

Figure S1 (continued)

ClpB_EhrCh	526	LKREVTESDIASIVSRWTGPIENMMSSEKEKLLRMEEEIGKTVIGQESAIKAVSDAVRR
ClpB_EColi	527	LNKVTDAEIAEVIARWTGIPVSRMMESEREKLLRMEQELHHRVIGQNEAVDAVSNAIRR
ClpB_TheThe	517	VRLEVTEEDIAEIVSRWTGIPVSKLIEGEREKLLRIEELHKRVVGGQDEAIRAVADAIRR
HSP104_SacCer	537	IQNVVDSDTISETAARLTGIPVKKLSESENEKLIHMERDLSSEVVGQMDAIAKAVSNAVRL
HSP101_AraTha	528	LTVNVPDHIAEIVSRWTGIPVIRLQNEKERLIGLADRLHKRVVGGQNAVNAVSEAILR
		<-- D1 --> D2
ClpB_EhrCh	586	SRAGVQDANKPLGSGFLFLGPTGVGKTELVKTLAEFLFCDKSALIRFDMSEFMEKHAVSRL
ClpB_EColi	587	SRAGLADPNRPVIGSGFLFLGPTGVGKTELCKALANFVFDSDAMVRIDMSEFMEKHSVSRL
ClpB_TheThe	577	ARAGLKDPNRPVIGSGFLFLGPTGVGKTELAKTLAATLFDTEEAMIRIDMTEYMEKHAVSRL
HSP104_SacCer	597	SRSGLANPROPAS-FLFLGLSGSGKTELAKKVAGFLFNDEDMMIRVDCSELSEKYAVSKL
HSP101_AraTha	588	SRAGLGRPOOPTGSGFLFLGPTGVGKTELAKALAEQLFDDENLLVRIDMSEYMEQHSVSRL
		Walker A D2
ClpB_EhrCh	646	IGAPPGYVGYDGGMLTESVRRRPYQVILFDEIEKAHGDI FNILLQVLDEGRLLTDNHGKL
ClpB_EColi	647	VGAPPGYVGYEEGGYL TEAVRRRPYSVILL DEVEKAHPDVFNILLQVLDDGRLLTDGQGR
ClpB_TheThe	637	IGAPPGYVGYEEGQL TEAVRRRPYSVILFDEIEKAHPDVFNILLQILDDGRLLTDSHGRT
HSP104_SacCer	656	IGTTAGYVGYDEGGFLTNQLQYKPYSVILFDEVEKAHPDVLTVMLQMLDDGRITSGQGKT
HSP101_AraTha	648	IGAPPGYVGHIEGGQL TEAVRRRPYCVILFDEVEKAHVAVFNTLLQVLDDGRLLTDGQGR
		Pore loop Walker B D2
ClpB_EhrCh	706	VDFRNTILVITSNLGQEILINNKED-VDGESVKKSI TSVLQHHFRPEFLNRLDEIIVFHR
ClpB_EColi	707	VDFRNTVIMTSNLGSDLIQERFGE-LDYAHMKELVLGVVSHNFRPEFINRIDEVVFVHP
ClpB_TheThe	697	VDFRNTVIIITSNLGSPILIEGLQKGWPYERIRDEVFVKVLOQHFPEFLNRLDEIVVFRP
HSP104_SacCer	716	IDCSNCIVIMTSNLGAEFINSQQGS-KIQESTKNLVMGAVRQHFPEFLNRISSIVIFNK
HSP101_AraTha	708	VDFRNSVIMTSNLGAEHLIAGLTGKVTMEVARDVMREVRKHFPELLNRLDEIVVFDPE
		Sensor 1 D2
ClpB_EhrCh	765	LTKEHTEKTIIDVQFSLLOKIIVAQ--KELETSLSSEAKSWLMNNGYDSL YGARPLKRIIQQ
ClpB_EColi	766	LGEQHIASIAQIQKRLYKRLEE--RGYEIHSDEALKLLSENGYDPVYGARPLKRAIQQ
ClpB_TheThe	757	LTKEQIQIQTVEIQLSYLRARLAE--KRISLEL TEAAKDFLAERGYDPVFGARPLRRVIQR
HSP104_SacCer	775	LSRKAIHKIIVDIRLKEEERFEQNDKHYKLNLTQEAKDFLAKYGYSDDMGARPLNRLIQN
HSP101_AraTha	768	LSHDQLRKVARIQMKDVAVRLAE--RGVALAVTDAALDYILAESYDPVYGARPIRRWMEK
		D2 Sensor 2
ClpB_EhrCh	823	KIQNSLAKLILANQVSKGDKLEVVLLNDDL IINKL-----
ClpB_EColi	824	QIENPLAQQILSGELVPGKVI RLEV NEDRI VAVQ-----
ClpB_TheThe	815	ELETPLAQKILAGEVKEGDRVQVDVGPAGLVFAV PARVEA-----
HSP104_SacCer	835	EILNKLALRILKNEIKDKETVNVV LKKGKSRDENVP EEAEECLEVLPNHEATIGADTLGD
HSP101_AraTha	826	KVVTLELSKMMVREEDENSTVYIDAGAGD LVYRVESGGLVDASTGKKS DVLIHIANGPKR
		D2
ClpB_EhrCh		-----
ClpB_EColi		-----
ClpB_TheThe		-----
HSP104_SacCer	895	DDNEDSMEIDDDLD-----
HSP101_AraTha	886	SDAAQAVKKMRIEEIEDDDNEEMIED
		D2 -->