

Supplementary Material

Quantitative proteomic analysis of biogenesis-based classification for extracellular vesicles

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Table S1. Transitions used for quantification

Table S2. AF4 conditions and method

Figure S1. The amino acid sequences of GP1, GP2, PLin, and PLout QconCATs

Table S1. Transitions used for quantification

Protein	Peptide	L/H	Precursor (m/z)	Product Ions (m/z)		
				1	2	3
Integrin alpha-IIb	FGSAIAPLGDLDR	L	666.4	688.4 (y6)	785.4 (y7)	856.5 (y8)
		H	674.3	697.3 (y6)	795.4 (y7)	867.4 (y8)
	GEAQVWTQLLR	L	650.9	816.5 (y6)	915.5 (y7)	1043.6 (y8)
		H	659.3	827.4 (y6)	927.5 (y7)	1057.6 (y8)
Integrin beta-3	VLEDRPLSDK	L	586.3	559.3 (y5)	715.4 (y6)	830.4 (y7)
		H	593.3	565.3 (y5)	725.4 (y6)	841.4 (y7)
	GSGDSSQVTQVSPQR	L	766.9	815.4 (y7)	914.5 (y8)	1042.6 (y9)
		H	777.3	827.4 (y7)	927.5 (y8)	1057.5 (y9)
GP Ib alpha	GLGELQELYLK	L	631.9	665.4 (y5)	793.4 (y6)	906.5 (y7)
		H	638.3	671.4 (y5)	801.4 (y6)	915.5 (y7)
	GVLQGHLESSR	L	591.8	728.4 (y6)	785.4 (y7)	913.4 (y8)
		H	600.3	739.3 (y6)	797.4 (y7)	927.4 (y8)
GP Ib beta	LSLTDPLVAER	L	607.3	684.4 (y6)	799.4 (y7)	900.5 (y8)
		H	614.3	693.4 (y6)	809.4 (y7)	911.4 (y8)
	LLPYLADELRL	L	666.4	732.4 (y6)	845.4 (y7)	1008.5 (y8)
		H	673.3	741.3 (y6)	855.4 (y7)	1019.5 (y8)
GP V	SIAPGAFDR	L	467.2	508.3 (y4)	565.3 (y5)	662.3 (y6)
		H	473.2	515.2 (y4)	573.2 (y5)	671.3 (y6)
	LPNLSSLTLR	L	600.9	676.4 (y6)	763.4 (y7)	876.5 (y8)
		H	608.3	685.4 (y6)	773.4 (y7)	887.5 (y8)
GP IX	GHGLTALPALPAR	L	637.4	737.5 (y7)	808.5 (y8)	909.6 (y9)
		H	646.3	747.4 (y7)	819.5 (y8)	921.5 (y9)
	TPEALLQVR	L	513.8	628.4 (y5)	699.5 (y6)	828.5 (y7)
		H	520.3	637.4 (y5)	709.4 (y6)	839.5 (y7)
P2Y purinoceptor 1	YSGVVYPLK	L	513.3	520.3 (y4)	619.4 (y5)	718.4 (y6)
		H	518.3	525.3 (y4)	625.4 (y5)	725.4 (y6)
	VYATYQVTR	L	550.8	666.4 (y5)	767.4 (y6)	838.4 (y7)
		H	557.3	675.3 (y5)	777.4 (y6)	849.4 (y7)
P2Y purinoceptor 12	IPYTLSQTR	L	539.8	604.3 (y5)	705.4 (y6)	868.5 (y7)
		H	546.3	613.3 (y5)	715.4 (y6)	879.4 (y7)
	SNFIIFLK	L	491.3	520.3 (y4)	633.4 (y5)	780.5 (y6)
		H	496.3	525.3 (y4)	639.4 (y5)	787.5 (y6)
EHD4	SISVIDSPGILSGEK	L	751.4	800.5 (y8)	887.5 (y9)	1002.5 (y10)
		H	759.4	809.4 (y8)	897.5 (y9)	1013.5 (y10)
	LDISDEFSEAIK	L	683.8	547.3 (y5)	694.4 (y6)	823.4 (y7)
		H	690.3	553.3 (y5)	701.4 (y6)	831.4 (y7)
IgG Fc receptor II-a	AAQFEPPGR	L	486.7	426.2 (y4)	555.3 (y5)	702.4 (y6)
		H	493.2	433.2 (y4)	563.3 (y5)	711.3 (y6)
	VTFFQNGK	L	470.7	446.2 (y4)	593.3 (y5)	740.4 (y6)
		H	476.2	453.2 (y4)	601.3 (y5)	749.3 (y6)
Integrin alpha-2	FVQGLDIGPTK	L	587.8	630.3 (y6)	743.4 (y7)	800.5 (y8)
		H	594.3	637.3 (y6)	751.4 (y7)	809.4 (y8)

	IGQTSSSVSFK	L	570.8	654.3 (y6)	741.4 (y7)	842.4 (y8)
		H	577.3	661.3 (y6)	749.4 (y7)	851.4 (y8)
P-selectin	YTDLVAIQNK	L	582.8	573.3 (y5)	672.4 (y6)	785.5 (y7)
		H	589.3	581.3 (y5)	681.4 (y6)	795.5 (y7)
	NEIDYLNK	L	504.8	537.3 (y4)	652.3 (y5)	765.4 (y6)
		H	510.2	543.3 (y4)	659.3 (y5)	773.4 (y6)
CYP5A1	DELNGFFNK	L	542.3	612.3 (y5)	726.4 (y6)	839.4 (y7)
		H	548.2	619.3 (y5)	735.3 (y6)	849.4 (y7)
	QVLVENFSNFTNR	L	784.4	885.4 (y7)	999.5 (y8)	1128.5 (y9)
		H	794.4	897.4 (y7)	1013.4 (y8)	1143.5 (y9)
COX-2	TVTINASSSR	L	518.3	507.3 (y5)	621.3 (y6)	734.4 (y7)
		H	525.3	515.2 (y5)	631.3 (y6)	745.3 (y7)
	VSQASIDQSR	L	545.8	618.3 (y5)	705.4 (y6)	776.4 (y7)
		H	553.3	627.3 (y5)	715.3 (y6)	787.4 (y7)
IgG Fc receptor I	ITSASVNDSGEYR	L	699.8	726.3 (y6)	840.3 (y7)	939.4 (y8)
		H	708.3	735.3 (y6)	851.3 (y7)	951.4 (y8)
	LVYINVLYYR	L	601.8	713.4 (y5)	827.4 (y6)	990.5 (y7)
		H	608.3	721.4 (y5)	837.4 (y6)	1001.5 (y7)

Transitions are listed for both unlabeled, light (L) and fully ¹⁵N-labeled, heavy (H) peptides. All precursors were +2 charge and product ions were +1 charge. Additionally, y-ion information is included.

Table S2. AF4 conditions and method

An Eclipse DualTec (Wyatt Technology, Santa Barbara, CA, USA) equipped with a degasser (Gastorr TG-14, Flom Co., Ltd, Tokyo, Japan), 1100-series isocratic pump (Agilent Technologies, Santa Clara, CA), 1260 ALS series autosampler (Agilent Technologies), 1200 series UV-vis absorbance diode array detector (Agilent Technologies), and a DAWN HELEOS II multi-angle light scattering detector with QELS operating at a laser wavelength of 661 nm (Wyatt Technology).

UV absorbance is measured at 280 nm using an extinction coefficient of 0.667 mL/(mg cm). The DAWN HELEOS is calibrated using toluene at the 90° detector, and the other 17 detectors are normalized using a Rayleigh scatterer (bovine serum albumin) in water. The 12-detector position is used for the online QELS detector providing DLS measurements at an angle of 99.9 °.

Fractionation experiments are conducted using the following experimental method: MALS cell temperature set at 25 °C, mobile phase consisting of phosphate buffered saline (PBS), short channel (145 mm length, Wyatt Technology) with a 350 µm trapezoidal mylar spacer, a 10 kDa (kg/mol) molecular weight cut-off regenerated cellulose membrane and an injection volume of 80 µL.

The fractionation method is summarized below in tabular format.

Type of flow	Duration (min)	Cross-Flow or Focus flow (mL/min)	Elution flow (mL/min)
Elution	3	-	0.5
Focus	2	1.5	-
Focus + injection (0.2 mL/min)	5	1.5	-
Elution	40	0.5-0.05 Linear decrease	0.5
Elution	10	0	0.5

AF4 data is collected and analyzed using OpenLab (Agilent Technologies) and Astra 6.1.4.25 (Wyatt Technology) software.

Figure S1. The amino acid sequences of GP1, GP2, PLin, and PLout QconCATs

GP1. Number of amino acids: 585; Molecular weight: 64 670.02; Theoretical pI: 9.93; Grand average of hydropathicity (GRAVY): -0.327.

MSAIGLKIGDTVSFSEAKVRGAPQEKEKSFTIKPVGFKDSLIVQTQLYGRFGSAIAPLG
DLDRDGYNDIPLSLPRGEAQVWTQLLRAL EERAVWVL RDVAQVPADR SAYAGARAAA
RLSLTDPLVAERAGTDESALSQGRGQDLLSTVSIRYSGHSLAEVGRVYLFLQPRGPHA
LGGPSGRGQVLVFLGQSEGLRSRPSQVDDAVVRFQYYEDSSGKSILYVVDVSNRLT
SLPLGALRGLGELQELYLKGNELKTLPPGLLTPTPKLEKLSLWLEDRTPEALLQVRAAS
PSLWVDARGHGLTALPALPARTRHLLLESTKKTIPELDQPPKLRGVLQGHLESSRNDP
FLHRNHIRSIAPGAFDRLPNLSSLTL SRNH LAFLPEQPSRLQDPVLVVSRLSGLWPVSE
ARVLEDRPLSDKSGSDSSQVTQVSPQRIALRLRLVPLRAWLAGRPERAPYRDLERAR
AKWDTANNPLYKEATSTFPALRGRLLPYLAEDELRAAAPGRLSRNKITHLPGALLDKI
VLLEQERARAKWDTHYAQSLRKWNQPVNLSRLRYLGVTLSPRLSALPQKLAAALEHH
HHHH

Peptides (marked red) with 6 amino acid residues flanking sequences on both sides (marked black) from 6 proteins listed below were randomly concatenated in GP1 sequence. 7 Cys and 2 Met were replaced with Ala and Ile, respectively (marked blue)

in the flanking sequences. 6 x His tag and linker sequence (marked orange) was from expression vector.

Integrin alpha-IIb (500 000 to 800 000 copies/platelet) (single-pass)

1. LAEVGRVYLFLQPRGPHALG
2. TQLYGRFGSAIAPLGDLDRDGYNDI
3. GGPSGRGQVLVFLGQSEGLRSRPSQV
4. PLSLPRGEAQVWTQLLRALEERA
5. PEQPSRLQDPVLVVSRLSGLWP

Integrin beta-3 (500 000 to 800 000 copies/platelet) (single-pass)

- 1/2. PVSEARVLEDRPLSDKSGDSSQVTQVSPQRIALRLR
- 3/4. SCMGLKIGDTVFSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQ
5. DDQVVRFQYYEDSSGKSILYVV
6. ERARAKWDTANNPLYKEATSTF
7. ERARAKWDTHYAQSLRKWNQPV

platelet glycoprotein Ib alpha chain (60 000 copies/platelet) (single-pass)

- 1/2/3. DVSFNRLTSLPLGALRGLGELQELYLKGNELKTLPPGLLTPTPKLEKLSL
- 4/5. LESTKKTIPELDQPPKLRGVLQGHLESSRNDPFLH
6. ALSQGRGQDLLSTVSIRYSGHSL

platelet glycoprotein Ib beta chain (60 000 copies/platelet) (single-pass)

1. RLVPLRAWLAGRPERAPYRDL
2. PALRGRLLPYLAEDELRAACAPG
3. ARAAARLSLTDPLVAERAGTDES
4. AVWVLRDVAQVPADR SAYCGA

platelet glycoprotein IX (60 000 copies/platelet) (single-pass)

1. LWVDCRGHGLTALPALPARTRHLL
2. LWLEDRTPEALLQVR CASPSL

platelet glycoprotein V (60 000 copies/platelet) (single-pass)

1. RLSRNKITHLPGALLDKMVILLEQ
- 2/3. HRNHIRSIAPGAFDRLPNLSSLTLNRNHLAFL
4. NLSRLRYLGVTLSPRLSALPQ

GP2. Number of amino acids: 566; Molecular weight: 64 983.79; Theoretical pI: 9.66; Grand average of hydropathicity (GRAVY): -0.579.

MSATYKGKR SIYAVFESDVNLKGIPVYRRPESKATNATLDPRSFLLRNPNDKYEPFWE
DEEKNESGLTEYRLVSINKNFLEK FVQGLDIGPTKTQVGLIQYANNPRVFNLTNTYKTK
EEITSDFRIGFGSFVEKTVIPYILENGKLSEGVITISYKSYAKNGQKTIKKQVVLEEGTIAF
KNWVKTGLQFAKRLQVNLLVKPSEKIQVLKLNVLNLKIPLLYDAEIHLTRSTNINFLVLRLR
SGEPQTFTLKFKRAEDINPLKIGQTSSSVSFKSENFRHDNILRFGIAVLGYLNRNALDTK
LSLTNKGEVFNELVGKQRISGNYHYSTKAYWNISRKYAQNR YTDLVAIQNKNEIDYLNK
VLPYYSSYYWIGIRKNNKTWTWVGTKKALTNEKINAKWDTGENPIYKSAVTTVLQAQT
RYGFDQFALYKEGDPAPERWYRASPIITVTAHSGTYRAYSFSSLPLTRKSNGGQDG
GRQDVHSREQVGTKVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGK
KTAKTNTNEFLIDVDKGENYAFKLAAALEHHHHHH

Peptides (marked red) with 6 amino acid residues flanking sequences on both sides (marked black) from 7 proteins listed below were randomly concatenated in GP1 sequence. 5 Cys and 3 Met were replaced with Ala and Ile, respectively (marked blue) in the flanking sequences. 6 x His tag and linker sequence (marked orange) was from expression vector.

platelet glycoprotein 4 (20 000 copies/platelet) (multi-pass)

1. QKTIKKQVLEE**GTIA**FKNWWKTG
2. LQFAKRLQVNLLVK**PSE**KIQVLKN
3. TYKGKR**SIYAVFES**DVNLKGIPVYR

P-selectin (10 000 copies/platelet) (single-pass)

1/2/3/4/5.

YHYSTK**AYWNIS**RKYCQNR**YTDLVAIQNKNEIDYLNKVL**PYYSSYYWIGIRKNNKTWT**WVGTK**KALTNE

Integrin beta-1 (2 000 to 4 000 copies/platelet) (single-pass)

1. LVLRLR**SGEPQT**FTLKFKRAED
2. ITSDFR**IGFGSF**VEKTVMPYI
3. LSLTNK**GEVFNE**LVGKQRISGN
4. ILENGK**LSEGV**TISYKSYCKNG
5. EKMNAK**WDTGEN**PIYKSAVTTV

Integrin alpha-2 (2 000 to 4 000 copies/platelet) (single-pass)

- 1/2/3. KNFLEK**FVQGLDIGPTKTQVGLIQYANNPRVVFNLNTYK**TKEEMI
4. HDNILR**FGIAVLGYLNR**NALDTK
5. NLVNLK**IPLLYDAEIH**LTRSTNINF
6. DINPLK**IGQTSSSV**SFKSENFH

Proteinase-activated receptor 1 (PAR-1) (2 500 copies/platelet) (multi-pass)

1/2/3. RRPESK**ATNATLDP**RSFLLRNPNDKYEP**FWEDEEKNESGLTEY**RLVSINK

Platelet glycoprotein VI (1 000 copies/platelet) (single-pass)

1. LQCQTRY**YGFDQF**ALYKEGDPAP
2. PERWYRASPIITV**TAAHSGTYR**CYSFSS
3. LPLTRK**SNGGQD**GGRQDVHSR

Tissue factor (single-pass and secreted)

1/2/3/4.

EQVGTK**VNVTVE**DERTLVR**RNNTFLSLR**DVFGK**DLIYTLYYWKSSSSG**KKTAK**TNTNE**
FLIDVDKGENYCF

PLin. Number of amino acids: 585; Molecular weight: 67 004.32; Theoretical pI: 9.53; Grand average of hydropathicity (GRAVY): -0.216.

MSLRELK**TILPLIN**FKVSSAKFAPTQEK**VTFEIYDPNLAFLR**FVVYEEPD**IIKQVL**VENFSN
FTNRIASGLEKLLGPK**NSEGLHSARDVPV**AILGSGGGRA**IVGFSILFNRVLG**VSGSQS
RGSTIEELLALLKW**YSTSAFSR**LEKLGLFQTSR**LILIGETIKIVIEDYHFKLK**FDPELLFNK
QFQYQNPKNR**DELNGFFNKLIR**NVIGTKGKK**QLPDAQLLARRFLLRRL**FQTTRL**LILIGE**
TIKIVIEEYFLQLKFDPELLFGV**QFQYRNRIA**IEGLLEV**KLTL**LHV**LHK**FRFQA**ADYGYKS**

WEAFSNLSYYTRALPPVPPAVQKVSQASIDQSRQIKYQSPDEFERIYEPLDVKSKKIHV
 LGSLARGILDNTYNNVVKAPQGKNLLTHGRWFEFVNATFIREILIRIKENVGKAWAED
 VLALVKHPLTANKLPFPKIDPYVFDREGLKEAYPKGQRVDSSNYDPFRLWL_{AGSYIQPT}
 KFVSFEFSAQKNRSYVISSFTELKAYDLLSKASVQFVDYNKRQISRIDPELIKTVTINASS
 SRSGLLDDIQGLIDKYEPSGINAQRGQLSPEKLA_{AALEHHHHHH}

Peptides (marked red) with 6 amino acid residues flanking sequences on both sides (marked black) from 6 proteins listed below were randomly concatenated in PLin sequence. 4 Cys and 9 Met were replaced with Ala and Ile, respectively (marked blue) in the flanking sequences. 6 x His tag and linker sequence (marked orange) was from expression vector.

Thromboxane-A synthase (CYP5A1) (multi-pass)

1. LLALLK_{WYSTSAFSR}LEKLGL
2. EPDMIK_{QVLVENFSNFTNR}MASGLE
3. LPNKNR_{DELNGFFNK}LIRNVI
4. GLLEVKL_{TLLHVLHK}FRFQAC

Prostaglandin G/H synthase 1 (COX-1) (peripheral)

1. LLTHGR_{WFEFVNATFIRE}MLMRI
2. GTKGKK_{QLPDAQLLARR}FLLRR
3. LFQTTR_{LILIGETIK}IVIEEY (common with COX-2)
4. YFLQLK_{FDPELLFGVQFQYR}NR_{IA}ME

Cytosolic phospholipase A2 (cytoplasmic vesicles)

- 1/2. KLLGPK_{NSEGLHSARDVPV}AILGSGGGR_{AM}VGFS
3. SILFNR_{VLGVSGSQSR}GST_{ME}E
4. PDEFER_{IYEPLDVK}SKKIHV
5. KLPFPK_{IDPYVFDREGLKE}C

1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 (exosomes)

1. SLRELK_{TILPLINFK}VSSAKF
2. LGSL_{CR}GILDNTYNNVVKAPQGKN
3. YPKGQR_{VDSSNYDPFRLWL}CGS
4. APTQEK_{VTFEIYDPNLAFLR}FVVYEE

1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-2 (exosomes)

1. KENVGK_{AWAEDVLALVK}HPLTAN
2. QGLIDK_{YEPSGINAQRGQLSPE}
- 3/4/5. YIQPTK_{FVSFEFSAQKNRSYVISSFTELK}AYDLLSK_{ASVQFVDYNKRQ}MSRI

Prostaglandin G/H synthase 2 (Cox-2) (peripheral)

1. ADYGYK_{SWEAFSNLSYYTRALPPVP}
2. LFQTSR_{LILIGETIK}IVIEDY (common with COX-1)
3. YHFKLK_{FDPELLFNK}QFQYQN
4. PPAVQK_{VSQASIDQSRQ}MKYQS
5. DPELIK_{TVTINASSSR}SGLDDI

PLout. Number of amino acids: 637; Molecular weight: 71 339.29; Theoretical pI: 9.69; Grand average of hydropathicity (GRAVY): -0.307.

MAARSNR**VTVP**IGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDFYASRLLDLVFLLDG
SSRLSEAEFEVLKAFVVDIPYASKGLYLETEAGYYKLSGEAYGFVARIDGSGNFQVLLS
DRYFNKTAAFNDRVYATYQVTRGLASLN~~EEIK~~SQFEGFVKDILNK~~SAHRYSGVVYP~~
LKSLGRLKSTDPVKAAQFEPPGRQIIAIRSVTVRLPGLHNSLVKLKHGAGSFEIQKGDQ
NPQIAAHVISEASSKTTSVLQWAEKGYYTISTPSYRITSASVNDSGEYRAQRGLSGRSD
PIQLEIHRGWLLLQVSSRVFTEGEPLALRAHAWKDKLVYNVLYYRNGKAFKFQIRSKSN
FIIFLKNTVISDKPLVKVTFFQNGKSQKFSHIKNSLKVA~~AI~~SESPVAEKSASTTYNKKYQY
YSNKHARGSTPFHFARIPYTLSQTRDVFDATFEA~~AHRAVSPLPYLRNARYDVR~~AI~~AI~~KT
TSGIHPKNIQSLEVIGKGTHANQALAVKTTSQVRPRHITSLEVIKAGPHAPDPQHERIITV
STNGSIHSPRFPHTYPFGRKSRVVDLNL~~LLTEEVRLYS~~ATPIKITFKSDDYFVAKPGFKIY
YSLLDALDKKIAEFDTVEDLLKYFNPESKLAAALEHHHHHH

Peptides (marked red) with 6 a.a. residues flanking sequences on both sides (marked black) from 12 proteins listed below were randomly concatenated in PLout sequence. 16 Cys and 6 Met were replaced with Ala and Ile, respectively (marked blue) in the flanking sequences. 6 x His tag and linker sequence (marked orange) was from expression vector.

Low affinity immunoglobulin gamma Fc region receptor II-a (single-pass)

1. DKPLVK**VTFFQNGK**SQKFSH
2. STDPVK**AAQFEPPGRQ**MI~~AI~~R

P2Y purinoceptor 12 (multi-pass)

1. FQIRSK**SNFIIFLK**NTVISD
2. PFHFARIPY**TL**SQTRDVFD~~CT~~

P2Y purinoceptor 1 (multi-pass)

1. ~~C~~ISAHRYSGVVYPLKSLGRLK
2. ~~C~~AFNDRVYATYQVTRGLASLN

Prostaglandin F2-alpha receptor (multi-pass)

1. IKNSLKVA~~AI~~SESPVAEKSAST

CD40 ligand (single-pass)

1. N~~C~~EEIK**SQFEGFVK**DIMLNK
- 2/3. SFEMQKGDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMS

Phospholipase A2, membrane associated (peripheral, cell membrane)

1. TTYNKKYQYY**SNKH**CRGST

Von Willebrand factor (secreted)

- 1/2/3. ~~M~~PYASKGLYLETEAGYYKLSGEAYGFVARIDGSGNFQVLLSDRYFNK~~TC~~
4. RSVTVRLPGLHNSLVKLKHGAG
5. FEACHRAV**SPLPYLRN**CRYDV
- 6/7. DFY~~C~~SRLLDLVFLLDGSSRLSEAEFEVLKAFVDM
- 8/9. AARSNR**VTVP**IGIGDRYDAAQLRILAGPAGDSNVVKLQRIED

Platelet basic protein (secreted)

- 1/2. ~~R~~CMCIK**TTSGIHPKNIQSLEVIGK**GTH~~C~~NQ

Platelet factor 4 (secreted)

1. QCLCVKT**TSQVRPRHITSLEVIK**AGPHCP

Platelet-derived growth factor C (secreted)

1. DPQHERIITV**STNGSIHSPR**FPHTYP

2. FGRKSR**VVDLNLLTEEVRLYS**CTP

Platelet-derived growth factor D (secreted)

1. IKITFK**SDDYFVAKPGFKI**YYSLL

2. DALDKK**IAEFDTVEDLLKY**FNPES

High affinity immunoglobulin gamma Fc receptor I (single-pass)

1/2/3/4/5.

STPSYR**ITSASVNDSGEYR**CQRGLSGR**SDPIQLEIHRGWLLLQVSSRVFTEGEPLALR**

CHAWKDK**LVYNVLYYR**NGKAFK