

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications	missed cleavages
1925.907	1925.947	0.039	(K)/YQWPVGESFALQMLEK/(F)	201-216		0

Matching peptides for specific cleavage:

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications	missed cleavages
1,526,505	1,526,837	0.331	(H)ILDFPRLSKYQ(P)	289-300		1
1,526,505	1,526,884	0.378	(K)PIVDLKMSRQRAL(A)	452-464		2
1,526,505	1,526,894	0.389	(P)NLKLNYPKPIVDL(K)	444-456		0
1,566,581	1,566,755	0.173	(D)ENLEPYKQQRDF(P)	220-231		1
1,566,581	1,566,806	0.225	(N)KTHQPYQVFGAYK/(R)	141-153		1
1,599,489	1,599,849	0.359	(F)ANKYQVTVIHANIE(I)	88-101		0
1,599,489	1,599,937	0.447	(E)LIQRFHTFKIPSI(H)	178-190		1
1,655,536	1,655,919	0.382	(L)KQFNIPLMVEIVPQ(W)	63-76		0
1,690,409	1,690,728	0.318	(L)IDGDLAANNGGWQWCA(S)	376-391		0
1,690,409	1,690,849	0.440	(G)WMHNRVRMIVAMF(L)	343-355		1
1,722,683	1,722,885	0.201	(D)AQVKYQWPVGESFAL(Q)	197-211		0

Matching peptides for unspecific cleavage:

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications	missed cleavages
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**Matching peptides for
unspecific cleavage:**

1,722,683	1,722,907	0.224	(N)KTHQPYQVFGAYKR/(A)	141-154		2
1,722,683	1,722,917	0.234	(H)LDAKIIHEPYAKNPN(L)	430-444		1
1,722,683	1,722,917	0.234	(L)DAKIIHEPYAKNPNL(K)	431-445		1
1,768,729	1,768,859	0.129	(K)/THQPYQVFGAYKRAC(Y)	142-156		1
1,768,729	1,768,913	0.183	(S)QKFDSQGNVIRKWWV(P)	411-424		2
1,768,729	1,769,003	0.273	(E)LKQFNIPLMVEIVPQ(W)	62-76		0
1,812,023	1,811,911	-0.111	(R)/EFYQHILFDFPRLS(K)	284-297		0
1,812,023	1,811,944	-0.079	(D)FPRLSKYQPFNLNTS(N)	293-307		1
1,850,311	1,849,933	-0.377	(D)FPNIDATSQLSPYLNLG(I)	231-247		0
1,850,311	1,849,942	-0.369	(N)LLIDWRKGEQWFMQ(H)	360-373		1
1,850,311	1,849,981	-0.330	(W)DDVPARLLTFANKYQV(T)	78-93		1

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications	missed cleavages
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**Matching peptides for
unspecific cleavage:**

1,850,311	1,849,999	-0.311	(A)MFLSKNLLIDWRKGE(Q)	354-368		2
1,850,311	1,850,007	-0.303	(Q)PHELIQRFHTFKIPS(I)	175-189		1
1,893,488	1,893,049	-0.438	(K)/VQPHELIQRFHTFKI(P)	173-187		1
1,893,488	1,893,096	-0.392	(S)VPQPLAVPKVQPHELIQ(R)	164-180		0
1,968,243	1,968,013	-0.230	(W)REFYQHILFDFPRLS(K)	283-297		1
1,990,409	1,990,003	-0.406	(L)LESHKVTVEYYHDRTI(F)	117-132		1
1,990,409	1,990,003	-0.406	(Q)TLLESHKVTVEYYHDR/(T)	115-130		1
1,990,409	1,990,003	-0.406	(T)LESHKVTVEYYHDRT(I)	116-131		1
1,990,409	1,990,102	-0.306	(K)/VQPHELIQRFHTFKIP(S)	173-188		1
2,025,698	2,025,924	0.225	(F)MQHLIDGDLAANNGGWQW(C)	372-389		0
2,025,698	2,025,962	0.264	(F)NLNTSNVPWRDAPDELNA(W)	303-320		0

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications
2,025,698	2,026,025	0.326	(R)/QDLRVRDNTALMEATR(H)	8-24	2
2,025,698	2,026,050	0.352	(F)DSQGNIRKWWPELAHL(D)	414-430	1
2,025,698	2,026,050	0.352	(D)SQGNIRKWWPELAHLD(A)	415-431	1
2,087,768	2,087,993	0.225	(V)PWRDAPDELNAWKFGQTG(I)	310-327	1
2,087,768	2,088,062	0.293	(Q)TGPIVDAGIRQMLETGWM(H)	326-344	0
2,087,768	2,088,106	0.337	(N)AWKFGQTGPIVDAGIRQM(L)	320-338	1
2,108,572	2,108,092	-0.479	(S)QKFDSQGNIRKWWPEL(A)	411-427	2
2,147,514	2,147,044	-0.469	(S)PEQWKLHDDAEIKIDFY(L)	35-51	1
2,147,514	2,147,067	-0.447	(S)KYQPFNLNTSNVPWRDAP(D)	298-315	1
2,147,514	2,147,070	-0.443	(R)/HGNTCAVVILSPEQWKLHD(D)	24-42	0
2,147,514	2,147,154	-0.359	(N)LIWFRQDLRVRDNTALM(E)	3-19	2
2,147,514	2,148,001	0.486	(G)WQWCASTGTDVVPYFRIF(N)	387-404	0
2,172,094	2,172,065	-0.029	(V)RDNTALMEATRHGNTCAVVI(L)	13-32	1
2,172,094	2,172,083	-0.010	(K)YQWPVGESFALQMLEK(F)	201-218	0
2,172,094	2,172,192	0.098	(L)AHLDAKIIHEPYAKNP(L)	428-446	2
2,172,094	2,172,221	0.126	(S)QLSPYLNLGIVSIRQCLAAI(F)	239-258	0
2,172,094	2,172,229	0.134	(P)ARLLTFANKYQVTVIHANI(E)	82-100	1
2,214,483	2,214,115	-0.367	(S)FALQMLEKFDENLEPYK/(Q)	209-226	1
2,214,483	2,214,128	-0.355	(K)/NLLIDWRKGEQWFMQHL(I)	359-375	1
2,214,483	2,214,239	-0.243	(A)HLDAKIIHEPYAKNP(L)	429-447	2
2,387,178	2,387,160	-0.017	(L)LIDWRKGEQWFMQHLIDGD(L)	361-379	1
2,387,178	2,387,160	-0.017	(L)IDWRKGEQWFMQHLIDGDL(A)	362-380	1
2,387,178	2,387,229	0.051	(W)REFYQHILFDFPRLSKYQ(P)	283-300	2
2,427,648	2,427,219	-0.429	(R)/DAPDELNAWKFGQTGPIVDAGI(R)	313-335	0
2,427,648	2,427,230	-0.417	(C)ASTGTDVVPYFRIFNPISQSQK/(F)	391-412	1
2,427,648	2,427,234	-0.413	(D)LRVRDNTALMEATRHGNTCAVV(I)	10-31	2
2,427,648	2,427,234	-0.413	(L)RVRDNTALMEATRHGNTCAVVI(L)	11-32	2
2,427,648	2,427,263	-0.385	(E)IELKQFNIPLMVEIVPQWDD(V)	60-79	0
2,427,648	2,427,274	-0.373	(P)LMVEIVPQWDDVPARLLTFAN(K)	69-89	0
2,477,148	2,477,141	-0.007	(L)YSDGQQTWLDELLWREFYQ(H)	269-287	0
2,477,148	2,477,188	0.040	(S)DGQQTWLDELLWREFYQHI(L)	271-289	0

**Matching peptides for
unspecific cleavage:**

Matching peptides for unspecific cleavage:

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications	missed cleavages
2,477,148	2,477,319	0.170	(P)QWDDVPARLLTFANKYQVTVI(H)	76-96		1
2,638,363	2,638,497	0.133	(E)IKIDFYLRQLKSLEIELKQFN(I)	46-66		3
2,638,363	2,638,497	0.133	(I)KIDFYLRQLKSLEIELKQFNI(P)	47-67		3
2,775,702	2,775,353	-0.349	(W)FRQDLRVRDNTALMEATR HGNTCA(V)	6-29		3
2,775,702	2,775,446	-0.255	(P)EQWKLHDDAEIKIDFYLRQLKS(L)	36-57		3
2,775,702	2,775,556	-0.146	(L)DAKIIHEPYAKNPNLKLNYPKPIV(D)	431-454		2
2,775,702	2,775,556	-0.146	(D)AKIIHEPYAKNPNLKLNYPKPIVD(L)	432-455		2
2,826,595	2,826,374	-0.221	(S)IRQCLAAIFSR SNGNFHLYSDGQQT(W)	251-275		1
2,826,595	2,826,421	-0.174	(F)RQDLRVRDNTALMEATR HGNTCAVV(I)	7-31		3
2,881,893	2,881,419	-0.474	(A)LQMLEKFVDENLEPYKQQRDFPN(I)	211-233		2
2,881,893	2,881,419	-0.474	(L)QMLEKFVDENLEPYKQQRDFPNI(D)	212-234		2
2,881,893	2,881,463	-0.429	(R)/IFNPISQSQKFDSQGN YIRKWWPE(L)	403-426		2
2,881,893	2,881,463	-0.429	(I)FNPISQSQKFDSQGN YIRKWWPEL(A)	404-427		2
2,881,893	2,881,475	-0.418	(Q)TGPIVDAGIRQMLETGWMHNRV RM(I)	326-350		2
2,881,893	2,881,478	-0.415	(N)LGIVSIRQCLAAIFSR SNGNFHLYSD(G)	246-271		1
2,881,893	2,881,495	-0.397	(L)TFANKYQVTVIHANIEIGV NELHRD(A)	86-110		1
2,881,893	2,881,536	-0.357	(I)VPQWDDVPARLLTFANKYQVTVIHA(N)	74-98		1
2,881,893	2,881,537	-0.356	(V)RMIVAMFLSKNLLIDWRKGEQWF(M)	349-371		3
2,881,893	2,881,593	-0.299	(D)DVPARLLTFANKYQVTVIHANIEIGV(N)	79-104		1
2,881,893	2,881,630	-0.263	(C)YEILNISVPQPLAVPKVQPHELIQR/(F)	157-181		1
2,932,518	2,932,520	0.002	(Q)VQTLLESHKVTVEYYH DRTIFPLGS(I)	113-137		1
2,932,518	2,932,667	0.149	(Q)PLAVPKVQPHELIQR FHTFKIPSIH(D)	167-191		2

User mass	DB mass	Δ mass (daltons)	peptide	position	modifications	missed cleavages
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Potentially modified peptides,
detected by mass difference and
conforming to rules (considering
only peptide
masses that have not matched
above):

2,537.90	1,941.94	-0.343	YQWPVGESFALQMLEK	201-216	1xTPO (THR)	
2,710.54	2,695.25	-0.281	SNGNFHLYSDGQQTWLDPELLWR	262-283	1xTPO (DEAME)	