# C-Met Proto-Oncogene (C-MET) ELISA Kit for Fish

## PRODUCT OVERVIEW

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| **Product Name** | C-Met Proto-Oncogene Protein, ELISA Kit |
| **Full Product Name** | Fish C-Met Proto-Oncogene Protein ELISA Kit |
| **Product Gene Name** | C-MET elisa kit |
| **Species Reactivity** | Fish |
| **Assay Type** | Sandwich |
| **Preparation and Storage** | Store all reagents at 2-8 degree C |
| **Molecular Weight** | 154,637 Da |
| **Chromosome Location** | Chromosome: 14; NC_006596.3 (55626435..55709875). Location: chromosome: 14 |
| **3D Structure** | ModBase 3D Structure for Q75ZY9 |
| **Related Product Information for C-MET elisa kit** | MBS040465 is a ready-to-use microwell, strip-or-full plate ELISA (enzyme-linked immunosorbent assay) Kit for analyzing the presence of the C-Met Proto-Oncogene Protein, ELISA Kit target analytes in biological samples. The concentration gradients of the kit standards or positive controls render a theoretical kit detection range in biological research samples containing C-MET. The ELISA analytical biochemical technique of the MBS040465 kit is based on C-MET antibody-C-MET antigen interactions (immunosorbency) and an HRP colorimetric detection system to detect C-MET antigen targets in samples. The ELISA Kit is designed to detect native, not recombinant, C-MET. Appropriate sample types may include undiluted body fluids and/or tissue homogenates, secretions. Quality control assays assessing reproducibility identified the intra-assay CV (%) and inter-assay CV(%). |
| **Other Notes** | Small volumes of C-MET elisa kit vial(s) may occasionally become entrapped in the seal of the product vial during shipment and storage. If necessary, briefly centrifuge the vial on a tabletop centrifuge to dislodge any liquid in the container`s cap. Certain products may require to ship with dry ice and additional dry ice fee may apply. |

## ADDITIONAL DETAILS

NCBI/Uniprot data below describe general gene information for C-MET. It may not necessarily be applicable to this product.

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| **NCBI GI #** | 25815188 |
| **NCBI GeneID** | 403438 |
| **NCBI Accession #** | BAC41197.1 |
| **UniProt Primary Accession #** | Q75ZY9 |
| **UniProt Secondary Accession #** | A0M8U9 |
| **UniProt Related Accession #** | Q75ZY9 |
| **NCBI Official Full Name** | c-Met |
| **NCBI Official Symbol** | MET |
| **NCBI Official Synonym Symbols** | c-Met |
| **UniProt Protein Name** | Hepatocyte growth factor receptor |
| **UniProt Synonym Protein Names** | HGF/SF receptor; Proto-oncogene c-Met; Scatter factor receptor; SF receptor; Tyrosine-protein kinase Met |
| **UniProt Gene Name** | MET |
| **UniProt Synonym Gene Names** | HGF receptor; SF receptor |

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| **UniProt Entry Name** | MET_CANFA |
| **NCBI Protein Information** | hepatocyte growth factor receptor; SF receptor; HGF receptor; HGF/SF receptor; proto-oncogene c-Met; scatter factor receptor; tyrosine-protein kinase Met; met proto-oncogene tyrosine kinase |
| **UniProt Comments for C-MET** | Function: Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to hepatocyte growth factor/HGF ligand. Regulates many physiological processes including proliferation, scattering, morphogenesis and survival. Ligand binding at the cell surface induces autophosphorylation of MET on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with the PI3-kinase subunit PIK3R1, PLCG1, SRC, GRB2, STAT3 or the adapter GAB1. Recruitment of these downstream effectors by MET leads to the activation of several signaling cascades including the RAS-ERK, PI3 kinase-AKT, or PLCgamma-PKC. The RAS-ERK activation is associated with the morphogenetic effects while PI3K/AKT coordinates prosurvival effects. During embryonic development, MET signaling plays a role in gastrulation, development and migration of muscles and neuronal precursors, angiogenesis and kidney formation. In adults, participates in wound healing as well as organ regeneration and tissue remodeling. Promotes also differentiation and proliferation of hematopoietic cells<br><br>By similarity. Ref.4<br><br>Catalytic activity: ATP + a [protein]-L-tyrosine = ADP + a [protein]-L-tyrosine phosphate.<br><br>Enzyme regulation: In its inactive state, the C-terminal tail interacts with the catalytic domain and inhibits the kinase activity. Upon ligand binding, the C-terminal tail is displaced and becomes phosphorylated, thus increasing the kinase activity<br><br>By similarity.<br><br>Subunit structure: Heterodimer made of an alpha chain (50 kDa) and a beta chain (145 kDa) which are disulfide linked. Binds PLXNB1. Interacts when phosphorylated with downstream effectors including STAT3, PIK3R1, SRC, PCLG1, GRB2 and GAB1. Interacts with SPSB1, SPSB2 and SPSB4. Interacts with INPP5D/SHIP1. When phosphorylated at Tyr-1357, interacts with INPPL1/SHIP2. Interacts with RANBP9 and RANBP10, as well as SPSB1, SPSB2, SPSB3 and SPSB4. SPSB1 binding occurs in the presence and in the absence of HGF, however HGF treatment has a positive effect on this interaction. Interacts with MUC20; prevents interaction with GRB2 and suppresses hepatocyte growth factor-induced cell proliferation. Interacts with GRB10<br><br>By similarity.<br><br>Subcellular location: Membrane; Single-pass type I membrane protein<br><br>By similarity.<br><br>Domain: The kinase domain is involved in SPSB1 binding<br><br>By similarity.The beta-propeller Sema domain mediates binding to HGF<br><br>By similarity.<br><br>Post-translational modification: Autophosphorylated in response to ligand binding on Tyr-1235 and Tyr-1236 in the kinase domain leading to further phosphorylation of Tyr-1350 and Tyr-1357 in the C-terminal multifunctional docking site<br><br>By similarity.Dephosphorylated by PTPRJ at Tyr-1350 and Tyr-1366<br><br>By similarity.Ubiquitinated. Ubiquitination by CBL regulates the receptor stability and activity through proteasomal degradation<br><br>By similarity.<br><br>Sequence similarities: Belongs to the protein kinase superfamily. Tyr protein kinase family.Contains 3 IPT/TIG domains.Contains 1 protein kinase domain.Contains 1 Sema domain. |
| **Research Articles on C-MET** | **1.** NFAT-dependent gene transcription is required for hepatocyte growth factor-induced cell scattering. |

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