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consensus	1	SKLTKDVKCTSVLLSVLQQLH. [3].	NSKLWACYVKLNDIL. [3]. DPTTEAFKFSVLLSVLLS. [5].	DLDALCELL	DN. [1].	TVLQ	85	
GNUR_C	2	SKMSDVKCTSVLLSVLQQLR. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINRCELML	DN. [1].	ATLQ	84
1YSY_A	3	SKMSDVKCTSVLLSVLQQLR. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINRCELML	DN. [1].	ATLQ	85
2ATQ_A	4	SKMSDVKCTSVLLSVLQQLR. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINRCELML	DN. [1].	ATLQ	86
6MTQ	5	SKMSDVKCTSVLLSVLQQLH. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINRCELML	DN. [1].	ATLQ	86
6WTC_C	4	SKMSDVKCTSVLLSVLQQLR. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINKCEML	DN. [1].	ATLQ	86
7BWC_C	2	SKMSDVKCTSVLLSVLQQLR. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINKCEML	DN. [1].	ATLQ	84
AAP33696	3837	SKMSDVKCTSVLLSVLQQLR. [3].	SSKLWAQCVLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DINRCELML	DN. [1].	ATLQ	3919
ADY69163	878	SKMSDVKCTSVLLSVLQQLR. [3].	NSKLTLCLVNLNDIL. [3].	DTTEAFKFSVLLSVLLS. [5].	DISKLCDTIM	EN. [1].	TVLQ	952
YP_009729438	4604	SKMSDVKCTSVLLSVLQQLR. [3].	NSRSLVCLVNLNDIL. [3].	DATEAFKFTLLSVLLS. [5].	DKTLCDVDF	EN. [1].	ATLQ	4886
PF_00870	100	SKMSDVKCTSVLLSVLQQLR. [3].	NSRSLVCLVNLNDIL. [3].	DATEAFKFTLLSVLLS. [5].	DKTLCDVDF	EN. [1].	ATLQ	4886
AOG38811	3742	SNMTLTKCTSVLLSVLQQLH. [3].	SSKLWSLCLVNEIL. [3].	DTTEAFKFSVLLSVLLS. [5].	NDELCSNLSI	EN. [1].	TVLQ	3824
AWG6738	3657	SRLTKLTKCTSVLLSVLQQLR. [3].	SSKLWALCVKMLNDIL. [3].	SADSAFESVLLSVLLS. [5].	NDELCSNLSI	EN. [1].	TVLQ	3739
AGT28265	3918	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWSHCVKMLNDIL. [3].	DPSAEAFKFPVALLTMS. [5].	DLDALASEL	DN. [1].	SVLQ	4080
QA749691	3853	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWSHCVKMLNDIL. [3].	DPSAEAFKFPVALLTMS. [5].	DLETLASEL	DN. [1].	TVLQ	3935
ALM68023	3844	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWAHCVKMLNDIL. [3].	DPSAEAFKFPVCLFATMT. [5].	DLBNLASEL	DN. [1].	AVLQ	3926
PCG649	3837	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWHCVKMLNDIL. [3].	DPSAEAFKFPVCLFATMT. [5].	DLBNLASEL	DN. [1].	AVLQ	3926
BFB68086	3947	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWAYCVKMLNDIL. [3].	DPTTEAFKFSVLLSVLLS. [5].	DLGLASOLF	DN. [1].	AVLQ	4929
ASL68951	3988	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWAMCVKMLNDIL. [3].	DPTTEAFKFSVLLSVLLS. [5].	DLGLASOLF	DN. [1].	TVLQ	4062
AVL62535	3874	SKLTKLTKCTSVLLSVLQQLH. [3].	NSKAWAMCVKMLNDIL. [3].	DPSAEAFKFPVCLFATMT. [5].	DLGLASOLF	DN. [1].	SVLQ	3956
PCQ63	3890	SKLTKLTKCTSVLLTVLQQLH. [3].	NSKAWMVCVKNLNEIL. [3].	DPTTEAFKFSVLLSVLLS. [5].	DLDALANDF	EN. [1].	SVLQ	3972
KN97C	3846	SKLTKLTKCTSVLLSVLQQLH. [3].	NSRAWAFVCVKNLNEIL. [3].	DPSAEAFKFSVLLSVLLS. [5].	DLDALANDF	EN. [1].	TVLQ	3928
AN65638	3939	SKLTKLTKCTSVLLTVLQQLH. [3].	NSKAWMVCVKNLNEIL. [3].	DPTTEAFKFPVCLFATMT. [5].	DLGLANDOLF	ET. [1].	TVLQ	3963
PA6964	3837	SKLTKLTKCTSVLLTVLQQLH. [3].	NSKAWHCVKMLNDIL. [3].	DPSAEAFKFPVCLFATMT. [5].	DLGLANDOLF	ET. [1].	TVLQ	3925
ACGA534	3875	SKLTKVCKANVLLNCLQHLH. [3].	NSKLWQVCSTLNEIL. [3].	DLSAFAFKQALLVILFS. [7].	KCLASIDEV	DO. [5].	TVLQ	3985
ATP65731	4225	SKLTKVCKANVLLNCLQHLH. [3].	NSKLWQVCSTLNEIL. [3].	DLGTAFAFKQALLVILFS. [7].	KCLASIDEV	DO. [5].	TVLQ	4313
PCQ670	3922	SRLTKVCKANVLLNCLQHLH. [3].	NSKLWQVCSTLNEIL. [3].	DLMSAFAFKQALLVILFS. [7].	KCLASIEVS	DO. [5].	TVLQ	4040

[illegible]

**Supplementary Figure S2. Multiple sequence alignment for nsp7 (A) and nsp8 (B) during conserved domain database (CDD) analysis.** The respective alignments from CDD consisted of 27 nsp7 protein sequences and their homologues and 30 nsp8 protein sequences and their homologues across different species. In nsp7, three critical interaction residues are identified: Lys-7, His-36, and Asn-37. In nsp8, the three critical interaction residues are: Lys-58, Pro-183, and Arg-190.