

Sequence listing-English
SEQUENCE LISTING

<110> Sichuan Huiyang Life Science & Technology Corp

<120> CRYSTALLINE RECOMBINANT INTERFERON WITH ALTERED SPATIAL CONFIGURATION, THREE-DIMENSIONAL STRUCTURE AND USES THEREOF

<130> UP-102099-59:58

<140> PCT/CN 2010/002055

<141> 2010-12-16

<150> CN200910259339.2

<151> 2009-12-18

<160> 5

<170> PatentIn version 3.5

<210> 1

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of recombinant interferon

<400> 1

Met Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu
1 5 10 15

Ile Leu Leu Ala Gln Met Arg Arg Ile Ser Pro Phe Ser Cys Leu Lys
20 25 30

Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln
35 40 45

Phe Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln
50 55 60

Thr Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu
65 70 75 80

Ser Leu Leu Glu Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp
85 90 95

Leu Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu
100 105 110

Met Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile
115 120 125

Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
130 135 140

Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln
145 150 155 160

Sequence listing-English

Glu Arg Leu Arg Arg Lys Glu
165

<210> 2
<211> 504
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding recombinant interferon

<400> 2
atgtgcgacc tgccgcagac ccactccctg ggtaaccgtc gtgctctgat cctgctggct 60
cagatgcgtc gtatctcccc gttctcctgc ctgaaagacc gtcacgactt cggtttcccg 120
caggaagaat tcgacggtaa ccagttccag aaagctcagg ctatctccgt tctgcacgaa 180
atgatccagc agaccttcaa cctgttctcc accaaagact cctccgctgc ttgggacgaa 240
tccctgctgg aaaaattcta caccgaactg taccagcagc tgaacgacct ggaagcttgc 300
gttatccagg aagttgggtg tgaagaaacc ccgctgatga acgttgactc catcctggct 360
gttaaaaaat acttccagcg tatcacctg tacctgaccg aaaaaaata ctccccgtgc 420
gcttggggaag ttgttcgtgc tgaaatcatg cgttccttct ccctgtccac caacctgcag 480
gaacgtctgc gtcgtaaaga ataa 504

<210> 3
<211> 504
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding recombinant interferon

<400> 3
tacacgctgg acggcgtctg ggtgaggac ccattggcag cagcagacta ggacgaccga 60
gtctacgcag catagagggg caagaggacg gactttcttg cagtgtgaa gccaaagggc 120
gtccttctta agctgccatt ggtcaaggtc ttctcagtc gatagaggca agacgtgctt 180
tactaggtcg tctggaagtt ggacaagagg tggtttctga ggaggcgacg aacctgctt 240
agggacgacc tttttaagat gtggcttgac atggctcgtc acttgctgga ccttcgaacg 300
caataggtcc ttcaaccaca acttctttgg ggcgactact tgcaactgag gtaggaccga 360
caatttttta tgaaggctgc atagtgggac atggactggc ttttttttat gaggggcacg 420
cgaacccttc aacaagcacg actttagtag gcaaggaaga gggacaggtg gttggacgtc 480
cttgacagcg cagcatttct tatt 504

<210> 4
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of AB loop

Sequence listing-English

<400> 4

Ser Pro Phe Ser Cys Leu Lys Asp Arg
1 5

<210> 5

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of BC loop

<400> 5

Asp Gly Asn Gln Phe Gln Lys Ala Gln
1 5

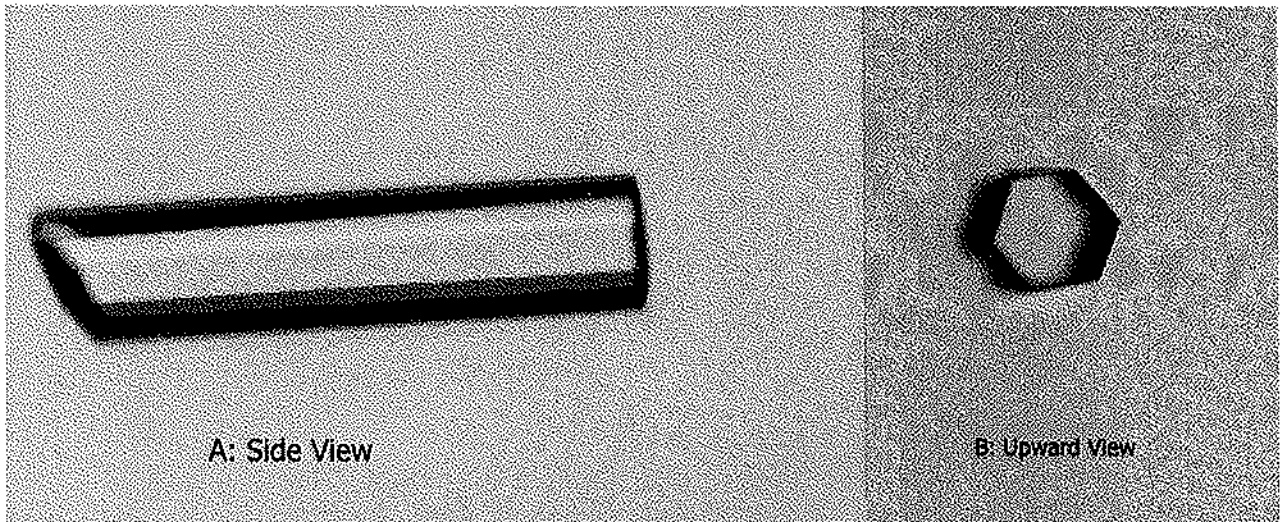


Figure 1

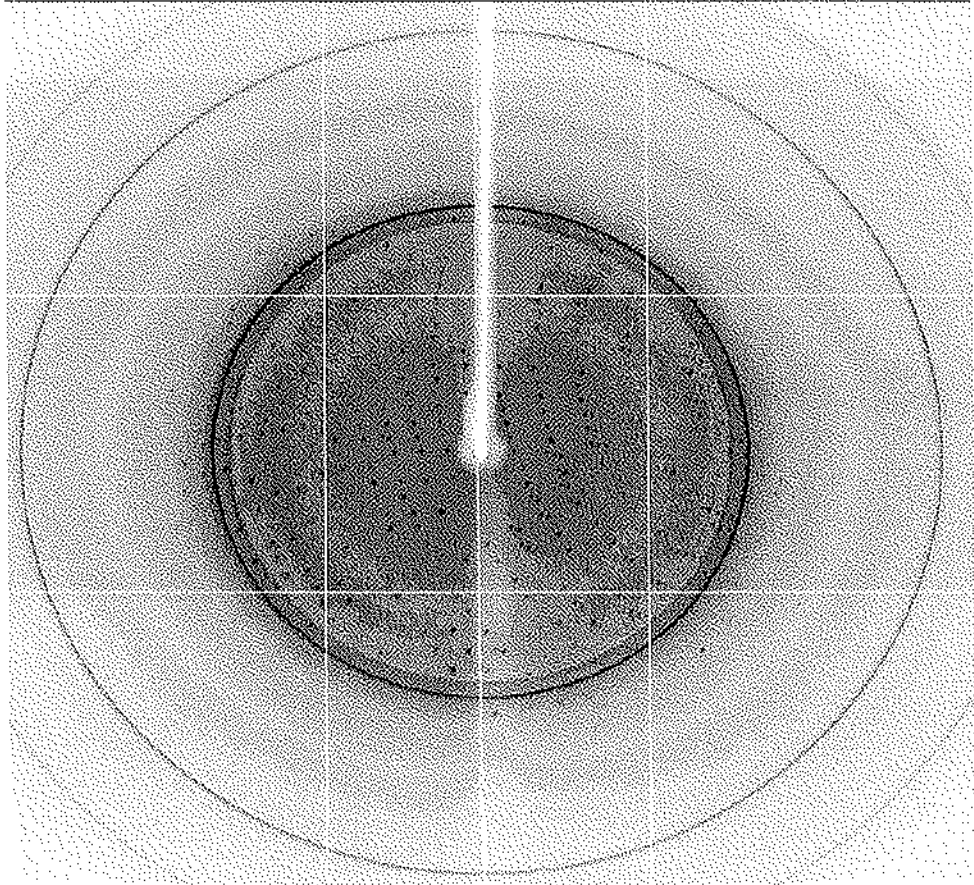


Figure 2

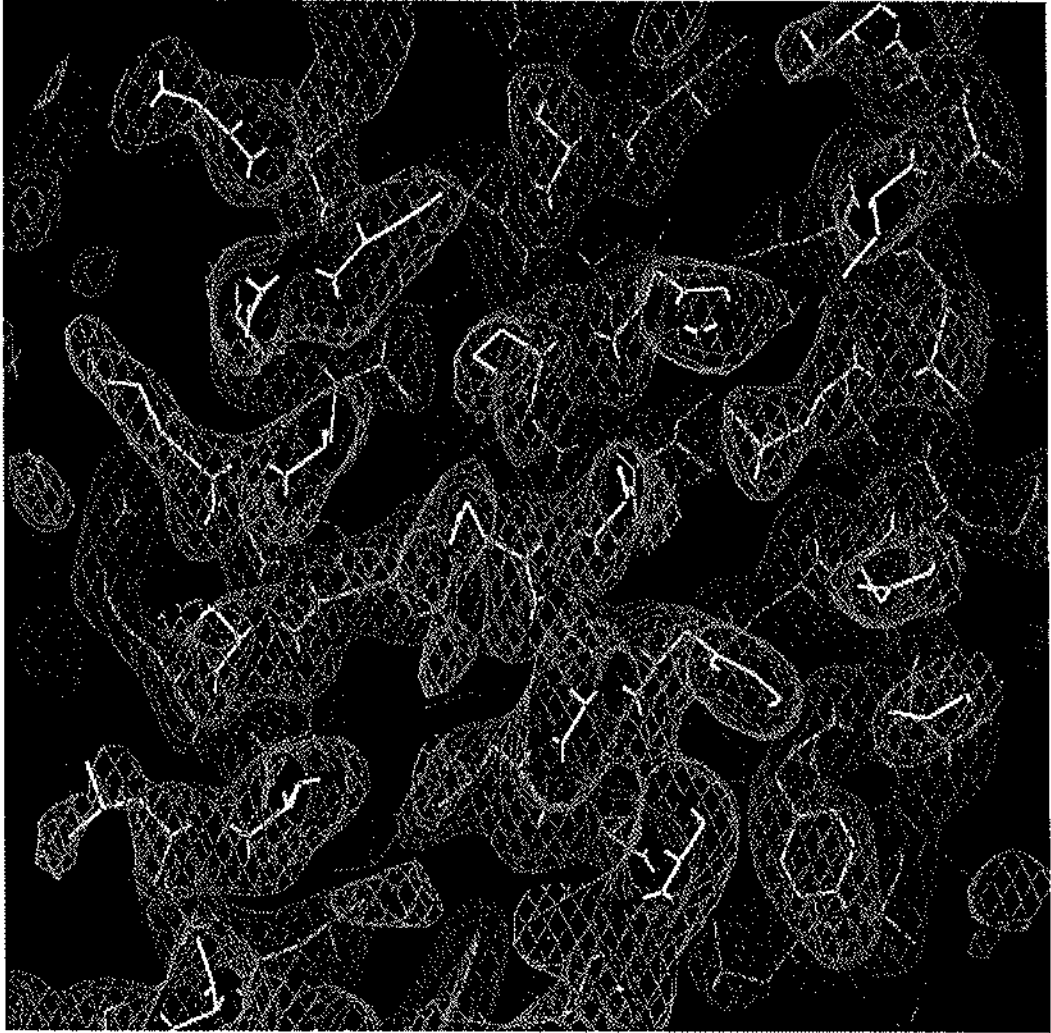


Figure 3

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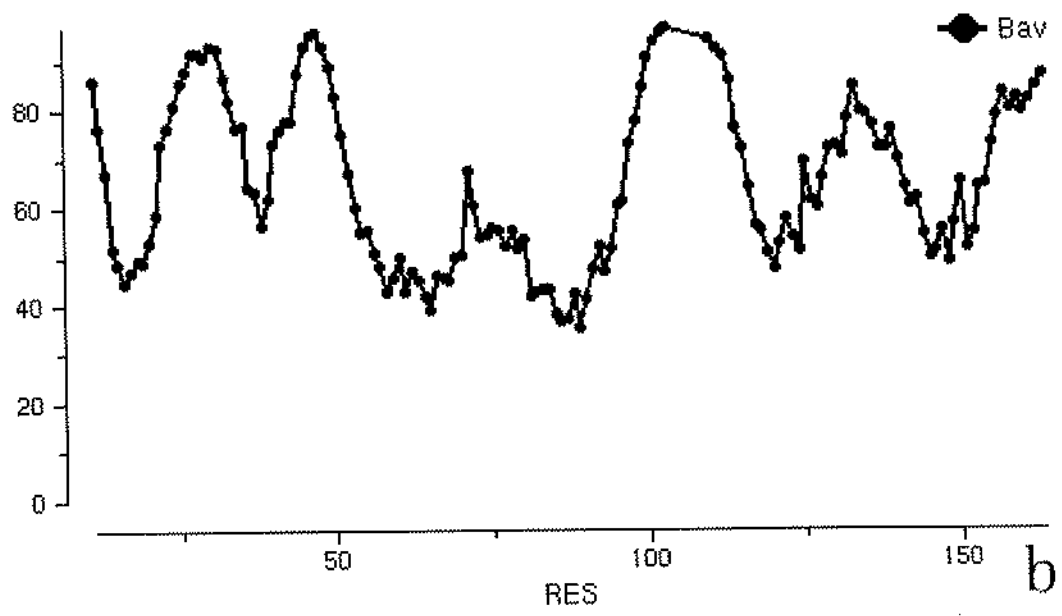
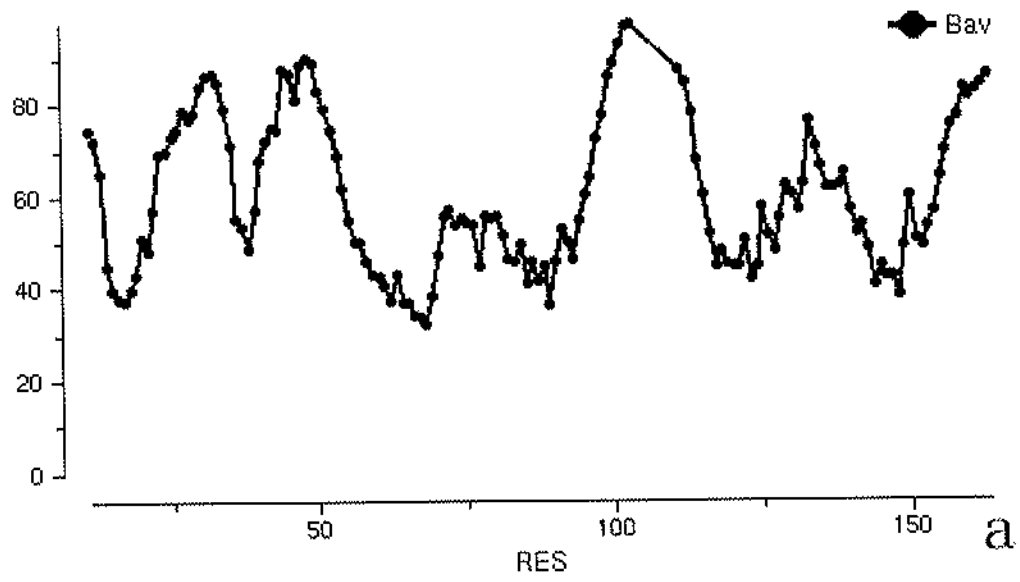
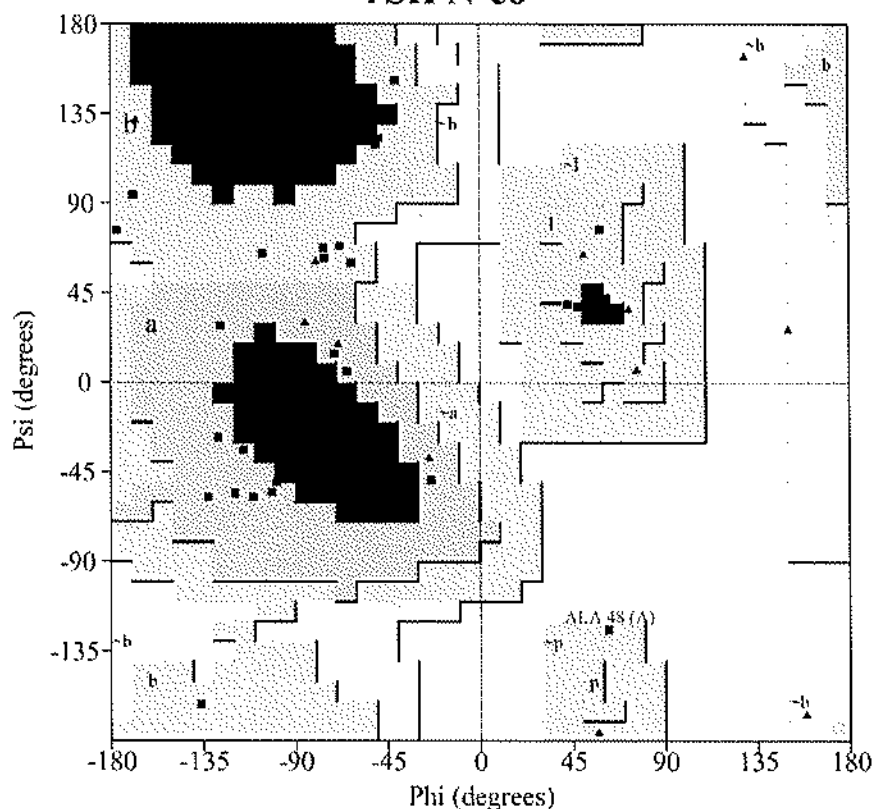


Figure 4

PROCHECK

Ramachandran Plot rSIFN-co



Plot statistics

Residues in most favoured regions [A, B, L]	240	90.6%
Residues in additional allowed regions [a, b, l, p]	24	9.1%
Residues in generously allowed regions [~a, ~b, ~l, ~p]	1	0.4%
Residues in disallowed regions	0	0.0%

Number of non-glycine and non-proline residues	265	100.0%
Number of end-residues (excl. Gly and Pro)	127	
Number of glycine residues	18	
Number of proline residues	6	

Total number of residues	416	

Based on an analysis of 118 structures of resolution of at least 2.0 Angstroms and R-factor no greater than 20%, a good quality model would be expected to have over 90% in the most favoured regions.

Figure 5

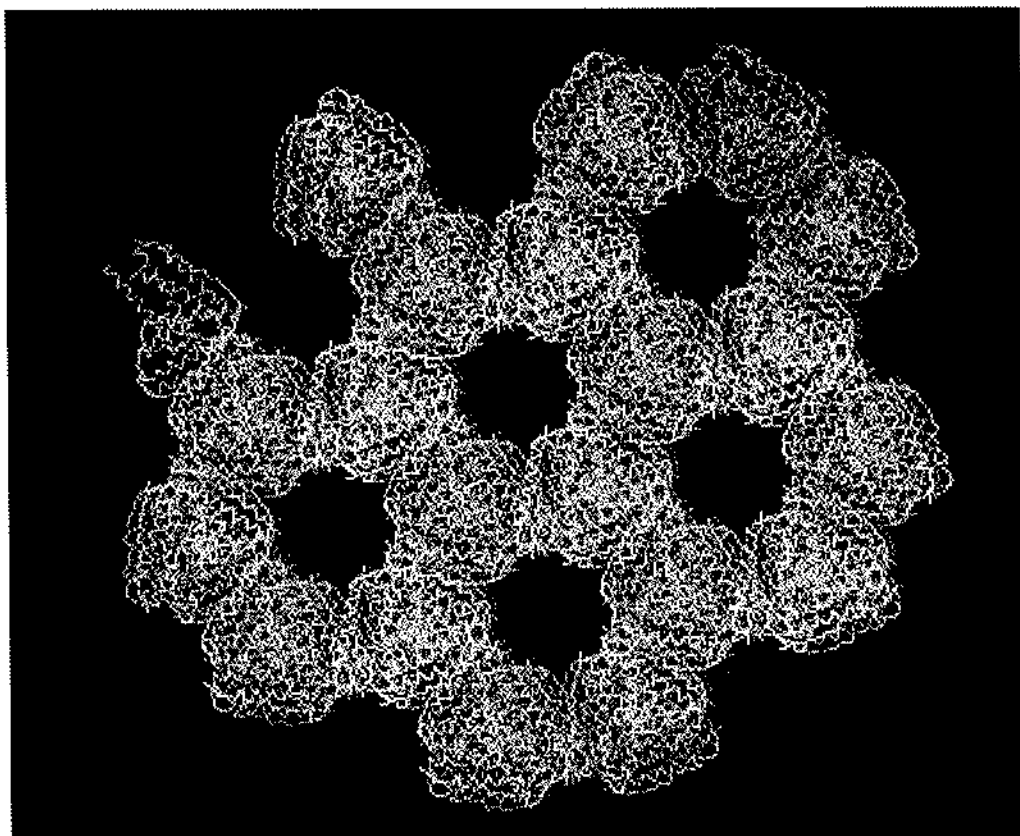


Figure 6

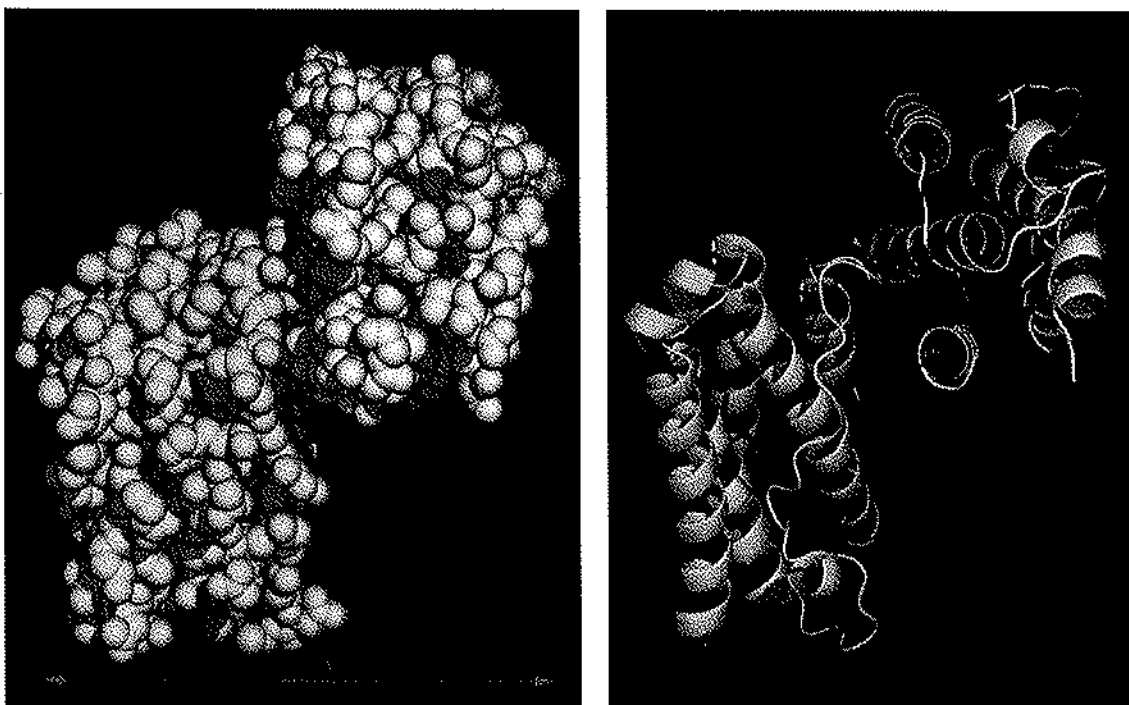


Figure 7

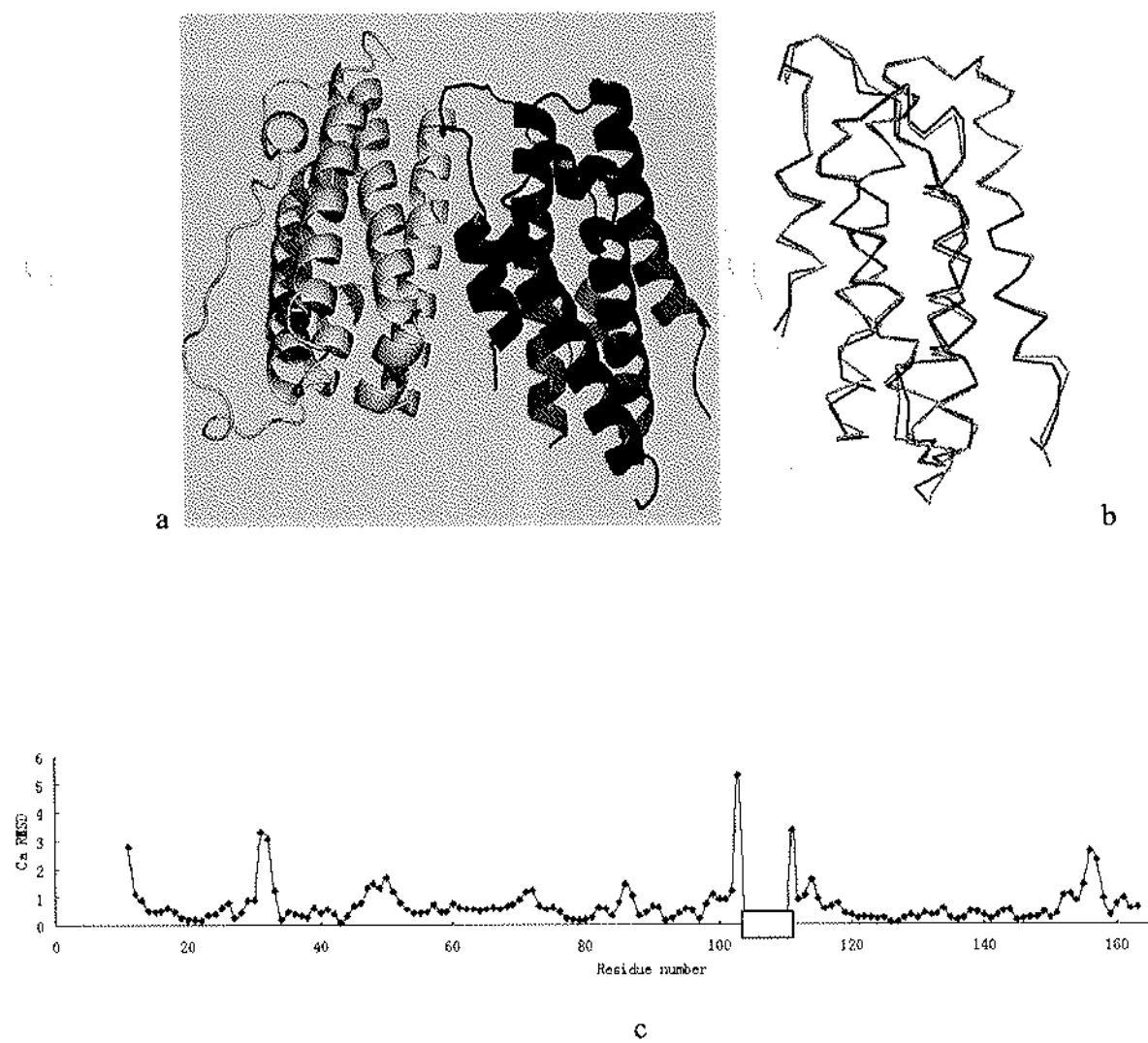
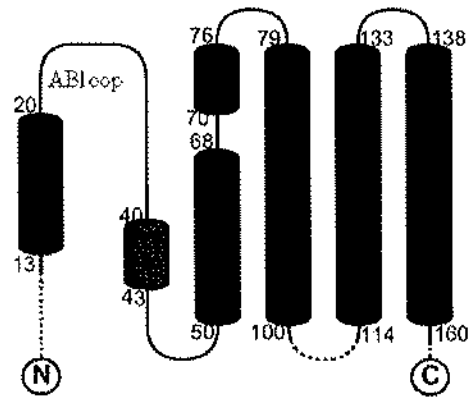
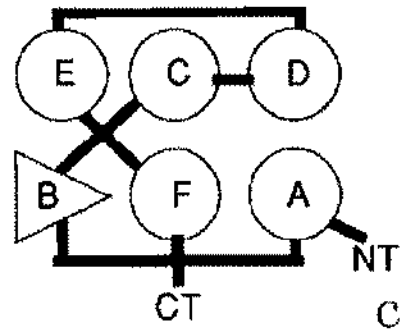
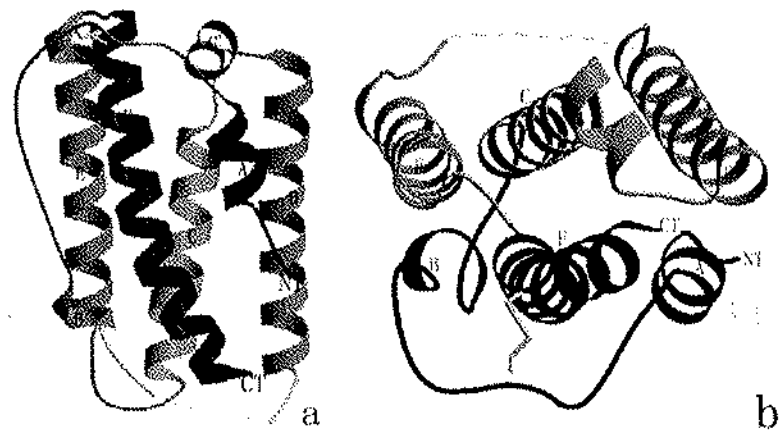


Figure 8



d

Figure 9

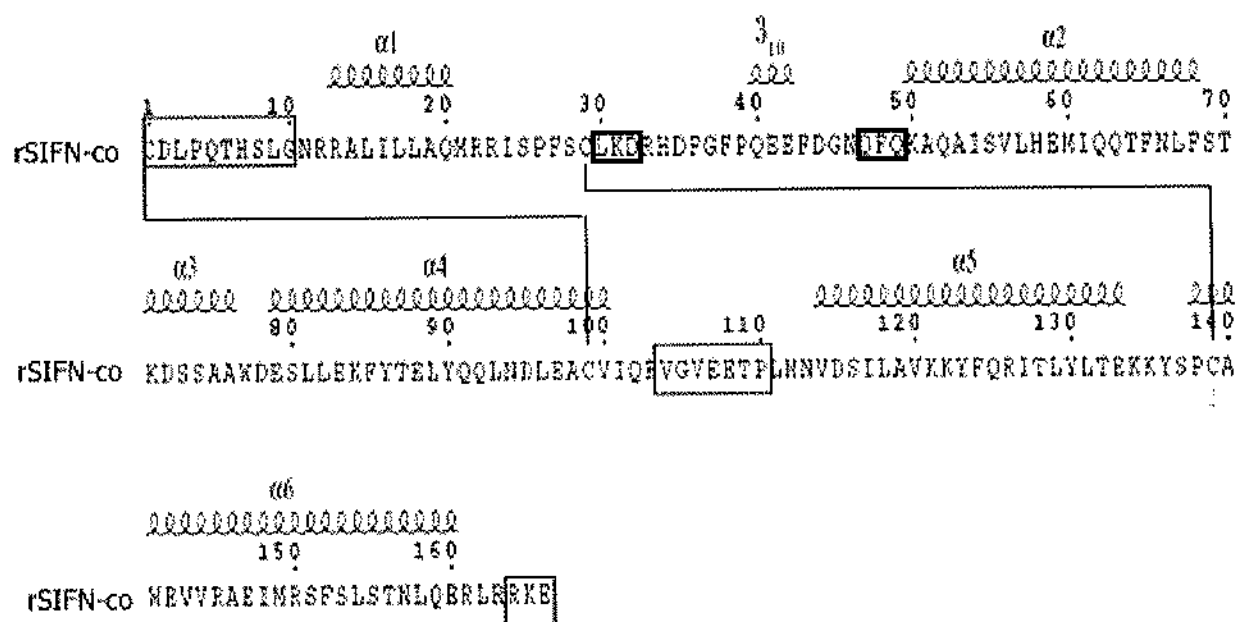


Figure 10

	1	10	20	30	40	50	60
rSIFN-co	...	CDLPQTHSLG	NRRA	DI	LLA	QMR	RIS
IFN-a2b	...	CDLPQTHSLG	SRRT	LM	LLA	QMR	RIS
IFN-a2a	...	CDLPQTHSLG	SRRT	LM	LLA	QMR	RIS
IFN-tau	...	CYLSR	KLM	LD	ARE	N	LK
hIFN-beta	MS	YN	LL	GF	LQ	RS	SN
mIFN-beta	IN	YK	OL	QL	QERT	NI	IK

	70	80	90	100	110	120	130
rSIFN-co	ES	TKD	SSA	AW	DES	LE	KE
IFN-a2b	ES	TKD	SSA	AW	DET	LL	DK
IFN-a2a	ES	TKD	SSA	AW	DET	LL	DK
IFN-tau	FY	TEH	SSA	AW	DT	TL	LE
hIFN-beta	FR	QDS	SS	TG	WN	ET	IV
mIFN-beta	FR	NN	FS	TG	WN	ET	IV

	140	150	160
rSIFN-co	PC	AW	EV
IFN-a2b	PC	AW	EV
IFN-a2a	PC	AW	EV
IFN-tau	DC	AW	EV
hIFN-beta	HC	AW	EV
mIFN-beta	SY	AW	EV

Figure 11

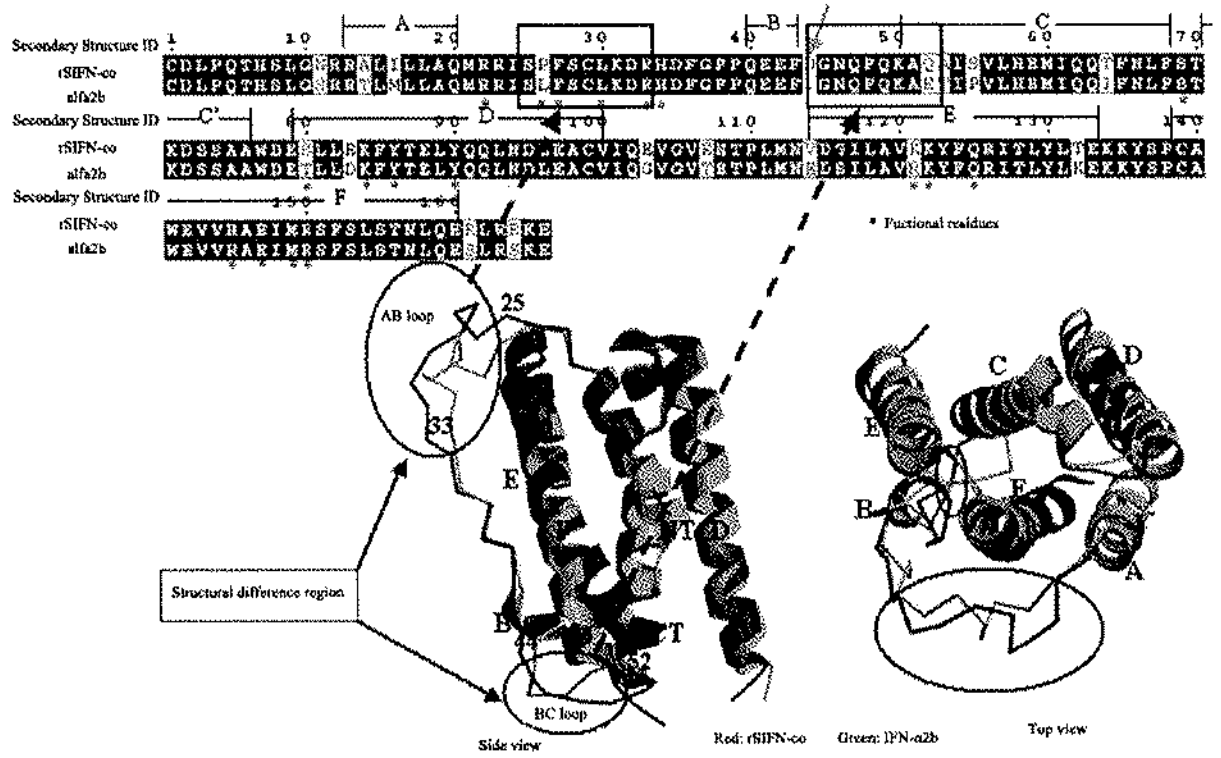


Figure 12

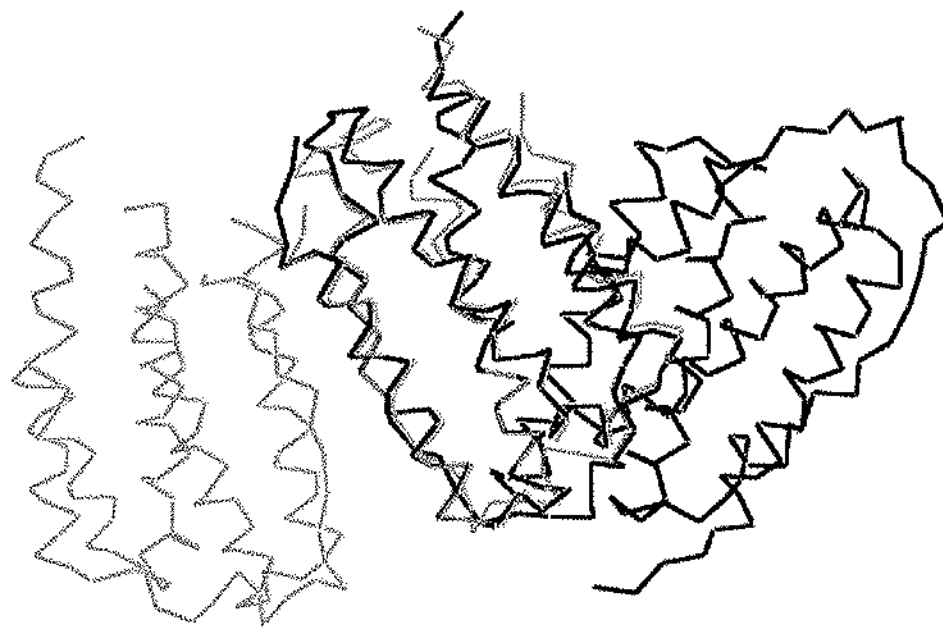


Figure 13

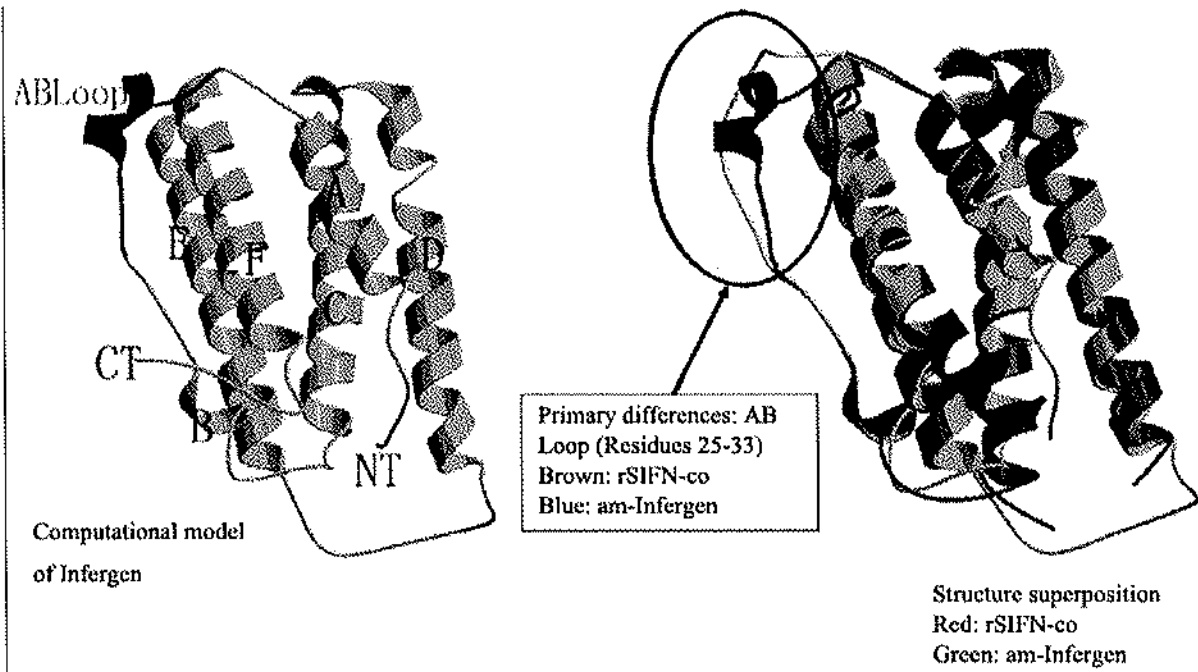


Figure 14

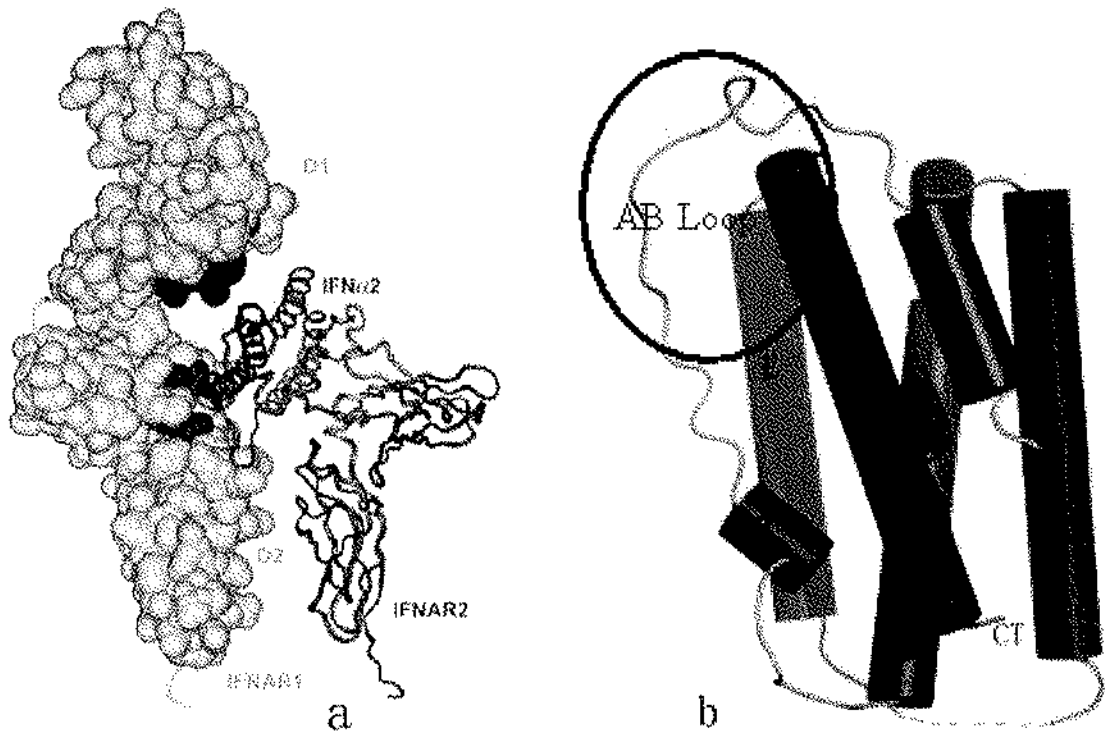


Figure 15

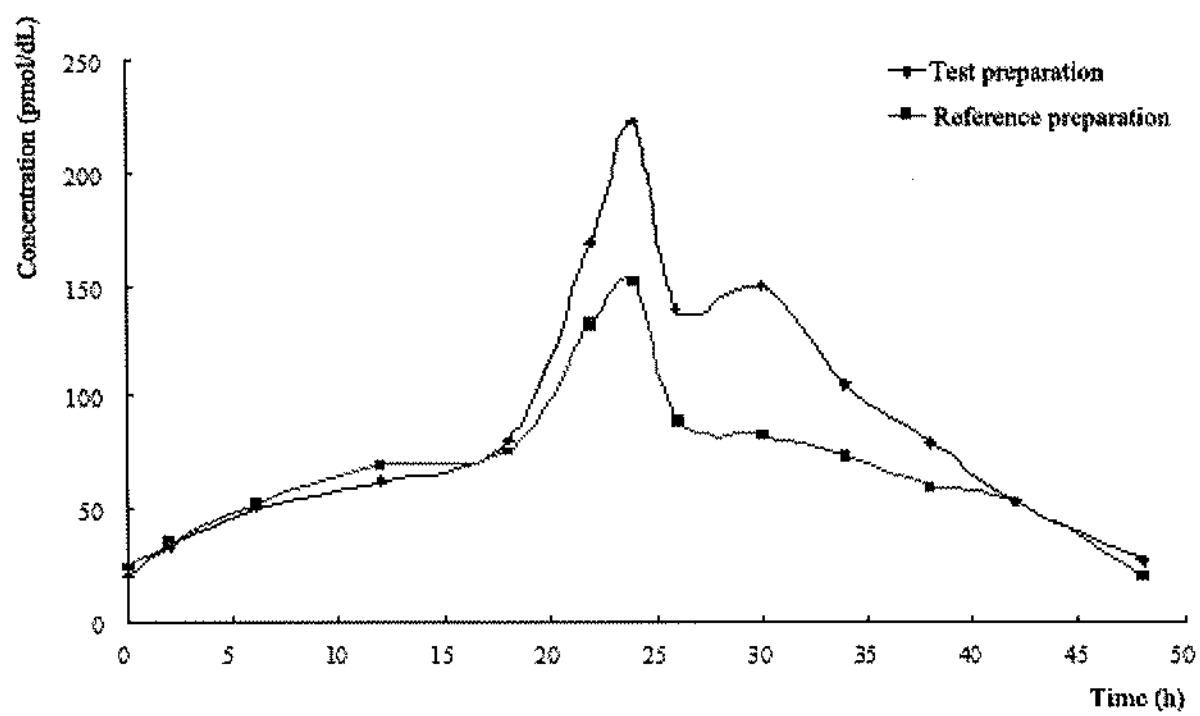


Figure 16