

```

#####
#
# Aligned_sequences: 2
# 1: 7btfA
# 2: region
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 1517
# Identity:      919/1517 (60.6%)
# Similarity:    919/1517 (60.6%)
# Gaps:          597/1517 (39.4%)
# Score: 4930.0
#
#
#

```

Fig. 4.6 Alignment of the subject sequence with the selected protein region of 4406–5900 of query polyprotein

4.7 Prediction of Disordered Sites Within the Protein Structure Based on GLOBPLOT

Inference: The above result of Globplot [5] indicates that the regions that are more prone for mutation or the regions of disorder are 2–7, 20–29, 213–236, 321–329, 413–420, 503507, 614–624, 673–688, 828–841. The longest region within these is 213–236 (Fig. 4.7).

Disordered by Russell/Linding definition

```

>none_Disorder 2-7, 20-29, 213-236, 321-329, 413-420, 503-507, 614-624, 673-688, 828-841
tFSADAQsfl nrvcgvsaar LTPCGTGTSt dvvyrafdiy ndkvagfakf lktncrcfqe kdeddnllids yfvvkrhtfs nyqheetiyn llkdcpvak hdfkfridg dmvpshisqr
lkytmdavl yalrhfdegn cdtlkeilvt nycdddyfn kkydydfven pdilrvyanl gervvqalk tvqfcdamn agivgvltd nqDLNGMWD FGDFIQTPG SGVPVdysy
sllmpiltit raltaashvd tdlkpylkw dlkydftee rklfdryfk ywdstyhpc vnclddrcil hcanfvlfz TVFFPTSFgp lvrkifvdvg pfvvtgtyhf relgvnhqd
vnlhssrlst kellyvaadp amhaasgnll ldkrttcfcv aaltmvafa tvKPGNFKD fydfavskgf fkegssvelk hffffaqgna aisdydyry nlpstccdirq ltrveevdk
yfcydggi nanovivnnl dkSAGFPfnk wkarlyyds asyedqdal f aytkrvnpt itqmkyai saknraetva gvscicstmta rqfhqllks iaatrgatv i gtskfyagw
hnmiktvsyd venPHLMGD YPKCdrampn mlrmaslvl arkhttcsl shrfyrlane caqlsevmv cgGSLVVKPG GISSGDAta yansvfnicq avtanvna11 stdgnkiadk
yvnnlqhrly eclyrndvd tdfvnefyay lkhfsmml sddavvcfn tyasqglvas iknfkslyy qnrvfaseak cutetdtlkg phefcsqhtv lvkagddVVV LPYDPSRIL
Gagcfvddiv ktdgtleier fvslaidayp ltkhpnqeya dvfhlylqi rklhdeltgh mldmvsmlt ndntsrwyep efyeamytp tvlqhhhhhh hhhh

```

Fig. 4.7 Partial output of Globplot