1. Phylogeny  
   SMG1 is a large serine/threonine‐protein kinase that belongs to the phosphatidylinositol 3‐kinase–related kinase (PIKK) family, a group that also includes ATM, ATR, DNA‑PKcs, and mTOR (grimson2004smg1isa pages 2-3). It is evolutionarily conserved in metazoans and is found in both Caenorhabditis elegans and humans, although no clear ortholog is present in budding yeast, which reflects an evolutionary adaptation associated with the increasing complexity of mRNA surveillance in higher eukaryotes (yamashita2001…3kinaserelatedprotein pages 1-2, ariaspalomo2011thenonsensemediatedmrna pages 1-3). Phylogenetic analyses place SMG1 as a distinct PIKK that has evolved in animals to support the intricate regulation of nonsense-mediated mRNA decay (NMD), a pathway not as elaborated in lower eukaryotes (grimson2004smg1isa pages 2-3, ariaspalomo2011thenonsensemediatedmrna pages 1-3). The placement of SMG1 within the PIKK subgroup underscores its conserved kinase core while also highlighting lineage‑specific adaptations such as its unique large insertion domain, which supports interactions with regulatory subunits SMG8 and SMG9 (ariaspalomo2011thenonsensemediatedmrna pages 6-7, zhu2019cryoemstructureof pages 1-2).
2. Reaction Catalyzed  
   SMG1 catalyzes the transfer of a phosphate group from ATP to serine or threonine residues on its substrate proteins, following the general reaction: ATP + [protein]‐(L‑serine/threonine) → ADP + [protein]‑(L‑serine/threonine)‑phosphate + H⁺ (yamashita2001…3kinaserelatedprotein pages 7-9). This reaction is exemplified during nonsense-mediated mRNA decay (NMD) when SMG1 specifically phosphorylates the RNA helicase UPF1 at conserved serine residues within SQ motifs, thereby modifying UPF1’s activity in downstream mRNA surveillance (langer2020structureofsubstratebound pages 2-5).
3. Cofactor Requirements  
   SMG1’s kinase activity is strictly ATP-dependent and requires divalent metal ions such as Mg²⁺ as a cofactor to coordinate ATP binding and catalysis (langer2020structureofsubstratebound pages 10-11, conti2021cryoemreconstructionsof pages 1-3). The presence of Mg²⁺ is essential for achieving the proper catalytic geometry within the active site of the kinase domain, and this cofactor requirement is consistent with the behavior of other members of the PIKK family (yamashita2005theroleof pages 5-6).
4. Substrate Specificity  
   SMG1 exhibits a strong substrate preference for serine/threonine residues immediately followed by a glutamine residue, thereby recognizing the [ST]-Q motif in its substrates; this is particularly evident in the phosphorylation of UPF1 during NMD (langer2020structureofsubstratebound pages 2-5, ariaspalomo2011thenonsensemediatedmrna pages 1-3). In addition, SMG1 shows enhanced phosphorylation efficiency when a hydrophobic residue, usually leucine, precedes the serine, forming an LSQ consensus sequence that has been mapped in UPF1 (langer2020structureofsubstratebound pages 2-5, ariaspalomo2011thenonsensemediatedmrna pages 12-13). Detailed structural and biochemical studies have established that this substrate recognition ensures selective modification of proteins involved in mRNA surveillance (langer2020structureofsubstratebound pages 5-6).
5. Structure  
   SMG1 is an exceptionally large kinase with a molecular mass of approximately 410 kDa and displays a modular domain organization characteristic of the PIKK family (ariaspalomo2011thenonsensemediatedmrna pages 1-3, zhu2019cryoemstructureof pages 1-2). Its N-terminal region is composed of numerous HEAT repeats, which form an elongated alpha‑solenoid structure that serves as a scaffold for protein–protein interactions and is critical for binding regulatory subunits such as SMG8 and SMG9 (conti2021cryoemreconstructionsof pages 6-8, ariaspalomo2011thenonsensemediatedmrna pages 6-7). Downstream of the HEAT repeats, SMG1 includes a FAT domain that is conserved among PIKKs and more centrally located is its catalytic kinase domain, homologous to phosphatidylinositol 3-kinases, which houses key catalytic motifs such as the activation loop, a conserved catalytic loop, and a hydrophobic spine essential for enzyme activity (langer2020structureofsubstratebound pages 5-6, conti2021cryoemreconstructionsof pages 27-36). C-terminal to the kinase domain, SMG1 contains a FATC domain that contributes to overall stability and proper folding of the kinase; moreover, a large insertion domain situated between the kinase domain and the FATC domain is unique to SMG1 and appears to have regulatory functions, including an autoinhibitory role that modulates substrate access (ariaspalomo2011thenonsensemediatedmrna pages 6-7, conti2021cryoemreconstructionsof pages 3-6). High-resolution cryo-electron microscopy studies have revealed various conformations of the SMG1-8-9 complex, including states in which the insertion domain occludes the active site, indicating a mechanism by which regulatory subunits such as SMG8 stabilize autoinhibition (conti2021cryoemreconstructionsof pages 8-11, langer2020structureofsubstratebound pages 10-11).
6. Regulation  
   The activity of SMG1 is subject to complex regulation mediated primarily through its assembly into a multiprotein complex often referred to as SMG1C, which is comprised of SMG1 together with regulatory subunits SMG8 and SMG9 (ariaspalomo2011thenonsensemediatedmrna pages 6-7, yamashita2009smg8andsmg9 pages 1-2). SMG8 contains a C-terminal kinase inhibitory domain (KID) that interacts with SMG1’s unique insertion region, effectively stabilizing an autoinhibited conformation that reduces its catalytic activity in the absence of appropriate stimuli (conti2021cryoemreconstructionsof pages 6-8, yamashita2009smg8andsmg9 pages 14-16). SMG9, which contains a predicted NTPase domain, is essential for the proper assembly of the SMG1C complex, thereby ensuring that SMG8 is recruited to SMG1 and can exert its inhibitory effect; this coordinated regulation modulates the kinase activity required for phosphorylation of UPF1 (yamashita2009smg8andsmg9 pages 9-10, llorcacardenosa2022smg8smg9heterodimerloss pages 7-8). In vitro biochemical assays have demonstrated that the inhibition imposed by SMG8 is overcome under conditions where the SURF complex assembles at stalled ribosomes during translation termination, permitting SMG1 to phosphorylate UPF1 and initiate NMD (ariaspalomo2011thenonsensemediatedmrna pages 7-9, conti2021cryoemreconstructionsof pages 17-19). Additionally, pharmacological agents such as wortmannin and caffeine have been shown to inhibit SMG1’s kinase activity, further underscoring the importance of regulatory control in maintaining mRNA surveillance (yamashita2001…3kinaserelatedprotein pages 9-11, yamashita2005theroleof pages 1-3). The interplay between autoinhibition by the insertion domain and relief of this inhibition upon proper complex assembly provides a robust regulatory mechanism that ensures SMG1 is active only when needed (conti2021cryoemreconstructionsof pages 3-6).
7. Function  
   SMG1 plays a central biological role in controlling the fidelity of gene expression through its regulation of nonsense-mediated mRNA decay (NMD) (ariaspalomo2011thenonsensemediatedmrna pages 1-3, yamashita2005theroleof pages 1-3). In the canonical NMD pathway, SMG1 phosphorylates the RNA helicase UPF1 on specific serine residues such as S1078 and S1096 within SQ motifs, a modification that is essential for the transition of the transient SURF complex (comprising SMG1, UPF1, eRF1, and eRF3) into a decay-inducing complex upon interaction with exon junction complexes (EJCs) (ariaspalomo2011thenonsensemediatedmrna pages 7-9, langer2020structureofsubstratebound pages 2-5). This phosphorylation event marks aberrant mRNAs containing premature termination codons for rapid degradation, thereby preventing the accumulation of potentially deleterious truncated proteins (yamashita2005theroleof pages 1-3, nicholson2010nonsensemediatedmrnadecay pages 6-7). Beyond its role in NMD, SMG1 also functions as a genotoxic stress-activated kinase; it can phosphorylate p53, which is required for the optimal activation of p53 following exposure to ionizing radiation and other DNA-damaging stimuli (zhu2019cryoemstructureof pages 1-2, nicholson2010nonsensemediatedmrnadecay pages 16-18). SMG1 is recruited to stalled ribosomes via its association with release factors and regulatory subunits SMG8 and SMG9, forming specialized complexes that couple aberrant translation termination with mRNA decay (ariaspalomo2011thenonsensemediatedmrna pages 6-7, yamashita2009smg8andsmg9 pages 3-4). The kinase activity of SMG1 thereby integrates signals from the translation machinery and the DNA damage response to maintain both mRNA quality and genome stability (zhu2019cryoemstructureof pages 1-2, usuki2013inhibitionofsmg8 pages 1-2). Expression studies indicate that SMG1 is widely expressed across mammalian tissues, consistent with its fundamental role in post-transcriptional quality control and stress response pathways (yamashita2005theroleof pages 6-8, nicholson2010nonsensemediatedmrnadecay pages 6-7).
8. Other Comments  
   Experimental inhibitors of SMG1, such as SMG1i and the broader PIKK inhibitor wortmannin, have been employed in research settings to dissect its kinase activity and its role in NMD, although these inhibitors are not entirely specific for SMG1 (yamashita2001…3kinaserelatedprotein pages 9-11, usuki2013inhibitionofsmg8 pages 1-2). Loss or depletion of the regulatory subunits SMG8 and SMG9, which form a heterodimer with SMG1, has been shown to modulate SMG1 activity; for instance, the SMG8/SMG9 complex maintains NMD robustness, and its disruption leads to altered kinase activity and, in certain contexts, drug resistance particularly to ATR inhibitors in cancer cells (yamashita2009smg8andsmg9 pages 14-16, llorcacardenosa2022smg8smg9heterodimerloss pages 7-8). SMG1’s involvement in both mRNA surveillance and genotoxic stress response has significant translational implications, with dysregulation linked to increased sensitivity to DNA-damaging agents and potential roles in tumorigenesis due to altered p53 activation (zhu2019cryoemstructureof pages 1-2, nicholson2010nonsensemediatedmrnadecay pages 16-18). Although no highly selective SMG1 inhibitors have yet reached clinical application, experimental modulation of SMG1 activity remains a promising strategy for correcting aberrant NMD in genetic diseases caused by premature stop codons (usuki2013inhibitionofsmg8 pages 1-2). Additionally, cross-linking mass spectrometry studies have contributed further insights into the SMG1-containing complexes by mapping interactions with UPF2 and SMG7, thereby expanding the understanding of its functional assemblies beyond the canonical NMD machinery (padariya2024invitrocrosslinking pages 15-16).
9. References
10. Arias-Palomo, E., Yamashita, A., Fernández, I. S., Núñez-Ramírez, R., Bamba, Y., Izumi, N., Ohno, S., & Llorca, O. (2011). The nonsense-mediated mrna decay smg-1 kinase is regulated by large-scale conformational changes controlled by smg-8. Genes & Development, 25(2), 153-164. (ariaspalomo2011thenonsensemediatedmrna pages 1-3; ariaspalomo2011thenonsensemediatedmrna pages 6-7; ariaspalomo2011thenonsensemediatedmrna pages 12-13).
11. Langer, L. M., Bonneau, F., Gat, Y., & Conti, E. (2021). Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, July 2021. (conti2021cryoemreconstructionsof pages 1-3; conti2021cryoemreconstructionsof pages 6-8; conti2021cryoemreconstructionsof pages 27-36).
12. Grimson, A., O’Connor, S., Newman, C. L., & Anderson, P. (2004). Smg-1 is a phosphatidylinositol kinase-related protein kinase required for nonsense-mediated mrna decay in caenorhabditis elegans. Molecular and Cellular Biology, 24, 7483-7490. (grimson2004smg1isa pages 1-2; grisom2004smg1isa pages 2-3; grisom2004smg1isa pages 3-4; grisom2004smg1isa pages 4-6; grisom2004smg1isa pages 6-7).
13. Langer, L. M., Gat, Y., Bonneau, F., & Conti, E. (2020). Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. (langer2020structureofsubstratebound pages 1-2; langer2020structureofsubstratebound pages 2-5; langer2020structureofsubstratebound pages 5-6; langer2020structureofsubstratebound pages 6-9; langer2020structureofsubstratebound pages 10-11; langer2020structureofsubstratebound pages 13-14; langer2020structureofsubstratebound pages 14-14).
14. Yamashita, A., Kashima, I., & Ohno, S. (2005). The role of smg-1 in nonsense-mediated mrna decay. Biochimica et Biophysica Acta, 1754(1-2), 305-315. (yamashita2005theroleof pages 1-3; yamashita2005theroleof pages 5-6; yamashita2005theroleof pages 6-8).
15. Yamashita, A., Izumi, N., Kashima, I., Ohnishi, T., Saari, B., Katsuhata, Y., Muramatsu, R., Morita, T., Iwamatsu, A., Hachiya, T., Kurata, R., Hirano, H., Anderson, P., & Ohno, S. (2009). Smg-8 and smg-9, two novel subunits of the smg-1 complex, regulate remodeling of the mrna surveillance complex during nonsense-mediated mrna decay. Genes & Development, 23, 1091-1105. (yamashita2009smg8andsmg9 pages 1-2; yamashita2009smg8andsmg9 pages 3-4; yamashita2009smg8andsmg9 pages 9-10; yamashita2009smg8andsmg9 pages 14-16).
16. Zhu, L., Li, L., Qi, Y., Yu, Z., & Xu, Y. (2019). Cryo-em structure of smg1–smg8–smg9 complex. Cell Research, 29, 1027-1034. (zhu2019cryoemstructureof pages 1-2).
17. Nicholson, P., Yepiskoposyan, H., Metze, S., Zamudio Orozco, R., Kleinschmidt, N., & Mühlemann, O. (2010). Nonsense-mediated mrna decay in human cells: mechanistic insights, functions beyond quality control and the double-life of nmd factors. Cellular and Molecular Life Sciences, 67, 677-700. (nicholson2010nonsensemediatedmrnadecay pages 6-7; nicholson2010nonsensemediatedmrnadecay pages 16-18).
18. Nicholson, P., Josi, C., Kurosawa, H., Yamashita, A., & Mühlemann, O. (2014). A novel phosphorylation-independent interaction between smg6 and upf1 is essential for human nmd. Nucleic Acids Research, 42, 9217-9235. (nicholson2014anovelphosphorylationindependent pages 14-15).
19. Padariya, M., Vojtěšek, B., Hupp, T. R., & Kalathiya, U. (2024). In vitro cross-linking ms reveals smg1–upf2–smg7 assembly as molecular partners within the nmd surveillance. International Journal of Molecular Sciences, Mar 2024. (padariya2024invitrocrosslinking pages 2-3; padariya2024invitrocrosslinking pages 15-16).
20. Usuki, F., Yamashita, A., Shiraishi, T., Shiga, A., Onodera, O., Higuchi, I., & Ohno, S. (2013). Inhibition of smg-8, a subunit of smg-1 kinase, ameliorates nonsense-mediated mrna decay-exacerbated mutant phenotypes without cytotoxicity. Proceedings of the National Academy of Sciences, 110, 15037-15042. (usuki2013inhibitionofsmg8 pages 1-2).
21. Llorca-Cardenosa, M. J., Aronson, L. I., Krastev, D. B., Nieminuszczy, J., Alexander, J., Song, F., Dylewska, M., Broderick, R., Brough, R., Zimmermann, A., Zenke, F. T., Gurel, B., Riisnaes, R., Ferreira, A., Roumeliotis, T., Choudhary, J., Pettitt, S. J., de Bono, J., Cervantes, A., Haider, S., Niedzwiedz, W., Lord, C. J., & Chong, I. Y. (2022). Smg8/smg9 heterodimer loss modulates smg1 kinase to drive atr inhibitor resistance. Cancer Research, 82, 3962-3973. (llorcacardenosa2022smg8smg9heterodimerloss pages 6-6; llorcacardenosa2022smg8smg9heterodimerloss pages 7-8).

References

1. (ariaspalomo2011thenonsensemediatedmrna pages 1-3): E. Arias-Palomo, A. Yamashita, I. S. Fernández, R. Núñez-Ramírez, Y. Bamba, Natsuko Izumi, S. Ohno, and O. Llorca. The nonsense-mediated mrna decay smg-1 kinase is regulated by large-scale conformational changes controlled by smg-8. Genes & development, 25 2:153-64, Jan 2011. URL: https://doi.org/10.1101/gad.606911, doi:10.1101/gad.606911. This article has 100 citations.
2. (ariaspalomo2011thenonsensemediatedmrna pages 6-7): E. Arias-Palomo, A. Yamashita, I. S. Fernández, R. Núñez-Ramírez, Y. Bamba, Natsuko Izumi, S. Ohno, and O. Llorca. The nonsense-mediated mrna decay smg-1 kinase is regulated by large-scale conformational changes controlled by smg-8. Genes & development, 25 2:153-64, Jan 2011. URL: https://doi.org/10.1101/gad.606911, doi:10.1101/gad.606911. This article has 100 citations.
3. (conti2021cryoemreconstructionsof pages 1-3): L. M. Langer, F. Bonneau, Y. Gat, and E. Conti. Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, Jul 2021. URL: https://doi.org/10.1101/2021.07.28.454180, doi:10.1101/2021.07.28.454180. This article has 31 citations and is from a domain leading peer-reviewed journal.
4. (conti2021cryoemreconstructionsof pages 8-11): L. M. Langer, F. Bonneau, Y. Gat, and E. Conti. Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, Jul 2021. URL: https://doi.org/10.1101/2021.07.28.454180, doi:10.1101/2021.07.28.454180. This article has 31 citations and is from a domain leading peer-reviewed journal.
5. (grimson2004smg1isa pages 2-3): Andrew Grimson, Sean O’Connor, Carrie Loushin Newman, and Philip Anderson. Smg-1 is a phosphatidylinositol kinase-related protein kinase required for nonsense-mediated mrna decay incaenorhabditis elegans. Molecular and Cellular Biology, 24:7483-7490, Sep 2004. URL: https://doi.org/10.1128/mcb.24.17.7483-7490.2004, doi:10.1128/mcb.24.17.7483-7490.2004. This article has 172 citations and is from a domain leading peer-reviewed journal.
6. (langer2020structureofsubstratebound pages 13-14): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
7. (langer2020structureofsubstratebound pages 5-6): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
8. (langer2020structureofsubstratebound pages 6-9): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
9. (yamashita2005theroleof pages 5-6): A. Yamashita, Isao Kashima, and S. Ohno. The role of smg-1 in nonsense-mediated mrna decay. Biochimica et biophysica acta, 1754 1-2:305-15, Dec 2005. URL: https://doi.org/10.1016/j.bbapap.2005.10.002, doi:10.1016/j.bbapap.2005.10.002. This article has 101 citations.
10. (yamashita2005theroleof pages 6-8): A. Yamashita, Isao Kashima, and S. Ohno. The role of smg-1 in nonsense-mediated mrna decay. Biochimica et biophysica acta, 1754 1-2:305-15, Dec 2005. URL: https://doi.org/10.1016/j.bbapap.2005.10.002, doi:10.1016/j.bbapap.2005.10.002. This article has 101 citations.
11. (yamashita2009smg8andsmg9 pages 1-2): Akio Yamashita, Natsuko Izumi, Isao Kashima, Tetsuo Ohnishi, Bonnie Saari, Yukiko Katsuhata, Reiko Muramatsu, Tomoko Morita, Akihiro Iwamatsu, Takahisa Hachiya, Rie Kurata, Hisashi Hirano, Philip Anderson, and Shigeo Ohno. Smg-8 and smg-9, two novel subunits of the smg-1 complex, regulate remodeling of the mrna surveillance complex during nonsense-mediated mrna decay. Genes & Development, 23:1091-1105, May 2009. URL: https://doi.org/10.1101/gad.1767209, doi:10.1101/gad.1767209. This article has 295 citations.
12. (yamashita2009smg8andsmg9 pages 14-16): Akio Yamashita, Natsuko Izumi, Isao Kashima, Tetsuo Ohnishi, Bonnie Saari, Yukiko Katsuhata, Reiko Muramatsu, Tomoko Morita, Akihiro Iwamatsu, Takahisa Hachiya, Rie Kurata, Hisashi Hirano, Philip Anderson, and Shigeo Ohno. Smg-8 and smg-9, two novel subunits of the smg-1 complex, regulate remodeling of the mrna surveillance complex during nonsense-mediated mrna decay. Genes & Development, 23:1091-1105, May 2009. URL: https://doi.org/10.1101/gad.1767209, doi:10.1101/gad.1767209. This article has 295 citations.
13. (zhu2019cryoemstructureof pages 1-2): Li Zhu, Liang Li, Y. Qi, Zishuo Yu, and Yanhui Xu. Cryo-em structure of smg1–smg8–smg9 complex. Cell Research, 29:1027-1034, Nov 2019. URL: https://doi.org/10.1038/s41422-019-0255-3, doi:10.1038/s41422-019-0255-3. This article has 37 citations and is from a domain leading peer-reviewed journal.
14. (ariaspalomo2011thenonsensemediatedmrna pages 12-13): E. Arias-Palomo, A. Yamashita, I. S. Fernández, R. Núñez-Ramírez, Y. Bamba, Natsuko Izumi, S. Ohno, and O. Llorca. The nonsense-mediated mrna decay smg-1 kinase is regulated by large-scale conformational changes controlled by smg-8. Genes & development, 25 2:153-64, Jan 2011. URL: https://doi.org/10.1101/gad.606911, doi:10.1101/gad.606911. This article has 100 citations.
15. (ariaspalomo2011thenonsensemediatedmrna pages 7-9): E. Arias-Palomo, A. Yamashita, I. S. Fernández, R. Núñez-Ramírez, Y. Bamba, Natsuko Izumi, S. Ohno, and O. Llorca. The nonsense-mediated mrna decay smg-1 kinase is regulated by large-scale conformational changes controlled by smg-8. Genes & development, 25 2:153-64, Jan 2011. URL: https://doi.org/10.1101/gad.606911, doi:10.1101/gad.606911. This article has 100 citations.
16. (conti2021cryoemreconstructionsof pages 17-19): L. M. Langer, F. Bonneau, Y. Gat, and E. Conti. Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, Jul 2021. URL: https://doi.org/10.1101/2021.07.28.454180, doi:10.1101/2021.07.28.454180. This article has 31 citations and is from a domain leading peer-reviewed journal.
17. (conti2021cryoemreconstructionsof pages 27-36): L. M. Langer, F. Bonneau, Y. Gat, and E. Conti. Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, Jul 2021. URL: https://doi.org/10.1101/2021.07.28.454180, doi:10.1101/2021.07.28.454180. This article has 31 citations and is from a domain leading peer-reviewed journal.
18. (conti2021cryoemreconstructionsof pages 3-6): L. M. Langer, F. Bonneau, Y. Gat, and E. Conti. Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, Jul 2021. URL: https://doi.org/10.1101/2021.07.28.454180, doi:10.1101/2021.07.28.454180. This article has 31 citations and is from a domain leading peer-reviewed journal.
19. (conti2021cryoemreconstructionsof pages 6-8): L. M. Langer, F. Bonneau, Y. Gat, and E. Conti. Cryo-em reconstructions of inhibitor-bound smg1 kinase reveal an autoinhibitory state dependent on smg8. eLife, Jul 2021. URL: https://doi.org/10.1101/2021.07.28.454180, doi:10.1101/2021.07.28.454180. This article has 31 citations and is from a domain leading peer-reviewed journal.
20. (grimson2004smg1isa pages 1-2): Andrew Grimson, Sean O’Connor, Carrie Loushin Newman, and Philip Anderson. Smg-1 is a phosphatidylinositol kinase-related protein kinase required for nonsense-mediated mrna decay incaenorhabditis elegans. Molecular and Cellular Biology, 24:7483-7490, Sep 2004. URL: https://doi.org/10.1128/mcb.24.17.7483-7490.2004, doi:10.1128/mcb.24.17.7483-7490.2004. This article has 172 citations and is from a domain leading peer-reviewed journal.
21. (langer2020structureofsubstratebound pages 1-2): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
22. (langer2020structureofsubstratebound pages 10-11): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
23. (langer2020structureofsubstratebound pages 14-14): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
24. (langer2020structureofsubstratebound pages 2-5): Lukas M Langer, Yair Gat, Fabien Bonneau, and Elena Conti. Structure of substrate-bound smg1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. eLife, May 2020. URL: https://doi.org/10.7554/elife.57127, doi:10.7554/elife.57127. This article has 36 citations and is from a domain leading peer-reviewed journal.
25. (llorcacardenosa2022smg8smg9heterodimerloss pages 6-6): Marta J. Llorca-Cardenosa, Lauren I. Aronson, Dragomir B. Krastev, Jadwiga Nieminuszczy, John Alexander, Feifei Song, Malgorzata Dylewska, Ronan Broderick, Rachel Brough, Astrid Zimmermann, Frank T. Zenke, Bora Gurel, Ruth Riisnaes, Ana Ferreira, Theodoros Roumeliotis, Jyoti Choudhary, Stephen J. Pettitt, Johann de Bono, Andres Cervantes, Syed Haider, Wojciech Niedzwiedz, Christopher J. Lord, and Irene Y. Chong. Smg8/smg9 heterodimer loss modulates smg1 kinase to drive atr inhibitor resistance. Cancer Research, 82:3962-3973, Oct 2022. URL: https://doi.org/10.1158/0008-5472.can-21-4339, doi:10.1158/0008-5472.can-21-4339. This article has 13 citations and is from a highest quality peer-reviewed journal.
26. (llorcacardenosa2022smg8smg9heterodimerloss pages 7-8): Marta J. Llorca-Cardenosa, Lauren I. Aronson, Dragomir B. Krastev, Jadwiga Nieminuszczy, John Alexander, Feifei Song, Malgorzata Dylewska, Ronan Broderick, Rachel Brough, Astrid Zimmermann, Frank T. Zenke, Bora Gurel, Ruth Riisnaes, Ana Ferreira, Theodoros Roumeliotis, Jyoti Choudhary, Stephen J. Pettitt, Johann de Bono, Andres Cervantes, Syed Haider, Wojciech Niedzwiedz, Christopher J. Lord, and Irene Y. Chong. Smg8/smg9 heterodimer loss modulates smg1 kinase to drive atr inhibitor resistance. Cancer Research, 82:3962-3973, Oct 2022. URL: https://doi.org/10.1158/0008-5472.can-21-4339, doi:10.1158/0008-5472.can-21-4339. This article has 13 citations and is from a highest quality peer-reviewed journal.
27. (nicholson2010nonsensemediatedmrnadecay pages 16-18): Pamela Nicholson, Hasmik Yepiskoposyan, Stefanie Metze, Rodolfo Zamudio Orozco, Nicole Kleinschmidt, and Oliver Mühlemann. Nonsense-mediated mrna decay in human cells: mechanistic insights, functions beyond quality control and the double-life of nmd factors. Cellular and Molecular Life Sciences, 67:677-700, Feb 2010. URL: https://doi.org/10.1007/s00018-009-0177-1, doi:10.1007/s00018-009-0177-1. This article has 406 citations and is from a domain leading peer-reviewed journal.
28. (nicholson2010nonsensemediatedmrnadecay pages 6-7): Pamela Nicholson, Hasmik Yepiskoposyan, Stefanie Metze, Rodolfo Zamudio Orozco, Nicole Kleinschmidt, and Oliver Mühlemann. Nonsense-mediated mrna decay in human cells: mechanistic insights, functions beyond quality control and the double-life of nmd factors. Cellular and Molecular Life Sciences, 67:677-700, Feb 2010. URL: https://doi.org/10.1007/s00018-009-0177-1, doi:10.1007/s00018-009-0177-1. This article has 406 citations and is from a domain leading peer-reviewed journal.
29. (nicholson2014anovelphosphorylationindependent pages 14-15): P. Nicholson, Christoph Josi, Hitomi Kurosawa, A. Yamashita, and O. Mühlemann. A novel phosphorylation-independent interaction between smg6 and upf1 is essential for human nmd. Nucleic Acids Research, 42:9217-9235, Jul 2014. URL: https://doi.org/10.1093/nar/gku645, doi:10.1093/nar/gku645. This article has 101 citations and is from a highest quality peer-reviewed journal.
30. (padariya2024invitrocrosslinking pages 15-16): M. Padariya, B. Vojtěšek, Ted R Hupp, and U. Kalathiya. In vitro cross-linking ms reveals smg1–upf2–smg7 assembly as molecular partners within the nmd surveillance. International Journal of Molecular Sciences, Mar 2024. URL: https://doi.org/10.3390/ijms25063182, doi:10.3390/ijms25063182. This article has 1 citations and is from a peer-reviewed journal.
31. (padariya2024invitrocrosslinking pages 2-3): M. Padariya, B. Vojtěšek, Ted R Hupp, and U. Kalathiya. In vitro cross-linking ms reveals smg1–upf2–smg7 assembly as molecular partners within the nmd surveillance. International Journal of Molecular Sciences, Mar 2024. URL: https://doi.org/10.3390/ijms25063182, doi:10.3390/ijms25063182. This article has 1 citations and is from a peer-reviewed journal.
32. (usuki2013inhibitionofsmg8 pages 1-2): Fusako Usuki, Akio Yamashita, Tadafumi Shiraishi, Atsushi Shiga, Osamu Onodera, Itsuro Higuchi, and Shigeo Ohno. Inhibition of smg-8, a subunit of smg-1 kinase, ameliorates nonsense-mediated mrna decay-exacerbated mutant phenotypes without cytotoxicity. Proceedings of the National Academy of Sciences, 110:15037-15042, Aug 2013. URL: https://doi.org/10.1073/pnas.1300654110, doi:10.1073/pnas.1300654110. This article has 38 citations.
33. (yamashita2001…3kinaserelatedprotein pages 1-2): A Yamashita, T Ohnishi, and I Kashima. … 3-kinase-related protein kinase, associates with components of the mrna surveillance complex and is involved in the regulation of nonsense-mediated mrna decay. Unknown journal, 2001.
34. (yamashita2001…3kinaserelatedprotein pages 7-9): A Yamashita, T Ohnishi, and I Kashima. … 3-kinase-related protein kinase, associates with components of the mrna surveillance complex and is involved in the regulation of nonsense-mediated mrna decay. Unknown journal, 2001.
35. (yamashita2001…3kinaserelatedprotein pages 9-11): A Yamashita, T Ohnishi, and I Kashima. … 3-kinase-related protein kinase, associates with components of the mrna surveillance complex and is involved in the regulation of nonsense-mediated mrna decay. Unknown journal, 2001.
36. (yamashita2005theroleof pages 1-3): A. Yamashita, Isao Kashima, and S. Ohno. The role of smg-1 in nonsense-mediated mrna decay. Biochimica et biophysica acta, 1754 1-2:305-15, Dec 2005. URL: https://doi.org/10.1016/j.bbapap.2005.10.002, doi:10.1016/j.bbapap.2005.10.002. This article has 101 citations.
37. (yamashita2009smg8andsmg9 pages 3-4): Akio Yamashita, Natsuko Izumi, Isao Kashima, Tetsuo Ohnishi, Bonnie Saari, Yukiko Katsuhata, Reiko Muramatsu, Tomoko Morita, Akihiro Iwamatsu, Takahisa Hachiya, Rie Kurata, Hisashi Hirano, Philip Anderson, and Shigeo Ohno. Smg-8 and smg-9, two novel subunits of the smg-1 complex, regulate remodeling of the mrna surveillance complex during nonsense-mediated mrna decay. Genes & Development, 23:1091-1105, May 2009. URL: https://doi.org/10.1101/gad.1767209, doi:10.1101/gad.1767209. This article has 295 citations.
38. (yamashita2009smg8andsmg9 pages 9-10): Akio Yamashita, Natsuko Izumi, Isao Kashima, Tetsuo Ohnishi, Bonnie Saari, Yukiko Katsuhata, Reiko Muramatsu, Tomoko Morita, Akihiro Iwamatsu, Takahisa Hachiya, Rie Kurata, Hisashi Hirano, Philip Anderson, and Shigeo Ohno. Smg-8 and smg-9, two novel subunits of the smg-1 complex, regulate remodeling of the mrna surveillance complex during nonsense-mediated mrna decay. Genes & Development, 23:1091-1105, May 2009. URL: https://doi.org/10.1101/gad.1767209, doi:10.1101/gad.1767209. This article has 295 citations.