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| Motif | Mutations | Organism | Equivalent to human residue | Ref. |
| Walker A | K40AK40RK40E | *S. cerevisiae* | K42AK42RK42E | [1] |
| Walker A(WA)& D-loop | R37AN38AD512ND512AE514QE515A | T4 bacteriophage | P37AN38AD1238ND1238AE1240QN1241A | [2] |
| ATP binding domain &Walker A | K6ES14PR20ME21KG39D (WA)K40E (WA)V63EQ79KK81IN97DQ99KE915VA930P | *S. cerevisiae* | K6ES14PK22MQ23KG41DK42ET65EQ81KR83IS99DV101KK921VS936P | [3] |
| ATP binding domain | K6E =K6EScK22M=R20MScR83I=K81Sc | *M. musculus* | K6EK22MR83I | [4] |
| Walker A,Walker B& Signature motif | K39R (WA)K39M (WA)D303N (WB)S270R (SM) | *D. radiodurans* | K42RK42MD1231NS1202R | [5] |
| ATPase binding domain&Walker B (WB)&Signature motif (SM) | K115EK175EK182ER94EK95ER765EE798Q (WB)S768R (SM)K99EK108EK109EK110ER125EK103EK104ER131ER1201EN190DS1205E+E1235Q | *T. maritima**S. cerevisiae* | K132ET191EC221EK105ES106EG1199EE1232QS1202RE110KE126KK127EK122EK126EK105ES106EK132ER1198ET191DS1202R+E1232Q | [6] |
| Zinc hook | S679RP682EV683R | *M. musclulus* | S679RP682EV683R | [7] |
| Zinc hook | C680GC681GC684GR686AC681G+C684GC680G+C681G+C684G | *H. sapiens*  | C680GC681GC684GR686A | [8] |
| Zinc hook  | C684NC685AP686AV6871C688RQ689S | *S. cerevisiae* | C680NC681AP682AV683IC684RQ685S | [9] |

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| Motif | Mutations | Organism | Equivalent to human residue | Ref. |
| Zinc hook &coiled coil domain (ATPase domain) | C288SC291SC312SK211PK351PS183C | T4 bacteriophage | C681SC684SC990SK256PN1028PM208C | [10] |
| Zinc hook&coiled coil domain (ATPase domain) | S685RY688EY688RL689RI680VK700QL703FV285AN607YN873IS193F | *S cerevisiae* | S679RP682EP682RV683RL673VL694QV697FM293AS603YQ886IQ194F | [11] |
| Zink hook | S635G  | *H. sapiens* | S635G | [12] |
| Signature motif &ATPase domain | R797GR805ER805WL802WL806FK155A | *P. furiosus* | K1206GR1214ER1214WL1211WL1215FQ174A | [13] |
| Signature motif | K1187AK1187ER1195AR1195E | *S.pombe* | K1206AK1206ER1214AR1214E | [14] |
| Signature motif & Q loop | S793RQ140H | *P. furiosus* | S1202RQ159H | [15] |
| Signature motif | S471AS471RS471ME472GE474QK475M | T4 bacteriophage | S1202AS1202RS1202MA1203GQ1205EK1206M | [16] |
| Signature motif | S1205RS793RS1202R | *S. cerevisiae**P. furiosus**H. sapiens* | S1202R | [17] |
| ATPase domain | R1093X | *H. sapiens* | R1093X | [18] |

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