

Fig. 1

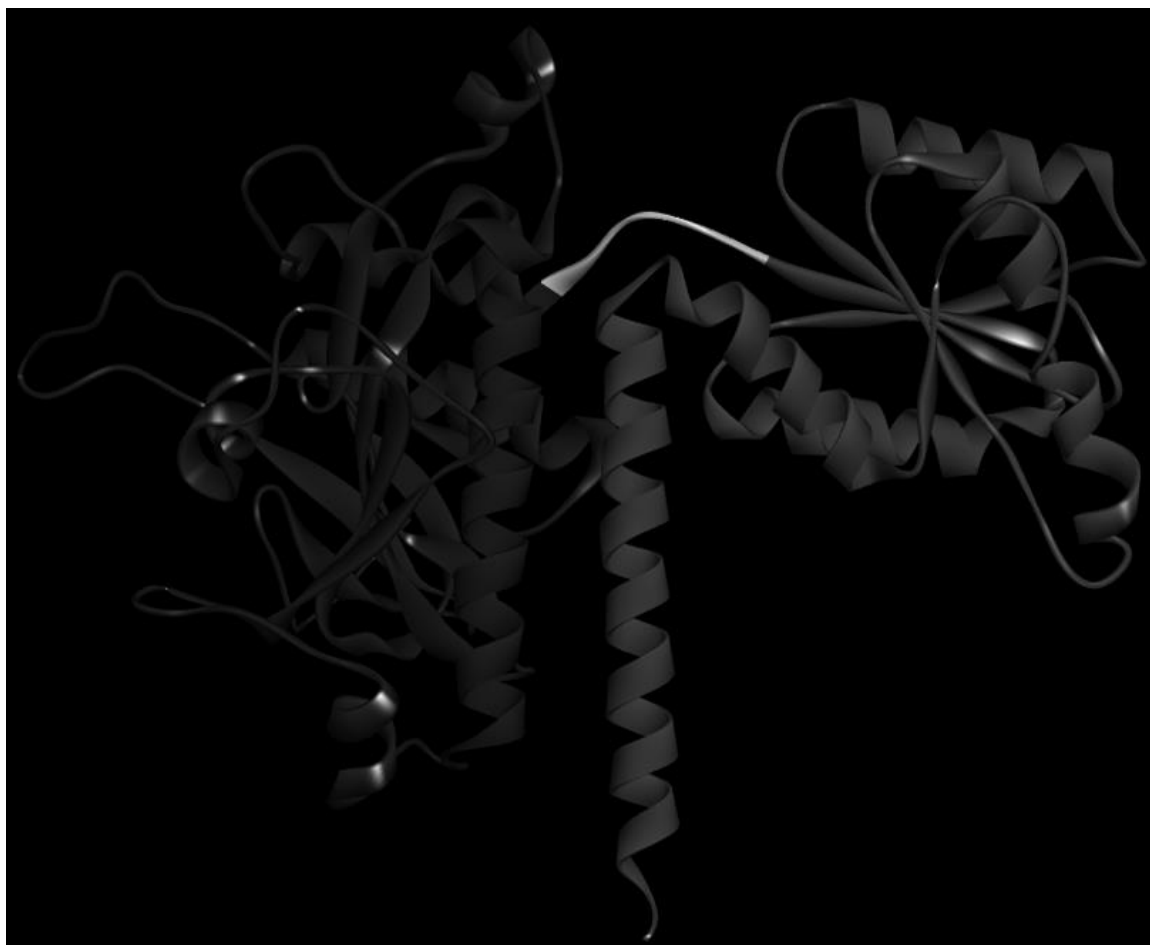
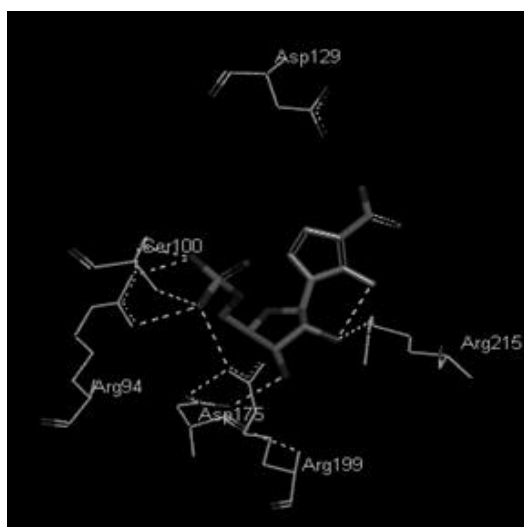
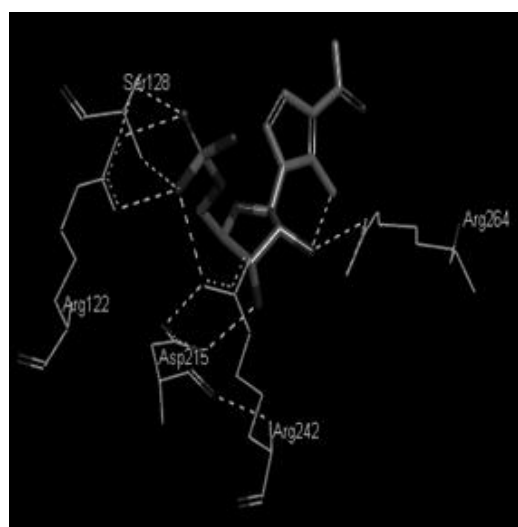


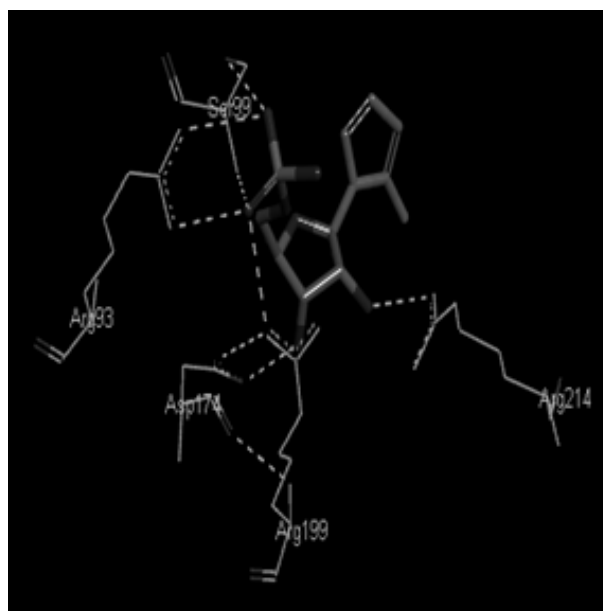
Fig. 2



(A)



(B)



(C)

Fig. 3

		Section 1									
		(1)	1	10	20	30	40	50	60	64	
2H31_Homo_PACIS	(1)	-----	MATAEVLNIGKKLYEGKTK	EVYELLDS	SPGKVL	LQSKDQ	ITAGNA	ARKNH			
4JA0_Bombyx mor_PACIS	(1)	-----	MSHPKQVQGYKLGKLLIEGKT	KQVEDV	PDOPGY	CLLNKDR	ITAGDGV	KAH			
1KUT_Thermotoga maritima_SAICAR synthase	(1)	-----	-----	MNYEGKTKIVKVTG	-----	DYALLEF	KDDITAGDGL	KHDV			
2GQR_Escherichia coli_SAICAR synthetase	(1)	-----	-----	MQKQAE	LYRGKAKTV	STEN	PDLLVLE	FRNDT	SAGDG	ARIEQ	
2YZL_Methanocaldococcus jannaschii_SAICAR synthetase	(1)	-----	-----	MEIKLEE	ILKKQPLYS	GKAKSIYE	IDD	DKVLIE	FRDDITAGN	GAKHDV	
3U54_Pyrococcus horikoshii_SAICAR synthetase	(1)	-----	-----	MVKLM	EVYEGKAKRM	IPID	DKLIME	FKDDATA	FDG	TKKAR	
2YVW_Geobacillus kaustophilus_SAICAR synthetase	(1)	-----	-----	GHMPT	KQQLLYEGKAKKI	YATD	PDVLWV	EVYKDS	ATAFN	GEKKAT	
3NUA_Clostridium perfringens_SAICAR synthetase	(1)	-----	-----	SNAMVN	QLEMLYEGKAKKI	YATD	EDMVI	VHYKDD	ATAFN	GEKKAT	
3KRE_Ehrlichia chaffeensis_SAICAR synthetase	(1)	MAHHHHH	MGTL	EAQTG	PGSGMEN	KEKLYEGKAKKI	IFATLN	PLEVIO	HFKDE	ITAFNN	KKAAI
1A48_Saccharomyces cerevisiae_SAICAR SYNTHASE	(1)	-----	-----	XSIRKTE	LDGILPLV	ARGKVRD	IEYVDA	GTLLF	VATDR	ISAYD	VIMENS
3R9R_Mycobacterium abscessus_SAICAR synthetase	(1)	-----	-----	GPFGMR	PSLSDY	QHVASG	KVRELY	RVDD	EHLLF	VATDR	ISAFD
Consensus	(1)	-----	-----	M	LYEGKAK	IY	VDD	D	LLL	FKDDITAFD	G
		Section 2									
		(65)	65	70	80	90	100	110	120	128	
2H31_Homo_PACIS	(50)	LEGKAA	ISNKITS	CFQLLE	-----	-----	AGIKTA	FRKCG	ETAF	LAPOCE	
4JA0_Bombyx mor_PACIS	(53)	LEGKAA	ISNQTNA	KVFILKS	-----	-----	AGIKTA	FRV	KIAS	TAFLSK	KCE
1KUT_Thermotoga maritima_SAICAR synthase	(36)	LTGKGS	ICAE	TTAILM	KYLSE	-----	-----	KGIKTH	LVEY	IPPTL	KVIFLK
2GQR_Escherichia coli_SAICAR synthetase	(43)	FDRKGM	VNNKFN	YFIMS	KLAE	-----	-----	AGIPT	CMER	LLSD	TEGLVKKLD
2YZL_Methanocaldococcus jannaschii_SAICAR synthetase	(49)	KQSGY	LYNAL	ISKLE	FEALDE	-----	-----	NGVKTH	YIKY	IEPRYN	IAKKE
3U54_Pyrococcus horikoshii_SAICAR synthetase	(42)	FKGK	GLNAQL	SVIF	FKLLE	-----	-----	HGKTH	HFIV	AGGN	RLIVKLD
2YVW_Geobacillus kaustophilus_SAICAR synthetase	(46)	IAGK	GRLN	NEITS	LLFL	KLKE	-----	-----	AGIAN	HFIK	LSPTOLVRRVT
3NUA_Clostridium perfringens_SAICAR synthetase	(47)	IESK	GVLN	NEITS	LLF	EMLNK	-----	-----	EGIKTH	HFV	KLNDRLCKEVE
3KRE_Ehrlichia chaffeensis_SAICAR synthetase	(64)	IHEK	GILNN	YIS	FLMK	KLID	-----	-----	KGIKTH	HFIS	LLNGREL
1A48_Saccharomyces cerevisiae_SAICAR SYNTHASE	(50)	IPER	GILL	TKLS	EF	FLSND	VNRN	HLVD	IA	PGKTI	FDYLP
3R9R_Mycobacterium abscessus_SAICAR synthetase	(50)	IPDK	GRIL	TAMS	VFF	EGLL	TVP	-----	-----	N	HLAG
Consensus	(65)	I	GKG	LNN	ISS	LF	L	E	GIKTH	FI	L
		Section 3									
		(129)	129	140	150	160	170	180	190	192	
2H31_Homo_PACIS	(93)	MIPIE	WVCR	RIATG	SFLKRN	-----	PGVKE	GK	FYP	PKVLE	FFKDD
4JA0_Bombyx mor_PACIS	(96)	MIPIE	WVTR	RLATG	SFLKRN	-----	PGVPE	GK	FRT	PKQET	FFKDD
1KUT_Thermotoga maritima_SAICAR synthase	(79)	MFPLE	EVVRL	KKAGS	FVRR	-----	YGA	EG	EDL	PLV	PLVE
2GQR_Escherichia coli_SAICAR synthetase	(86)	MVPVE	CVVR	NRAAG	SLVKR	-----	LGIE	EG	IEL	NPL	FL
2YZL_Methanocaldococcus jannaschii_SAICAR synthetase	(92)	IIPIE	EVIV	RNIAG	SLCRR	-----	YFE	EG	KEL	FP	IVQ
3U54_Pyrococcus horikoshii_SAICAR synthetase	(85)	MYPLE	EVVR	NVAV	SLKRR	-----	LPL	PE	G	YEL	PE
2YVW_Geobacillus kaustophilus_SAICAR synthetase	(89)	IIPLE	EVVR	NVAV	SLAKR	-----	IGLE	EG	T	PLE	AP
3NUA_Clostridium perfringens_SAICAR synthetase	(90)	IVPLE	EVVR	NVAV	SLAKR	-----	LGLE	EG	YEL	KT	V
3KRE_Ehrlichia chaffeensis_SAICAR synthetase	(107)	IIPLE	EVVR	NVAV	SLAKR	-----	LGLE	EG	YEL	KT	V
1A48_Saccharomyces cerevisiae_SAICAR SYNTHASE	(114)	LIPLE	EVIV	RNIAG	SLCRR	-----	YFE	EG	KEL	FP	IVQ
3R9R_Mycobacterium abscessus_SAICAR synthetase	(99)	MIPVE	CVVR	NRAAG	SLVKR	-----	LGIE	EG	IEL	NPL	FL
Consensus	(129)	MIPLE	EVVR	NVAV	SLAKR	-----	IGLE	EG	T	PLE	AP
		Section 4									
		(193)	193	200	210	220	230	240	250	256	
2H31_Homo_PACIS	(152)	FAGLL	IGQTE	VDIM	SHATQ	ATFEILE	KSWLP	QNCT	LVD	MKIE	EF
4JA0_Bombyx mor_PACIS	(155)	YNGLL	IGRDE	VDIM	MRKAT	ITILFEILE	KAWAL	RDCAL	DMKIE	EF	FG
1KUT_Thermotoga maritima_SAICAR synthase	(137)	T-----	KKQAE	KMKEA	AVKIT	LALKE	FFERAN	FELWD	IKYE	FG	LD
2GQR_Escherichia coli_SAICAR synthetase	(144)	S-----	KEND	ARMKE	LYKAND	VLLKLE	DDAG	ILVDF	KLE	FG	LY
2YZL_Methanocaldococcus jannaschii_SAICAR synthetase	(150)	T-----	REELN	KIKEL	IALKV	NEVLK	LEDEK	KGIL	VDF	KIE	IG
3U54_Pyrococcus horikoshii_SAICAR synthetase	(143)	-----	LDEIK	KIEEL	ALKVNE	ILKDY	LAKG	ILVDF	KLE	FG	RD
2YVW_Geobacillus kaustophilus_SAICAR synthetase	(147)	S-----	REEVA	ALQ	ALAV	NDVLR	LHFA	ERN	VRL	DF	KLE
3NUA_Clostridium perfringens_SAICAR synthetase	(148)	T-----	FEELN	KIYE	ITAKV	NEILKE	AFKKQ	INIL	DF	KLE	FG
3KRE_Ehrlichia chaffeensis_SAICAR synthetase	(165)	T-----	NQELE	KIKIL	SLKINN	ILSE	LEFN	VNG	KLV	DF	KLE
1A48_Saccharomyces cerevisiae_SAICAR SYNTHASE	(178)	QAAEL	VGED	LSRR	VAE	AVKLY	SKCKDY	AKKGI	IAD	TK	FE
3R9R_Mycobacterium abscessus_SAICAR synthetase	(163)	AVVGL	VGA	VRAN	OLRDE	TIKIY	TRAA	AHAL	HKG	IL	AD
Consensus	(193)	T	EEL	KIKET	TLKINE	ILK	F	KGI	LVDF	KLE	FG
		Section 5									
		(257)	257	270	280	290	300	310	320		
2H31_Homo_PACIS	(214)	WRLWP	SG	-----	DRSQ	QDKQS	YRDL	KEVT	PEGL	QMVK	KN
4JA0_Bombyx mor_PACIS	(216)	WRLWP	SG	-----	DKRL	MVDQ	VYRN	LT	VTAA	LD	LT
1KUT_Thermotoga maritima_SAICAR synthase	(192)	FRIR	-----	KKGE	IFDK	DVYRR	DLG	PLKKY	REVL	ELC	RS
2GQR_Escherichia coli_SAICAR synthetase	(198)	SRLWD	-----	ETLE	KMDK	DRFR	QSLG	GLIE	AYE	AVARR	IG
2YZL_Methanocaldococcus jannaschii_SAICAR synthetase	(205)	MRLWD	-----	ETRD	VYLD	KDVR	FRKDL	GLDV	IAKY	RI	VA
3U54_Pyrococcus horikoshii_SAICAR synthetase	(197)	CRFWDA	-----	KT	KRS	LDK	DVFR	FDK	GLIE	AYE	AVARR
2YVW_Geobacillus kaustophilus_SAICAR synthetase	(202)	CRFWDA	-----	KT	NEK	LDK	DVFR	FDK	GLIE	AYE	AVARR
3NUA_Clostridium perfringens_SAICAR synthetase	(202)	CRFWDA	-----	TT	GEK	MKD	DRFR	DMGN	VING	YRE	VL
3KRE_Ehrlichia chaffeensis_SAICAR synthetase	(223)	CRFWDI	-----	ST	NKR	LDK	DRYR	LN	GNV	IEG	YRE
1A48_Saccharomyces cerevisiae_SAICAR SYNTHASE	(241)	SRFWNGA	-----	SY	KVG	SOD	S	YDK	QFL	RD	WT
3R9R_Mycobacterium abscessus_SAICAR synthetase	(225)	SRFWDA	-----	AHY	QPG	VQDS	FDK	QFVR	NW	IT	GP
Consensus	(257)	RLWDA	-----	T	E	LDK	D	FR	I	G	LI

Fig. 4

