

ScRad54	1	MA-----RRRLPDRPPNGIGAGERP-----RLVPRPINVQDSVNRLTK	38
		.       . .:... ...   .       ...   :... .. .	
PfRad54	1	MRKYNGNVKRSRDDEYEENENVNGERTSITLVRATLLPI-LSIGKNEKTT	49
ScRad54	39	PFRVPYKNTHIPPAAGRIATGSDNIVGGRSLRKRSATVCYSGLDINADEA	88
		. .  :  . : .....: ... .....:.....: .	
PfRad54	50	LFH-PFKNP-LPGFVSDKTLYLKKTLGVKVRRTGWINLMKNSIPRRSDET	97
ScRad54	89	EYNSQDISFSQ-----LTKRRKDALSAQRLAKDPTRLSH---IQYTLRR	129
		...:.....:       . ... :.....:..... ... : :.....	
PfRad54	98	EEQEKIEEVIKKHEPLILYKDENDKIEVDPILAQYLREHQREGVQFVFEC	147
ScRad54	130	SFTVP---IKGYVQRHSLPLTLGMKKKITPEPRP	160
		...:.       . :.....: ...:.        .....	
PfRad54	148	LMNIKDDKISGCILADDMGLGKTLQS-ITVLYTL	180

**Region A**  
**Identity: 22%**  
**Positives : 29%**  
**E value : 0.35**

Fig S1: Alignment of various domains (A, B and C represented in Fig 1A) of PfRad54 with ScRad54 using BLAST analysis showing percent identity, positives and E values.

ScRad54	261	VVIDPKLAKILRPHQVEGVRFLYRCVTGLVMKDYLEAEAFNTSSSEDPLKSDEKALTESQK	320
		+ +DP LA+ LR HQ EGV+F++ C+ + D+K	
PfRad54	123	IEVDPILAQYLREHQREGVQVFVECLMNI-----KDDKI-----	156
ScRad54	321	TEQNNRGAYGCIMADEMGLGKTLQCIALMWTLLRQGPQGKRLIDKCIIVCPSSLVNNWAN	380
		GCI+AD+MGLGKTLQ I +++TLL+QG K + +C+I+CP+SL+NNW +	
PfRad54	157	-----SGCILADDMGLGKTLQSIITVLYTLLKQGFHKKCAVRRCLILCPASLINNWND	208
ScRad54	381	ELIKWLGPNLTPLAVDGGKSSMGGNTTVSQAIHAWAQAQGRNIVKPVLIISYETLRRN	440
		E+ KW+ PN V N + I + + +I VLI SYE R N	
PfRad54	209	EISKWI-PNRCNVTCV-----NDNAKEKIVSKLEGFKYDIQSTVLIICSYECFRIN	257
ScRad54	441	VDQLKNCNVGLMLADEGHRLKNGDSLTF TALDSISCPRRVILSGTPIQNDLSEYFALLSF	500
		+ L ++ +++ DE HRLKN + T+T++ +++ +R++LSGTPIQNDL E++AL+S	
PfRad54	258	NEFLDKSSIDMIICDEAHLKNDKTKTYTSIYNLTAKKRLLSGTPIQNDLGEFYALISL	317
ScRad54	501	SNPGLLGSRAEFRKNFENPILRGRDADATDKEITKGEAQLQKLSTIVSKFIIRRTNDILA	560
		NP L FRK F NPIL GRD DAT+KE +L +LS I +KFI+RRTN++L+	
PfRad54	318	CNPDLFDDINLFRKKFANPILIGRDKDATEKEQEIASERLTELSNITNKFILRRTNLLS	377
ScRad54	561	KYLPCKYEHVIFVNLKPLQNELYNKLIKSRVKKVVKGVGGSQPLRAIGILKKLCNHPNL	620
		K LP KY IF+ L P+Q LY +K +++ K L I L+K+CNHP L	
PfRad54	378	KVLPVKYLINIFIKLNP IQEALYVFLKDKKILKNDNTNKNVNLINIKKLEKICNHPLL	437
ScRad54	621	LN FED 625	
		LN D	
PfRad54	438	LN VND 442	

**Region B**  
**Identity: 42.5%**  
**Positives : 56%**  
**E value : 2e-72**

ScRad54	638	DYNMPGSK-----ARDVQTKY---SAKFSILERFLHKIKTESDDKIVLISNYTQTLDLIE	689
		DYN P + RD+ Y S KF +L L IK ++DK+V++SNYTQTLD +E	
PfRad54	585	DYNKPVKRIIEECKRDIYRSYNNFSCFKLLLHFLLNKNIKQNTNDKVIVSNYTQTLDYME	644
ScRad54	690	KMCRYKHYSVRLDGTMSINKRQKLVDRFNDPEGQEFIFLLSSKAGGCGINLIGANRLIL	749
		+C+ Y VRLDG ++I KR K+++ F FIFLLSSK+GGCGINLI +NRLIL	
PfRad54	645	ILCKENMYKFVRLDGGINIKRHKVINDFTHS-ADIFIFLLSSKSGGCGINLISSNRLIL	703
ScRad54	750	MDPDWNPAADQQALARVWRDQKKDCFIYRFISTGTIEEKIFQRQSMKMSLSSCVVDAKE	809
		+DPDWNPA D+QALARVWR+GQKK C+IYR TGTI+EK++QRQ K LS+ +V	
PfRad54	704	LDPDWNPAANDKQALARVWREGQKKICYIYRLFCTGTIDEKVYQRQISKDGLSNMIVTTN	763
ScRad54	810	DVERLFSSDNLRQLFQKNENTICETHETHYCKRCNAQG 847	
		+ S +N+++LF NT+ ETH+ C RCN G	
PfRad54	764	LSKDQMSDENVKKLFNYKMNTVSETHDNIECNRCNLNG 801	

**Region C**  
**Identity: 52%**  
**Positives : 66%**  
**E value : 1e-56**

**Fig. S1 cont.)**