

Supplementary Data for “Bacterial Pleckstrin Homology Domains: a Prokaryotic Origin for the PH Domain”

FIGURE LEGENDS

Fig. S1. C^α superimposition of monomers in the asu PHb1(*sl*) (**a**), PHb1(*sa*) (**b**) and PHb2 (**c**).

The first monomer in each panel was colored from blue to red from N-terminus to C-terminus.

(d) Superimposition of all PHb domains (PHb1(*sl*): blue, PHb1(*sa*): red, PHb2: cyan), shown in stereo view.

Fig. S2. Crystal packing environments of PHb1(*sl*) (**a**), PHb1(*sa*) (**b**) and PHb2 (**c**).

Fig. S3. Electrostatic potentials of PHb1(*sl*) monomer (**a**), pentamer (**b**), and PHb2 dodecamer (**c**) mapped to their protein surfaces. The color is scaled from -5 to 5kT for oligomeric assemblies (blue, positive; red, negative electrostatic potential), and -3 to 3 kT for the PHb1(*sl*) monomer.

Fig. S4. Multiple sequence alignments of uncharacterized families that are likely to possess a PHb-like fold. Alignments show the UniProt accession number followed by the start and end coordinate of the domain in the sequence. For each alignment a secondary structure prediction is shown based on a JPred3¹ prediction of the first sequence in the alignment (extended (E), helical (H) and other (-) types of secondary structure). Coloring of conservation has been carried out with the CHROMA software² (Conserved aliphatic residues are shown in bold black fonts with yellow background, residues with large side chains are shown in bold purple fonts with light yellow background, polar residues in blue text, and residue with small side chains are shown in green fonts). **(a)** Alignment of family DUF304. **(b)** Alignment of Family DUF1200. **(c)** Alignment of family DUF2244.

Supplementary References

1. Cole, C., Barber, J. D. & Barton, G. J. (2008). The Jpred 3 secondary structure prediction server. *Nucleic Acids Res.* **36**, W197-201.
2. Goodstadt, L. & Ponting, C. P. (2001). CHROMA: consensus-based colouring of multiple alignments for publication. *Bioinformatics*, **17**, 845-846.

Table S1. Data collection and phasing statistics for PHb1(sl)

Structure (PDB ID)	<i>S. loihica</i> PHb1 (3dcx)		
Beamline	SSRL BL 11-1		
Space group	P2 ₁ 2 ₁ 2 ₁		
Unit cell parameters	a=61.07 Å b=75.32 Å c=139.40 Å		
Data collection	3dcx-infl	3dcx-rem	3dcx-peak
Wavelength (Å)	0.9793	0.9184	0.9787
Resolution range (Å)	29.83-2.00	29.26-2.00	29.26-2.12
Number of observations	177,704	177,123	149,911
Number of unique reflections	43,831	43,614	37,021
Completeness(%) ^a	99.1(97.9) ^a	99.2(97.8)	99.3(98.2)
Mean I/σ (I) ^a	13.9(2.3) ^a	13.6(2.2)	14.7(2.7)
R _{sym} on I (%) ^a	6.7(68.4) ^a	7.4(71.0)	7.6(58.3)
Highest resolution shell	2.11-2.00	2.11-2.00	2.23-2.12
Phasing			
Resolution (Å)		30-2.0	
Number of Se sites		16	
Mean FOM		0.32	

^a Statistics for the highest resolution shell in parentheses.

$$R_{\text{sym}} = \frac{\sum_{\text{hkl}} \sum_i |I_i(\text{hkl}) - \langle I(\text{hkl}) \rangle|}{\sum_{\text{hkl}} \sum_i I_i(\text{hkl})}$$

Table S2. Data collection and phasing statistics for PHb1(sa)

Structure (PDB ID)	<i>S. amazonensis</i> PHb1 (3hsa)			
Beamline	SSRL 9-2			
Space group	P2 ₁ 2 ₁ 2 ₁			
Unit cell parameters	a=33.23 Å b=129.49 Å c=138.73 Å a=33.01 Å b=129.63 Å c=138.96 Å			
Data collection	3hsa-peak	3hsa-infl	3hsa-rem	3hsa-peak
Wavelength (Å)	0.9792	0.9793	0.9184	0.9792
Resolution range (Å)	47.4-2.0	43.6-2.7	47.4-2.7	43.6-2.7
Number of observations	150,785	61,112	61,189	61,111
Number of unique reflections	41,702	17,022	17,004	17,030
Completeness(%) ^a	98.9(98.6)	98.4(94.3)	98.4(94.3)	98.4(94.3)
Mean I/σ (I) ^a	12.1(2.6)	13.0(3.2)	13.6(3.3)	16.1(4.1)
R _{sym} on I (%) ^a	8.8 (49.3)	9.1(42.0)	8.6(41.6)	7.2(32.6)
Highest resolution shell	2.10-2.0	2.84-2.7	2.84-2.7	2.84-2.7
Phasing				
Resolution (Å)		47.4-2.7		
Number of Se sites		14		
Mean FOM		0.37		

^a Statistics for the highest resolution shell in parentheses.

$$R_{\text{sym}} = \frac{\sum_{\text{hkl}} \sum_i |I_i(\text{hkl}) - \langle I(\text{hkl}) \rangle|}{\sum_{\text{hkl}} \sum_i I_i(\text{hkl})}$$

Table S3. Data collection and phasing statistics for PHb2

Structure (PDB ID)	PHb2 (3b77)		
Beamline	ALS 8.2.2		
Space group	P4		
Unit cell parameters	a=150.99 Å b=150.99 Å c=76.20 Å		
Data collection	3b77-infl	3b77-rem	3b77-peak
Wavelength (Å)	0.9799	1.000	0.9795
Resolution range (Å)	47.73-2.42	47.73-2.47	47.73-2.56
Number of observations	245,189	230,496	207,778
Number of unique reflections	65,459	61,521	55,605
Completeness(%) ^a	99.7(99.8)	99.7(99.9)	99.8(99.8)
Mean I/σ (I) ^a	10.6(1.9)	13.9(2.1)	10.4(2.0)
R _{sym} on I (%) ^a	8.1(76.1)	7.1(70.4)	9.2(73.2)
Highest resolution shell	2.55-2.42	2.60-2.47	2.70-2.56
Phasing			
Resolution (Å)	44-2.42		
Number of Se sites	20		
Mean FOM	0.27		

^a Statistics for the highest resolution shell in parentheses.

$$R_{\text{sym}} = \frac{\sum_{\text{hkl}} \sum_i |I_i(\text{hkl}) - \langle I(\text{hkl}) \rangle|}{\sum_{\text{hkl}} \sum_i I_i(\text{hkl})}$$

Table S4. Structural comparisons between monomers of PHb1(sl) pentamer

RMSD	3dcx-B	3dcx-C	3dcx-D	3dcx-E
3dcx-A	2.72 Å (113) ^a	1.50 (115)	2.24 (113)	1.70 (103)
3dcx-B		3.16 (113)	1.76 (113)	0.96 (103)
3dcx-C			2.55 (113)	1.80 (103)
3dcx-D				1.03 (103)
3dcx-E				

^aNumber of aligned C^α atoms in parenthesis.

Table S5. Structural comparisons between monomers of PHb1(sa) pentamer

RMSD	3hsa-B	3hsa-C	3hsa-D	3hsa-E
3hsa-A	3.62 (124) ^a	1.46 (112)	2.48 (113)	1.91 (111)
3hsa-B		2.03 (112)	2.24 (113)	1.94 (111)
3hsa-C			2.31 (112)	2.17 (111)
3hsa-D				2.00 (111)
3hsa-E				

^aNumber of aligned C^α atoms in parenthesis.

Table S6. Structural comparisons between monomers of PHb1(sa) and PHb1(sl)

RMSD	3dcx-A	3dcx-B	3dcx-C	3dcx-D	3dcx-E
3hsa-A	3.29 (116) ^a	2.15 (113)	3.62 (115)	2.20 (113)	1.38 (103)
3hsa-B	3.80 (116)	1.72 (113)	3.65 (115)	1.74 (113)	0.97 (103)
3hsa-C	2.69 (111)	1.45 (111)	3.06 (111)	1.53 (111)	1.32 (102)
3hsa-D	2.14 (112)	2.36 (112)	2.62 (112)	2.02 (112)	1.63 (103)
3hsa-E	2.14 (110)	2.49 (110)	2.39 (110)	2.00 (110)	1.20 (101)

^aNumber of aligned C^α atoms in parenthesis.

Table S7. Structural comparisons between PHb2-PH domain and monomers of**PHb1(sa)/PHb1(sl)**

RMSD	3dcx-A	3dcx-B	3dcx-C	3dcx-D	3dcx-E
3b77-A	3.0 (111) ^a	3.35 (105)	3.08 (108)	3.10 (107)	2.94 (97)
	3hsa-A	3hsa-B	3hsa-C	3hsa-D	3hsa-E
3b77-A	3.12 (110)	3.38 (108)	3.27 (107)	3.00 (106)	2.75 (102)

^aNumber of aligned C^α atoms in parenthesis.

Fig. S1.

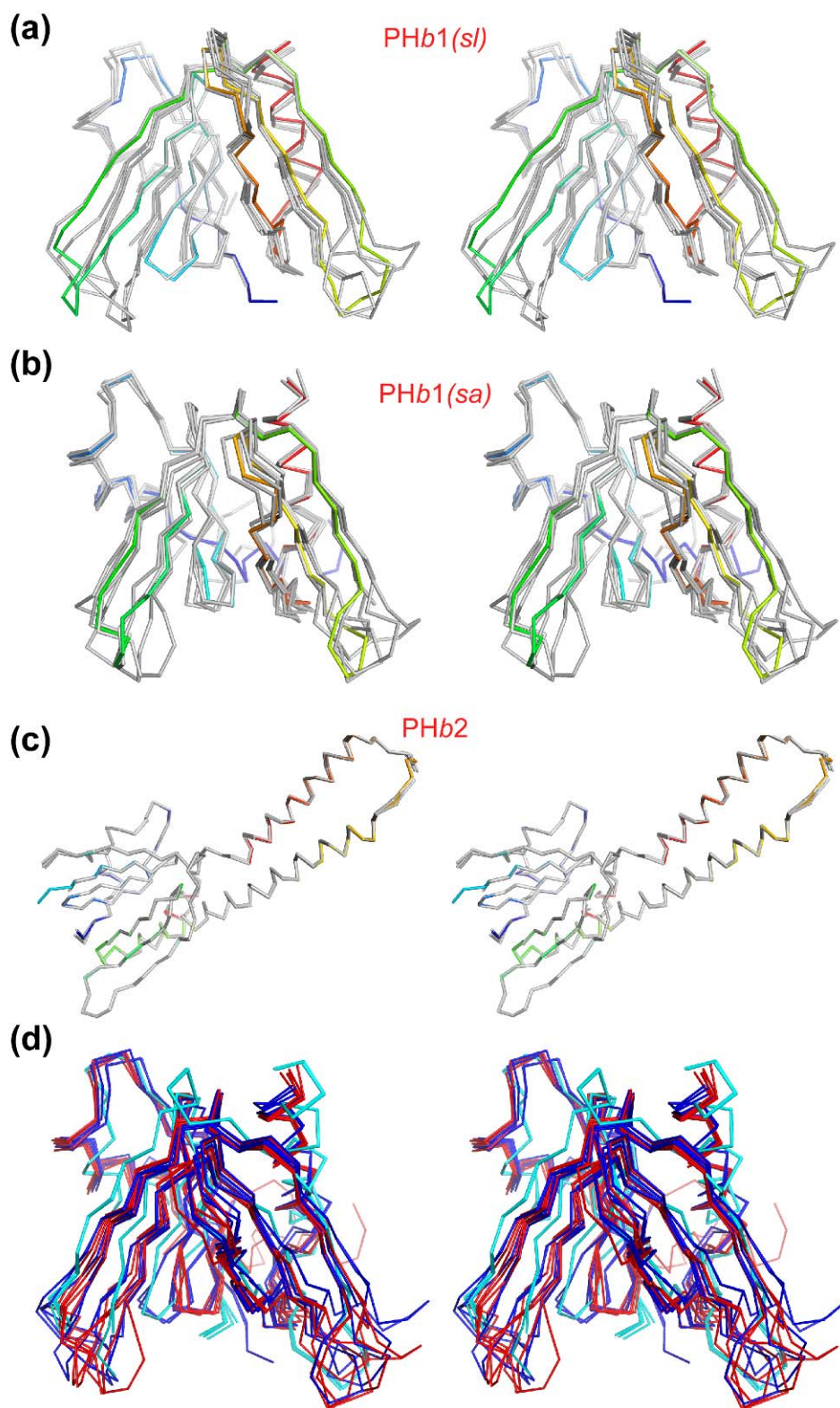


Fig. S2.

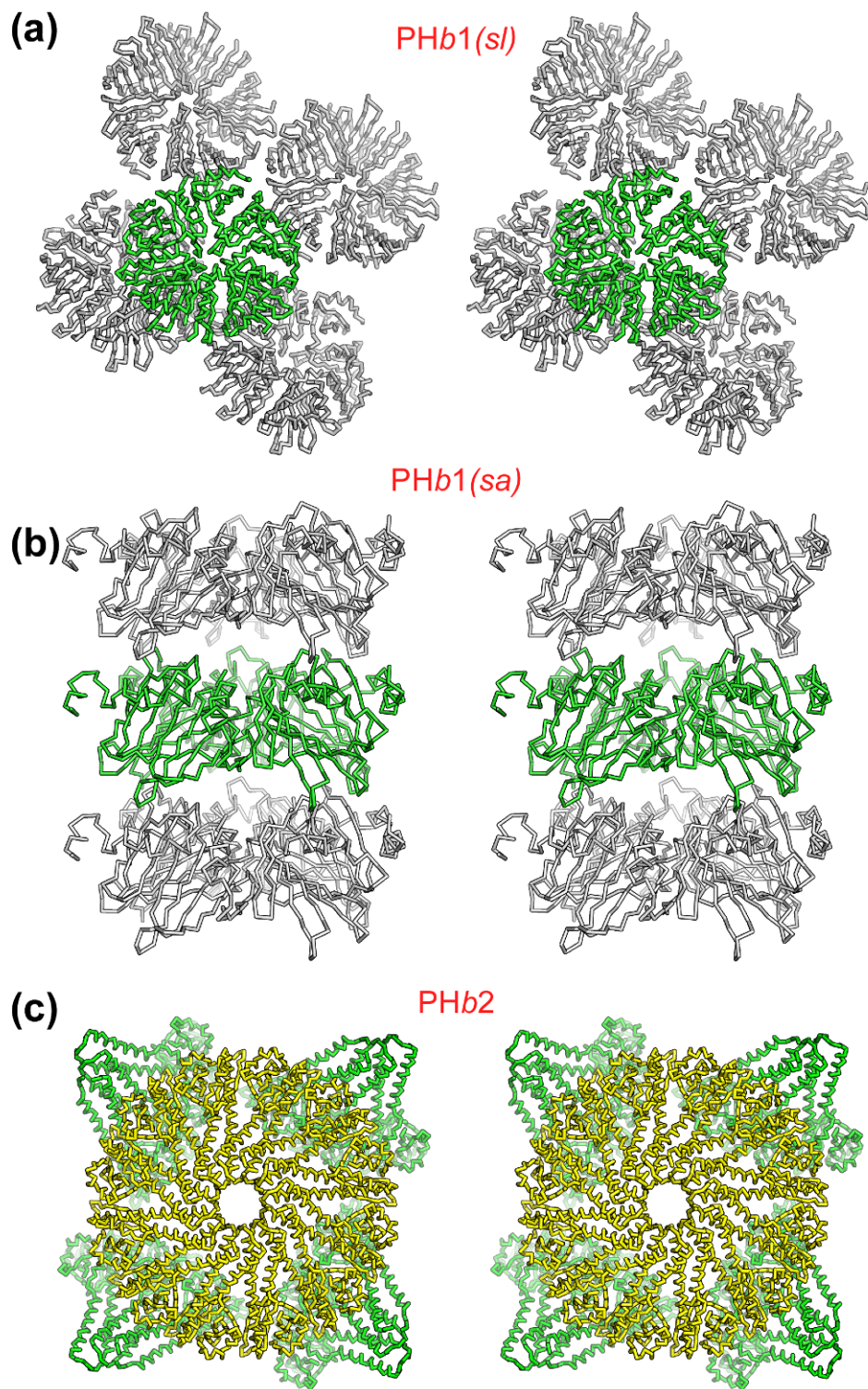


Fig. S3.

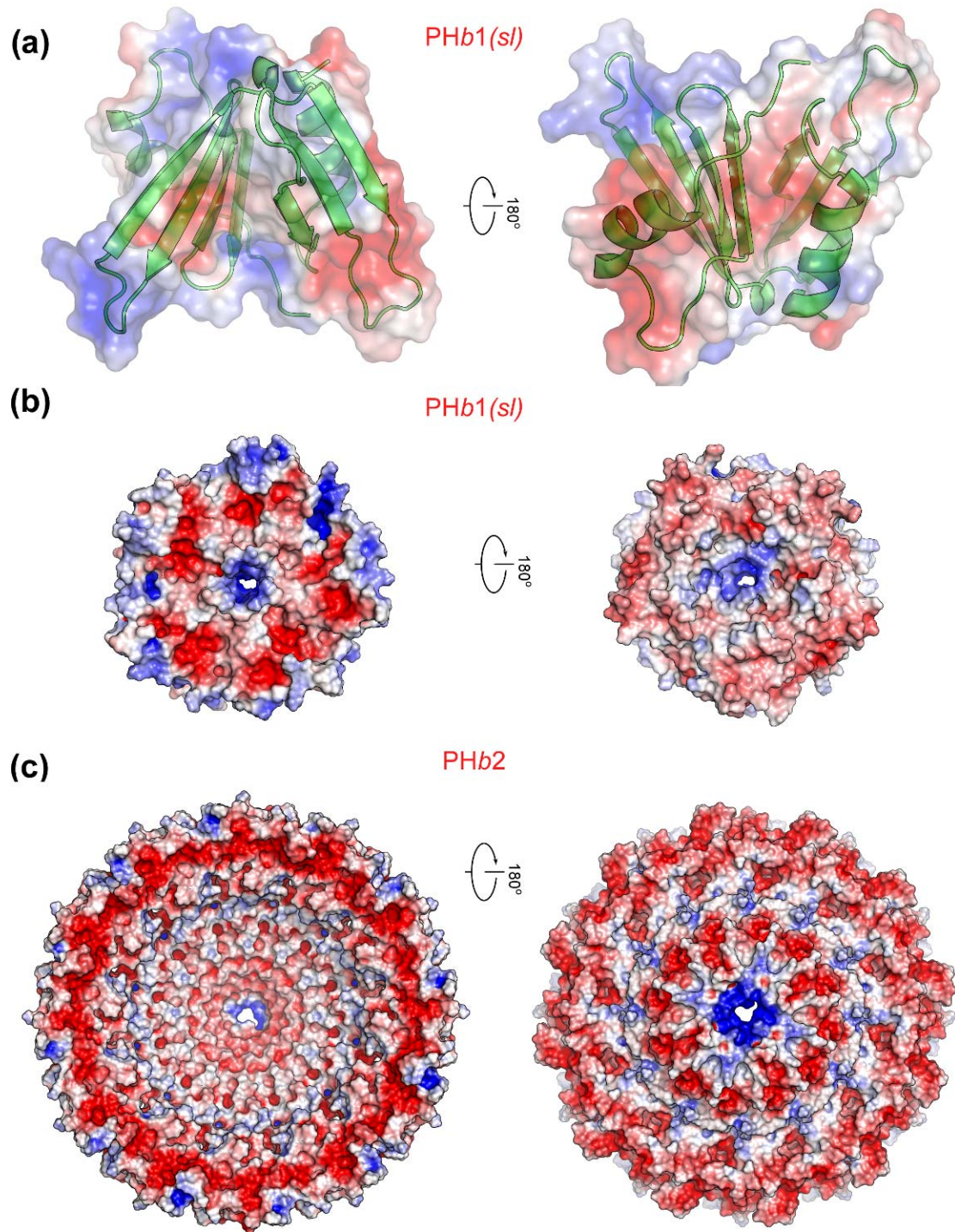


Fig. S4

(a)

```
Secondary Struct.  --EEEEEEEEEE---EEEEEEEE-EEEEEEEE---EEEEEEE--HHHH--EEEEEEEE-----EEEE-----HHHH-HHHH-H---
A0NKK3_1_75-160  ALFRYIFFAYRFDEN-SLTTDSGV-FVRHHEHIPFNKIQTIOHKQWFFLQPFGLSELSSETAGHND-GKAEAILPV---IPLKIS-NFLE-KLN
Q5HEC8_1_63-143  QIVGIMNTRYWIEDN-YFILTGTI-FNKKRKELNIKRIQSVDMTQGVVNIIGGVLDLQIKTP-----SDGIVLSV---ISKKQG-EYLE-RYI
A0M124_1_402-482  QLLYYRSLRSLSFSEE-FILKNSGV-WEKKQQYLEIWKLQAVSMSQPLWYRKKNLVNLIFHSA-----GGDVRFEL---IDRNKA-ESLM-DYV
A3CWW6_1_68-152  IPLYHESIVYRLTVT-EVTVRRGV-WFRQTGIVPYNRIITNDIVQGPLMRFSSFSAVRVQTAGYS--AQAQAEIVL---NGIADP-KDLQ-ETI
A5N1P5_1_58-140  QFLAWRKNFFIVKTN-SIYHEEGI-FSIKKIEIPLDRINTIDISQKLLERIFKVATIKIDTGDTN--KDSELKFT----LDKDKT-ETLK--NI
Q721T2_1_399-484  GVASYRATGV-FTDKHTLLVQSRPIFSKLTTHIRKERIQGLSLRQSIWMEKGGSRHLNWLKSGS--TSAEAYVRY---INQDLA-IKVV-NWY
A6CG36_1_169-250  WWLQTRFRSVTVTSK-RTLYTQGI-FSKQTSEVQHDDVRNMQVNSFFDRILVGVGHIAISSS-----GQDDMEIDV---RGLKSP-QRVI-DII
Q2S4T2_1_276-363  HVARYYNFRWLWDGD-KLRKRHGL-FTVTEGTIPLDKVQALILRNPFRAFGWYELKVQITIGL(4)QGHRVIAPF---AGAERI-LELA-RQV
Q8XM54_1_452-535  SILKGRNINLKIEEN-KVHAVTGG-FFRTIHILKGDIAQVGFNTNPIQEKNNIGKIVIDYSE---NSEEIKLPY---MNKNYV-EVLL-NSS
Q5KZA4_1_390-472  GIRRFQIAGWSLSK-QLALRSVG-FRQTTYILKRHVQSLSETSATWQKRKRLATISAVMP---LGTFRVRVVD---VDEADA-ASVY-RWL
A0Y0J7_1_79-160  ASIKLQGV--MRQH-DIAFKKGI-IWRRVTILPLARVQHTIHRGPIQLKLSNPLRQLLKRYEINVIKGY(4)KEQIIMYPI---GNDKEV-QNII-REF
Q73CA2_1_384-464  AYARYTSSGYMIRDNLQVMVYRG--LAKYTGIMRRRHVQAVGYSQSYFQKDELCTAVVSV-----GHPYKVKH---MQKEDA-LCIY-NWY
A9NAV6_1_80-166  AYTIVYRTSEYGVTDK-RVIMKKGW-IRRNSLEIFLRRLEGVVNVQTVTGRILGYGLVLSGMGSRDYTYTNPQPL---MFRKYV-QRQV-DLL
A4ILF0_1_378-461  RIREYRHTAFRLEDT-HVQLRSCA-FTVETLVTKRAKLELQFERSLLRMFQVMSVKLTNR---AHPVHVTTL---LDIDSSLQPLITSWF
Q0TSV7_1_307-394  YFIKYNFNTLLKEGE-NIKIKYGF-FSTKEFSFKENSIKLTKLKSPLRQLLKRYEINVIKGY(4)KEQIIMYPI---GNDKEV-QNII-REF
A0JUF8_1_82-161  RVLRWHTAQVLTSR-RIIARYGM-LRRRDIQIPLAHVHHIGVQSLSLWQRIILSGNISLDTG---QGADAVI---PDVPEA-VRFR-NFV
A7GLR9_1_265-351  TFFTYKNFKVQRSTF-GIDISYGL-IDKKEVSLAKHDIRAVEIVQVPIYRLFVYSKIHLQLI-G(4)KSKIIVLIPS---IQSSEV-SSLF-KKY
A4C2S8_1_256-345  VLLRHFNLRVYLKDN-ALEIYQGL-ITKKSIVLKKDKVQHTTISHNPIKKKLGISFITFKQAVS(4)KKQDKIKI---VGCKKEQIAIITNLL
A7B794_1_64-144  PYFRYNRYYSINEE-CIDIREGY-LFVKRNIVPIERLHKLEISKGPIDQIFHVAKVTVTA-----GGDVTLEF---LEEEKA-EKIA-ENL
A6G2U2_1_82-163  TYVTHVSTKYKVTGR-RIETEHGV-ISKSVDSLELWRVLDVKYNQSLLDRLVNGKTIILIST-----DQSDPNLEL---HGLPNH-RELF-EKL
A7B9U4_1_402-484  DPLVYKRRAFGLTDA-VFAIRDGF-FNLRFSIIPLTRIQSVSLHQGPIQRWRRVASVRAALVP---GPVASMAGEH---VEVGRS-LELW-AQL
B4RX55_1_450-530  LTLRWWRWGISYDNK-YVYIIRSR-IGIDYQCFEPHKVQVIVKQSVFMKRRKLATIKFVLA-----SGAVTVPF---LPEQYV-FTLA-NNV
A0QQT0_1_64-149  GLARWFTTYRIEIPN-EVQLRTGV-LQRKVLAVPRNIRISVSTDARLLHRVMGLTVLRISTGQEAKEGDAEFALDA---VEAGQV-PRLR-AIL
Q8L2A0_1_48-129  RYLVIHISIRYEITTE-RIRFHRGV-LNRKMDETELRVRDYSIRRPFHLLIFHLATLHIDTK-----DVRHSTIDM---IGIRNA-EQVI-TML
O26822_1_86-166  DVISWRNRRYIITDQ-RVMVEEGV-LWKRYYINHRKIVDVFSFSQSITERLLDSADLEHGG-----HEGTNIIL---RDAPSP-SKIE-YHI
Q3BNL4_1_405-490  AQRQVQRMAYAVDAR-YVAVRGGW-WKRWWRLAELDKLQALQLQRSPLDRLSGTATLWLDTVGASA-TGPALRLRF---VPLAQA-QALQ-AQL
A7A966_1_18-101  CRTPTFTTVYALTDK-ELSVKTCI-LNENFNLIKLFIVDISVERTFQLRIFGMSTIVLDTRDQ---LNENFNLIKLFIVDISVERTFQLRIFGMSTIVLDTRDQ---SSNGVVAL---KNVLNG-FEVR-KVL
A7GLR9_1_62-145  SFLIWKNNVFIFYED-ILSVREGV-WSKEYSDIHYTKVKSISIDRTFVKRILNVSNNVETVGG---DTIQIVVSN---KKLSYI-KSIL-NRH
A6PLN6_1_81-162  IILLRKNQFYTISTQ-SITSEGSV-LIRFNHTLRRNQIQSVSYTQTLIQQLLGCNIVVSTA-----ASSRGGIIL---TNIDHV-QEYI-KAI
Q26E06_1_268-354  SINKFYDFKMELRDE-HLEVRMGL-LNKKEIKIPLSKIQILEFHSNPLRKILDFKTARTYQA-Q(4)QISSVEVPA---CHAHIQ-AQLQ-YLI
Q1VZX2_1_419-499  SILKVKKSSIGINPT-FINVRNCS-IETIHKLIEIHKLQSVKLRNIFQQYNGHADLILETA-----SGSLNIEY---LKVEEA-RKIL-NYL
Q0RP62_1_82-163  KVADWQFDHLMITDK-RLKVSGL-FFRKKVQTMPLSKITDLYNRPDLGRLLYGGEFVESA-----GQDQALSKI---QFLPRP-DRLY-LTL
B1YH17_1_231-317  FVLRVYGSFRATRDKQ-RMTTGYGL-LNRTEIVFHQDKVQALVIEBSWIKRRLKRAHLSLHII---SASGBEEKLLLHPFIRTSEI-DDFL-SRF
```


(b)

```
Secondary struct_-EEEE-E-EEEE-----EE E-----EEEE-----HHH-----EEEE-----EEEE-----HHHHHHHHHHH-
P37523_2_60-136 LKVVTL--KEHHLIKAG-LIKHQ-IPYENDKVVQKKLWSG-FRLIGSRHAITYYQ---GGWGH-AVTSFQKSEEFHKLKKN
A6T2Q0_1_61-134 TRVYTL--EASRLVQSG-PFKWT-IPLADKNITPNSNPLS---SPALSLDRLEHYG---NRNA-LMISFKDKEQLLDLEAAR
Q5WJG5_1_65-143 IKFVTL--TEEHLIKSG-PFKRK-ILYPNIKVVPTTDRFTG-YQISSSDKGIELRYKT-ANATRT-IKILEKDKLKFISELRKRC
Q5WLL6_1_65-138 TGVYTL--SGSRKIVYG-PIRKT-IDIHDRTIRSKIDPFI---DPALSMDKIENYQ---QFET-ISISFKRKDEFSKLLKKN
Q6HLV3_1_52-125 TKYIV--GEETITIRSG-FVKKH-IFIRDKQISNTKNPIA---AYALSFDRLLEVYQ---AHQT-EIISFKDKEQFINHVKNKN
Q8A2X0_1_53-129 TVVTV--STDGVLEISTGRFMRKVIPIAEATAIRKYHSMKF---GKFSVTNYVLEHYG---NGKFAASVMFKEREVELEKRM
Q9K9B1_1_42-116 TYDRI--DGDRFAISG-PFRWS-IPIQDRSIEKRKNLLS---GPSLSLDRLTLYG---VGYDI-IVISFEKEDVPLQLLDKN
A6KZD8_1_54-130 STVYTL--TADGKVVYGRFYKGTIPLTDTDVELKRSSGF---GGIMPSKYVLEHYE---KKNLLSLEVKPEEINALVKRL
A5WI48_1_64-136 IKYTL--TADTLVKNG-FSTQS-ISLEDTHITPTSSTLS---AAALSLDRIEHYE---GGSI--VISEKDKDRFYHAIQERV
Q8ELH5_1_56-129 TRVRI--DNNTIRISYG-PMKWS-ININEKSIRKTTNLFV---GPCLSVHREHYG---NYKV-IQISFKRMQLFIEKIQKIN
A4BZG7_1_58-133 TSYKI--ENNEFIYRSG-FLRKG-IGIPNKEILKEKTMWSG-IKPALARNGLIKFN---KYDE-IYIAEENNELISDLLKVN
Q9KEX6_1_65-138 TGVTV--TEDWVIEYG-PFKKK-VEIETESIRETKNPFII---DPALSMNKLQLYG---NSRH-IAISFQEKHEFKKQLVKRN
Q67SW8_1_62-135 TGVAV--TENEVIRSA-FLTWR-IPLAAARRVRPTRSPLT---SPALSMRLEVRTN---KGSAPLISERNRSEFLALLRERC
A7UYW5_1_53-129 TTYTV--TPDGKVLSPGRFSRSKEILMKDTSVERASSMQV---GRFAVMRYVLVKYG---EGKCVVLEVKEEFIRLLEERR
Q813R4_1_53-128 SHYNI--TESSVVKHGFIFHTE-IPFEDRHVKYSGKKLH---SKKWTRQOLEHYN---LFDVTTTFVLEEEKFISLLKENC
Q5WM07_1_64-139 TKVVLKPDSTRIVVVFQ-FYKKT-ININTNAMRCTKDFFA---SPALSSNKIEEYS---HSNL-IRISFKKQLFIEQVKKIN
Q8ETD0_1_64-141 LCYIF--FYDYLVKSG-FFRFH-IKYSQMTKIEATSNFLIG-TRAMMATNGIVYYS---SGITGELKLEDDQDAFLKILQERA
A7AH02_1_54-129 TWYKI--TADGHIHCSIFPEKK-PISESAVEVTMPVS---SYALSLDRLEHYG---DTQWLLISEVVKQDFVKKLKKHN
A4ASP1_1_60-135 TNYEL--HKDGFYRSG-PINGK-ISIDRYEIVKGRTLWMG-SRPATAKGLIKYD---AYNE-IYISEKTNEKFEKILELN
A6KZD7_1_56-123 TIVIV--KDNGVLEIKPQ--WGNR-ICVDGRKVSYN-----PNAIGMQKVKDEHA-----QGFVMINEPKPLEFVEALREID
A4CQ29_1_54-128 IRYEL--REETHVHGSFLVKLH-IPVRESIRRSYNPLA---SPAGSLKRLAVRYG---DSGM-TLISEKDEADFISTLKALN
A6EQ87_1_59-133 TRVKI--LGTEQITCFPFYDKK-VAIDSKKVAFSRSIMS---SPAPSLDRIEFFN---TYDS-VIISEKDKEQMDHLKQIN
A4ANC2_1_53-127 TYVVI--DGKTKVKSFIWNKS-FEINRIKISETNNPIS---APAASLDRLEKLD---SKRS-VIISEKDKHEFIEELKKN
A3J6N6_1_59-136 TFYKI--ENTCWHWSG-PFYGE-IDIQKNKIEYHKGIIIV(4)KPALSHIGTIITYN---KYDD-IYISEEKQEEFIATLQRLN
Q64WH9_1_55-123 CKYIV--KQNGDQIVND-FFRQK-RTFSHTDVTYT-----RHALGMQKIKRHA-----TGFVMIDEQSPRELKALQKTN
Q5WDR5_1_61-138 ITYEL--KEEGFVQAG-LISRF-YSYESMTALEPMGSPFSGKERIVGSSQGFNKHN---GPKGEVKVSEERMEEFKQELKRA
Q8EQJ6_1_52-125 TGVRI--DNDKILIIYG-PVKQT-VKIKDEVIFKTKFPLT---SPALSFDRMQKSG---KYDI-VTISEEEKESPLQQLMDIN
A6CHZ7_1_57-130 TCVIF--KEQKILIRYG-PFRWR-LLIKDKSIRKVKSPFT---SPALAVNRLEHYQ---KYEV-VQISEQDQDAFINYCNQN
Q7USX7_1_65-137 CRVYTL--LDDASIRCG-LICYQ-VAYADTEAIPSSTWIS---GPAMSLKRVIVRTA---KRDH--ILISEEERERFIEELMDRV
A6CKW3_1_69-152 TYVET--NDRVRIVAG-PIRYT-TEIERKSVRPSRNPLS---SPALSLDRLEHYYS(10)SWNT-ILISEKNKERFIDELLVN
Q8CV26_1_61-135 TGVYI--VNDIVKVKAG-PFKKT-INIQENKISKRKSVWT---AAALATDRLVQYG---KYNLDILVSERNESDFIKLLLSKK
```

(c)

Secondary Struct. ----EEEEEE---EEEEEE---EEEEEE---EEEEEE-----EEEEEE---EEEEEE-----HHHHHHHHHHH---
A3SQM8_1_77-159 RSGETREELCIDPERAVLIRSNPDGREQRWQANSYVWEAR IYPKGGP-VPQYITLRGEGREVE LGAFSEPERARLITELTTAL
Q2NYF1_1_75-150 RSGEREEARVGEAVVEVFPSPG--HAPPAPQAHPHWVRLCMERDD-----RVLLVSSGKQIEIGSFGPAERVELAMTKRLL
Q2K411_1_76-158 RAGRVREQVTVSRTDVSVRK FAPSGRMVEHFNPNFWARFLVRRHQEI-GILSMHIFGEGRRTDIGSFPNPDRESFAKAFRGAL
Q2J311_1_78-160 ARGRATEEISMTSPSELVRRTSPRGQVAEWVLPNPLWVRL EKIVHAEF-GIEQLYLVSRRVSVASFGAEEKASFANATAAL
A4AAP7_1_72-154 WKLEYRHVITLDD-SVVSIDKGYHAPKRWRFRKRDQVALAITPEKHPWEGPGLSVHGNETVVRVGEFNRDDCLSLMALLRKEL
A5XSB1_1_70-148 RHAVDYERIRLFFP-HRLVIERMSAERLTQIELNPNWVREVPASPRD----PITLVSRCESVVVQGHQAQYRRAQFARELRASL
A4GJG9_1_73-153 KWSKREKIFISQ-DKVTIEKGIHKADYRWEFRFTSFHVTKDINK--VLKLSFRSKGEDVEVGAFNEDDKNVLKEEVSNII
A7IFT4_1_85-167 RSARAREHILVTPSVIEVRREPARGRRITRLNPNWTRLTREDDH-GTLDVALVSGPRTVPGRF GPDQKAAALATDLSRAL
Q168L9_1_76-158 KARNIVEVLTNDEEARLIRTEPTGATREWDCNRYWTTITKYEKDGP-IPHYVTLKGMGREVEIGAFSEEEERVALYDELQRAW
Q60AH5_1_74-156 RQSAVREVITVTD-ADVMLERGI RGPDETYRFRRAWLGLSLDGPAAGHPSRLCLKRHGRKIEIGRPFVSEEREALYRELKKELE
Q0C0K4_1_71-152 RQQQEETRVVTARAI CLHMKDAKGREKRAELPSAFARVLEEPAGP--ASWLRTEHGKTAWIIGRFP TPPERSDFAKALRQAL
Q7W345_1_81-163 RHARDGEDIELRADGLVVEVHDGERVSRHVFDRGRARVIRHRAWSA-ADESLWLHCGRQRVRLARYDRRRTCAFETDIRQAL
A3RSA3_1_84-162 LHTSDHERTELEDD-DALVIEQVFANQRVRFVFNPNWVRELGEPLRE---QVALCSSGRVVRVGRFPDPAGRRLADELSRCL
A3UIN0_1_74-156 RDGRRMESKLTREIRVIRFPFTGHLIQVLPSPAWVRLVEGEGERP--DVQTRLTAMGKSLIVGSWSPRERESLADALRDAL
A1VTB4_1_93-172 LHAADGEQISFSPEGQLAIEVVRGLDTRHYRMNPAWAHLERGGPRKD---RLWLCCSPLRVEVATQ GAGEKRRVERELKQAL
Q9A236_1_68-149 RAARRVERIQVTAEAVTVSR EDEK GARTVWTSPTAFTRVGVEQGEH--EVRVRLMIHRKRLTLARALGPDQRLEFGAALQDAI
A2SKP6_1_95-173 RHAADRELTLLP-GRLVVEHLNGGRIERAFFVPDWRVREPRDDRS---LIELSGQGVIAVGRYVRPELRRALAEFFRTAL
Q0BPC5_1_89-170 RAVRQTEIIVTISGTGPGIAHIDARGRSRHMKIRPQWLRRLRLEECGPR--VPQLILSSRDGEFELARS GEDKRALAETLQDAL
A4BQS4_1_74-156 QRAYDTEVVHVSE-SKVEIDKGRRRPERHWSFDRLWSEVILAGP GHPWYPTRLAVRSRGEQVELGRFPADEERARVAGELRRWI
A4SZC5_1_63-141 RHALDCETEIDG-TRLIVK KFIGYKETIYEFNSRWAKLEPPIAGSK----TFHIIQSNLRVELGQFIRHEQQMALIASIRPHL
A0P3P2_1_83-165 HSARTFEEVVSRHEIARIRKVGPGKKYQYERFNPNFWRLTVDRIDE-GVVKVTLQSRGKVDLGNFNPDDRTSFAGAMANAL
A3NFM1_1_145-225 RHAVDYDCVALTE-QRLEVIQCDCGQLRRYDWNPLVAVDLDAAHAR--DPTIRIRHGSETALVGRHVTLARRRHVARELNAAL
A1B3D8_1_80-159 GTAR--EVMLEDRDRLLILTRSDPGRPDRIWQTNPNVWRLALRQN-GP-VEDYLVITDGKREVE LGAFAPERMALRNDLARRL
A5G1G0_1_85-166 RGAKASEVIVLTDEALTIITRTTPGRRSEVRLEAGWLRVDVEEQAGT-N-PIVSVANREARQIVGMA GDAERRDFADAKAAI
A3VQB4_1_95-176 AQGRRHRELITD DALWVIRVLP SGHETRWKLT PAFVRLDIARPIEH--DSQLCLRECCKTLVIGSFPAPKERGEVAAELERVLE
A3VHI7_1_90-172 RDGEILLELTIWTD RMHLSRTGPRRQHAEW DANPHVSVVQVHKDGGP-VKHYLITLKGNGREVEIGSFPSEDERPLLREELERAL
A6F2F8_1_72-154 RRCQRREVLTFAP-ELIRLEKGLTRKEQEWELPRRHTRVWQDMPRHPWTPPKLHLQFRGEEISLAPFNIDTTELVAILERHG
Q2YZX7_1_124-204 RRTDVIETVELSP-RDITVHRRRELGREETKVFPAYWAHVDFSGSPTQ--NGTLELRSHGEAIEIGRFSASEKDR TAWKLNVDL
A6GLS2_1_97-175 RHAADYEMIELQP-NQLTLVMADGKTLTQLEWSPQWAKLSYNGKYKA---PLLF SHKGQVVKIGKFI AEKDKSALHRELKAAI
A7HZ34_1_77-158 KAARAHETVQLTDDLELLVRRVDAKGRARAFAPQYVWRLALRKEPDE--TTHLHLLSHGROLEVAASPPERESFMHALAAL
Q3J6Q7_1_74-156 RRAQHCEIITIGQ-EEIEIFRGRETTGETWKFHRYWARVRIELPPYAWHMSRLIIGSHGHEVEIGVFLSEEERLRLAKELOAVC
B7L1X4_1_84-166 RRGRSFEVVAISPLEVFLARIDPRGVREWRFNPLWTKLSRIDDEF-GLRTLTLTSRREHV VVARDASPEDERAI VADGLTRAL
Q28SZ7_1_86-168 RDMDLYEDVMIWDDLIRVERHERRHALRDWEANPNVWVRLVHLAKGGP-VPNYLTLQGGPREVE LGAF TPLERVELKQLDRNL
A1TT19_1_80-163 RHALDGLLVLLDNGELEICCLRGAQE QHYRFPAAWCRVCEVPGRHRASGLCTACGRHRIALGAWGSPRADRLAGEIRAAA
Q2SMB1_1_74-155 KRCASQEVLLITP-LEVICIKGMAQPERTWTFPRWYTRIIILVEGGRN-GHICVMTACKGEEVEIGAWAEGDRKALIA TLRSLV
A3JQ23_1_89-171 LDGQLREVLHWEDRITLTHIPRKGTAAFWQANPNYVWVKLVKHD TGGR-VPEYITLEGSGKIVELGAFAPERRELYIYLRNAL
Q3SLX6_1_78-159 ERKDDYERLTIDG-DRVVLEWRSRKREGRELRNRWTRV RCTCAAPG-RNCRVGVCCYGRETLVGQYSDEARLRLAATLRSKL