

Scc1_Hs_HR21spA_KIA0078	MFVAHFVLSKRGCP-LAKIWLAAHWDK	-----KLTk-A-HVFEcNLESSVESITSPKV-----	-----KMAkRTSGHLLLGvVRIYHRKAKVLLADcNEAFIKIKMAFRPGV	93
Rec8_Hs_HR21spB	MFVYPNVLQRHTGCFATIWLAAATRGs	-----RLVk-R-EYLRVNVVKTCEEILNvYLVVRVQPPQ-----	-----PGLPRPRFSLYLsAQlQIGVIRVYSQCQVlVEDIQHILERLHRAQLQIR	107
Scc1_Dm	MFVEHIIlLARKGCP-LARIWLAAHWDK	-----KITk-A-HVFEIcNIEKsVSEILQPKV-----	-----KLALRTSGHLLLGvVRIYsRKAKVLLADcNEAFVVKIKMAFRPGM	93
Rec8_Dm_Mei-910	SAFQQLNRNEIAD-VDVVAcCKQITE	-----LIEE-N-ALKkRQKRSNVLAARNRQ-----	-----NVlFKDISRLVFGVADIFRCQVdLLlGDTKvLLDQCcTRTnLDVY	116
Scc1_Ce_A_K08A8_3	MFVADFLVLSKKGCP-LSKVWLAAHWK	-----KLSk-A-QIPEIcVDVEAVNEIMPSQ-----	-----KLALRTTGHLLLGICrVYSRKTkVLLADcNEAFkIKLkVFRSGA	93
Rec8_Ce_B_W02A2_6	AEVIRKDAVFHVA-----WILGTGDSK	-----KLSR-R-EIldQNLPELcHSITIEMVPERHRG-----	-----SATKGLYLLSLlTYGvVlLHQVQVDFLKRdVEKlELMKKsFILL	102
Scc1_Sp_Rad21	MFVSEAILSKKGP-LAKVWLAAHWK	-----KLSk-V-QLLHcSIEQsVHAIVTEET-----	-----APMALRLSGQLMLGvVRIYsRKARVLLEDcTEALMRlKMSFPQ	94
Rec8_Sp	FYNQDVLTKKKGCG-MGVlWLAAATLGSKH	-----LRLkLHK-K-DIMsVdIDEAcDFVAFsPE-----	-----PLALRLSSNLMIgVTRVWAHQYsFFHSQVSTLHLRkVRELdHFT	99
Scc1_Sc_YDL003w	RLVLRlLATNKGP-LAQIWLASNMS	-----NIPR-C-SVlQcHIAESAKETAKAScQDDES-----	-----GDNEYITlRTSGELlQGlVIRVYSKQAFLLTDIKDlTKlSMLFKTSQ	108
Rec8_Sc_YPR007c_Spo69	LSLNFKDDKKYKGL-LTlVWLlSALGNlVKEsNNYYSNKsNSlGNlSSS	-----TVKK-K-DIVNlSIPKcTcDElQNFEN-----	-----DFSLRYlSNLLYGVlIcYNKkTEVlVNDLNLHLVQLQKNDVYAF	119
Scc1_Leishmania	MFFSYVLTlTKKGP-LAKVWLAAHWDK	-----RLTR-H-EVkvVdLSQTLlLHVlRfVV-----	-----FlALRTSGELlVGVVRIYkKkVHLkEATeAlFLFRVTTlATK	93
Scc1_At_A	MFVSHlLlARKGCP-LGTVWCAAHVHQ	-----RLKk-S-QYTSINlPDTVDNlMfPEV-----	-----FlALRTSSHLlVGVVRIYsKkVdYlVNDWNLlNTVAKAFVSTQ	93
Rec8_At_SYN1	MFVSHQlLARKAP-LGQlWMAATLHA	-----KINR-K-KlDKDlDlQlCEElNPSV-----	-----FMAALRLSGlMGVvIYERkVLLFDVdVNRfVlEINcAWRTKS	93
Scc1_E_cuniculi	MSKAMGALCLANP-QDVLFAIFVER	-----RLSR-H-HLKEVSlSAlILRVMEEN-----	-----ISVKDGLlTALGSLRlLlRkLRYlLDEcNEVvHKlCRKdMDRE	112
CtDsl1_Hs	-----MEDVEARFAHLLQ-----PIR	-----DLTKNW-EVDVAQlGEYlEELDQlCSfDE-----	-----GKTlMNFIEAAlLlQGSACVYsKkVYlVlSlVYQAlDFISGKRRAQ	93
CtDsl1_At	-MlSHGGGGERGERlHTVQ-----PER	-----DLVANW-EVdLSEKLEAYlLkICSGETlGNEE-----	-----DGQlEVNFAEAlLLQGSVQVYsKkVYlVlVlRlLEFlSLKEDQEQ	100
CtDsl1_Dm_CG14685-PB	VAKCIRAYDEQDlASlVVLLEELs	-----KNTD-Y-SlDLRlSlGvYIEELRHClGRND-----	-----VSRRSAlVAAGSAlQYcGkIYGRdVEYlCQVvEHQIEAlLTSelQKE	133
CtDsl1_Ce_C29E4_2	AlMTRNAPPGQES-IDLAWLlPAK	-----DLVENF-SIDVlKAlAGYlEVlRQESEDTDNQVD-----	-----AAATTYRLDFQRACRlIIGcSACVYGRKkVdHVlELISVVDlVENKcQDD	202
CtDsl1_Plasm_falc	-----MSlTDELNLlIQNLQ-----KCN	-----NlNECl-NFDLSSlIQGfLNCldRNVlENIDKGLG-----	-----ENYEKEVVDNFtSAAIFVENcVklFSpQlEHLHNLAHNTlYNYKENKHS	104
CtDsl1_Cryptosporidium_1	---MENl---PllKsV---ENK	-----DPSlNW-NIDVSAELKYLsAlELLEDdMNYsQSTeANGYGNNEENlSNG	-----SYMqMNFVEAAlIIGNSlSlYSKkIEHLHSlVDFAFHLLSTcKsQLN	112
scpA_B_subtilis	EEVQVKlDlTFEGP-LDlLLHLINRL	-----EIDl-Y-DlPVAklTEQYlLYVHTMR-----	-----VLEdIASEYlVMAATLlSIKSRMLlPKQEEELFEDELLEEDP	93
scpA_Thermotoga	MDLVFKlLVFEGP-LDlLLYLVRKk	-----KVdI-R-ElPISQlADEfVEYlEHMK-----	-----KlDMKITSDFlEMASTlMELKsKMLlPRVREEEKESlDRKKEEL	92
DHFR_scpA_Mycoplasma	LSFNvFLDYNGT-LFNlLEllLIDK	-----KFNL-H-QVDIAklTQYlHLlINTNL-----	-----NKQAEFlTDVlVlSRlVEQkANNlLQINDlAlDSDFLdNKlRD	251
scpA_Pseudomonas	--MEVFlEAFEGP-LDlLLYLlRkQ	-----NIDl-L-DlPVAElTRQYMGYVlELMK-----	-----AVRLElAAEYlVMAAMlAEIKSRMLlPSRAEAEeEEDPRAElT	90
scpA_Chloroflexus	MPVAVTlPEFTGP-LDlLLRLlERa	-----ElDl-T-TlAlASVADQYlAHVRTLE-----	-----EVEPRElAEFVSMARlLlIKSRALLPRSPPTlPAEAcDDEDAGQl	92
scpA_Pyrococcus	--MERFEPEVTP-VDlLLQlVKMG	-----KVdP-W-NIDVlDELTEKYlKMLREMO-----	-----ELdLRlSARAlLAAslVlRMKsEAlLREDEERNEEKEERlRVE	89
scpA_Methanococcus	--MlDSNFdVlVW-VRMIKEGlEKk	-----NlNP-W-DVNIAlEADYlYlQKlKELK-----	-----KFDlRLSADVlVAGlLLRMKsEAlVDEcKVEEEDYDcDDYV	90
scpA_Thermosynechococcus	PPVMSQSFADTA-IDlIlLElAERG	-----EIDP-W-DlQVVDVcDRClAEAlLARRG-----	-----EPNlSESQAFlYAAMLVLLKsDRlVAVTEPSPAEGEPEPEIA	100
scpA_Cytophaga	ASFEIQlPLFAGP-FDlLLFFlERD	-----ElDl-Y-DlPISKlINDFlEYlIHRLE-----	-----KMNVdIASEFlVAATlMRlKAKlLLPRPDIDPQcNEIDPREEL	96
scpA_Mycobacterium	AGFRVRLTNFEGP-FDlLLQlFAH	-----QlDv-T-EVALHQVlDDFlAYlKAIG-----	-----ARLEElEETAFVlVAATlLdLkARllPAGQVdDEEDlAlLEVRD	113
scpA_Treponema	PVQEFKlSQFEGP-LDlLLFlIKKk	-----ElSl-Y-DlPICEITAQYlQYVdQTV-----	-----SPDLRGLTEFVMAAVlLYlKsCMLlPMELDlDGEDIEDPRQSl	100
scpA_Aquifex	--MKVFFHFTEEHP-FSlVlPLIEEG	-----KlDP-W-EVDlVlELANlMYEELKkLE-----	-----VLDLRVPARAlLAAFlLlRkKIElTlFPKPPRkTKRKYTlQEVl	90
scpA_Fusobacterium	EEVVKlLNNFEGP-FDlLLNLlEKk	-----KMKI-S-DlNISQlDlEYlEVLRVSK-----	-----RENlEIKSDFlIIEASElEIKlLNLNLdKdKEENlNRRlRE	93
scpA_Thermoplasma	MRlDRSVDlPKSl-IlElLlSlCSDG	-----RlDP-W-DVdLLKFAElMNSFFGNs-----	-----FIDPQFAGKAlADAWRlRlKsDMsPKEQDRQMDIIGCEFPEDT	120
scpA_Prochlorococcus	LNRGADSGARLA-IRlLQDAAERG	-----ElDP-W-DVDVlAVDQfLdQLRQRIEVlPQQVAAQ-----	-----VQRQGGsYEQDlADsSEAFLAASVlVSlKAEVLEAQlFPPEFlFEFGFAEL	117
scpA_Archaeoglobus	-----MA-----KRG	-----EIDP-W-NIDVDVlDRFlRkIEDAK-----	-----KlDLRVSGVlLYAAIlVlRMKABAlLEAlGGDEEEElEMYDYD	73
scpA_Rhodospirillum	-----MLlTLARSQ	-----KVdL-T-KlSlLRLAElQYlAFVARAR-----	-----QlHLElAGDvLVMAAWlAYlKsRlLlPAPKNEQEPsGEDMAAl	77
Barren_Encephal	-----MSN-----DDlGtWlKAAAE	-----KITTKNWkSTLIDHFTNIDEFRERQ-----	-----GlnFQKASClDGCakVYSTRVdVdVSENAMRlLEGSGREARkK	86
Barren_At	ESDPCFDKQqILElFQNCIKLASEN	-----KINQKNWELNLIDHLCElIKVEDENN-----	-----TElNFKASClEAGVKIYSMRVdSVHSEAYKlVGGITRAGHDDG	161
Barren_Dm_B	HRSSlLESIEDNElIKNCLELYNGN	-----KVSKDNAWNlMLIDSlANlLlDHHKkR-----	-----MSNFKAGSsLEASsKVYGLRVdSIYlDAMRlSAGlSARTlLTDK	143
Barren_Plasm_f	NKVDKNVKEINDVFKNCMVAlSHNK	-----lCTR-NAFDlHIEHLEDlLNLNDEE-TPeELNDE-----	-----MIENGfNlSfTRASKAlEGATkVYGYRVEAlVDQlYNFlTNMNLAKQFL	162
Barren_Hs	ATlPKFNTQITEHYSTClKlSTEN	-----KITTKNAFGlHLIDfMSElLQKQDTE-----	-----PtnfKVAAGlLDASTkIYAVRVdAVHADVYRlVGLGkDAPSlE	197
Barren_Sc	-----MM-----ANFEEWIKMATDN	-----KINSRNWNfAlIDVfYdLDVlKdGEN-----	-----NINfQKASAlLDGCIKlYSSRVdSVTETGKlLSGLAQKRTNGA	86
Barren_Sp	SPFNSSHQVfVLSNFEEWIKLATDN	-----KINSNTWNfAlIDVfYdHMSlLlRdGE-----	-----DINfQKASClLDGCVKlYTSRlDSVATETGKlLSGLANDSKVlQ	151