

Table1. Potential caspase cleavage sites

position	site	N fragment	C fragment	frequency score	similarity maxscore	similarity maxsite	average score
479 to 483	TESD.G	53.1 kD	86.2 kD	4.269	81.481	TEEDG	347.826
684 to 688	SEED.S	75.9 kD	63.3 kD	3.692	69.565	SESDA	256.829
48 to 52	ELPD.S	6.0 kD	133.2 kD	3.260	62.963	SFPDS	205.229
868 to 872	ISAD.G	96.7 kD	42.6 kD	1.231	59.259	FEADG	72.927
731 to 735	SSSD.N	81.5 kD	57.7 kD	0.931	69.565	SSTDS	64.786
261 to 265	TVQD.S	30.0 kD	109.3 kD	1.048	56.000	TVADG	58.671
1248 to 1252	HLLD.G	137.5 kD	1.8 kD	0.658	65.385	HLADS	43.026
132 to 136	WFTD.S	15.4 kD	123.9 kD	0.299	81.250	WFKDS	24.322
741 to 745	EGTD.L	82.5 kD	56.8 kD	0.306	69.231	DGVDL	21.156
749 to 753	DFED.N	83.5 kD	55.7 kD	0.267	71.429	DMQDN	19.055
752 to 756	DNGD.R	83.8 kD	55.4 kD	0.191	82.143	DQGDR	15.653
707 to 711	SRRD.S	78.7 kD	60.5 kD	0.200	70.833	AQRDS	14.136
61 to 65	FSPD.R	7.5 kD	131.8 kD	0.200	64.000	ISPDS	12.772
508 to 512	LEYD.R	56.4 kD	82.9 kD	0.173	60.870	LSVDR	10.534
814 to 818	VIGD.G	90.7 kD	48.6 kD	0.154	60.000	TVADG	9.230
1255 to 1259	SRGD.A	138.1 kD	1.2 kD	0.133	60.870	SESDA	8.098
1114 to 1118	SGED.A	123.4 kD	15.8 kD	0.150	52.174	SESDA	7.809
213 to 217	IPID.G	24.5 kD	114.7 kD	0.135	54.167	AAVDG	7.291
324 to 328	PHQD.S	36.8 kD	102.4 kD	0.116	61.290	PHLDG	7.135
114 to 118	GCLD.G	13.3 kD	126.0 kD	0.094	66.667	SALDG	6.267

Position: aa position within the sequence

Site: identified sequence

N fragment: size of N-terminal protein fragment derived from cleavage

C fragment: size of C-terminal protein fragment derived from cleavage

frequency score: indicates whether the aa of the potential cleavage site are likely to occur at that position

similarity maxscore: similarity score of the potential cleavage sites to the known cleavage sites

similarity maxsite: site from the list of known cleavage sites that is most similar to the site

average score: frequency score x similarity maxscore