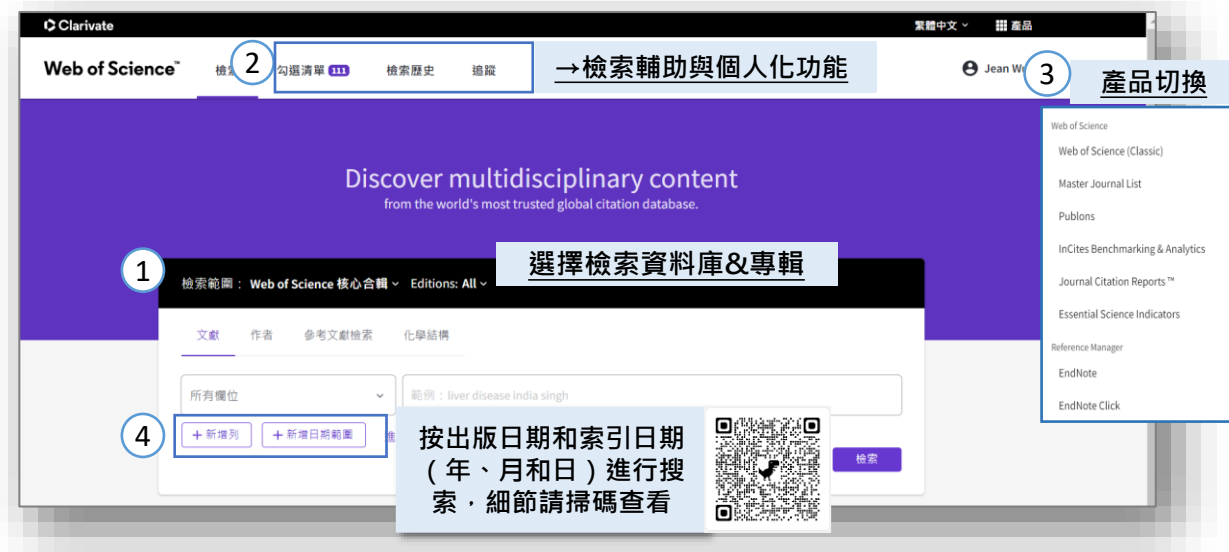


New Web of Science 更新重點索引

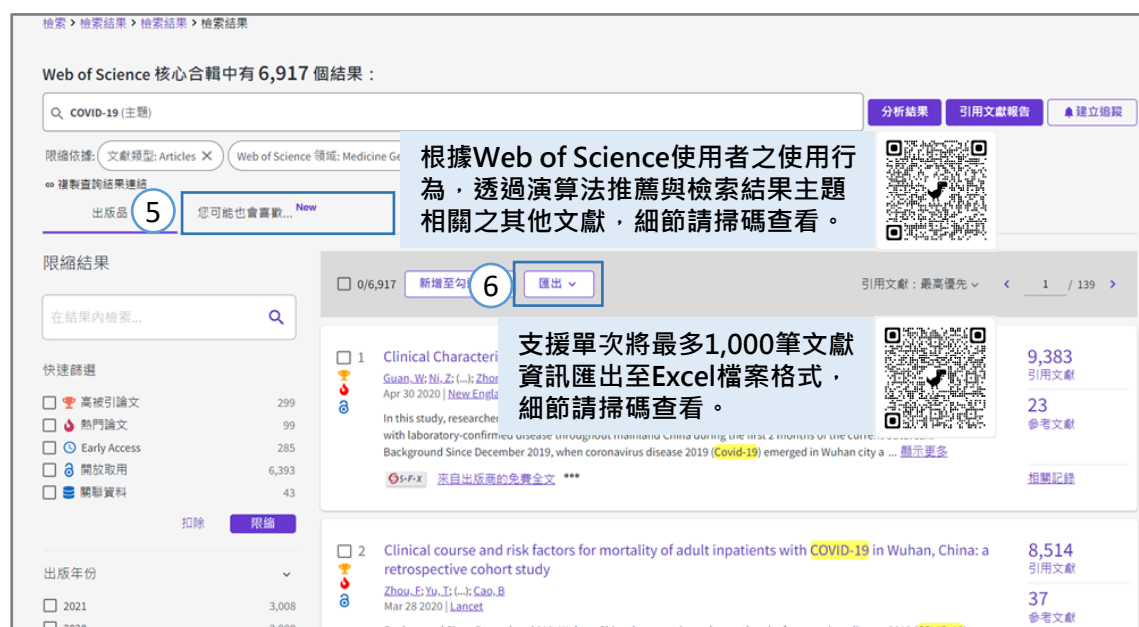
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Structural basis of receptor recognition by SARS-CoV-2

關聯資料

作者: Shang, J (Shang, Jian)¹; Ye, G (Ye, Gang)¹; Shi, K (Shi, Ke)²; Wan, YS (Wan, Geng, QB (Geng, Qibin)¹; Auerbach, A (Auerbach, Ashley)¹; Li, F (Li, Fang)¹
檢視 Web of Science ResearcherID 和 ORCID (Clarivate 提供)

NATURE
卷冊: 581 期: 7807 頁面: 221-+
DOI: 10.1038/s41586-020-2179-y
出版時間: MAY 2020
早期取閱: MAR 2020
文獻類型: Article

摘要
The crystal structure of the receptor-binding domain of the SARS-CoV-2 spike in complex with human ACE2, sheds light on the structural features that increase its binding affinity to ACE2. A key to tackling this pandemic is to understand the receptor recognition and host range. SARS-CoV-2 and SARS-CoV recognize the same receptor-angiotensin-converting enzyme 2 (ACE2). In comparison with the SARS-CoV RBD, an ACE2-binding ridge in SARS-CoV-2 stabilizes two virus-binding hotspots at the RBD-ACE2-binding affinity. Additionally, we show that RaTG13, a bat coronavirus that is closely related to SARS-CoV-2, has a different ACE2 recognition site. The differences among SARS-CoV-2, SARS-CoV and RaTG13 in ACE2 recognition shed light on the evolution of the virus. This study provides guidance for intervention strategies that target receptor recognition.

關鍵字
Keywords Plus: ACUTE RESPIRATORY SYNDROME; SARS-CORONAVIRUS; SPIKE PROTEIN; RECEPTOR; TARGET; COV

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領域/分類
研究領域: Science & Technology - Other Topics

關聯資料 1 (來自 Data Citation Index)

7

Author Impact Beamplots 提供作者影響力指標，協助評估研究人員影響力，細節請掃碼查看。

8

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