

Synthesis of kinase inhibitors containing a pentafluorosulfanyl moiety.

Supojjane Sansook^a, Cory A. Ocasio^a, Iain J. Day^a, Graham J. Tizzard^b, Simon J. Coles^b, Oleg Fedorov^c, James M. Bennett^c, Jonathan M. Elkins^{c,d}, John Spencer^{a,*}

^a*Dept of Chemistry, School of Life Sciences, University of Sussex, Falmer, BN1 9QJ, UK.*

^bUK National Crystallography Service, Chemistry, University of Southampton, Highfield, Southampton, SO17 1BJ, U.K. ^cStructural Genomics Consortium, Nuffield Department of Clinical Medicine, University of Oxford, Oxford, OX3 7DQ, UK. ^dStructural Genomics Consortium, Universidade Estadual de Campinas, Campinas, SP 13083-886, Brazil

^eStructural Genomics Consortium, Universidade Estadual de Campinas, Campinas, SP 13083-886, Brazil.

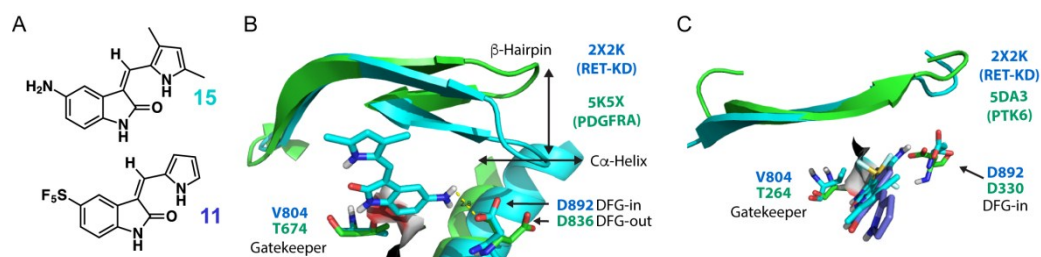


Figure S1. Structural studies comparing binding modes of methylidene indolinone-based kinase inhibitors **11** and **15** (A) with active and inactive kinase domains. Compound **15** (A) was co-crystallised with RET kinase domain (B, PDB: 2X2K) forcing a “DFG-in” kinase conformation. This **15**-bound RET conformation was aligned with the PDGFRA crystal structure (B, PDB: 5K5X) revealing gross conformational shifts around the ATP-binding pocket, particularly between the RET and PDGFRA b-hairpin and Ca-helix (B), and compared to RET, the PDGFRA DFG catalytic-motif aspartic acid is pointing outside of the ATP-binding pocket; evidence for an inactive kinase conformation. Compound **11** displayed the greatest potency in the series against PDGFRA, a receptor tyrosine kinase containing a threonine gatekeeper. RET has a valine gatekeeper, and thus PTK6 (C, PDB: 5DA3), a non-receptor tyrosine kinase containing a threonine gatekeeper, was selected for docking studies with compound **10** - **11** (Fig. 5, main article) to ascertain the molecular determinants for the superior potency of **11** vs **10**. The alignment between **15**-bound RET and **11**-docked PTK6 (C) reveals very similar binding modes between compounds **11** and **15** and an agreement in PTK6 and RET kinase conformation, both in the active state.

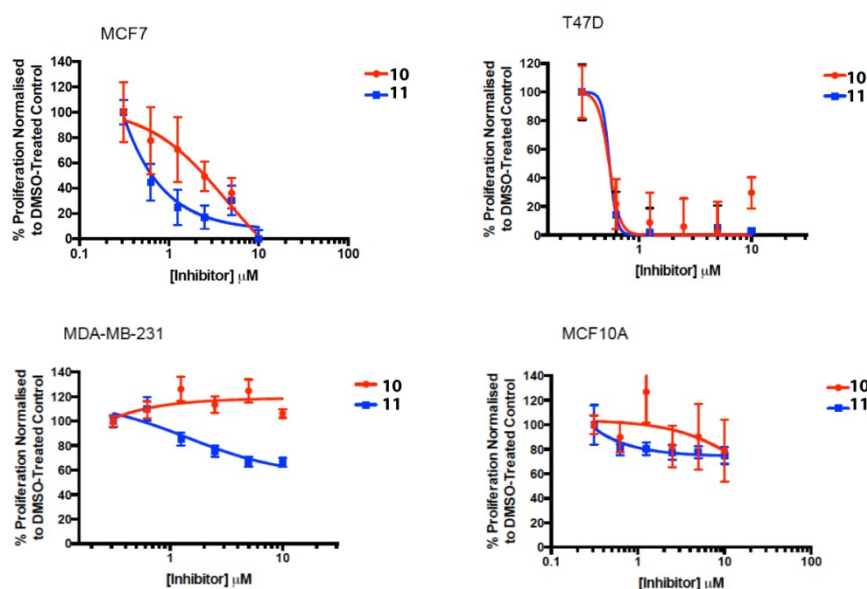
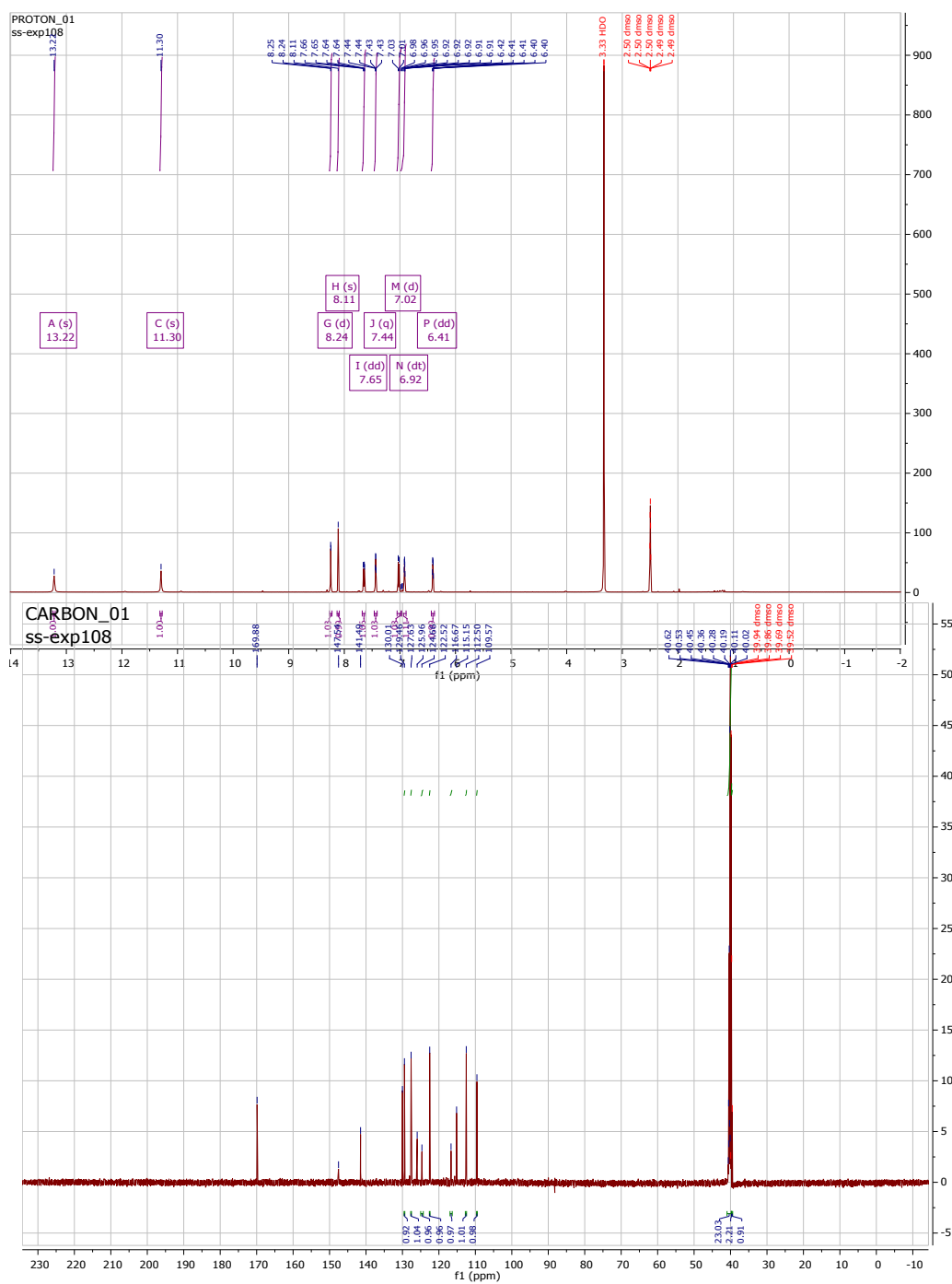
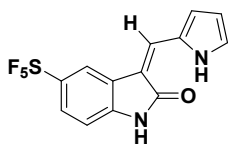
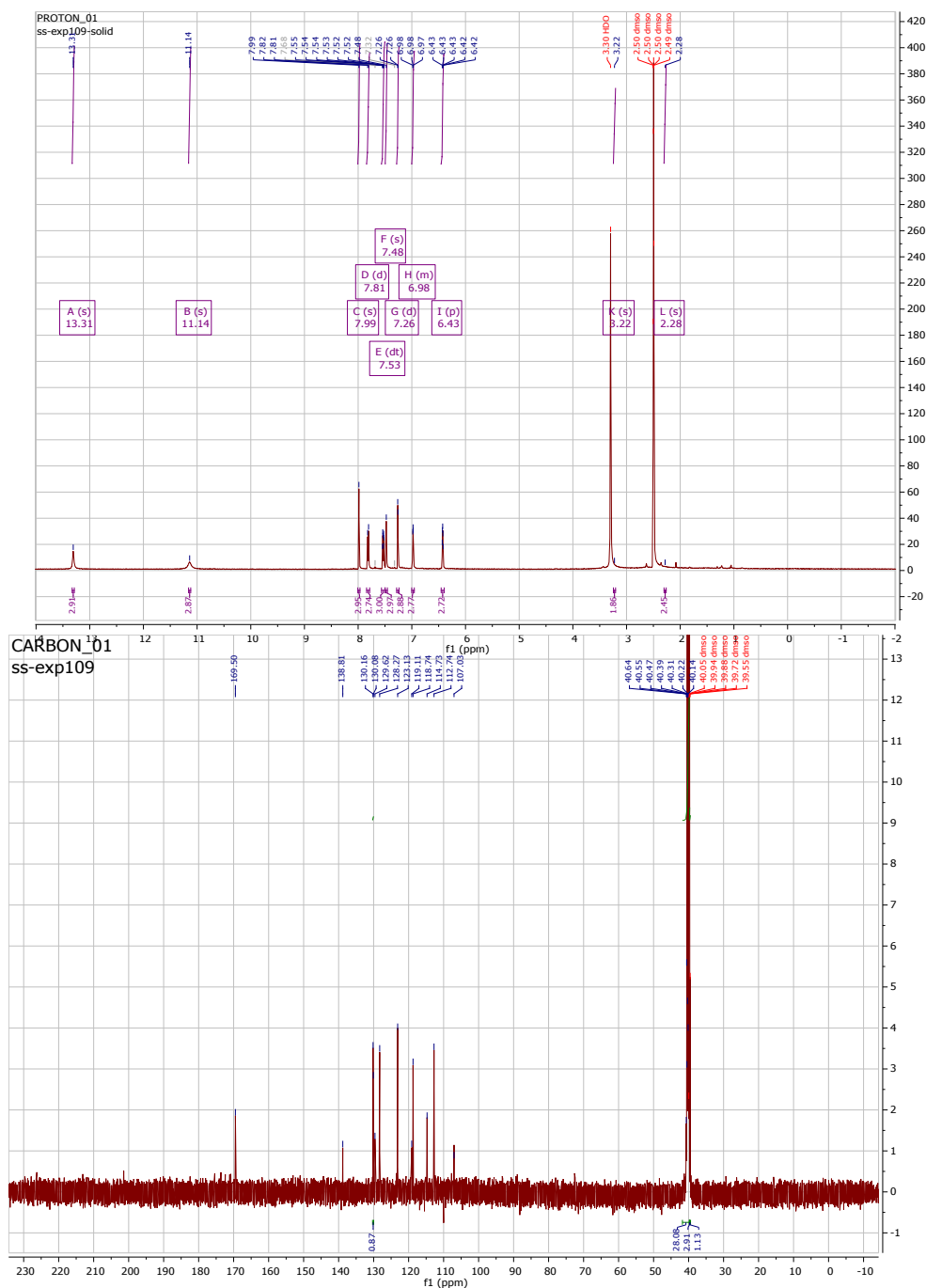
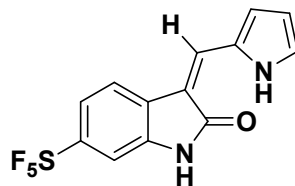


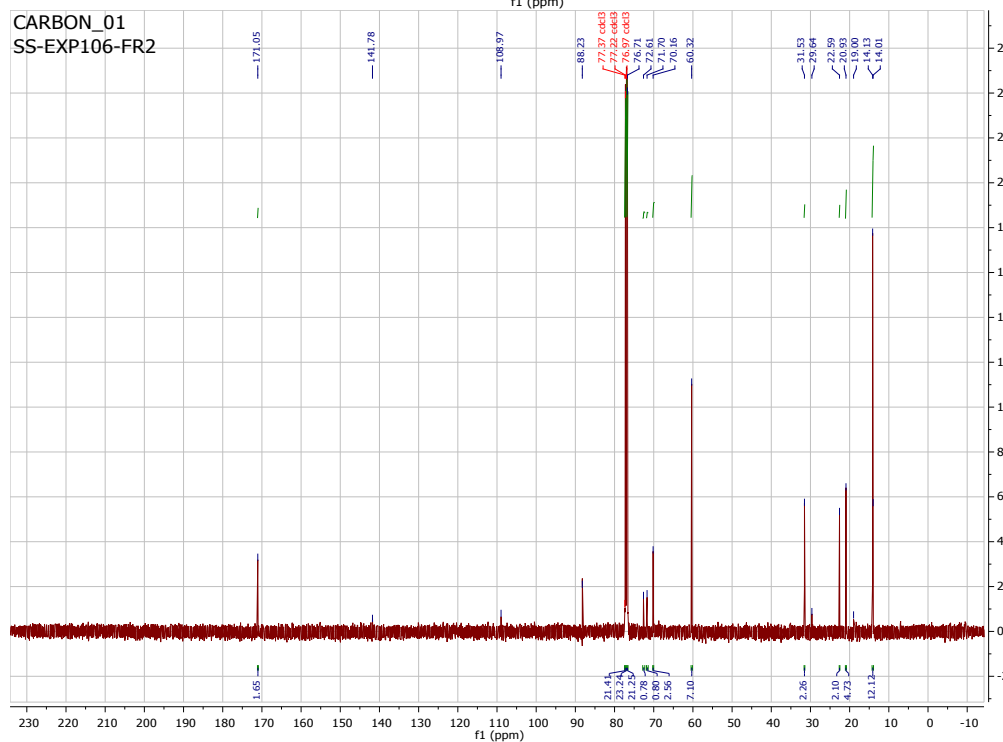
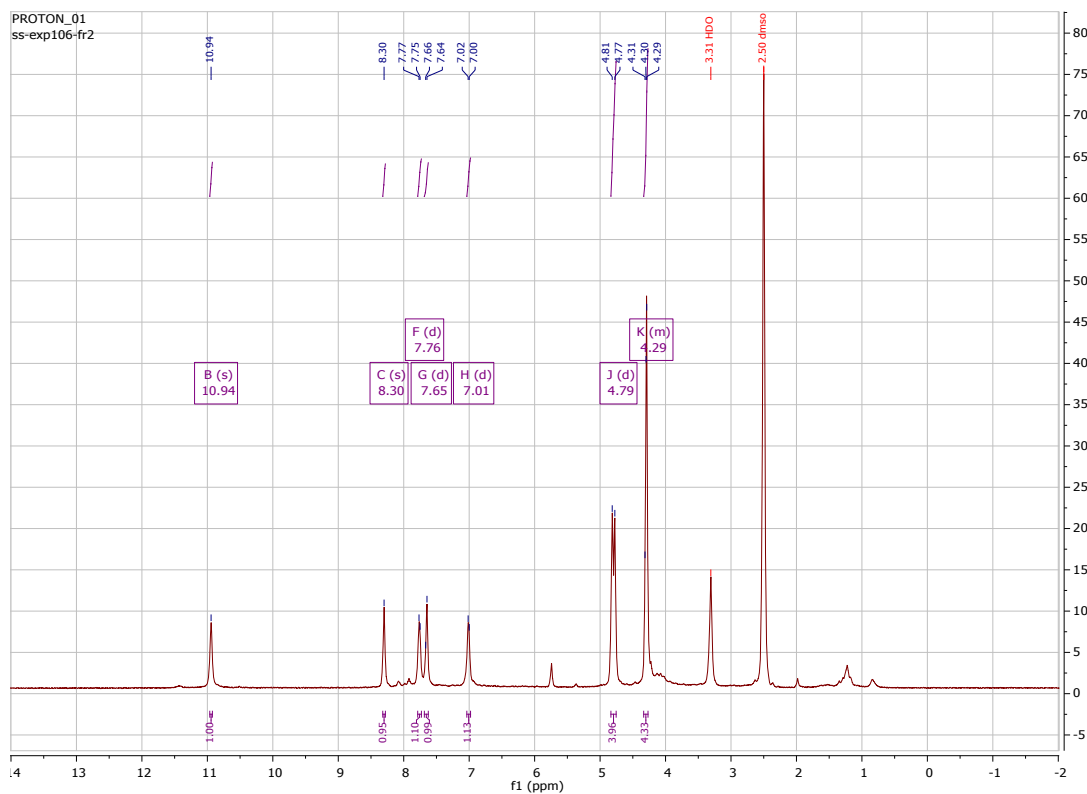
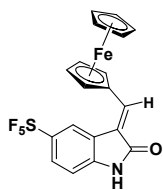
Figure S2. Proliferation assays. Dose-dependent inhibition of MCF7, T47D MDA-BM-231 and MCF10A cells by compounds **10** and **11**.

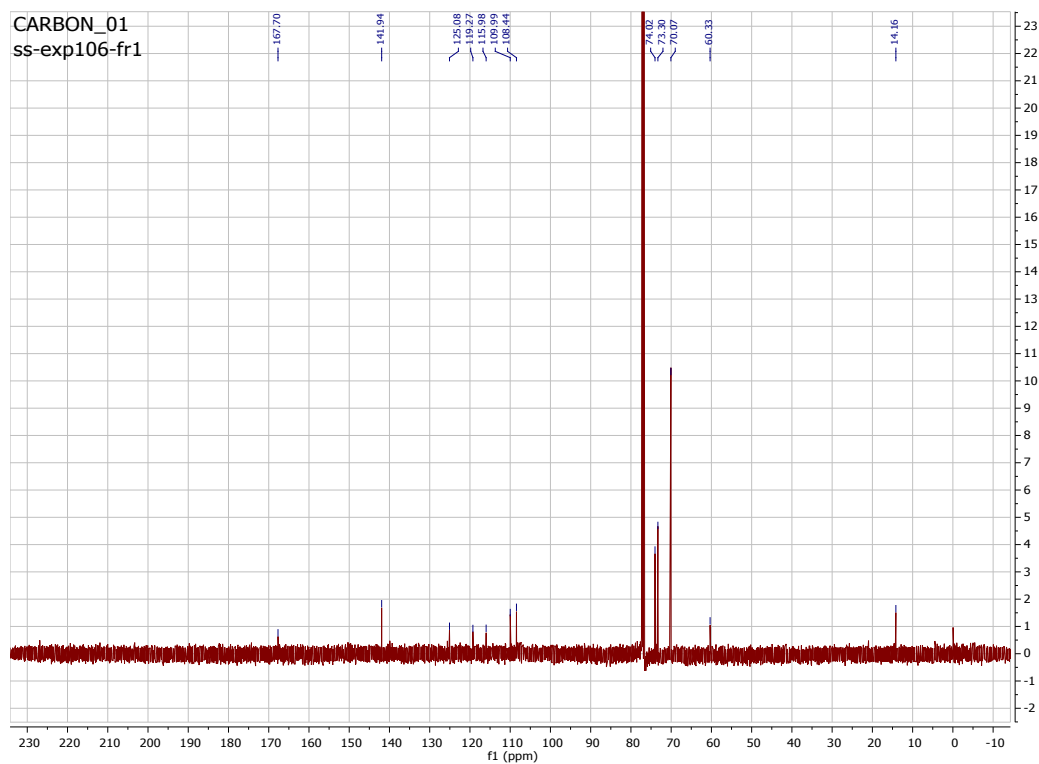
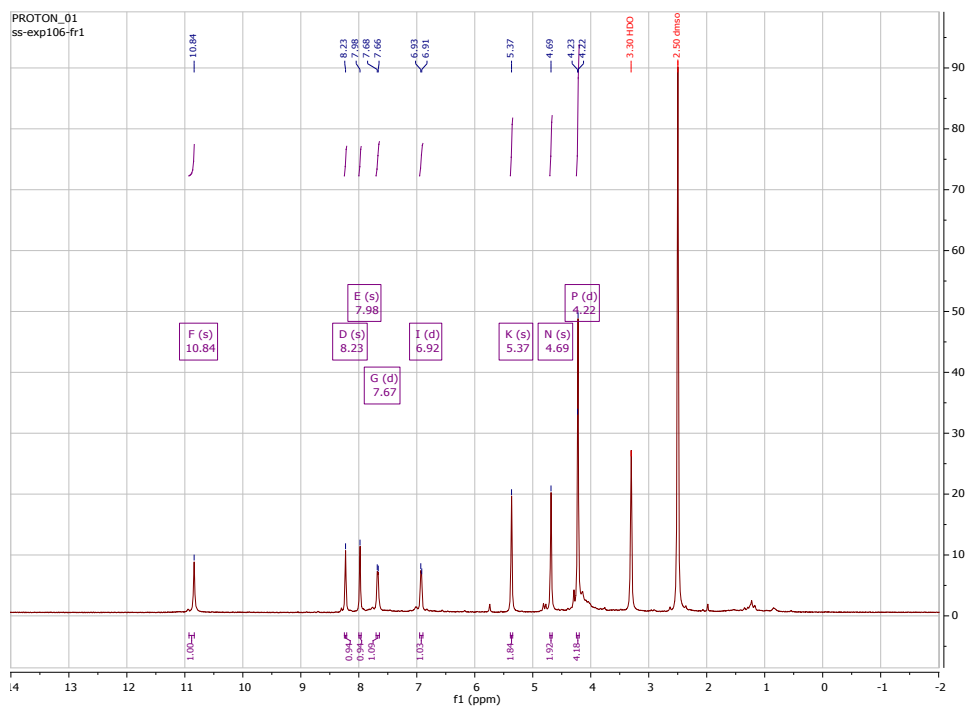
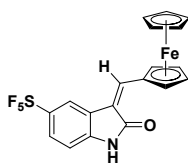
Fig S3. NMRs

(Z)-3-((1H-Pyrrol-2-yl)methylene)-5-pentafluorosulfonylindoline-2-one

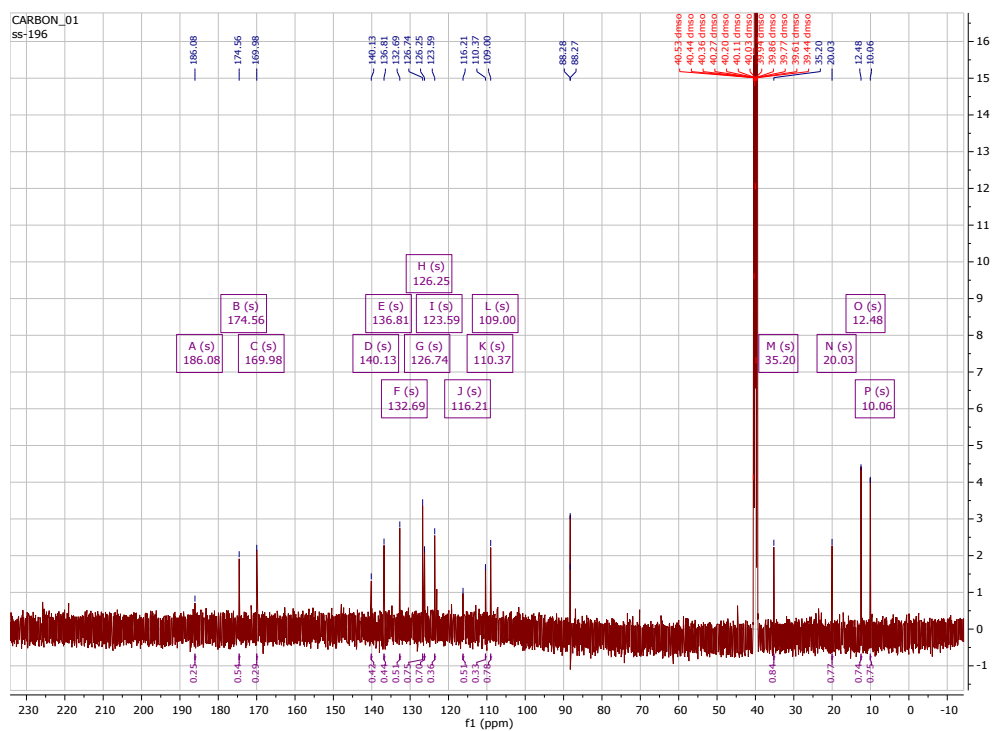
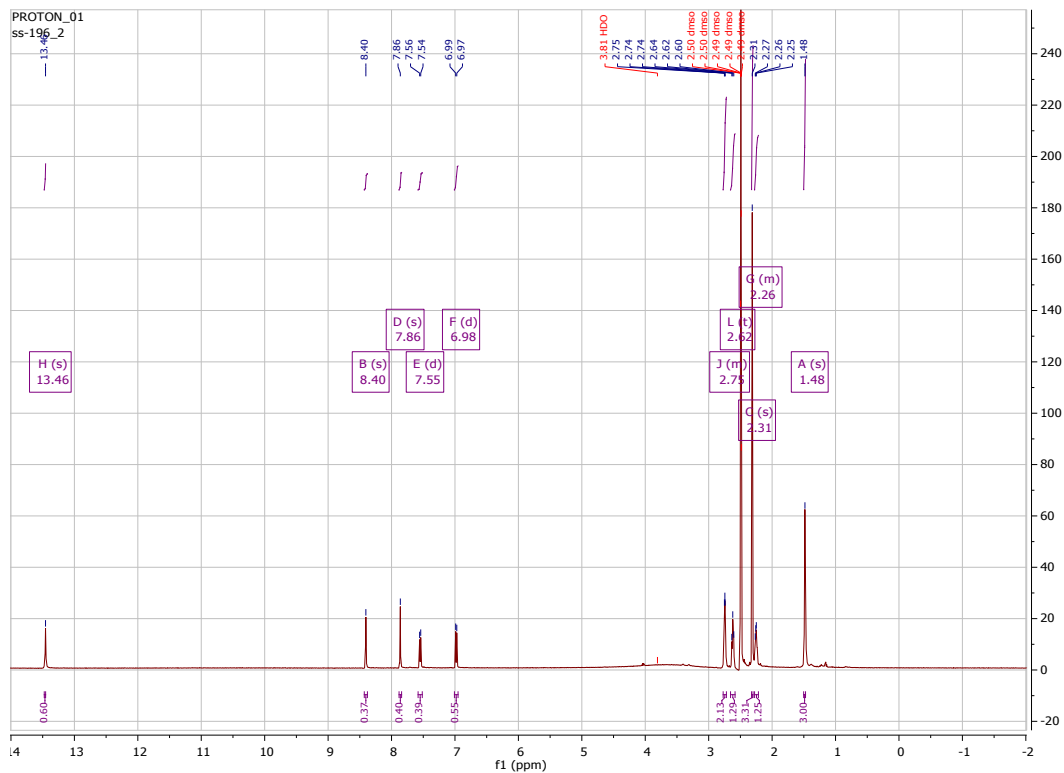
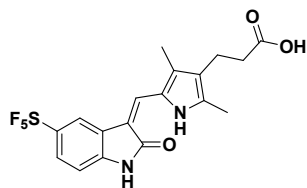
(Z)-3-((1H-Pyrrol-2-yl)methylene)-6-pentafluorosulfanylindoline-2-one



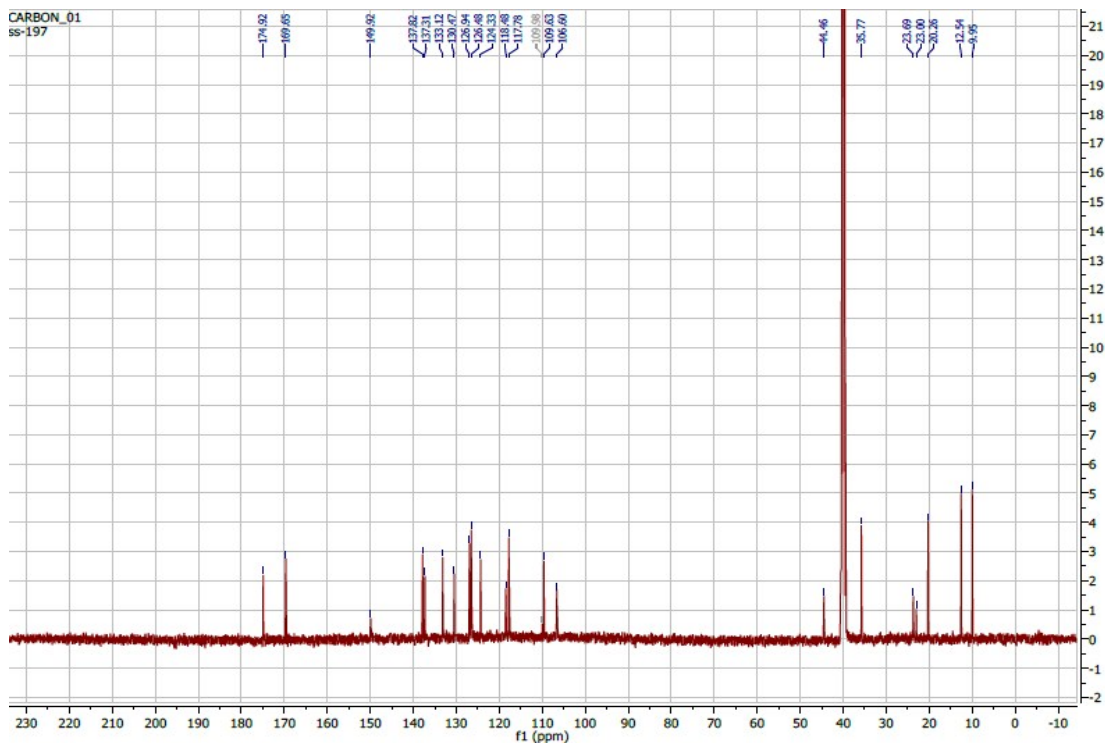
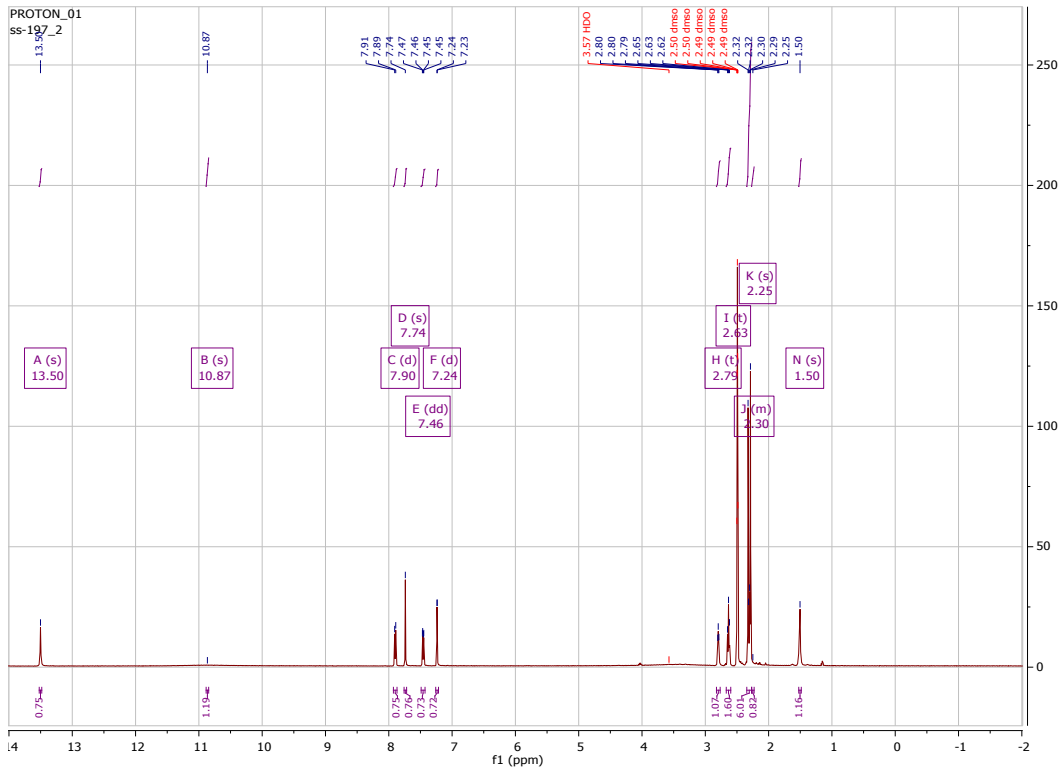
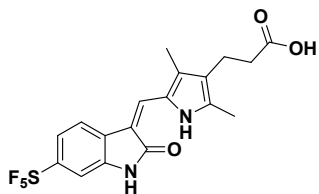
(E)-5-Pentafluorosulfanyl-3-ferrocenylindolin-2-one**(Z)-5-Pentafluorosulfanyl-3-ferrocenylindolin-2-one**



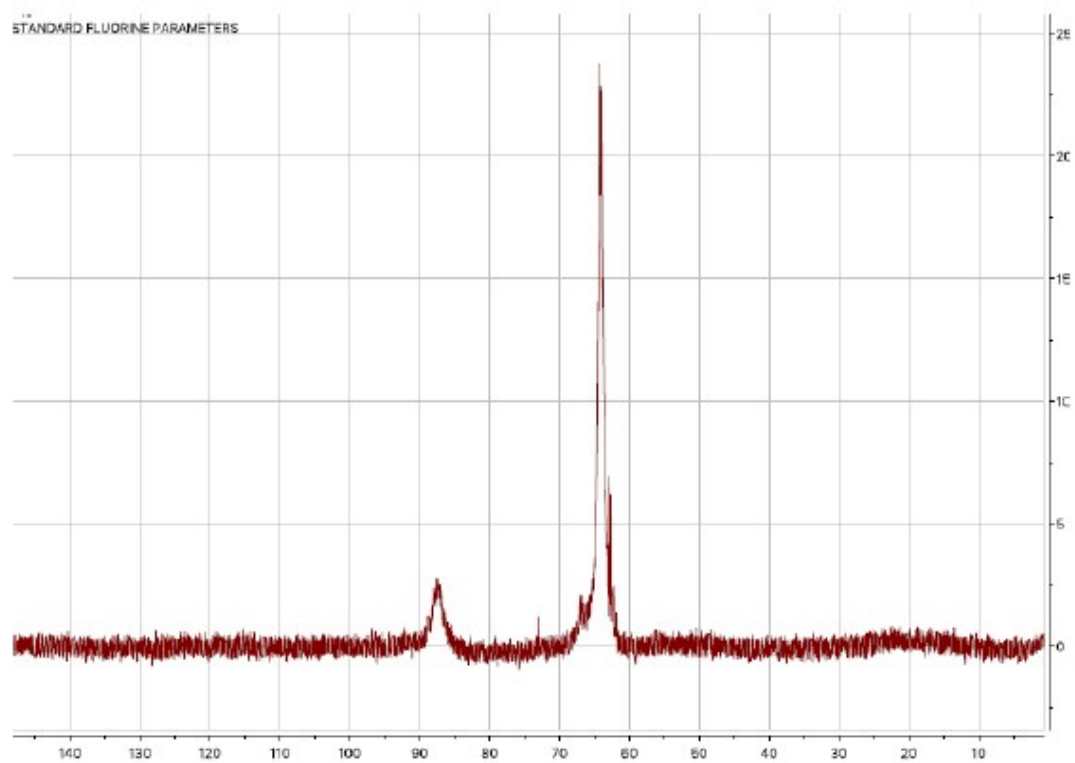
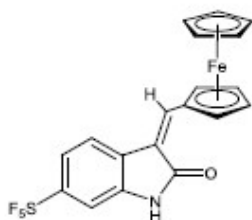
(Z)-3-(2,4-dimethyl-5-((5-pentafluorosulfanyl-2-oxindolin-3-ylidene)methyl)-1H-pyrrol-3-yl)propanoic acid

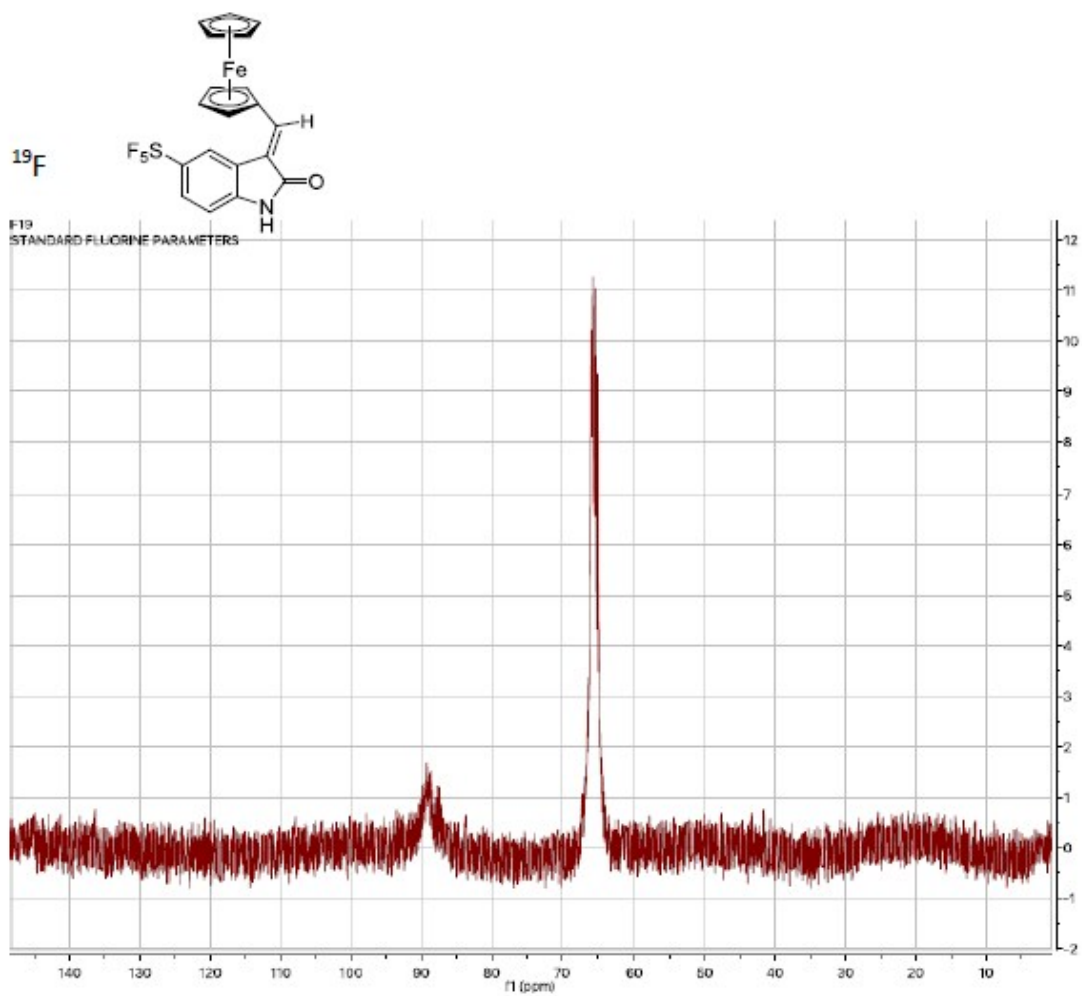


(Z)-3-(2,4-dimethyl-5-((6-pentafluorosulfanyl-2-oxoindolin-3-ylidene)methyl)-1H-pyrrol-3-yl)propanoic acid



^{19}F : (broad)





^{19}F 