

**Figure S1. Secondary structure prediction of SASP14 by different methods.** Secondary structural organization of wild-type SASP14 was predicted by different methods, secondary structural elements are shown by different color: yellow,  $\beta$ -strand; red,  $\alpha$ -helix; active site motif residues, black and bold. The additional helical insert was predicted by PredictProtein, JPred4 and SOPMA prediction algorithms, while the consensus helix and three C-terminal  $\beta$ -sheets were predicted by all methods.

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PredictProtein	SMGKG <u>GYLKGKI</u> GK <u>VPVRFLV</u> DSGAQVSVVH <u>PNLWEEV</u> TDGDLDLTLQPFEN <u>VVK</u> VANGAEM <u>KILGVWD</u>
JPred4	SMGKG <u>GYLKGKI</u> GK <u>VPVRFLV</u> DSGAQVS <u>VVH</u> <u>PNLWEEV</u> TDGDLDLTLQPFEN <u>NVVKV</u> ANGAE <u>MKILGVWD</u>
DSC	SMGKG <u>GYLKG</u> KIGK <u>VPVRFLV</u> DSGAQVSVVH <u>PNLWEEV</u> TDGDLDLTLQPFEN <u>NVVKV</u> ANGAE <u>EMKILGVWD</u>
SOPMA	SMGKG <u>GYL</u> KGKIGKVP <u>VRFLV</u> DSGAQVS <u>VH</u> <u>PNLWEEV</u> TDGDLD <u>TL</u> QPFEN <u>NVVKV</u> ANGAE <u>MKILGVWD</u>
GOR4	SMGKG <u>GYLKG</u> KIGK <u>VPVRFLV</u> DSGAQVS <u>VH</u> PNLW <u>EEV</u> TDGDLDLTLQPF <u>FENVVKV</u> ANGA <u>EMKILGVWD</u>
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PredictProtein	<u>TAVSL</u> GKLK <u>LKAQFLVANASAEAAII</u> G <u>TDVLQD</u> HNA <u>ILD</u> FEHR <u>TCTL</u> KGKK <u>FRL</u> LPVGGSLDEFDLE
JPred4	<u>TAVSL</u> GKL <u>LKLKAQFLVANASAEAAII</u> G <u>TDVLQD</u> HNA <u>ILD</u> FEHR <u>TCTL</u> KGKK <u>FRL</u> LPVGGSLDE <u>FDLE</u>
DSC	<u>TAVSL</u> GKL <u>LKLKAQFLVANASAEAAII</u> G <u>TDVLQD</u> HNA <u>ILD</u> FEHR <u>TCTL</u> KGKK <u>FRL</u> LPVGGSLDEFDLE
SOPMA	<u>TAVSL</u> GKL <u>LKLKAQFLVANASAEAAII</u> G <u>TDVLQD</u> HNA <u>ILD</u> FEHR <u>TCTL</u> KGKK <u>FRL</u> LPVGGSLDE <u>FDLE</u>
GOR4	<u>TAVSL</u> GKLK <u>LKAQFLVANASAEAAII</u> G <u>TDVLQD</u> HNA <u>ILD</u> FEHR <u>TCTL</u> KGKK <u>FRL</u> LPVGGSLDE <u>FDLE</u>