**Table S1. Details of primers used in qPCR validation of gene targets.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene name | Accession ID  | Forward (5'-3') | Reverse (5'-3') | Amplicon size (bp) | Annealing temperature (°C) |
| 18S | NR\_003286.4 | GTAACCCGTTGAACCCCATT | CCATCCAATCGGTAGTAGCG | 150 | 60 |
| AKR1B1 | NM\_001628.4 | CTCCAACTTCAACCATCTCCAG | ACCACGATGCCTTTGGACT | 143 | 58 |
| FLNA | NM\_001456.3 | GCATCCAAAGTGGCACCAC | AGCCTCATAAGGGATGTACTCG | 166 | 60 |
| GFPT2 | NM\_005110.4 | GCTCATCGTGATTGGCTGT | CCATCACAGGAAGCTCAGTC | 88 | 62 |
| ITGA1 | NM\_181501.2 | CAGACGCTCAGTGGAGAACA | TGTACATAGGGGCTCCGACT | 111 | 60 |
| ITGA2 | NM\_002203.4 | ATCATTCTCCCTGCCGGTT | GCTTGGAAACTGAGAGACGC | 179 | 60 |
| ITGAV  | NM\_002210.5 | AGGAGAAGGTGCCTACGAAG | GCACAGGAAAGTCTTGCTAAGG | 104 | 60 |
| SNAI1 | NM\_005985.4 | GGTTCTTCTGCGCTACTGCT | TAGGGCTGCTGGAAGGTAAA | 146 | 60 |
| SQSTM1 | NM\_003900.5 | GGTGCACCCCAATGTGATC | TCGCAGACGCTACACAAGTC  | 101 | 60 |
| TGFBI | NM\_000358.3 | TAACGGCCAGTACACGCTT | TGTTCAGCAGGTCTCTCAGG | 112 | 62 |

**Table S2. Clinical information on platinum-resistant, platinum-sensitive, initial diagnosed and relapsed patients.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Patient**  | **Diagnosis** | **Age at diagnosis (years)** | **Stage at diagnosis** | **Grade** | **Platinum-sensitive/ resistant** | **Progression-free survival (months)** |
| 1 | Serous ovarian carcinoma | 66 | 3C | 3 | resistant | 8.5 |
| 2 | Serous ovarian carcinoma | 59 | 3C | 3 | sensitive | 13.6 |
| 3 | Serous ovarian carcinoma and tubal cancer | 69 | 3C | 3 | sensitive | 24.9 |
| 4 | Serous ovarian carcinoma | 62 | 3C | 3 | resistant | 7.2 |
| 5 | Serous ovarian carcinoma | 62 | 1C | 3 | sensitive | 46.1 |
| 6 | Serous ovarian carcinoma | 84 | 2A | 2 | resistant | 8.7 |
| 7 | Serous ovarian carcinoma | 81 | 3 | 2 | resistant | 4.1 |
| 8 | Serous ovarian carcinoma | 44 | 3C | 3 | sensitive | 12.9 |
| 9 | Serous ovarian carcinoma | 61 | 3C | 3 | sensitive | 13.4 |
| 10 | Peritoneal cancer | 43 | 3C | 3 | sensitive | 28.6 |
| 11 | Serous papillary carcinoma of the ovary | 75 | 3C | 3 | sensitive | 23.8 |
| 12 | Serous papillary carcinoma of the ovary | 46 | 3 | 3 | sensitive | 51.0 |
| 13 | Serous papillary carcinoma of the ovary | 42 | 3c | 3 | sensitive | 37.4 |
| 14 | Serous papillary carcinoma of the ovary | 42 | 3c | 3 | sensitive | 41.0 |
| 15 | Serous carcinoma of gynaecologi-cal origin | 63 | 3c | 3 | resistant | 13.1 |
| 16 | Serous papillary carcinoma of the ovary | 60 | 3c | 3 | sensitive | 16.5 |
| 17 | Serous papillary carcinoma of the ovary | 78 | 3a | 3 | resistant | 9.6 |
| 18 | Serous papillary carcinoma of the ovary | 46 | 3c | 3 | resistant | 8.5 |
| 19 | Serous carcinoma of the ovary  | 61 | 3c | 3 | sensitive | 35.3 |
| 20 | Serous carcinoma of the peritoneum | 48 | 3a | 3 | resistant | 0.0 |
| 21 | Serous papillary carcinoma of the ovary | 66 | 3c | 3 | sensitive | 23.1 |
| 22 | Serous papillary carcinoma of the ovary | 63 | 2c | 3 | resistant | 10.2 |
| 23 | Serous papillary carcinoma of the ovary  | 52 | 3c | 3 | resistant | 8.8 |
| 24 | Serous carcinoma of the ovary | 60 | 2a | 3 | sensitive | NA |
| 25 | High grade serous carcinoma of the ovary | 66 | 4 | 3 | sensitive | 8.4 |

Platinum-sensitive: n=15

Platinum-resistant: n=10

**Matching relapsed samples-**

**At Diagnosis**  **Relapsed**

5 26

12 27

14 28

17 29

**Table S3 (A): Peptide profile of proteins upregulated in OVCAR5CBPR compared to OVCAR5 cell line.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession ID | Gene names | Protein names | Peptide sequence | Sequence coverage | Protein score | Fold change (CBPR/Control) | p value |
| P32455 | GBP1 | Interferon-induced guanylate-binding protein 1 | EKEIEVERESMTDAILQTDQTLTEKGFSLGSTVQSHTKSSPDENENEVEDSADFVSFFPDFVWTLRAIAHYEQQMGQKDVDHLFQK | 14.5 | 37.293 | 3.92 | 0.0011 |
| P11413 | G6PD | Glucose-6-phosphate 1-dehydrogenase | CISEVQANNVVLGQYVGNPDGEGEATKDGLLPENTFIVGYARDNIACVILTFKDVMQNHLLQMLCLVAMEKPASTNSDDVRDEKEELFQGDAFHQSDTHIFIIMGASGDLAKEMVQNLMVLRGGYFDEFGIIRGPTEADELMKGSTTATFAAVVLYVENERGYLDDPTVPRIDHYLGKIFGPIWNRIFTPLLHQIELEK KPGMFFNPEESELDLTYGNRLEDFFARLFYLALPPTVYEAVTKLILDVFCGSQMHFVRLNSHMNALHLGSQANRLPDAYERLQFHDVAGDIFHQQCKLSNHISSLFRLTVADIRNIHESCMSQIGWNRNSYVAGQYDDAASYQRQSEPFFKRVGFQYEGTYKTQVCGILRVGFQYEGTYKWDGVPFILR | 73.4 | 184.37 | 3.64 | 0.0002 |
| P17301 | ITGA2 | Integrin alpha-2 | AGDISCNADINPLKCPVDLSTATCEKDCGEDGLCISDLVLDVRFGIAVLGYLNRFVQGLDIGPTKIGQTSSSVSFKIPLLYDAEIHLTRSVACDVGYPALKTSHGHLIFPKVDISLENPGTSPALEAYSETAK | 11.3 | 80.444 | 3.61 | 0.0001 |
| Q16555 | DPYSL2 | Dihydropyrimidinase-related protein 2 | AITIANQTNCPLYITKFQLTDCQIYEVLSVIRFQMPDQGMTSADDFFQGTKGIQEEMEALVKGLYDGPVCEVSVTPKGTVVYGEPITASLGTDGSHYWSKIAVGSDADLVIWDPDSVKIVLEDGTLHVTEGSGRKGTVVYGEPITASLGTDGSHYWSKMVIPGGIDVHTRTHNSSLEYNIFEGMECRVFNLYPRMDENQFVAVTSTNAAKQIGENLIVPGGVK | 35 | 64.638 | 3.58 | 0.0005 |
| Q12913 | PTPRJ | Receptor-type tyrosine-protein phosphatase eta | AVSISPTNVILTWKDFIATQGPLPNTLKGASDTYVTYLIRGDPLGTEGGLDASNTERGLIDGAESYVSFSRNNEVSFSQIKPKSPDGASEYVYHLVIESKVENFEAYFKVITEPIPVSDLR | 9.1 | 30.007 | 3.24 | 0.0208 |
| Q15582 | TGFBI | Transforming growth factor-beta-induced protein ig-h3 | DLLNNHILKEGVYTVFAPTNEAFRGDELADSALEIFKIPSETLNR LTLLAPLNSVFKNSLCIENSCIAAHDKQAGLGNHLSGSERQHGPNVCAVQKSPYQLVLQHSRSTVISYECCPGYEKVISTITNNIQQIIEIEDTFETLRVLTPPMGTVMDVLKYGTLFTMDRYLYHGQTLETLGGK | 26.5 | 89.138 | 3.13 | 0.0135 |
| Q15738 | NSDHL | Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating | CTVIGGSGFLGQHMVEQLLARDPQLVPILIEAARFFLGDLCSRGVNTVFHCASPPPSSNNKGYAVNVFDIQQGFDNPQVRILTGLNYEAPKTHLTEDTPKVALAGTFHYYSCERVNADIEK | 32.4 | 63.853 | 3.05 | 0.0005 |
| P15121 | AKR1B1 | Aldose reductase | DYPFHEEFGIVVTAYSPLGSPDRPWAKGIVVTAYSPLGSPDRPWAKPEDPSLLEDPRHIDCAHVYQNENEVGVAIQEKLDYLDLYLIHWPTGFKPGKLIQYCQSKLLLNNGAKLWCTYHEKNLVVIPKPAVNQIECHPYLTQEKSPPGQVTEAVKVAIDVGYRVCALLSCTSHKVFDFELSSQDMTTLLSYNRYKPAVNQIECHPYLTQEKTTAQVLIR | 58.2 | 105.9 | 3.00 | 0.0017 |
| P51572 | BCAP31 | B-cell receptor-associated protein 31 | AENQVLAMRKYMEENDQLKKYMEENDQLKKLDVGNAEVKLLEEHAKLQAAVDGPMDKLVTLISQQATLLASNEAFKVNLQNNPGAMEHFHMKYMEENDQLKK | 33.3 | 44.299 | 2.89 | <0.0001 |
| Q13642 | FHL1 | Four and a half LIM domains protein 1 | AITSGGITYQDQPWHADCFVCVTCSKAIVAGDQNVEYKCLHPLANETFVAKDCFTCSNCKFCANTCVECRFDCHYCRFTAVEDQYYCVDCYKFWHDTCFRGEDFYCVTCHETKQVIGTGSFFPK | 38.4 | 128.24 | 2.59 | 0.0227 |
| P06756 | ITGAV | Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain | AGTQLLAGLRDLALSEGDIHTLGCGVAQCLKEPVGTCFLQDGTKEQLQPHENGEGNSETGGLMQCEELIAYLRILACAPLYHWRIYIGDDNPLTLIVKMFLLVGAPKQAHILLDCGEDNVCKPKSAILYVKSHQWFGASVRSTGLNAVPSQILEGQWAARTVEYAPCRVRPPQEEQER | 17 | 35.81 | 2.52 | 0.0014 |
| P00492 | HPRT1 | Hypoxanthine-guanine phosphoribosyltransferase | DLNHVCVISETGKFFADLLDYIKFVVGYALDYNEYFRNVLIVEDIIDTGKSIPMTVDFIRSVGYKPDFVGFEIPDKSYCNDQSTGDIKTMQTLLSLVRVFIPHGLIMDRVIGGDDLSTLTGKVASLLVK | 59.2 | 62.136 | 2.48 | 0.0008 |
| Q13636 | RAB31 | Ras-related protein Rab-31 | EYAESIGAIVVETSAKFVQDHFDHNISPTIGASFMTKGSAAAVIVYDITKNAINIEELFQGISRFLIWDTAGQERVCLLGDTGVGK | 44.3 | 16.503 | 2.45 | 0.0146 |
| Q13501 | SQSTM1 | Sequestosome-1 | AGEARPGPTAESASGPSEDPSVNFLKCSVCPDYDLCSVCEGKDHRPPCAQEAPREAALYPHLPPEADPRFSFCCSPEPEAEAEAAAGPGPCERIALESEGRPEEQMESDNCSGGDDDWTHLSSKLAFPSPFGHLSEGFSHSRLIESLSQMLSMGFSDEGGWLTRLTPVSPESSSTEEKNMVHPNVICDGCNGPVVGTRNVGESVAAALSPLGIEVDIDVEHGGKNYDIGAALDTIQYSKPGPTAESASGPSEDPSVNFLKRFSFCCSPEPEAEAEAAAGPGPCERSSSQPSSCCSDPSKPGGNVEGATQSLAEQMRVAALFPALR | 63.6 | 157.11 | 2.12 | 0.0293 |
| P56199 | ITGA1 | Integrin alpha-1 | EDTIYEADLQYRFEYQMSLEPIKTIVHYSPNLVFSGIEAIQKVIQDCEDENIQRVMVIVTDGESHDNHRYSSTEEVLVAAK | 6.9 | 27.575 | 2.10 | 0.0478 |
| O94808 | GFPT2 | Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2 | EITYMHSEGILAGELKETDCGVHINAGPEIGVASTKGSPLLIGVRGYDVDFPRQVLEELTELPVMVELASDFLDRCQNALQQVTAREIFEQPESVFNTMREIFETLIKETEDITFSTLVERGYDSAGVAIDGNNHEVKGYEFESETDTETIAKGYNYATCLEGALKLSTEQIPILYRWATHGVPSAVNSHPQR | 28.3 | 53.837 | 2.07 | 0.0086 |
| P07099 | EPHX1 | Epoxide hydrolase 1 | DVELLYPVKEDDSIRPFKGGHFAAFEEPELLAQDIRIEGLDIHFIHVKPPQLPAGHTPKNHGLSDEHVFEVICPSIPGYGFSEASSKVETSDEEIHDLHQRYLEDGGLER | 24.2 | 24.912 | 2.02 | 0.0216 |
| P21333 | FLNA | Filamin-A | AEAGVPAEFSIWTRAEGPGLSRAEISFEDRAFGPGLQGGSAGSPARAGNNMLLVGVHGPRAGQSAAGAAPGGGVDTRAHEPTYFTVDCAEAGQGDVSIGIKALGALVDSCAPGLCPDWDSWDASKPVTNARALTQTGGPHVKANLPQSFQVDTSKAPSVANVGSHCDLSLKASGPGLNTTGVPASLPVEFTIDAKATCAPQHGAPGPGPADASKAYGPGIEPTGNMVKCAPGVVGPAEADIDFDIIRCSGPGLSPGMVRCSYQPTMEGVHTVHVTFAGVPIPRDAGEGGLSLAIEGPSKDAGEGLLAVQITDPEGKDAGEGLLAVQITDPEGKPKDAPQDFHPDRDGSCGVAYVVQEPGDYEVSVKDGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFKDKGEYTLVVKDNGNGTYSCSYVPRDQEFTVKDVDIIDHHDNTYTVKEAGAGGLAIAVEGPSKEAMQQADDWLGIPQVITPEEIVDPNVDEHSVMTYLSQFPKEATTEFSVDAREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSKEGPYSISVLYGDEEVPRENGVYLIDVKETGEHLVHVKFGGEHVPNSPFQVTALAGDQPSVQPPLRFNEEHIPDSPFVVPVASPSGDARFNGTHIPGSPFKFVPAEMGTHTVSVKGAGSYTIMVLFADQATPTSPIRGAGTGGLGLAVEGPSEAKGEYTLVVKGLVEPVDVVDNADGTQTVNYVPSRGTVEPQLEARHTAMVSWGGVSIPNSPFRIANLQTDLSDGLRIPEISIQDMTAQVTSPSGKIVGPSGAAVPCKKDGSCGVAYVVQEPGDYEVSVKLDVQFSGLTKLPQLPITNFSRLQVEPAVDTSGVQCYGPGIEGQGVFRLTVSSLQESGLKLVSNHSLHETSSVFVDSLTKLYSVSYLLKMDCQECPEGYRNGHVGISFVPKRAEFTVETRRAPSVANVGSHCDLSLKRLTVSSLQESGLKSADFVVEAIGDDVGTLGFSVEGPSQAKSAGQGEVLVYVEDPAGHQEEAKSPFEVYVDKSPFSVAVSPSLDLSKSPYTVTVGQACNPSACRSSFTVDCSKTFSVWYVPEVTGTHKTGVAVNKPAEFTVDAKTGVELGKPTHFTVNAKTHIQDNHDGTYTVAYVPDVTGRTPCEEILVKVANPSGNLTETYVQDRVAQPTITDNKVAQPTITDNKDGTVTVRVDVGKDQEFTVKVEPGLGADNSVVRVGSAADIPINISETDLSLLTATVVPPSGRVHGPGIQSGTTNKPNKVHSPSGALEECYVTEIDQDKVHSPSGALEECYVTEIDQDKYAVRVLPTHDASKVNQPASFAVSLNGAKVNVGAGSHPNKVPVHDVTDASKVQVQDNEGCPVEALVKVTAQGPGLEPSGNIANKVTVLFAGQHIAKVTYTPMAPGSYLISIKVYGPGVAKYAPSEAGLHEMDIRYGGDEIPFSPYRYGGPYHIGGSPFKYGGQPVPNFPSKYNEQHVPGSPFTARYTPVQQGPVGVNVTYGGDPIPKYWPQEAGEYAVHVLCNSEDIRQMQLENVSVALEFLDRDLAEDAPWKDLAEDAPWKKIQQNTFTRLIALLEVLSQKLLGWIQNKLVSIDSKWCNEHLKGQHVPGSPFQFTVGPLGEGGAHKIECDDKGDGSCDVRNDNDTFTVK | 57.9 | 323.31 | 2.01 | 0.0028 |

**Table S3 (B): Peptide profile of proteins downregulated in OVCAR5CBPR compared to OVCAR5 cell lines.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Accession ID | Gene names | Protein names | Peptide sequence | Sequence coverage | Protein score | Fold change (CBPR/Control) | p value |
| O95810 | SDPR | Serum deprivation-response protein | DNSQVNAVTVLTLLDKGIQNDLTKLENNHAQLLRLVNMLDAVQENQHKRLENNHAQLLRSDGDPVQPAVLQVHQTSVLIFQEENEIPASVFVKYEGSYALTSEEAERYQASTSNTVSK | 25.4 | 104.96 | 7.10 | 0.0172 |
| P22676 | CALB2 | Calretinin | AGPQQQPPYLHLAELTASQFLEIWKELENFFQELEKGFLSDLLKHFDADGNGYIEGKLLPVQENFLLKLQEYTQTILRSGYIDEHELDALLK | 33.9 | 37.604 | 5.76 | 0.0033 |
| Q16822 | PCK2 | Phosphoenolpyruvate carboxykinase [GTP], mitochondrial | AIDTTQLFSLPKCLHSVGQPLTGQGEPVSQWPCNPEKEGALDLSGLRETPIGLVPKEVLAELEALERGQLGNWMSPADFQRGVPLVYEAFNWRLCQPEGIHICDGTEAENTATLTLLEQQGLIRLGTPVLQALGDGDFVKSYLTEQVNQDLPKVECVGDDIAWMRVLDWICRVLSGDLGQLPTGIREIISFGSGYGGNSLLGK | 31.7 | 67.532 | 4.78 | 0.0403 |
| Q13740 | ALCAM | CD166 antigen | ADIQMPFTCSVTYYGPSGQKQIGDALPVSCTISASRSSNTYTLTDVRSSPSFSSLHYQDAGNYVCETALQEVEGLKSVQYDDVPEYKYEKPDGSPVFIAFR | 17.3 | 21.726 | 3.68 | 0.0216 |
| Q86UP2 | KTN1 | Kinectin | AAGDTTVIENSDVSPETESSEKAHVQEVAQHNLKDAVSNTTNQLESKDLLTELQKEEELKDIQNMNFLLKEEIGNVQLEKEHNVFQNKENEVQSLHSKLLEEQLQHEISNKLQALANEQAAAAHELEKLQTLVSEQPNKQNDQVSFASLVEELKKQQQVEAVELEAKRQEALPLHQETKSVLAETEGILQKTAEHEAAQQDLQSKTQLLQDVQDENKWLQDLQEENESLK | 16.9 | 139.2 | 3.54 | 0.0399 |
| Q14141 | SEPT6 | Septin-6 | AATDIAREDSYKPIVEFIDAQFEAYLQEELKFEGEPATHTQPGVQLQSNTYDLQESNVRLTIVSTVGFGDQINKSLDDEVNAFKTAAELLQSQGSQAGGSQTLKVLHTYHDSR | 40.1 | 38.387 | 3.44 | 0.0393 |
| Q16658 | FSCN1 | Fascin | DELFALEQSCAQVVLQAANERDVPWGVDSLITLAFQDQRFLIVAHDDGRGEHGFIGCRLINRPIIVFRLSCFAQTVSPAEKLVARPEPATGYTLEFRNASCYFDIEWRQIWTLEQPPDEAGSAAVCLRVTGTLDANRWSLQSEAHRYAHLSARYFGGTEDRYLAADKDGNVTCERYLAPSGPSGTLKYLTAEAFGFKYSVQTADHRYWTLTATGGVQSTASSK | 45.2 | 164.69 | 2.66 | 0.0052 |
| Q13085 | ACACA | Acetyl-CoA carboxylase 1;Biotin carboxylase | ATLVDHGIRDIIVIGNDITYRDLAEWLEKDPSLPLLELQDIMTSVSGRDPTLTDELLNILTELTQLSKDVDDGLQAAEEVGYPVMIKECCQPVLVYIPPQAELREEGIGPENLRIDTGWLDRIGSFGPQEDLLFLRIIEEAPATIATPAVFEHMEQCAVKIIQQAGQVWFPDSAFKILNVPQELYEKLGGIPVGVVAVETRLLETESFQMNRLLLEDLVKLPELLLKLTFLVAQKMMYGVSPWGDSPIDFEDSAHVPCPRRVDPVYIHLAERSVHSSVPLLNSKTDCDIEDDRLAAMFRVDWQENDFSKVEVGTEVTDYRVLQAELKVNNADDFPNLFRVSALNSVHCEHVEDEGESRYLYLTPQDYKDFTVASPAEFVTREEAISNMVVALKFGAYIVDGLRITSENPDEGFKPSSGTVQELNFR | 18.2 | 62.384 | 2.34 | 0.0003 |
| Q9NP81 | SARS2 | Serine--tRNA ligase, mitochondrial | DGSVLVPPALQSYLGTDRFCACPEEAAHALELRFDIEAWMPGRFGEVTSASNCTDFQSRITAPTHVPLQYIGPNQPRLLIALLESNQQKLPNQTHPDVPVGDESQARVLDMPTQELGLPAYR | 23.6 | 51.46 | 2.32 | 0.0059 |
| Q9Y570 | PPME1 | Protein phosphatase methylesterase 1 | DFSPVPWSQYFESMEDVEVENETGKDLTIGQMQGKFQMQVLPQCGHAVHEDAPDKGLSNLFLSCPIPKLDKDLTIGQMQGKLLLLAGVDRLPSRPPLPGSGGSQSGAKQCEGITSPEGSKSIVEGIIEEEEEDEEGSESISKSIVEGIIEEEEEDEEGSESISKRSLENAIEWSVKVAEAVATFLIRVKNPEDLSAETMAKVSMVGQVKYWDGWFR | 47.7 | 172.61 | 2.30 | 0.0118 |
| Q14315 | FLNC | Filamin-C | DLAEDAPWKDLAEDAPWKKIQQNTFTRLIALLEVLSQKLLGWIQNKLVSIDSKWCNEHLKGQHVPGSPFQFTVGPLGEGGAHKIECDDKGDGSCDVRNDNDTFTVKEAGAGGLSIAVEGPSKGAGTGGLGLTVEGPCEAKAEIAFEDRAPLQVAVLGPTGVAEPVEVRAPSGNEEPCLLKCSGPGLGAGVRDGSCGVSYVVQEPGDYEVSIKDNGDGTHTVHYTPATDGPYTVAVKEVGEHVVSVRFNDEHIPDSPFVVPVASLSDDARGDYILIVKGGLVGTPAPFSIDTKGVAGVPAEFSIWTRLGSFGSITRLSGGHSLHETSTVLVETVTK QAPSIATIGSTCDLNLKTPCEEVYVKTSQLNVGTSTDVSLKVAVGQEQAFSVNTRVCAYGPGLKVDITYDGHPVPGSPFAVEGVLPPDPSKVEAAEIVEGEDSAYSVRVEESTQVGGDPFPAVFGDFLGRVHTPSGAVEECYVSELDSDKVHTPSGAVEECYVSELDSDKHTIRVYNVTYTVK | 17.9 | 61.61 | 2.25 | 0.0192 |
| P13726 | F3 | Tissue factor | CFYTTDTECDLTDEIVKDLIYTLYYWKGENYCFSVQAVIPSRSTDSPVECMGQEKTILEWEPKPVNQVYTVQISTKTNTNEFLIDVDK | 29.8 | 140.55 | 2.20 | 0.0359 |
| Q15084 | PDIA6 | Protein disulfide-isomerase A6 | ALDLFSDNAPPPELLEIINEDIAKDGELPVEDDIDLSDVELDDLGKDELDVIELTDDSFDKGESPVDYDGGRGSTAPVGGGAFPTIVERGSTAPVGGGAFPTIVEREPWDGRHHSLGGQYGVQGFPTIKKDVIELTDDSFDKLAAVDATVNQVLASRNLEPEWAAAASEVKNSYLEVLLKTCEEHQLCVVAVLPHILDTGAAGRTGEAIVDAALSALR | 43 | 96.534 | 2.13 | 0.047 |
| P24666 | ACP1 | Low molecular weight phosphotyrosine protein phosphatase | EDFATFDYILCMDESNLRIELLGSYDPQKLVTDQNISENWRSPIAEAVFRSVLFVCLGNICRVDSAATSGYEIGNPPDYR | 50.6 | 18.531 | 2.11 | 0.0112 |