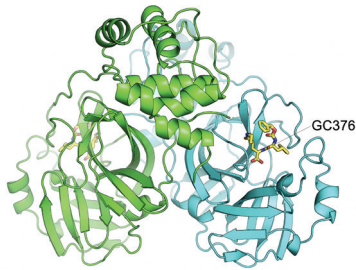
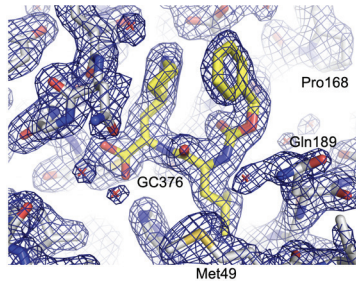


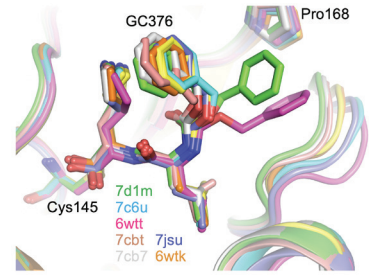
a



b



c



d

M49

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SARS2 SCFRKMAHPSCKVECCMVQVTCGTTLNGLWLDLVVYCPRHVICSEMLNENMEDLLIRKSNENSLMOAGN...VQIRVICHSONCVLKKVDTANEKTPKYKIVRIQPGOTHSVLAC 117
SARS2 SCFRKMAHPSCKVECCMVQVTCGTTLNGLWLDLVVYCPRHVICSEMLNENMEDLLIRKSNENSLMOAGN...VQIRVICHSONCVLKKVDTANEKTPKYKIVRIQPGOTHSVLAC 117
HKU9 ACGLTRMAHPSCLVBPCLVKNVYCSMLNLNGIWLIDNFIICPRHVICSRDELANDPPIISMRAAYDHHSONG...HNIRVICHTEGSLIKLIVDNNKTPAHSIRVSTQAMSLILAC 117
MHV SCIVRVAHSTKVEPCLVSVTICNMNLGLWLDLVVYCPRHVICSSALMTDIPFNICRVTSDDCMHSGR...MSTIVMSYQCCQVIVTLDQNNPKHSQVVRREPTVLA 117
MERS SCLMNSHESDVEACVQVTCGSMNLGLWLDLVVYCPRHVICPADQLSDENPDALLISIMNHSQORHIGAPANRVAHACQITLKLIVDANISSTFAHTTIVKREASVILAC 120
229E ACLKMAQPSGCVKCVVRRVYCGNTVNLGLWLDLVVYCPRHVICIASN.TTTSATVDHEYSIMRILNNSISLISGT...AFICVVCATVHCVTIKIKVQTNMHTPRHSRITLKEEGNLLAC 116
NL63 SCLKMAQPSGCVKCVVRRVYCGSTVNLGLWLDLVVYCPRHVICIASN.TTTLIDVDHAYSTRILNNSISLISGT...VFLCVVSVTLHC SVIRIKVQSNVHTPRHSRITLKEEGNLLAC 116
IBV ACFRKLVSSESAVEKCIIVSVSRGNLNLGLWLDLVVYCPRHVICIASN.TTTSATVDHEYSIMRILNNSISLISGT...VFLCVVSVTLHC SVIRIKVQSNVHTPRHSRITLKEEGNLLAC 115
    
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P168

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SARS2 VNCSESGVYQCAMRPNFTIKGSFINGSCGSGVGNIDY.DCVSFCYMHMEIPICVFACTDLECKFYCFVDRQTACAAGTDTTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 230
SARS1 VNCSESGVYQCAMRPNFTIKGSFINGSCGSGVGNIDY.DCVSFCYMHMEIPICVFACTDLECKFYCFVDRQTACAAGTDTTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 230
HKU9 VDCPLGAVYTCITLRSKCHMRASFCGSCGSECFVHNG.KEVCFYDHLLELPCVHAGDDESQVYCFVDRQVFLAAPHCTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 230
MHV VNCSESGVYQCAMRPNFTIKGSFINGSCGSGVGNIDY.DCVSFCYMHMEIPICVFACTDLECKFYCFVDRQTACAAGTDTTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 230
MERS VNCSESGVYQCAMRPNFTIKGSFINGSCGSGVGNIDY.DCVSFCYMHMEIPICVFACTDLECKFYCFVDRQTACAAGTDTTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 233
229E VDCCAQCFVGNMRENIWIKGSFINGSCGSGVGNIDY.DCVSFCYMHMEIPICVFACTDLECKFYCFVDRQVFLAAPHCTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 229
NL63 VECIASVFCVGNIRNFTIKGSFINGSCGSGVGNIDY.DCVSFCYMHMEIPICVFACTDLECKFYCFVDRQVFLAAPHCTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 230
IBV VCCTVICLVPVIMRNSCHIRASFTIACACGSGVGNIEK.GVNVNFCYMHMEIPICVFACTDLECKFYCFVDRQVFLAAPHCTITVNVLAWLAAVINGDR.....WFINRFTTLLNDF 234
    
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Q189

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SARS2 NLVVMKYNYEPLTQDHVDILGPTSAQTCIAVLDMCASLKEFLQNGMNCRTILGSALELEDFTEFDVVRCCSGVTHC 306
SARS1 NLVVMKYNYEPLTQDHVDILGPTSAQTCIAVLDMCASLKEFLQNGMNCRTILGSALELEDFTEFDVVRCCSGVTHC 306
HKU9 NCVVMKYNYEPLTQDHVDILGPTSAQTCIAVLDMCASLKEFLQNGMNCRTILGSALELEDFTEFDVVRCCSGVTHC 306
MHV VVMVMKYNYEPLTQDHVDILGPTSAQTCIAVLDMCASLKEFLQNGMNCRTILGSALELEDFTEFDVVRCCSGVTHC 306
MERS NRRLLANQTEFFVCT..OSVDMLAVKTCVAVLEQLYAIQVYTTGQCKKILGYSSEDEFTEFLAEVVKMCGVNLG 302
229E NRRLLANQTEFFVCT..DAFSLAAKTCVAVLEQLYAIQVYTTGQCKKILGYSSEDEFTEFLAEVVKMCGVNLG 302
NL63 NRRLLANQTEFFVCT..ECYSILAAKTCVAVLEQLYAIQVYTTGQCKKILGYSSEDEFTEFLAEVVKMCGVNLG 303
IBV NRRLLANQTEFFVCT..TAITKLSAITCVDVCKLRTIMVKS.AQWSDPILCQYNEDEFTEFLAEVVKMCGVNLG 307
    
```

Legend:
 non conserved
 ≥ 50% conserved

e

