

Supplementary material: Rad50, SMC and MutS sequence proteins highlight Walker A, Signature and Walker B domains in this order.

>AAEL005802-PA.NBD1

MDS AFLQFIEVDNFKSYRGKV TIGPLKKFSAVI **CNGSGKS** NFM DAIS FVM GEKTTSLRV RKL NELI HGA
SIGRPV SNRASV MAFI ITD QEGN QT SKSF QR SVI GSS SEY RING SV VTTNAYL QE LEHIG I NVKA KNFL
VFQG AVESIA MKA KERT ALFEE ISG SGL LKEE YNKL KHEM QMA EET QFTY QKKG JIAA ERKE ALEK Q
EADRYARLKDEYAEKQI QYQLYR LYHNE KETKRL YEDMESK QQL DLTIE KKKE ADDVL KEK KKEAG KTA
RDLAKNEQEIREVESEMSKKHPMFIAKEKVAHTKKKLDSAMKTLEQARKADEAHQADIRKLEDELKGIE
AKMKT FEDA IAGESKKRGSNVHLEQNLVQYEYDRLKQKADATSGY LIK L DSVNRE QKSDQ DLLS EINKK
AQIEEN YKKY E SERNEAAKRQ EK LIDHI KASK QALEE QNRL KQEL S QDV GSS KERI LE LQAE LD DV REQL
GDAK IDK HEDARRKKQEV VELFKQEV PGVYDRM INMC QPT HKR YNV AVT KVLG KYME AIVD TEKT ARR
CIQILKEKML DVETFLPLDYLQKKPLKERLRNIEDPRNVKLIYDVLKFSP PQIEPAVLFA TNNA LV C ET P
DDAM KVAYEIDRSRYDALALDGT FYQKSGIISGGSHDLARKAKRWDEKHMAQLKAQKEKITEELKEVMKK
TRRQGE LTTVESQIRGLENRLKYSQNDL DASK KNIKEYDKKLA ALQ LE DQIGPKISEIERRMQQRDLKI
QEIKENMNNVEDDVYAEFCARIGVANIRQFEERE LVLQ QERAKKRAE FEQQIDRINNNLE FERSKDTSKN
VTRWERAVQDDEDSLET FKQAE ARQRQ EIEKDKERIEKMKV DKA KKA A VD AMEE EMA KARR DVQQ QAKE
LAAVHQ QIAGIESK IETMKNKRHNLLMQCKMDAIEIPMKRGKMNDIVEQTGGNESETTPLSTIYEREAKI
EIDYSSLPKNLNPSEPDQVKVGDGLARELQS KLD TLEKIQT PNLKAMQK LDRVTEKIQT TNEE FEAAR
KKAKKA AAF EKIKNERCTLFTNCCNHISDAIDGIYKQ LARNE AAQAYLGPDNPEEPYLDGINYN C VAPG
KRFQPMSN **LSGGEKTI** AAL ALLFAIHSFQ PAP **FFVLD** EIDA ALDNTNIGKV ASYIREKCTNLQTVVISL
K EEFY SHADILIGICPEPAECLVSQ TLIYDLEQFTP HS

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QGE LTTVESQIRGLENRLKYSQNDL DASK KNIKEYDKKLA ALQ LE DQIGPKISEIERRMQQRDLKI QEI
KENMNNVEDDVYAEFCARIGVANIRQFEERE LVLQ QERAKKRAE FEQQIDRINNNLE FERSKDTSKNVTR
WERAVQDDEDSLET FKQAE ARQRQ EIEKDKERIEKMKV DKA KKA A VD AMEE EMA KARR DVQQ QAKE LAA
VHQ QIAGIESK IETMKNKRHNLLMQCKMDAIEIPMKRGKMNDIVEQTGGNESETTPLSTIYEREAKI EID
YSSLPKNLNPSEPDQVKVGDGLARELQS KLD TLEKIQT PNLKAMQK LDRVTEKIQT TNEE FEAARKKA
KKAKKA AAF EKIKNERCTLFTNCCNHISDAIDGIYKQ LARNE AAQAYLGPDNPEEPYLDGINYN C VAPG KRF
QPM SN **LSGGEKTI** AAL ALLFAIHSFQ PAP **FFVLD** EIDA ALDNTNIGKV ASYIREKCTNLQTVVISL
KEEF YSHADILIGICPEPAECLVSQ TLIYDLEQFTP HS

>AAEL003449-PA.NBD1

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PNFLIMQGRITKVLNMKPQE ILSMIEAAGTSV YEA KREHS I K LIEKKDAKLN ELYTVLREEIEPKLEKL
RKERAHYIEYQKICRDIEYLTRLYISHKYLQHVKS VENSEKAIAALNDV ISGH R NKIEAHITESKEIEQS
AKALQ E LIDTEGGGALAE LAELSAESKKE ATASAERD STKENIGAEQRKLKNLQKSIR DDE NALQKKEA
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MELKHCQQLLKEQGD MNSSDAAYLEDKKKLTKAESQI QSITAELQKIDYEGSIEQLHERKQVLSHEIR
NLKSELDRKNAYRWEFQYRDP EPNFDRSSVHGMVAKLVAV RDKKYALSLGT AAGGSL YSVVVDSDT VGKK
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SKLERIAH RY NQLKEQ QDM MN YELKTLQ QRLA QTSYQQA QQEIEELKAKI ETLK QTMVDARQ AQTQANAK
VKDL TAKIADSKGHRERELKA AEDELKRAKKSEESRKNWKKHEQS FETL RLIEELQKG IATAKEQAAK
LEETIA ELQRKLQ AASSEN SAEMN KAVA AVKQ KIKEH KDKI NSQN KELK AYH HRD KLLQ NEEMELDIKK
KENEI QKVRN ENKD GY NKIS ALEEKY PW ISEDKEFFGVKNTRYDYNKEDPQEAGR KLNKLQDSKEKMSRN
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QAQLKPPDG VDFMKGLEV KVG NGMWKESL TE **LSGGQRS** LVALS LILA MLKYK PAP **LYI** LDEV D AAL DLS
HTQ NIGNMLKAHFTNSQF VIVSLK DGMF NNANVL FRTK FIDG MSGV RTV NVAHAKAAGR

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>AAEL001655-PA.NBD1

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>AAEL002581-PA.NBD1

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DKRRQYHYRVVQAKNDVEIDMRGR**CSAGOKV**LASLIIRMALAETFSNNCG**VMA**DEPTTNLDRENIASLC
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TEEIPKLKEQLEETERKLVQASSDLEECQMSILEPNSSVQLINSILGDMSILDESVRDIDRMKKGienLK
IEVAVKTPEGTTASLDDIKLREALRGELEXVERISIDAMQNKIDEETERLNNLHQRYNQNMKEKKIQLQES
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DYIRIKTEDESKPDKVTDKRRQYHYRVVQAKNDVEIDMRGR**CSAGOKV**LASLIIRMALAETFSNNCG**VMA**
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