

Human	MST ASSSSSSSSSSQT PHPPSQR MRSAAGSPPAVAAAGSGNGAGGGGVGCAPAAGAGRL
Mouse	MST ASSSSS---SQTPHSAPQR MR RSTAGSPP--AAAGSGTGPAG---SCAPAAGAGRL
Zebrafish	MSASP VHS-----ARVRRSNDGSPINTSSSASSS-----SSSSSTGNTSR
Human	LQPIRATVPYQLL RGSQHSPTR PPVAAA-----AASLGSLPGPGAARGPSPSSPTPPAA
Mouse	LQPIRATVPYQLL RGSQHSPTR AAAAAT---AAAALGSLSGPGGARGPSPSSPTPPPA
Zebrafish	LQPIRATVPYQLL RGSQHSPTR PASFSTPSSSSSI VGNSNTEPTASAQHSN TPGSPTL
Human	AAPAEQAP---RAKGRPRRSPESHRRSSSPERRSPGSPVCR-ADKA KSQ QVR T S T IRRT
Mouse	AAPAEQAP---RAKGRPRRSPESHRRSSSPERRSPGSPVCR-VDRPKS Q HIRT S STIRRT
Zebrafish	ASPAGSASLDGRLI PRQR SPPEHR--SSPER-CPHSPVLAVERSKSQQVR STGA IRRRT
Human	SSLDTITGPYLTGQWPRD PHV HYPSCMKD KAT QT P SCWAEEGA EKRS -HQ RS ASWGSDQ
Mouse	SSLDTITGPYLTGQWPRD PHV HYPSCMRD KAT QT P SCWAEEGA EKRS -HQ RS ASWGSDQ
Zebrafish	SSLGAITGPYLTGQWPRESHLHNPLCMKD KST QT P CWSDESEEKRSTHQ RS ASWGSDH
Human	IKE Q IAKLRQQLQRSKQSS-RHSKE-KDRQSP L HGNHITISHTQATG-----SRS
Mouse	IKE-IAKLRQQLQRSKQSS-RHSKE-KDRQSP L HGNHITISHTQAI G -----SRS
Zebrafish	IKE-IAKLR L Q Q R N KQ GG GR Q CKDS K ECL S PLH C CT T TT T ATTISTASQAPSSMSKS
Human	VPMPLSNISVPKSSVS R PCNVEG I SP E LEKV F IKENNGKEEVSKPLDI PD GRRAP L PAH
Mouse	VPMPLSNISVPKSSVS R PCNVEG I SP E LEKV F IKENNGKEEVSKPLDI PD GRRAP L PAH
Zebrafish	AQMPLSNITVPKPSI R V P S M E G INHELEKV F IKDN G E K EEL-KALEV P DGRAP F PQ
Human	YRSSSTRSIDTQ TP SVQERSSSCSSH S PCVSPFC P ESQDGSPC S TED L LYDRDKD S GSS
Mouse	YRSSSTRSIDTQ TP SVQERSSSCSSH S PCVSPFC P ESQDGSPC S TED L LYDRDKD S GSS
Zebrafish	QRSSSSRGIDTQ TP SV P GRSSSSCSSL S PCP S AC P R S H D GSPY S TDEM L DD R KD S GSS
Human	SPLPKYASSPKPNNSYMFKRE P PEGC E RV K VFEEMASRQ P I S APLF S CPDKNKVNFIPTG
Mouse	SPLPKYASSPKPNNSYMFKRE P PEGC E RV K VFEEMASRQ P I S APLF S CPDKNKVNFIPTG
Zebrafish	SPLPKFASSPKPNNSYMFKRE P PEGCE K IKVFEEMTSRQ S TTVPLF S CPDKNKVNFIPTG
Human	SAFCPV K LLGP L PASD I MLKN S PNSGQSS S ALATLT V EQ L SSRV S FT S LSDD T STAGS M E
Mouse	SAFCPV K LLGP L PASD I MLKN S PNSGQSS S ALATLT V EQ L SSRV S FT S LSDD T STADS L E
Zebrafish	SAFCPV K LP G SM I QHSSSQ Q EDEERE-PTQ A GPSALHHHMPTQV S T S TD D P-----
Human	ASVQQPSQQQQQLQ E LOGEDH I SAQNYVII
Mouse	PSAQQPSQQQQQLQ D LQ V VEEHV S TQNYVMI
Zebrafish	--PESPSQO---QEAPSESGS Q PONFEVS

Supplementalry Figure.1

Alignment of amino acid sequences of human, mouse and zebrafish Glcc1 predicted from their nucleotide sequences. The amino acid same with human, mouse and zebrafish are marked by shading.

Supplementary Table 1. Identification of protein sequences in peptides obtained from the 70 kDa and 150 kDa protein fractions in the urine of proteinuric zebrafish embryos using mass spectrometry sequencing. Only the 10 most prominent peptide sequences identified in each fraction are shown.

A.	150 kDa fraction	
Accession	Protein name	Hits
Q1LWN5_DANRE	Novel protein similar to vitellogenin 1 Vg1 Flags Fragment	420
A2VCZ6_DANRE	Zgc 136383 protein Flags Fragment	433
Q1LWN2_DANRE	Vitellogenin 1	383
Q1LWN4_DANRE	Novel protein similar to vitellogenin 1 Vg1 Flags Fragment	328
Q90YN8_DANRE	Vitellogenin 1	369
Q8JH37_DANRE	Vitellogenin 1 Flags Fragment	294
Q1LWN1_DANRE	Novel protein similar to vitellogenin 1 Vg1 Flags Fragment	294
A8WGJ7_DANRE	Zgc 136383 protein Flags Fragment	315
A4VCF4_DANRE	Vtg1 protein Flags Fragment	240
A3KMS4_DANRE	Vtg7 protein	269

B.	70 kDa fraction	
Accession	Protein name	Hits
Q1LWN5_DANRE	Novel protein similar to vitellogenin 1 Vg1 Flags Fragment	586
A2VCZ6_DANRE	Zgc 136383 protein Flags Fragment	597
Q1LWN2_DANRE	Vitellogenin 1	557
Q90YN8_DANRE	Vitellogenin 1	535
Q1LWN4_DANRE	Novel protein similar to vitellogenin 1 Vg1 Flags Fragment	473
Q8JH37_DANRE	Vitellogenin 1 Flags Fragment	385
Q1LWN1_DANRE	Novel protein similar to vitellogenin 1 Vg1 Flags Fragment	380
A4VCF4_DANRE	Vtg1 protein Flags Fragment	330
Q1MTC6_DANRE	Novel protein similar to vitellogenin 1 Vg1	422
Q1MTC4_DANRE	Novel protein similar to vitellogenin 1 Vg1	244

Supplementary Table 2. Identification of protein sequences in peptides obtained from the 70 kDa and 150 kDa protein fractions in the serum of adult wild type zebrafish using mass spectrometry sequencing. Only the 10 most prominent peptide sequences identified in each fraction are shown.

A. 150kDa fraction

Accession	Protein name	Hits
IPI00508594	vtg1;vtg5 Vitellogenin 1	228
IPI00919379	vtg7 149 kDa protein	215
IPI00975348	vtg7 149 kDa protein	223
IPI00858854	vtg6 vitellogenin 6	209
IPI00866006	vtg7 Vtg7 protein	191
IPI00920458	vtg7 124 kDa protein	157
IPI00503804	vtg3 vitellogenin 3, phosvitinless	67
IPI00500668	vtg2 Novel protein similar to vitellogenin 1	62
IPI00615908	Novel protein similar to complement component 3	42
<u>IPI00506519</u>	<u>cp Ceruloplasmin</u>	<u>49</u>

B. 70kDa fraction

Accession	Protein name	Hits
IPI00972722	tfa Transferrin	154
IPI00505602	Complement component c3b	56
IPI00773000	fetub fetuin B	54
IPI00513243	lmnb2 Lamin B2	39
IPI00835213	si:dkey-76b14.4 185 kDa protein	41
IPI00963174	si:dkey-76b14.4 Novel protein	40
IPI00864674	191 kDa protein	34
IPI00975348	vtg7 149 kDa protein	21
IPI00858854	vtg6 vitellogenin 6	20
<u>IPI00866006</u>	<u>vtg7 Vtg7 protein</u>	<u>21</u>