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APPENDICES

New FindPept Search

PeptideMass

FindMod

GlycoMod

Biograph



FindPept documentation

Mass values and considered PTMs

Matching peptides for unspecific cleavage:

User mass	DB mass	Δ mass (daltons)	peptide	position modifications	misse cleavages
118.458	118.086	-0.371	V(I)	1-1	0
118.458	118.086	-0.371	(L)V(V)	16-16	0
118.458	118.086	-0.371	(V)V(A)	17-17	0
118.458	118.086	-0.371	(A)V(Y)	19-19	0
118.458	118.086	-0.371	(G)V(L)	32-32	0
118.458	118.086	-0.371	(W)V(I)	40-40	0
118.458	118.086	-0.371	(L)V(F)	54-54	0
118.458	118.086	-0.371	(P)V(N)	99-99	0
118.458	118.086	-0.371	(I)V(G)	117-117	0
118.458	118.086	-0.371	(R)V(M)	123-123	0
118.458	118.086	-0.371	(D)V(L)	135-135	0
118.458	118.086	-0.371	(R)V(L)	167-167	0
118.458	118.086	-0.371	(I)V(A)	198-198	0
118.458	118.086	-0.371	(W)V(N)	224-224	0
118.458	118.086	-0.371	(N)V(I)	227-227	0
203.685	204.098	0.412	(C)AN(I)	144-145	0
203.685	204.098	0.412	(G)NA(T)	231-232	0
203.685	204.134	0.449	(K)KG(R)	164-165	0
230.985	231.170	0.185	VI(G)	1-2	0
230.985	231.170	0.185	(G)VL(L)	32-33	0
230.985	231.170	0.185	(W)VI(T)	40-41	0
230.985	231.170	0.185	(D)VL(S)	135-136	0
230.985	231.170	0.185	(R)VL(C)	167-168	0
230.985	231.170	0.185	(N)VI(A)	227-228	0
230.985	231.170	0.185	(F)LV(V)	15-16	0
230.985	231.170	0.185	(N)LV(F)	53-54	0
230.985	231.170	0.185	(P)IV(G)	116-117	0
230.985	231.170	0.185	(G)IV(A)	197-198	0
245.650	245.186	-0.464	(V)LL(I)	33-34	0
245.650	245.186	-0.464	(L)LI(H)	34-35	0
245.650	245.186	-0.464	(M)LI(R)	92-93	0
245.650	245.186	-0.464	(P)LI(C)	188-189	0
245.650	246.145	0.494	(V)IGG(D)	2-4	0

245.650	246.145	0.494	(C)NI(N)	8-9	0
245.650	246.145	0.494	(M)NL(V)	52-53	0
245.650	246.145	0.494	(A)NI(N)	145-146	0
245.650	246.145	0.494	(I)NL(H)	147-148	0
245.650	246.145	0.494	(N)IN(E)	9-10	0
245.650	246.145	0.494	(R)LN(K)	95-96	0
245.650	246.145	0.494	(S)IN(R)	129-130	0
245.650	246.145	0.494	(N)IN(L)	146-147	0
248.706	249.072	0.365	(F)DD(E)	65-66	0
248.706	249.127	0.420	(R)VM(G)	123-124	0
250.036	250.086	0.049	(L)CAG(D)	169-171	0
279.025	279.134	0.108	(R)YP(K)	71-72	0
279.025	279.170	0.145	(R)FL(V)	14-15	0
279.025	279.170	0.145	(T)FI(C)	27-28	0
279.025	279.170	0.145	(G)LF(R)	157-158	0
327.604	327.166	-0.437	(S)NPP(I)	113-115	0
327.604	327.166	-0.437	(G)PNP(C)	202-204	0
334.884	335.120	0.235	(S)DSGG(P)	183-186	0
334.884	335.120	0.235	(C)NSD(S)	181-183	0
334.884	335.138	0.254	(I)CGGV(L)	29-32	0
353.656	354.115	0.459	(F)TMC(H)	152-154	0
353.656	354.148	0.492	(V)FGM(H)	55-57	0
356.602	356.156	-0.445	(T)AEH(C)	43-45	0
361.562	361.172	-0.390	(V)IGGD(E)	2-5	0
364.117	364.165	0.047	(R)CNK(T)	79-81	0
371.558	371.167	-0.390	(G)TNH(T)	23-25	0
371.558	371.167	-0.390	(T)NHT(F)	24-26	0
374.796	375.181	0.384	(E)PRC(A)	141-143	0
374.796	375.187	0.391	(C)AGDL(R)	170-173	0
374.796	375.187	0.391	(N)INE(R)	9-11	0
374.796	375.206	0.410	(K)MPK(K)	161-163	0
374.796	375.206	0.410	(R)KMP(K)	160-162	0
374.796	375.224	0.427	(P)IVGS(D)	116-119	0
376.236	376.171	-0.064	(D)EDI(M)	88-90	0
376.236	376.226	-0.009	(D)IML(I)	90-92	0
376.236	376.226	-0.009	(I)MLI(R)	91-93	0
380.229	380.218	-0.011	(H)TFI(C)	26-28	0
383.307	383.204	-0.103	(I)NLH(N)	147-149	0
383.307	383.204	-0.103	(N)LHN(F)	148-150	0
387.660	387.224	-0.436	(I)APLS(L)	106-109	0
387.660	387.260	-0.399	(L)VAV(Y)	16-19	0

387.660	387.271	-0.388	(G)RVL(C)	166-168	0
387.660	388.129	0.468	(A)EHC(A)	44-46	0
400.901	401.214	0.313	(D)EPR(C)	140-142	0
400.901	401.276	0.374	(F)LVVA(V)	15-18	0
400.901	401.276	0.374	(G)GVLL(I)	31-34	0
400.901	401.287	0.386	(M)LIR(L)	92-94	0
400.901	401.287	0.386	(L)IRL(N)	93-95	0
402.559	402.246	-0.313	(I)VARG(P)	198-201	0
402.559	402.246	-0.313	(I)RLN(K)	94-96	0
402.559	402.246	-0.313	(S)INR(R)	129-131	0
402.559	402.257	-0.301	(C)ARR(R)	47-49	0
406.877	407.156	0.279	(T)SWD(E)	85-87	0
406.877	407.159	0.282	(A)TCSP	233-236	0
406.877	407.229	0.351	(R)YPK(K)	71-73	0
409.629	409.169	-0.460	(F)MRC(N)	77-79	0
409.629	409.208	-0.420	(E)KFD(D)	63-65	0
418.105	418.175	0.070	(N)PCAQ(P)	204-207	0
418.105	418.175	0.070	(P)CAQP(N)	205-208	0
418.105	418.204	0.099	(I)NER(R)	10-12	0
418.105	418.208	0.103	(D)WVN(N)	223-225	0
422.354	422.152	-0.202	(N)SDSGG(P)	182-186	0
422.354	422.152	-0.202	(C)NSDS(G)	181-184	0
423.605	423.118	-0.486	(G)GDEC(N)	4-7	0
423.605	423.224	-0.381	(S)EKF(D)	62-64	0
432.182	432.172	-0.009	(S)DSGGP(L)	183-187	0
432.182	432.220	0.038	(E)QER(Y)	68-70	0
434.284	434.254	-0.029	(F)RKM(P)	159-161	0
446.422	446.218	-0.204	(E)PRCA(N)	141-144	0
446.422	446.247	-0.175	(G)RRD(S)	176-178	0
450.763	450.282	-0.480	(L)FRK(M)	158-160	0
450.763	451.255	0.492	(V)VAVY(E)	17-20	0
463.248	463.178	-0.069	(V)NNSE(H)	100-103	0
463.248	463.197	-0.051	(E)CNIN(E)	7-10	0
463.248	463.208	-0.039	(P)RCAN(I)	142-145	0
463.248	463.255	0.007	(K)PALY(T)	211-214	0
465.332	465.176	-0.155	(A)GNATC(S)	230-234	0
465.332	465.213	-0.119	(R)CNKT(R)	79-82	0
467.302	467.214	-0.088	(A)VYEG(T)	19-22	0
467.302	467.225	-0.077	(Q)ERY(P)	69-71	0
467.302	467.250	-0.051	(P)ALYT(S)	212-215	0
469.097	469.193	0.095	(V)YEGT(N)	20-23	0

593.466	593.260	-0.206	(P)IVGSDC(R)	116-121	0
599.887	600.237	0.350	(V)NNSEH(I)	100-104	0
604.072	604.337	0.265	(E)DIMLI(R)	89-93	0
611.514	611.326	-0.188	(V)ARGPNP(C)	199-204	0
622.750	623.245	0.495	(I)AGNATCS(P)	229-235	0
635.562	635.215	-0.346	(F)DDEQE(R)	65-69	0
635.562	635.288	-0.273	(I)DVLSSD(E)	134-139	0
640.563	640.188	-0.375	(R)DSCNSD(S)	178-183	0
642.139	642.325	0.186	(E)HCARR(R)	45-49	0
644.023	644.315	0.292	(I)NLHNF(T)	147-151	0
647.895	647.413	-0.482	(R)FLVVAV(Y)	14-19	0
647.895	648.329	0.433	(C)RVMGW(G)	122-126	0
650.241	650.245	0.003	(G)GDECNI(N)	4-9	0
650.241	650.297	0.055	(V)MGWGS(I)(N)	124-129	0
650.241	650.326	0.084	(K)TRTSW(D)	82-86	0
652.353	652.389	0.035	(L)HGIVAR(G)	195-200	0
654.470	654.357	-0.113	(A)QPNKPA(L)	207-212	0
654.470	654.357	-0.113	(C)AQPNKP(A)	206-211	0
656.948	657.427	0.478	(D)LRGRR(D)	173-177	0
661.436	661.280	-0.156	(F)TMCHGL(F)	152-157	0
661.436	661.367	-0.068	(H)CARRR(M)	46-50	0
666.851	667.320	0.468	(I)HPEW(I)	36-40	0
670.277	670.280	0.002	(Y)FMRCN(K)	76-80	0
670.277	670.315	0.038	(N)NSEHIA(P)	101-106	0
674.583	674.391	-0.192	(F)ICGGVLL(I)	28-34	0
674.583	674.391	-0.192	(I)CGGVLLI(H)	29-35	0
676.161	676.290	0.128	(D)DEQER(Y)	66-70	0
676.161	676.305	0.143	(E)GTNHTF(I)	22-27	0
679.088	679.366	0.278	(L)VVAVYE(G)	16-21	0
679.088	679.377	0.289	(S)EHIAPL(S)	103-108	0
681.153	681.262	0.109	(R)RDSCNS(D)	177-182	0
681.153	681.335	0.182	(L)IHPEW(V)	35-39	0
681.153	681.368	0.214	(C)ANINLH(N)	144-149	0
683.564	683.372	-0.191	(S)NPPIVGS(D)	113-119	0
683.564	683.372	-0.191	(P)SNPPIVG(S)	112-118	0
686.609	686.293	-0.316	(R)GPNPCAQ(P)	201-207	0
686.609	686.304	-0.305	(T)AEHCAR(R)	43-48	0
686.609	686.383	-0.225	(W)VNNVIAG(N)	224-230	0
689.838	689.388	-0.450	(R)RRMNL(V)	49-53	0
689.838	689.399	-0.439	(C)ARRRM(N)	47-51	0
689.838	690.288	0.449	(S)DEPRCA(N)	139-144	0

689.838	690.305	0.467	(L)SSDEPR(C)	137-142	0
689.838	690.313	0.474	(P)PIVGSDC(R)	115-121	0
689.838	690.335	0.497	(P)RCANIN(L)	142-147	0
695.942	696.338	0.396	(H)TFICGGV(L)	26-32	0
698.279	698.310	0.031	(C)NEELHG(I)	191-196	0
698.279	698.387	0.108	(R)YPKKY(F)	71-75	0
701.915	702.401	0.485	(W)GSINRR(I)	127-132	0
701.915	702.414	0.499	(R)RIDVLS(S)	132-137	0
722.030	722.361	0.331	(R)CNKTRT(S)	79-84	0
724.050	724.326	0.276	(D)EQERY(P)	67-71	0
724.050	724.374	0.323	(A)NINLHN(F)	145-150	0
731.173	731.299	0.126	(I)YDYRD(W)	218-222	0
732.842	732.361	-0.481	(M)CHGLFR(K)	154-159	0
732.842	732.367	-0.474	(G)TNHTFI(C)	23-28	0
732.842	732.379	-0.463	(G)WGSINR(R)	126-131	0
732.842	732.405	-0.437	(A)RRRMN(L)	48-52	0
734.499	734.329	-0.170	(N)HTFICGG(V)	25-31	0
734.499	734.329	-0.169	(T)NHTFIC(G)	24-29	0
736.116	736.257	0.140	(S)CNSDSGGP(L)	180-187	0
736.116	736.329	0.213	(V)IAGNATCS(P)	228-235	0
736.116	736.388	0.271	(L)VAVYEG(T)	16-22	0
738.390	738.357	-0.033	(D)YRDWV(N)	220-224	0
738.390	738.367	-0.023	(V)VAVYEGT(N)	17-23	0
738.390	738.414	0.024	(E)ELHGIVA(R)	193-199	0
745.649	745.355	-0.294	(G)GPLICNE(E)	186-192	0
745.649	745.363	-0.286	(I)NLHNFT(M)	147-152	0
745.649	745.373	-0.276	(N)SDSGGPLI(C)	182-189	0
747.119	747.382	0.262	(V)LCAGDLR(G)	168-174	0
749.363	749.361	-0.001	(P)IVGSDCR(V)	116-122	0
749.363	749.365	0.002	(R)VMGWGSI(N)	123-129	0
751.370	751.338	-0.032	(D)CRVMGW(G)	121-126	0
751.370	751.428	0.058	(H)GLFRKM(P)	156-161	0
764.791	764.310	-0.481	(T)SWDEDI(M)	85-90	0
764.791	764.331	-0.460	(I)DVLSSDE(P)	134-140	0
764.791	764.340	-0.451	(V)MGWGSIN(R)	124-130	0
764.791	764.419	-0.372	(K)PALYTSI(Y)	211-217	0
766.531	766.409	-0.121	(N)SEHIAPL(S)	102-108	0
766.531	766.409	-0.121	(S)EHIAPLS(L)	103-109	0
770.460	770.404	-0.055	(P)SNPPIVGS(D)	112-119	0
776.820	777.320	0.499	(S)SDEPRCA(N)	138-144	0
785.775	785.372	-0.402	(V)ARGPNPCA(Q)	199-206	0

787.992	787.497	-0.494	(F)RKMPKK(G)	159-164	0
787.992	788.456	0.463	(R)RRMNLV(F)	49-54	0
795.928	796.289	0.360	(R)RDSCNSD(S)	177-183	0
795.928	796.358	0.430	(K)PVNNSEH(I)	98-104	0
795.928	796.420	0.491	(N)EELHGIV(A)	192-198	0
797.397	797.477	0.079	(H)IAPLSLPS(N)	105-112	0
797.397	797.536	0.138	(M)PKKGRVL(C)	162-168	0
803.419	803.379	-0.039	(Y)RDWVNN(V)	221-226	0
803.419	803.389	-0.029	(V)LSSDEPR(C)	136-142	0
803.419	803.419	0.000	(P)RCANINL(H)	142-148	0
803.419	803.442	0.022	(C)ARRRMN(L)	47-52	0
803.419	803.456	0.036	(K)KGRVLCAG(D)	164-171	0
803.419	803.492	0.072	(P)KKGRVLC(A)	163-169	0
803.419	803.514	0.094	(R)RFLVVAV(Y)	13-19	0
806.441	806.335	-0.106	VIGGDECN(I)	1-8	0
806.441	806.441	0.000	(P)NKPALYT(S)	209-215	0
806.441	806.463	0.022	(L)HGIVARGP(N)	195-202	0
806.441	806.471	0.029	(L)FRKMPK(K)	158-163	0
829.266	829.475	0.209	(A)GDLRGRR(D)	171-177	0
833.202	833.343	0.141	(K)YFMRCN(K)	75-80	0
833.202	833.382	0.180	(V)IAGNATCSP	228-236	0
833.202	833.397	0.195	(N)HTFICGGV(L)	25-32	0
833.202	833.407	0.205	(P)LICNEEL(H)	188-194	0
835.666	835.377	-0.289	(G)TNHTFIC(G)	23-29	0
835.666	835.398	-0.268	(N)VIAGNATCS(P)	227-235	0
839.941	839.546	-0.394	(L)IRLNKPV(N)	93-99	0
839.941	840.367	0.425	(G)PNPCAQPN(K)	202-209	0
852.435	852.400	-0.035	(D)YRDWVN(N)	220-225	0
852.435	852.410	-0.025	(V)VAVYEGTN(H)	17-24	0
854.632	854.419	-0.213	(N)PCAQPNKP(A)	204-211	0
854.632	854.488	-0.143	(E)RYPKKY(F)	70-75	0
909.243	909.442	0.199	(K)PVNNSEHI(A)	98-105	0
909.243	909.479	0.235	(H)RKSEKFD(D)	59-65	0
914.633	914.404	-0.229	(L)ICNEELHG(I)	189-196	0
914.633	914.404	-0.229	(I)CNEELHGI(V)	190-197	0
917.588	917.379	-0.209	(I)YDYRDW(V)	218-223	0
917.588	917.415	-0.173	(S)DEPRCANI(N)	139-146	0
917.588	917.436	-0.151	(Y)TSIYDYR(D)	215-221	0
919.598	919.419	-0.179	VIGGDECNI(N)	1-9	0
919.598	919.547	-0.050	(E)LHGIVARGP(N)	194-202	0
919.598	919.555	-0.043	(G)LFRKMPK(K)	157-163	0

921.599	921.402	-0.196	(S)WDEDIML(I)	86-92	0
921.599	921.504	-0.095	(A)PLSLPSNPP(I)	107-115	0
923.936	923.520	-0.416	(L)SLPSNPPIV(G)	109-117	0
923.936	924.399	0.462	(L)YTSIYDY(R)	214-220	0
926.241	926.488	0.246	(G)IVARGPNPC(A)	197-205	0
928.739	928.576	-0.162	(K)MPKKGRVL(C)	161-168	0
941.007	941.487	0.480	(P)CAQPNKPAL(Y)	205-213	0
942.512	942.479	-0.032	(C)ANINLHNF(T)	144-151	0
948.883	948.443	-0.440	(R)MNLVFGMH(R)	51-58	0
948.883	948.501	-0.382	(C)NINERRF(L)	8-14	0
948.883	948.526	-0.356	(E)QERYPKK(Y)	68-74	0
950.827	950.352	-0.475	(I)GGDECNINE(R)	3-11	0
950.827	950.519	-0.307	(F)LVVAVYEGT(N)	15-23	0
952.356	952.390	0.034	(G)RRDSCNSD(S)	176-183	0
952.356	952.489	0.132	(I)HPEWVITA(E)	36-43	0
952.356	952.630	0.274	(M)LIRLNKPV(N)	92-99	0
961.996	961.504	-0.492	(L)VFGMHRKS(E)	54-61	0
961.996	962.425	0.428	(N)SDSGGPLICN(E)	182-191	0
961.996	962.425	0.428	(S)CNSDSGGPLI(C)	180-189	0
961.996	962.425	0.428	(C)NSDSGGPLIC(N)	181-190	0
961.996	962.495	0.498	(D)LRGRRDSC(N)	173-180	0
964.330	964.449	0.119	(F)TMCHGLFR(K)	152-159	0
966.144	966.443	0.298	(D)YRDWVNN(V)	220-226	0
966.144	966.525	0.381	(N)SEHIAPLSL(P)	102-110	0
966.144	966.577	0.433	(R)RFLVVAVY(E)	13-20	0
967.579	967.427	-0.152	(Y)DYRDWVN(N)	219-225	0
967.579	967.484	-0.094	(N)NSEHIAPLS(L)	101-109	0
967.579	967.485	-0.093	(R)RMNLVFGM(H)	50-57	0
969.157	969.534	0.376	(Y)PKKYFMR(C)	72-78	0
971.775	971.582	-0.193	(M)PKKGRVLC(A)	162-170	0
976.604	976.452	-0.152	(V)NNVIAGNATC(S)	225-234	0
976.604	976.496	-0.107	(R)YPKKYFM(R)	71-77	0
976.604	976.546	-0.057	(S)EHIAPLSLP(S)	103-111	0
976.604	976.576	-0.027	(H)GLFRKMPK(K)	156-163	0
977.865	977.436	-0.429	(V)LSSDEPRCA(N)	136-144	0
982.214	982.484	0.269	(L)PSNPPIVGSD(C)	111-120	0
984.059	984.478	0.419	(P)EWWITA(EH)	38-45	0
985.281	985.540	0.258	(C)HGLFRKMP(K)	155-162	0
988.219	988.440	0.221	(P)SNPPIVGSDC(R)	112-121	0
990.286	990.525	0.239	(Q)PNKPALYTS(I)	208-216	0
998.432	998.506	0.074	(T)AEHCARRR(M)	43-50	0

998.432	998.611	0.178	(S)INRRIDVL(S)	129-136	0
1001.042	1000.620	-0.422	(F)RKMPKKGR(V)	159-166	0
1001.042	1000.634	-0.408	(D)IMLIRLNK(P)	90-97	0
1001.042	1001.541	0.499	(C)AQPKNPALY(T)	206-214	0
1004.750	1004.435	-0.314	(S)DSGGPLICNE(E)	183-192	0
1004.750	1004.447	-0.303	(S)SDEPRCANI(N)	138-146	0
1004.750	1004.508	-0.241	(W)DEDIMLIR(L)	87-94	0
1010.528	1010.418	-0.109	(V)GSDCRVMGW(G)	118-126	0
1010.528	1010.418	-0.109	(G)SDCRVMGWG(S)	119-127	0
1010.528	1010.418	-0.109	(S)DCRVMGWGS(I)	120-128	0
1010.528	1010.484	-0.044	(V)ARGPNPCAQP(N)	199-208	0
1013.306	1013.472	0.166	(I)CNEELHGIV(A)	190-198	0
1016.088	1015.594	-0.493	(C)ARRRMNLV(F)	47-54	0
1016.088	1016.447	0.359	(I)YDYRDWV(N)	218-224	0


Peptides are displayed with the adjoining residues before cleavage greyed out and in parentheses.

Unmatched masses:

11.370
21.382
29.998
35.814
38.528
41.135
55.579
57.842
66.422
68.531
70.556
74.623
80.786
82.882
93.177
134.850
151.340
157.559
193.817
200.368
227.615
238.496
242.804
265.954

268.046
298.730
309.154
325.594
354.872
395.238
453.798
470.631
522.331
527.869
566.944
577.922
586.024
668.354
672.344
827.184
831.225

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Workunit: P002378 Title:

 1 236

Go to: [Template Selection] [Alignment] [Modelling Log] [Evaluation]

Print/Save this page as Model Details:  Segment 1

Model info:

modelled residue range: 1 to 236

based on template 2aiqA (1.54 Å)

Sequence Identity [%]: 53

Evaluate: 1.52e-66

display model: as pdb - as DeepView project

download model: as pdb - as Deepview project - as text

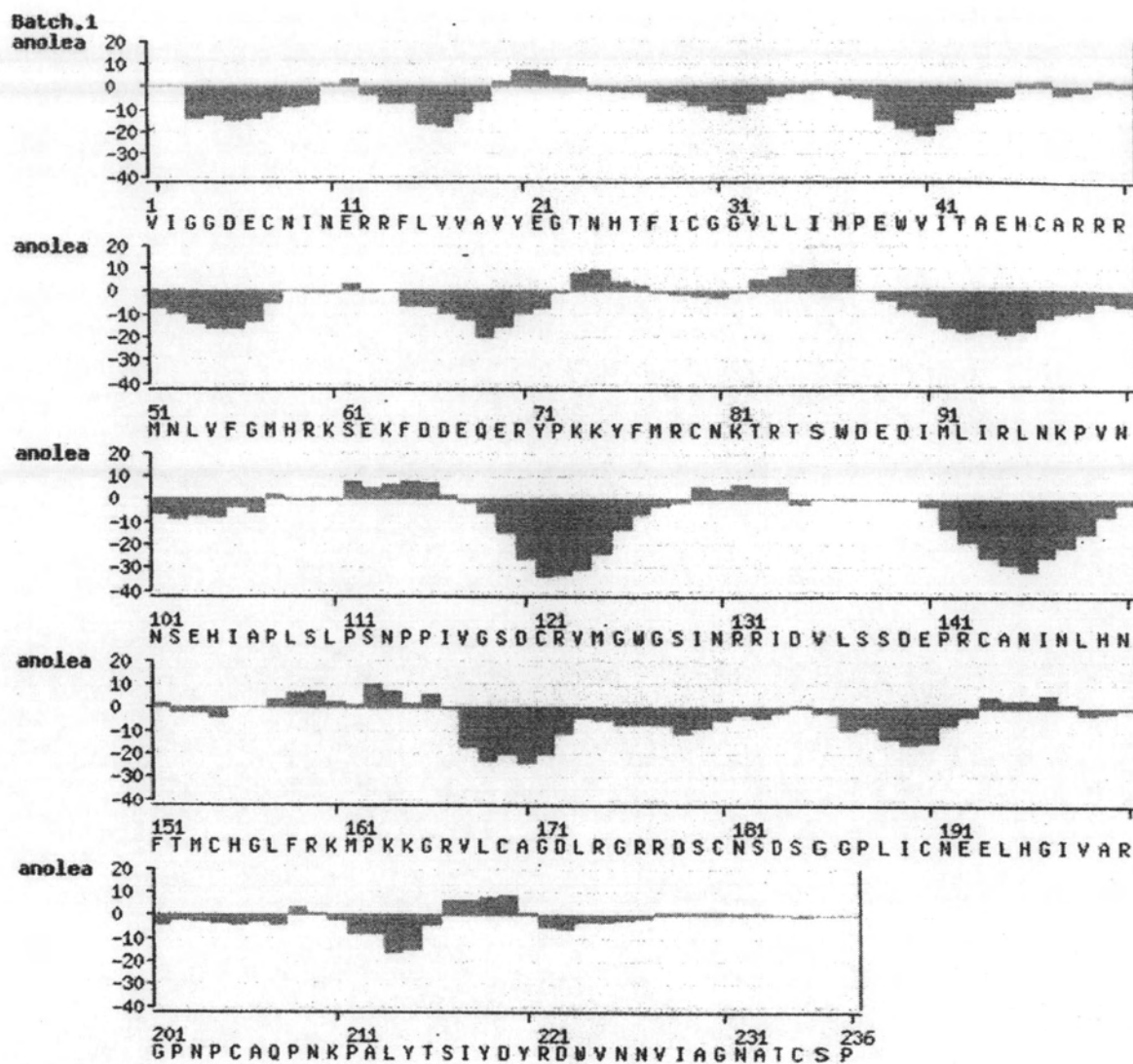
Alignment  [top]

TARGET	1	VIGGDECN	INERRFLVVA	VYEGTNHTPI	CGGVLLIHPE	WVITAEHCAR
2aiqA	16	viggdecn	inehrflal-	vyangs---	1 cggtl-inqe	wvltarhcdr

TARGET		SSS	SSSSS S	SSSS	S SSSS
2aiqA		SSS	SSSS SSS S	S SSSSS S S SSSS	

TARGET	49	RRMNLVFGMH	RKSEKFDDEQ	ERYP-KKYFM	RCNKTRTSWD	EDIMLIRLNK
2aiqA	62	gnmriylgmh	nlkvinkdal	rpfpekyfc	lntrndtiwd	kdimlirlnr

TARGET		SSSS	S SS	SSSSS
2aiqA		SSSS	S SSSSSSSS	SSSSSS



Modelling log [\[top\]](#)

3.70 (SP3)

Loading Template: 2aiqA.pdb

Loading Raw Sequence

Aligning Raw Sequence

Refining Raw Sequence Alignment

ProModII: doing simple assignment of backbone

ProModII: adding blocking groups

Adding Missing Sidechains

AddPolar H

BuildDeletedLoopsModel

```

TARGET 98 PVNNSEHIAP LSLPSNPPIV GSDCRVMGWG SINRRIDVLS SDEPRCANIN
2aiqA 111 pvrnsahiap lslpsnppsv gsvcrimgwg titspnatlp -dvphcanin

TARGET                                     sssssss sssssss
2aiqA                                     sssssss sssssss

TARGET 148 LHNFTMCHGL FRKMPKGRV LCAGDLRGRR DSCNSDSGGP LICNEELHGI
2aiqA 162 ildyavcqaa ykglA--att lcagileggk dtckgdsggp licngqfqqi

TARGET      ss hhhhhh          ss ssss          ss sss sssss
2aiqA      ss hhhhhh          ss ssss          ss sss sssss

TARGET 198 VARGPNPCAQ PNKPALYTSI YDYRDWVNNV IAGN--ATCS P
2aiqA 213 lsvggnpcaq prkpgiytkv fdytdwqsi isgntdatcp p-

TARGET      ss          ssssss h h hh h
2aiqA      ss          ssssss h hhhhhh h

```

Anolea / Gromos / Verify3D [top]

anolea: on off gromos: on off verify3d: on off

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ScanProsite Results Viewer

This view shows ScanProsite results together with ProRule-based predicted intra-domain features (help).

[show hits of frequently occurring signatures](#)

Hits for all PROSITE (release 20.0) motifs on sequence USERSEQ1 :

found: 17 hits in 1 sequence

USERSEQ1 (236 aa)

```
VIGGDECINERRFLVVAVYEGTnHTFIcGGVLLIHPEWVITAEHCARRRMLVFGMHRKSEKFD
EQERYPKKYPMRCNKTRTSWDEDIMLIRLNKPVNNEHIAPLSLP--SN
PPIVGSDCRVMGWGSINRRIdVLSSDEPRCANINLHNFTnCHGLFRKMPKGRVLCAGDL
RGRDSCNSDsgGPLIC----NEELHGIVARGpNPcAQPKNKALYTSIYDyRDWVNNVIA
```

ruler: 1 100 200 300 400 500 600 700 800 900 1000

hits by profiles: [1 hit (by 1 profile) on 1 sequence]

Hits by PS50240 **TRYPSIN_DOM** Serine proteases, trypsin domain profile :

USERSEQ1  (236 aa)

1 - 229: score = 27.296

```
VIGGDECINERRFLVVAVYEGTnHTFIcGGVLLIHPEWVITAEHC-----ARRRMLV
GHRKSEKFDDEQERYPKKYPMRCNKTRTSWDEDIMLIRLNKPVNNEHIAPLSLP--SN
PPIVGSDCRVMGWGSINRRIdVLSSDEPRCANINLHNFTnCHGLFRKMPKGRVLCAGDL
RGRDSCNSDsgGPLIC----NEELHGIVARGpNPcAQPKNKALYTSIYDyRDWVNNVIA
```

Predicted features:

DISULFID	29	46	By similarity	[condition: C-x*-C]	
ACT_SITE	45		Charge relay system (By similarity)	[condition: H]	[group: 1]
ACT_SITE	89		Charge relay system (By similarity)	[condition: D]	[group: 1]
DISULFID	121	190	By similarity	[condition: C-x*-C]	
DISULFID	154	169	By similarity	[condition: C-x*-C]	
DISULFID	180	205	By similarity	[condition: C-x*-C]	
ACT_SITE	184		Charge relay system (By similarity)	[condition: S]	[group: 1]

hits by patterns with a high probability of occurrence or by user-defined patterns: [16 hits (by 7 distinct

patterns) on 1 sequence]

USERSEQ1  (236 aa)

PS00008 **MYRISTYL** *N-myristoylation site :*

3 - 8: GGdeCN

22 - 27: GTnhTF

230 - 235: GNatCS

PS00001 **ASN_GLYCOSYLATION** *N-glycosylation site :*

24 - 27: NHTF

80 - 83: NKTR

100 - 103: NNSE

150 - 153: NFTM

231 - 234: NATC

PS00005 **PKC_PHOSPHO_SITE** *Protein kinase C phosphorylation site :*

61 - 63: SeK

PS00007 **TYR_PHOSPHO_SITE** *Tyrosine kinase phosphorylation site :*

63 - 71: KfddEgerY

PS00006 **CK2_PHOSPHO_SITE** *Casein kinase II phosphorylation site :*

84 - 87: TswD

85 - 88: SwdE

137 - 140: SedE

216 - 219: SiyD

PS00009 **AMIDATION** *Amidation site :*

174 - 177: rGRR

PS00004 **CAMP_PHOSPHO_SITE** *cAMP- and cGMP-dependent protein kinase phosphorylation site :*

176 - 179: RRdS


Legend:



disulfide bridge active site other 'ranges' other sites

horizontal scaling: 0.6
do not show text labels:
do not show sites in hits:
do not show ranges in hits:

redisplay

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BIOGRAPHY

Mr. Piboon Pornmanee was born on March 20, 1975 in Phattalung province, Thailand. He graduated with a Bachelor's Degree in Medical technology from Chulalongkorn University in 1997, Master's Degree in Biotechnology from Chulalongkorn University in 2001 and continued his Ph.D study in Biotechnology Program in the Faculty of Science Chulalongkorn University and complete the program in 2007.