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Is There a Preponderance of Novel Folds in the SARS Coronavirus Proteome? Jeremiah S. Joseph, Kumar S. Saikatendu, Vanitha Subramanian, Benjamin W. Neuman, Michael J. Buchmeier, Raymond C. Stevens and Peter Kuhn, Depts. of Cell Biology and Molecular Biology, The Scripps Research Institute, 10550 N. Torrey Pines Rd, La Jolla, CA, 92122 USA.

The SARS coronavirus has a ~29.7kb genome with 14 ORFs yielding ~28 mature proteins, many with very low sequence similarity to other proteins. Several NMR and crystal structures of full length viral proteins and/or their constituent domains have been determined by us and others. We observe that even at the structural level, SARS-CoV proteins appear to comprise of a significant number of new folds. To date, out of the 10 proteins with available 3-D structural information (ADRP and PLP domains of nsp3, nsp5, nsp7, nsp8, nsp9, nsp10, sars2, sars7a, N-terminal domain of sars9a), five contain new folds. These novel structures allow us to model and understand structure-function relationships in several new families of proteins, including those in other pathogenic coronaviruses affecting humans. As more structures of the SARS-CoV proteome and those of other viruses are structurally characterized, it will also be interesting to see if the preponderance of uncommon folds is unique to coronaviruses or true of viruses in general. This study was supported by NIAID/NIH Contract #HHSN 266200400058C “Functional & Structural Proteomics of the SARS-CoV”.