

188

248

ASAPALTSQLDRLEVLLNPKDEISLNSGKP-----FRELESELLSRRKKDLQQIYAEERENYLGKLE
 -PAPSLTRSQLDRVEALLSPEDKISLNMAKP-----FRELEPELVTRRKNDQFQLRYTNRDREDYLGKLE
 TSAPALTKGQLDRLEGGLSPKDEISLDSEKP-----FRELESELLSRRKKDLKRQIYAEERENYLGKLE
 ASAPALTQSIDRQLQGLSPKDEISLDLSGTP-----FRKLESELLSRRRKDLQIYAEEREHYLGKLE
 VPEVKVYTPSQUIERLKLTMSPDDKIPQDELPE----FKVLEKELIQRRRDDLKMYYEDREDRLGKLE
 -LSSFWTKVQYQRKLKELNASGEQLEMGSFDALSRDRAFGQIEHQLMQSQGRHLQEQLRTVKRPALLELE
 -MSIGWTEIQQARLIELAADEAQLAGQFENAASRDKAYQQLEKQLVKIQRRKLQLLRDGPRRPGICRLE

*side chains that hydrogen bond with pyl

✓ side chains that form the hydrophobic pocket

- residues forming the putative tetramer interface

PIKIFEI**G**PYRKESDGKEHLEEFTMLNFCQMGSG--CTRENLESIITDFLNHLGI-DFKIVGDS*C*MVYG
 PIKIFE**V**GPCYRKESDGKEHLEEFTMVNFQCMGSG--CTRENLEAI**E**FLDYLEI-DFEIVGDS*C*MVYG
 PIKIFEI**G**PYRKESDGKEHLEEFTMLNFCQMGSG--CTRENLEAI**I**TEFLNHLDI-DFE**I**IGDS*C*MVYG
 PIKIFEI**G**PYRKESDGKEHLEEFTMLNFCQMGSG--CTRENLEAI**I**KDFLDLYLGI-DFEIVGDS*C*MVYG
 PIRIFEI**G**PYRKESDGSSHLEEFTMVNFQCMGSG--CTRENMEALIDEFLHLGI-EYE**I**EADNC*C*MVYG
 PIRIFE**I**GTCYRKESQGA**Q**HNLNEFTMLNL**T**ELGTPLEERHQRL**R**LED**M**ARWV**L**EAAG**I**REFELV**T**ESSVVYG
 PVRIFE**I**GSSCFRKESQGA**Q**HNS**E**FTMLNL**V**EMGLAEDQRQSRL**E**MAALVTAA**G**VDDY**I**Q**T**ESSAVYG

35 36 α6 37

386 V V MOTIF 3 454

DTLDVMHGD--LELSSAVVGPVPLDREWGIDKPWIAGFGLERLLKVHDFKNIKRAARSESYYNGISTNL
 DTLDIMHGD--LELSSAVVGPVSLDREWGIDKPWIAGFGLERLLKVMHGFKNIKRASRSESYYNGISTNL
 NTLDVMHDD--LELSSAVVGPVLDREWGIDKPWIAGFGLERLLKVMHGFKNIKRASRSESYYNGISTNL
 DTLDVMHGD--LELSSAVVGPVPMDRDWGINKPWIAGFGLERLLKVMHNFKNIKRASRSESYYNGISTNL
 DTDIMHGD--LELSSAVVGPVPLDREWGVNPWMPAGFGLERLLKVRHNNTIRRASRSELYYNGINTNL
 DTVDVMKGD--LELASGAMGPFLDEKEWIVDPWVLGLFGLERLLMIREGTQHVQSMARSLSYLDGVRLNI
 ETIDILAGEDRMEIGSAMGPFLWDQAWQVTDAMWGIIGFGLERLLMILENSRSRSLGRMGRSLGYLGDGIRLN

B8 B9 α7 β10 α8