

IPI00296337 (100%), 469,095.5 Da
Isoform 1 of DNA-dependent protein kinase catalytic subunit
14 unique peptides, 14 unique spectra, 155/4128 amino acids (4% coverage)

MAGSSGAGVRC S L LR L Q E T L S A A D R C G A A L A G H Q L I R G L G Q E C V L S S S P A V L A L Q T S L V F S R D F G L L V F V R
K S L N S I E F R E C R E E I L K F L C I F L E K M G Q K I A P Y S V E I K N T C T S V Y T K D R A A K C I P A L D L F R S
S R L M D E F K I G E L F S K F Y G E L A L K K K I P D T V E L E K V Y E L L G L L G E V H P S E M I N N A E N L F R A F L G E L L K T Q M T S
A V R E P K L P V L A G C L K G L S S L L C N F T K S M E E D P Q T S R E I F N F V L K A I R V P Q I D L K R Y A V P S A G L R L F A L H A S
Q F S T C L L D N Y V S L F E V L L K W C A H T N V E L K K A A L S A L E S F L K Q V S N M V A K N A E M H K N K L Q Y F M E Q L F Y G I I R
N V D S N N K E L S I A I R G Y G L F A G P C K V I N A K D V D F M Y V E L I Q R C K Q M F L T Q T R C K Q M F L A L A A D T G D D R V Y Q M P S F L Q S V A S V
L L Y L D T V P E V Y T P V L E H L V V M Q I D S F P Q Y S P K M Q L V C C R A I V K V F L A L A A K G P V L R N C I S T V V H Q G L I R I
C S K P V V L P K G P E S E S E D H R A S G E V R T G K W K V P T Y K D Y V D L F R H L L S S D Q M M D S I L A D E A F F S V N S S S E S L
N H L L Y D E F V K S V L K I V E K L D L T L E I Q T V G E Q E N G D E A P G V W M I P T S D P A A N L H P A K P K D F S A F I N L V E F C
R E I L P E K Q A E F F E P W V Y S F S Y E L I L Q S T R L P L I S G F Y K L L S I T V R N A K K I K Y F E G V S P K S S A F I N L V E F C
Y S C F A L F V K F G K E V A V K M K Q Y K D E L L A S C Y L T F L L S L P H N I I E L D V R A Y V P A L Q M A F K L G L S Y T P L A E V G L
N A L E E W S Y I Y I D R H V M Q P Y Y K D I L P C L D G Y L K T S A L S D E T K N N W E V S A L S R A A Q K G F N K V V L K H L K K T K N L
S S N E A I S L E E I R I R V V Q M L G S L G G Q I N K N L L T V T S S D E M M K S Y V A W D R E K R L S F A V P F R E M K P V I F L D V F T
L P R V T E L A L T A S D R Q T K V A A C E L L H S M V M F M L G K A T Q M P E G G Q G A P P M Y Q V D S T L R D F C G R L A C D V D Q V T
R Q L Y E P L V M Q L I H W F T N N K K F E S Q D T V A L L E A I L D G I V D P E A I L D G I V D P V D S T L R D F C G R I K Q I T P Q Q E
K S P V N T K S L F K R L Y S L A L H P N A F K R L G A S L A F N N I Y R E F R E E E S L V E Q F V F E A L V I Y M E S L A L A H A D E K S
L G T I Q Q C C D A I D H L C R I I E K N H V S L N K A K K R R L P R G F P P S A S L C L L D L V K W L L A H C G R P Q T E C R H A S I E L
F Y K F V P L L P G N R S P N L W L K D V L K E E G V S F L I N T F E G G G C G Q P S G I L A Q P T L L Y L R G P F S L Q A T L C W L D L L
L A A L E C Y N T F I G E R T V G A L Q V L G T E A Q S S L L K A V A F F L E S I A M H D I I A A E K C F G T G A A G N R T S P Q E G D E R Y
N Y S K C T K V V R I M E F T T T L L N T S P E G W K L L K L D L C N T H L M R V L V Q T L C E P A S I G F N I G D V Q V M A H L P D V C V
N L M K A L K M S P Y K D I L E T H L R E K I T A Q S I E E L C A V N L Y G P D A Q V D R S R L A A V V S A C K Q L H R A G L L H N I L P S
Q S T D L H S V G T E L L S L V Y K G I A P G D E R O C L P S L D L S C K Q L A S G L L E L A F A F G G L C E R L V S L L L N P A V L S T
A S L G S S Q G S V I H F S H G E Y F Y S L F S E T I N T E L L K N L D L A V L E L M Q S S V D N T K M V S A V L N G M L D Q S F R E R A N
Q K H Q G L K L A T T I L Q H W K K C D S W W A K D S P L E L K M A V L A L L A K I L Q I D S S V S F N T S H G S F P E V F T T Y I S L L A
D T G L Y E P L V M Q L Q A V T L L P F F T S L T G G D S L E E L R R V L E Q L I V A R R V L E Q L I V A P G T P R F N N Y V D C M K K F L D A L
E L S Q S P M L L E C M T E V L C R E E Q Q H V M E E L F Q S S F R R I A R R G S C V T Q V G L L E S V Y E M F R K D D V M R L S F T R Q S F V
D R S L L T L L W H C S L D A L R E F F S T I V V D A I D V L K S R R F T K L N E S T F D T Q I T K K M G Y Y K I L D D P Y S R L P K D D V H
A K E S K I N Q V F H G S C I T E G N E L T K T L I K L C Y D A F T E N M A G E N Q L L E R R R L Y H C A A Y N C A I S V I C C V F N E L K
F Y Q G F L F S E K P E K N L L I F E N L I D L K R R Y N F P V E V E V P M E R K K K Y I E I R K E A R E A A N G D S D G P S Y M S S L Y
L A D S T L S E E M S Q F D F S T G V Q S Y S Y S Q D P R P A T G V F R R R E L E L E M D E L N R G E C M A P L T A L G H S Y M S S L Y
V K H M H R S L G P P Q G E E D S V P R D L P S W M K F L H G K L G N P I V P L N I R L F L A K L V I N T E E V F R P Y A K H W L S P L L Q
L A A S E N N G G E G I H Y M V V E I V A T I L S W T G L A T P T G V P K D E V T P T G V P K D E V N I R L L N F L M K H V F H P K R A V F R H N L E I K T
L V E C W K D C L S I P Y R L I F E K F S G K D P N S K D N S V G I Q L L G I V S V G I Q L L G I V M A N D L P P Y D P Q C G I Q S S E Y F Q A L V N N M S F V
R Y K E V Y A A A A E V L G L I L R Y V M E R K N I L E E S L C E L V A K Q L K Q H Q N T M E D K F I V C L N K V T K S F P P L A D R F M N
A V F F L L P K F H G V L K T L C L E V V L C R V E G M T E L Y F Q L K K S K D F V Q V M R H R D D E R Q K V C L D I I Y K M M P K L K P V E
L R E L L N P V V E F V S H P S T T C R E Q M Y N I L M W I H D N Y R D P E S E T D N D S Q E I F K L A K D V L I Q G L I D E N P G L Q L I
I R N F W S H E T R L P S N T L D R L L A L N S L Y S P K I E V H F L S L A T N F L L E M T S M S P D Y P N P M F E H P L S E C E F Q E Y T
I D S D W R F R S T V L T P M F V E T Q A S Q G T L Q T R I Q E G S L S A R W P Q E G S L S A R W P V A G O I R A T Q Q Q H D F T L T Q T A D G R S S F D W L T
G S S T D P L V D H T S P S S D S L L F A H K R S E R L Q R A P L K S V G P D F G K K R L G L P G D E V D N K V K G A A G R T D L L R L R
R F M R D Q E K L S L M Y A R K G V A E Q K R E K E I K S E L K M K Q D A Q V V L Y R S Y R H G D L L Y R S Y R H G D L I T P L Q A V A Q R
D P I I A K Q L F S S L F S G I L K E M D K F K T L S E K N N I T Q K L L Q D F N R F L N T T F S F F P P F V S C I Q D I S C Q H A A L L S
L D P A A V S A G C L A S L Q Q P V G I R L L E E A L L R L Q P A E L P A K R V R G K A R L P P D V L R W V E L A K L Y R S I G E Y D V L R
G I F T S E I G T K Q I T Q S A L L A E A R S D Y S E A A K Q Y D E A L N K Q D W V D G E P T E A E K D F W E L A S L D C Y N H L A E W K S
L E Y C S T A S I D S E N P P D L N K I W S E P F Y Q E T Y L P Y M I R S K L L L L L Q G E A D Q S L L T F I D K A M H G E L Q K A I L E L
H Y S Q E L S L L Y L L Q D D V D R A K Y Y I Q N G I Q S F M Q N Y S S I D V L L H Q S R L T K L Q L H Q S R L T K L Q S V Q A L T E I Q E F I S F I S K Q G N
L S S Q V P L K R L L N T W T N R Y P D A K M D P M N I W D D I I T N R C F F L S K I E E K L T P L P E D N S M N V D Q D G D P S D R M E V
Q E Q E E D I S S L I R S C K F S M K M K M I D S A R K Q N N F S L A M K L L K E L H K E S K T R D D W L V S W V Q S Y C R L S H C R S R S
Q G C S E Q V L T V L K T V S L L D E N N V S Y S L S K N I L A F R D Q N I L L G T T Y R I I A N A W S C G P A A G V I L S S E P A C L A E I E E D K A R R I
E L S G S S S E D S E K V I A G L Y Q R A F Q H L S E A V N A A E E E A Q P P S I I E R Y P E E T L D A Y M T L A D F C D Q Q L R K E E E N
A S V I D S A E L Q A Y P A L V Y E K M L K A L K L N S A N E A R L K F P R L L Q I I E R Y P E E T L S L M T K E I S S V P C W Q F I S W I S
H M V A L L D K D Q A V A V Q H S V E E I T D N Y P Q A I V Y P F I I S S E S Y S F K D T S T G H K N K E F V A R I K S K L D Q G G V I Q D
F I N A L D Q L S N P E L L F K D W S N D V R A E L A K T P V N K K N I E K M Y E R M Y A A L G D P K A P G L G A F R R K F I Q T F G K E F
D K H F G Q G S K L L R M K L S D F N D I T N E L L K M K N K S K P P G N L K E C S P W M S D F K V E F L R N E L E I P G Q Y D G R G K
P L P R E Y H V R I A G F D E R V T V M A S L R R P K R I I R G H D E R E H P F L V K G G E D L R Q D Q R V E Q L F Q V M N G I L A Q S D A
C S Q R A L Q L R T Y S V V P M T S R L G L I E W L E N T V G L I E W L E N T V S Q E E K A A Y L S D P R A P P C E Y K D W L T K M S G K H
D V G A Y M L M Y K G A N R T E T V T S F R K R E S K V P A D L L K R A F V R M D L L K R A F V R M I C I S H W I L G I
G R S H L N N F M V A M E T G G V I G I D F G H A F G S A T Q F L P V P E L M P F R L T R Q F I N L M L P M K E T G L M Y S I M V H A L R A
F R S D P G L L T N T M D V F V K E P S F D W K N F E Q K M R Q K I C Y A K R K L A G A N P A V I T
C D E L L L G H E K A P A F R D Y V A V A R G S K D H N I R A Q E P E S G L S E E T Q V K C L M D Q A T D P N I L G R T W E G W E P W M

IPI00456969 (100%), 532,405.6 Da
 Cytoplasmic dynein 1 heavy chain 1
 10 unique peptides, 10 unique spectra, 10 total spectra, 119/4646 amino acids (3% coverage)

MSEPGGGGGE	DGSAGLEVS A	VQNVADVSVL	QKHLRKLVP L	LLEDGGGEAPA	ALEAALEEK S	ALEEQMRKFLS
DPQVHTVLE	RSTLKEEDVGD	EGEEEEKEFIS	YNINIDIHYP L	VKSNKLAFLK	RTPVLDADKNI	VSSQLRVLTLH
SEDSPTNVA	SFISNAVAPF	FKSYIREESGK	ADRDGDGKMAP	SVKEKIAELE	MGLLHLPASNGT	EIQEISLFWLNL
PMITPNYAKQC	YERGEKPKVVT	DFGDKVEDPPT	FLNQ LQSGVNV	RWIKREIQKVT	KLDRDPASDFFP	ALNDLLSATEL
LERALYRIQE	KRESPEVLLT	LDILKHKGRF	HATVSRDFTDT	GLKQALLETVN	DYNPLMKDFE	LNMHVAYEEVF
DKIRQALVAI	FTHLRKIRNT	KYPIQRALRL	VEAISRDLS S	QLLKVVLGTRK	LMHVAYEEVF	KVMVACFEVF
QTWDDYEYK L	QVLLRDI VKR	KREENLKMVW	RINPAHRKLLQ	ARLDKQMRKFR	RQHEQLRAVI	VRVLRPQVTA
VAQQNQGEVP	EPQDMKVAEV	LFDAADANA I	EENVLAYENV	KEVDGLDVSK	EGTEAWEAAMH	KRYLDERIDRV
ETRITARLRD	QLGTAKNANE	MFRIFSRFNA	LFVVRPHIRGA	IREYQTQLIQ	RVKDDIESLH	DKFKVQY PQS
QACKMSHVRD	LPPVSGSIIW	AKQIDRQLTA	YMKRVEDVVLG	KGWENHVEGQ	KLKQDGD SFR	MKLNTQE I FD
DWARKVVQQRN	LGVSGRI FTI	ESTRVRGERTG	NVLKLVGNFL	PEIITLSKEV	RNLKWLGF RV	PLAIVNKAHQ
ANQLYPPFAIS	LIESVRTYER	TCEKVEGERTN	ISLLVAGLKK	EVQALIAEGI	ALVWESYKLD	PYVQR LAETV
FNFAQEKVDDL	LIIEEEKIDLE	VRSLET CMYD	HKTFS EILNLR	VQKAVDDLNL	HSYSNLP I W	NKLDMEIER I
LGVRLQAGLR	AWTQVLLGQA	EDKAQVDMDT	DAPQVSHKPG	GEPKIKNVVH	ELRITNQVIY	LNPPIEEECRY
KLYQEMFAWK	MVVL SLPRIQ	SQRVQVGVHY	EALTEEEKFYR	NALTRMPDGP	VALEESYSAV	MGIVSEVEQY
VKVVLLQYQCL	WDMQAENIYN	RLGEDLNKWR	ALLVQIRKAR	GTFDNAETKK	EFGPVVIDYQ	KVQSKVNLKY
DSWHKVEVLSK	FGQMLGSNMT	EFHSGEISKSR	QELQHSVDT	ASTSDAVETFI	TYVQSLK RKI	KQFEKQVLEFY
RNGQRLLLEKQ	RFQFP P SWLY	IDNIEGEGWA	FNDIMRRKDS	AIQQQVANLQ	MKIVQEDRAV	ESRTTDL L TD
WEKTKPVTGN	LRPEEALQAL	TIYEGKFGRL	KDDR EKCAKA	KEALELTDTG	LLSGSEERVQ	VALLEQLQDLK
GVWSLELSK V W	EQIDQMKEQP	WVSVQPRKLR	QNLDALLNLQ	KSFIPARLRGY	ASYEFVQRLL	KGYMKINMLV
IELKSEALKKD	RHWKQLMKRL	HVNWV V SELT	LGQIWDV DLQ	KNEAIVKDV L	LVAQGE M ALE	EFLKQIREVW
NTYELDLVNY	QNKCR LIRGW	DDL FNTKVKEH	INSVSAMKLS	PYKVFEEEDA	LSWEDKLNRI	MALFDVVIDV
QRRWVYLEG I	FTGSADIKHL	LPVETQRFQS	I STEFLALMK	KVSKSPLVMD	VLNIQGVQRS	LERLADLLGK
IQKALG EYLE	RERS S FPRFY	FVGDEDDLLEI	IGNSKNVAKL	QKHFKKMFAG	VSS IILNEDN	SVVLG I S SRE
GEEVAMFKT PV	SITEHPKINE	WLTLVVEKEMR	VTLAKLLAES	VTEVEVIFGKA	TSIDPNTYIT	WIDKYQAQLV
VLSAQIAWSE	NVETALSSMG	GGGDAAPLHS	VLSNVEVTLN	VLADSVLFMEQ	PPLRRRRLKLEH	LITELVAHQRD
VTRS L I KSK I	DNAKSF EWL S	QMRFYFDPKQ	TDLVQLQLS IQ	MANAKFNYGF	EYLGVDKLV	QTPLTDRCYL
TMTQALLEARL	GGSPFGPAGT	GKT ESVKALG	HQLGRFVLSV	NCDETFDFQF	MGRIFVGLCQ	VGAWGCFDFE
NRL EERMLSA	VSQQVQCIQE	ALREHSNPNY	DKTSAPI TCE	LLNKQVKVSP	DMAIFITMNP	GYAGR SNLPD
NLKKLFRSLA	MTKPDRLI A	QVMVLSQGF	TAEVELANKIV	PFCKLDCDEQL	SSQSHYDFGL	RALKSVLVSA
GNVKKRERIQK	IKREKEERGE	AVDEGEIAEN	LPEQEILIQIS	VCEFTMVPKLV	AEDIPLLFSL	LSDVFPGVQY
HRGEMTALRE	ELKKVVCQEMY	LTYGDCGEEVG	GMWVEKVLQL	YQITQINHGL	MMVGP SSGSK	SMAWRVLLKA
LERLEGEVGLD	AHIIDPKAIS	KDHLVGTLDLP	NTREWTDGLF	THVLRKVIDS	VRGELQKRQW	IVFDGDVDP E
WVENLNSVLD	DNKLLTL P NG	ERL SLP P NVR	IMFEVQDLKY	ATLATVSRCG	MVWFS EDVLS	TDMIFNFLA
RLRSLIPLDEG	EDEAQR RRKG	KEDEGE E AAS	PMLQIQRDAA	TIMQVYFTSN	GLVTKALEHA	FQLEHIMDLT
RLRCLGLS LFS	MLHQACRNVA	QYNANHPDFP	MQIEQLERYI	QRYLVAATLW	SLSGDSRLKM	RAELG EYIRR
ITTVPLPTAP	NIP I IDYEVS	ISGEWSPWQA	KVPPQIEVETH	KVAAPDVVVP	TLDTVR HEAL	LYTWLAEHKP
LVLCGPGSG	KTMTLTF SALR	ALPDMQV VGL	NFSSATTP EL	LLKTFDHYCE	YRRTPNGVVL	APVQLGKWL V
LFCDEINLPD	MDKYGTQRVI	SFIRAMVEH G	GFYRTSDQ TW	VKLERIQFVG	ACNPPTDPGR	KPLSHRFLRH
VPVVYVDY PG	PASLTQ IYGT	FNRAMLRLIP	SLRTYAEPLT	AAMVEFYTMS	QERFTQDTP	HYIYSPREMT
RWVRGIF EAL	RPLETLPVEG	LIRIWAHEAL	RLFDRLVLED	EEERR WTDENI	DTVALK HFPN	GDRLEKAMSRP
ILYSNLVSKD	YIPVDQEELR	DYVKARLKV F	YEEELDVPLV	LFNEVL DHVL	RIDRIFRQPQ	GHLLLIGVSG
AGKTTLSRFV	AWMNGLSVYQ	IKVHRKYTGE	DFDEDLRTVL	RRSGCKNEKI	AFIMDES NVL	DSGFLERMNT
LLANGEV PGL	FEGDEYATLM	TQCKE GAKKE	GMLDLSHEEL	YKWF T SQVIR	NLHVFTMNP	SSEGLKDRAA
TSPANL FNR CV	LNWFGDWSTE	ALYQVQKEFT	SKMDLSEPNY	IVPDMPLVVY	DKLPQPPSHR	EAI VNSCFV
HQTLHQANAR	LAKRGGRTMA	ITPRHYLD F I	NHYANLFHEK	RSELEEQQM H	LNVG L R K I KE	TVDQVEELRR
DLRIKVSQEL E	VKNA AANDKL	KKMVKDQQE A	EKKKVM SQEI	QEQLHKQ QEV	IADKQMSVKE	DLDKVESP AVI
EAQNAVKS I K	KQH LVEVRSM	ANPPAAVKLA	LESICLLLGE	STTDWKQIRS	IIMRENFIPT	IVNFSAE EIS
DAIREKMKKN	YMSNPSYNYE	I VNRASLACG	PMVKWAI AQL	NYADM LKRVE	PLRNE LQKLE	DDAKDNQQA
NEVEQMKIRD L	EAS IARYKEE	YAVLISEAQ A	IKADLAAVEA	KV NRSTALLK	SLSAERERWE	KTSETFKNQ M
STIAGDC LLS	AAFIAYAGYF	DQQMRQNLFT	TWSHHLQ QAN	IQFRTDIART	EYLSNADERL	RWQASSLPAD
YDLC TENA IML	KRFNRYP L I I	DPSSGQAT E F I	MNEYKDRKIT	RTSFLDDA FR	KNLESALRFG	NPLLVQDVES
DLPVTLN PVLN	REVRRY T GGRV	LITLGDQDID	LSPSFKVIFLS	TRDPTVEFPP	DLCSRVT FVN	FTVTR SSLQS
QLNEVLK AE	RPDVDEKRS D	LLKLQGEFQL	RLRQL EKSL L	QALNEVKGR I	LDDD T I ITTL	ENLKR EAAEV
TRKVEETD I V	MQEVETV SQQ	YLP LSTACSS	IYFTMESL LKQ	IHF LTYQVSLQ	FFLDIYHNVL	YENPNLKGVT
DHTQRLS I I T	KDLFQVAFNR	VARGMLHQDH	ITFAMLLARI	KLKGTQYGEPT	YDAEFQHF LR	GNEIVLSAGS
TPR IQGLTVE	QAEAVVRLS C	LPAFKDL IAK	VQADEQFGI W	LDS S S PEQTV	PYLWSEETPA	TPIGQA IHR L
LLIQAFR PDR	L LAMAHM FVS	TNLGESFMS I	MEQPLDLTH I	VGTEV K PNT P	VLMCSVPGYD	ASGHVEDLAA
EQNTQ I T S I A	I GSAE G F NQA	DKAINTAVK S	GRWVALLK N H	LAPGWLKMQLE	KKLHSLQPH A	CFR L F L T M E I

IPI00014898 (100%), 531,783.9 Da
Isoform 1 of Plectin
2 unique peptides, 2 unique spectra, 26/4684 amino acids (1% coverage)

MVAGMLMPRIAD QLRRAIYEVLLF REEGVMSVAKKRD RRPVSLHMPV P GVTNLQVVMR AASLRAARGL VRETFEACHVF
YWYLTLMKPRD HLRQYLHLPLP EIVPASLQQRV RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RRKLEELNEVSP RRKLEELNEVSP RTILARPGLQRPV RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
HNLIISLLEEVSL HNLIISLLEEVSL RMRFRHKLRQNV RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
FQISLSDIQVSG FQISLSDIQVSG LLLWSQRMVVE RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
TNLENLLDQAF TNLENLLDQAF RLLDFPSSVFEV RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
YRELVLQLLQ YRELVLQLLQ SVAERHTAAGFE RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
QLKLVPPGYPHP QLKLVPPGYPHP LDVGEKEWGWKLD RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RLLLAAGKVPQ RLLLAAGKVPQ LDAGEVERDLD RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AGVAAAPKATPV AGVAAAPKATPV RAQVTLQSVQR RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
SIEEEFRAKIE SIEEEFRAKIE RASRSDENQGLS RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
EKEEEFVAKFD EKEEEFVAKFD RASDRNTNMTA RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
WSWMLKGLSCG WSWMLKGLSCG IEAHLKKNAA RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
LNEYKQLLSS LNEYKQLLSS LAKRAKAVVQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
SSGSEAAVPS SSGSEAAVPS VCFLLVPPPNQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
FRITLKEPEEQR FRITLKEPEEQR QALHSLCELHY RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RCISLQVDFIR RCISLQVDFIR LQLEACELETRT RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
PEPSPAPAPTL PEPSPAPAPTL RSELELELETRT RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
ELEAATKASLKE ELEAATKASLKE RLRAQAEEAQQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
QTDVQRQRELE QTDVQRQRELE QYLRGRLRYR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
KVEECCQRFKAK KVEECCQRFKAK QYINAIKDYE RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
IKFISETLRRR IKFISETLRRR MEERLAEER RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RELEAALRDAQQE RELEAALRDAQQE QKREAIQRLEEQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
EELQALRAAE EELQALRAAE QAEEAQRARQV RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
QAEEEAERLR QAEEEAERLR QAEEAERERLER RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AQQQAEEERA AQQQAEEERA REEKAERQLAEG RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
VRQRLEAEQE VRQRLEAEQE MEVLLLASAKAR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AAARLKAEEER AAARLKAEEER ELAELKLAAG RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RLAQLKAKASD RLAQLKAKASD SELERQKGLR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
QAELLEAAQR QAELLEAAQR SLEAAEERRR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RQLQLAAQEA RQLQLAAQEA QKRRLQAEEKA RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AAQSTRQKVAE AAQSTRQKVAE AVELKQSAEE RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AAEQTLRQVAAQ AAEQTLRQVAAQ QLEELTLRL RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
KARIEAENRA KARIEAENRA LILKAEAEELLQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
EKMQAVQENRA EKMQAVQENRA RAQAARAEEDA RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
ELKLRVAEMS ELKLRVAEMS QAQKLQLKKS RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
VAKAAQKLEEE VAKAAQKLEEE QQRQAALQMEQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
LRAEQQLLLEE LRAEQQLLLEE QHQAALAHSE RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
LSAEELQLLALA LSAEELQLLALA QGHHTTVDELA RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AASGFLLDTPV AASGFLLDTPV RNRRLTVNEA RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RLLLEAQIATG RLLLEAQIATG GVIDPVHSHR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
DPETGLCLLP DPETGLCLLP LTKKAAKGG RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
QFRTRITVE QFRTRITVE KVIKIIITVV RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
DTVRRALRGAGA DTVRRALRGAGA NVIAGVWLEE RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
AGLVGPFHGA AGLVGPFHGA KLLSAEKAVT RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
LDVACARGCL LDVACARGCL DEETSRAALS RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
LYSELQARET LYSELQARET FEKTPVEVPV RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
EVETLRQERL EVETLRQERL SFSGLRAPVP RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
DTKKEKVIYEDT KKEKVIYEDT AMRRGLLRAT RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
TGYRDDPYSGS TGYRDDPYSGS TISLFLQAMQK RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
DPSDDTQGGFF DPSDDTQGGFF DPNTHENLTY RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
IPGGGSHGGS IPGGGSHGGS TMSLWVVMQS RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RRRLTAVEDLFL RRRLTAVEDLFL EARLISLETY RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
LLSAEAVARLL LSAEAVARLL LEAQAATGFL RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
QAMKELIPT QAMKELIPT EEALRLLDQAQ RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RLSYTKLLRR RLSTYTKLLRR ECRDDGTGQL RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
NLQKFLFGTS NLQKFLFGTS CIAGVFDAT RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
GIVGPEFEGDK GIVGPEFEGDK LLSAERAVTG RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
EVAYKRKGLFD EVAYKRKGLFD EEMNEILTDP RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
SSVAKRRVVI SSVAKRRVVI VDPSETGKEMS RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
DIDDAIRKVD DIDDAIRKVD IDRSALDQYR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
TEETGPVAGI TEETGPVAGI LDTETLEKVS RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
IMVDRINLAQ IMVDRINLAQ TKFCGFEDPR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
RGTVDARTAQ RGTVDARTAQ KLRDVGAYS RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF
GSTAGSRTGS GSTAGSRTGS RTGSRAGSRR RRPVSLHMPV P RRPVSLHMPV P RRTVNLQVVMR AASLRAARGL VRETFEACHVF

IPI00018971 (100%), 54,169.5 Da
 Isoform 1 of E3 ubiquitin-protein ligase TRIM21
 8 unique peptides, 8 unique spectra, 8 total spectra, 96/475 amino acids (20% coverage)

M A S A A R L T M M	W E E V T C P I C L	D P F V E P V S I E	C G H S F C Q E C I	S Q V G K G G G S V	C P V C R Q R F L L	K N L R P N R Q L A
N M V N N L K E I S	Q E A R E G T Q G E	R C A V H G E R L H	L F C E K D G K A L	C W V C A Q S R K H	R D H A M V P L E E	A A Q E Y Q E K L Q
V A L G E L R R K Q	E L A E K L E V E I	A I K R A D W K K T	V E T Q K S R I H A	E F V Q Q K N F L V	E E E Q R Q L Q E L	E K D E R E Q L R I
L G E K E A K L A Q	Q S Q A L Q E L I S	E L D R R C H S S A	L E L L Q E V I I V	L E R S E S W N L K	D L D I T S P E L R	S V C H V P G L K K
M L R T C A V H I T	L D P D T A N P W L	I L S E D R R Q V R	L G D T Q Q S I P G	N E E R F D S Y P M	V L G A Q H F H S G	K H Y W E V D V T G
K E A W D L G V C R	D S V R R K G H F L	L S S K S G F W T I	W L W N K Q K Y E A	G T Y P Q T P L H L	Q V P P C Q V G I F	L D Y E A G M V S F
Y N I T D H G S L I	Y S F S E C A F T G	P L R P F F S P G F	N D G G K N T A P L	T L C P L N I G S Q	G S T D Y	

IPI00179473 (100%), 47,687.4 Da
 Isoform 1 of Sequestosome-1
 4 unique peptides, 4 unique spectra, 4 total spectra, 75/440 amino acids (17% coverage)

M A S L T V K A Y L	L G K E D A A R E I	R R F S F C C S P E	P E A E A E A A A G	P G P C E R	L L S R	V A A L F P A L R P	G G F Q A H Y R D E
D G D L V A F S S D	E E L T M A M S Y V	K D D I F R I Y I K	E K K E C R R D H R	P P C A Q E A P R N	M V H P N V I C D G	C N G P V V G T R Y	
K C S V C P D Y D L	C S V C E G K G L H	R G H T K L A F P S	P F G H L S E G F S	H S R W L R K V K H	G H F G W P G W E M	G P P G N W S P R P	
P R A G E A R P G P	T A E S A S G P S E	D P S V N F L K N V	G E S V A A A L S P	L G I E V D I D V E	H G G K R S R L T P	V S P E S S S T E E	
K S S S Q P S S C C	S D P S K P G G N V	E G A T Q S L A E Q	M R K I A L E S E G	R P E E Q M E S D N	C S G G D D D W T H	L S S K E V D P S T	
G E L Q S L Q M P E	S E G P S S L D P S	Q E G P T G L K E A	A L Y P H L P P E A	D P R L I E S L S Q	M L S M G F S D E G	G W L T R L L Q T K	
N Y D I G A A L D T	I Q Y S K H P P P L						

IPI00023122 (100%), 49,844.4 Da
 Isoform 1 of PDZ and LIM domain protein 7
 4 unique peptides, 4 unique spectra, 4 total spectra, 45/457 amino acids (10% coverage)

M D S F K V V L E G	P A P W G F R L Q G	G K D F N V P L S I	S R L T P G G K A A	Q A G V A V G D W V	L S I D G E N A G S	L T H I E A Q N K I
R A C G E R L S L G	L S R A Q P V Q S K	P Q K A S A P A A D	P P R Y T F A P S V	S L N K T A R P F G	A P P P A D S A P Q	Q N G Q P L R P L V
P D A S K Q R L M E	N T E D W R P R P G	T G Q S R S F R I L	A H L T G T E F M Q	D P D E E H L K K S	S Q V P R T E A P A	P A S S T P Q E P W
P G P T A P S P T S	R P P W A V D P A F	A E R Y A P D K T S	T V L T R H S Q P A	T P T P L Q S R T S	I V Q A A A G G V P	G G G S N G N K T P
V C H Q C H K V I R	G R Y L V A L G H A	Y H P E E F V C S Q	C G K V L E E G G F	F E E K G A I F C P	P C Y D V R Y A P S	C A K C K K K I T G
E I M H A L K M T W	H V H C F T C A A C	K T P I R N R A F Y	M E E G V P Y C E R	D Y E K M F G T K C	H G C D F K I D A G	D R F L E A L G F S
W H D T C F V C A I	C Q I N L E G K T F	Y S K K D R P L C K	S H A F S H V			

IPI00218398 (100%), 65,895.8 Da
 Matrix metalloproteinase-14
 2 unique peptides, 2 unique spectra, 2 total spectra, 17/582 amino acids (3% coverage)

M S P A P R P P R C	L L L P L L T L G T	A L A S L G S A Q S	S S F S P E A W L Q	Q Y G Y L P P G D L	R T H T Q R S P Q S	L S A A I A A M Q K
F Y G L Q V T G K A	D A D T M K A M R R	P R C G V P D K F G	A E I K A N V R R K	R Y A I Q G L K W Q	H N E I T F C I Q N	Y T P K V G E Y A T
Y E A I R K A F R V	W E S A T P L R F R	E V P Y A Y I R E G	H E K Q A D I M I F	F A E G F H G D S T	P F D G E G G F L A	H A Y F P G P N I G
G D T H F D S A E P	W T V R N E D L N G	N D I F L V A V H E	L G H A L G L E H S	S D P S A I M A P F	Y Q W M D T E N F V	L P D D D R R G I Q
Q L Y G G E S G F P	T K M P P Q P R T T	S R P S V P D K P K	N P T Y G P N I C D	G N F D T V A M L R	G E M F V F K E R W	F W R V R N N Q V M
D G Y P M P I G Q F	W R G L P A S I N T	A Y E R K D G K F V	F F K G D K H W V F	D E A S L E P G Y P	K H I K E L G R G L	P T D K I D A A L F
W M P N G K T Y F F	R G N K Y Y R F N E	E L R A V D S E Y P	K N I K V W E G I P	E S P R G S F M G S	D E V F T Y F Y K G	N K Y W K F N N Q K
L K V E P G Y P K S	A L R D W M G C P S	G G R P D E G T E E	E T E V I I I E V D	E E G G G A V S A A	A V V L P V L L L L	L V L A V G L A V F
F F R R H G T P R R	L L Y C Q R S L L D	K V				

IPI00021263 (100%), 27,745.9 Da
 14-3-3 protein zeta/delta
 2 unique peptides, 2 unique spectra, 2 total spectra, 26/245 amino acids (11% coverage)

M D K N E L V Q K A	K L A E Q A E R Y D	D M A A C M K S V T	E Q G A E L S N E E	R N L L S V A Y K N	V V G A R R S S W R	V V S S I E Q K T E
G A E K K Q Q M A R	E Y R E K I E T E L	R D I G N D V L S L	L E K F L I P N A S	Q A E S K V F Y L K	M K G D Y Y R Y L A	E V A A G D D K K G
I V D Q S Q Q A Y Q	E A F E I S K K E M	Q P T H P I R L G L	A L N F S V F Y Y E	I L N S P E K A C S	L A K T A F D E A I	A E L D T L S E E S
Y K D S T L I M Q L	L R D N L T L W T S	D T Q G D E A E A G	E G G E N			

IPI00010796 (100%), 57,118.1 Da

Protein disulfide-isomerase

2 unique peptides, 2 unique spectra, 2 total spectra, 19/508 amino acids (4% coverage)

MLRRALLCLA	VAAALVRADAP	EEEDHVLVLR	KSNFAEALAA	HKYLLVEFYA	PWCGHCKALA	PEYAKAAGK	L
KAEGSEIR LA	KVDATEEESDL	AQQYGVRGYP	TIKFFRNGDT	ASPKEYTAGR	EADDIVNWLK	KRTGPAATTL	
PDGAAAESLV	ESSEVAVIGF	FKDVESDSAK	QFLQAAEAID	DIPFGITSNS	DVFSKYQLDK	DGVVLFKKFD	
EGRNNFEGEV	TKENLLDFIK	HNQLPLVIEF	TEQTAPKIFG	GEIKTHILLF	LPKSVSDYDG	KLSNFKTAAE	
SFKGKILFIF	IDS DHTDNQR	I L E F F G L K K E	ECPAVRLITL	EEEMTKYKPE	SEELTAERIT	EFCHRFLLEGK	
IKPHLMSQEL	PEDWDKQPVK	VLVGKNFEDV	AFDEKKNVVF	EFYAPWCGHC	KQLAPIWDKL	GETYKDHENI	
VIAKMDSTAN	EVEAVKVHSF	PTLKFFPASA	DRTVIDYNGE	RTL D G F K K F L	ESGGQD G A G D	DDDLEDELEEA	
E E P D M E E D D D	Q K A V K D E L						