Supplementary Data

Figure S1. Sequence alignment of the FAR proteins used for the construction of the phylogenetic tree given in Figure 1. Signal peptide sequences are omitted. The alignment includes N. americanus recently identified FAR proteins (NECAME_09996; GI:568291396, NECAME_04475; GI:568275026, NECAME_14205; GI:568270857, NECAME_14203; GI:568270856, NECAME_14206; GI:568270855), the free living nematode Caenorhabditis elegans (CefAR-1 to CefAR-8; CefAR-1; GI:3875446, CefAR-2; GI:3875447, CefAR-3; GI:3875959, CefAR-4; GI:3875958, CefAR-5; GI:31043795, CefAR-6; GI:4008403, CefAR-7; GI:261824478, CefAR-8; GI:351065871), the free living nematode Onchocerca volvulus (OvFAR-1; GI:68052030, Brugia malayi (BmFAR-1; GI:68052234), animal parasitic nematodes Ancylostoma caninum (AcFAR-1; GI:22164324 and AcFAR-2; GI:22532421), Ancylostoma ceylanicum (AcFAR-1; GI:22164324), Ostertagia ostertagi (OoFAR-1; GI:18104159) and Heligmosomoides. 

Structure of Necator americanus FAR protein
Rey-Burusco et al.
polygyrus (Hp-FAR-1; GI:14289131), and the plant parasitic nematodes *Globodera pallida* (Gp-FAR-1; GI:5457299) and *Meloidogyne javanica* (Mj-FAR-1; GI:429201020). The sequence for NECAME_04475 shown is our revision of the conceptual splicing and translation of NECAMEDFT Contig65 with the coding sequence comprised of the complement of nucleotides 1-38, 97-268, 326-445, 523-629 and 689-782 that results in a shorter polypeptide that possesses a predicted N-terminal secretion signal.

Figure S2. Backbone amide $^{15}$N relaxation data for Na-FAR-1 at 14.1 Tesla. The backbone amide T$_1$, T$_2$ and heteronuclear NOE ($I_{sat}/I_{ref}$) data are shown for each residue. A cartoon depicting the locations of the alpha-helices is shown below. The anisotropic tumbling of the protein is evident from the depressed T$_1$s, and raised T$_2$s of the backbone amides of $\alpha$4, which lies almost perpendicular to the other helices. Evidence of internal motion is seen at the N- and C-termini of the protein and in several loops, e.g. the raised T$_2$s and depressed heteronuclear NOEs in the $\alpha$4-$\alpha$5 loop.
**Figure S3. Na-FAR-1 ligand chain length preference.** Each saturated fatty acid with chain lengths ranging from C10:0 to C19:0 were added to final concentrations between 0.5 and 50 μM to 2 ml of 1.5 μM Na-FAR-1 solution containing 1 μM DAUDA in the fluorescence cuvette. The excitation wavelength was 345 nm and fluorescence monitored at 470 nm (points). To illustrate the trends in the data, for each ligand, the data are fitted with a simple single site saturation binding model (lines).