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Workunit: P000021 Title:Saxiphilin



Go to: [Template Selection] [Alignment] [Modelling Log] [Evaluation]

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Model Details: Segment 1



Model info:
 modelled residue range: 26 to 382
 based on template: 3mc2A (2.40 Å)
 Sequence Identity [%]: 44.258
 Evaluate: 0.00e-1

display model: as pdb - as DeepView project
 download model: as pdb - as Deepview project - as text

Alignment [top]

3mc2A	3	ektirwcvvs	dheatkcssf	rdnmkkvlpa	gdpavtcvrk	mshpecirdi
3mc2A		sssss	hhhhhhhh	hhhhhh	sssss	hhhhhhhh
3mc2A	53	sankvdavtv	dgalvaeadl	phhslkpima	eyygskdppk	thyyvvamak
3mc2A		hh	sss	sssss	ss	ssssssss
3mc2A	103	kgtgfqlnql	rgkkschtgl	gwsagwyvpl	stllpsgsre	taaatffsss
3mc2A		s	sss	hhh	h	h hh
3mc2A	153	cvpcadgkmf	pslcqlcagk	gtdkcacssr	epyfgswgal	kclqdgtdav
3mc2A				hhhhh	hh	s
3mc2A	203	sfvkhltvfe	amptkadrq	yellcmdntr	rpveeyeqcy	larvpshvvv
3mc2A		ssssshh	s	sssss	ss s	sss ssss
3mc2A	253	arsvdgkeds	iqellrvaqe	hfgkdksspf	qlfgsphged	llftdaahgl
3mc2A		s	hhh	hhhhhh	h	ss
TARGET	26			PSKKNV	RWCTINKLEK	MKCDDWSAVS
3mc2A	303	lrpvrkidis	lylgyeflsa	frnlkrsqrq	kwcavggqer	tkcdqwsavs
TARGET					hhh	hhhhhhhh
3mc2A		sss	hh hh	hhhhh	hhhhh	s ssssss hhh hhhhhhhhh
TARGET	52	GGAIACEAS	CPKGCVKQIL	KGEADAVKLE	VQYMYEALMC	GLLPAVEEYH
3mc2A	357	ggalacatee	tpedciaatm	kgeadamsld	ggfayvaghc	glvpvlaeny
TARGET			hhhhhhhh	h	sss	hhhhhhhh
3mc2A		sssssss	hhhhhhhh	h	sss	hhhhhhhh
TARGET	102	NKDDFGPKT	PGSPYDFGT	LRAVALVKKS	NKDINWNNIK	GKKSCHTGVG

```

3mc2A      407  lsthssgrlg skcvnapleg yyvvavvkks dvgitwkslq gkkschtavg
TARGET
3mc2A      hh          sssssssss          sss
          hh          sssssssss          sss

TARGET     152  DIAGWVIPVS LIRRQNDNSD IDSFEGESCA PGSDTKSNLC KLCIGDPKNS
3mc2A     457  tsegwnvpmg liydqtgsck fdaffsrscs pgsdpdpslc alcvggmn--
TARGET
3mc2A      hhhh  hhhh          hhh  sss          ss s
          hhhh  hh   h          hhh  sss          ss s

TARGET     202  AANTKCSLSD KEAYYGNQGA FRCLVEKGDV AFVPHTVVFE NTDGKNPAVW
3mc2A     505  -pahmcaann aeegyhgsga lrclvekgdv afmkhptvlq ntdgknpepw
TARGET
3mc2A      hhhh  hhhh          s  sssss
          hhhh  hhhh          s  sssss  hh

TARGET     252  AKNLKSEDFE LLCLDGSRAP VSNYKSKKLS GIPPPAIVTR EESISDVVRI
3mc2A     554  akglkhedfe llclldgtrkp vteaqschla rvpnravfsr kdkadvrri
TARGET
3mc2A      sss sss  sss          s ss  sssss          hhhhhh
          sss sss  sss          s ss  sssss          hhhhhh

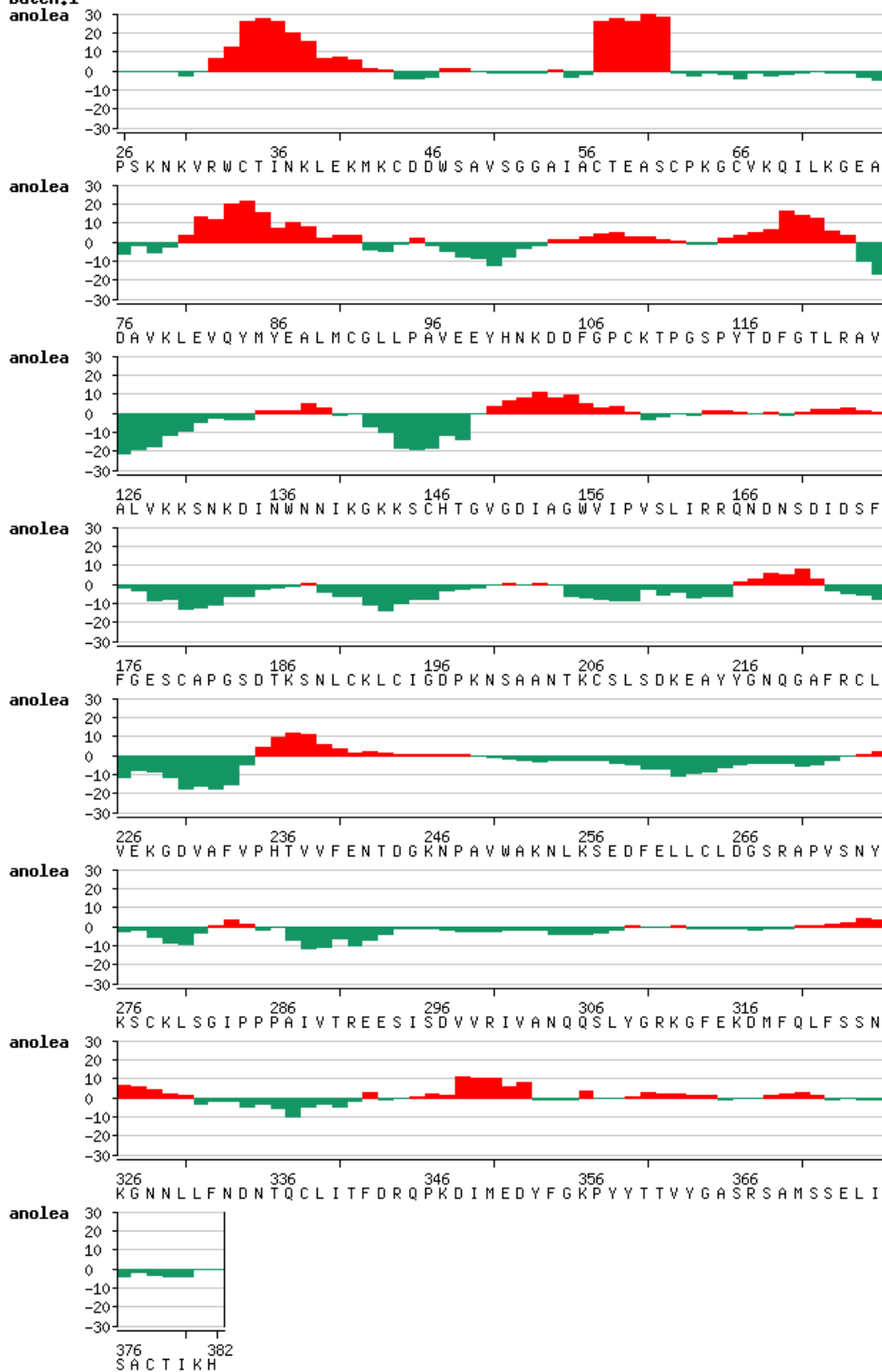
TARGET     302  VANQQSLYGR KGF EKDMFQL FSSNKGNLL FNDNTQCLIT FDRQPKDIME
3mc2A     604  lfnqqelfgr ngfeymmfqm fes-sakdll fsdteclsn lqd--ktyk
TARGET
3mc2A      hhhhhh          sss          hh
          hhhhhh          sss          hh

TARGET     352  DYFGKPYTT  VYGASRSAMS SELISACTIK H
3mc2A     651  tylgpqyltl mdnfrq-cls selldactfh ky
TARGET
3mc2A      hh  hhhh  hh          hhhhhh
          hh  hhhh  hhhh          hhhhhh
    
```

Anolea / Gromos  [\[top\]](#)

anolea: on off gromos: on off

Batch.1



Download raw data: [\[Anolea Data\]](#)

Modelling log [\[top\]](#)

3.70 (SP3)
 Loading Template: 3mc2A.pdb
 Loading Raw Sequence
 Renumber target sequence starting from (26)
 Loading Alignment: ./NXXX.align.submit.fasta
 Removing HET groups from template structure
 Refining Raw Sequence Alignment
 ProModII: doing simple assignment of backbone
 ProModII: adding blocking groups
 Adding Missing Sidechains

