

Pattern	Human_recognition_domain_n	Domain_p	unique_position	Human_p	matc
KRRK	Armadillo-like helical	0.000799	B4URF7_736_739	P52294	
KRRK	Armadillo-type fold	0.000799	B4URF7_736_739	P52294	
E.V..G.{0,2}N.{0,1}Q	WD40/YVTN repeat-like-contai	0.008178	B4URF7_342_350	O95163	
KR.{0,1}L.{0,1}V.G	MAGE homology domain	0.214057	B4URF7_663_669	Q12816	
E.V..G.{0,2}N.{0,1}Q	WD40/YVTN repeat-like-contai	0.014231	C5E527_342_350	O95163	
KRRK	Importin-alpha, importin-beta-l	3.66E-05	E5LBT9_339_342	O60684	
KRRK	Armadillo-like helical	3.66E-05	E5LBT9_339_342	O60684	
KRRK	Armadillo-type fold	3.66E-05	E5LBT9_339_342	O60684	
KRRK	Importin-alpha, importin-beta-l	3.66E-05	E5LBT9_339_342	P52294	
KRRK	Armadillo-like helical	3.66E-05	E5LBT9_339_342	P52294	
KRRK	Armadillo-type fold	3.66E-05	E5LBT9_339_342	P52294	
KRK	Importin-alpha, importin-beta-l	3.66E-05	E5LBT9_339_341	P52292	
KRK	Armadillo-like helical	3.66E-05	E5LBT9_339_341	P52292	
KRK	Armadillo-type fold	3.66E-05	E5LBT9_339_341	P52292	
KRRK	Importin-alpha, importin-beta-l	0.004127	F5HE15_93_96	O60684	
KRRK	Armadillo-like helical	0.004127	F5HE15_93_96	O60684	
KRRK	Armadillo-type fold	0.004127	F5HE15_93_96	O60684	
KRRK	Importin-alpha, importin-beta-l	0.004127	F5HE15_93_96	P52294	
KRRK	Armadillo-like helical	0.004127	F5HE15_93_96	P52294	
KRRK	Armadillo-type fold	0.004127	F5HE15_93_96	P52294	
KRK	Tetratricopeptide-like helical d	0.001106	I6T1Z2_219_221	Q9Y2X3	
KRK	Armadillo-like helical	0.013001	O92837_203_205	P52292	
KRK	Armadillo-type fold	0.013001	O92837_203_205	P52292	
DSG	WD40/YVTN repeat-like-contai	0.016842	P03070_656_658	Q9UKB1	
DSG	WD40-repeat-containing doma	0.016842	P03070_656_658	Q9UKB1	
KRK	Importin-alpha, importin-beta-l	0.007473	P03070_129_131	O60684	
KRK	Armadillo-like helical	0.007473	P03070_129_131	O60684	
KRK	Armadillo-type fold	0.007473	P03070_129_131	O60684	
DSG	WD40/YVTN repeat-like-contai	0.016842	P03070_656_658	Q9Y297	
DSG	WD40-repeat-containing doma	0.016842	P03070_656_658	Q9Y297	
KRK	Importin-alpha, importin-beta-l	0.007473	P03070_129_131	P52292	
KRK	Armadillo-like helical	0.007473	P03070_129_131	P52292	
KRK	Armadillo-type fold	0.007473	P03070_129_131	P52292	
KRK	Armadillo-like helical	0.013123	P03087_5_7	P52292	
KRK	Armadillo-type fold	0.013123	P03087_5_7	P52292	
KRK	Armadillo-like helical	3.04E-06	P03101_484_486	P52292	
KRK	Armadillo-like helical	3.04E-06	P03101_499_501	P52292	
KRK	Armadillo-like helical	3.04E-06	P03101_502_504	P52292	
KRK	Armadillo-type fold	3.04E-06	P03101_484_486	P52292	
KRK	Armadillo-type fold	3.04E-06	P03101_499_501	P52292	
KRK	Armadillo-type fold	3.04E-06	P03101_502_504	P52292	
[ST].[LV]\$	PDZ domain	1.87E-05	P03126_156_158	Q12959	matc
[DE]T.[ILV]\$	PDZ domain	1.87E-05	P03126_155_158	Q14160	matc
ET..\$	PDZ domain	1.87E-05	P03126_155_158	P26045	matc
[KR][KR][KR][KR]	Importin-alpha, importin-beta-l	0.012399	P03211_458_461	O60684	

[KR][KR][KR][KR]	Armadillo-like helical	0.012399	P03211_458_461	O60684	
[KR][KR][KR][KR]	Armadillo-type fold	0.012399	P03211_458_461	O60684	
RKR	Armadillo-type fold	0.085193	P03427_737_739	O00505	
KR.R	PDZ domain	0.045749	P03428_736_739	Q92997	matc
KR.R	PDZ domain	0.045749	P03428_752_755	Q92997	matc
KR.R	PDZ domain	0.038157	P03431_669_672	Q92997	
[ST].V\$	PDZ domain	0.034288	P03496_228_230	O14908	
LR.{0,2}G.G.T	Double-stranded RNA-binding c	0.004605	P03496_43_49	Q96SI9	
KRK	Armadillo-like helical	0.000104	P04012_493_495	P52292	
KRK	Armadillo-type fold	0.000104	P04012_493_495	P52292	
[HR][HK]R.R	RNA recognition motif domain	0.108667	P04015_238_242	Q07955	
[HR]KR.R	RNA recognition motif domain	0.108667	P04015_238_242	Q16629	
T.AP..S..T	Zinc finger, RING/FYVE/PHD-ty	0.009411	P04015_219_228	Q9NRL2	
PAP	P-loop containing nucleoside tri	0.002011	P04487_7_9	Q00839	
DSG	WD40/YVTN repeat-like-contai	0.013911	P05919_51_53	Q9UKB1	
DSG	WD40-repeat-containing doma	0.013911	P05919_51_53	Q9UKB1	
DSG	WD40/YVTN repeat-like-contai	0.013911	P05919_51_53	Q9Y297	
DSG	WD40-repeat-containing doma	0.013911	P05919_51_53	Q9Y297	
[ST].[LV]\$	PDZ domain	4.55E-06	P06427_147_149	Q12959	
[DE]T.[ILV]\$	PDZ domain	4.55E-06	P06427_146_149	Q14160	
DY.[FY]	P-loop containing nucleoside tri	0.004633	P06461_67_70	P09543	
[ST].[LV]\$	P-loop containing nucleoside tri	7.65E-06	P06463_156_158	Q12959	matc
[DE]T.[ILV]\$	PDZ domain	0.000159	P06463_155_158	Q14160	matc
ET..\$	PDZ domain	0.000159	P06463_155_158	P26045	matc
E..QR..E	Armadillo-like helical	0.011427	P06463_148_155	Q99460	matc
E..QR..E	Armadillo-type fold	0.011427	P06463_148_155	Q99460	matc
E.DE	PDZ domain	0.115665	P06464_36_39	Q9NR12	
DL.CHE	Cyclin-like	0.001668	P06788_24_29	Q08999	
G.V.{0,1}G.{0,1}S	Keratin type II head	0.155327	P06921_404_409	P02538	
G[KR].RGR	Histone deacetylase domain	0.001411	P08393_339_344	O15379	
Q..H..RE..D	GroEL-like apical domain	0	P09992_402_412	P78371	
Q..H..RE..D	GroEL-like equatorial domain	0	P09992_402_412	P78371	
D.T..K..S	Armadillo-like helical	0.017386	P0C1C7_85_93	O00629	
D.T..K..S	Armadillo-type fold	0.017386	P0C1C7_85_93	O00629	
[ST].[LV]\$	PDZ domain	0.00011	P0C213_351_353	Q12959	
[DE]T.[ILV]\$	PDZ domain	0.00011	P0C213_350_353	Q14160	
[DE]..V\$	PDZ domain	0.00011	P0C213_350_353	Q96RT1	
P..P.P.D	P-loop containing nucleoside tri	0.001532	P0C739_28_35	P51148	
E.LG.D	GroEL-like apical domain	0.216951	P0DOE9_131_136	P10809	
[ST].[LV]\$	PDZ domain	0.004431	P16717_146_148	Q12959	
T.L\$	PDZ domain	0.004431	P16717_146_148	Q14160	
[ST].[LV]\$	PDZ domain	0.021123	P17386_147_149	Q12959	
[ST].[LV]\$	Guanylate kinase-like domain	0.021123	P17386_147_149	Q12959	
[ST].[LV]\$	Guanylate kinase/L-type calciur	0.021123	P17386_147_149	Q12959	
[ST].[LV]\$	P-loop containing nucleoside tri	0.021123	P17386_147_149	Q12959	
[ST].[LV]\$	PDZ domain	0.004535	P21735_156_158	Q12959	

[DE]T.[ILV]\$	PDZ domain	0.004535	P21735_155_158	Q14160
[ST].[LV]\$	PDZ domain	0.004474	P24835_156_158	Q12959
[DE]T.[ILV]\$	PDZ domain	0.004474	P24835_155_158	Q14160
[ST].[LV]\$	P-loop containing nucleoside triphosphate-binding motif	0.004489	P26555_147_149	Q12959
[ST].[LV]\$	PDZ domain	0.004536	P27228_147_149	Q12959
[DE]T.[ILV]\$	PDZ domain	0.004536	P27228_146_149	Q14160
C..PG	P-loop containing nucleoside triphosphate-binding motif	0.000619	P30119_4_8	P62191
KRKR	Importin-alpha, importin-beta-like domain	0.000105	P31345_736_739	O60684
KRKR	Armadillo-like helical domain	0.000105	P31345_736_739	O60684
KRKR	Armadillo-type fold	0.000105	P31345_736_739	O60684
KRKR	Importin-alpha, importin-beta-like domain	0.000105	P31345_736_739	P52294
KRKR	Armadillo-like helical domain	0.000105	P31345_736_739	P52294
KRKR	Armadillo-type fold	0.000105	P31345_736_739	P52294
PT..S.[ST]	Armadillo-type fold	0.025747	P36780_233_239	Q7Z6Z7
PT..S.[ST]	Armadillo-type fold	0.025747	P36780_320_326	Q7Z6Z7
[ST].[LV]\$	PDZ domain	0.000103	P50804_156_158	Q12959
[DE]T.[ILV]\$	PDZ domain	0.000103	P50804_155_158	Q14160
[DE]..V\$	PDZ domain	0.000103	P50804_155_158	Q96RT1
PE.AEA	Protein kinase domain	0.004562	P89462_325_330	Q13546
PE.AEA	Protein kinase-like domain	0.004562	P89462_325_330	Q13546
PE.AEA	RHIM domain	0.004562	P89462_325_330	Q13546
[ST].V\$	PDZ domain	0.008636	Q0A2H0_228_230	O14908
[ST].V\$	SH3 domain	0.008636	Q0A2H0_228_230	P78352
[ST].V\$	PDZ domain	0.008636	Q0A2H0_228_230	P78352
LR.{0,2}G.G.T	Double-stranded RNA-binding domain	4.83E-06	Q0A2H0_43_49	Q96SI9
LR.{0,2}G.G.T	Double-stranded RNA-binding domain	3.35E-07	Q20MH3_43_49	Q96SI9
V.ESM..E	Armadillo-type fold	3.21E-06	Q20MH8_68_75	O60518
E.[LV].QL	Tetratricopeptide-like helical domain	0.010229	Q2MG95_260_265	P49792
[ST].[ILV]\$	PDZ domain	0.003137	Q2PJP0_223_225	Q14160
[ST].V\$	PDZ domain	0.003137	Q2PJP0_223_225	O14908
[ST].V\$	PDZ domain	0.003137	Q2PJP0_223_225	P78352
[DE]..V\$	PDZ domain	0.003137	Q2PJP0_222_225	Q96RT1
LR.{0,2}G.G.T	Double-stranded RNA-binding domain	5.68E-06	Q2PJP0_43_49	Q96SI9
[GS].[FV]..I[IL].R	SKP1/BTB/POZ domain	0.097665	Q2PJP1_7_15	Q13105
[GS].[FV]..I[IL].R	Zinc finger, RING/FYVE/PHD-type	0.097665	Q2PJP1_7_15	Q13105
[GS].[FV]..I[IL].R	Zinc finger C2H2-type	0.097665	Q2PJP1_7_15	Q13105
LR.{0,2}G.G.T	Double-stranded RNA-binding domain	1.85E-07	Q3SBS4_43_49	Q96SI9
EI[IV]QQ	EF-hand domain	0.111539	Q5EP37_112_116	Q9BRK5
EI[IV]QQ	EF-hand domain pair	0.111539	Q5EP37_112_116	Q9BRK5
KR.R	PDZ domain	0.014138	Q67296_736_739	Q92997
KR.R	PDZ domain	0.014138	Q67296_752_755	Q92997
[ST].V\$	PDZ domain	0.001519	Q6DP93_223_225	O14908
[ST].V\$	PDZ domain	0.001519	Q6DP93_223_225	P78352
[DE]..V\$	PDZ domain	0.001519	Q6DP93_222_225	Q96RT1
LR.{0,2}G.G.T	Double-stranded RNA-binding domain	5.27E-07	Q6DP93_43_49	Q96SI9
S.{0,1}V\$	RNA recognition motif domain	6.14E-06	Q6VGS8_126_128	Q9NZI8

V.ESM..E	Armadillo-like helical	0.000146	Q76353_150_157	O60518
V.ESM..E	Armadillo-type fold	0.000146	Q76353_150_157	O60518
EE..[KR].[LV]	PH domain-like	0.080346	Q77M19_3_9	O14654
[HR][HK]R.R	RNA recognition motif domain	0.102478	Q77UU1_237_241	Q07955
[HR]KR.R	RNA recognition motif domain	0.102478	Q77UU1_237_241	Q16629
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_156_161	O95816
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_222_227	O95816
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_24_29	O95816
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_288_293	O95816
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_354_359	O95816
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_420_425	O95816
L.{0,1}Q.LR	BAG domain	0.079879	Q8AZK7_90_95	O95816
[KR]P.L.[AS]..S	S-adenosyl-L-methionine-depen	0.152174	Q8JPQ9_42_50	P22061
P.R.[KR]..[ST]	Tubulin/FtsZ, GTPase domain	0.00624	Q8JPQ9_40_47	P68371
P.R.[KR]..[ST]	Tubulin/FtsZ, C-terminal	0.00624	Q8JPQ9_40_47	P68371
P.R.[KR]..[ST]	Tubulin/FtsZ, 2-layer sandwich	0.00624	Q8JPQ9_40_47	P68371
D.T..K..S	Importin-alpha, importin-beta-l	0.094025	Q997F2_85_93	O00629
D.T..K..S	Armadillo-like helical	0.094025	Q997F2_85_93	O00629
D.T..K..S	Armadillo-type fold	0.094025	Q997F2_85_93	O00629
E..R.Y	Basic-leucine zipper domain	0	Q9DGW5_296_301	P15336
P..P.[HKR]	Protein kinase domain	1.22E-05	Q9QPN3_72_77	P12931
P..P.[HKR]	SH2 domain	1.22E-05	Q9QPN3_72_77	P12931
P..P.[HKR]	Serine-threonine/tyrosine-prote	1.22E-05	Q9QPN3_72_77	P12931
P..P.[HKR]	SH3 domain	1.22E-05	Q9QPN3_72_77	P12931
P..P.[HKR]	Protein kinase-like domain	1.22E-05	Q9QPN3_72_77	P12931
PE.AEA	Protein kinase domain	0.004536	U5TQE9_320_325	Q13546
PE.AEA	Protein kinase-like domain	0.004536	U5TQE9_320_325	Q13546
PE.AEA	RHIM domain	0.004536	U5TQE9_320_325	Q13546