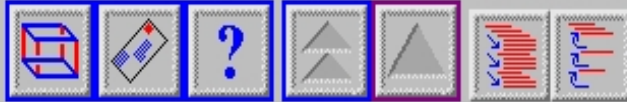


SCOP: Structural Classification of Proteins

Structural Classification of Proteins



Protein: Platelet factor 4, PF4 from Cow (*Bos taurus*)

Lineage:

1. Root: [scop](#)
2. Class: [Alpha and beta proteins \(a+b\)](#)
Mainly antiparallel beta sheets (segregated alpha and beta regions)
3. Fold: [II8-like](#)
beta(3)-alpha
4. Superfamily: [Interleukin 8-like chemokines](#)
form dimers with different dimerisation modes
5. Family: [Interleukin 8-like chemokines](#)
6. Protein: Platelet factor 4, PF4
7. Species: [Cow \(*Bos taurus*\)](#)

PDB Entry Domains:

1. [1plf](#)  
complexed with tcn
 1. [chain a](#)  
 2. [chain b](#)  
 3. [chain c](#)  

Murzin *et al.* 1995

Il8-like Domain

MMS-Code : 54117
Class : *Alpha and Beta Proteins (a+b)*
Number of Members : 2
Average Size : 71

Percentage Identity Matrix

	1ikl-	1huma
1ikl-	100.0	21.0
1huma	21.0	100.0

Alignment Based On Similarities In Structural Features in Interleukin Superfamily

1ik1- elrçqçikTyskpfhpkfIkeL
 1huma apmgsdpptaç-çfsytarklp~~rnf~~Vvdy
 * * *

1ik1- rviesgphçanteIiVklsdg
 1huma yeTs1çsqpAvVFqTkrs---
 bb bbbb

1ik1- relÇLdpknwVqrvvekflkraens
 1huma kqvçAdpseswVqeyvydleln
 bb aaaaaaaaa
 * ** * *** *

Alignment with Homologues in HOMSTRAD database

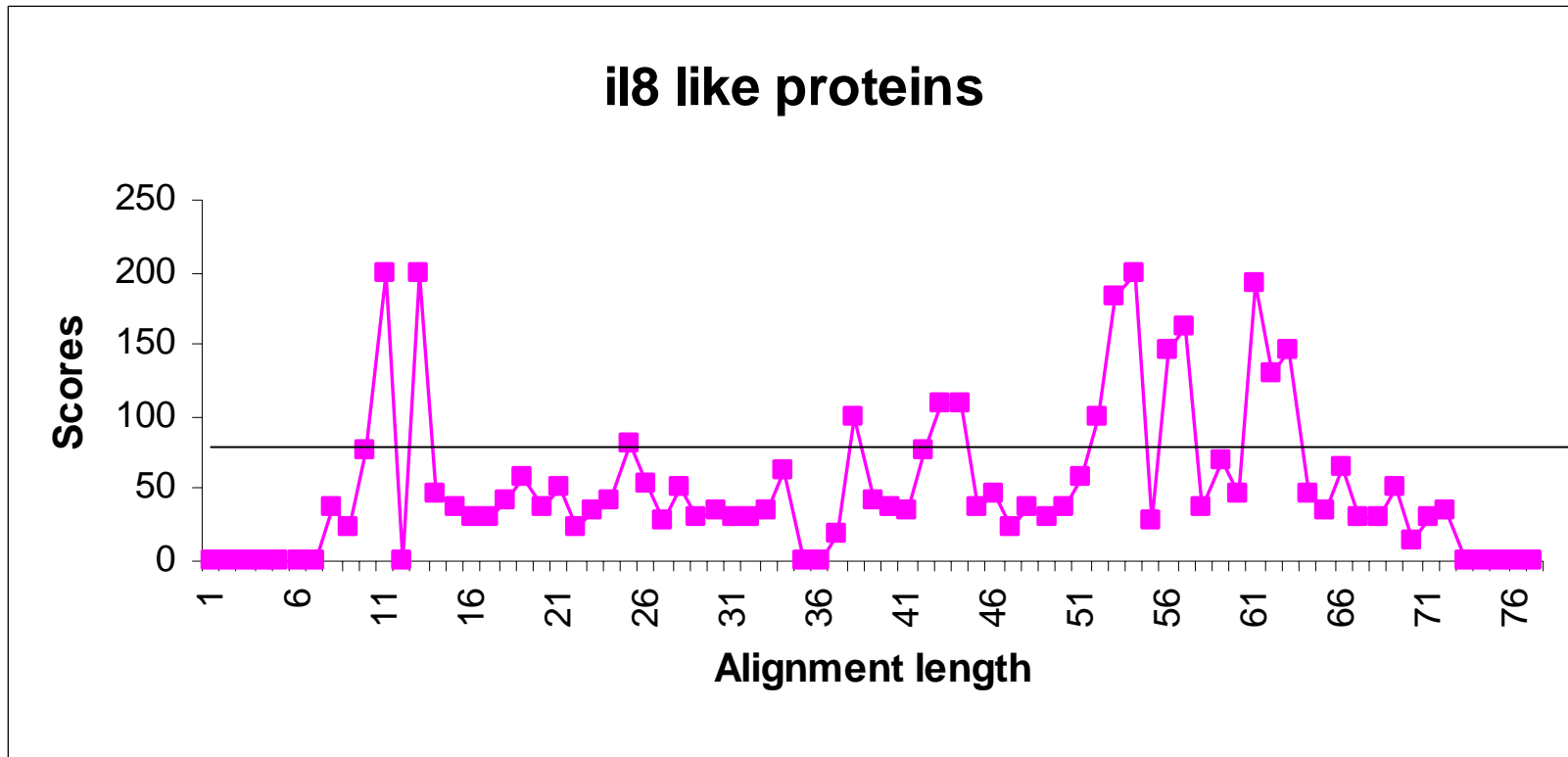
```

          10          20          30          40          50
1huma ( 1 ) apmgsdp---ptaççfsytarklprnfVvdyyeT-ss-lçsqpAvVFgTk
1b3aa ( 2 ) p y s s - d --- t t p ç Ç f a y i a r p l p r a h I k e y f y T - s g - k Ç s n p A V V F v t r
2eot ( 1 ) g p a s v p t t Ç ç f n l a n r k i p l q r L e s y r r i t s g - k ç p q k a V i F k t k
1plfa ( 23 ) l q ç v ç l k t t s - g i n p r h I s s L e v i g a g l h Ç p s p q L i A t l k
1rhpa ( 7 ) d I ç ç I Ç v k t t s - q V r p r h I t s L e v i k a g p h Ç p t a Q L I A t l k
1tvxa ( 23 ) l r ç l Ç i k t t s - g i h p k n I q s l e v i g k g t h ç n g v e V i A t l k
1mgsa ( 1 ) a s v a t e l r ç ç Ç l q t l q - G i h p k n I q s v n v k s p g p h Ç a q t E V i A t l k
1mi2a ( 1 ) a v v a s e l r ç ç ç l k t l p - r V d F k n I q s l s v t p p g p h Ç a q t E V i A t l k
1roda ( 1 ) s a k e l r ç ç ç i k t Y s k p f h p k f i k e l r v i e s g p h Ç a n t e i i V k L s
1il8a ( 2 ) a k e l r ç ç Ç i k t y s k p f h P k f I k e l r v i e s g p h Ç a n t e i i V k l s
1sdf ( 1 ) k p v s l s y r ç p Ç r f f e s - h V a r a n V k h l k i l n t - p n ç - a l g i V a r L k
          333bbbbbbb          bbbbbb

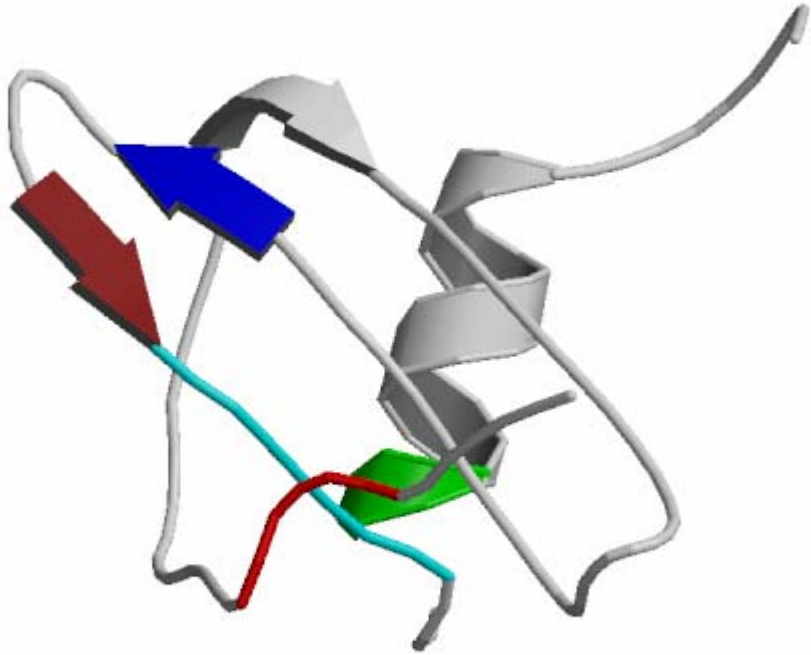
          60          70          80
1huma ( 46 ) r - s k q v ç A d p s e s w V q e y v y d l e l n
1b3aa ( 45 ) k - m r q v ç A n p e k k w V r e y I n s l e m s
2eot ( 45 ) l - a k d i Ç A d p k k w V q d S m k y l d q k s p t p k p
1plfa ( 62 ) t - g r k i ç L d q q n p l y k k I i k r l l k s
1rhpa ( 47 ) n - g r k i ç L d l g a p l y k k I i k l l e s
1tvxa ( 62 ) d - g r k i ç L d p d a p r I k k I v q k k l a g d
1mgsa ( 46 ) n - g r k a ç L n p a s p i V k k I i e k m l n s d k s -- n
1mi2a ( 46 ) g - g q k v Ç L d p e A p l v g k i i q k i l n k g k a -- n
1roda ( 45 ) d - g r e l ç L d p a s p i v k k i i e k m l n s d k s -- n
1il8a ( 45 ) d - g r e l ç L d p k e n w V q r v v e k f l k r a e n -- s
1sdf ( 44 ) n n z r q v ç I d p k l k w I q e y l e k a l n
          bbbb          aaaaaaaaaa

```

Alignment Score of il8-like Superfamily



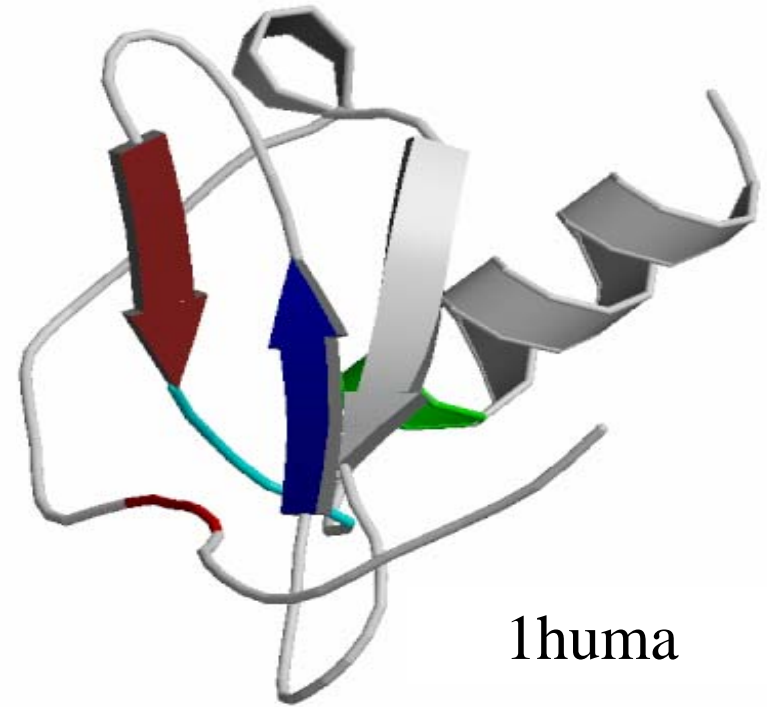
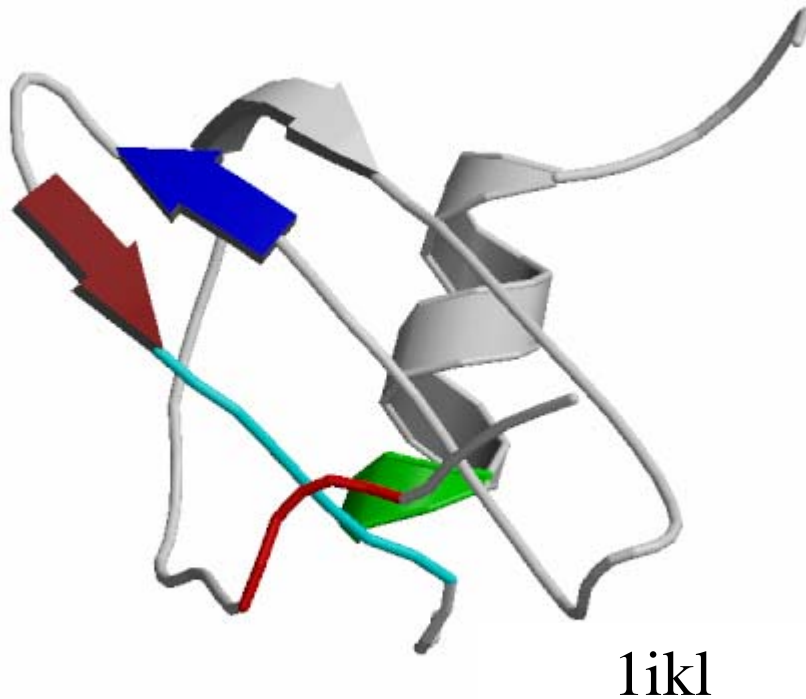
Interacting Motifs of the il8 superfamily



1ikl-	(4)		<div style="display: flex; align-items: center;"> <div style="border: 1px solid black; padding: 2px;">elrççik</div> Tyskpf <div style="border: 1px solid black; padding: 2px;">hpkfIke</div> Lrviesgp <div style="border: 1px solid black; padding: 2px;">hçante</div> <div style="border: 1px solid black; padding: 2px;">eIiVkl</div> sdg </div>
1huma	(1)		<div style="display: flex; align-items: center;"> <div style="border: 1px solid black; padding: 2px;">apmg</div> sdpptaç- <div style="border: 1px solid black; padding: 2px;">çfsytarklp</div> rnfVv <div style="border: 1px solid black; padding: 2px;">dyyeT</div> ss--lçsqpA <div style="border: 1px solid black; padding: 2px;">vVFg</div> Tkrs </div>
				bb	bbbb
1ikl-	(47)		<div style="display: flex; align-items: center;"> <div style="border: 1px solid black; padding: 2px;">relÇLdp</div> kenw</div> <div style="border: 1px solid black; padding: 2px;">Vqr</div> vve

kfl

Conservation of the motifs in the structures



Bhaduri, A., Ravishankar, R. & Sowdhamini, R.,
Proteins Structure, Function and Genetics (in press)

Employing structural motifs for sensitive sequence searches

Step 1:

Homologous sequences of individual superfamily members are aligned and amino acid exchanges at individual positions were scored for conservation.

Step 2:

Homologous sequences of individual superfamily members are aligned and amino acid exchanges at individual positions were scored for conservation.

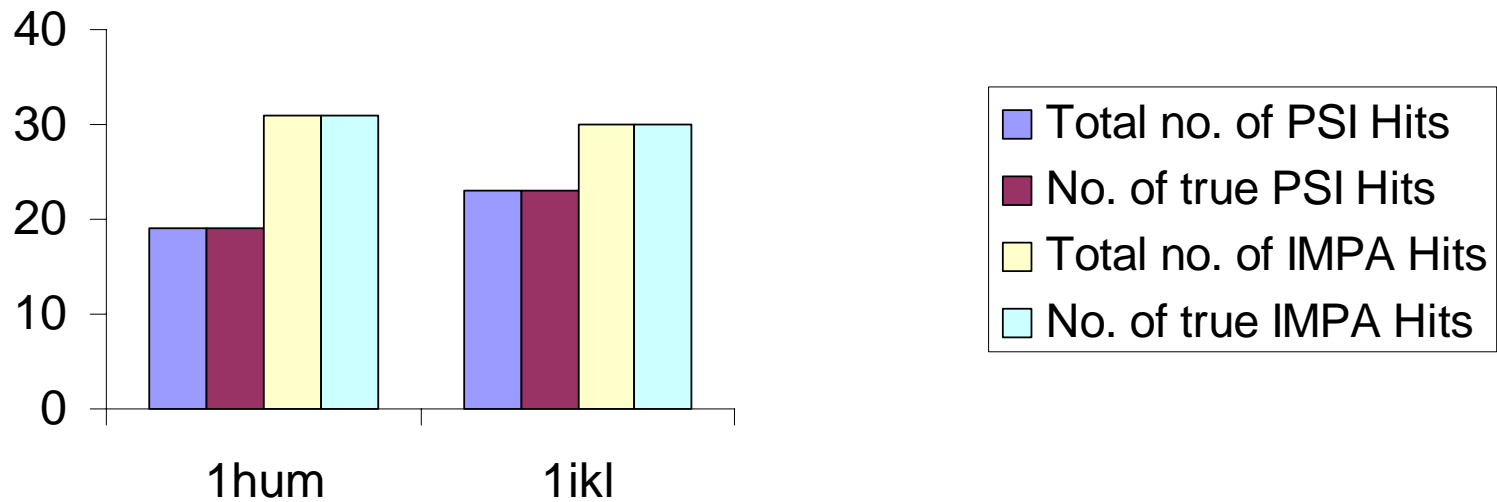
Step 3:

Spatially interacting motifs, when mapped on the superfamily alignment if in equivalent positions are considered for constrained sequence searches

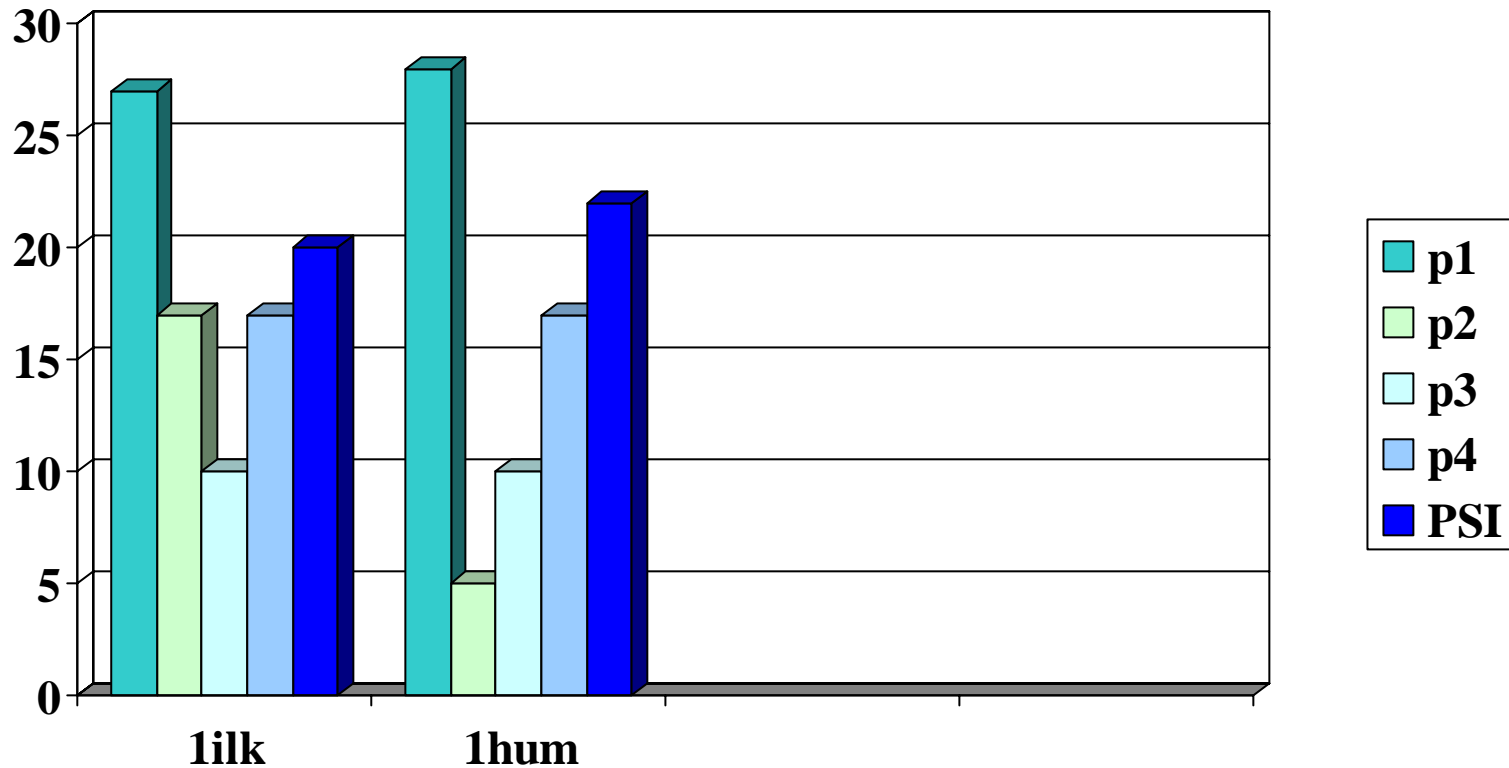
Interacting Motif Pattern Assisted (IMPA) Search: PHI-Blast Parameters

- Patterns obtained from Interactive Motifs
- E –value 1 (Standard value 0.0001)
- Iterations used 1(Standard value 3 or 5)
- Each superfamily Member of CAMPASS was used as a query Sequence

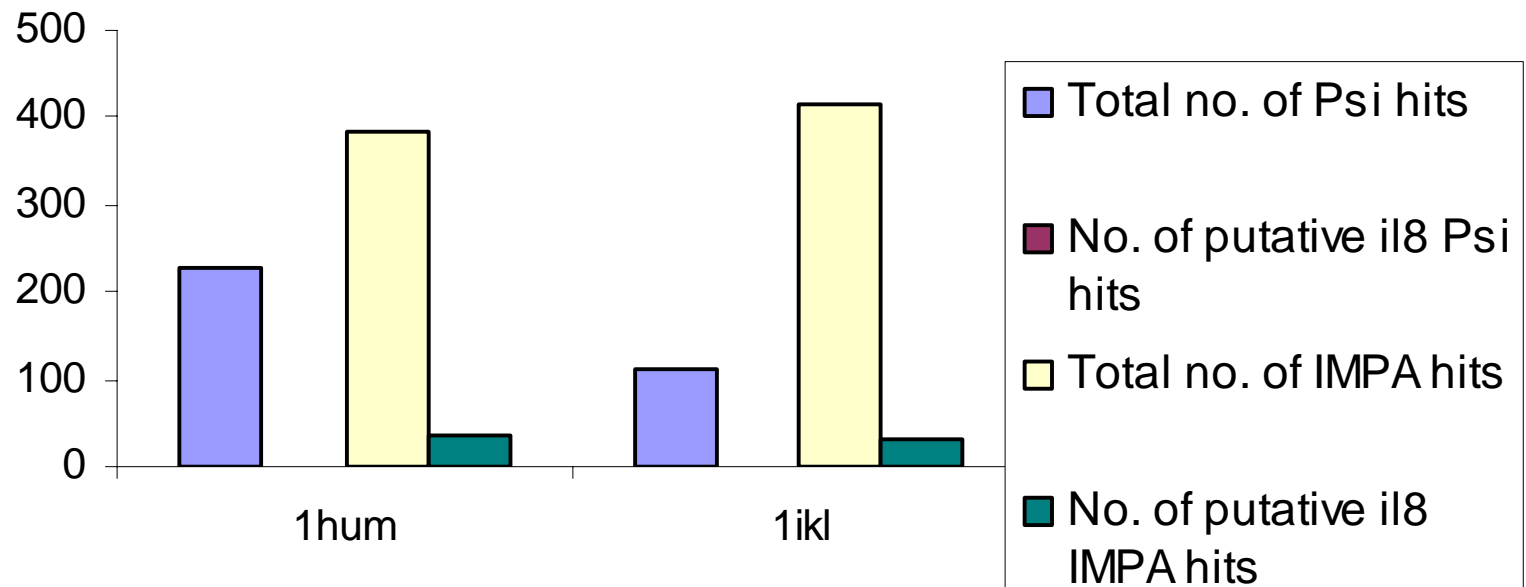
Blast analysis on PDB for il8-like proteins



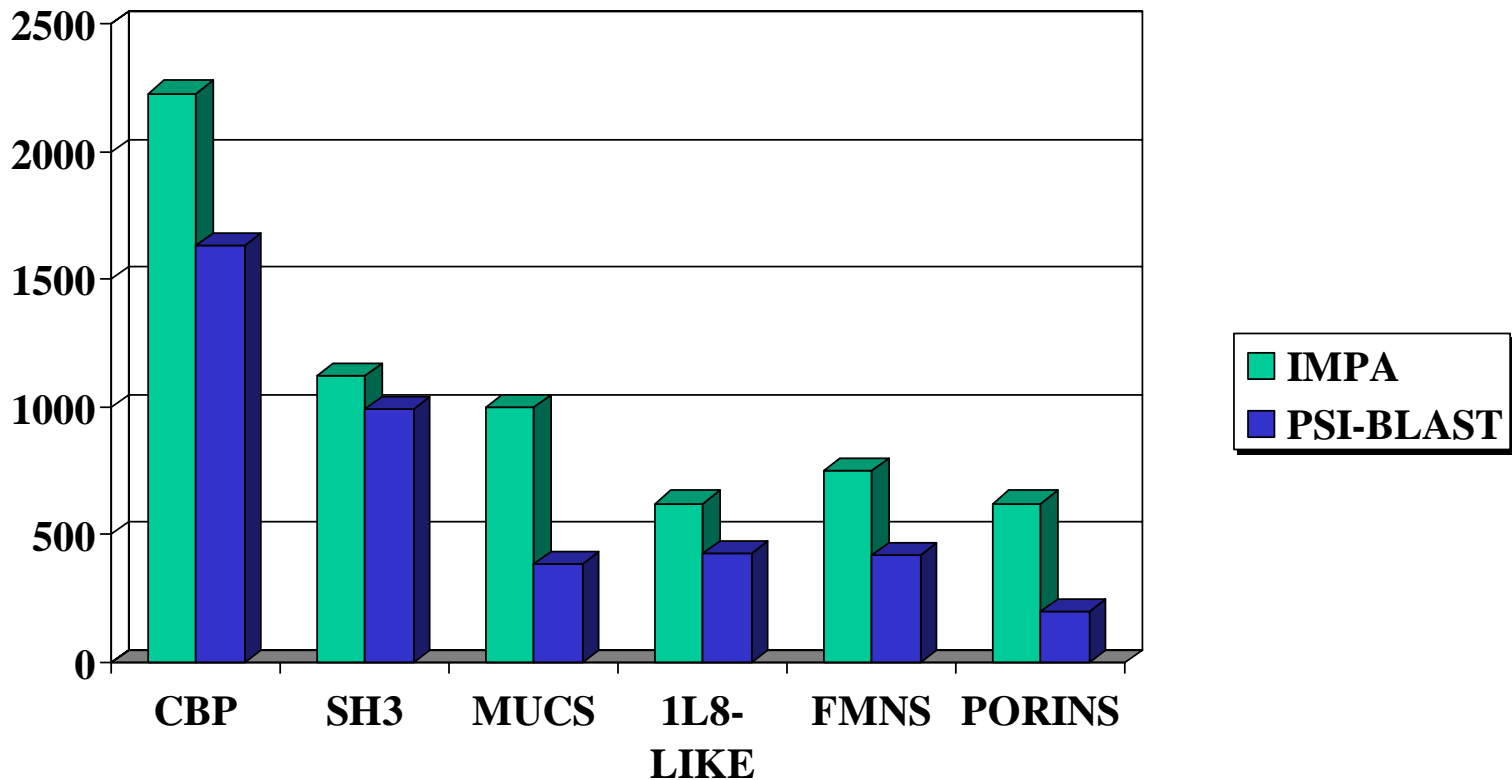
Contribution of individual motifs of the il8-like proteins



Blast analysis on Genomes



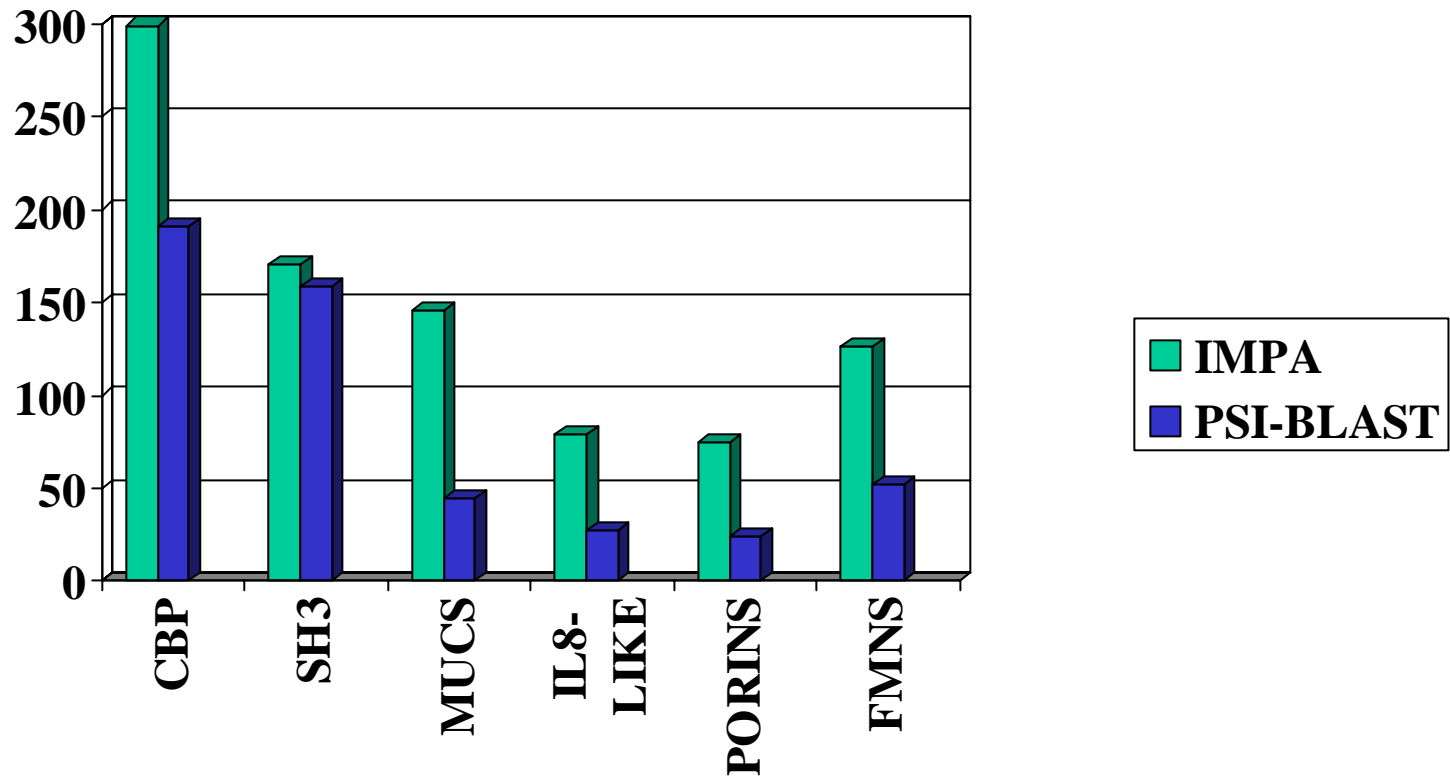
Genome Distribution across 91 Genomes



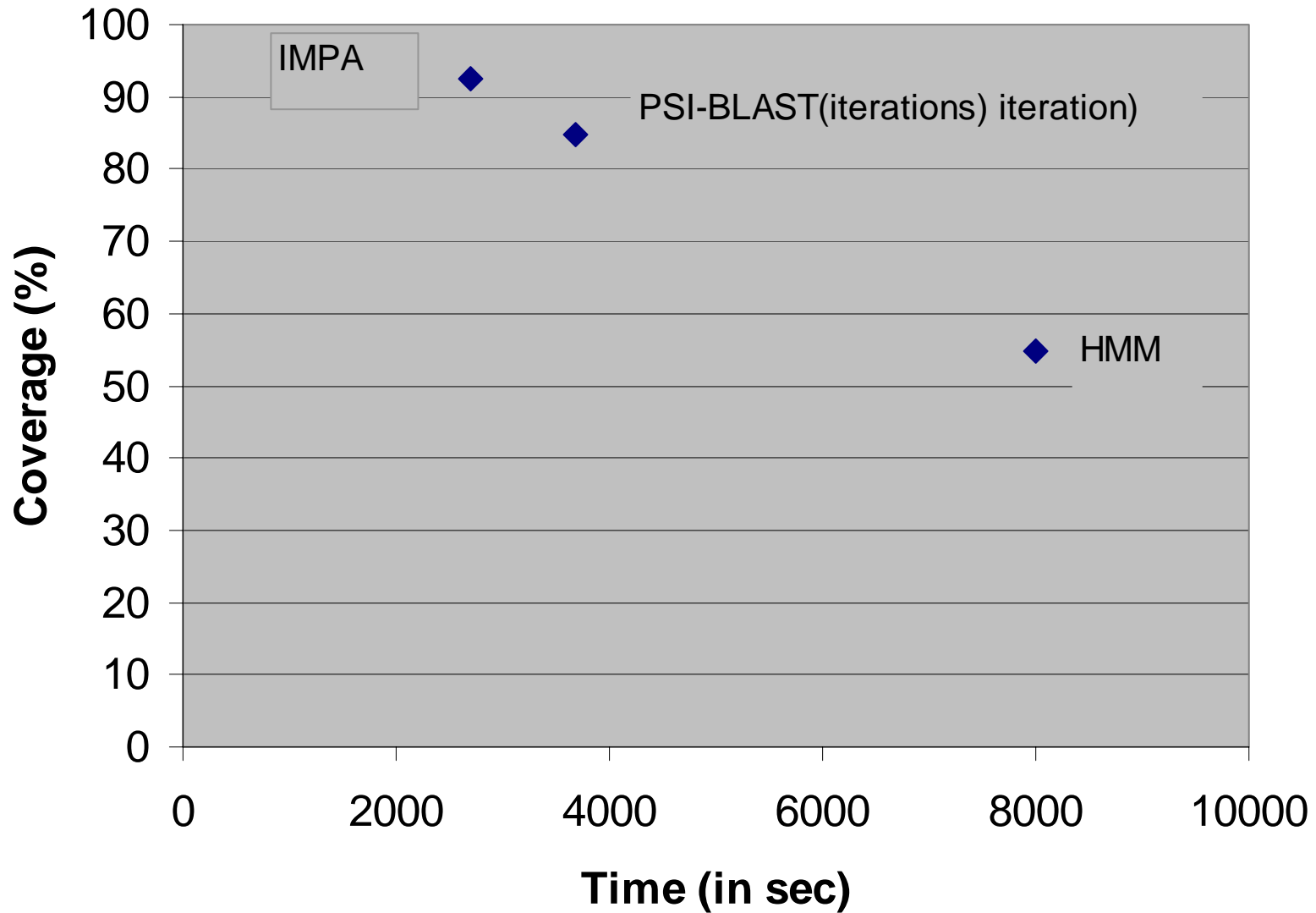
Bhaduri *et al.*, (in press)

Proteins Structure, Function and Genetics

Distribution of Hypothetical Proteins in the genome : Putative members of the Superfamily



Performance with respect to time



Testing of The Coverage against SCOP

Superfamily	IMPALA	BLAST	IMPA	TOTAL
SH3	58	54	56	67
Porins	31	24	33	33
Mucs	20	18	18	20
FMNs	17	5	16	18
Il8-like	34	34	34	35
CBP	111	99	105	125

Bhaduri et al., (in press)

Proteins Structure, Function and Genetics