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| --- | --- | --- | --- | --- |
| Motif | Mutation | Score | Affected PROSITE and ELM Motifs | |
| Walker A | P37A | 0.536 | PS00008  PS00017 | -N-myristoylation site  -ATP/GTP-binding site motif A (P-loop) |
| N38A | 0.963 | PS00017 | -ATP/GTP-binding site motif A (P-loop) |
| G41D | 0.961 | ELME000052  ELME000064  PS00008  PS00017 | - FHA phosphopeptide ligands  - CK2 Phosphorylation site  -N-myristoylation site  -ATP/GTP-binding site motif A (P-loop) |
| K42R | 0.852 | ELME000052, ELME000062, ELME000064, ELME000220,  PS00008,  PS00017 | - FHA phosphopeptide ligands  - PKA Phosphorylation site  - CK2 Phosphorylation site  - FHA phosphopeptide ligands  -N-myristoylation site  -ATP/GTP-binding site motif A (P-loop)  -ATP/GTP-binding site motif A (P-loop) |
| K42M | 0.930 | ELME000052, ELME000064, ELME000220,  PS00008,  PS00017 | - FHA phosphopeptide ligands  - CK2 Phosphorylation site  - FHA phosphopeptide ligands  -N-myristoylation site  -ATP/GTP-binding site motif A (P-loop) |
| K42E | 0.939 | ELME000052, ELME000064, ELME000147, ELME000220,  PS00008,  PS00017 | - FHA phosphopeptide ligands  - CK2 Phosphorylation site  - Polo-like kinase phosphorylation site  - FHA phosphopeptide ligands  -N-myristoylation site  -ATP/GTP-binding site motif A (P-loop) |
| K42A | 0.956 | ELME000052  ELME000064  ELME000220  PS00008  PS00017 | - FHA phosphopeptide ligands  - CK2 Phosphorylation site  - FHA phosphopeptide ligands  -N-myristoylation site  -ATP/GTP-binding site motif A (P-loop) |
| Q-loop | Q159H | 0.466 | None | None |
| Zinc hook | S635A | 0.088 | None | None |
| S635G | 0.133 | None | None |
| S679R | 0.250 | None | None |
| C680G | 0.671 | ELME000070, ELME000085,  PS00001,  PS00008 | - N-glycosylation site  - Glycosaminoglycan attachment site  -N-glycosylation site  -N-myristoylation site |
| C680N | 0.740 | ELME000070  PS00001 | - N-glycosylation site  -N-glycosylation site |
| C681G | 0.760 | ELME000070 | - N-glycosylation site |
| C681A | 0.709 | ELME000070 | - N-glycosylation site |
| C681S | 0.640 | ELME000070, ELME000136, ELME000159 | - N-glycosylation site  - Proline-directed phosphorylation  - MAPK Phosphorylation Site |
| P682R | 0.599 | None | None |
| P682E | 0.536 | ELME000064  PS00006 | - CK2 Phosphorylation site  -Casein kinase II phosphorylation site |
| P682A | 0.385 | None | None |
| V683R | 0.606 | None | None |
| V683I | 0.127 | None | None |
| C684G | 0.847 | None | None |
| C684A | 0.798 | None | None |
| C684R | 0.868 | ELME000012 | di Arginine retention/retrieving signal |
| C684S | 0.738 | ELME000202  PS00005 | - PIKK phosphorylation site  - Protein kinase C phosphorylation site |
| Q685S | 0.674 | ELME000197  ELME000239 | - BRCT phosphopeptide ligands  - USP7 binding motif |
| R686A | 0.796 | None | None |
| Signature motif | S1202A | 0.780 | ELME000062, ELME000085 | - PKA Phosphorylation site  - Glycosaminoglycan attachment site |
| S1202R | 0.937 | ELME000062, ELME000085 | - PKA Phosphorylation site  - Glycosaminoglycan attachment site |
| S1202M | 0.927 | ELME000062, ELME000085 | - PKA Phosphorylation site  - Glycosaminoglycan attachment site |
| A1203G | 0.780 | ELME000062, ELME000085 | - PKA Phosphorylation site  - Glycosaminoglycan attachment site |
| Q1205E | 0.835 | ELME000062, ELME000064,  PS00006 | - PKA Phosphorylation site  - CK2 Phosphorylation site  - Casein kinase II phosphorylation site |
| K1206M | 0.833 | None | None |
| K1206A | 0.901 | None | None |
| K1206E | 0.873 | ELME000117, ELME000193 | - TRAF2 binding site  - NES Nuclear Export Signal |
| K1206G | 0.919 | PS00008 | N-myristoylation site |
| L1211W | 0.914 | ELME000335 | - SUMO interaction site |
| R1214A | 0.961 | PS00211 | - ATP-binding cassette, ABC transporter-type, signature and profile |
| R1214E | 0.956 | ELME000333,  PS00211 | - SUMO interaction site  - ATP-binding cassette, ABC transporter-type, signature and profile |
| R1214L | 0.952 | ELME000045, ELME000335,  PS00211 | - Nuclear receptor box  - SUMO interaction site  - ATP-binding cassette, ABC transporter-type, signature and profile |
| R1214W | 0.950 | PS00211 | - ATP-binding cassette, ABC transporter-type, signature and profile |
| L1215F | 0.889 | None | None |
| Walker B | D1231N | 0.931 | ELME000333 | - SUMO interaction site |
| E1232Q | 0.882 | ELME000052, ELME000333 | -FHA phosphopeptide ligands  - SUMO interaction site |
| D-loop | D1238N | 0.895 | ELME000052, ELME000220,  PS00006 | - FHA phosphopeptide ligands  -FHA phosphopeptide ligands  - Casein kinase II phosphorylation site |
| D1238A | 0.931 | ELME000052, ELME000220,  PS00006 | - FHA phosphopeptide ligands  - FHA phosphopeptide ligands  - Casein kinase II phosphorylation site |
| E1240Q | 0.492 | None | None |
| N1241A | 0.900 | ELME000239 | -USP7 binding motif |
| ATPase domain | K6E | 0.134 | None | None |
| S14P | 0.941 | ELME000235 | RRM domain ligands |
| K22M | 0.317 | None | None |
| Q23K | 0.664 | ELME000137, ELME000233 | - PP1-docking motif RVXF  - MAPK docking motifs |
| T65E | 0.845 | ELME000053, ELME000155,  PS00008 | - GSK3 phosphorylation site  - SH3 ligand  - N-myristoylation site |
| Q81K | 0.814 | ELME000137, ELME000233 | - PP1-docking motif RVXF  - MAPK docking motifs |
| R83I | 0.754 | ELME000137 | - PP1-docking motif RVXF |
| S99P | 0.739 | ELME000053, ELME000155 | - GSK3 phosphorylation site  - SH3 ligand |
| V101K | 0.254 | None | None |
| Q174A | 0.423 | None | None |
| T191D | 0.515 | ELME000337  PS00005 | - PP1-docking motif RVXF  - Protein kinase C phosphorylation site |
| Q194S | 0.420 | None | None |
| M208C | 0.216 | None | None |
| K256P | 0.215 | None | None |
| M293A | 0.347 | None | None |
| S603Y | 0.211 | None | None |
| K921V | 0.397 | None | None |
| L673V | 0.289 | None | None |
| L694Q | 0.579 | ELME000220, ELME000313 | - FHA phosphopeptide ligands  - Actin-binding motifs |
| V697F | 0.300 | None | None |
| Q886I | 0.639 | None | None |
| S936P | 0.395 | None | None |
| C990S | 0.209 | None | None |
| N1028P | 0.237 | None | None |
| K132E | 0.862 | ELME000063, PS00005 | - CK1 Phosphorylation site  -Protein kinase C phosphorylation site |
| T191E | 0.561 | ELME000117, ELME000337, PS00005 | - TRAF2 binding site  - NEK2 phosphorylation site  - Protein kinase C phosphorylation site |
| C221E | 0.269 | None | None |
| K105E | 0.430 | None | None |
| S106E | 0.152 | None | None |
| G1199E | 0.945 | ELME000012, ELME000062 | - di Arginine retention/retrieving signal  - PKA Phosphorylation site |
| E110K | 0.362 | None | None |
| K126E | 0.340 | None | None |
| V127E | 0.590 | ELME000233 | -MAPK docking motifs |
| K122E | 0.475 | None | None |
| R1198E | 0.944 | ELME000012 | - di Arginine retention/retrieving signal |
| Y1184R | 0.961 | ELME000012, ELME000102, ELME000103, ELME000108, ELME000120 | - di Arginine retention/retrieving signal  - NRD cleavage site  - PCSK cleavage site  - PCSK cleavage site  - PCSK cleavage site |
| SNPs | K616E | 0.314 | None | None |
| T191I | 0.387 | None | None |
| R1038G | 0.406 | None | None |
| K973M | 0.477 | None | None |
| V842A | 0.158 | None | None |
| V127I | 0.107 | None | None |
| V697A | 0.174 | None | None |
| R224H | 0.140 | None | None |
| Y964H | 0.436 | None | None |
| R193W | 0.537 | ELME000337  PS00005 | - NEK2 phosphorylation site  - Protein kinase C phosphorylation site |
| I94L | 0.195 | None | None |
| G469A | 0.326 | None | None |
| V315L | 0.227 | None | None |