ss_pred HhhhcccCccchHHHHHHHHhCccchHHHHHHHHhcc-CCCCCHHHHHHHHHhCCHHHHHHHHHHHHHHhC

Q ss_pred CCHHHHHHHHHhccCHHHHHHHHHhhHHHHHHccccCccccCHHHHHHHHHH

Q Fri_Mar_04_23: 550 GNYLSEYQNLGLGSSYDLAEIAVTSGLPRLLSNNPVQNNELKTLREILNE 601 (712)

Q Consensus 550 gd~~~e~~~Ll~A~~~eAH~v~v~~~laP~~~II~~~~~d~~~L~~~Ll~~~ 601 (712)








|+.+.+.+.+|+|+.+.+.+|= .+---.+.+.+ +.+-+-.+|.+.+.+

T Consensus 521 g~~g~AL~~~rA~d~~~V~~~i~~~l~~~l~~~g~~~D~~~L~~~lv~~~ 568 (715)

T 4xmm_D 521 HNIIESIANFSRAGKYELVKSYSW-LLFEASCMEE--GQKDDPVLNAIVSK 568 (715)

T ss_dssp ---CHHHHHHC-----CHHHHHH-HHHHHHHHH---HHC---CHHHHHHC

T ss_pred CCHHHHHHHHHhCCHHHHHHHHH-HHHHHHHhC---CCCCCHHHHHHHHHhC

No 9       

3jrp_A Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic vesicle, endoplasmic reticulum; 2.60A {Saccharomyces cerevisiae}

Probab=97.47 E-value=2.8e-05 Score=84.14 Aligned_cols=58 Identities=100% Similarity=1.383 Sum_probs=0.0

```

Q ss_pred HHHhccccchHHHHhccccccccCccchhhccCcccecccccccccecccccc
Q Fri_Mar_04_23: 122 IDLLFSECNDEIDNAKLIMKERRFTASYTFKFTSGSMLTKDIVGKSGVSIKRLPTE 179 (712)
Q Consensus 122 ~LLF~fn~~~k~~~r~~~l~~~f~~~l~~~l~~~ 179 (712)
++++|++|+.+.+.+|+|+++|+|++++|+|++|++|+++|++|+.+.+.+
T Consensus 322 ~F~~~i~~~i~~~r~~~~~d~~~e~~~v~~~WLe~~~a~~~~~W~~~T~~~ 379 (379)
T 3jrp_A 322 IDLLFSECNDEIDNAKLIMKERRFTASYTFKFTSGSMLTKDIVGKSGVSIKRLPTE 379 (379)
T ss_dssp -----CTHHHHHHHTTCTTCCCEEEETTTEEEETTSSSSSEEEECCECC
T ss_pred hhhhHHHHHHHHHHHHHHhHHhccCccEEEEcCccEEEEcCccCccEEEEcCCECC

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No 10       

3iko_C Nucleoporin NUP84; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore complex, nucleus, phosphoprotein; 3.20A {Saccharomyces cerevisiae} PDB: 4xmm_F 4xmn_F 3jro_C

Probab=96.24 E-value=0.05 Score=61.34 Aligned_cols=267 Identities=13% Similarity=0.135 Sum_probs=0.0

```

Q ss_pred HhHHHHHHHHhCcccccccc-----CCChHHHHHH---HHHHHHHHHHHHHHHH
Q Fri_Mar_04_23: 231 DYNLWKLSSILFDVPYSPYK-----TDNDQVKMAL---LKKERHCRLTSWIVSQI 277 (712)
Q Consensus 231 e~vW~L~saLfd~~~~~TDNDQVKMAL---LKKERHCRLTSWIVSQI 277 (712)
|...|+|...|+.....+ .+.+.+.+ .+.+.+.+|+|+...
T Consensus 71 E~tW~Ll~L~r~~~r~~~~~d~~~e~~~v~~~WLe~~~a~~~~~W~~~T~~~ 150 (460)
T 3iko_C 71 EARFWHLVLELLVFNADLDLDEMELHPYNSRGLFEKLMQDNQKLYQIIVIMVWLKENTYVMERPKNVPTSKWLNSITS 150 (460)
T ss_dssp HHHHHHHHHHHHHHHHHCCCCCCCCCTTSCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred HHHHHHHHHHHHHhccCccccccccCCCCCHHHHHHHHHhCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

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Q ss_pred -----HHHHHHHHhccCHHHHHHHHHhCCHHHHHHHHHHHCCCCCHHHHH
Q Fri_Mar_04_23: 278 GPEIEEKIRNSSNEIQIFLYLLNDVVRASKLAIESKNGHLSVLI 323 (712)
Q Consensus 278 ~v~~~l~~~l~~~e~if~L~g~I~~~A~~~Ai~~~gn~rLA~Ll~~~~~ 323 (712)
++...+.+.+.+.+|+|+|+|+++|+.+.+|+.+.+|...
T Consensus 151 g~v~~LDpDap~R~~~l~~~D~~~e~~~lw~~~if~lLR~G~~~eA~e~~~~~wra~~~L~g~~~~~p~~~~~ 230 (460)
T 3iko_C 151 GGLKSCDLDFPLRENTNVLVDVKDEEDHIFPKYIYELILAGAIDEALEEAKLSDNISCMILCGIQBYLNPNVIDTQIANE 230 (460)
T ss_dssp SCCSCCSTTHHHHSCGGGSCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred CCCcccCCCCccccCCCCcchHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

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Q ss_pred --HHHhCCHhHHHHHHHHHHHHHHCC---C-cCHHHHHHHHHhCccccccccchhhccCHHHHHHHHH---
Q Fri_Mar_04_23: 324 --SYLGSNDPRIRDLAELQLQKWSGG---C-SIDKNISKIYKLLSGSPFEGFLSKLESEFSWLCLLNLTL 390 (712)
Q Consensus 324 ~sq~gs~~~~~r~~~~~QL~~~W~~~~~I~~~~~kIY~LLAG~~~e~~~~~i~e~LdW~raIgL~L~~~~~ 390 (712)
...|... ..|+... - .+++-.+|.+.+|.+.+ .+.+.+|+|+...
T Consensus 231 l~~~~g~~~~~r~lw~~~~~la~~~~~d~yerAvY~~~L~g~~~~~s~~~l~v~~~swED~LW~~~l~~~~~ 295 (460)
T 3iko_C 231 FNTQQGIKK-----HSLWRRTVVSLSQAGLDPYERATYSYLSGAI---PNQEVQLQYSDWESDLHIHLNQILQ 295 (460)
T ss_dssp CSSCBSBTT-----HHHHHHHHHHHHHSSSCHHHHHHHHHHHHTSC---CCHHHHTTCCCHHHHHHHHHHHHH
T ss_pred cccccCchh-----HHHHHHHHHHhCccCCHHHHHHHHHhCcc-----hhhhccccCHHHHHHHHHHHHH

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Q ss_pred -----HcCCC-CCC---CHHHHHHHHHhCccccCHHHHHHHhCccccCHHHhCccccCCCCccc---
Q Fri_Mar_04_23: 391 -----CYGOI-DEY--SLESVQSLHDKFSLPYDDPIGVIFQLYAAENTEKLYKVRQRTNALD 447 (712)

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No 11

Q >2pm7_A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces cerevisiae}; PDB: 2pm6_A 3mz1_B
Probab=96.23 E-value=0.066 Score=59.33 Aligned_cols=219 Identities=12% Similarity=0.005 Sum_probs=0.0

Q ss_pred CCHHHHHHHHCCCCCCCCCCCCCCcCCHHHHHHHCCCCcCCHHHHHHHHHCCCCcCCHHHHHHHhCCccc
Q Fri_Mar_04_23: 289 NRIEQIFLYLLNDVVVRASKLAIESKNGHLVSLVSYLGSNDPRIRDLAEQLQKWSTGGCSIDKNISKIYKLSGSPFE 368 (712)
Q Consensus 289 ---e-if--L-g-I-A---Ai--gn-rLA-Llsq-gs-----r-----QL-W-----I-----kIY-LLAG---e 368 (712)
+++.+|-.|+|.++++|++|.++|.---|++|+..||+. +...+=...+....++..+..+|.+.+|++
T Consensus 144 ---l--L-l-G---Av-al-----a-ALLLA---gd-----l--v---a-----l--ll-v----- 217 (399)
T 2pm7_A 144 GNIEQTISKNLVSGNKKSAVKNSLENDLMMEAMVTALDSNNNE---RLKESVKNAYFAKYGSKSSLRILYISISKREV-- 217 (399)
T ss_dssp HHHHHHHHHHTTCCHHHHHHHHHHTTTCTHHHHHHHTTCCCH---HHHHHHHHHHHTTSCCHHHHHHHHHHTTCC--
T ss_pred HHHHHHHHHHHCCCCCCCCCCCCCCcCCHHHHHHHCCCCcCCH---HHHHHHHHhhccCCCcCHHHHHHHhCCH--

Q ss_pred cccccchhccCC-CHHHHHHHHHCCCCCCCCCHHHHHHHHHhCCCCcCCHHHHHHHhCCCCCHHHh-----
Q Fri_Mar_04_23: 369 GLFSLKELESEF-SWLCLNLTLCYGOIDEYSLESLSVQSHLDKFSLPYDDPIGVIFOLYAANENTFKL----- 435 (712)
Q Consensus 369 -----i-e-L-dW-raIg-L-LWYg-----sl--av-y-----P---D---LLkLyA---le-v----- 435 (712)
..+..++ +|+.+++++-|+.+++++..+..+ +.....+|-.|+...+++.+
T Consensus 218 ---v---l-Wre-la-iltn-----l---LGdrL---g---AA-CVL-a---k-v-iw-----e 292 (399)
T 2pm7_A 218 ---DDLVENLDVSQWKFIKATQNLYPNDAQRNMIMTKLGDRM---KENGHRQSDITLYLAAGSLDKVASIWLSEFPDLE 292 (399)
T ss_dssp ---HHHHHHBCCGGHHHHHHHHHHHTTCTHHHHHHHTTCCCH---HTTCTHHHHHHHTTSCCHHHHHHHHTTCC--
T ss_pred ---HHHHhCCHHHHHHHHHHHHHCCCCcChHHHHHHHHHH---HhCCCChhhHHhhhhCCHhHHHHHHhhhhcccc

Q ss_pred ----hCccccCCCCccccchHHHHHHHHhC--CccecCchHHHHHHHHHHHHCCCCcHHHHHHHHhCCHHHHHHH
Q Fri_Mar_04_23: 436 ----YKEVRQRTNALDVQFCWYLITQLRFN--GTRVPFSKETSDSATFAAQLEFAQLHGHSFLVSCFLNDDKAEDPTI 508 (712)
Q Consensus 436 ----L-p-s-t---lD-rLsW-L-VL-a---gs-----d-lt-sfa-QLe-Glw-AVFVllHl-d---R-aI 508 (712)
-++..++..+++...=.+...+++ +.....+.....+||-|...|+...|=+-+..+++.....
T Consensus 293 ---l---l-e-ieK-v---a-----l---l-yA--LA--G--A--Yl--i-----l 372 (399)
T 2pm7_A 293 DKLKDNKIYEAHSECMTFIERETVFSNFINGSSITNNEQLIAKLFELINLTSTGNFELATEFFLNLSLPDNEEVKTE 372 (399)
T ss_dssp HHHHTTCTHHHHHHHHHHHHHHHTTSCC---CCCHHHHHHHHHHTTCTHHHHHHHHHTTCTHHHHHHHTTCTHHHHHH
T ss_pred cccccCCHCCCCcHHHHHHHHHHHHHHCCCCCCCCCHHHHHHHHHHHCCCCcCHHHHHHHhCCHHHHHHH

Q ss_pred HHHHHhhccc
Q Fri_Mar_04_23: 509 KRLVMREITL 518 (712)
Q Consensus 509 r-LL-R---- 518 (712)
|+=|.++..
T Consensus 373 --Rl--a--- 382 (399)
T 2pm7_A 373 KARVLIASGK 382 (399)
T ss_dssp HHHHHHHHC-
T ss_pred HHHHHhCccc

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Q ss_pred -----hCcccCCCCccccchHHHHHHHHHHhC---CcCccCchHHHHHHHHHHHHHHHHCCCCcHHHHHHHHhCCCcHHHHHHH
Q Fri Mar 04 23: 436 -----YKEVRRTNALDVOFCWYLIQTLRFN---GTRVFSKETSD EATFAFAAQLEFAQLHGHSLFVSCFLNDDKA AED 506 (712)

Q ss_pred		HHHHHHHH	
Q Fri_Mar_04_23:	507	TIKRLVMR	514 (712)
Q Consensus	507	aIr-LL-R	514 (712)
		.. += .+	
T Consensus	735	r-r-r	742 (1273)
T 4bzj_A	735	TEKARVLT	742 (1273)
T ss_dssp		HHHHHHHH	
T ss_pred		HHHHHHHH	

```
Q ss_pred          HHHHHHHHhCCCHHHHHHHhhCCCCcHHHHHHH-----hCCCCCHHHHHHHHHHHHHHHCCC-----
Q Fri_Mar_04_23:  292 IEIQFYLLYLLGIVVRRASKLAIESKNGHLSSLVLISy-----LGSNDPRIRDLAELQLQKWSGTGC-   349 (712)
Q Consensus        292 -e-if-L-g-I--A-Ai-gn-L-Llsq-----gs-T-----QL-W-----           349 (712)
                  +.+|.+.|+|++++|++|.+.|++|.||.-.....+.+.+.|.|.-
T Consensus        347 ---if-lLR-G---eA-eLC---gq-WRAAsL-G-1-dp-----Gn-R-L-----WK-C--la----- 418 (925)
T 5a9q_4           347 LKYLFTLIRAGMTBEAQRLCKRCQGAWRAATLEGWKLHYDHPNVNGGTLELPVEGN-PYRRI-----WKISCWRMAEDE 418 (925)
T ss_dssp          HHHHHHHHHHTCTHHHHHHHHHHHTCTHHHHHHHHHTTSBVCBTTCCTTCSSCBSB-SCHNH-----HHHHHHHHHC
T ss_pred          HHHHHHHHhCCCHHHHHHHhhCcHHHHHHcCchhhCccccCcccccccccC-hhhhh-----HHHHHHHHhCC
```

Q ss_pred		cCCCHHHHHHHHhCCCcccccccchhhccCCHC-----HHHHHHHHH-----cCCCCC----CCHHHH	
Q Fri_Mar_04_23:	350	SIDKNISKIYKLLSGSPFEGFLFSKELESEFWS-----LCLNLTLT-----YGQIDE-----YSLES	403 (712)
Q Consensus	350	-I-----KIY-LLAG--e-----l-e-LdW-----ralgLTW-----Yg-----sl-a	403 (712)
		.+++.=+.[. + .++ +. + .++..+++= +++++	
T Consensus	419	--yERAIYg-Lsgddl -1vc--SWeD-LwA-nld-ev-l -lp-----tlt-i	492 (925)
T 5a9_q_4	419	LFNRYERAIIYAALSGNL-----KQLLPVCD-TWEDTVWAYFRVMVDLSVEEQIQTSVATLDTEELPREYLGNWTLEKV	492 (925)
T ss_dssp		SSCHHHHHHHHHHTTC-----CSNHHHTC-CCHHHHHHHHHHHHHHHHHHHHHHTTSCGGGCGCCSC---CCCCCHHH	
T ss_pred		CCHHHHHHHHHHhCCc-----hHHhhCcC-CCHHHHHHHHHHHHHHHHHHHHHhCcCCCCcccChhhccCcCCHHHH	













Q ss_pred		HHHHHHhhhCCC-----ccCHHHHHHHhhhCCC-----CHHHhhCcccCCCCCccccchHHHHHHHHHHhCCCCcCchhHHH			
Q Fri_Mar_04_23:	404	VQSHLDKFSLP-----YDDPIGVIFQLYAAANE-----NTEKLYKEVRQRTNALDVPFCWYLIQTRFNQTRVFSKETSDS		473	(712)
Q	404	v-y-y-P-----D-----LkLKlyA-----le-v-P-s-t-----ld-rlSw-L--vL-a-g-s-----d		473	(712)
T Consensus		++-...-+... Q-+...- . . .+...++- . +.. +.. +.. . . .+...+			
T	493	f-L-----v-ea-----p-r-IQ-----i-i-ll-----LRF-aHL-L-l-r-lg-----		571	(925)
T 5a9_q_4	493	FEELQATDKKRVLLENQEHYHHVQKFLILGDIDGLMDEFSKWLSSKSRNNLPGLHLLRFMTHLILFFRTLGL-LQTKEEVSIE		571	(925)
T ss_dssp		HHHHHHCC-----CHHHCHHHHHHHHHHHSSCHHHHHHHHHCC-----CCSSCHHHHHHHHHHHHHHHHHHHSS-SCSCHHHHHH			
T ss_pred		HHHHHccCccCchhhHhCCCHHHHHHHHHccCHHHHHHHHHhhcCHCCcChhHHHHHHHHHHhhcCCHccHHHHHH			

Q ss_pred		HHHHHHHHHHHCCcCCHHHHHHHHHHCCCHHHHHHH-----HHHHHHhhccccchHHHHH	
Q Fri_Mar_04_23:	474	ATFAFAAQLEFAQLGHGSFLVSCFLNDKKAEDT-----IKRLVMREITLLRASTNDHI	527 (712)
Q Consensus	474	Lt-sfa-QLe-Glw-AvFVlllH-d-R-a-Ir-L-RL--L	527 (712)
		+--+ + - ... +.-+ -+.+ +.....+ ...+.+.+.+.+.+	
T Consensus	572	II-YI-L-l-eLIPlYas-Lp-e-Ys-L-i-d-eR--L-la-gldV-i-k-ve-i-	925 (925)
T 5a9q_4	572	VLKTYIQLLIREKHNTLIAFYFTCHLPQDLAVAQYALFESVTEFEQRHHCLLELAKEADLDVATITKTVVENIRKKDNGEF	651 (925)
T ss_dssp		HHHHHHHHHHHTCCGGGHHHHTCCGGGGTC-----	
T ss_pred		HHHHHHHHHHHCCCcChCCHHHHHHHHHHHHHHHHHccCCHHHHHHHHHHHhCCHHHHHHHHHHHHHccccccc	

[illegible]

```
Q ss_pred          HHHHHHHHHHCCCCCCHHHHHHHHHHCCHHHHHHHHHhhccccccchHHHHHHHHHCCcCHHH-----  
Q Fri_Mar_04_23:   473 EATFAAQAQLFQAQLGHGSLFVSCFLNDDKAAEDTIKRLLVRREITLLRASNDHLILNRKLPQSILT      538 (712)  
Q Consensus        473 -L-tS-a-QL-e-Glw-AvFVLlHl-d--R-air-ll-R-----L-e-L-lP-WI-----      538 (712)  
                  +...+.+|.+.|..+|-.-.+    +...+-++-.+=+--+.....+.  
T Consensus        277 -i~A-L-g-eA-y-kag-----kAie-y-a-w-A-la-l-----l~~LA~l~~~~      349 (622)  
T 5cqr_A           277 DISIAyGEHLMQHMYEPAGLMfARCGA-----HEKALSAFLTGCNWKAQCVAAlNFTKDQLVGLGRtLAGKLVEQ     349 (622)  
T ss_dssp          HHHHHHHHHHTTTCTHHHHHHHHHHHTCT-----HHHHHHHHHTTCCHHHHHHHHTTTCTCHHHHHHHHHHHHHHHHT  
T ss pred          HHHHHHHHHHCCCCHHHHHHHHHC-----HHHHHHHHHcccCHHHHHHHHCcCCHHHHHHHHHHHHHHHHC
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Q ss_pred ---HHHHHHHHHHhCCCCHHHHHHHHHHccCHHHHHHHHHhhHHHHH
Q Fri_Mar_04_23: 539 ---FNAQALKDRYEGN⁵³⁹YLSEVQN⁵⁴⁰LLLGSSYDLAE⁵⁴¹MAIV⁵⁴²TSLGPRLL 581 (712)

Q Consensus	539	---eAkAl-ar--gd---e---Ll-A---eAh-v-v--laP~-I	581 (712)
T Consensus	350	g---eA-----l-d---AI-ll-a---eA--La-----dl-	395 (622)
T 5cqr_A	350	RKHIDAAAMVLEECADYEEAVLLLEGAWEALRLVYKYNRLDII	395 (622)
T ss_dssp		TCHHHHHHHHHHHSCCHHHHHHHHHHTTCHHHHHHHHHHTTCTHHH	
T ss_pred		CCHHHHHHHHHHcCCHHHHHHHHHCCCHHHHHHHHHhChHHHH	
<div>No 17</div> <div></div> <div><input type="checkbox"/> >5cqs_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A {Saccharomyces cerevisiae}</div> <div>Probab=76.91 E-value=8 Score=43.15 Aligned_cols=109 Identities=16% Similarity=0.113 Sum_probs=0.0</div>			
Q ss_pred		HHHHHHHHHHCCCHHHHHHHHHCCCHHHHHHHHH----HHhccccchHHHHHHHHCCc---HHHHHHHHHH	
Q Fri_Mar_04_23:	473	EATFAFAAQLEFAQLHGHSLFVSCFLNDDKAEDTTRKRL---VMRITLLRASTNDHILNRLKIP---SGLIFNAQAL	544 (712)
Q Consensus	473	-Lt-sfA-QLe--Glw--AvFvllHl-d---R-aIr-l-----L-R-----L-e-L-IP-----WI-eAkAl	544 (712)
T Consensus	109	-i---A--L---g---eA---Y-kag--kAie-y--w--al-la--l-----l--la--l---g---A--l	188 (435)
T 5cqs_A	109	VIIYNIYAKHLSNQMYTDAAVAYEMLGKLEAMGAYQSAKRWRREAMSTIAVQKPEEVESVAEELISSLFFEHRRVDAADI	188 (435)
T ss_dssp		HHHHHHHHHHHTTCTHHHHHHHHHTTCHHHHHHHHHHTTCHHHHHHHHHHTTCTHHHHHHHHHTTCHHHHHHH	
T ss_pred		HHHHHHHHHHcCCHHHHHHHHHCCCHHHHHHHHHccCHHHHHHHHHcChHHHHHHHHHHHHCCCHHHHHHH	
Q ss_pred		HHhCCCHHHHHHHHHccCHHHHHHHHHhhHHHH	
Q Fri_Mar_04_23:	545	KDRYEGNYLSEVQNLLGSSYDLAEMAIVTSLGPRLL	581 (712)
Q Consensus	545	-ar--gd---e---Ll-A---eAh-v-v--laP~-I	581 (712)
T Consensus	189	y-----d---AI--l-----eA--La-----dl-	225 (435)
T 5cqs_A	189	QLEYLDNVKKAVALYCKAYRYDIASLVAIKAKKDEL	225 (435)
T ss_dssp		HHHHHCCCHHHHHHHHHHTTCHHHHHHHHHHTTCTHHH	
T ss_pred		HHhCCCHHHHHHHHHCCCHHHHHHHHHcChHHH	
<div>No 18</div> <div></div> <div><input type="checkbox"/> >2qx5_A Nucleoporin NIC96; mRNA transport, nuclear pore complex, nucleus, protein transport, translocation, transport, transport protein; 2.50A {Saccharomyces cerevisiae} PDB: 2rfo_A</div> <div>Probab=70.71 E-value=1.1e+02 Score=36.23 Aligned_cols=271 Identities=10% Similarity=0.036 Sum_probs=0.0</div>			
Q ss_pred		HHHHHHCCCHHHHHHHHHCCc-----CHHHHH---HHhCCCHHHHHHHHHHHCCcCHHHHHHHHHc	
Q Fri_Mar_04_23:	295	IFLYLLELDNVVRASKLAIESKNG---HLSVLI---SYLGSNDPRIRDLAELQKQKSTGGCSIDKNISKIYKLLS	363 (712)
Q Consensus	295	if--L-g--I--A--Ai--gn-----rLA-Ll--sq-gs---r---QL--W---I---kIY-LLA	363 (712)
T Consensus	159	IyY-LR-G---eA-----F--l-----L--ey--r---DpyK-avY-iig	238 (661)
T 2qx5_A	159	IFYLLRAGLKEALQVLVKNKANIKKVQSFLTYFKAYASSKDHGLPVEYSTKLHTEYNQHIKSSLDGDPYRLAVYKLG	238 (661)
T ss_dssp		HHHHHTTCTHHHHHHHHHTTGGGC-----CHHHHHHHc-----CHHHHHHHCCcC	
T ss_pred		HHHHHHcCCHHHHHHHHHhhHH	
Q ss_pred		CCccccccccchhccCCHHHHHHHHHcCCCCCCCCHHH---HHHHHHHHhC---CCcCCHHHHHHHHHcCCCCHHHH	
Q Fri_Mar_04_23:	364	GSPFEGFLSKLESEFSWLCLNLTLCYQYIDYLSLES---LVQSHLDKFS---LPYDDPIGVIFQLYANENYTEKL	435 (712)
Q Consensus	364	G---e---i-e-LdW-raLg-L-WYg-----sl-----av-y-----P---D---LLkLya---le-v	435 (712)
T Consensus	239	-...+.-.....= . =++ ---...+.+.+. .+...+.+. ...+.+. ---+.+. . ..	
T 2qx5_A	239	RCDLRSKNIPAVTSLIEDWL---WMHMLLIKEDAEADPVYERYSLDFQNIITISYGPSRFSNYVLQTLLELGS--LYGLA	313 (661)
T ss_dssp		CCCCGGCCCGGGCCSHHHHH---HHHHHTCCC---CCCHHHHHHHHHHHCGGGGTCTHHHHHHHTT---CHHHH	
T ss_pred		CCccccchHHhCCCHHHHH---HHHHHHccccccccccccHHHHHHHHHHhhhhccccHHHHHHHHh--HHHHH	
Q ss_pred		hCccccCCCCccccCHHHHHHHHHhCccccCc-----hhHHHHHHHHHHHHCCcCHHHHHHHHHCCCH---	
Q Fri_Mar_04_23:	436	YKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSK-----ETSDAETFAFAAQLEFAQLHGHSLFVSCFLNDD	501 (712)
Q Consensus	436	L-p-s-t---lD-rLsW-L--vL-a-g-----s-----d-Lt-sfA-QLe--Glw--AvFvllHl-d---	501 (712)
T Consensus	314	I--L---vd---AVH-AIaL---gLL-----lls-----lnfarLI--Yt--F--d--Al-Y--li---d-	388 (661)
T 2qx5_A	314	IDYTYTF-SEMD---AVHLAIGLASLKFIDSSRLTKKPKRDIRFANILANYTKSFRYS-DPRVAVYVLVLTINLNGP	388 (661)
T ss_dssp		HHHHHTT-CHHH---HHHHHHHHHTTCT-----CHHHHHHHHHHTTTTCT-CHHHHHHHHHGGGSCCH	
T ss_pred		HHHHHHc-Cchh---HHHHHHHHHHCCCCCCCCccccCCCCCHHHHHHHHHhC-CCHHHHHHHHHHHCCCC	
Q ss_pred		---HHHHHHHHHHHHhC-----ccccchH---HHHH---HHhCcCHHHHHHHHHHHHHCCCHHHHHHH	
Q Fri_Mar_04_23:	502	---KAAEDTIKRLVMREI---TLLRAST-----NDHIL-----NRLKIPSQLIFNAQALKDRYEGNYLSEVQN	558 (712)
Q Consensus	502	---R--aIr-lL-R-----L-----L-IP---WI-eAkAl-ar--gd---e---	558 (712)
T Consensus	389+ ++++-..- +.+.+. + + .. +++- ...+.+ -.+.+.+.+.+.+.+	
T 2qx5_A	389	TDVELCHEALRELVLVETKEFTVLGKIGRDGARIPGVIEERQPLLVHVRDEKEFL--HTITEQA-ARRADEGRIYDSILL	465 (661)
T ss_dssp		HH	
T ss_pred		HHHHHHHHHHHHhccccHHHHCCCCCCCCcCccHHHHccccccccHHHH---HHHHHH---HHHHHHCCCCHHHHHH	
Q ss_pred		HHhCCCHHHHHHHHHHHhhH	
Q Fri_Mar_04_23:	559	LLLGSSYDLAEMAIVTSLGP	578 (712)
Q Consensus	559	Ll-A---eAh-v-v--laP~-I	578 (712)
T Consensus	466	Y-La---d-vl-lln--Ls-	485 (661)
T 2qx5_A	466	YQLAEYDIVITLVNSLLSD	485 (661)
T ss_dssp		HHHTTCHHHHHHHHHHHHH	
T ss_pred		HHhCCCHHHHHHHHHHHHH	

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