### **Supplementary Information**

Acute-phase proteins during inflammatory reaction by bacterial infection: Fishmodel

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# Attachment 1 (SDS-PAGE polyacrylamide gel)



**Figure I.** SDS-PAGE polyacrylamide gel during acute inflammatory response in tilapias 6 and 24 HPI. Highlighted in red the area presented in the Figure 1.



**Figure II.** SDS-PAGE polyacrylamide gel demonstrating the cut areas (highlighted in red) submitted to in gel trypsin digestion coupled to mass spectrometric analysis resulting in the identification of proteins present in the bands (Figure 1). (1) ceruloplasmin; (2) complement C3; (3)  $\alpha_2$  macroglobulin; (4) albumin; (5) transferrin; (6) haptoglobin; (7) apolipoprotein Eb and complement C3 isoform X1; (8) complement factor 3 and apolipoprotein Eb; (9) apolipoprotein A1.

# Attachment 2 (Protein comparative analysis)

XP_019212735.1	1	. MDRIWILSCTICVILSWIHVDQAVAE <mark>PQYLVAIPAVI</mark> EAGAEAKFCATIRQPSGTIVM
sp P01023 A2MG_HUMAN	1	MGKNKILHPSLVILLIVLLPTDASVSGKPQYMVLVPSLLHTETTEKGCVLISYLNETVTV
XP_019212735.1	59	TVTEMSREKNTTLETHTSNE.AFQTCVQFKAPLVQKEVQHFQVEVRGDTFYSKQVTKV
sp P01023 A2MG_HUMAN	61	SASLESVRGNRSLETDLEAENDVLHCVAFAVDKSSSNEEVMFLTVQVKGPTQEFKKRTTV
XP_019212735.1	116	MIQTYDPFTFIQTDKPIYLPGQKVNFRVVTMDNKMRPANOLYDVIELQDPNSNRIGOWLN
sp P01023 A2MG_HUMAN	121	MVKNEDSLVFVQTDKSIYKPGQTVKFRVVSMDENFHPINELIPLVYIQDPKGNRIAQWQS
XP_019212735.1	176	ETSSSRILQLSYSIDTEAREGPYQIIVSMGER.KISHNEKVEKYVLPKEDVTVNTSEEVS
sp P01023 A2MG_HUMAN	181	FQLEGGLKQFSEPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEVLPKFEVQVTVPKILT
XP_019212735.1	235	IGQEDTEAKVCAK <mark>YTYGQPVPGRVTVNVCR</mark> PIKYFFHGVSV <mark>HSED</mark> DLALLQISAPGHTET
sp P01023 A2MG_HUMAN	241	ILEEEMNVS <mark>VC</mark> GL <mark>YTYG</mark> K <mark>PVPGHVTVSICR</mark> KYSDASDCHGEDSQAFCEKFS
XP_019212735.1 2	295	KOADKTGCATFSFNMSIFTKVDQKVLHDVLDIRAKVEEEGTGISHPQEKRIRISYVLGKV
sp P01023 A2MG_HUMAN 2	292	GOLNSHGCFYQQVKTKVFQLK.RKEYEMKLHTEAQIQEEGTVVELTGRQSSEITRTITKL
XP_019212735.1 3	355	SFINMPKVWERGSNVEGKVRAVYHNNTPVCDAPVYLFTGQMRQTHSLONLTTDSNGVASF
sp P01023 A2MG_HUMAN 3	351	SFVKVDSHFRQGIPFFGQVRLVDGKGVPLPNKVIFIRGNEANYYSNATTDEHGLVQF
XP_019212735.1	415	SFSTDNFDQDIQLHASLTPTVDYPRYRAAFYDRGFHTLSMSQPSSPDIKTISSLEVQTND
sp P01023 A2MG_HUMAN	408	SINTTNVMGTSLTVRVNYKDRSPCYGYQWVSEEHEEAHHTAYLVFSPS <mark>K</mark> SFVH <mark>LE</mark> PMS
XP_019212735.1	475	KAVACDAEEDISVNYTIVGESPGSVDVI <mark>YLVISRG</mark> AVTMOGOKOVEVODRSVTEGOV
sp P01023 A2MG_HUMAN	466	HELPCGHTQTVQAHYILNGGTLLGLKKLSFY <mark>YLIM</mark> AKGGIVRTGTHGLLVK.QEDMKGHF
XP_019212735.1	532	SFKVRVSPEMAPEFOVVAYAVLPSEDVIAHSADFSTDKCFSNKVSVEFSPSSAVPGEETN
sp P01023 A2MG_HUMAN	525	SISIPVKSDIAPVARLLIYAVLPTGDVIGDSAKYDVENCLANKVDLSFSPSOSLPASHAH
XP_019212735.1 9	592	MOVMALPHSLCGVSAIDKSVLIKEPGKTLDADKIFDLFPLKKSSGIPYEVDDATECLNVR
sp P01023 A2MG_HUMAN 9	585	LRVTAAPOSVCALRAVDOSVLLMKPDAELSASSVYNLLPEKDLTGFPGPLNDODNEDCIN
XP_019212735.1	652	PKRYVLPYPRQEQNDAYAIFQKVGLKMATNLLIRLPSCLQFKGKFYHERSHRVY
sp P01023 A2MG_HUMAN	645	RHNVYINGITYT <mark>P</mark> VSSTNEK <mark>DMY</mark> SFLEDMGLKAFTNSK <mark>IR</mark> KPKMCPQLQQYE
XP_019212735.1 7	706	YAMAPRERDNSIRLSSPVAASAGNLAPEPAPI <mark>etvr</mark> sf <b>epetwiwdlv</b> evgdd <mark>g</mark> krgvsl
sp P01023 A2MG_HUMAN 6	697	Mhgpegl <mark>r</mark> vgfyesdvmgrgh <mark>a</mark> rlvhv <mark>e</mark> epht <mark>etvr</mark> k <mark>yppetwiwdlv</mark> vvnsa <mark>g</mark> vaevgv
XP_019212735.1 7	766	TVPDTITTWETEAFCLSSQG.FGLAPRKEMKVFQPFFLELTMPYSIIRGEHEE <mark>LKATV</mark> FN
sp P01023 A2MG_HUMAN 7	757	TVPDTITEWKAG <mark>AFCLS</mark> EDAGL <mark>G</mark> ISSTASLRAFQPFFVELTMPYSVIRGEAFTLKATVLN
XP_019212735.1 8	825	YLTSCIMVTVTPGPSSDYTLTPLSGDLYTSCLCANERKTLRWTMIPTALGAVNVTVSAEA
sp P01023 A2MG_HUMAN 8	817	YLPKCIRVSVOLEASPAFLAVPVEKEOAPHCICANGROTVSWAVTPKSLGNVNFTVSAEA
XP_019212735.1 8	885	VASHVSCONEVVSVPDRGRIDVVTKSLIVKAEGTEMTKTYNWLLCPKGSPLTEEAEIHLP
sp P01023 A2MG_HUMAN 8	877	LESQELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTPNSLLCPSGGEVSEELSLKLP
XP_019212735.1 9	945	E <mark>NVIEGSARTSVSVLGDILGRALK</mark> NLDGLLQMPYGCGEQNMALLAPNIYILHYLKGTQQL
sp P01023 A2MG_HUMAN 9	937	P <mark>NVVE</mark> ESARASVSVLGDILGSAMQNTQNLLQMPYGCGEQNMVLFAPNIYVLDYLNETQQL
XP_019212735.1 10	005	TTAIMEKATNELTSGYQRQLNYKSADGAYTTEGTGPGNTWLTAEVVRSESKAQSEV
sp P01023 A2MG_HUMAN 9	997	TPEIKS <mark>KA</mark> IG <mark>YLNTGYQRQLNYK</mark> HY <mark>DGSYSTEG</mark> ERY <mark>G</mark> RNQG <mark>NTWLTAEVLKTE</mark> AQ <mark>A</mark> RA <u>YI</u>
XP_019212735.1 10	061	YIDPRKIEESKSWLQHKQQENGCFEKSGKLFNNRMKGGVSDEVTLSAYVTAAFLEMNTSQ
sp P01023 A2MG_HUMAN 10	057	FIDEAHITQALIWLSQRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTV
XP_019212735.1 1: sp P01023 A2MG_HUMAN 1:	121	HDPVMNKSLACLKESLSDLSNTYTTALLAYVFTLAGDVETRAHDLQHDTVAVR THPVVRNALFCLESAWKTAQEGDHGSHVYTKALLAYAFALAGNQDKRKEVUKSUNEEAVK
xP_019212735.1 11 sp P01023 A2MG_HUMAN 11	175	EGGFILYWSQTAAETSASLSVELSSYVLLAKLSASPTAEDLGYASGIIR KDNSVHWERPQKPKAPVGHFYEPQAP <mark>SAEVEMTSYVLLAYLTAQ</mark> PA <mark>PTSEDLTSATNIVK</mark>
XP_019212735.1 12 sp P01023 A2MG_HUMAN 12	223	WLTGQQNYYGGFSSTQDTVVALQALALYSTLVPSPEGWSTVTVQAPSSQLT HDVNQSN WITKQQNAQGGFSSTQDTVVALHALSKYGAATETRTGKAAQVTIQSSGTFSSKEQVDNNN
AF_019212735.1 12   sp P01023 A2MG_HUMAN 12   XP_019212735.1 13	297 340	RELLOQUES UPELPGEYSMKVTGEGCUYLOTSLKYNILPEKEEFPFALGVOTLPOTCDBPK RELLOQUESUPELPGEYSMKVTGEGCUYLOTSLKYNILPEKEEFPFALGVOTLPOTCDBPK
sp P01023 A2MG_HUMAN 13	357	
sp P01023 A2MG_HUMAN 1	417	IYLDKVSNQT.LSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNAPCSKDLGNA

**Figure III.** Structural comparison of the alpha-2-macroglobulin between *Oreochromis niloticus* and *Homo sapiens*. The FASTA files related to tilapia and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).

XP_021322235.1	1	MALIVSCCLKGFFTTFTCVNGNKTRPIFMVTFPAVTESGSDAKLCASTLKPNKTLFM
sp P01023 A2MG_HUMAN	1	MGKNKLLHPSLVLLLIVTLPTDASVSGKPQYMVLVPSLLHTETTEKGCVLTSYLNETVTV
XP_021322235.1	61	NIYLVHSNQŠ.TLLLQEKABOEFHRCFNBOAD.LAEABSVOKIKVELQGESFNMTEERKV
sp P01023 A2MG_HUMAN	61	SASLesvrgnrSlftdlbaendvlhcvabavdksssnbevmfltvovkGptoefkkrttv
XP_021322235.1	119	MFKSYHPLTFIOMDKPFYIA <mark>GQTV</mark> NFRVVTMDKSERPLDQQYSAVVLEDSQDNRIGQWTN
sp P01023 A2MG_HUMAN	121	MVKNEDSLVFVQTDKSIYKPGQTVKFRVVSMDENFHPLNELIPLVYLQDPKGNRIAQWQS
XP_021322235.1	179	VSSTRWILORSYDINPEARECTYKVKAFIG.ERMISHDEDVKKYVLPKEGVEVISENPVS
sp P01023 A2MG_HUMAN	181	Foleggikofsepissepfocsykvvvokksggrtehpetveefvlpkfevovtvekiit
XP_021322235.1	238	IDDEFMVIE <mark>vcgkytygkpvlgksSvkvcrk</mark> tldthSplcvkeSteisktgCa
sp P01023 A2MG_HUMAN	241	ILEEEMNVS <mark>vcglytygkpv</mark> pgHvTvsIcrkysdasdchgedsQafCekFSgQLNshGCF
XP_021322235.1	291	NHTLALSVEFYPTHHQLLNDLHIEATTTEEETEITMTQSNTISLTYEIGKVTETDLPKTY
sp P01023 A2MG_HUMAN	301	YQQVKTKVFQLK.RKEYEMKLHTEAQIQEEGTVVELTGRQSSEITRTITKLSEVKVDSHF
XP_021322235.1	351	EYGSVIEGKVKLARFRGTAVPGKHIYLENYSWPPKVLLNLTTDSNGLANESLNTLRFVK
sp P01023 A2MG_HUMAN	360	RQGIPFFGQVRLVDGKGVPIBNKVIFIRGNEANYYSNATTDEHGLVQFSINTTNVMG
XP_021322235.1	411	SDINLMASAYPGYRSMFQKSPMFNTDBKTVQFFPKPAASYTPTFSELIIENTEQPUKCGT
sp P01023 A2MG_HUMAN	417	ISLTVRVNYKDRSPCMGMQWVSBEHEEAHHTAYLVFSBSKSFVHLBPMSHETPCCH
XP_021322235.1	471	EITATVKYYFVKETVK.IFNADIVYMVLSRGVIIHHGYEKVEVKSSNAVASGTMSFKLSV
sp P01023 A2MG_HUMAN	473	TQTVQAHYILNGGTLLGLKKLSFYYLIMAKGGIVRTGTHGLLVKQEDMKGHFSISIPV
XP_021322235.1	530	GADVAPLVQILAYCVLPSENIAIHSENFHVEKCLKNKVSLQFSPAKAVPGEKNTLQLSAQ
sp P01023 A2MG_HUMAN	531	KSDIAPVARLLIYAVLPTGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTA
XP_021322235.1	590	EGSLCGLSAVDQSVLMLESGKRUDADKIFNLLEVKYGSGYESSLPDEKECFYMMAVPI
sp P01023 A2MG_HUMAN	591	POSVCALRAVDQSVLLMKPDAELSASSVYNLLPEKDLIGFEGPINDQDNEDCINRHNVYI
XP_021322235.1	648	EN <mark>I</mark> FKSSKR <mark>IGLKMATNLAVR</mark> SGTSTCEMYKKFSMFAILPVDLFRDI
sp P01023 A2MG_HUMAN	651	NG <mark>I</mark> TYTPVSSTNEKDMYSFLED <mark>MGLKA</mark> F <mark>TN</mark> SK <mark>IR</mark> KPKMCPQLQQYEMHGPEGLRVGFYES
XP_021322235.1	695	GLAEDSVPHWTLFEENVRSVFPKTWLWQLIEISDSGSAEVPVTVPDTITSMETEAF
sp P01023 A2MG_HUMAN	711	DVMGRGHARLVHVEEPHTET <mark>VR</mark> KYFPETWIWDLVVVNSA <mark>GVAEVGVTVPDTIT</mark> BWKAGAF
XP_021322235.1	751	CLSSTG.LGLAPP <mark>AQLTVFQPFFLELSLPYSIIRGEMFELKATVFNYLSKCIMVKVS</mark> PAP
sp P01023 A2MG_HUMAN	771	CLSEDAGLGISST <mark>ASLRAFQPFFVELTMPYSVIRGEAFTLKATVL</mark> NYLPKCIRVSVQLEA
XP_021322235.1	810	SSDYTLKASSDDOYSS <mark>CLCANGRKTFKWILTP</mark> SV <mark>IGVVNVTVRAEAEASOTVC</mark> DNEIVSV
sp P01023 A2MG_HUMAN	831	SPAFLAVPVEKEOAPH <mark>CICANGROT</mark> VSWAVTPKSLGNVNFTVSAEALESOELCGTEVPSV
XP_021322235.1	870	PERGRIDTVTRSLLVQAEGIKKAKTNSWLLCPKGDSLLEEIDLTLPKDMIEGSVTSSVSV
sp P01023 A2MG_HUMAN	891	PEHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVSEELSLKLPPNVVEESARASVSV
XP_021322235.1	930	IGDIVGRSLKKLHRTLWRIYRSGN <mark>ONIAILSPSIYIHOYLENWKOLT</mark> SAIREKASSFLKS
sp P01023 A2MG_HUMAN	951	LGDILGSAMQNTQNLLQMPYGCGE <mark>QNMVL</mark> FAPNIYVLDYLNETQQLTPEIKSKAIGYLNT
XP_021322235.1	990	GYQRQLKYRHRNGAYSTFGNGKGNAWLTAFVLKSFVKAQKYIYIDPQIIKSAKKWL
sp P01023 A2MG_HUMAN	1011	GYQRQLNYKHYDGS <mark>YSTFG</mark> ERYGRNQGNTWLTAFVLKTFAQARAYIFIDEAHITQALIWL
XP_021322235.1	1046	IGTQDPEGCFIQHGRLFNNRLKGGVSDHVTMTAYITASLLELETSVTDPVIIKGLSCLRS
sp P01023 A2MG_HUMAN	1071	SQRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTVTHPVVRNALFCLES
XP_021322235.1	1106	VIKDVKNTYTTALLAYTESLARDTNTRQQLENKLEDLAISDGPLVHWSQSAS
sp P01023 A2MG_HUMAN	1131	AWKTAQEGDHGSHVYTK <mark>ALLAY</mark> A <mark>FALA</mark> GNQDK <mark>R</mark> KEVLKSLNEEAVKKDNS <mark>VHW</mark> ERPQKPK
XP_021322235.1	1158	ADDSD <mark>SLDVEISSYVLLAVLTA</mark> D.SL <mark>TTADL</mark> GF <mark>ANRIVSWLVKQQNAYGGFSS</mark>
sp P01023 A2MG_HUMAN	1191	APVGHFYEPQAP <mark>SAEVEMTSYVLLAYLTA</mark> QPAPTSEDLTSATNIVKWITKQQNAQGGFSS
XP_021322235.1	1210	TODTVVALOALSLYATKVFSSDGSSTVTVQŠAGDSHYFNVNQDNKLVYOEKOLANVPG
sp P01023 A2MG_HUMAN	1251	TODTVVALHALSKYGAATFIRTGKAAQVTIQSSGTFSSKFOVDNNNRLLLOQVSLPELPG
XP_021322235.1	1268	KYKTEVKCSACVSVOMAQFYNIITPKEVKTLSTDVKIEGDCKKTFGNKLLLEFTVNYD
sp P01023 A2MG_HUMAN	1311	Eysmkvtgegcvylotslkyniipekeefpfalgvotlpotcdepkahtsfolslsvsyt
XP_021322235.1	1326	GPHETTNMLIVDVKLLSGFTADDT <sup>WMF</sup> GSSSGFVVPLVEQVDVKDDHVIVVLKEVPKHFP
sp P01023 A2MG_HUMAN	1371	GSRSA <mark>SNMAIVDVKMVSGF</mark> IPLKPWVKMLERSNHVSRTEVSSNHVLIVLDKVSNQT.
XP_021322235.1	1386	VNYQIQMKQVLHVMNLKPAVIKVYDYYQTSDQSETEYYFHC
sp P01023 A2MG_HUMAN	1427	LSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNAPCSKDLGNA

**Figure IV.** Structural comparison of the alpha-2-macroglobulin between *Danio rerio* and *Homo sapiens*. The FASTA files related to zebrafish and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

	1 10	20	30	4 Q	5 Q	60
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	MGKHRLRSLA MGKNKL 70	LLPLLLRLLLL LHPSLVLLLLV 80	LLPTDASAPQK LLPTDASVSGK 90	PIYMVMVPSLL PQYMVLVPSLL 100	HAG <mark>TPEKAC</mark> F HTE <mark>TTEK</mark> GCV 110	LFSHLNE LLSYLNE
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN 12	TVAVRVSLES TVTVSASLES 20 13	VRGNOSLFTDL VRGN <mark>RSLFTDL</mark> 0 140	VVDKDLFHCTS EAENDVLHCVA 150	FTVPQSSS.DE FAVPKSSSNEE 160	VMFFTVQVKG VMFLTVQVKG 170	ATH <mark>EF</mark> RR P <b>TQEF</b> KK
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN 1	RSTVLVKKKE RTTVMVKNED 80 19	SLVFAQTDKPI SLVFVQTDKSI 0 200	KPGQTV <mark>RFRV</mark> KPGQTV <mark>K</mark> FRV 210	VSLDESFHPLN VSMDENFHPLN 220	ELIPL <mark>LYIQD</mark> ELIPLVYIQD 230	PK <mark>NNRIA</mark> PK <mark>GNRIA</mark>
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	QWQNFNLEGG QWQSFQLEGG	LKQLSFPLSSE LKQFSFPLSSE	PTQGSYKVVI PFQGSYKVVVQ	ATE <mark>SG</mark> RTV <mark>EHPF</mark> OKK <mark>SG</mark> GRT <b>EHPF</b>	SVEEFVLPKF TVEEFVLPKF	EVRVTVP EVQVTVP
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	ET <mark>ITILEEEM</mark> KI <b>ITILEEEM</b>	NVSVCGIYTYG NVSVCGLYTYG	KPVPGRVTVNI KPVPGHVTVSI	CRKYSNPSNCF CRKYSDASDCH	GEESVAFCEK GEDSQAFCEK	L <mark>SQQL</mark> DG F <b>SGQL</b> NS
3 0 sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	RGCFSQLVKT HGCFYQQVKT	9 320 KS <mark>FQLKR</mark> QEYEN KV <mark>FQLKR</mark> KEYEN	330 QLDVHAKIQE KLHTEAQIQE	<b>340</b> EGTGVEETGKG EGTVVELTGRQ	350 LTKITRTITK S <mark>S</mark> EITRTITK	LSFVNVD LSFV <mark>KVD</mark>
3 sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	60 37 SHFRQGIPFV SHFROGIPFF	0 380 GOVLLVDGRGT GOVRLVDGKGV	390 PIPYETIFIGA PIPNKVIFIRG	400 DEANLYINTTT NEANYYSNATT	410 DKHGLARFSI DEHGLVOFSI	NTDDIMG
4 sp   P06238   A2MG_RAT	20 43 TSLTVRAKYK TSLTVRUNYK	0 440 DSNACYGFRWL	450 TEENVEAWHTA	460 YAVFSPSRSFL	470 HLESLPDKLR	DOTLEV
sp P01023 A2MG_R0MAX 4 8 sp P06238 A2MG_RAT	QAHYILNGEA	QE <mark>LK</mark> ELV <mark>FYYI</mark>	510 M <mark>MAKGGIVR</mark> A	520 510 <mark>GTH</mark> VLPL <mark>KO</mark> GQ	530 530 M <mark>RGHFSI</mark> LIS	METDLAP
sp P01023 A2MG_HUMAN 54	QAHYILNGGT 40 55	LG <mark>LK</mark> KLSFYYI 0	JIMAKGGIVRT 570	GTHGLLVKQED 580	MKGHFSISIP 590	VKSDIAP
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN 6	VARLVLYAIL VARLLIYAVL	PNGEVVGDTAK PTGDVIGDSAK .0 620	YEIENCLANKV Y <u>DVENCLANKV</u> 630	DLVFRPNSGLP DLSFSPSQSLP 640	ATRALLSVMA A <u>SHA</u> HLRVTA 659	SPQSLCG APQSVCA
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN 6	LRAVDOSVLL LRAVDOSVLL 60 67	MKPETELSASL MKPDAELSASS 0 680	IYDLLPVKDLT VYNLLPEKDLT 690	GFPQGADQREE GFPGPLNDQ 700	DTNGCVKOND DNEDCINRHN 710	T <b>YINGI</b> L V <b>YINGI</b> T
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN 7:	YSPVQNTNEE YTPVSSTNEK 20	DMYGFLKDMGL DMYSFLEDMGL 730	KVFTNSNIRKP KAFTNSKIRKP 740	KVCERLRDNKG KMCPQLQQYEM	IPAAYHL <mark>V</mark> SQ: HGPEGLRVGF 760	SHM <mark>D</mark> AFL YES <b>DV</b> MG 770
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	ESS RGHARLVHVE	ESPTETRRSYFI EPHTETVRKYFI	PETWIWDLVVV PETWIWDLVVV	DSAGVAEVEVT NSAGVAEVGVT	VPDTITEWKA VPDTITEWKA	GAFCLSN GAFCLSE
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	DTGLGLSPVV DAGLGISSTA	FQAFQPFFVEI SLR <mark>AFQPFFVE</mark> I	TMPYSVIRGE TMPYSVIRGE	AFTLKATVLNY AFTLKATVLNY	PTCIRVAVQI PKCIRVSVQI	LEASPDF LEASPAF
DIP062381A2MG RAT	840	850 HCTCMNORHTA	860 SWAV⊺PKSLG	870 NVNETVSAEAL	880 ISKELCGNEVE	890 VVPEOG
p P01023 A2MG_HUMAN	LAVPVEKEQAP 900	HCICANGROTV 910	SWAV 920	NVNFTVSAEAL 930	SQELCGTEVE 940	SVPEHG 950
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	KKDTIIKSLLV RKDTVIKPLLV 960	· /EPEGLENEVTE /EPEGLEKETTE 970	NSLLCPMGAE NSLLCPSGGE	VSELTALKLPSI VSEELSLKLPPM	VVEESARAST	TVLGDI SVLGDI
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	LGSAMQNTQD LGSAMQNTQN	LLKMPYGCGEQN LLOMPYGCGEQN	MVLFAPNIYV MVLFAPNIYV	LDYLNETQQLT LDYLNETQQLT	EIKTKAIAYI EIKSKAIGYI	LNTGYQR LNTGYQR
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	QLNYKHRDGS QLNYKHYDGS	YSTFGDKPGRN YSTFGERYGRN	HANTWLTAFVL GNTWLTAFVL	KSFAQARKYIF KTFAQARAYIF	IDEVHITQALI IDEAHITQALI	WLSQQQ WLSQRQ
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	1080 KDNGCFRSSG KDNGCFRSSG	1090 Sllnnamkggvi Sllnnaikggvi	1100 Edevtlsayit Edevtlsayit	1110 IALLEMSLPVTI IALLEIPLTVTI	1120 HPVVRNALFCI HPVVRNALFCI	1130 DTAWKS ESAWKT
sp P06238 A2MG_RAT	1140 Arg <mark>g</mark> ag <mark>gshv</mark> Aofgdhgshv	1150 YTKALLAYAFA YTKALLAYAFA	1160 LAGNODTKKEI LAGNODKEKEV	1170 LKSLDEEAVKE	1180 EDSVHWTRPOI	1190 KPSVSVA KPKAPVG
spiP06238 A2MG RAT		1210 EVEMTAYVLLA		1230 DLTAAMLIVKW	1240 TKOONSHGGE	1250 SSTODT
sp P01023 A2MG_HUMAN	HFYEPQAPSA 1260	EVEMTSYVLLA 1270	LTAQPAPTSE	DLTSATNIVKW 1290	ITKQQNAQGGI 1300	SSTODT 1310
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	VVALHALSKY VVALHALSKY 1320	GSATFTRAKKA GAATFTR 1330	AQVTIHSSGTF AQVTIQSSGTF 1340	STKFQVNNNNQI SSKFQVDNNNRI 1350	LLORVTLPT LLOOVSLPEI 1360	PGDYTV PGEYSM 1370
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	KVTGEGCVYL KVTGEGCVYL	QTSLKYSVLPRI QTSLKYNILPEI	EEFPFTVVVQ KEEFPFALGVQ	TLPGTCEDPKAI	HTSFQISLNIS HTSFQISLSVS	YTGSRS YTGSRS
sp P06238 A2MG_RAT sp P01023 A2MG_HUMAN	ESNMAIADVK Asnmaivdvk	MVSGFIPLKPT MVSGFIPLKPT	VKMLERSVHVS VKMLERSNHVS	RTEVSNNHVLI RTEVSSNHVLI	YLDKVSNQTVI YLDKVSNQTL	NLSFTVQ SLFFTVL
sp P06238 A2MG_RAT sp P01023 A2MG_HUMA		LKPAVVKVYD LKPAIVKVYD	YYEKDEFAVA YYEKDEFAVA YYETDEFAIA	KYSAPCSTDY KYNAPCSKDI	GNA GNA	

**Figure V.** Structural comparison of the alpha-2-macroglobulin between *Rattus norvegicus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

sp Q6GQT1 A2MG_MOUSE sp P01023 A2MG_HUMAN	1	MGKRWLPSLALLPLPPPLLLLLLLLPTNASAPQKPIYMVMVPSLLHAGTPEKGCLLFNH MGKNKLLHPSLVLLLVLLPTDASVSGKPQYMVLVPSLLHTETTEKGCVLLSY
sp Q6GQT1 A2MG_MOUSE	61	LNETVTVKVSMESVRGNQSLFTDLVVDKDLFHCASFIVPQSSSNE.VMFLTVQVKGPTHE
sp P01023 A2MG_HUMAN	54	LNETVTVSASLESVRGNRSLFTDLEAENDVLHCVAFAVPKSSSNEEVMFLTVQVKGPTQE
sp Q6GQT1 A2MG_MOUSE	120	FRRRSTVLIKTKESLVFAQTDKPIYKPGQMVRFRVVSLDENFHPLNELIPLLYIQDSKKN
sp P01023 A2MG_HUMAN	114	F <u>KKRTTVMVKNEDSLVFVQTDK</u> SIYKPGQTVKFRVVSMDENFHPLNELIPLVYIQDPKGN
sp Q6GQT1 A2MG_MOUSE	180	RIAQWQNFRLEGGLKQLSFPLSSEPTQGSYKVVIRTESGRTVEHPFSVKEFVLPKFEVKV
sp P01023 A2MG_HUMAN	174	RIAQWQSFQLEGGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEHPFTVEEFVLPKFEVQV
sp Q6GQT1 A2MG_MOUSE	240	AVPETITILEEEMNVSVCGIYTYGKPVPGHVTV <mark>N</mark> ICRKYSNPSSCFGEESLAFCEKFSQQ
sp P01023 A2MG_HUMAN	234	TVPKIITILEEEMNVSVCGLYTYGKPVPGHVTV <mark>S</mark> ICRKYSDASDCHGEDSQAFCEKFSGQ
sp Q6GQT1 A2MG_MOUSE	300	LDGRGCFSQLVKTKSFQLKRQEYEMQLDVNAKIQEEGTGVEETGKGLTKITRTITKLSFV
sp P01023 A2MG_HUMAN	294	LNSHGCFYQQVKTKVFQLKRKEYEMKLHTEAQIQEEGTVVELTGRQSSEITRTITKLSFV
sp Q6GQT1 A2MG_MOUSE	360	NVDTHFRQGIPFVGQVLLVDGRGTPIPYEMIFIGADEANQNINTTTDKNGLARFSINTDD
sp P01023 A2MG_HUMAN	354	KVDSHFRQGIPFFGQVRLVDGKGVPIPNKVIFIRGNEANYYSNATTDEHGLVQFSINTTN
sp Q6GQT1 A2MG_MOUSE	420	IMGTSLTVRAKYKDSNVCYGFRWLTEENVEAWHTANAVFSPSRSFVHLESLPYKLRCEQT
sp P01023 A2MG_HUMAN	414	VMGTSLTVRVNYKDRSPCYGYQWVSEEHEEAHHTAYLVFSPSKSFVHLEPMSHELPCGHT
sp Q6GQT1 A2MG_MOUSE	480	LA <mark>VQAHYILN</mark> DEA <mark>VLERKELVFYYLMMAKGGIVRAGTHVLPVTQ</mark> GHKKGHFSILISMETD
sp P01023 A2MG_HUMAN	474	QT <mark>VQAHYILN</mark> GGT <mark>LL</mark> GIKKLS <mark>FYYLIMAKGGIVR</mark> T <mark>GTH</mark> GLLVKQEDMKGHFSISIPVKSD
sp Q6GQT1 A2MG_MOUSE	540	LAPVARLVLYTILPNGEVVGDTVKYEIEKCLANKVDLVFHPNIGLPATRAFLSVMASPQS
sp P01023 A2MG_HUMAN	534	IAPVARLLIYAVLPTGDVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAAPQS
sp Q6GQT1 A2MG_MOUSE	600	LCGLRAVDQSVLLTKPEAELSASLVYDLLPVKDLTGFPKGVNQQEEDTNGCLKQNDTYIN
sp P01023 A2MG_HUMAN	594	VCALRAVDQSVLLMKPDAELSASSVYNLLPEKDLTGFPGPLNDQDNEDCINRHNVYIN
sp Q6GQT1 A2MG_MOUSE	660	GIL <mark>YSPVQNTNEEDMYGFLKDMGLKVFTN</mark> LN <mark>IRKPKVC</mark> ERLGVNKIPAAYHLVSQGHMDA
sp P01023 A2MG_HUMAN	652	GITYTPVSSTNEKDMYSFLEDMGLKAFTNSKIRKPKMCPQLQQYEMHGPEGLRVGFYESD
sp Q6GQT1 A2MG_MOUSE	720	FIESSESPTETTRSYFPETWIWDLVIVDSTGVAEMEVTVPDTITEWKAGAFC
sp P01023 A2MG_HUMAN	712	VMGRGHARLVHVEEPHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDTITEWKAGAFC
sp Q6GQT1 A2MG_MOUSE	772	LSNDTGLGLSPVIDFQAFQPFFVDLTMPYSVIRGEAFTLKATVLNYLQTCIRVGVQLEAS
sp P01023 A2MG_HUMAN	772	LSEDAGLGISSTASLR <mark>AFQPFFVELTMPYSVIRGEAFTLKATVLNYL</mark> PK <mark>CIRV</mark> SVQLEAS
sp Q6GQT1 A2MG_MOUSE	832	PDFLATPEEKEQKSHCICMNERHTMSWAVIPKSLGNVNFTVSAEALDSKELCRNEVPVVP
sp P01023 A2MG_HUMAN	832	PAFLAVPVEKEQAPHCICANGRQTVSWAVTPKSLGNVNFTVSAEALESQELCGTEVPSVP
sp 26G2T1 A2MG_MOUSE	892	ERGKKDTIIKSLLVEPEGLENEVTFNSLLCPTGAEVSEQISLKLPSDVVEESARASVTVL
sp P01023 A2MG_HUMAN	892	EHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVSEELSLKLPPNVVEESARASVSVL
sp Q6GQT1 A2MG_MOUSE	952	GDILGSAMQNTQDLLKMPYGCGEQNMVLFAPNIYVLDYLNETEQLTQEIKTKAITYLNTG
sp P01023 A2MG_HUMAN	952	GDILGSAMQNTQNLLQMPYGCGEQNMVLFAPNIYVLDYLNETQQLTPEIKSKAIGYLNTG
sp Q6GQT1 A2MG_MOUSE	1012	YQRQLNYKHRDGSYSTFGDKPGRSHANTWLTAFVLKSFAQARRYIFIDESHITQALTWLS
sp P01023 A2MG_HUMAN	1012	YQRQLNYKHYDGSYSTFGERYGRNQGNTWLTAFVLKTFAQARAYIFIDEAHITQALIWLS
sp Q6GQT1 A2MG_MOUSE	1072	QQQKDNGCFRSSGSLLNNAMKGGVEDEVTLSAYITIALLEMSLPVTHPVVRNALFCLDTA
sp P01023 A2MG_HUMAN	1072	QRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTVTHPVVRNALFCLESA
sp Q6GQT1 A2MG_MOUSE	1132	WKSARRGASGNHVYTKALLAYAFALAGNQDTKKEILKSLDEEAVKEDNSVHWTRAQKPRV
sp P01023 A2MG_HUMAN	1132	WK <mark>TA</mark> QE <mark>GDHGSHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVK</mark> KDNSVHWERPQKPKA
sp Q6GQT1 A2MG_MOUSE	1192	PADLWYQPQAPSAEVEMTAYVLLAYLTTELVPTREDLTAAMLIVKWLTKQQNSHGGFSST
sp P01023 A2MG_HUMAN	1192	PVGHFYEPQAPSAEVEMTSYVLLAYLTAQPAPTSEDLTSATNIVKWITKQQNAQGGFSST
sp Q6GQT1 A2MG_MOUSE	1252	QDTVVALHALSKYGAATFTRAKKAAHVTIQSSGAFYTKFQVNNDNQLLLQRVTLPTVPGD
sp P01023 A2MG_HUMAN	1252	QDTVVALHALSKYGAATFTRTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVSLPELPGE
sp Q6GQT1 A2MG_MOUSE	1312	YTAKVAGEGCVYLQTSLKYSVLPREKEFPFALVVQTLPGTCEDLKAHTTFQISLNISYIG
sp P01023 A2MG_HUMAN	1312	YSMKVTGEGCVYLQTSLKYNILPEKEEFPFALGVQTLPQTCDEPKAHTSFQISLSVSYTG
sp Q6GQT1 A2MG_MOUSE	1372	SRSDSNMAIADVKMVSGFIPLKPTVKMLERS <mark>VHVSRTEVSNNHVLIYLDKVSNQMLTLFF</mark>
sp P01023 A2MG_HUMAN	1372	SRS <mark>A</mark> SNMAIVDVKMVSGFIPLKPTVKMLERS <mark>NHVSRTEVSSNHVLIYLDKVSNQTLS</mark> LFF
sp Q6GQT1 A2MG_MOUSE	1432	MVQQDIPVRDLKPAIVKVYDYYE <mark>KDEFAVA</mark> KYSAPCSAGYGNA
sp P01023 A2MG_HUMAN	1432	TVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNAPCSKDLGNA

**Figure VI.** Structural comparison of the alpha-2-macroglobulin between *Mus musculus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).

tr 17J7R5 17J7R5_ORENI	1	MKFVALALTLULÄVGSQAASLQADAPSQLAQIRSAVDVYLTQÄKEGAIKALDQLDDT
sp P02647 APOA1_HUMAN	1	MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
tr 17J7R5 17J7R5_OREN1	58	PY.QEFKVILAQRLEDLHTQVKALQGSVAPVTDSVFTTVSEARAELRSNTATDIBALRTE
sp P02647 APOA1_HUMAN	61	ALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLBEVKAK
tr 17J7R5 17J7R5_OREN1	117	LEPKRAHLREVIDRHI <mark>E</mark> DYRSRLQPVISEYYAKHTAEMD <mark>EI</mark> KT <mark>KLEPIMTELREKIR</mark> TNV
sp P02647 APOA1_HUMAN	121	VQPYLDDFQKKWQEEM <mark>ELYRQKV</mark> EPLRAELQEGARQKLH <mark>EL</mark> QEKLSPLGE <mark>EMRDRAR</mark> AHV
tr 17J7R5 17J7R5_OREN1	177	EETKAALTPIVESIRARVATHVEQAKAMLAPYVEEYKEQIRQAYDHAHNVRAEDITALRA
sp P02647 APOA1_HUMAN	181	DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRQ
tr 17J7R5 17J7R5_OREN1	237	KIN <mark>PLAB</mark> DI <mark>K</mark> TKLQQIFAILSETFTKS
sp P02647 APOA1_HUMAN	241	GLL <mark>PVLB</mark> SF <mark>K</mark> VSFL <u>SA</u> LEEY <u>T</u> KKLNTQ

**Figure VII.** Structural comparison of the apolipoprotein A1 between *Oreochromis niloticus* and *Homo sapiens*. The FASTA files related to tilapia and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

sp 042363 APOA1_DANRE	1	MKFVALALTLLLALGSQANLFQADAPTQLEHYKAAALVYLNQVKDQAEKAIDNLDGT
sp P02647 APOA1_HUMAN	1	MKA <mark>AVL</mark> TLAVLFLT <mark>GSQA</mark> RHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
sp 042363 APOA1_DANRE	58	DY.EQYKLQLSESLTKLQEYAQTTSQALTPYAETISTQLMENTKQLRERVMTDVBDLRSK
sp P02647 APOA1_HUMAN	61	AlgkQlnlkllDnwdsVTstFsklreqLgeVtqefwdnleketeglrqemskDlbevkak
sp 042363 APOA1_DANRE	117	LEPHRAELYTALOKHIDE <mark>YREKLEP</mark> VFQ <mark>B</mark> YSALN <mark>RO</mark> NAEQIRAKIEPIMDDIRKAFESNI
sp P02647 APOA1_HUMAN	121	VQPYLDDFQKKWQEEMELYRQKVEPIRABLQEGAROKIHEIQEKISPIGEEMRDRARAHV
sp 042363 APOA1_DANRE	177	EETKSKVVPMVEAVRTKLTERLEDLRTMAAPYAEEYKEQIVKAVEEAREKIABHTQDIQT
sp P02647 APOA1_HUMAN	181	Dal <u>rthlap</u> ysdel <mark>rqrl</mark> aarlealkenggarla <mark>ey</mark> hakatehistis <mark>eka</mark> kpaledirq
sp 042363 APOA1_DANRE	237	RMEPYMENVRTTFAQMYETIAKAIQA.
sp P02647 APOA1_HUMAN	241	GLLPVLESFKVSFLSALEEYTKKLNTQ

**Figure VIII.** Structural comparison of the apolipoprotein A1 between *Danio rerio* and *Homo sapiens*. The FASTA files related to zebrafish and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).

sp P04639 APOA1_RAT	1	MKAAVLAVALVFLTGCQAWEFWQQDEP.QSQWDRVKDFATVYVDAVKDSGRDYVSQFESS
sp P02647 APOA1_HUMAN	1	MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSGRDYVSQFEGS
sp P04639 APOA1_RAT	60	TLGKQLNLNLLDNWDTLGSTVGRLQEQLGPVTQEFWANLEKETDWLRNEMNKDLENVKQK
sp P02647 APOA1_HUMAN	61	AlgkqlnlklldnwdsVTSTFSKLREQLGPVTQEFWDNLEKETEGLRQEMSKDLEEVKAK
sp P04639 APOA1_RAT	120	MQPHLDEFQEKWNEEVEAYRQKLEPLGTELHKNAKEMQRHLKVVAEEFRDRMRVNA
sp P02647 APOA1_HUMAN	121	VQPYLDDFQKKWQEEMELYRQKVEPLRABLQEGARQKLHELQEKLSPLGEEMRDRARAHV
sp P04639 APOA1_RAT	176	DALRAKFGLYSDOMRENLAORLTEIKNHPTLIEYHTKASDHLKTLGEKAKPALDDLGO
sp P02647 APOA1_HUMAN	181	DALRTHLAPYSDELRORLAARLEALKENGGARLAEYHAKATEHLSTLSEKAKPALEDLRO
sp P04639 APOA1_RAT	234	GLMPVLEAWKAKIMSMIDEAKKKLNA.
sp P02647 APOA1_HUMAN	241	GLLPVLESEKVSFLSALEEYTKKLNTQ

**Figure IX.** Structural comparison of the apolipoprotein A1 between *Rattus norvegicus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).



**Figure X.** Structural comparison of the apolipoprotein A1 between *Mus musculus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).

tr I3JNN4 I3JNN4_ORENI sp P00450 CERU_HUMAN	1	MLRLD <b>L</b> RÄVILLECVVNCVSGMRRENFIKTEEVSWNNAPTGRNIIQNRSIQDDEEASTEL MKILILGIFLELCSTPAWAKEKHNYIGIIETTWDYASDHGEKKLISVDTEHSNIYL
tr I3JNN4 I3JNN4_ORENI	61	KSGPQRIGSTYKKAVYKQYSDATYRTEVIKAEWLGYLGPLLMAEEGDTLIVHLKNTASRP
sp P00450 CERU_HUMAN	57	QNGPDRIGRLYKKALYLQYTDETERTTIEKPVWLGFLGPIIKAETGDKVYVHLKNLASRP
tr I3JNN4 I3JNN4_ORENI	121	YSAHPHGLNYTKGNEGALYPDGTGPELKRDDSVAPGQTVTYEWTLAESHGPTSHDSNCMT
sp P00450 CERU_HUMAN	117	YTFHSHGITYYKEHEGAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVT
tr I3JNN4 I3JNN4_ORENI	181	RFYHSHVSPPKDINSGLIGPLIVCKRGTLDLHGDSSGDYQYALLFMVSDENFSWYLDENI
sp P00450 CERU_HUMAN	177	RIYHSHIDA <mark>PKDI</mark> ASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDNI
tr I3JNN4 I3JNN4_ORENI	241	RTYITNPARNLKEDEDFIESNKMHGINGLLYGN <mark>D</mark> RGLSMCQGNKIQWHLFALGNEVDMHS
sp P00450 CERU_HUMAN	237	KTYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSDPGLSMCAEDRVKWYLFGMGNEVDVHA
tr I3JNN4 I3JNN4_ORENI	301	VHFHGQILTTMNHHTDTISLFPASSTTAEMVADNPGHWLLTCSVNDHLMAGMQALFEIKK
sp P00450 CERU_HUMAN	297	AFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCONLNHLKAGLQAFFQVQE
tr I3JNN4 I3JNN4_ORENI	361	CFPNVHKPRPHG.ELROYFIAAEEEVWDYAPTVPTDGTAETFVTRGONRT
sp P00450 CERU_HUMAN	357	CNKSSSKDNI <mark>RG</mark> KH <mark>VR</mark> HYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRI
tr I3JNN4 I3JNN4_ORENI	410	GSRYKKVRYVEYTDNTFMTKILRSPEEQ <mark>HLGILGPVL</mark> KAEEKDTIRVVFKNKASRPYTIQ
sp P00450 CERU_HUMAN	417	GGS <u>YKKL</u> VYR <mark>EYTD</mark> ASFTNRKERGPEEHLGILGPVIWAEVGDTIRVTFHNK <mark>GAYPLSI</mark> E
tr I3JNN4 I3JNN4_ORENI	470	PHGVQYSVEQDGTLYHNELEESYTDKKLRELKRLPRVVT <mark>PPPAALVRP</mark> GMVHI <mark>YEWMVP</mark> V
sp P00450 CERU_HUMAN	477	PIGVRFNKN <mark>NEGT</mark> YYSPNYNPQSRSV <mark>PPSA</mark> SHVAPTETFTYEWTVPK
tr I3JNN4 I3JNN4_ORENI	530	GAGPVEGEADCLTYLYYSAVDEVKDTSSGLVGPLLICRPKSLKKG.VQKNYNKEFHLMAT
sp P00450 CERU_HUMAN	524	EVgetnadpvClakmyysavdptkdiftGligemkicKkgSlhangr <u>ok</u> dvdkefylfpt
tr I3JNN4 I3JNN4_ORENI	589	VFDENLSWYLDDNIRTFTTAPNTVNKEDEGFIESNKMHAINGFVYNNLPGLTMCKGDKVS
sp P00450 CERU_HUMAN	584	VFDENESLLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMCKGDSVV
tr I3JNN4 I3JNN4_ORENI	649	WHLSGLGSETDIISLYFOGNRFIYEQNRRDTISVFPHISHTVTMEPDSMGOFEVVSATVN
sp P00450 CERU_HUMAN	644	WYLFS <mark>AGNEADV</mark> HG <mark>IYFSGN</mark> T <u>YLW</u> RGE <mark>RRDTANLFPOTSLTLHMWPDTEGTFNV</mark> ECLTTD
tr I3JNN4 I3JNN4_ORENI	709	HYRNGMRANYTVEKCSILHROSEMMLHSKTYYIAAMEIDWDYAPNRTWEVEMFRGME
sp P00450 CERU_HUMAN	704	HYTG <mark>GML</mark> OKYTVNQCRRQSEDSTFYLGE <mark>RTYYIAAVEVEWDY</mark> SP <mark>OR</mark> EWEKELHHLOE
tr 13JNN4 13JNN4_OREN1	769	P.IFLDKQGGFIGSRYKKVVYROFTSDKFTKQVERTADMEHLGIVGPMIHANVGDKV
sp P00450 CERU_HUMAN	764	SN <mark>AFLDK</mark> GEFY <mark>IGSKYKKVVYROYT</mark> DSTFRVP <mark>VERKAEEEHLGILGPOLHADVGDKV</mark>
tr I3JNN4 I3JNN4_ORENI	828	FKNMATRPYSIHAHGVKTENPSVHOTOPGEIHTYTWYVNKNTGPTTEQEECSVSAYY
sp P00450 CERU_HUMAN	824	FKNMATRPYSIHAHGVOTESSTVTPTLPGETLTYVWKIPERSGAGTEDSACIPWAYY
tr I3JNN4 I3JNN4_ORENI	888	DVAKDLYSGLIGPLVVCRRSWGRTLGLKKEVEEFALLFLVFDENESWYLDENIRAQI
sp P00450 CERU_HUMAN	884	DQVKDLYSGLIGPLIVCRRPYLKVFNPR.RKL <mark>EFALLFLVFDENESWYLDD</mark> NIKTYS
tr I3JNN4 I3JNN4_ORENI	948	RPNLKDDEDFIESNKMHAINGYVYGNLNGLNMEVGDKVYWYLMGMGNEVDIHTAHWH
sp P00450 CERU_HUMAN	943	EKVNKDDEEFIESNKMHAINGRMFGNLOGLIMHVGDEVNWYLMGMGNEIDLHTVHFH
tr I3JNN4 I3JNN4_ORENI	1008	VE <mark>YK</mark> LG <mark>G</mark> GÄHRA <mark>DVYELFPATFOT</mark> VKMRPQYPGTWLLHCHVTDHIKAGMEAMYTVTE
sp P00450 CERU_HUMAN	1003	FQYKHRG.VYSS <b>DVFDIFPGTYQTLEMFP</b> RTPGIWLLHCHVTDHIHAGMETTYTVLQ
tr I3JNN4 I3JNN4_ORENI	1068	KSGIFG
sp P00450 CERU_HUMAN	1062	TKSG

**Figure XI.** Structural comparison of the ceruloplasmin between *Oreochromis niloticus* and *Homo sapiens*. The FASTA files related to tilapia and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

tr Q6P3G1 Q6P3G1_DANRE	1	MKGLQFALLGVLCCAGIASSITREYFFATKEIQWDYAPSGKNLIQNKTVQQDEAARVFL
sp P00450 CERU_HUMAN	1	.MKILILGIFLFICSTPAWAKEKHYYIGIIETTWDYA
tr Q6P3G1 Q6P3G1_DANRE	61	RGEQRIGRVYKKAVYHQYTDATYRQEIDKPKWLGYLGPIISAEEDDTVIVHLKNMARRAY
sp P00450 CERU_HUMAN	58	NGPDRIGRUYKKALYLQYTDETERTTIEKPVWLGELGPIIKAETGDKVYVHLKNLASRPY
tr Q6P3G1 Q6P3G1_DANRE	121	SLHAHGLSYNKTNEGALYPDSSEKVEKHDDSVAPGTTFTYIWTLPASHAPGKDDTNCLTR
sp P00450 CERU_HUMAN	118	TFHSHGITYYKEHEGALYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVTR
tr Q6P3G1 Q6P3G1_DANRE	181	IYHSHVNAPKDIASGLIGPLIVCKKGSLDVHGDKTGDYLYTLMFTVSDENLSWYLDENIK
sp P00450 CERU_HUMAN	178	IYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDNIK
tr Q6P3G1 Q6P3G1_DANRE	241	TYCSAPAKVNKDDEAFQESNKMHSINGYVYGNLPDLSMCTGNKIHWHLFGMGNEVDIHSA
sp P00450 CERU_HUMAN	238	TYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFGMGNEVDVHAA
tr Q6P3G1 Q6P3G1_DANRE	301	FFHGQILTDKRQHVDTVSLFPATFVNVEMVADNPGQWLLSCQVNDHLEAGMQAFFEIKK
sp P00450 CERU_HUMAN	298	FFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQEG
tr Q6P3G1 Q6P3G1_DANRE	361	FPNVHKPRPFG.EVROYYIAAEEIIWDYGPTEINOYTMKKLVDDIVS.DTFFDNRNDRIG
sp P00450 CERU_HUMAN	358	NKSSSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIG
tr Q6P3G1 Q6P3G1_DANRE	419	GKYKKVQYVEYTDDTFTKRKEKTPEEOHLGILGPVIRAEEEDTIKVTFRNKASRPFSIQE
sp P00450 CERU_HUMAN	418	GSYKKLVYREYTDASFTNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNKGAYPLSIEE
tr Q6P3G1 Q6P3G1_DANRE	479	HGVQYNIDMDG71YHNVLEESYTDKKLRELKKQPRVIEPLPAAMVRPDT7YKYEWVVPKD
sp P00450 CERU_HUMAN	478	IGVRENKNNEGTYYSPNYNPQSRSVPPSASHVAPTETETYEWTVPKE
tr Q6P3G1 Q6P3G1_DANRE	539	GGPTEKDPDCLTYLYYSAVDPIRDTNSGLVGPLLICKPKTLKS.GKQKNVDKEFHLLATV
sp P00450 CERU_HUMAN	525	VGPTNADPVCLAKMYYSAVDPTKDIFTGLIGPMKICKKGSLHANGRQKDVDKEFYLFPTV
tr Q6P3G1 Q6P3G1_DANRE	598	FDENLSWYLDDNINRYAKQPKSVNKEDADFQESNKMHSLNGYMYCNLKGLNMCKGDKVSW
sp P00450 CERU_HUMAN	585	FDENESLILEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGEMYGNQPGLIMCKGDSVVW
tr Q6P3G1 Q6P3G1_DANRE	658	HLSGLGSETDIHGLYFEGNRFLYKETRRDTINVFPHISHTVIMEPDSMGOFEVNCKTTDH
sp P00450 CERU_HUMAN	645	YLFSAGNEADVHGIYFSGNT <u>YLWR</u> GERRDTANLFPOTSLTLHMWPDIEGTFNVECLTTDH
tr Q6P3G1 Q6P3G1_DANRE	718	YH <mark>GGM</mark> RAN <mark>YTV</mark> EK <mark>CR</mark> FWNRQSETMLHQKK <mark>YYIAAVEMDWDYSPTRTWE</mark> DKMHNGLKESPG
sp P00450 CERU_HUMAN	705	YT <mark>GGMK</mark> QK <mark>YTV</mark> NQ <mark>CR</mark> RQSEDSTFYLGERT <u>YYIAAVEVEWDYSPQR</u> EWEKELHHLQEQNVS
tr Q6P3G1 Q6P3G1_DANRE	778	NEFLKKEGKFIGSKYKKVLYKEYTDETFIKLKERTADMEHLGIMGPMIHGKVGEKVKIVF
sp P00450 CERU_HUMAN	765	NAFLDKGEFYIGSKYKKVVYRQYTDSTFRVPVERKAEBEHLGILGPQLHADVGDKVKIIF
tr Q6P3G1 Q6P3G1_DANRE	838	KNMARRPYSIHAHGVKTDSPOVALTRPGETOTYTWYLPKNSGPTEBOEECSVG <mark>AYYSTVD</mark>
sp P00450 CERU_HUMAN	825	KNMAT <mark>RPYSIHAHGVOTES</mark> STVTPTLPGETLTYVWKIPERSGAGTEDSACIPW <mark>AYYSTVD</mark>
tr Q6P3G1 Q6P3G1_DANRE	898	V <mark>IKDMYSGLVGPLVIC</mark> KKSLARTLGLKKEVE <b>EFALLFMVFDENESWYLEENIKT</b> HVKNPP
sp P00450 CERU_HUMAN	885	Q <mark>VKDLYSGLIGPLIVCRR</mark> PYLKVFNPR.RKL <mark>EFALLFLVFDENESWYLDDNIKT</mark> YSDHPE
tr Q6P3G1 Q6P3G1_DANRE	958	KALTEDQQFIESNKMHGINGLVFGNLKGLNMKVGDKVYNYLMGLGNEVDIHTAHFHGHSF
sp P00450 CERU_HUMAN	944	KVNKDDEEFIESNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHSF
tr Q6P3G1 Q6P3G1_DANRE	1018	DYKVSGTHRADVFDLVPGTFQTVTMRPLYSGTWLLHCHVTDHIQAGMETTYTVLEKDGRK
sp P00450 CERU_HUMAN	1004	QYKHRGVYSS <mark>DVFDIFPGTYQTLEMFP</mark> RTPGIWLLHCHVTDHIHAGMETTYTVLQNEDTK
tr Q6P3G1 Q6P3G1_DANRE	1078	R <mark>G</mark> FLGIFGSG
sp P00450 CERU_HUMAN	1064	S <mark>G</mark>

**Figure XII.** Structural comparison of the ceruloplasmin between *Danio rerio* and *Homo sapiens*. The FASTA files related to zebrafish and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

sp P13635 CERU_RAT	1	MKFLLLSÄLLFLHSSLAWTREKHYYIGITEAVWDYASGSEEKELISVDTEQSNFYLRNGP
sp P00450 CERU_HUMAN	1	MKILILGIFLFLCSTPAWAKEKHYYIGIIETTWDYASDHGEKKLISVDTEHSNIYLQNGP
sp P13635 CERU_RAT	61	DRIGRKYKKALYSEYTDGTFTKTIDKPAWLGFLGPVIKAEVGDKVSVHVKNFASRPYTFH
sp P00450 CERU_HUMAN	61	DRIGRLYKKALYLQYTDETFRTTIEKPVWLGFLGPIIKAETGDKVYVHLKNLASRPYTFH
sp P13635 CERU_RAT	121	AHGVTYTKANEGAIYPDNTTDFQRADDKLFPGQQYLYVLRANEP.SPGEGDSNCVTRIYH
sp P00450 CERU_HUMAN	121	ShGITYYKEHEGAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVTRIYH
sp P13635 CERU_RAT	180	SHVDAPKDIASGLIGPLIICKKGSLHKEKEENIDQEFVIMFSVVDENLSWYLEDNIKTFC
sp P00450 CERU_HUMAN	181	SHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDNIKTYC
sp P13635 CERU_RAT	240	SEPEKVDKDNEDFQESNRMYS <mark>I</mark> NGYTFGSLPGLSMCAEDRVKWYLFGMGNEVDVH <mark>SEL</mark> FH
sp P00450 CERU_HUMAN	241	SEPEKVDKDNEDFQESNRMYS <mark>V</mark> NGYTFGSLPGLSMCAEDRVKWYLFGMGNEVDVH <mark>AAF</mark> FH
sp P13635 CERU_RAT	300	GQALTSKNYHTDIINLFPATLIDVSMVAQNPGVWMLSCQNLNHLKAGLQAFFQVRDCNKP
sp P00450 CERU_HUMAN	301	GQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQECNKS
sp P13635 CERU_RAT	360	SPDDDIQDRHVRHYYIAAEETIWDYAPSGTDTFTGENFTSLGSDSRVFFEQGATRIGGSY
sp P00450 CERU_HUMAN	361	SSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIGGSY
sp P13635 CERU_RAT	420	KKLVYREYTDDSFTNRKERGPDEEHLGILGPVIWAEVGDIIRVTFHNKGQFPLSIQPMGV
sp P00450 CERU_HUMAN	421	KKLVYREYTDASFTNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNKGAYPLSIEPIGV
sp P13635 CERU_RAT	480	RFTKENEGTYYGPDGRSSKQASHVAPKETFTYEWTVPKEMGPTYADPVCLSKMYY
sp P00450 CERU_HUMAN	481	RFNKNNEGTYYSPNYNPQSRSVPPSASHVAPTETFTYEWTVPKEVGPTNADPVCLAKMYY
sp P13635 CERU_RAT	535	SGVDLTKDIFTGLIGPMKICKKGSLLADGROKDVDKEFYLFATVFDENESLLLDDNIRMF
sp P00450 CERU_HUMAN	541	SAVDPTKDIFTGLIGPMKICKKGSLHANGROKDVDKEFYLFPTVFDENESLLLEDNIRMF
sp P13635 CERU_RAT	595	TTAP <mark>EN</mark> VDKEDEDFQESNKMHSMNGFMYGN <mark>L</mark> PGLNMCLGESIVWYLFSAGNEADVHGIYF
sp P00450 CERU_HUMAN	601	TTAPDQVDKEDEDFQESNKMHSMNGFMYGN <mark>Q</mark> PGLTMC <mark>KGDSV</mark> VWYLFSAGNEADVHGIYF
sp P13635 CERU_RAT	655	SGNTYLS <mark>KGERRDTANLFPHKSLTLLMTPDTEGSFDVECLTTDHYTGGMKQKYTVNQCK</mark> G
sp P00450 CERU_HUMAN	661	SGNTYLW <mark>R</mark> GERRDTANLFPQTSLTLHMWPDTEGTFNVECLTTDHYTGGMKQKYTVNQC <mark>R</mark> R
sp P13635 CERU_RAT	715	QFEDVTLYCGERTYYIAAVEVEWDYSP <mark>SRDWE</mark> MELHHLQEQNVSNAFLDK <mark>E</mark> EFFIGSKYK
sp P00450 CERU_HUMAN	721	QSEDSTFYLGERTYYIAAVEVEWDYSP <mark>RR</mark> WE <mark>MELHHLQEQNVSNAFLDK</mark> GEFMIGSKYK
sp P13635 CERU_RAT	775	KVVYREFTDSTFREOVKRRAEEEHLGMLGPLIHADVGAKVK <mark>VV</mark> FKNMATRPYSIHAHGVK
sp P00450 CERU_HUMAN	781	KVVYR <mark>OY</mark> TDSTFR <mark>VFVBRK</mark> AEEEHLG <mark>H</mark> LGPOLHADVGDKVKII <mark>I</mark> FKNMATRPYSIHAHGVO
sp P13635 CERU_RAT	835	TKSSTVAPTLPGEVRTYIWOIPERSGAGTEDSPCIPWAYYSTVDRVKDLYSGLIGPLIVC
sp P00450 CERU_HUMAN	841	TESSTVTPTLPGETLTYWKKIPERSGAGTEDSACIPWAYYSTVDOVKDLYSGLIGPLIVC
sp P13635 CERU_RAT	895	RKSYVKVFNPKKKMEFSLLFLVFDENESWYLDDNI <mark>nty</mark> pdhpekdnkd <mark>neefiesnkmha</mark>
sp P00450 CERU_HUMAN	901	RRPylkvFnp <mark>RRkLefa</mark> llflvfdeneswylddni <mark>ktys</mark> dhpekvnkddeefiesnkmha
sp P13635 CERU_RAT	955	ING <mark>KMFGNLQGLTMHVGDEVNWYVMA</mark> MGNEIDLHTVHFHGHSFQYKHRG <mark>IH</mark> SSDVFD <mark>F</mark> FP
sp P00450 CERU_HUMAN	961	ING <mark>R</mark> MFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHSFQYKHRG <mark>V</mark> YSSDVFD <mark>I</mark> FP
sp P13635 CERU_RAT	1015	GTYQTLEMFPQTPGIWLLHCHVTDHIHAGMVTTYTVLPNQETKSG
sp P00450 CERU_HUMAN	1021	GTYQTLEMFPRTPGIWLLHCHVTDHIHAGMETTYTVLONEDTKSG

**Figure XIII.** Structural comparison of the ceruloplasmin between *Rattus norvegicus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

sp Q61147 CERU_MOUSE sp P00450 CERU_HUMAN	1	MKFLLLSTETFLYSSLALARDKHYFIGITEAVWDYASGTEEKKLISVDTEQSNFYLQNGP MKILILGIFLFLCSTPAWAKEKHYYIGIIETTWDYASDHGEKKLISVDTEHSNIYLQNGP
sp Q61147 CERU_MOUSE	61	DRIGR <mark>KYKKALY</mark> FEYTDGTFSKTIDKPAWLGFLGPVIKAEVEDKVYVHLKNLASRIYTFH
sp P00450 CERU_HUMAN	61	DRIGR <mark>L</mark> YKKALYLQYTDETFRTTIEKPVWLGFLGP <mark>I</mark> IKAETGDKVYVHLKNLASRPYTFH
sp Q61147 CERU_MOUSE	121	AHGVTYTKEYEGAVYPDNTTDFQRADDKVLPGQQYVYVLHANEP.SPGEGDSNCVTRIYH
sp P00450 CERU_HUMAN	121	SHGITYYKEHEGAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVTRIYH
sp Q61147 CERU_MOUSE	180	SHVDAPKDIASGLIGPLILCKKGSLYKEKEKNID <mark>QEFVLMFSVVDENLSWYLEDNIKTFC</mark>
sp P00450 CERU_HUMAN	181	SH <mark>I</mark> DAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDEN <mark>FSWYLEDNIKTYC</mark>
sp Q61147 CERU_MOUSE	240	SEPEKVDKDNEDFQESNRMYS <mark>I</mark> NGYTFGSLPGLSMCA <mark>A</mark> DRVKWYLFGMGNEVDVH <mark>S</mark> AFFH
sp P00450 CERU_HUMAN	241	SEPEKVDKDNEDFQESNRMYS <mark>V</mark> NGYTFGSLPGLSMCA <mark>E</mark> DRVKWYLFGMGNEVDVH <mark>A</mark> AFFH
sp Q61147 CERU_MOUSE	300	GQALTSRNYQTDIINLFPATLIDAYMVAQNPGVWMLSCQNLNHLKAGLQAFFQVRDCNKP
sp P00450 CERU_HUMAN	301	GQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQECNKS
sp Q61147 CERU_MOUSE	360	SPEDNIQDRHVRHYYIAAEEVIWNYAPSGTDIFTGENLTALESDSRVFFEQGATRIGGSY
sp P00450 CERU_HUMAN	361	SSKDNIRG <mark>KHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQG</mark> TTRIGGSY
sp Q61147 CERU_MOUSE	420	KKMAYREYTD <mark>GSFTNRKORGPDEEHLGILGPVIWAEVGDTIK</mark> VTFHNKG <mark>OH</mark> PLSIOPMGV
sp P00450 CERU_HUMAN	421	KK <mark>LVYREYTDA</mark> SFTNRKERGPEEHLGILGPVIWAEVGDTI <mark>R</mark> VTFHNKG <mark>AY</mark> PLSIEPIGV
sp Q61147 CERU_MOUSE	480	SFTAENEGTYYGPPGRSSQQAASHVAPKETFTYEWTVPKEMGPTYADPVCLSKMYY
sp P00450 CERU_HUMAN	481	RFNKNNEGTYYSPNYNPQSRSVPPS <mark>ASHVAP</mark> TETFTYEWTVPKEMGPTNADPVCLAKMYY
sp Q61147 CERU_MOUSE	536	S <mark>GVDPTKDIFTGLIGPMKICKKGSLLAD</mark> GRQKDVDKEFYLFPTVFDENESLLLDDNIRMF
sp P00450 CERU_HUMAN	541	S <mark>AVDPTKDIFTGLIGPMKICKKGSLHAN</mark> GRQKDVDKEFYLFPTVFDENESLLL <mark>B</mark> DNIRMF
sp Q61147 CERU_MOUSE	596	TTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGL <mark>NMCLGEST</mark> VWYLFSAGNEADVHGIYF
sp P00450 CERU_HUMAN	601	TTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMC <mark>KGD</mark> SWVWYLFSAGNEADVHGIYF
sp Q61147 CERU_MOUSE	656	SGNTYLSKGERRDTANLFPHKSLTLLMNPDTKGTFDVECLTTDHYTGGMKQKYTVNQCQR
sp P00450 CERU_HUMAN	661	SGNTYLWRGERRDTANLFPQTSLTLHMWPDTEGTFNVECLTTDHYTGGMKQKYTVNQCRR
sp Q61147 CERU_MOUSE	716	QEEDETWYLGERTYYVAAVEVEWDYSPSRAWEKELHHLQEQNVSNVFLDKEEFFIGSKYK
sp P00450 CERU_HUMAN	721	QSEDSTFYLGERTYYIAAVEVEWDYSPOREWEKELHHLQEQNVSNAFLDKGEFYIGSKYK
sp Q61147 CERU_MOUSE	776	KVVYROFTDSSFREQVKRRAEDEHLGILGPPIHANVGDKVKVVFKNMATRPYSIHAHGVK
sp P00450 CERU_HUMAN	781	KVVYROTDSTFRVPVERKAEEEHLGILGPOLHADVGDKVKIIFKNMATRPYSIHAHGVQ
sp Q61147 CERU_MOUSE	836	TESSTVVPTLPGEVRTYTWQIPERSGAGREDSACIPWAYYSTVDRVKDLYSGLIGPLIVC
sp P00450 CERU_HUMAN	841	TESSTVTPTLPGETLTYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLIGPLIVC
sp Q61147 CERU_MOUSE	896 901	RKSYVKVFSPKKKMEFFLLFLVFDENESWYLDDNIKTYSEHPEKVNKDNEEFLESNKMHA BEDDVIKVENBERKIEFALLFLVFDENESWYLDDNIKTYSDHPEKVNKDDEEFTESNKMHA
sp Q61147 CERU_MOUSE	956	INGEMFGNLQGLTMHV <mark>K</mark> DEVNWYVMGMGNEIDLHTVHFHGHSFQYKHRGVYSSDVFD <mark>H</mark> FP
sp P00450 CERU_HUMAN	961	INGEMFGNLOGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHSFQYKHRGVYSSDVFD <mark>H</mark> FP
sp Q61147 CERU_MOUSE	1016	GTYQTLEMFPOTPGTWLLHCHVTDHVHAGMATTYTVLPVEQETKSG
SPIFOUASUICERO_NOMAN	1021	GITYILEMPPRINGIWILMCHVIDHIMAGMENTITVMYNMDIRSG.

**Figure XIV.** Structural comparison of the ceruloplasmin between *Mus musculus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

tr I3KHS6 I3KHS6_ORENI	1	.RTRLWLLASLAFLSLIFLTDGSPMKVMSAPNLLGVGTAQNIFVECODCTDESDIMVEIT
sp P01024 CO3_HUMAN	1	mgptsgpsllllllthlplalgspmyslitpnilrleseetmvlsahdaqgDvpvtvt
tr I3KHS6 I3KHS6_ORENI	60	VMSYDTKSKRIISTSVNLTSANKFQAFGQIKIPT.EGFSRDPORKQYVYLQAQFPDVKLE
sp P01024 CO3_HUMAN	59	VHDFPGKKLVISSEKTVLTPATNHMGNVTFTIPANREFKSEKGRNKFVTVQATFGTQVVE
tr I3KHS6 I3KHS6_ORENI	119	KIVLVSFHSGYLFIQTDKTLYTPNSKVHYRLFALTPNMEPVERDNSTISDTSVAIQFVNP
sp P01024 CO3_HUMAN	119	KVVLVSLQSGYLFIQTDKTIYTPGSTVLYRIFTVNHKLLPVGRTVMVNIENP
tr I3KHS6 I3KHS6_ORENI	179	EGVIFPLDTVSVKSGIHSGHFQLNEIVSTGLWKVMASFQSKPQLSYSAEFEVKDYVLP
sp P01024 CO3_HUMAN	171	EGIPVKQDSLSSQNQLGVLPLSWDIPELVNMGQWKIRAYYENSPQQVFSTEFEVKEYVLP
tr I3KHS6 I3KHS6_ORENI	237	NFEVKLTNENPEFYVDSDE.LTINIKATYLFGEEVDGSAFGVFGVLHQDOKTNFQASLQK
sp P01024 CO3_HUMAN	231	SFEVIVEPTEKFYMIYNEKGLEVTITARFLYGKKVEGTAFVIFGIQDGEORISLPESLKR
tr I3KHS6 I3KHS6_ORENI	296	VSIENGVGTVTLKKEHIKQTFENISSLVGSSIFAAVNVLTDSGSEMAEAELIGIQIVT
sp P01024 CO3_HUMAN	291	IPIEDGSGEVVUSRKVLLDGVQNPRAEDLVGKSLYVSATVILHSGSDMVQAERSGIPIVT
tr I3KHS6 I3KHS6_ORENI	354	SPYTIHFKKTSRYFKPGMSFDVVIEVLNPDGSPAQGVAVMIDPGD.VQGFTAANGMARLT
sp P01024 CO3_HUMAN	351	SPYQIHFTKTPKYFKPGMPFDLMVFVTNPDGSPAYRVPVAVQGEDTVQSLTQGDGVAKLS
tr I3KHS6 I3KHS6_ORENI	413	INTUNNPOPMKITAKTKOVKISPEROASATMTALPYASQSNSYIHIGVOTAEVKNGON
sp P01024 CO3_HUMAN	411	INTHPSOKPLSITVRTKKQELSEAEQATRTMOALPYSTVGNSNNYLHLSVLRTELRPGET
tr I3KHS6 I3KHS6_ORENI	471	MKINIHLSRQQNVQNDITYLLLSRGQLVKYG.RYRTSGQIMISLITTVTKDLLPSFR
sp P01024 CO3_HUMAN	471	LNVNFLLRMDRAHEAKIRYYTYLIMNKGRLLKAGRQVREPGQDLVVLPLSITTDFIPSFR
tr I3KHS6 I3KHS6_ORENI	527	IIAYYHPNDNEVVSDSVWVDVEDTCMGLLQLQS.EGGSKFYEPRKIFRLKITGDPE
sp P01024 CO3_HUMAN	531	LVAYYTLIGASGQREVVADSVWVDVKDSCVGSLVVKSGQSEDRQPVPGQQMTLKIEGDHG
tr I3KHS6 I3KHS6_ORENI	582	ATVGLVAVDKGVYILNSKHRLTOKKIWDTVENYDTGCTPGGGKDSMSVFYDAGLLFESNI
sp P01024 CO3_HUMAN	591	Arvvlvavdkgvfvlnkknkltoskiwdvvekadigctpgsgkdyagvfsdagltftss
tr I3KHS6 I3KHS6_ORENI	642	ASGTPYRQELKCLTPNRRKRSVDMMNVTTTLLSQYKDKLEHDCCLDGIRETPTSSNCEKR
sp P01024 CO3_HUMAN	651	GQQTAQRAELQCPQPARRRRSVQLTEKRMDKVGKYPKELRKCCEDGMRENPMRFSCQRR
tr I3KHS6 I3KHS6_ORENI	702	SEFITD.TACFEAFTHCCKEMEKKRAERKEDGLKLARSEDDDSSFMDSNELVSRTNFPES
sp P01024 CO3_HUMAN	711	TRFISLGEACKKVPLDCCNYLTELRRQHARASHLGLARSNLDEDIIAEENLVSRSEFPES
tr I3KHS6 I3KHS6_ORENI	761	WLWSDIKLPACPEENAKCETESVLRNIPLODSITTWOLTGISLSKTHGICVGDPLEIVVR
sp P01024 CO3_HUMAN	771	WLWNVEDLKEPPKNGISTKLMNIFLKDSITTWEILAVSMSDKKGICVADPFEVTVM
tr I3KHS6 I3KHS6_ORENI	821	KDFFVDLKLEDSAVRGEQLEIKAVIHNHGPN.LYTVRVDLTEAEHVCSAASKRGRYRQEM
sp P01024 CO3_HUMAN	827	QDFFIDLRLEYSVVRNEQVEIRAVLYNYRQNQELKVRVELLHNPAFCSLATTKRRHQQTV
tr I3KHS6 I3KHS6_ORENI	880	ĸ <mark>vGaksirSvSftifftkeG</mark> qhR <mark>ieikaav</mark> keseisdGivKmL <mark>rvvpeGi</mark> LVkSShtitL
sp P01024 CO3_HUMAN	887	Tippksslsvpyv <mark>tvp</mark> lktGlqev <u>evkaav</u> yhhfisdGvrksLkvvpeGirMnktvavrt
tr I3KHS6 I3KHS6_ORENI	940	DPKQRDGRQVEILNSKIPVIDFVPNSPTSTQISLIGKQQRNVLKNTISGBSMGGLIYQ
sp P01024 CO3_HUMAN	947	LDPERLGREGVQKEDIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDABRLKHLIVT
tr I3KHS6 I3KHS6_ORENI	998	PSGCGEENMIHMTLPVIAITYLDRADLWEIVNIDQRHQALQHITTGYHNQLEYSKKDGSF
sp P01024 CO3_HUMAN	1007	PSGCGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAF
tr I3KHS6 I3KHS6_ORENI	1058	ARTQDVPS <mark>STWLTAYVVKVF</mark> ALANNLIAVQSEVICNAVRFLIVNTQQPNGMEMBVGSVSH
sp P01024 CO3_HUMAN	1067	Aafvkrap <mark>stwltayvvkvf</mark> slav <mark>nliai</mark> dsqvlcgavkwlilekokpdgveqedapvih
tr I3KHS6 I3KHS6_ORENI	1118	KEILGDVLDTDS.DASFTAFCVISMQESRTICAPTVHNLQASIDKAVGYLERRLPSLVNP
sp P01024 CO3_HUMAN	1127	QEMIGGLRNNNEKDMALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRS
tr I3KHS6 I3KHS6_ORENI	1177	YAVAITSYAMANENKUNRETFFKFSSPDSSYMPAPAGRVFTVEATAYALLALVRAKAF
sp P01024 CO3_HUMAN	1187	YTVAIAGYALAOMGRLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLOLKDF
tr I3KHS6 I3KHS6_ORENI	1235	DEARPIVRWFNKQIRENGGYGSAQATMTVYQAIAEYWTSE.KEPEYDLNVDILLPGRSKP
sp P01024 CO3_HUMAN	1247	DFWPBVVRWLNEGRYYGGGYGSTQATFMVFQALAQYQKDAPDHQBLNUDVSLQLPSRSSK
tr I3KHS6 I3KHS6_ORENI	1294	DKYNFNWDNHFATRTSKINVINQDVKVSATGPGEATLTITSLYYELPKEKENNCQKFNLS
sp P01024 CO3_HUMAN	1307	ITHRIHWESASLLRSEET.KENEGFTVTAEGKGQGTLSVVTMYHAKAKDQLT.CNKFDLK
tr I3KHS6 I3KHS6_ORENI	1354	VQILPESLGDDENIYNLKIKVFYKNKERNATTPVLDIGLLTGFTVSTKDIDLQAK
sp P01024 CO3_HUMAN	1365	VTIKPAPETEKRPQDAKNTMILEICTRYRG.DQDATMSILDISMMTGFAPDTDDLKQLAN
tr I3KHS6 I3KHS6_ORENI	1409	GHARTISKYRLŃSES. ERRLITIYLNKVPYT. ELEIAFRVHOKLKVGILOPAAVYVYEFS
sp P01024 CO3_HUMAN	1424	GVDRYISKYBLDKAFSDRNTLIIYLDKVSHSEDDCLAFKVHOYFNVELIOPGAVKVYAYY
tr I3KHS6 I3KHS6_ORENI	1467	DQLQNTKCVRFYHPERKAGELLRLCRNDECICAEENCSMQK.KGKINNDERKDKICESTV
sp P01024 CO3_HUMAN	1484	NLEESCTRFYHPEKEDGKLNKLCRDELCRCAEENCFIQKSDDKVTLEERLDKACEP
tr I3KHS6 I3KHS6_ORENI	1526	RSKIDYAYKVSVEQFADGLSTDIYTVQVLEVIKEGSYDVGAQGRQRTFLGYPHCRMALDL
sp P01024 CO3_HUMAN	1540	GVDYVYKTRLVKVQLSNDFDEYIMAIEQTIKSGSDEVQVG.QQRTFISPIKCREALKL
tr I3KHS6 I3KHS6_ORENI	1586	GVGKTFLMMGTSGDIFKDEKSQSYQYVLGERTWIEYWPTVTECTTEEHNSTCSAIDEMVN
sp P01024 CO3_HUMAN	1597	EEKKHYLMWGLSSDFWGEKPNLSYIIGKDTWVEHWPEEDECQDEENQKQCQDLGAFTE
tr I3KHS6 I3KHS6_ORENI	1646	EYMIR <mark>GCRN</mark>
sp P01024 CO3_HUMAN	1655	SMVVF <mark>GC</mark> PN

**Figure XV.** Structural comparison of the complement C3 between *Oreochromis niloticus* and *Homo sapiens*. The FASTA files related to tilapia and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

tr F1QYN0 F1QYN0_DANRE	1	.MHGCLVCVAAVIDSLPLLSFCQPLYILSAPNKLKDCSAERVFVEAQDYAGASLNVRISV
sp P01024 CO3_HUMAN	1	MGPTSGPSLLLLLDTHLPLALG <mark>SPMY</mark> SIIT <b>PNILRDSSEETMVLEA</b> HDAQCDVP.VTVTV
tr F1QYN0 F1QYN0_DANRE	60	RREKDDQREVASTSVTLTAGKNFQELVEIEVESN.SETFDKSAQQYAVLQAQFPNKLLQK
sp P01024 CO3_HUMAN	60	HDEPGKKLVLSSEKTVLTPATNHMGNVTFTIPANREEKSEKGRNKEVTVQATEGTQVVEK
tr F1QYN0 F1QYN0_DANRE	119	QILVTFQSGHIVLQTDKTIYTPDSTVHYRVFSLSPGMTRPFQSGVRVEILTPDGISLESK
sp P01024 C03_HUMAN	120	VVLVSLQSGYLFIQTDKTIYTPGSTVLYRIFTVN.HKLLPVGRTVMVNIENPEGIPVKQD
tr F1QYN0 F1QYN0_DANRE	179	SVFPDGGVVSGTFGITDPASPGLWKLVAWHKNSPQKNFTSEFEVKEYVLPSFEVSLSP
sp P01024 CO3_HUMAN	179	SLSSQNQLGVLPLSWDIPELVNMGQWKIRAYYENSPQQVFSTEFEVKEYVLPSFEVIVEP
tr F1QYN0 F1QYN0_DANRE	237	HKAFFYVNDD.SLLVDIHAKYLFGETVNGHG <mark>FVVFGV</mark> VTEDKG <mark>KISIPGSLORVQIWDGS</mark>
sp P01024 CO3_HUMAN	239	TEKFYYIYNEKGLEVTIT <mark>ARFLYG</mark> KKVEGTAFVIFGIQDGEQ.RISLPESLKRIPIEDGS
tr F1QYN0 F1QYN0_DANRE	296	GTAQLTKRQIHQTFPEIRQLVGKSLYISVSLLTESGSEMVEAHKKGIHIVTSPYTIYF
sp P01024 CO3_HUMAN	298	GEVVLSRKVLLDGVQNPRAEDLVGKSLYVSATVILHSGSDMVQAERSGIPIVTSPYQLHF
tr F1QYN0 F1QYN0_DANRE	354	KRTPOFFKPGMPFDVSVYVTNPDETPAKNVKVEVN.PGGVSGOTKANGIAKVTINTPGGS
sp P01024 CO3_HUMAN	358	TKTPKYFKPGMPFDLMVFVTNPDGSPAYRVPVAVOGEDTVOSLTOGDGVAKLSINTHPSO
tr F1QYN0 F1QYN0_DANRE	413	STLEITARTSDPQLTSRQQAEKKMTAHAYVPKGGSRNYLHIGIDAAELRIGDSMKVNLNL
sp P01024 CO3_HUMAN	418	KPLSITYRTKKQELSEAEQATRTMQALPYSTVGNSNNYLHLSVLRTELRPGETLNVNFLL
tr F1QYN0 F1QYN0_DANRE	473	GQSPGVRDQDFTYMILSRGQIVQANRFKRR.GQTLVSLSLPVTKDMVPSFRFVAYYHV
sp P01024 CO3_HUMAN	478	RMDRAHE <u>AK</u> IRYYTYLIMNKGRLLKAGRQVREPGQDLVVLPLSITTDFIPSFRIVAYYTL
tr F1QYN0 F1QYN0_DANRE	530	GSS <mark>EVV</mark> S <mark>DSVWVDVKDTCMGSLKV</mark> EVHDP.VEVYE <mark>PG</mark> EEFE <mark>LRITGDPGAKVGLVA</mark>
sp P01024 CO3_HUMAN	538	IGASGQR <mark>EVVADSVWVDVKDSCVGSL</mark> VV <mark>K</mark> SGQSEDRQPV <mark>PG</mark> QQMT <mark>LKIEGDHGARVVLVA</mark>
tr F1QYN0 F1QYN0_DANRE	585	VDKGVYVLNNKHRITQSKIWDVVESHDTGCTAGSGKNSMQVFSDAGLLFESSSAGGTSVR
sp P01024 CO3_HUMAN	598	VDKGVFVLNKKNKLTQSKIWDVVEKADIGCTPGSGKDYAGVFSDAGLTFTSSSGQQTAQR
tr F1QYN0 F1QYN0_DANRE	645	TNSECPSSSRRERERETIVNLHKTLLDKYSGLARECCVDGLKALDVLDFSCEYRSSFILD
sp P01024 CO3_HUMAN	658	AelocpopaarrersvoltekrmdkVgKypkelerccedgmr.enpmrfscorriefisl
tr F1QYN0 F1QYN0_DANRE	705	GKECRDAFLDCCNRLTSHR.EEPAEEEIFLGRTGEDEEFVNSDDIVSRTLFPESWLWEEV
sp P01024 CO3_HUMAN	717	GEACKKVFLDCCNYITELRRQHARASHLGLARSNLDEDIIAEENIVSRSEFPESWLWNVE
tr F1QYN0 F1QYN0_DANRE	764	MLPKCLG <mark>NRQCQTTTLPKDGLWLKDSITTWEITAISLS</mark> NTHGICVADVHEMIVAKNFFID
sp P01024 CO3_HUMAN	777	DLKEPPK <mark>NGISTKLMNIFLKDSITTWEILAVSMS</mark> DK <mark>KGICVAD</mark> PFEVTVMQDFFID
tr F1QYN0 F1QYN0_DANRE	824	LKIPYSAVENCOIEIKAIIHNLYS.KAVKVVELKEIKDICSPASNKGRYAVVVASKS
sp P01024 CO3_HUMAN	833	LRIPYSVVRNEOVEIRAVIYNYRONOEIKVRVELLHNPAFCSLAIIKRBHOOTVTIPPKS
tr F1QYN0 F1QYN0_DANRE	883	SYSVEEVIVPLALGRHAIEVKAAASGRGN.DGVKKDLLVVSEGVLT.KISENLOFNEFKK
sp P01024 CO3_HUMAN	893	SLSVEYVVVPLKTGLQEVEVKAAVYHHFISDGVRKSLKVVPEGIRMNKTVAVRTLDPERL
tr F1QYN0 F1QYN0_DANRE	941	GETIVTROSHILKDOAPNTPSSTYVQAIGDTITITIEKAISGAAMGSLIIOPGGCCE
sp P01024 CO3_HUMAN	953	GregvokedippadisdovPdreserrillogtpmaqmtedavdaerikhlivtPsgcge
tr F1QYN0 F1QYN0_DANRE	998	QNMMGLIMPVIATHYLDKTNQWHTVRAGLRQTATEYIRKGYNQELAYRKSDGSFAAWINR
sp P01024 C03_HUMAN	1013	QNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAFAAFVKR
tr F1QYN0 F1QYN0_DANRE	1058	PSSTWLTAYVAKVFAMASDIIHIDQNVICSALRWLIMNROLPNGVFRENAPVIHGEMIGN
sp P01024 CO3_HUMAN	1073	APSTWLTAYVVKVFSLAVNLIAIDSQVLCGAVKWLILEKOKPDGVFQEDAPVIHQEMIGG
tr F1QYN0 F1QYN0_DANRE	1118	VQCSNS.EASMTAFVTIALQEGRSRCNG <mark>QVSSL</mark> DSSTYKAIAYLKSOLQGLINPYAVAMA
sp P01024 CO3_HUMAN	1133	LRNNNEKDMALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIA
tr F1QYN0 F1QYN0_DANRE	1177	SYALANANSLNKQVLMSKASADKSHNPVPGSSSFTLEASSYALLALVKLHDYQNTAPI
sp P01024 CO3_HUMAN	1193	Gyalaomgrlkgpllnkflttakdknrwedpgkolynveatsyallallolkdfdfvppv
tr F1QYN0 F1QYN0_DANRE	1235	VNWLNNOROYNGGYGTTOATIMVFOAVAEYRIHAKNIKOLDLEISTRVEG.VRPTVFTFS
sp P01024 CO3_HUMAN	1253	VRWLNEORYYGGGYGSTOATFMVFOALAOYOKDAPDHOELNLDVSLOLPSRSSKITHRIH
tr F1QYN0 F1QYN0_DANRE	1294	KNNDH <mark>D</mark> SQTAKIPSNKGITISAKGFGEASVTVVTEYYAKPKESSSTCKNFELELTFEK
sp P01024 CO3_HUMAN	1313	WESASLIRSEETKENEGFTVTAEGKGQGTLSVVTMYHAKAKD.QLTCNKFDLKVTIKPAP
tr F1QYN0 F1QYN0_DANRE	1352	DNEVRYOGATESYKLTINTRYLSADRDATMSILDVSLLTGFVVDENDLKALSTGRDKLIQ
sp P01024 CO3_HUMAN	1372	ETEKRPODAKNTMILEICTRYR.GDODATMSILDISMMTGFAPDTDDLKQLANGVDRYIS
tr F1QYN0 F1QYN0_DANRE	1412	KFEMNKQLSERGSLIIYLDKISHTRKDRVAFRLHRIMNGGFLQPAGVIVYEYYSIENRCV
sp P01024 CO3_HUMAN	1431	KYELDKAFSDRNTLIIYLDKVSHSEDDCLAFKVHQYFNVELIQPGAVKVYAYYNLEESCT
tr F1QYN0 F1QYN0_DANRE	1472	KFYHFTRKE <mark>C</mark> GIOKICKNDVCQCAEDNCSLQK.KEKIQEAHRNKKACESKINYVYKAVLL
sp P01024 CO3_HUMAN	1491	RFYHPEKEDCKLNKLCRDELCRCAEENCFIQKSDDKVTLEERLDKACEPGVDYVYKTRLV
tr F1QYN0 F1QYN0_DANRE	1531	GQDEDASTVS <mark>YYMRIQQALKIGPED</mark> DVEGKRRTETVQISCKEALDLKRGESYLIMGQSED
sp P01024 CO3_HUMAN	1551	KVQLSNDFDEYIMAIEQTIKSGSDEVQVGQQRTEISPIKCREALKLEEKKHYLMWGLSSD
tr F1QYN0 F1QYN0_DANRE	1591	VQLEGKVG <mark>QYALG</mark> ERTWLEFWPSLEQSKTSAELKLCDYIMSESKNSSSAGCKN
sp P01024 C03_HUMAN	1611	FWGEKPNLSYIIGKDTWVEHWPEEDECQDEENQKQCQDLGAFTESMVVFGCPN

**Figure XVI.** Structural comparison of the complement C3 between *Danio rerio* and *Homo sapiens*. The FASTA files related to zebrafish and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

sp P01026 CO3_RAT sp P01024 CO3_HUMAN	1	MGPTSGSQLL <mark>VLLLLL</mark> ASSL <mark>LALGSPMYSIITPNVLRLESEETFILEAHDAQGDVPVTVT</mark> MGPTSGPSLLLLLLTHLPLALGSPMYSIITPN <mark>I</mark> LRLESEET <mark>MVLEAHDAQGDVPVTVT</mark>
sp P01026 CO3_RAT	61	VODFLKKOVLTS, EKTVLTGATGHLNRVFIKIPASKEFNADKG, HKYVTVVANFGATVVE
sp P01024 CO3_HUMAN	59	VHDFPGKKLVLSSEKTVLTPATNHMGNVTFTIPANREFKSEKGRNKFVTVOATFGTOVVE
sp P01026 CO3_RAT	119	K <mark>RVLVSFQSGYLFIQTDKTIYTPGSTVF</mark> YRIFTVDNNLLPVGKTVVIVIETPDGVPIKRD
sp P01024 CO3_HUMAN	119	KVVLVSLQSGYLFIQTDKTIYTPGSTVLYRIFTVNHKLLPVGRTVMVNIENPEGIPVKQD
sp P01026 CO3_RAT	179	ILSSHNQYGILPLSWNIPELVNMGQWKIRAFYEHAPKQTFSAEFEVKEYVLPSFEVIVEP
sp P01024 CO3_HUMAN	179	SLSSQNQLGVLPLSWDIPELVNMGQWKIRAYYENSPQQVFSTEFEVKEYVLPSFEVIVEP
sp P01026 CO3_RAT	239	TEKFYYIHGPKGLEV <mark>S</mark> ITARFLYGKN <mark>VDGTAFVIFGV</mark> QDEDKKISLALSLTRVLIEDGSG
sp P01024 CO3_HUMAN	239	TEKFYYIYNEKGLEV <mark>T</mark> ITARFLYGK <mark>KVEGTAFVIFGIQD</mark> GEQRISLPESLKRIPIEDGSG
sp P01026 CO3_RAT	299	E <mark>AVLSRKVLMDGV</mark> RPSSPE <mark>ALVGKSLYVSVTVILHSGSDMVE</mark> AERSGIPIVTSPYQIHFT
sp P01024 CO3_HUMAN	299	E <mark>VVLSRKVLL</mark> DGVQNPRAEDLVGKSLYVSATVILHSGSDMVQAERSGIPIVTSPYQIHFT
sp P01026 CO3_RAT	359	KTPKFFKPAMPFDLMVFVTNPDGSPARRVPVVTQGSD.AQALTODDGVAKLSVNTPNNRQ
sp P01024 CO3_HUMAN	359	KTPKYFKPGMPFDLMVFVTNPDGSPAYRVPVAVQGEDTVQSLTQGDGVAKLSINTHPSQK
sp P01026 CO3_RAT	418	PLTITVSTKKEGIPDAROATRTMOAOPYSTMHNSNNYLHLSVSRVELKPGDNLNVNEHLR
sp P01024 CO3_HUMAN	419	PLSITVRTKKOELSEABOATRTMOALPYSTVGNSNNYLHLSVLRTELRPGETLNVNFLLR
sp P01026 CO3_RAT	478	TDAGQEAKIRYYTYLVMNKGKLLKAGRQVREPGQDLVVLSLPITPEFIPSFRLVAYYTLI
sp P01024 CO3_HUMAN	479	MdraheakiryytylimnkgrllkagrqvrepgqdlvvlplsitTdfipsfrlvayytli
sp P01026 CO3_RAT	538	GANGQREVVADSVWVDVKDSCVGTLVVKGDPRDNRQPAPGHQTTLRIEGNQGARVGLVAV
sp P01024 CO3_HUMAN	539	GA <mark>SGQREVVADSVWVDVKDSCVG</mark> SLVVK <mark>SGQSEDRQPWPGQQMTLKIEGDHGARVVLVAV</mark>
sp P01026 CO3_RAT	598	DKGVFVLNKKNKLTQSKIWDVVEKADIGCTPGSGK <mark>NYAGVFMDAGLTF</mark> KTNOGLQTDQRE
sp P01024 CO3_HUMAN	599	DKGVFVLNKKNKLTQSKIWDVVEKADIGCTPGSGK <mark>D</mark> YAGVFSDAGLTFT <mark>SSSGQQT</mark> AQRA
sp P01026 CO3_RAT	658	DPECAKPAARRRRSVQLMERRMDKAGQYTDKGLRKCCEDGMRDIPMPYSCQRRARLITQG
sp P01024 CO3_HUMAN	659	ELQCPQPAARRRRSVQLTBKRMDKWGKYP.KBLRKCCEDGMRENPMRFSCQRRIRFISLG
sp P01026 CO3_RAT	718	ESCLKAFMDCCNYITKLREQHRRDHVLGLARSDVDEDIIPEEDIISRSHFPESWLWTIEE
sp P01024 CO3_HUMAN	718	EACKKVFLDCCNYITELRRQHARASHLGLARSNLDEDIIAEENIVSRSEFPESWLWNVED
sp P01026 CO3_RAT	778	LKEPEKNGISTK <mark>V</mark> MNIFLKDSITTWEILAVS <mark>I</mark> SDKKGICVADP <mark>YEI</mark> TVMQDFFIDLRLPY
sp P01024 CO3_HUMAN	778	LKEP <mark>P</mark> KNGISTKLMNIFLKDSITTWEILAVS <mark>M</mark> SDKKGICVADP <mark>FEV</mark> TVMQDFFIDLRLPY
sp P01026 CO3_RAT	838	SVVRNEQVEIRAVLENYREQEKLKVRVELLHNPAFCSMATAKKRYYQTIEIPPKSSVAVP
sp P01024 CO3_HUMAN	838	SVVRNEQVEIRAVLYNYRQNQELKVRVELLHNPAFCSMATTKRRHQQTVTIPPKSSLSVP
sp P01026 CO3_RAT	898	YVIVPLKIGLQEVEVKAAVENHFISDGVKKILKVVPEGMRVNKTVAVRTLDPEHLNQGGV
sp P01024 CO3_HUMAN	898	YVIVPLKTGLQEVEVKAAVYHHFISDGV <mark>RKS</mark> LKVVPEGIRMNKTVAVRTLDPERLGREGV
sp P01026 CO3_RAT	958	Q <mark>REDVNAADLSDQVPDTDSETRILLQGTPVAQM</mark> AEDAVD <mark>GERLKHLIVTPSGCGEQNMIG</mark>
sp P01024 CO3_HUMAN	958	QKEDIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDAERLKHLIVTPSGCGEQNMIG
sp P01026 CO3_RAT	1018	MTPTVIAVHYLD <mark>O</mark> TEQWEKFGLEKRO <mark>E</mark> ALELIKKGYTQQLAFKOPISAYAAFNNRPPSTW
sp P01024 CO3_HUMAN	1018	MTPTVIAVHYLD <mark>E</mark> TEQWEKFGLEKRO <mark>G</mark> ALELIKKGYTQQLAFROP <mark>SSAF</mark> AAFVKRAPSTW
sp P01026 CO3_RAT	1078	LTAMWSRSFSLAANLIAIDSQVLCGAVKWLILEKQKPDGVFQEDGPVIHQEMIGGFRNTK
sp P01024 CO3_HUMAN	1078	LTAYVVKVFSLAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQEMIGGLRNNN
sp P01026 CO3_RAT	1138	EADVSLTAFVLIALQEARDICEGQVNSLPGSINKAGEYLEASYLNLQRPYTVAIAGYALA
sp P01024 CO3_HUMAN	1138	EKDMALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYALA
sp P01026 CO3_RAT	1198	LMNKLEEPYLTKFINTAKDRNRWEEPGQQLYNVEATSYALLALLLLKDFDSVPPVVRWLN
sp P01024 CO3_HUMAN	1198	QMGRLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLN
sp P01026 CO3_RAT	1258	DERYYGGGYGSTQATFMVFQALAQYRADVPDHKDLNMDVSLHLPSRSSPTVFRLLWESGS
sp P01024 CO3_HUMAN	1258	Eqryygggygstqatfmvfqalaqyqkdapdhqelnldvslqlpsrsskithrihwesas
sp P01026 CO3_RAT	1318	LLRSEETK <mark>onegfsltakgrgogtlsvvtvyhakvk</mark> gkt <mark>tckkfdlrvtikpapetakkp</mark>
sp P01024 CO3_HUMAN	1318	Llrseetk <mark>enegftvta</mark> e <mark>grgogtlsvvtmyhakak</mark> dol <mark>tcnkfdlkvtikpapet</mark> ek <mark>r</mark> p
sp P01026 CO3_RAT	1378	QDAKSSMILDICTRYLGDVDATMSILDISMMTGFIPDTNDLELLSSGVDRYISKYEMDKA
sp P01024 CO3_HUMAN	1378	QDAKNTMILEICTRYR <mark>GDQDATMSILDISMMTGFAPDT</mark> DDLKQLANGVDRYISKYBLDKA
sp P01026 CO3_RAT	1438	FSNKNTLIIYLEKISHSEEDCLSFKVHQFFNVGLIQPGSVKVYS <mark>yynleesctrfyhpek</mark>
sp P01024 CO3_HUMAN	1438	FSDRNTLIIYLDKVSHSEDDCL <mark>AFKVHQYFNVE</mark> LIQPGAVKVYA <mark>yynleesctrfyhpek</mark>
sp P01026 CO3_RAT	1498	DDGMLSKLCHNEMCRCAEENCFMHQSQDQVSLNERLDKACEPGVDYVYKTKLTTIELSDD
sp P01024 CO3_HUMAN	1498	EdgKLnklcrdelcrcaeencfiqksddkvtleerldkacepgvdyvyktrlvkVqlsnd
sp P01026 CO3_RAT	1558	FDEYIMTIEQVIKSGSDEVQAGQERRFISHVKCRNALKLQKGKQYLMWGLSSDLWGEKPN
sp P01024 CO3_HUMAN	1558	FDEYIMAIEQTIKSGSDEVQVGQQRTFISPIKCREALKLEEKKHYLMWGLSSDFWGEKPN
sp P01026 CO3_RAT	1618	TSYIIGKDTWVEHWPE <mark>AEERQD</mark> QKNQKQCEDLGAFTETMVVFGCPN
sp P01024 CO3_HUMAN	1618	LSYIIGKDTWVEHWPEEDECQDEENQKQCQDLGAFTESMVVFGCPN

**Figure XVII.** Structural comparison of the complement C3 between *Rattus norvegicus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1 1 MGPASG <mark>S</mark> QI MGPT <mark>S</mark> GP	. 9 LVLLLLA SLLLLLT	20 SS <b>PLALG</b> IP HL <b>PLALG</b> SP	30 Mysiitpnv Mysiitpni	4 0 LRLESEETIVL LRLESEETMVL	50 EAHDAQGD EAHDAQGD	60 IPVTVT VPVTVT
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	VQDFLKR.Q VHDFPGKKI	70 VLTSEKTV VLSSEKTV	80 LTGASGHLF LTPATNHMG	90 SVSIKIPAS NVTFTIPAN	100 KEFNSDKEGH <mark>K</mark> REFKSEKGRNK	110 YVTVVANE FVTVQATE	GETVVE GTovve
1 sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	2 Q KAVMVSFQS KVVLVSLQS	30 GYLFIQTD GYLFIQTD	140 KTIYTPGST KTIYTPGST	150 VLYRIFTVD VLYRIFTVN	160 NN <mark>LLPVGKTV</mark> V HK <b>LLPVGRTV</b> M	170 ILIETPDG VNIENPEG	IPVKRD IPVKOD
1 sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	80 ILSSNNOHO SLSSONOLO	I 90 I LPLSWN I VLPLSWD I	200 Pelvnmgor Pelvnmgor	210 KIRAFYEHA KIRAYYENS	220 PKQIFSAEFEV PQQVFSTEFEV	230 Keyvlpsf Keyvlpsf	EVR <mark>VEP EV</mark> IVEP
2 sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	40 TETFYYIDI TEKFYYIYI	250 DPN <mark>GLEVSI</mark> NEK <mark>GLEVTI</mark>	260 I <mark>AKFLYGK</mark> N T <mark>ARFLYGK</mark> B	270 VDGTAFVIF VEGTAFVIF	280 GVQDGDKKISL GIQDGEQRISL	290 AH <mark>SL</mark> T <mark>RV</mark> V PE <b>SL</b> KRIP	IEDGVG IEDGSG
3 sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	DAVLTRKV EVVLSRKV	<b>310</b> LMEGVRPSN LLDGVQNPH	320 ADALVGKSI RAEDLVGKSI	330 LYVSVTVILH LYVSATVILH	340 SGSDMVEAERS SGSDMVQAERS	350 GIPIVTSP GIPIVTSP	YQIHFT YQIHFT
3 sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	60 3 KTPKFFKPA KTPKYFKPG	70 MPFDLMVF MPFDLMVF	380 VTNPDGSPA VTNPDGSPA	390 SKVLVVTQG YRVPVAVQG	400 S.NAKA <b>LTO</b> D EdTVQS <b>LTO</b> GD	410 GVAKLSINT GVAKLSINT	PN <mark>S</mark> RQ HP <b>S</b> QK
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	420 PLTITVRTK PLSITVRTK	430 Kdtlpesr Kqelseae	440 OATKTMEAH OATRTMOAL	450 PYSTMHNSNI PYSTVGNSNI	460 NYLHLSVSRME NYLHLSVLRTE	470 LKPGDNLN LRPGETLN	VNFHLR VNFLLR
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	480 TDPG <mark>HEAK</mark> MDRA <b>HEAK</b>	490 IRYYTYLVN IRYYTYLIN	500 ANKGKLLKA ANKGRLLKA	510 GRQVREPGQD GRQVREPGQD	520 LVVLSLPITPE LVVLPLSITT	530 FIPSFRLV FIPSFRLV	AYYTLI AYYTLI
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	540 GASGQREV GASGQREV	550 VADSVWVDV VADSVWVDV	560 /KDSCIGTL /KDSCVGSL	<b>570</b> /VK.GDPRDN /VKSGQSEDR	580 HL <mark>APGQQTTL</mark> R QP <b>VPGQQMTL</b> K	590 IEGNQ <mark>GAR</mark> IEGDH <mark>GAR</mark>	VG <mark>LVAV</mark> VVLVAV
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	600 DKGVFVLN DKGVFVLN	610 KKNKLTQSI KKNKLTQSI	620 KIWDVVEKA KIWDVVEKA	630 DIGCTPGSGK DIGCTPGSGK	640 N <mark>YAGVF</mark> MDAGI D <mark>YAGVF</mark> SDAGI	650 AFKTSQGL TFTSSSGQ	QT <mark>E</mark> QRA QT <mark>AQRA</mark>
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	660 DLECTKPA ELQCPQPA	670 ARRRRSVQI ARRRRSVQI	680 MERRMDKA TEKRMDKV	690 GQYTDKGLRK GKYP.KELRK	700 CCEDGMRDIPM CCEDGMRENPM	710 RYSCORRA RFSCORRT	RLITQG RFISLG
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	ENCIKAFII EACKKVFLI	CCNHITKI CCNYITEI	REQHERDHV RROHARASH	LGLARSELE LGLARSNLD	EDIIPEEDIIS EDIIAEENIVS	RSHFPQSW RSEFPESW	LWTIEE LWNVED
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	780 LKEPEKNG LKEPPKNG	790 ISTKVMNIE ISTKLMNIE	800 ILKDSITTWI ILKDSITTWI	810 EILAVSLSDK EILAVSMSDK	820 KGICVADPYEI KGICVADPFEV	830 RVMQDFFI TVMQDFFI	DLRLPY DLRLPY
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	SVVRNEQVE SVVRNEQVE	IRAVLENY IRAVLYNY	REQEELKVR RQNQELKVR	VELLHNPAF VELLHNPAF	CSMATAKNRYF CSLATTKRRHQ	QTIKIPPK QTVTIPPK	SSVAVP SSLSVP
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	900 YVIVPLKIO	910 GOOEVEVKA GLOEVEVKA	920 AVFNHFISI AVYHHFISI	930 GVKKTLKVV GVRKSLKVV	940 PEGMRINKTVA PEGIRMNKTVA	950 IHTLDPEK VRTLDPER	LGQG <mark>GV</mark> LGREGV
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	OKVDVPAA OKEDIPPA	DLSDQVPD1 DLSDQVPD1	980 DSETRIIL ESETRILLO	OGSPVVOMAE OGTPVAOMTE	DAVDGERLKHI DAVDAERLKHI	IVTPAGCG IVTPSGCG	EQNMIG EQNMIG
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1020 MTPTVIAV MTPTVIAV	1030 HYLDQTEQU HYLDETEQU	1040 Wekfgiekr Wekfglekr	1050 De <mark>alelikko</mark> Dg <mark>alelikko</mark>	1060 YTQQLAFKQPS YTQQLAFROPS	1070 SAYAAFNN SAFAAFVK	R P P S T W R A P S T W
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1080 LTAYVVKVE LTAYVVKVE	1090 SLAANLIA SLAVNLIA	1100 IDSHVLCGA IDSQVLCGA	1110 VKWLILEKQ VKWLILEKQ	1120 KPDGVFQEDGP KPDGVFQEDAP	1130 VIHQEMIG VIHQEMIG	GF <mark>RN</mark> AK GL <mark>RN</mark> NN
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1140 EADVSLTAE EKDMALTAE	1150 VLIALQEA VLISLQEA	1160 RDICEGOVI KDICEEQVI	1170 Slpgsinka Slpgsitka	1180 GEYIEASYMNI GDFL <mark>EA</mark> NYMNI	1190 QRPYTVAI QRSYTVAI	AGYALA Agyala
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	LMNKLEEP QMGRLKGP	1210 YLG <mark>KFLNT</mark> LLNKFLTT	1220 AKDRNRWEEI AKDKNRWEDI	1230 DO <mark>OLYNVEA</mark> GK <mark>OLYNVEA</mark>	1240 TSYALLALL TSYALLALLOI	1250 KDFDSVPP KDFDFVPP	VVRWLN VVRWLN
sp P01027 C03_MOUSE sp P01024 C03_HUMAN	1260 EQRYYGGG EQRYYGGG	1270 YGSTQATFI YGSTQATFI	1280 MVFQALAQY MVFQALAQY	1290 QTDVPDHKDI QKDAPDHQEI	1300 NMDVSFHLPSF NLDVSLQLPSF	1310 RSSATTFRL RSSKITHRI	L <mark>WEN</mark> GN H <mark>WES</mark> AS
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1320 LLRSEETKC LLRSEETKE	1330 NEAFSLTA NEGETVTA	1340 K <mark>GKG</mark> R <mark>GTLS</mark> EGKGOGTLS	1350 VVAVYHAKL VVTMYHAKA	1360 KSKVTCKKFDI KDOLTCNKFDI	1370 RVSIRPAP KVTIKPAP	ETA <mark>K</mark> KP ETEKRP
sp P01027 C03_MOUSE sp P01024 C03_HUMAN	1380 EEAKNTMF QDAKNTMI	1390 EICTKYLC EICTRYRC	1400 DVDATMSII	1410 DISMMTGFA DISMMTGFA	1420 PDTKDLELLAS PDTDDLKQLAN	1430 GVDRYISK GVDRYISK	YEMNKA YELDKA
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1440 FSNKNTLI FSDRNTLI	1450 Ylekisht Yldkvshs	1460 EEDCLTFK EDDCLAFK	1470 HQYENVGLI HQYENVELI	1480 OPGSVKVYSYY OPGAVKVYAYY	1490 NLEESCTR NLEESCTR	FYHPEK FYHPEK
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1500 DDGMLSKL EDGKLNKL	1510 CHSEMCRC2 CRDELCRC2	1520 AEENCFMQQ AEENCFIQK	1530 SQEKINLNVR SDDKVTLEER	1540 LDKACEPGVDY LDKACEPGVDY	1550 VYKTELTN VYKTRLVK	IELLDD VQLSND
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	I 5 6 0 FDEYTMTI FDEYIMAI	1570 QQV <mark>IKSGSI</mark> EQT <mark>IKSGSI</mark>	1580 DEVQAGQQR DEVQVGQQR	1590 K <mark>FIS</mark> H <mark>IKCR</mark> N F <b>IS</b> PIKCRE	1600 ALKLQKG <mark>KKYI</mark> ALKLEEK <mark>KHYI</mark>	1610 MWGLSSDL MWGLSSDF	W G E K P N W G E K P N
sp P01027 CO3_MOUSE sp P01024 CO3_HUMAN	1620 T <mark>syiigkd</mark> L <mark>syiigkd</mark>	1630 TWVEHWPE TWVEHWPE	1640 AEECODOKY EDECODEEN	1650 OKOCEELGA OKOCODLGA	1660 FTESMVVYGCE FTESMVVFGCE	N N	

**Figure XVIII.** Structural comparison of the complement C3 between *Mus musculus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

tr I3J4H8 I3J4H8_ORENI sp P00738 HPT_HUMAN	1	MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT
tr 13J4H8 13J4H8_ORENI sp P00738 HPT_HUMAN	61	EGDGVYTLNDKKQWINKAVGDKLPECEADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRTE
tr I3J4H8 I3J4H8_ORENI sp P00738 HPT_HUMAN	1 121	
tr 13J4H8 13J4H8_OREN1	35	IAESILDGGYAGGA <b>LI</b> SDRWVLTAGRNLFVKKSREAIQGKEPVIPK <mark>VYLG</mark> ITKKDDANSS
sp P00738 HPT_HUMAN	181	SHH <mark>N</mark> ITTGAT <mark>LINEOWLLT</mark> TAKNLFLNHSENATAKDIAPTLTLYVGKKQ
tr 13J4H8 13J4H8_OREN1	95	SEVAVEKVVLHEGFONOSDWNNDLALIQLKOPVVINDKVTPIPLEERGODLAKAVHGSGI
sp P00738 HPT_HUMAN	230	.LVEIEKVVLHENYSQVDIGLIKLKOKVSVNERVMPICLESKDYAEVGRVGY
tr I3J4H8 I3J4H8_ORENI	155	ITGWGWGPLLTPSPFLKHIVVPLANHSECRAEYESLALTPTVDDDMIC
sp P00738 HPT_HUMAN	281	VSGWGRNANFKFTDH <mark>LK</mark> YVMLPVADQDQCIRHYEGSTVPEKKTPKSPVGVQPILNEHTFC
tr 13J4H8 13J4H8_ORENI	203	TA <mark>ATKYQE</mark> NV <mark>CEGDAGGALAV</mark> TDPETGDIYAAGILSYDKSCTRYKHAVYMKLSSYLPWTH
sp P00738 HPT_HUMAN	341	AG <u>MSKYQE</u> DT <mark>CYGDAG</mark> SAFAVHDLEEDTWYATGILSEDKSCAVAEYG <mark>VYVKVTS</mark> IQDWVQ
tr I3J4H8 I3J4H8_ORENI	263	SIMRGDTDTSTAVRFKAMSSMYRRQE
sp P00738 HPT_HUMAN	401	KTIAEN

**Figure XIX.** Structural comparison of the haptoglobin between *Oreochromis niloticus* and *Homo sapiens*. The FASTA files related to tilapia and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).



**Figure XX.** Structural comparison of the haptoglobin between *Danio rerio* and *Homo sapiens*. The FASTA files related to zebrafish and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).

sp P06866 HPT_RAT	1	MRALGAVVTLLLWGQLFAVELGNDATDIEDDSCPKPPEIAN
sp P00738 HPT_HUMAN	1	MSALGAVIALLLWGQLFAVDSGNDWTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT
sp P06866 HPT_RAT sp P00738 HPT_HUMAN	42 61	
sp P06866 HPT_RAT	62	GDGIYTLN <mark>SEKQWVNPAA</mark> GDKLP <mark>KCEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI</mark>
sp P00738 HPT_HUMAN	121	GDGVYTLN <u>NEKQWINKAV</u> GDKLP <mark>E</mark> CEAVCGKPKNPANPVQRILGGHLDAKGSFPWQAKMV
sp P06866 HPT_RAT	122	SRHGLTTGATLI <mark>SDQWLLTTAQ</mark> NLFLNHSENATAKDIAPTLTLYVGK <mark>NQLVEIEKVVLHP</mark>
sp P00738 HPT_HUMAN	181	SHHN <mark>LTTGATLINEQWLLTTAK</mark> NLFLNHSENATAKDIAPTLTLYVGK <mark>KQLVEIEKVVLHP</mark>
sp P06866 HPT_RAT	182	ER <mark>SVVDIGLIKLKQKVLVTEKVMPICLPSKDYVAPGRMGYVSGWGRNVNFRFTERLKYVM</mark>
sp P00738 HPT_HUMAN	241	NYS <mark>QVDIGLIKLKQKVS</mark> V <mark>NERVMPICLPSKDYAEVGRVGYVSGWGRNANFKFTDHLKYVM</mark>
sp P06866 HPT_RAT	242	LPVADQEKCELHYEKSTVPEKKGAVSPVGVQPILNKHTFCAGLTKYEEDTCYGDAGSAFA
sp P00738 HPT_HUMAN	301	LPVADQDQCIRHYEGSTVPEKKTPKSPVGVQPILNEHTFCAGMSKYQEDTCYGDAGSAFA
sp P06866 HPT_RAT	302	VHDTEEDTWYAAGILSFDKSCAVAEYGVYVRATDLKDWVQETMAKN
sp P00738 HPT_HUMAN	361	VHDLEEDTWYATGILSFDKSCAVAEYGVYV <mark>KVT</mark> SIQDWVQKTIAEN

**Figure XXI.** Structural comparison of the haptoglobin between *Rattus norvegicus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).



**Figure XXII.** Structural comparison of the haptoglobin between *Mus musculus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).

tr 13J919 13J919_ORENI	1	MO <mark>G</mark> FYPILLFSIFVCS <mark>V</mark> SAKKMRWCTVSDPEORKCAELAKALAAVVSPAILAAFARL
sp P02787 TRFE_HUMAN	1	MRLAVGALLVCAVLGLCLAVPDKTVRWCAVSEHBATKCOSFRDHMKSVIPSDGPSV
tr 13J919 13J919_OREN1	58	S <mark>CIRAYSTTDCINRIKANRADIVTLDAGEIY</mark> SAVKQFD.LVAIAKEIYSDDLSTGGCTLS
sp P02787 TRFE_HUMAN	57	A <mark>CVK</mark> KA <mark>SYL<mark>DCI</mark>RA<mark>IAANEADAVTLDAG</mark>LVYDAYLAPNNLKPVVAEFYGSKEDPQTFYYA</mark>
tr 13J919 13J919_OREN1	117	VAVVRNNS.LDIRSLQGRRSCHSGVRWTAGWSLPLGFLLSRNYLSWAKEHPLSQDVSTFF
sp P02787 TRFE_HUMAN	117	VAVVKKDSGFQMNQLRGKKSCHIGLGRSAGWNIPIGLLYCDLPEPRKPLKAVANFF
tr 13J919 13J919_ORENI	176	SASCIPGAGAMALP, LCTLCOGLKSYIRQKNYHCETSHSEPFYNNOGALRCLRRCICDVA
50 P02 /8 /   TREE_HUMAN	1/4	
sp P02787 TRFE_HUMAN	223	EVUHLALEI. ILEESEKDEFKLIGSDGTQAPISQHKSCNIGGGGGGMIKVNFKNVVKK EVKHSTIFENLANKADRDQYELLCLDNTRKEVDEYKDCHLAQVESHTVVARSMGGKEDLI
tr 13J919 13J919_OREN1	293	FLATV <mark>O</mark> TLFGRQGRERQRFQLFSSSSFGEN <b>DLLFRD</b> VTEKLVVLQDDIDVSQVLGLDYVA
sp P02787 TRFE_HUMAN	283	WELLNQAQEHFGKDKSKE <mark>FQLFSS</mark> PHGK <mark>DLLFKD</mark> SAHGFLKVPPRMDAKMYLGYEYV
tr I3J919 I3J919_ORENI	353	LLKGLGHEGSSLEDSVIRWCCISYAEQKKCEQWALSIKSDPLVCVRAISMRDCTEK
sp P02787 TRFE_HUMAN	341	AIRNLREGTCPEAPTDECKPVKWCALSHHERLKCDEWSVNSVG.KIECVSAETTEDCIAK
tr 13J919 13J919_ORENI	409	IKRD <mark>BVDAVSLD</mark> ATHSF <b>IAGKCGLVPVV</b> TEYYGKNCVPAEG <mark>S</mark> THLETDVFPSVVGL <b>AVAK</b>
sp P02787 TRFE_HUMAN	400	IMNG <mark>EADAMSLD</mark> GGFV <mark>YIAGKCGLVPV</mark> LAENYNKSDNCEDTPEAGYFAIAVVK
tr 13J919 13J919_OREN1	469	H <mark>S</mark> SRNIFIG <mark>NLGGRRSCHS</mark> NTYSP <mark>AGW</mark> LIPYRHSLSLA <mark>N</mark> NSSSPCDPDKVYNEVFWKSCL
sp P02787 TRFE_HUMAN	453	KSASDLTWDNLKGKKSCHTAVGRTAGWNIPMGLLYNKINHCRFDEFFSEGCA
tr I3J919 I3J919_ORENI	529	<mark>PGSK</mark> GNLCKVCIGGTGETATKRCTENHNERYYGNMGALRCLVGDRSGKSY <mark>GDVAF</mark> LEQ
sp P02787 TRFE_HUMAN	505	PGSKKDS <mark>SLCKLCMG</mark> SGLNLCEPNNKEGYYGYTGAFRCLVEKGDVAFVKH
tr 13J919 13J919_OREN1	587	HSIHTNILGINTTGWAEGWSSSDFELLCADGRRAPISDWETCNIGVIPPNTVMTRPVITA
sp P02787 TRFE_HUMAN	555	QTVPQNTGGKNPD <mark>PWA</mark> KNINEKDYELLCIDGTRKPVEEYANCHIARAPNHAVVTRKDKEA
tr I3J919 I3J919_ORENI	647	RVYDF <b>I</b> MKSQEALAVNSNTEFRLFESHQYGES <mark>DLLFKDATQCFA</mark> HTSHMD.YRSI <b>LGEE</b> F
sp P02787 TRFE_HUMAN	615	CVHKIIRQQQHLFGSNVTDCSGNFCLFRSETKDLLFRDDTVCLAKLHDRNT <mark>Y</mark> EKY <mark>LGEE</mark> Y
tr 13J919 13J919_ORENI	706	YTHADTVFNCTHSDILEFCNQDVC
sp P02787 TRFE_HUMAN	675	VKAVG <mark>NL</mark> RKCSTSSLLEACTFRRP

**Figure XXIII.** Structural comparison of the serotransferrin between *Oreochromis niloticus* and *Homo sapiens*. The FASTA files related to tilapia and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).



**Figure XXIV.** Structural comparison of the serotransferrin between *Danio rerio* and *Homo sapiens*. The FASTA files related to zebrafish and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).



**Figure XXV.** Structural comparison of the serotransferrin between *Rattus norvegicus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (<u>http://www.uniprot.org</u>).



**Figure XXVI.** Structural comparison of the serotransferrin between *Mus musculus* and *Homo sapiens*. The FASTA files related to rodent and human proteins were acquired on the UNIPROT search platform (http://www.uniprot.org).

## Attachment 3 (Blood analysis- Manual counting)

#### Results and discussion for blood analysis (manual counting)

Fish inoculated with *A. hydrophila* showed a significant decrease (p < 0.05) in erythrocyte, leukocyte and granulocyte counts 6 HPI when compared to animals inoculated with saline (Figure XXVII and XXVIII). No difference was observed in the number of circulating lymphocytes, thrombocytes and monocytes 6 and 24 HPI (Figure XXVIII). The study of hematocrit, MCV, hemoglobin and MCHC did not demonstrate significant variations during the experimental period (Figure XXVII). Similar to our results, Inoue et al.<sup>1</sup> showed correlation between manual counting and flow cytometry of fish blood cells. According to these authors, this technique presented advantages, because it is a simple and rapid method for analysis of fish blood cells.

Automatic counting methods have been routinely used for the diagnosis of diseases in mammals. However, the techniques applied to mammalian blood depend on lysing the erythrocytes, and then the remaining leukocytes can be counted automatically by the machine. In fish, these techniques are not precise, since their erythrocytes are nucleated, and the glutinous nature of released chromatin from red blood cells interferes with automated counting<sup>2</sup>. On the other hand, the limitations of the use of flow cytometry would be the high costs of the analysis, such fact difficult its use in routine clinical analysis, besides the need for technical training to carry out the sampling.

### Material and Methods for blood analysis

Blood samples were drawn from the caudal vessel. Red (RBC) and white blood cell (WBC) counts were made using a haemocytometer and Natt and Herrick solution. The haemoglobin concentration (Hb) was determined with Drabkin's reagent read at 540 nm and haematocrit (Ht) by a microhaematocrit centrifugation technique. Mean cell volume (MCV) and cell haemoglobin concentration (MCHC) were calculated from the Ht, [Hb] and RBC. Blood smears for differential leukocyte counts were stained with a combination of May-Grünwald Giemsa and Wright's Method<sup>3</sup>.



**Figure XXVII.** Mean values ( $\pm$ SE) and ANOVA for hematological parameters: (A) Number of erythrocytes; (B) Hematocrit; (C) MCV - Mean corpuscular volume; (D) Hemoglobin; (E) MCHC – Mean corpuscular hemoglobin concentration. Mean values (n=10) and ANOVA observed for total cells and differential counting of cells present in the blood during acute inflammatory response in tilapias 6 and 24 HPI. Means followed by the same letter do not differ by the Tukey test (P<0,05). The variance analysis is represented by capital letters to compare the different treatments within each experimental period, lowercase letters to compare the evolution of each treatment in the different experimental periods. Different letters indicate significant difference (p < 0.05).



**Figure XXVIII.** Mean values ( $\pm$ SE, data transformed in Log x+1) and ANOVA for thrombocyte and leukocyte counts: (A) Number of thrombocytes; (B) Number of leukocytes; (C) Number of lymphocytes; (D) Number of neutrophils; (E) Number of monocytes. Mean values (n=10) and ANOVA observed for total cells and differential counting of cells present in the blood during acute inflammatory response in tilapias 6 and 24 HPI. Means followed by the same letter do not differ by the Tukey test (P<0,05). The variance analysis is represented by capital letters to compare the different treatments within each experimental period, lowercase letters to compare the evolution of each treatment in the different experimental periods. Different letters indicate significant difference (p < 0.05).

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