

CCT	CSA	GAG	CTG	TCA	ACA	GAG	GCT	GAG	GAA	TCT	CAA	GGC	CCA	GTG	CTC	AAG	ATG	CCT	AGC	60	
Pro	Arg	Glu	Leu	Ser	Thr	Gln	Ala	Glu	Glu	Ser	Gln	Gly	Pro	Val	Leu	Lys	Met	Pro	Asp	120	
GAG	CSA	GCA	GGG	AGC	TTC	CCC	CTG	ACC	AGG	TCC	CAG	TCC	TGT	GAG	ACG	AAG	CTA	CTT	GAC	120	
Gln	Arg	Ala	Arg	Ser	Phe	Pro	Leu	Thr	Arg	Ser	Gln	Ser	Cys	Glu	Thr	Lys	Leu	Leu	Asp	130	
GAA	AAG	ACC	AGC	AAA	CTC	TAT	TCT	ATC	AGC	AGC	CAA	GTG	TCA	TGG	GCT	GTC	ATG	AAA	TCC	130	
Glu	Lys	Thr	Ser	Lys	Leu	Tyr	Ser	Ile	Ser	Ser	Val	Ser	Val	Ser	Ala	Met	Lys	Ser	Leu	140	
TTG	CTG	TCC	CTT	CCA	TCT	TCT	ATC	TCC	TGT	GCC	CAG	ACT	CCC	TCC	ATC	CCC	AAG	GAA	GGG	140	
Leu	Leu	Cys	Leu	Pro	Ser	Ser	Ile	Ser	Cys	Ala	Gln	Thr	Pro	Cys	Ile	Pro	Lys	Glu	Gly	150	
GCA	TCT	CCA	ACA	TCA	TCA	TCC	AAC	GAA	GAC	TCA	GCT	GCA	AAT	GGT	TCT	GCT	GAA	ACA	TCT	150	
Ala	Ser	Pro	Thr	Ser	Ser	Ser	Asn	Glu	Asp	Ser	Ala	Ala	Asn	Gly	Ser	Ala	Glu	Thr	Ser	160	
GCC	TTG	GAC	ACA	GGG	TTC	TGG	CTC	AAC	CTT	TCA	GAG	CTG	AGA	GAA	TAT	ACA	GAG	GCT	CTC	160	
Ala	Leu	Asp	Thr	Gly	Phe	Ser	Leu	Asn	Leu	Ser	Glu	Leu	Arg	Glu	Tyr	Thr	Glu	Gly	Leu	170	
ACG	GAA	GCC	AAG	GAA	GAC	GAT	GAT	GGG	GAC	CAC	AGT	TCC	CTT	CAG	TCT	GGT	CAG	TCC	GTT	170	
Thr	Glu	Ala	Lys	Glu	Asp	Asp	Asp	Gly	Asp	His	Ser	Ser	Leu	Gln	Ser	Gly	Gln	Ser	Val	180	
ATC	TCC	CTG	CTG	AGC	TCA	GAA	GAA	TTA	AAA	AAA	CTC	ATC	GAG	GAG	GTG	AAG	GTT	CTG	GAT	180	
Ile	Ser	Leu	Leu	Ser	Ser	Glu	Glu	Leu	Lys	Lys	Leu	Ile	Glu	Val	Lys	Val	Leu	Leu	Asp	190	
GAA	GCA	ACA	TTA	AAG	CAA	TTA	GAC	GGC	ATC	CAT	CTC	ACC	ATC	TTA	CAC	ACG	ATC	GAA	GCT	190	
Glu	Ala	Thr	Leu	Lys	Gln	Leu	Asp	Gly	Ile	His	Val	Thr	Ile	Leu	His	Lys	Glu	Gly	Leu	200	
GCT	GCT	CTT	GGG	TTC	AGC	TTG	GCA	GGG	AGA	GCA	GAT	CTA	GAA	AAC	AAG	GTG	ATT	ACG	GTT	200	
Ala	Gly	Leu	Gly	Phe	Ser	Leu	Ala	Gly	Gly	Ala	Asp	Leu	Glu	Asn	Lys	Val	Ile	Thr	Val	210	
CAG	AGA	GTG	TTT	CCA	AAT	GGG	CTG	GCC	TCC	CAG	GAA	GGG	ACT	ATT	CAG	AAG	GCC	AAT	GAG	210	
His	Arg	Val	Phe	Pro	Asn	Gly	Leu	Ala	Ser	Gln	Glu	Gly	Thr	Ile	Gln	Lys	Gly	Asn	Glu	220	
GTT	CTT	TCC	ATC	AAC	GGC	AAG	TCT	CTC	AAG	GGG	ACC	ACG	CAC	CAT	GAT	GCC	TTG	GCA	ATC	220	
Val	Leu	Ser	Ile	Asn	Gly	Lys	Ser	Leu	Lys	Gly	Thr	His	His	Ser	Ala	Leu	Ala	Ile	Ser	230	
CTC	CGC	CAA	GCT	CGA	GAG	CCC	AGG	CAA	GCT	GTG	ATT	GTC	ACA	AGG	AAG	CTG	ACT	CCA	GAG	230	
Leu	Arg	Gln	Ala	Arg	Glu	Pro	Arg	Gln	Ala	Val	Ile	Val	Thr	Arg	Lys	Leu	Thr	Glu	Glu	240	
GCC	ATG	CCT	GAC	CTC	AAC	TCC	TCC	ACT	GAC	TCT	GCA	GCC	TCA	GCC	TCT	GCA	GCC	AGT	GAT	240	
Ala	Met	Pro	Asp	Leu	Asn	Ser	Ser	Thr	Asp	Ser	Ala	Ala	Ser	Ala	Ser	Ala	Ser	Asp	Asp	250	
GGT	TCT	GTA	GAA	TCT	ACA	GCA	GAG	GCC	ACA	GTC	TCC	ACG	GTG	ACA	CTG	GAG	AAG	ATG	TCG	250	
Val	Ser	Val	Glu	Ser	Thr	Ala	Glu	Thr	Val	Thr	Val	Thr	Val	Thr	Leu	Gly	Met	Ser	Ser	260	
GCA	GGG	CTG	GGC	TTC	AGC	CTG	GAA	GGG	AAG	GCC	TCC	CTA	CAC	GCA	GAG	ACT	CTC	CTC	CTC	260	
Ala	Gly	Leu	Gly	Phe	Ser	Leu	Glu	Gly	Gly	Lys	Gly	Ser	Leu	His	Gly	Asp	Lys	Pro	Leu	270	
ACC	ATT	AAC	AGG	ATT	TTC	AAA	GCA	GCC	TCA	GAA	AGT	GAG	ACA	GTC	CAG	CGT	CGT	CGT	CGA	270	
Thr	Ile	Asn	Arg	Ile	Phe	Lys	Gly	Ala	Ala	Ser	Glu	Gln	Ser	Glu	Thr	Val	Gln	Pro	Gly	280	
GAT	GAA	ATC	TTG	CAG	CTG	GCT	GGC	ACT	GCC	ATG	CAG	GGC	CTC	ACA	CGG	TTT	GAA	CGC	GGG	280	
Asp	Glu	Ile	Leu	Gln	Leu	Gly	Gly	Thr	Ala	Met	Gln	Gly	Leu	Thr	Arg	Phe	Glu	Ala	Trp	290	
AAC	ATC	ATC	AAG	GCA	CTG	CCT	GAT	GGG	CCT	GTC	ACC	ATT	GTC	ATC	AGG	AGA	AAA	AGC	CTC	290	
Asn	Ile	Ile	Lys	Ala	Leu	Pro	Asp	Gly	Pro	Val	Thr	Ile	Val	Ile	Arg	Arg	Lys	Ser	Leu	300	
CAG	TCC	AAG	GAA	ACC	ACA	GCT	GCT	GGG	GAC	TCC	TGG	Gln	Ser	Lys	Glu	Thr	Ala	Ala	Gly	Asp	310

The 1,173 base pairs in the human IL-16 cDNA. The first Met residue, the five Cys and the GLCF-motif-like repeats are boxed. Dots above corresponding proteins indicate the three nucleotides not present in the previously published sequence⁵. Details of our sequence determination are available on request.

protein (encompassing the DHR3 module of the 40,000-*M_r* LCF) to CD4, causing some activating events and cytoskeletal reorganization. This could explain the upregulation of interleukin-2 receptors, and the general increase in CD4⁺ cell motility^{2-5,11,12}; antibody blocking of CD4 would diminish these effects. Moreover, blockade of CD4 by LCF/IL-16 binding (even if this were a nonspecific event) could inhibit HIV entry into these cells, perhaps explaining the recent observations of Baier *et al.*¹. Although this does not necessarily detract from the potential therapeutic use of this polypeptide, the notion that it represents an endogenous cytokine⁵ useful as a natural HIV inhibitor¹ must be scrutinized further.

J. Fernando Bazan
Thomas J. Schall

Departments of Molecular Biology and Immunology, DNAX Research Institute, Palo Alto, California 94304, USA

SIR — Cruikshank *et al.*⁵ described interleukin-16 as a 130-residue protein encoded by one main open reading frame of a 2,150-base-pair-long complementary DNA. A biologically active protein is expressed by this DNA even when it has a truncated 5' end (as originally cloned)⁵, indicating that one functional domain of interleukin-16 is in a 390-base-pair coding region. A 130-amino-acid fragment derived from *Escherichia coli* based on this sequence is

active as a lymphocyte chemoattractant⁵ and as an inhibitor of HIV replication¹.

Nevertheless, our nucleotide sequence comparison of interleukin (IL)-16 cDNA clones from non-human primates reveals that the previously postulated ATG start codon⁵ is mutated in two out of six species tested — saimiri and aotus monkeys. Because evolutionarily highly conserved genes probably use the same ATG, we decided to reanalyse the published 5'-untranslated region⁵. We found one large 1,173-bp open reading frame, which includes at its 3' end the 390 bp of the original IL-16 sequence⁵ (see figure).

The first ATG in this open reading frame at position 52 is probably where translation starts¹⁴, and would therefore represent the most likely start codon of this putative IL-16 precursor (prIL-16),

with a predicted relative molecular mass of 39,358. This protein is detectable in correspondingly transfected COS-7 cells with a molecular mass of about 42,000 (M.B. *et al.*, manuscript in preparation).

The prIL-16 sequence contains five cysteine residues and two repeats, which resemble GLGF motifs¹⁵ (see figure). Sequence database searches reveal no significant homologies between the prIL-16 sequence and that of other proteins (except those that carry the GLGF motif). As for the originally published IL-16, there is no consensus signal sequence in prIL-16 (also missing, for example, in IL-1 α and - β) and the secretion pathway for prIL-16 or its processed products is unknown.

Both the 130-amino-acid and the naturally purified versions of IL-16 have a relative molecular mass of 17,000 as measured by SDS gels⁵. This method would not exclude small size differences between the proteins. Although the primary structure of prIL-16 does not resemble a secreted protein, it is conceivable that processing of prIL-16 could lead to the 17,000 form of IL-16 that is detectable in cell culture supernatants of histamine- or mitogen-induced CD8⁺ cells¹⁶. Knowledge of the precise amino terminus of naturally processed and secreted IL-16 is important for investigating its chemoattractant and anti-HIV activities, as altered amino termini can be critical for the biological properties of proteins. Processing of the native prIL-16 may well be essential for generat-

ing properly folded IL-16, which is difficult to obtain in *E. coli* expression systems¹. We are now investigating the processing of prIL-16 and the properties of both prIL-16 and the carboxy-terminal domain of IL-16 from primary lymphocytes to elucidate the biological functions of this protein.

Norbert Bannert
Michael Baier
Albrecht Werner
Reinhard Kurth
Paul-Ehrlich-Institut, Paul-Ehrlich-Str. 51-59, D-63225 Langen, Germany

Three-dimensionally preserved insects

SIR — The Tertiary limestones of Riversleigh (northwest Queensland) have yielded an assemblage of beetles (including larvae), flies and millipedes preserved in three dimensions, in addition to the already diverse range of vertebrates so far reported¹. These arthropods were recovered from the Upper Site (Late Oligocene/ Early Miocene), which represents a small, shallow, lime-rich pool in a tropical rainforest¹. Scavengers were inhibited by the high salinity, and the conditions for exceptional preservation were enhanced by microbial mats^{1,2}. The arthropods are preserved by mineralization in calcium phosphate (carbonate fluorapatite) without collapse or compaction. They were recovered by acid digestion of the vertebrate-packed limestone; they are preserved in remarkable detail, particularly of the eyes. The only other well-known three-dimensionally phosphatized terrestrial arthropods are from the slightly older Quercy Phosphorites of France, but these specimens have been diagenetically recrystallized or encrusted³.

Replication of soft tissues is more rapid in calcium phosphate than in any other authigenic mineral, and therefore preserves the highest fidelity of detail⁴⁻⁶. The

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