in diameter) RNA viruses that have an icosahedrally systematic capsid. This capsid contains 60 copies of each of four coat proteins VP1, VP2, VP3, and VP4. Several structures of picornaviruses have been determined to date, however, no three-dimensional structure is currently available for CVB1. We report here the crystallization, X-ray diffraction analysis, and structure determination of CVB1 complexed to a potent antiviral agent.

Crystals of CVB1 complexed to an antiviral agent in the SCH 47020 series were grown in the presence of Li$_2$SO$_4$ and PEG using a modification of the vapor diffusion technique. Small triangular blocks appear in 2-5 days, the largest measuring 0.2 x 0.2 x 0.3 mm. These crystals diffract X-rays to at least 2.6 ˚A resolution on CHESS. Data analysis indicates that these crystals belong to space group $P6_1221$, with cell dimensions of $a=345.7$, $b=497.2$, and $c=585.9$ ˚A, and $\alpha=\beta=90^\circ$, $\gamma=106.5^\circ$.

Molecular replacement was used to solve the structure using a starting model of coxsackievirus B3. Rotation and translation functions indicate that the particle is rotated 54.8° around the $y$-axis relative to a standard icosahedral orientation and that the position of the particle center is at $y=0.19$. After the molecular replacement solution was determined, thirty-fold non-crystallographic symmetry averaging was used to improve the electron density and the phases. Electron density consistent with bound antiviral agent is present in the drug binding pocket. Details of the interactions between the antiviral agent and the virus will be presented, as well as a comparison between CVB1 and other picornaviruses.

**PS04.09.11 INTERACTION OF INTERCELLULAR ADHESION MOLECULE-1 (ICAM-1) AND HUMAN RHINOVIRUS (HRV) AND THE ROLE OF CHARGE.** Prasanna R. Kolatkar, Jordi Bella, Wai-ming Lee*, Roland Rueckert* and Michael G. Rossmann ,Department of Biological Sciences, Purdue University, W. Lafayette, IN 47906*Institute of Molecular Virology, University of Wisconsin, Madison, WI 53706.

Intercellular Adhesion Molecule-1 (ICAM-1) is the receptor used by the majority of human rhinoviruses (HRVs). We have previously reported a cryo-electron microscopy reconstruction of the ICAM-1:HRV complex (PNAS, 1992) which shows the general features of the binding. Well-diffracting crystals of ICAM-1 expressed in baculovirus are now being used for crystallographic studies. Nevertheless the crystals have somewhat variable cell constants which change by as much as 10 Å and make MIR phasing problematic. The variability in cell constants is likely attributed to the significant amount of glycosylation. We (Chris Marlor, Jeff Greve; Bayer Inc., W. Haven, CT 06516) have introduced one selenomethionine into ICAM-1 to allow MAD phasing. In addition we are using MAD data collection at the absorption edges of heavy atom derivatives to obtain phase information. We will report the progress of the structure determination of ICAM-1 and its relevance to understanding virus-receptor binding interactions.

The charge surface potentials of several human rhinoviruses have been calculated using X-ray coordinates of HRVs. We have employed site-directed mutagenesis of certain charged residues within the canyon and which overlap with the ICAM-1 footprint determined from the EM reconstruction. The results are consistent with the observed HRV:ICAM-1 interactions.

**PS04.09.12 STRUCTURAL STUDIES OF THE ROUS SARCOMA VIRUS (RSV) CAPSID PROTEIN.** Ladiasau C. Kovanli, Cory Momany, Faith Miyagil, Rui Zhao*, Stephen Campbell, Bao Yong, Volker M. Vogt*, Michael G. Rossmann, Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA, *Institute of Biochemistry, Molecular and Cell Biology, Cornell University, Ithaca, NY 14853, USA

The RSV and HIV virus capsid (CA) proteins exhibit structural and functional similarities. Secondary structural predictions suggest that the two capsid proteins share the same fold. Knowledge of the CA protein structure should prove useful in designing anti-retroviral agents that inhibit viral uncoating, assembly, maturation or release.

Crystals of RSV CA diffract X-rays to 3.5 Å resolution. The crystals belong to the monoclinic space group C2 with unit cell parameters $a = 374.4$ Å, $b = 128.1$ Å, $c = 200.2$ Å and $\beta = 121.8^\circ$. An asymmetric unit of the crystal should contain 20 to 30 molecules based on reasonable $V_M$ values. Diffraction data of native and heavy atom derivatives were collected on frozen crystals at home and at CHESS. Self rotation functions suggest that RSV CA crystallizes as a helical array.