

Do SNPs in glutathione S-transferase-omega allow predictions of the susceptibility of vertebrates to SARS-CoV-2?

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Short title: COVID-19 and GST

Abstract

Infection with the SARS-Cov-2 virus causes COVID-19 in humans, and is the cause of the pandemic around the world in 2020 and on. However, some animals have been found to be susceptible to the virus too. This has included the non-human primates, dogs, cats and mustelids. Mink, and very recently hamsters and deer, have been shown to be able to contract the virus and pass it back to humans. However, which animals are susceptible to the virus has been very hard to predict. Many groups have looked at the sequence homology of the angiotensin converting enzyme 2 receptor (ACE2) across species, but this has had limited success. Similar work on other proteins such as Transmembrane Serine Protease 2 (TMPRSS2), neuropilin-1 and furin have also been unfruitful. Recently it has been suggested that single nucleotide polymorphisms (SNPs) in the glutathione S-transferase-omega (GSTO) genes of humans could alter viral susceptibility. Therefore, here, the presence of related sequences in vertebrates has been investigated. The SNPs in the GST-omega-1 (GSTO1) gene reported to increase COVID-19 in humans do not appear in the vertebrate species. However, the GST-omega-2 (GSTO2) SNP is represented in several vertebrate species known to have contracted the SAR-CoV-2 virus. Of course, animals may contain

unknown SNPs at disruptive points in these genes too. In summary, GST-omega-1 genes are unlikely, at least at the moment, to be of value in predicting the susceptibility of an animal to the SARS-CoV-2 virus or disease progression, but a further study of the GST-omega-2 genes would be worthwhile. Therefore, more work on SARS-CoV-2 infections on vertebrates is recommended.

Keywords: ACE2; COVID-19; GST; polymorphisms; SARS-CoV-2; SNPs.

Introduction

The SARS-CoV-2 virus caused the COVID-19 pandemic which has spread across the world. At present (28th February 2022) there have been 435,626,514 confirmed cases and 5,952,215 deaths worldwide¹. The virus is an RNA-containing enveloped virus, and has been shown to be transmitted through respiratory droplets and being deposited on surfaces². The virus interacts and then enters the host cells through the interaction of the viral surface proteins with the cell surface. This involves spike proteins³ which protrude out of the virus and give it its image, and hence name, as being a coronavirus. The host cell protein of note that the virus interacts with is the angiotensin converting enzyme 2 receptor (ACE2)⁴, although other proteins are also involved, such as neuropilin⁵. Severe COVID-19 is underpinned by what is termed the cytokine storm⁶, and this can lead to death.

The SARS-Cov-2 is thought to have derived from a virus from a bat⁷, but exactly how it entered the human population is still contested⁸. However, regardless of its origin, it is known that several species of animals have been found to be SARS-CoV-2 positive. Susceptible animal species include non-human primates, dogs, cats and mustelids. This has been reviewed before⁹⁻¹³. However, two factors are important here. Firstly, contraction of the virus has been found to be fatal in some animals. For example, lions have died at zoos in Honolulu¹⁴ and Chennai, India¹⁵. Secondly, the virus can be passed from animal to animal, such as has been found in cats¹⁶, but more concerning, it can be passed back to humans. This was first reported in mink^{17,18}, and led to a mass euthanasia programme for mink in several

mink farms, for example in Denmark¹⁹. More recently hamsters were thought to have given the virus back to humans in a pet shop in Hong Kong²⁰, and were subsequently culled, whilst deer were a worry for the same reason in Canada²¹. The main concern for human health is the potential for the virus to mutate in the animal before re-transmission back to humans, and therefore the efficacy of vaccines may be compromised, and for animals' health in relation to the impact on endangered populations which may be susceptible, such as black footed ferrets (*Mustela nigripes*), and the culling of domestic species during an outbreak.

There is, therefore, a need to be able to predict which animals are susceptible to the SARS-Cov-2 virus. This has in the past concentrated on looking at the ACE2 receptor, which is the primary protein which interacts with the viral spike proteins⁴. Similarity analysis between the human ACE sequences and those found in animal genomes has been carried out extensively by others^{9,22,23}. However, the predictions do not appear to match reality. Animals which have been reported to be SARS-CoV-2 susceptible do not show sequence similarities in their ACE2 genes. Therefore, other proteins were examined too, including Transmembrane Serine Protease 2 (TMPRSS2), neuropilin-1 and furin¹⁰. Again, limited usefulness was found. Not surprisingly, the animals most similar to humans, such as non-human primates, were predicted to be susceptible to the virus, and this has been borne out in reality²⁴. At the lower end of the vertebrate evolutionary scale, reptiles, fish, amphibians and birds all seem to be predicted to not be susceptible to SARS-CoV-2, and there have been to date no reports of such animals being infected with the SARS-CoV-2 virus. However, in between this range of animals, viral susceptibility seems hard to predict. For example, the mustelids such as mink were not predicted to be highly susceptible and yet mink is one of the species most affected. Similarly, the susceptibility to the virus of dogs and cats does not jump out of the sequence alignment data reported, and yet again, these animals seem to be being tested positive for the virus more than predicted. Being companion animals, this may be due to their close contact with infected people. Therefore, there is a need for more analysis of the proteins involved in the SARS-Cov-2 infection process.

Recently, single nucleotide polymorphisms (SNPs) within the genes of two isoforms of glutathione S-transferase- Omega (GST-omega; GSTO) have been found to correlate with COVID-2 severity²⁵. Therefore, these gene sequences were aligned in animal species to see if there was any evidence that the SNPs were represented and therefore could lead to a better understanding as to why certain animals are SARS-CoV-2 susceptible.

Methods

Representative vertebrate species were chosen and the sequences for GSTO1 and GSTO2 were obtained from the National Center for Biotechnology Information (NCBI) database. For some animal species there were several isoforms or variants available and these were extracted too (see Tables 1 & 2). Alignments of the sequences were undertaken using Clustal Omega²⁶. The multiple sequence alignment tool, Clustal Omega, is based on seeded guide trees and Hidden Markov Model (HMM) profile-profile techniques. Further analysis of functional and control sequences were undertaken using Prosite²⁷.

Results

Previous analysis of the GSTO SNPs

Glutathione-S transferase (GST) is a superfamily of proteins²⁸. GST proteins have a range of roles. They are involved in antioxidant metabolism, and hence reactive oxygen species (ROS) metabolism, and are instrumental in many cell signalling pathways and in the detoxification of certain molecules²⁹. In mammals there are eight classes of cytosolic GST enzymes: alpha ((α)-*GSTA*); mu ((μ)-*GSTM*); pi ((π)-*GSTP*); omega ((ω)-*GSTO*); theta ((θ)-*GSTT*); sigma ((σ)-*GSTS*); kappa ((κ)-*GSTK*); zeta ((ζ)-*GSTZ*). Of relevance here GSTO1 has a role in chronic obstructive pulmonary disease (COPD), through its action as an antioxidant and its control of glutathione (GSH) homeostasis. GSTO1 activity also impacts in the inflammatory response through its action on the lipopolysaccharide (LPS)/Toll-like receptor (TLR-4) and the subsequent downstream activation of nuclear factor-kappa B (NF-

κB), and hence gene expression. There is also a physiological inhibitor of GSTO1 which can impact the inflammatory response²⁵. Therefore, it appears that this enzyme has a significant role in inflammation: COVID-19 severity in humans involves a cytokine storm, and hence loss of control of the inflammatory response. However, even though some animals are reported to be virus positive, this does not necessarily result in a cytokine storm, with some animals appearing to have less severe symptoms. However, GSTO1 polymorphisms were the focus of a recent study²⁵. GSTO2, meanwhile, is also involved in redox homeostasis and control of vitamin C levels. Vitamin C has been shown to be beneficial for patients with severe COVID-19³⁰. As discussed below, again a SNP in this enzyme's gene sequence was analysed with respect to COVID-19 severity too²⁵.

The idea of GST SNPs being important in the onset and severity of COVID-19 has been reported before. For example, it was found that patients with the GSTT1^{-/-} genotype (i.e., lacking the theta 1 form) had high mortality³¹. However, recently a paper focused on SNPs in the GST-omega genes and how their presence correlates with the susceptibility and severity of SARS-Cov-2 infection in humans²⁵. Interestingly, it was found that polymorphisms in the ACE2 receptor (rs4646116) were not useful as a predictor of susceptibility, similar to that reported previously¹⁰. However, SNPs in GSTO1 (rs4925) and GSTO2 (rs156697) correlated with COVID-19 infection. 255 COVID-19 patients and 236 matched healthy individuals were assessed, and the correlation of disease severity and presence of polymorphisms analysed²⁵. Haplotype analysis was used to confirm the findings. The authors say that the presence of these SNPs in GSTO1 or GSTO2 reached a “statistically significant association” with the development of the disease. The presence of GSTO1*AA (as opposed to GSTO1*CC) showed significantly increased COVID-19 development (2.45 fold), whilst presence of the GSTO2*GG SNP (as opposed to GSTO2*AA) led to a 3.7 increase in disease development.

In GSTO1 the rs4925 SNP leads to the amino acid change of A140D, whilst the GSTO2 SNP rs156697 leads to a N142D (or N142Y) change in the amino acid sequence of

that polypeptide. Therefore, if, as stated, these changes can increase the development and disease severity of COVID-19 in humans, are these “new” amino acid sequences present in the GSTO genes of animals and can their presence be used as a predictor of COVID-19 in those animal species?

Analysis of GSTO genes, SNPs and animals

As stated above, the GSTO1 SNP (rs4925) leads to a nucleotide change of C to A, and this translates to an amino change of A140D (Ala to Asp). Here, three GSTO1 isoforms from humans were aligned with homologous sequences from twenty vertebrate species (Table 1).

Table1: GSTO1 sequences used for alignments

Species	Latin name	Sequence used
Human isoform 1	<i>Homo sapiens</i>	NP_004823
Human isoform 3	<i>Homo sapiens</i>	NM_001191003
Human isoform 2	<i>Homo sapiens</i>	NM_001191002
Chimpanzee	<i>Pan troglodytes</i>	NP_001233486
Gorilla (western lowland) isoform X1	<i>Gorilla gorilla gorilla</i>	XP_004050100
Gorilla (western lowland) isoform X2	<i>Gorilla gorilla gorilla</i>	XP_018890528
Rhesus monkey	<i>Macaca mulatta</i>	NP_001247484
Dog	<i>Canis lupus familiaris</i>	XP_535007
Cow (cattle)	<i>Bos taurus</i>	NP_001068682
Mouse (house)	<i>Mus musculus</i>	NP_034492
Rat (Norway)	<i>Rattus norvegicus</i>	NP_001007603
Chicken	<i>Gallus gallus</i>	NP_001264304
Zebrafish	<i>Danio rerio</i>	NP_001002621
Bat (large flying fox)	<i>Pteropus vampyrus</i>	XP_011362082
Bat (Myotis)	<i>Myotis myotis</i>	XP_036191958
Bat (Kuhl's pipistrelle)	<i>Pipistrellus kuhlii</i>	XP_036294846
Ferret (domestic)	<i>Mustela putorius furo</i>	XP_004749360
Mink (American)	<i>Neogale vison</i>	CCP84655
Whale (killer)	<i>Orcinus orca</i>	XP_033276967
Dolphin (common bottlenose) isoform X1	<i>Tursiops truncatus</i>	XP_033697527
Hamster (Chinese) isoform X1	<i>Cricetulus griseus</i>	XP_003515091
Hamster (Chinese) isoform X2	<i>Cricetulus griseus</i>	XP_007653253
Hamster (Chinese) isoform X3	<i>Cricetulus griseus</i>	XP_035294030
Hamster (Chinese) isoform X4	<i>Cricetulus griseus</i>	XP_007653254
Hamster (Chinese) isoform X5	<i>Cricetulus griseus</i>	XP_027262854
Hamster (Chinese) isoform X6	<i>Cricetulus griseus</i>	XP_027262855
Hamster (Chinese) isoform X7	<i>Cricetulus griseus</i>	XP_027262856
Frog (tropical clawed) isoform X1	<i>Xenopus tropicalis</i>	XP_012821965
Crocodile (Australian saltwater)	<i>Crocodylus porosus</i>	XP_019411533
Squirrel (grey)	<i>Neosciurus carolinensis</i>	MBZ3873070

Snake	Not found	
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Some animal species had more than one isoform in the NCBI database, so these were also included. For example, as hamsters are thought to be a species able to cause animal-to-human viral transmission, seven isoforms were analysed here. The human SNP of interest is A140D, and is highlighted as yellow in Figure 1. Although the Ala was conserved in humans and non-human primates there was little conservation of this amino acid across species, many have a Ser in this position. None analysed had the Asp which would have predicted greater disease progression. Therefore, looking for the presence of this amino acid change in GSTO1 appears to have little use in prediction of SARS-Cov-2 infection in vertebrates.

To further investigate the protein, the human isoform 1 sequence of GSTO1 was analysed using Prosite, to find domains and sequences of interest in functionality and possible control of the polypeptide. The reported SNP at residue 140 is well within the C-terminal functional domain of the protein, as shown in purple (Figure 1). Several amino acids are predicted to be phosphorylated, suggesting possible control, along with amidation and *N*-myristoylation sites. However, none of these seem to be impinged upon by the SNP, at least as predicted by this rather limited analysis (no structure was analysed here).

Similar analysis was carried out with GSTO2. The SNP here (rs156697) was at amino acid 142. This led to changes of N142D or N142Y. Interestingly, when all the human GST sequences were aligned the two SNPs are in the same region of the protein (adjacent amino acids), as can be seen in Figure 2 (highlighted in yellow and purple). This region is missing from three of the isoforms, and although there are some conserved amino acids in this section of the protein (shown in blue), the area is not overall heavily conserved.

To analyse the possible use of the GSTO2 SNP (rs156697) in SARS-Cov-2 infections in animals the four human isoform sequences were aligned with those of fifteen animal species (Table2). The SNP is shown in yellow in Figure 3.

Table 2: GSTO2 sequences used for alignments

Species	Latin name	Sequence used
Human isoform 1	<i>Homo sapiens</i>	NP_899062
Human isoform 2	<i>Homo sapiens</i>	NP_001177942
Human isoform 3	<i>Homo sapiens</i>	NP_001177943
Human isoform 4	<i>Homo sapiens</i>	NP_001177944
Gorilla	<i>Gorilla gorilla gorilla</i>	XP_004050103
Rhesus monkey	<i>Macaca mulatta</i>	NP_001276891
Mouse (house)	<i>Mus musculus</i>	NP_084327
Rat (Norway)	<i>Rattus norvegicus</i>	AAH79295
Whale (killer)	<i>Orcinus orca</i>	XP_033276969
Ferret (domestic)	<i>Mustela putorius furo</i>	AER99471
Dolphin (common bottlenose)	<i>Tursiops truncatus</i>	XP_019795507
Hamster (golden) isoform X1	<i>Mesocricetus auratus</i>	XP_040599162
Hamster (golden) isoform X2	<i>Mesocricetus auratus</i>	XP_040599171
Hamster (golden) isoform X3	<i>Mesocricetus auratus</i>	XP_040599174
Frog (tropical clawed)	<i>Xenopus tropicalis</i>	NP_001005086
Cow (cattle)	<i>Bos taurus</i>	NP_001193084
Dog isoform X1	<i>Canis lupus familiaris</i>	XP_038296425
Dog isoform X2	<i>Canis lupus familiaris</i>	XP_038296426
Cat (domestic) isoform X1	<i>Felis catus</i>	XP_023096662
Cat (domestic) isoform X2	<i>Felis catus</i>	XP_044896585
Cat (domestic) isoform X3	<i>Felis catus</i>	XP_044896586
Bat (greater spear-nosed)	<i>Phyllostomus hastatus</i>	XP_045710275
Bat (common vampire)	<i>Desmodus rotundus</i>	XP_045047595
Bat (big brown)	<i>Eptesicus fuscus</i>	XP_008142501
Reptile	Not found	
Mink	Not found	

As mentioned above, not all the human isoforms of GSTO2 have the regions in which the SNP falls, but it does occur in isoforms 1 & 3. The SNP manifests as changes from N to D or Y. Interestingly, although Y at residue 142 is not represented at all in the vertebrate analysis here, many animals have a D at this position. Interestingly, gorilla and Rhesus monkey have identical sequences around the SNP but have the N142D alteration. As this increases COVID-19 development and disease severity in humans²⁵ it is tempting to suggest this would have the same effect in these primate species and that non-human primates are more susceptible to the SARS-CoV-2 virus. The D at position 142 is also found in cats, dogs, and ferrets, all of which are known to contract the virus. It is also represented in two of the hamster sequences (X1 & X2, but not X3), again, a species known to become infected. It is also found in rats and mice, suggesting that rodents may be more susceptible, although the region of the protein is not completely conserved. The susceptibility of mice to the SARS-CoV-2 virus appears to be strain specific³². Interestingly, two of the bat species analysed

retained the N at position 142, but one also had the D substitution (big brown bat). Does this suggest that some bat species are more susceptible than others? Also of note, perhaps, is that marine mammals have the D at position 142, and it is suggested here that these species ought to be monitored more closely in the future. The frog sequence appears to be quite different in this region, and amphibians are known, at least to date, to be free from SARS-CoV-2 infections.

Again, using the human isoform 1 as a model, the GSTO2 protein was analysed by Prosite. As with GSTO1, the SNP in GSTO2 was not in a region which appears to conflict with predicted phosphorylation and other modification sites (Figure 3). However, further analysis of the gene sequence of GSTO2 may be of use in the prediction of whether vertebrates are susceptible to the SARS-CoV-2 virus.

Discussion and Conclusions

The factors which lead to severe COVID-19 in humans has been looked at by the analysis of of genomes. 7,491 critically ill patients were compared to 48,400 controls, and sixteen independent factors which can lead to severe outcome were identified. Many of these were involved in the immune response, for example in interferon signalling, but GST was not listed³³. However, GST-omega SNPs were highlighted by the work of Djukic *et al.*²⁵ and these are the focus here.

One of the manifestations of a SARS-CoV-2 infection is the onset of a cytokine storm, where there is hyperactivation of immune cells and elevated levels of circulating cytokines³⁴. There is also a rise in the accumulation of ROS and accompanied oxidative stress, and it has been suggested that there is a vicious circle of the rise of ROS and cytokines, which will lead to Acute Respiratory Distress Syndrome (ARDS) and potentially death³⁵. GSTO has a role in dampening the oxidative stress response, which can have profound effects on disease³⁶. Oxidative stress during COVID-19 can lead to the oxidation of

cellular components, such as lipids, which can be part of the disease mechanism³⁷. GST homologues, including GSTO, are known to be involved in reducing oxidative stress and to catalyse the reduction of oxidative factors in a variety of animal species^{38,39}. Because of their structures, and having a Cys in the active site, GSTOs catalyse reactions which cannot be carried out by other GST enzymes, and GSTOs are often involved in thiol transferase and reduction reactions⁴⁰. Therefore, they are instrumental in redox signaling and ROS metabolism. GSTOs are also involved in mediating aspects of apoptosis and autophagy⁴¹. Downstream effects of GSTO1-1 in macrophages, for example, were mediated by *c-Jun* N-terminal kinases (JNK), which were upstream of the cytochrome *c*/caspase pathway. Therefore, GSTOs will have an important role in the onset and maintenance of COVID-19, as well as other diseases which have a redox element to their manifestation.

Predicting the susceptibility of animals to the SARS-CoV-2 virus is turning out to be very hard to do, and little sequence analysis seems to be helpful. Despite sequence alignments across a wide range of vertebrates, using the sequence of ACE2^{9,10,22}, there was little correlation with predictions and the reality of the animals reported to be SARS-CoV-2 positive. This was more recently confirmed by Djukic *et al.*²⁵. Therefore, other proteins were also investigated by sequence alignment, including TMPRSS2, neuropilin-1 and furin¹⁰. Again, little prediction could be made, with some of the sequences being well conserved across vertebrate species. Therefore, here, the report that GST-omega gene sequences can predict COVID-19 severity in humans²⁵ seemed like an observation worth investigating across vertebrate species. Although little could be predicted from the GSTO1 sequences, the GSTO2 genes may give an indication of viral susceptibility in animals.

There are some species which are not represented in the study here. For example, no snake sequence could be found for GSTO1, and neither mink nor reptiles were found for GSTO2. There are obviously thousands of species not analysed here: estimates suggest around 65000 vertebrate species exist. Furthermore, there will be SNPs in the animal species which are not looked at either. Therefore, the lack of finding a predictive use here,

for example with the GSTO1 sequences, does not rule out that some animal GST sequences cause an animal species, or an individual animal, to be more SARS-CoV-2 susceptible. The same will be true for all the other proteins analysed in this way, including ACE2, TMPRSS2, neuropilin-1 and furin^{9,10,22}. Of course, in the analysis shown here there was no structural analysis of the polypeptides which would potentially highlight the significance of amino acid changes. However, although structural analysis would be better here, it is both more complex and long-winded. On the other hand, such a quick prediction by sequence analysis would be useful to guide structural work, especially considering how many vertebrate species there are. Here it is suggested that further analysis of the GSTO2 sequences would be worthwhile. There are many factors which dictate the viral entry into the cells and the production of new viruses which can be subsequently released. A simple analysis of some of the proteins involved, especially GST-omega-2 isoforms, at the present time seems like a useful pursuit.

There are now at least three animal species which are thought to be able to transmit the virus back to humans. These are mink¹⁸, hamsters²⁰ and deer²¹. There is a need therefore to have a way to predict which animals are likely to be susceptible. There are many circumstances in which humans and animals are in close contact, including companion animals, zoos and at conservation sites. There are also many vertebrate species which may be at risk but have had little investigation. These include the marine mammals, which have been predicted to be susceptible⁴², and may be exposed through human waste^{43,44} which is a potential source of infection. Here, the data from the GSTO2 genes may be useful to inform future monitoring and research.

Although the virus probably originated in a bat⁴⁵, and then possibly infected humans through an intermediate host, this has been disputed⁸. Bat species are not the only ones which need to be considered as able to transmit the virus to humans. SARS-CoV-2 is the latest in a series of coronavirus outbreaks, which includes SARS and MERS⁴⁶. Therefore, the COVID-19 pandemic is unlikely to be the last. Any work which can be used to predict, or

be ruled out as a method for prediction, which animals (including humans) are likely to be affected by coronaviruses in the future should aid in epidemic/pandemic control. Therefore, there needs to be far more of a focus on the impact of the SARS-CoV-2 virus in animal populations, both in monitoring what is happening in the real world and how to predict what happens, or may happen, during this and future pandemics. As already suggested by others⁴⁷, a One Medicine approach needs to be taken where the impact of epidemics/pandemics on human and animal populations are considered holistically. Certainly, it is likely that new coronaviruses will emerge and work is being undertaken to predict in which animal hosts this might take place⁴⁸. With more genomic analysis and more awareness of the interactions of animals with other species, and with humans, on the spread of viruses, such as SARS-CoV-2, amongst humans and animals, we will be better prepared for future challenges.

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References

- 1- WHO Coronavirus (COVID-19) Dashboard: <https://covid19.who.int/> (accessed 23/02/22)
- 2- Tizaoui, K., Zidi, I., Lee, K.H., Ghayda, R.A., Hong, S.H., Li, H., et al. Update of the current knowledge on genetics, evolution, immunopathogenesis, and transmission for coronavirus disease 19 (COVID-19). *Int. J. Biol. Sci.*, **16**, 2906–2923 (2020)
- 3- Huang, Y., Yang, C., Xu, X., Xu, W., Liu, S.W. Structural and functional properties of SARS-CoV-2 spike protein: Potential antiviral drug development for COVID-19. *Acta Pharmacol. Sin.*, **41**, 1141–1149 (2020)

- 4- Hoffman, M., Kleine-Weber, H., Schroeder, S., Krüger, N., Herrler, T., Erichsen, S., et al. SARS-CoV-2 Cell entry Depends on ACE2 and TMPRSS2 and is blocked by a clinically proven protease inhibitor. *Cell*, **181**, 271–280 (2020)
- 5- Daly, J.L., Simonetti, B., Klein, K., Chen, K.-E., Williamson, M.K., Antón-Plágaro, C., et al. Neuropilin-1 is a host factor for SARS-CoV-2 infection. *Science* **370**, 861-865 (2020)
- 6- Wang, J., Jiang, M., Chen, X., Montaner, L.J. Cytokine storm and leukocyte changes in mild versus severe SARS-CoV-2 infection: Review of 3939 COVID-19 patients in China and emerging pathogenesis and therapy concepts. *J. Leukoc. Biol.* **108**, 17-41 (2020)
- 7- Zhou, P., Yang, X.-L., Wang, X.-G., Hu, B., Zhang, L., Zhang, W., et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*, **579**, 270–273 (2020)
- 8- Chan, A. Ridley, M. *Viral: The Search for the Origin of Covid-19*. Fourth Estate (2021)
ISBN: 978-0008487492
- 9- Damas, J., Hughes, G.M., Keough, K.C., Painter, C.A., Persky, N.S., Corbo, M., et al. Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. *Proc. Nat. Acad. Sci. USA*, **117**, 22311–22322 (2020)
- 10- Hancock, J.T., Rouse, R.C., Stone, E. and Greenhough, A. Interacting proteins, polymorphisms and the susceptibility of animals to SARS-CoV-2. *Animals*, **11**, 797 (2021)
- 11- Coronavirus: Four lions test positive for Covid-19 at Barcelona Zoo:
<https://www.bbc.co.uk/news/world-europe-55229433> (accessed 23/02/22)
- 12- Mathavarajah, S. Dellaire, G. Lions, tigers and kittens too: ACE2 and susceptibility to COVID-19. *Evol. Med. Public Health* **2020**, 109–113 (2020)
- 13- Shi, J., Wen, Z., Zhong, G., Yang, H., Wang, C., Huang, B., et al. Susceptibility of ferrets, cats, dogs, and other domesticated animals to SARS–coronavirus 2. *Science*, **368**, 1016–1020 (2020)

- 14- Lion at Honolulu Zoo dies after contracting COVID in case prompting broader concern:
<https://www.hawaiinewsnow.com/2021/10/16/lion-honolulu-zoo-dies-after-contracting-covid-case-prompting-broader-concern-facility/> (Accessed 23/02/22)
- 15- Second lion dies of Covid at Indian zoo:
<https://www.independent.co.uk/news/science/covid-india-lion-death-zoo-b1867681.html> (Accessed 23/02/22)
- 16- Gaudreault, N.N., Trujillo, J.D., Carossino, M., Meekins, D.A., Morozov, I., Madden, D.W., et al. SARS-CoV-2 infection, disease and transmission in domestic cats. *Emerg. Microbes Infect.*, **9**, 2322–2332 (2020)
- 17- Oude Munnink, B.B., Sikkema, R.S., Nieuwenhuijse, D.F., Molenaar, R.J., Munger, E., Molenkamp, R., et al. Jumping back and forth: Anthroozoonotic and zoonotic transmission of SARS-CoV-2 on mink farms. *bioRxiv* 2020.
- 18- Oude Munnink, B.B., Sikkema, R.S., Nieuwenhuijse, D.F., Molenaar, R.J., Munger, E., Molenkamp, R., et al. Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans. *Science*, **371**, 172-177 (2020)
- 19- Dyer, O. Covid-19: Denmark to kill 17 million minks over mutation that could undermine vaccine effort. *BMJ*, **371**, m4338 (2020)
- 20- Hong Kong seizes hamsters from pet store for mass cull:
<https://www.bbc.co.uk/news/world-asia-china-60038551> (Accessed 23/02/22)
- 21- Pickering, B., Lung, O., Maguire, F., Kruczkiewicz, P., Kotwa, J.D., Buchanan, T., et al. Highly divergent white-tailed deer SARS-CoV-2 with potential deer-to-human transmission *bioRxiv* **2022.02.22.481551** (2022)
- 22- Kumar, A., Pandey, S.N., Pareek, V., Narayan, R.K., Faig, M.A., Kumari, C. Predicting susceptibility for SARS-CoV-2 infection in domestic and wildlife animals using ACE2 protein sequence homology. *Zoo Biol.* **40**, 79-85 (2020)
- 23- Senapati, S., Banerjee, P., Bhagavatula, S., Kushwaha, P.P., Kumar, S. Contributions of human ACE2 and TMPRSS2 in determining host–pathogen interaction of COVID-19. *Journal of Genetics*, **100**, 1-16 (2021)

24- Captive gorillas test positive for coronavirus:

<https://www.sciencemag.org/news/2021/01/captive-gorillas-test-positive-coronavirus>
(accessed on 01/03/22).

25- Djukic, T.; Stevanovic, G., Coric, V., Bukumiric, Z., Pljesa-Ercegovac, M., Matic, M., et al. GSTO1, GSTO2 and ACE2 polymorphisms modify susceptibility to developing COVID-19. *J. Pers. Med.*, **12**, 458 (2022)

26- Sievers, F., Wilm, A., Dineen, D., Gibson, T.J., Karplus, K., Li, W., et al. Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Mol. Syst. Biol.*, **7**, 539 (2011)

27- Sigrist, C.J.A., Cerutti, L., Hulo, N., Gattiker, A., Falquet, L., Pagni, M., et al. PROSITE: a documented database using patterns and profiles as motif descriptors. *Brief Bioinform.*, **3**, 265-274 (2002)

28- Vaish, S., Gupta, D., Mehrotra, R., Mehrotra, S., Basantani, M.K. Glutathione S-transferase: a versatile protein family. *3 Biotech.*, **10**, 321 (2020)

29- Singh, R.R., Reindl, K. M. Glutathione S-Transferases in cancer. *Antioxidants (Basel, Switzerland)*, **10**, 701 (2021)

30- Majidi, N., Rabbani, F., Gholami, S., Gholamalizadeh, M., BourBour, F., Rastgoo, S., et al. The effect of Vitamin C on pathological parameters and survival duration of critically ill coronavirus disease 2019 patients: A randomized clinical trial. *Front. Immunol.*, **12**, 717816 (2021)

31- Abbas, M., Verma, S., Verma, S., Siddiqui, S., Khan, F.H., Raza, S.T., et al. Association of GSTM1 and GSTT1 gene polymorphisms with COVID-19 susceptibility and its outcome. *Journal of Medical Virology*, **93**, 5446-5451 (2021)

32- Why mice are man's best friend in the fight against COVID-19, at:

<https://sciencenordic.com/animal-testing-epidemic-health/why-mice-are-mans-best-friend-in-the-fight-against-covid-19/1667209> (Accessed 24/03/22)

- 33- Kousathanas, A., Pairo-Castineira, E., Rawlik, K., Stuckey, A., Odhams, C.A., Walker, S., et al. Whole genome sequencing reveals host factors underlying critical Covid-19. *Nature*, 1-10 (2022)
- 34 - Fajgenbaum, D.C., June, C.H. Cytokine storm. *New England Journal of Medicine*, **383**, 2255-2273 (2020)
- 35 - Meftahi, G.H., Bahari, Z., Jangravi, Z., Iman, M. A vicious circle between oxidative stress and cytokine storm in acute respiratory distress syndrome pathogenesis at COVID-19 infection. *Ukrainian Biochemical Journal*, **93**, 18-29 (2021)
- 36 - Bilgin, E., Can Demirdöğen, B., Türkanoğlu Özçelik, A., Demirkaya, Ş., Adalı, O. Association analysis of Glutathione S-transferase omega-1 and omega-2 genetic polymorphisms and ischemic stroke risk in a Turkish population. *Neurol. Res.* **41**, 118-124 (2019)
- 37 - Sorokin, A.V., Karathanasis, S.K., Yang, Z.H., Freeman, L., Kotani, K., Remaley, A.T. COVID-19-associated dyslipidemia: Implications for mechanism of impaired resolution and novel therapeutic approaches. *FASEB J.* **34**, 9843-9853 (2020)
- 38 - Meng, F., Zhang, Y., Liu, F., Guo, X., and Xu, B. Characterization and mutational analysis of omega-class GST (GSTO1) from *Apis cerana cerana*, a gene involved in response to oxidative stress. *PLoS One*, **9**, e93100 (2014)
- 39 - Balakrishnan, B., Su, S., Wang, K., Tian, R., Chen, M. Identification, expression, and regulation of an Omega Class glutathione S-transferase in *Rhopalosiphum padi* (L.) (Hemiptera: Aphididae) under insecticide stress. *Front Physiol.*, **9**, 427 (2018)
- 40 - Board, P.G. The omega-class glutathione transferases: structure, function, and genetics. *Drug Metabolism Reviews*, **43**, 226-235 (2011)
- 41 - Paul, S., Jakhar, R., Bhardwaj, M., Kang, S.C. Glutathione-S-transferase omega 1 (GSTO1-1) acts as mediator of signaling pathways involved in aflatoxin B1-induced apoptosis–autophagy crosstalk in macrophages. *Free Radical Biology and Medicine*, **89**, 1218-1230 (2015)

- 42- Nabi, G. Risk of COVID-19 pneumonia in aquatic mammals. *Environ. Res.*, **188**, 109732 (2020)
- 43- Quilliam, R.S., Weidmann, M., Moresco, V., Purshouse, H., O'Hara, Z., Oliver, D.M. COVID-19: The environmental implications of shedding SARS-CoV-2 in human faeces. *Environ. Int.*, **140**, 105790 (2020)
- 44- Maal-Bared, R., Sobsey, M., Bibby, K., Sherchan, S.P., Fitzmorris, K.B., Munakata, N., et al. Pandemic danger to the deep: The risk of marine mammals contracting SARS-CoV-2 from wastewater. *Sci. Total Environ.*, **2020**, 144855 (2020)
- 45- Nova, N. Cross-species transmission of coronaviruses in humans and domestic mammals, what are the ecological mechanisms driving transmission, spillover, and disease emergence? *Frontiers in Public Health*, **9** (2021)
- 46- Hu, T., Liu, Y., Zhao, M., Zhuang, Q., Xu, L., He, Q. A comparison of COVID-19, SARS and MERS. *PeerJ*, **8**, e9725 (2020)
- 47- Stout, A.E., André, N.M., Jaimes, J.A., Licitra, B.N., Whittaker, G.R. One Medicine: a comparative approach to investigating human and animal coronavirus infections. *Journal of Feline Medicine and Surgery*, **23**, 267-268 (2021)
- 48- Wardeh, M., Baylis, M., Blagrove, M.S. Predicting mammalian hosts in which novel coronaviruses can be generated. *Nature Communications*, **12**, 1-12 (2021)

Figure 1: Clustal Omega alignments GSTO1 across animal species. Sequence details are in Table 1. "*" indicates sequence identity (":" indicates a conserved change, whilst "." Indicates less of a conserved change). Position of SNP indicated in yellow. The predicted (using Prosite and human isoform 1 sequence) N-terminal GST domain is highlighted in green, whilst the N-terminal domain is highlighted in purple. Predicted interesting sites in human isoform 1 are marked (from Prosite: protein kinase C target: grey; tyrosine phosphorylation: brown; amidation site: bright blue; Casein kinase II phosphorylation site: red; cAMP-dependent kinase: light blue: myristoylation;dark green)

CLUSTAL O(1.2.4) multiple sequence alignment

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Frog-(tropical-clawed) -----
MAGPTKSLAKGSPAPGVPDGVIRAYI 27
Zebrafish -----
MAASQKCLGKGSPPAPGVPKDHIRLYS 27
Hamster-isoform-X1 -----
MSGASSRSLGKGSPPGVPPEGLIRVYS 28
Hamster-isoform-X7 -----
MSGTSSRSLGKGSPPGVPPEGLIRVYS 28
Hamster-isoform-X5 -----
MSGASSRSLGKGSPPGVPPEGLIRIYS 28
Hamster-isoform-X2 -----
MSGASSRSLGKGSPPGVPPEGLIRVYS 28
Hamster-isoform-X3 -----
MSGASSRSLGKGSPPGVPPEGLIRIYS 28
Hamster-isoform-X4 -----
MSGASSRSLGKGSPPGVPPEGLIRVYS 28
Hamster-isoform-X6 -----
MSGASSRSLGKGSPPGVPPEGLIRIYS 28
Whale-(killer) -----
MSGGSARSLGKGEACLPRFAATLRRVSGPGGGWAAPERSHAGGSAPPQVPEGLIRVYS 60
Dolphin-(common-bottlenose) -----
MSGGSARSLGKGEACLPRFAATLRRVSRPGGGWAAPERSHAGGSAPPQVPEGLIRVYS 60
Cow-(cattle) -----
SARSLGKGSAPPGPVPEGLIRVYS 28
Bat-(Myotis-myotis) -----
SDKSLEKGSAPPGPVPEGLIRVYS 28
Bat-(Kuhl's-pipistrelle) -----
SAKSLDKGSAPPGPVQGLIRVYS 28
Squirrel -----
SARSLAKGSAPPGPVPEGLIRVYS 28
Bat-(large-flying-fox) -----
SARSLGKGSAPPGPVPEGLIRLYS 28
Rhesus-monkey -----
SARSLGKGSAPPGPVPEGSIRVYS 28
Human-GSTO1-isoform-2 -----
SARSLGKGSAPPGPVPEGSIRIYS 28
Chimpanzee -----
SARSLGKGSAPPGPVPEGSIRVYS 28
Human-GSTO1-isoform-1 -----
SARSLGKGSAPPGPVPEGSIRIYS 28
Human-GSTO1-isoform-3 -----
----- 0 -----
Gorilla-isoform-X1 -----
SARSLGKGSAPPGPVPEGSIRVYS 28
Gorilla-isoform-X2 -----
----- 0 -----
Dog -----
SARSLAKGSAPPGPVPEGLIRVYS 28
Ferret-(domestic) -----
SDRSLAKGSAPPGPVPEGLIRVYS 27
Mink-(American) -----
SARSLAKGSAPPGPVPEGLIRVYS 27
Mouse -----
MSGESSRSLGKGSAPPGPVPEGQIRVYS 28

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Rat	-----	
MSGASARS ¹ SLGKGSAPP ² GPVPEGQIRVYS		28
Chicken	-----	
MAGDHSRSLGKGSAA ³ GPVPEGVIRLYS		28
Crocodile	-----	
MAGAMSRSRGKGSAA ⁴ GPVPEGLIRLYS		28
Frog- (tropical-clawed)		
MRFCPFAQRAHLILVAKGIKHEL ⁵ VYINTLNKPDWFF ⁶ EKSPFGQVPAIETSKGQLIYESQI		87
Zebrafish		
MRFCPFAQRT ⁷ RLV ⁸ LN ⁹ AKGIKYDTININLNK ¹⁰ PDW ¹¹ FLEKNPLGLVPVLETQSGQVIYESPI		87
Hamster-isoform-X1		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ¹² PEWFLKKNPTGLVPVLEDSKGR ¹³ LISESVI		88
Hamster-isoform-X7		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ¹⁴ PEWFLKKNPTGLVPVLEDSKGR ¹⁵ LISESVI		88
Hamster-isoform-X5		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ¹⁶ PEWFLKKNPTGLVPVLEDSKGR ¹⁷ LISESVI		88
Hamster-isoform-X2		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ¹⁸ PEWFLKKNPTGLVPVLEDSKGR ¹⁹ LISESVI		88
Hamster-isoform-X3		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ²⁰ PEWFLKKNPTGLVPVLEDSKGR ²¹ LISESVI		88
Hamster-isoform-X4		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ²² PEWFLKKNPTGLVPVLEDSKGR ²³ LISESVI		88
Hamster-isoform-X6		
MRFCPFAQRALMVLKAKGIRHEIVNINLNK ²⁴ PEWFLKKNPTGLVPVLEDSKGR ²⁵ LISESVI		88
Whale- (killer)		
MRFCPFAKRTLLVLKAKGIGHEVININLNK ²⁶ PEWFFKKNPFGLVPVLENSQGQVIYESAI		120
Dolphin- (common-bottlenose)		
MRFCPFAKRTLLVLKAKGIGHEVININLNK ²⁷ PEWFFKKNPFGLVPVLENSQGQVIYESAI		120
Cow- (cattle)		
MRFCPYAQR ²⁸ TRLVLTAKGIRHEVININLNK ²⁹ PEWFFKKNPSGLVPVLETSQGQLICESAI		88
Bat- (Myotis-myotis)		
MRFCPFAQR ³⁰ TRLV ³¹ LKAKGIRHEVVNINLNK ³² PEWFFKKNPAGLVPVLENSQGH ³³ LICESAI		88
Bat- (Kuhl's-pipistrelle)		
MRFCPFAQR ³⁴ TLLVLKAKGIRHEVININLNK ³⁵ PEWFFKKNPAGLVPVLENTQGQLICESAI		88
Squirrel		
MRFCPFAQR ³⁶ TLLVLKAKGIEHEVININLNK ³⁷ PEWFFKKNPLGLVPVLENSKGQLIYESTI		88
Bat- (large-flying-fox)		
MRFCPFAQR ³⁸ TRLV ³⁹ LKAKGIRHEIININLNK ⁴⁰ PEWFFKKNPFGLVPVLENSKGQLVCD ⁴¹ SAI		88
Rhesus-monkey		
MRFCPFAERTLLVLKAKGIRHEVININLNK ⁴² PEWFFKKNPFGLVPVLENSQGQLIYESPI		88
Human-GST01-isoform-2		
MRFCPFAERTRLVLKAKGIRHEVININLNK ⁴³ PEWFFKKNPFGLVPVLENSQGQLIYESAI		88
Chimpanzee		
MRFCPFAERTRLVLKAKGIRHEVININLNK ⁴⁴ PEWFFKKNPFGLVPVLENSQGQLIYESAI		88
Human-GST01-isoform-1		
MRFCPFAERTRLVLKAKGIRHEVININLNK ⁴⁵ PEWFFKKNPFGLVPVLENSQGQLIYESAI		88
Human-GST01-isoform-3		
MRFCPFAERTRLVLKAKGIRHEVININLNK ⁴⁶ PEWFFKKNPFGLVPVLENSQGQLIYESAI		60
Gorilla-isoform-X1		
MRFCPFAERTRLVLKAKGIRHEVININLNK ⁴⁷ PEWFFKKNPFGLVPVLENSQGQLIYESAI		88
Gorilla-isoform-X2		
MRFCPFAERTRLVLKAKGIRHEVININLNK ⁴⁸ PEWFFKKNPFGLVPVLENSQGQLIYESAI		60
Dog		
MRFCPFAQR ⁴⁹ TLLVLKAKGIRHEIININLNK ⁵⁰ PEWFFKKNPFGLVPVLENSQGQLIYESPI		88
Ferret- (domestic)		
MRFCPYAQR ⁵¹ TLLVLKAKGIRHEIININLNK ⁵² SKPEWFFKKNPFGLVPVLENSQGQLIYESAI		87
Mink- (American)		
MRFCPYAQR ⁵³ TLLVLTAKGIRHEIININLNK ⁵⁴ SKPEWFFKKNPFGLVPVLENSQGQLIYESAI		87
Mouse		
MRFCPFAQR ⁵⁵ TLMVLKAKGIRHEVININLNK ⁵⁶ PEWFFEKNPLGLVPVLENSQGH ⁵⁷ LVTESVI		88
Rat		
MRFCPFAQR ⁵⁸ TLMVLKAKGIRHEIININLNK ⁵⁹ PEWFFEKNPFGLVPVLENTQGH ⁶⁰ LITESVI		88
Chicken		
MRFCPFAQR ⁶¹ TRLVLRKAKGIRHEVVNINLNK ⁶² PDWIFEKNPDGLVPVLET ⁶³ SKGQLIYESPI		88
Crocodile		
MRFCPFAERTRLVLKAKGINHEIININLNK ⁶⁴ PDWFFEKNPFGLVPVLET ⁶⁵ SKGQLIYESPI		88

*****.*.*: :.* ***** :. : ** .**:*:*:*.* * * *.*

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Frog- (tropical-clawed)
VCDYLDEVF**G**GKKLTPQDPFQKAQQKMLLEHFSKASTVAFKIVGAKKNNEDI**S**ALKAEFL 147
Zebrafish
TCEYLDEVY**E**EKKLLPFPDFERAQQRMLELFSKVTPYFYKIPVNRTKGEDV**S**ALETELK 147
Hamster-isoform-X1 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFIRG-
NKEDR**S**ALKEELR 146 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFIRG-
Hamster-isoform-X7 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFIRG-
NKEDR**S**ALKEELR 146 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFIRG-
Hamster-isoform-X5 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
KKEDH**P**ALKEELT 146 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
Hamster-isoform-X2 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
KKEDH**P**ALKEELT 146 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
Hamster-isoform-X3 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
KKEDH**P**ALKEELT 146 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
Hamster-isoform-X4 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
KKEDH**P**ALKEELT 146 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
Hamster-isoform-X6 ICEYLDEAY**D**DKKLPDDP**V**EKARQKMTLESFSKVPPLVT-RFVRG-
KKEDH**P**ALKEELT 146
Whale- (killer) TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMFELFSKVPPLLL-
SFLRRQNKEDC**S**GLKEELH 179 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMFELFSKVPPLLL-
Dolphin- (common-bottlenose) SFLRRQNKEDC**S**GLKEELH 179
Cow- (cattle) TCEYLDEAY**G**GKKLLPGDP**V**EKACQKMLEFSKVPPLIL-
KILRTQNKEDC**S**GLKEELH 147 TCEYLDEAY**E**EKKLLPADP**V**EKACQKMFELFSKVPPLVG-
Bat- (Myotis-myotis) RFTRSKNKEDC**S**DLKEEFR 147 TCEYLDEAY**E**EKRLLPADP**V**EKACQKMFELFSKVPPLVG-
Bat- (Kuhl's-pipistrelle) RFTRSKTKEDR**S**GLKEEFR 147 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI FELFSKVPPLLA-
Squirrel NFIRGQNKNDW**P**GLKEELK 147 TCEYLDEAY**G**GKKLLPEDP**V**EKACQKMSFELFSKVPPLGG-
Bat- (large-flying-fox) SYIRNKNKEDC**S**GIKEELR 147 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
Rhesus-monkey SFIRSNKEDY**A**GLKEEFR 147 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
Human-GST01-isoform-2 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI LELFSK-----
----- 122
Chimpanzee TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
SFIRSNKEDY**A**GLKEEFR 147 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
Human-GST01-isoform-1 **SFIRSNKEDYAGLKEEFR** 147
Human-GST01-isoform-3 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
SFIRSNKEDY**A**GLKEEFR 119 TCEYLDEAY**T**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
Gorilla-isoform-X1 SFIRSNKEDY**A**GLKEEFR 147 TCEYLDEAY**T**GKKLLPDDP**V**EKACQKMI LELFSKVPPLVG-
Gorilla-isoform-X2 SFIRSNKEDY**A**GLKEEFR 119 TCEYLDEAY**G**GKKLLPDDP**V**EKACQKMFELFSKVPPLVT-
Dog GFLRRQNKEDC**S**GLKEELR 147 TCEYLDDVY**G**GKKLLPDDP**V**EKARQKMFELFSKVPPLVI-
Ferret- (domestic) SLLRKQNEEDC**S**GQKEELR 146 TCEYLDDVY**G**GKKLLPDDP**V**EKARQKMFELFSKVPPLVT-
Mink- (American) SLLRKQNEEDC**S**GQKEELR 146 TCEYLDEAY**E**EKKLPDDP**V**EKARQKMTLESFSKVPPLIA-
Mouse SFVRSKRKED**S**PNLREALE 147 TCEYLDEAY**E**EKKLPDDP**V**EKACQKMTFELFSKVPPLVT-
Rat SFIRAKRKEDH**P**GIKEELK 147 TCEYLDEAF**G**GRKLMPSDP**V**ERALQKMLLEHFSKITSVISK---
Chicken ALKEGGD**L**TALTAELA 145
Crocodile TCDYLDEAY**G**GKKLLPEDP**V**ERAYQKMLLEHFSKLTPLAYKHFMAIQNGED**S**TALKAEFS 148
..*:.* :.* * *.*:* *.* :.* *

Frog- (tropical-clawed)
EKLVDQVQVAKL**N**TPYVGGSS**V**SMADYMILPIFERFDIFGVKDCLE**K**T**P**HLLQWYQLML 207

Zebrafish
DKL S QFNEILLKKK S KFFGGDS I T MIDYMMWPFERLETMNLKHCLDGT PELKKWTERMM 207
Hamster-isoform-X1
KEYFKLEEAL TDCQ S EFRIGDAV S MTDYLMWPFQRL EALELNECVAHT PPKLKGWMAAMQ 206
Hamster-isoform-X7
KEYFKLEEAL TDCQ S EFRIGDAV S MTDYLMWPFQRL EALELNECVAHT PPKLKGWMAAMQ 206
Hamster-isoform-X5
KEYFKLEEAV TTKYKKDFRVGDAV S MTDYLMWPFQWLEALELKECVAHT PPKLKGWMAAMQ 206
Hamster-isoform-X2
KEYFKLEEAM TTKYKKDFRVGDAV S MTDYLMWPFQWLEALELKECVAHT PPKLKGWMAAMQ 206
Hamster-isoform-X3
KEYFKLEEAM TTKYKKDFRVGDAV S MTDYLMWPFQWLEALELKECVAHT PPKLKGWMAAMQ 206
Hamster-isoform-X4
KEYFKLEEAM TTKYKKDFRVGDAV S MTDYLMWPFQWLEALELKECVAHT PPKLKGWMAAMQ 206
Hamster-isoform-X6
KEYFKLEEAV TTKYKKDFRVGDAV S MTDYLMWPFQWLEALELKECL SIRSSTT----- 199
Whale- (killer)
KEF S KLEEVLTNKK T TFFGGSS L S MIDYLIWPFWEVLVALELNEYVNHT PNLKLWMEAMM 239
Dolphin- (common-bottlenose)
KEF S KLEEVLTNKK T TFFGGSS L S MIDYLIWPFWEVLVALELNEYVNHT PNLKLWMEAMM 239
Cow- (cattle)
KEI S KLEEVLTDKK T TFFGGNS L S MIDYLIWPFERLEALELNECVDHAPT LKLWMAAMK 207
Bat- (Myotis-myotis)
QEF S KLEEVLTNKK T TFFGGNS L S MIDYLIWPFERLEALELNECIDHT PPKLKLWMAAMR 207
Bat- (Kuhl's-pipistrelle)
QEF S KLEEVLTNKK T TFFGGNS I S MIDYLIWPFERLEALELNECIDHT PPKLKLWVAAMR 207
Squirrel
KEF S KLEEVLTNKK T TFFGGNS L S MIDYLIWPFERLEALELNECVAHT PPKLKLWIAAMK 207
Bat- (large-flying-fox)
KEF S KLEEVLTNKK T TFFGGNS L S MIDYLIWPFERLEALELSECVDHT PPKLKLWMAAMR 207
Rhesus-monkey
KEF S KLEEVLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLYECVDHT PPKLKLWMAAMK 207
Human-GST01-isoform-2
VLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLNCEVDHT PPKLKLWMAAMK 174
Chimpanzee
KEF S KLEEVLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLNCEVDHT PPKLKLWMAAMK 207
Human-GST01-isoform-1
KEF S KLEEVLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLNCEVDHT PPKLKLWMAAMK 207
Human-GST01-isoform-3
KEF S KLEEVLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLNCEVDHT PPKLKLWMAAMK 179
Gorilla-isoform-X1
KEF S KLEEVLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLNCEVDHT PPKLKLWMAAMK 207
Gorilla-isoform-X2
KEF S KLEEVLTNKK T TFFG NSI S MIDYLIWPFERLEAMKLNCEVDHT PPKLKLWMAAMK 179
Dog
KEF S KLEEVLTNKK T TFFGGNS L S MIDYLIWPFERLEALELNDCEVDHT PPKLKLWMAAMR 207
Ferret- (domestic)
KEI S KLEEVLTNKK T TFFGGNS L S MIDYLIWPFERMEILELNDCEVDHT PPKLKLWMAAMR 206
Mink- (American)
KEI S KLEEVLTNKK T TFFGGNS L S MIDYLIWPFERMEILELNDCEVDHT PPKLQWMAAMR 206
Mouse
KSFLLGGDS P S MVDYLTWPFQRL EALELKECLAHT PPKLKLWMAAMQ 206
Rat
KEF S KLEEAMAKKR T AFFGGNS L S MIDYLIWPFQRL EALELNECIDHT PPKLKLWMATMQ 207
Chicken
EKFGKLDEIL SQRN T VFFGGDS T S LIDYMMWPFERLEAFQLKDVLR T PPKLQRWMEAMR 205
Crocodile
EKLGKFEEILANRQ S VFFGGDS V S MFDYLIWPFERLEAFQLYDCLGHT PPKLKCWMDAMK 208
: . . : * . : : * : * * : : : . . :

Frog- (tropical-clawed) QDPAVKATHIKPEALEGGFFKLYLQGNPESVDYDI 241
Zebrafish EDPTVKATMF S TETYMVFYKSYMEGNP-NYDYGL 240
Hamster-isoform-X1 KDPTVSSH LIDAKTYRGFVNLYLQDNPEACDYGL 240
Hamster-isoform-X7 KDPTVSSH LIDAKTYRGFVNLYLQDNPEACDYGL 240
Hamster-isoform-X5 KDPTVSSH LIDAKTYRGFVNLYLQDSPEACDYGL 240
Hamster-isoform-X2 KDPTVSSH LIDAKTYRGFVNLYLQDSPEACDYGL 240
Hamster-isoform-X3 KDPTVSSH LIDAKTYRGFVNLYLQDSPEACDYGL 240
Hamster-isoform-X4 ----- 199

Hamster-isoform-X6	-----	199
Whale-(killer)	KDPAVSSLFIDPKAFRGFLDLYLQNNLEACDYGL	273
Dolphin-(common-bottlenose)	KDPAVSSLFIDPKAFRGFLDLYLQNNLEACDYGL	273
Cow-(cattle)	KDPTVSSLLTDVKTFQGFFNLYLQNNPEAYDYGL	241
Bat-(Myotis-myotis)	KDPTVSALLTDVKTFQGFLNLYLQNSLEACDYGL	241
Bat-(Kuhl's-pipistrelle)	KDPTVSALITDGKTFQGFLNLYLQNSVEACDYGL	241
Squirrel	EDPPVSALLHDVKTHQGFLGLYLQNSLEAFDYGL	241
Bat-(large-flying-fox)	EDPTVSALLTDAKTFRGYLDLYLQNSVEACDYGL	241
Rhesus-monkey	EDPTVSALLISGKDWQGFLELYLQNSPEACDYGL	241
Human-GSTO1-isoform-2	EDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL	208
Chimpanzee	EDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL	241
Human-GSTO1-isoform-1	EDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL	241
Human-GSTO1-isoform-3	EDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL	213
Gorilla-isoform-X1	EDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL	241
Gorilla-isoform-X2	EDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL	213
Dog	EDPAVSALLNEANTLRGFLNLYLQNSPEACDYGL	241
Ferret-(domestic)	KDPAVSALLMEPKALRGFLNLYLQNSPEACDYGL	240
Mink-(American)	KDPAVSALLMEPKALRGFLNLYLQNSPE-----	234
Mouse	QDPVASSHKIDAKTYREYLNLYLQDSPEACDYGL	240
Rat	EDPVASSHFIDAKTYRDYLSLYLQDSPEACDYGL	241
Chicken	KDPAVKDTITDTQTFRSFLQLYFKNSPEACDYGL	239
Crocodile	QDPAVKATMTDFQTFKGYLQLYVKNSPEACDYGL	242

Figure 2: Alignments of seven isoforms of human GSTO1 and GSTO2, showing positioning of relevant SNPs. rs4925 in yellow and rs156697 in purple. Conserved residues in that region are highlighted in blue. Sequences from Tables 1 & 2.

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CLUSTAL O(1.2.4) multiple sequence alignment

Human-GSTO1-isoform-2
MSGESARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLKAKGIRHEVININLKNKP      60
Human-GSTO1-isoform-1
MSGESARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLKAKGIRHEVININLKNKP      60
Human-GSTO1-isoform-3
MRFCPFAERTRLVLKAKGIRHEVININLKNKP      32
human-GSTO2-isoform-1
MSGDATRTLGLKGSQPPGPVPEGLIRIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNKP      60
human-GSTO2-isoform-3
MRFCPYSHRTRLVLKAKDIRHEVVNINLRNKP      32
human-GSTO2-isoform-2
MSGDATRTLGLKGSQPPGPVPEGLIRIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNKP      60
human-GSTO2-isoform-4
MRFCPYSHRTRLVLKAKDIRHEVVNINLRNKP      32

*****:.*****.*****:****:*

Human-GSTO1-isoform-2
EWFFKKNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKLLPDDPYEKACQKMILELF      120
Human-GSTO1-isoform-1
EWFFKKNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKLLPDDPYEKACQKMILELF      120
Human-GSTO1-isoform-3
EWFFKKNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKLLPDDPYEKACQKMILELF      92
human-GSTO2-isoform-1
EWYYTKHPFGHIPVLETSQCQLIYESVIACEYLDDAYPGRKLFPPYDPYERARQKMILLELF      120
human-GSTO2-isoform-3
EWYYTKHPFGHIPVLETSQCQLIYESVIACEYLDDAYPGRKLFPPYDPYERARQKMILLELF      92
human-GSTO2-isoform-2
EWYYTKHPFGHIPVLETSQCQLIYESVIACEYLDDAYPGRKLFPPYDPYERARQKMILLELF      120
human-GSTO2-isoform-4
EWYYTKHPFGHIPVLETSQCQLIYESVIACEYLDDAYPGRKLFPPYDPYERARQKMILLELF      92
                                                                    **::.*:*** :***** ** *****.*:*****:*****:**:* *****:*
***:***

Human-GSTO1-isoform-2      SK-----
VLTNKKTTFFGGNSISMIDYLIWP      146
Human-GSTO1-isoform-1      SKVPSLVGSFIR-
SQNKEDYArs4925GLrs156697KEEFrs4925RKEErs156697TKLEEVLTNKKTFFGGNSISMIDYLIWP      179
Human-GSTO1-isoform-3      SKVPSLVGSFIR-
SQNKEDYArs4925GLrs156697KEEFrs4925RKEErs156697TKLEEVLTNKKTFFGGNSISMIDYLIWP      151
human-GSTO2-isoform-1
CKVPHLrs4925TKECLVALRCRECTrs156697NLKAALrs4925ROEFrs156697SNLEEILEYQNTTFFGGTCISMIDYLLWP      180
human-GSTO2-isoform-3
CKVPHLrs4925TKECLVALRCRECTrs156697NLKAALrs4925ROEFrs156697SNLEEILEYQNTTFFGGTCISMIDYLLWP      152
human-GSTO2-isoform-2      CK-----
ILEYQNTTFFGGTCISMIDYLLWP      146
human-GSTO2-isoform-4      CK-----
ILEYQNTTFFGGTCISMIDYLLWP      118
                                                                    .*
:*****.*****:*

Human-GSTO1-isoform-2
WFERLEAMKLNrs4925ECVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQNSPEACDY      206
Human-GSTO1-isoform-1
WFERLEAMKLNrs4925ECVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQNSPEACDY      239
Human-GSTO1-isoform-3
WFERLEAMKLNrs4925ECVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQNSPEACDY      211
human-GSTO2-isoform-1
WFERLDVYGILDCVSHTPALRLWISAMKWDPTVCALLMDKSIrs4925FQGFrs156697LNLrs4925YFQNNPNAFDF      240

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human-GSTO2-isoform-3
 WFERLDVYGILDCVSHTPALRLWISAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDF 212
 human-GSTO2-isoform-2
 WFERLDVYGILDCVSHTPALRLWISAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDF 206
 human-GSTO2-isoform-4
 WFERLDVYGILDCVSHTPALRLWISAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDF 178

*****:. : :*.*** *:**.:*** *****.*** ..
 :****:*.**:*.*: * *:

Human-GSTO1-isoform-2	GL-	208
Human-GSTO1-isoform-1	GL-	241
Human-GSTO1-isoform-3	GL-	213
human-GSTO2-isoform-1	GLC	243
human-GSTO2-isoform-3	GLC	215
human-GSTO2-isoform-2	GLC	209
human-GSTO2-isoform-4	GLC	181

**

Figure 3: Clustal Omega alignments GSTO2. Sequence details are in Table 2. “*” indicates sequence identity (“:” indicates a conserved change, whilst “.” indicates less of a conserved change). Position of SNP indicated in yellow. The predicted (using Prosite) N-terminal GST domain (of human GST isoform 1) is highlighted in green, whilst the N-terminal domain is highlighted in purple. Predicted phosphorylation sites are marked (from Prosite: protein kinase C: grey; tyrosine phosphorylation: brown; amidation site: bright blue; Casein kinase II phosphorylation site: red; N-glycosylation site: teal; myristoylation; dark green).

CLUSTAL O(1.2.4) multiple sequence alignment

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Frog -
MTGSEKSLAKGSPAPGPVSEETIRVYSMRFCPYAQRARLVLAAGIKHEVININLNKPK 59
Hamster-isoform-X2 -----MEI-----
DVWGCDDQKLGERYEVININLNKPK 27
Hamster-isoform-X1
MSGDATRSLGRGSSPPGPVPEGVIRIYSMRFCPYSHRARLVLKAKGIRYEVININLNKPK 60
Hamster-isoform-X3
MSGDATRSLGRGSSPPGPVPEGVIRIYSMRFCPYSHRARLVLKAKGIRYEVININLNKPK 60
Bat- (big-brown)
MGEDASRSLGKGSVPPGPVPEGLIRIYSMRFCPPFAHRTRLVLLAKGISHEVININLRNPK 60
Bat- (greater-spear-nosed)
MAEDASRALGKGSHPGPVPEGLIRIYSMRFCPYAHRTRLVLQAKGISHEVININLRNPK 60
Bat- (common-vampire)
MAEDASRALGKGSHPGPVPEGLIRIYSMRFCPYAHRTRLVLQAKGIRHEVININLRNPK 60
Cow
MTDDATRTLKGKSIPPGVPPEGVIRLYSMRFCPYAHRTRLVLRKAGIRHEVININLRNPK 60
Whale
MTDDAARTLGRGSAPPGPVPEGLIRLYSMRFCPYAHRTRLVLQAKGIRHEVININLRNPK 60
Dolphin
MTDDAARTLGRGSAPPGPVPEGLIRLYSMRFCPYAHRTRLVLQAKGIRHEVININLRNPK 60
Dog-isoform-X1 -
MEDASRTFGKGSPPGPVPEGLIRIYSMRFCPYAHRTRLVLRKAGIRHEVININLRNPK 59
Dog-isoform-X2 -
MEDASRTFGKGSPPGPVPEGLIRIYSMRFCPYAHRTRLVLRKAGIRHEVININLRNPK 59
Ferret -----
HEVVNINLRNPK 12
Cat-isoform-X1 -
MEDATRTFGKGSPPGPVPEGLIRVYSMRFCPPFAHRTRLVLRKAGIRHEVININLRNPK 59
Cat-isoform-X2 -
MEDATRTFGKGSPPGPVPEGLIRVYSMRFCPPFAHRTRLVLRKAGIRHEVININLRNPK 59
Cat-isoform-X3 -
MEDATRTFGKGSPPGPVPEGLIRVYSMRFCPPFAHRTRLVLRKAGIRHEVININLRNPK 59
Rhesus-monkey
MSQDATRTLKGKSQPPGPVPEGLIRIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNPK 60
Human-GSTO2-isoform-2
MSGDATRTLKGKSQPPGPVPEGLIRIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNPK 60
Human-GSTO2-isoform-4 -----
MRFCPYSHRTRLVLKAKDIRHEVVNINLRNPK 32
Gorilla
MSEDATRTLKGKSQPPGPVPEGLIRIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNPK 60
Human-GSTO2-isoform-1
MSGDATRTLKGKSQPPGPVPEGLIRIYSMRFCPYSHRTRLVLKAKDIRHEVVNINLRNPK 60
Human-GSTO2-isoform-3 -----
MRFCPYSHRTRLVLKAKDIRHEVVNINLRNPK 32
Mouse
MSGDLRCLGKGSPPGPVPEGVIRIYSMRFCPYSHRARLVLKAKGIRHEVININLKSKE 60
Rat
MSGDLRCLGKGSPPGPVPEGVIRIYSMRFCPYSHRARLVLKAKSIRHEIININLNKPK 60

:::****:..**

Frog
DWFIEKSPFGLVPSLETSSGQVIYESPIVCDYLDEVYGRKLTVPVDPFQKAQQKMIVEHF 119
Hamster-isoform-X2
EWYFTKHPFGQIPVLENSQGQLIYESVIACEYLLDDLYGRKLFPPDPYERARQKMLLELF 87

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Hamster-isoform-X1	EWYFTKHPPFGQIPVLENSQGQLIYESVIACEYLDDLYGRKLFPPDPYERARQKMLLELF	120
Hamster-isoform-X3	EWYFTKHPPFGQIPVLENSQGQLIYESVIACEYLDDLYGRKLFPPDPYERARQKMLLELF	120
Bat- (big-brown)	DWYTKHPPFGQIPVLENSRCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	120
Bat- (greater-spear-nosed)	DWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPPDPYERARQKMLLELF	120
Bat- (common-vampire)	DWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPPDPYERARQKMLLELF	120
Cow	EWYFTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	120
Whale	EWYFTKHPPFGKIPVLENSKCQLIYESVIACEYLDDAYGRKLYPCDSYERARQKMLLDLF	120
Dolphin	EWYFTKHPPFGKIPVLENSKCQLIYESVIACEYLDDAYGRKLYPCDSYERARQKMLLDLF	120
Dog-isoform-X1	EWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	119
Dog-isoform-X2	EWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	119
Ferret	EWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	72
Cat-isoform-X1	EWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	119
Cat-isoform-X2	EWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	119
Cat-isoform-X3	EWYTKHPPFGQIPVLENSKCQLIYESVIACEYLDDAYGRKLYPYDPYERARQKMLLELF	119
Rhesus-monkey	EWYTKHPPFGHIPVLETSQCQLIYESVIACEYLDDAYGRKLFPHDPYERARQKMLLELF	120
Human-GSTO2-isoform-2	EWYTKHPPFGHIPVLETSQCQLIYESVIACEYLDDAYGRKLFPPDPYERARQKMLLELF	120
Human-GSTO2-isoform-4	EWYTKHPPFGHIPVLETSQCQLIYESVIACEYLDDAYGRKLFPPDPYERARQKMLLELF	92
Gorilla	EWYTKHPPFGHIPVLETSQCQLIYESVIACEYLDDAYGRKLFPPDPYERARQKMLLELF	120
Human-GSTO2-isoform-1	EWYTKHPPFGHIPVLETSQCQLIYESVIACEYLDDAYGRKLFPPDPYERARQKMLLELF	120
Human-GSTO2-isoform-3	EWYTKHPPFGHIPVLETSQCQLIYESVIACEYLDDAYGRKLFPPDPYERARQKMLLELF	92
Mouse	DWYTKHPPFGQIPVLENSQCQLVYESVIACEYLDDVYGRKLFPPDPYERARQKMLLELF	120
Rat	DWYTKHPPFGQVPVLENSQCQLIYESVIACEYLDDVYGRKLFPPDPYERARQKMLLELF	120

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Frog	SKISTLFYKILLAKKNNEDVSGVKAEVQEKLVLKLE-----
----- 155	
Hamster-isoform-X2	CKVPHLAKECLVALRCGRECMDLKTALRQEFRNLEE-----
----- 123	
Hamster-isoform-X1	CKVPHLAKECLVALRCGRECMDLKTALRQEFRNLEE-----
----- 156	
Hamster-isoform-X3	CKV-----
----- 123	
Bat- (big-brown)	YKVPHLTKECLVALRCGKECCDLKLALREEFCNLEE-----
----- 156	
Bat- (greater-spear-nosed)	YKIPHLTKECLVALRCGKECANLKLALREEFCNLEE-----
----- 156	
Bat- (common-vampire)	YKIPHLTKECLVALRCGKECGNLKLALREEFCNLEE-----
----- 156	
Cow	YKVPHLTKECLVALRCGRDCGDLKLALRQEFRNLEE-----
----- 156	
Whale	YKVPHLTKECLIASRCGRECADLKLALRQEFRNLEE-----
----- 156	
Dolphin	YKVPHLTKECLIASRCGRECADLKLALRQEFRNLEE-----
----- 156	

Dog-isoform-X1 YKVPHLTKECLVALRCGRECTD LKLALRQEFNCLEE-----
----- 155
Dog-isoform-X2 YK-----
----- 121
Ferret YKVPHLTKECLVALRCGRECAD LKLALRQEFNCLEE-----
----- 108
Cat-isoform-X1 YKVPHLTKECLVAIRCGRACAD LKLALRQEFNCLEEVFPVVISSTAFTNRKSSTPSGEME 179
Cat-isoform-X2 YKVPHLTKECLVAIRCGRACAD LKLALRQEFNCLEE-----
----- 155
Cat-isoform-X3 YK-----
----- 121
Rhesus-monkey CKVPHLTKECLVALRCGRECTD LKAALRQEFNCLEE-----
----- 156
Human-GSTO2-isoform-2 CK-----
----- 122
Human-GSTO2-isoform-4 CK-----
----- 94
Gorilla CKVPDLTKECLVALRCGRECTD LKAALRQEFNCLEE-----
----- 156
Human-GSTO2-isoform-1 CKVPHLTKECLVALRCGRECTN LKAALRQEFNCLEE-----
----- 156
Human-GSTO2-isoform-3 CKVPHLTKECLVALRCGRECTN LKAALRQEFNCLEE-----
----- 128
Mouse CKVPPLSKECLIALRCGRDCTD LKVALRQELCNMEE-----
----- 156
Rat CKVPQLSKECLVALRCGRDCTD LKVALRQELCNLEE-----
----- 156

*

Frog -----
ILAKQGLFFGSDV MVDYMIWPWFERLIIFDSKDCLNKTPHIDKWI 203
Hamster-isoform-X2 -----
VLEYQITFFGDRIMIDYLFWPWFERLDVYGLSDCVSHTPMLRLWI 171
Hamster-isoform-X1 -----
VLEYQITFFGDRIMIDYLFWPWFERLDVYGLSDCVSHTPMLRLWI 204
Hamster-isoform-X3 -----
LEYQITFFGDRIMIDYLFWPWFERLDVYGLSDCVSHTPMLRLWI 170
Bat- (big-brown) -----
ILSYQITVFFGDCIMIDYLFWPWFERLDVYIADCVNHTPALRLWI 204
Bat- (greater-spear-nosed) -----
ILSYQITVFFGPCIIMIDYLFWPWFERLDVYIADCVNHTPALRLWI 204
Bat- (common-vampire) -----
ILSYQITVFFGPCIIMIDYLFWPWFERLDVYIADCVNHTPALRLWI 204
Cow -----
ILGYQITVFFGDCIMIDYLFWPWFERLEVYIADCVNHTPALRLWI 204
Whale -----
ILGYQITVFFGDCIMIDYLFWPWFERLDVYIADCVNHTPALRLWI 204
Dolphin -----
ILGYQITVFFGDCIMIDYLFWPWFERLDVYIADCVNHTPALRLWI 204
Dog-isoform-X1 -----
ILGYQITVFFGDCIMIDYLFWPWFERLEVYIADCLNHTPALRLWT 203
Dog-isoform-X2 -----
ILGYQITVFFGDCIMIDYLFWPWFERLEVYIADCLNHTPALRLWT 169
Ferret -----
ILGYQITVFFGDCIMIDYLFWPWFERLDVYIADCLNHTPALRLWT 156
Cat-isoform-X1 -----
NIFFHPRSITLKILGYQITVFFGDCIMIDYLFWPWFERLDVYIADCLNHTPALRLWT 239
Cat-isoform-X2 -----
ILGYQITVFFGDCIMIDYLFWPWFERLDVYIADCLNHTPALRLWT 203
Cat-isoform-X3 -----
ILGYQITVFFGDCIMIDYLFWPWFERLDVYIADCLNHTPALRLWT 169
Rhesus-monkey -----
ILEYQITVFFGTCTMIDYLLWPWFERLDVYIADCVSHTPALRLWI 204
Human-GSTO2-isoform-2 -----
ILEYQITVFFGTCTMIDYLLWPWFERLDVYILDCVSHTPALRLWI 170
Human-GSTO2-isoform-4 -----
ILEYQITVFFGTCTMIDYLLWPWFERLDVYILDCVSHTPALRLWI 142

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Gorilla -----
ILEYQNTTFFFGTCIEMIDYLLWPWFERLDVYILDCVSHTPALRLWI 204
Human-GSTO2-isoform-1 -----
ILEYQNTTFFFGTCIEMIDYLLWPWFERLDVYILDCVSHTPALRLWI 204
Human-GSTO2-isoform-3 -----
ILEYQNTTFFFGTCIEMIDYLLWPWFERLDVYILDCVSHTPALRLWI 176
Mouse -----
ILEYQNTTFFFGDCIEMIDYLVWPWFERLDVYGLADCVNHTPMLRLWI 204
Rat -----
ILEYQNTTFFFGDSIEMIDYLVWPWFERLDVYGLADCVNHTPMLRLWI 204
* ** ***** **.*:.****** :.
**.:** : *

Frog QQMLQDPAVKATYIEPDLLLGFFKLYSQNDVEACDYGL----- 241
Hamster-isoform-X2 STMKQDPTVCALLTDKNIFLGFLHLYFQNNPCAFDFGLCAPAIR 215
Hamster-isoform-X1 STMKQDPTVCALLTDKNIFLGFLHLYFQNNPCAFDFGLCAPAIR 248
Hamster-isoform-X3 STMKQDPTVCALLTDKNIFLGFLHLYFQNNPCAFDFGLCAPAIR 214
Bat- (big-brown) EAMKQDPTVCALLIDKNIFLGFLNLYFQNHDPADFYGLSC---- 244
Bat- (greater-spear-nosed) AAMKRDPTVCALLIDKNIFLGFLNLYFQNHPEAFDYGLSC---- 244
Bat- (common-vampire) AAMKRDPTVCSLLIDKNIFLGFLNLYFQNHPEAFDYGLSC---- 244
Cow AAMKQDPTVCSLLTDKNIFLGFLNLYFQNNPGADFYGLSC---- 244
Whale AAMKQDPTVCALLIDKNIFLGFLNLYFQNNPDAFDYGLSC---- 244
Dolphin AAMKQDPTVCALLIDKNIFLGFLNLYFQNNPDAFDYGLSC---- 244
Dog-isoform-X1 AAMKQDPTVCALLIDKSVFSGFLNLYFQNNPDAFDYGLIC---- 243
Dog-isoform-X2 AAMKQDPTVCALLIDKSVFSGFLNLYFQNNPDAFDYGLIC---- 209
Ferret AAMKQDPTVCALLIDKNIFLGFLNLYFQNNPDAFDYGLA---- 195
Cat-isoform-X1 AAMKQDPTVCALLIDRSIFLGFLNLYFQNNPDAFDYGLTC---- 279
Cat-isoform-X2 AAMKQDPTVCALLIDRSIFLGFLNLYFQNNPDAFDYGLTC---- 243
Cat-isoform-X3 AAMKQDPTVCALLIDRSIFLGFLNLYFQNNPDAFDYGLTC---- 209
Rhesus-monkey SAMKWDPTVCALLTDKSI FQGFLNLYFQNNPNAFDFGLC----- 243
Human-GSTO2-isoform-2 SAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDFGLC----- 209
Human-GSTO2-isoform-4 SAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDFGLC----- 181
Gorilla SAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDFGLC----- 243
Human-GSTO2-isoform-1 SAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDFGLC----- 243
Human-GSTO2-isoform-3 SAMKWDPTVCALLMDKSI FQGFLNLYFQNNPNAFDFGLC----- 215
Mouse ASMKQDPAVCALHTDKSVFLGFLNLYFQNNPCAFDFGLCNPIIR 248
Rat SSMKQDPAVCALHIDKNIFLGFLNLYFQNNPCAFDFGLCGPIVR 248
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