Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P42592
Date	Thu Jan 5 12:01:39 GMT 2012
Unique Job ID	34cc4bd31f07a4dc

Secondary structure and disorder prediction

Sequence 1–60: MKIKTILTPVTCALLISFSAHAANADNYKNVINRTGAPQYMKDYDYDDHQRFNPFFDLGA

Sequence 61–120: WHGHLLPDGPNTMGGFPGVALLTEEYINFMASNFDRLTVWQDGKKVDFTLEAYSIPGALV

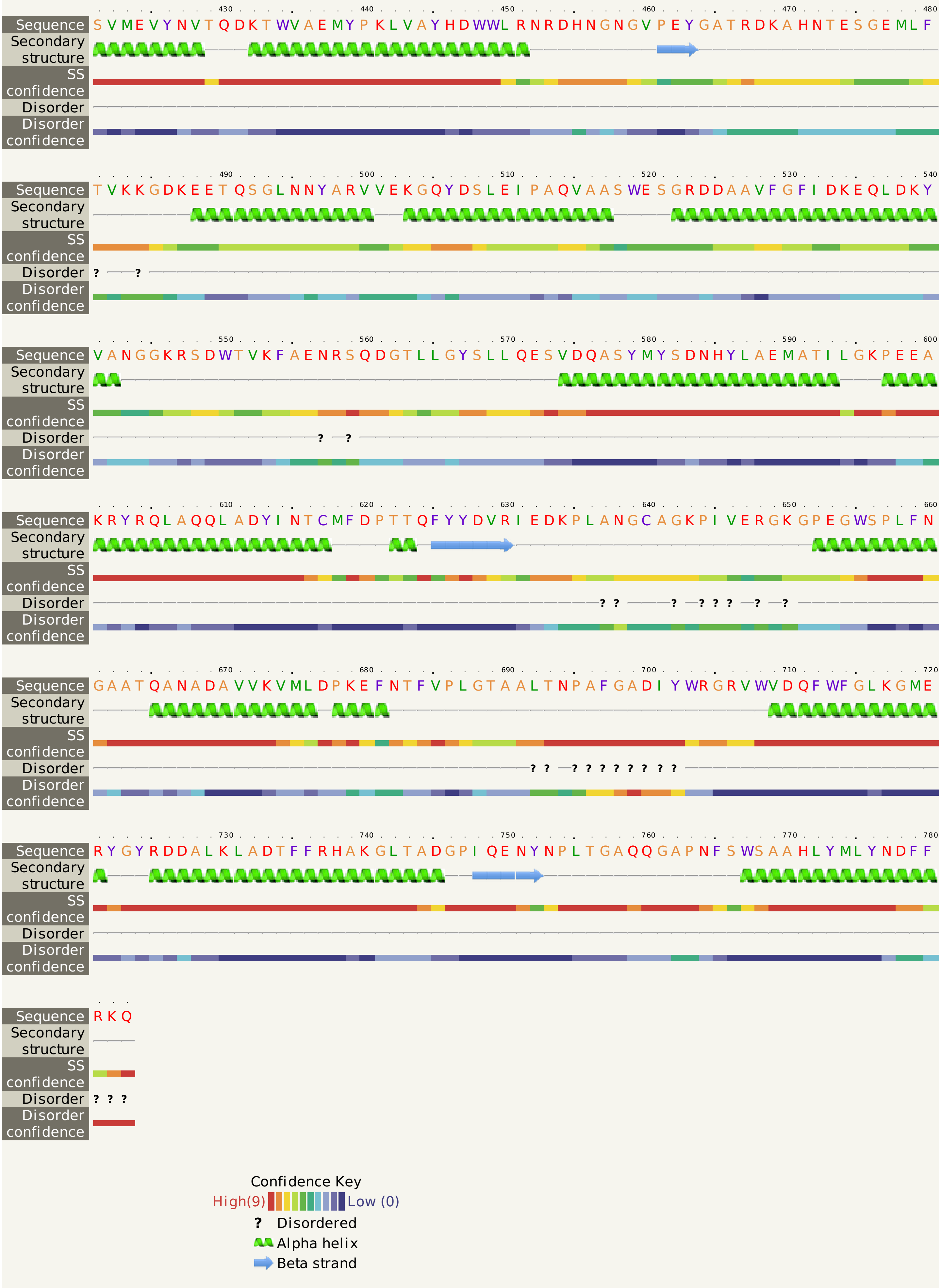
Sequence 121–180: QKLTAKDVQVEMTLRFATPRTSLLETKITSNKPLDLVWDGELLEKLEAKEGKPLSDKTIA

Sequence 181–240: GEYPDYQRKISATRDGLKVTFGKVRATWDLLTSGESEYQVHKSLPVQTEINGNRFTSKAH

Sequence 241–300: INGSTTLYTTYSHLLTAQEVSKEQMQIRDILARPAFYLTASQQRWEEYLKKGLTNPDATP

Sequence 301–360: EQTRVAVKAIETLNGNWRSPGGAVKFNTVTPSVTGRWFSGNQTWPWDTWKQAFAMAHFNP

Sequence 361–420: DIAKENIRAVFSWQIQPGDSVRPQDVGFVPDLIAWNLSPERGGDGGNWNERNTKPSLAAW


Sequence
Secondary structure
SS confidence
Disorder
Disorder confidence
430 440 450 460 470 480
SVMEVYNVTQDKTWVAEMYPKLVAYHDWWLRNRDHNGNGVPEYGATRDKAHNTESGEMLF
490 500 510 520 530 540
TVKKGDKEETQSGLNNYARVVEKGQYDSLEIPAQVAASWESGRDDAAVFGFIDKEQLDKY
550 560 570 580 590 600
VANGGKRSDWTVKFAENRSQDGTLLGYSLLQESVDQASYMYSDNHYLAEMATILGKPEEA
610 620 630 640 650 660
KRYRQLAQQLADYINTCMFDPTTQFYYDVRIEDKPLANGCAGKPIVERGKGPEGWSPLFN
670 680 690 700 710 720
GAATQANADAVVKVMLDPKEFNTFVPLGTAALTNPAFGADIYWRGRVWVDQFWFGLKGME
730 740 750 760 770 780
RYGYRDDALKLADTFFRHAKGLTADGPIQENYNPLTGAQQGAPNFSWSAAHLYMLYNDFF
RKQ
Confidence Key
High(9)
Low (0)
? Disordered
Alpha helix
Beta strand