

Supplementary Materials

Caption Clustering. The captions extracted from the PDF articles were clustered using TF-IDF representation and then running K-means. We also estimate the number of cluster in the captions using the Elbow method. We found out the correct number of clusters to be 13. In the Table 2 we share the top terms in those clusters. Table 3 shows some samples belonging to there corresponding clusters.

Cluster ID : Name	Top-5 Terms	# of Cluster Members
0 : Infection statistics about the virus	data, virus, results, infection, analysis	62155
1 : RNA	rna, lanes, protein, gel, viral, cells	3355
2 : Research on Mice	mice, group, day, infected, days	3824
3 : Protein Sequencing	sequences, amino, acid, residues, protein	7591
4 : Demographic Understanding	characteristics, demographic, patients, clinical, baseline	1683
5 : Oligonucleotide sequences	primers, study, pcr, sequences, oligonucleotide	1004
6 : Pandemic Outbreak Modelling	model, parameters, values, data, epidemic	2457
7 : SARS related research	patients, respiratory, acute, clinical, syndrome	3615
8 : Confirmed Cases tracking	cases, number, confirmed, reported, cumulative	2285
9 : Laboratory reports	continued, laboratory, previous, parameters, page	570
10 : Influeza Related Research	influenza, pandemic, virus, ahn, seasonal	3482
11 : Cell Specific Research	cells, infected, expression, control, infection	11353

Table 2: Clusters of the extracted captions and there corresponding top-5 terms.

Keyphrase extraction and similar paper recommendations We have deonstrated our keyphrase extraction capabilities in the Table 4. Users can filter there search results based on them using our Faceted Search feature. Table 5 demonstrates our similar paper recommendation based on SciBERT re-ranking on title and abstract similarity.

Caption	Cluster ID	Figure																								
Table 2. Comparative analysis of results tests for detection of Chikungunya virus in suspected cases of Chikungunya infection.	0:Infection statistics	<table><tr><th></th><th colspan="4">Test, no. (%) of cases</th></tr><tr><th></th><th></th><th>Detection of IgM antibodies</th><th>Virus isolation</th></tr><tr><th>Result</th><th>RT-PCR (n = 296)</th><th>RT-LAMP (n = 296)</th><th>(n = 65)</th><th>(n = 32)</th></tr><tr><td>Positive</td><td>144 (48.6)</td><td>164 (55.4)</td><td>14 (21.5)</td><td>20 (62.5)</td></tr><tr><td>Negative</td><td>152 (51.4)</td><td>132 (44.6)</td><td>51 (78.5)</td><td>12 (37.5)</td></tr></table>		Test, no. (%) of cases						Detection of IgM antibodies	Virus isolation	Result	RT-PCR (n = 296)	RT-LAMP (n = 296)	(n = 65)	(n = 32)	Positive	144 (48.6)	164 (55.4)	14 (21.5)	20 (62.5)	Negative	152 (51.4)	132 (44.6)	51 (78.5)	12 (37.5)
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NOTE. RT-LAMP, real-time loop-mediated isothermal amplification.																										

Figure 2.4 Expression of SARS-CoV 1-259 nsp13 in E. coli BL21 (DE3): A, the protein with a C-terminal 6His tag (construct 4); B, the protein without a 6His tag (construct 5).	1:RNA	
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Figure 3. Long-term CTL memory responses in infected/treated animals versus control mice.	2:Research on Mice	
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Fig 1. Alignment of predicted amino acid sequences within exon 1 of CXCL16 proteins from seven different mammalian species.

3:Protein Sequencing

Species	Amino Acid Sequence
Equus caballus (EqCXCL16)	DNGSGIAGSCNRYTPSDSPAVDPMEHFRRLQGYDRCGYVRFQLSRVVC
Equus caballus (EqCXCL16)F.....H.....
Ceratotherium simus	DNGSGVAGSCNRYTPSDSPAVDPMEHFRRLQGYDRCGYVRFQLSRVVC
Homo sapiens	NGNGSVTSGCYGCKRISDSFFVQIMRLKRLRAHRCILYTRFQLSRVVC
Bos taurus	NGNGSVTSGCYGCKRISDSFFVQIMRLKRLRAHRCILYTRFQLSRVVC
Canis lupus familiaris	DNGSGVAGSCNRYTPSDSPAVDPMEHFRRLQGYDRCGYVRFQLSRVVC
Rattus norvegicus	DNGSGVAGSCNRYTPSDSPAVDPMEHFRRLQGYDRCGYVRFQLSRVVC
Loxodonta africana	DNGSGVAGSCNRYTPSDSPAVDPMEHFRRLQGYDRCGYVRFQLSRVVC

Table 2: Oligonucleotide sequences of the primers and probes used in the GPV FQ-PCR method	5:Oligonucleotide sequences	Name	Sequence 5' to3'	Position	Amplicon size (bp)
		GPV-F	GTGCCGATGGAGTGGGTAAT	3084-3103	60
		GPV-R	ACTGTGTTCCCACTCATGG	3122-3143	
		GPV-FP	#FAM-FTCCGATCCCA	3098-3120	
			ATTTCCTGAGG-1A9A		
		VP1-1	AGGCTTTGAATGCGAGGAGGA	3008-3033	1658
		VP1-2	GGATCCCGCAGGAAGTCTTATTGA	4637-4665	
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Figure 3. Inferring epidemic dynamics in China (excluding Hubei province). (A) Prediction using stage II data. (B) Model-fitting and testing with stage II data.	6:Outbreak Modelling	
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Table 3: Random samples from the caption clusters. We show only the first sentence in the captions.

Paper Title	Top-10 Keyphrases
Evolution and variation of 2019-novel coronavirus	nCoV, nucleotide, coronavirus, nucleotide substitution, outbreak, substitution rate, nucleotide substitution rate, phylogenetic trees, amino acid, amino
Self-assembly of Severe Acute Respiratory Syndrome Coronavirus Membrane Protein	Membrane, Protein, Coronavirus, VLP, SARSCoV, Syndrome Coronavirus, Coronavirus Membrane, Golgi, Respiratory Syndrome, Selfassembly
Respiratory viral infections in institutions from late stage of the first and second waves of pandemic influenza A (H1N1) 2009, Ontario, Canada	outbreak, LTCF, HN, influenza, pdm, late stage, viral infections, Ontario, Respiratory viral infections, wave
Biogenesis and Dynamics of the Coronavirus Replicative Structures	viruses, viral RNA synthesis, vesicle, synthesis, infection, Structures, Replicative, RNA viruses, Replicative Structures, RNA
Infection with human coronavirus NL63 enhances streptococcal adherence to epithelial cells	adherence, coronavirus NL, human coronavirus, coronavirus, bacterial pathogens, human coronavirus NL, pathogens, Infection, HCoVNL, NL

Table 4: Top-10 keyphrases of research paper selected by CeKE-Citing model

Paper Title	Top-5 Similar Papers
Middle Eastern Respiratory Syndrome Coronavirus (MERS-CoV)	<ol style="list-style-type: none"> 1. Middle East Respiratory Syndrome coronavirus (MERS CoV): Update 2013 2. A novel coronavirus capable of lethal human infections: an emerging picture 3. Structure, Immunopathogenesis and Vaccines Against SARS Coronavirus 4. Hantaviruses in the Americas and Their Role as Emerging Pathogens 5. Zika fever and congenital Zika syndrome: An unexpected emerging arboviral disease
Coronavirus Receptors	<ol style="list-style-type: none"> 1. Crystal structure of murine sCEACAM1a[1,4]: a coronavirus receptor in the CEA family 2. The nucleocapsid protein of the SARS coronavirus is capable of self-association through a C-terminal 209 amino acid interaction domain 3. C-terminal domain of the MERS coronavirus M protein contains a trans-Golgi network localization signal 4. Structural and functional analysis of the S proteins of two human coronavirus OC43 strains adapted to growth in different cells 5. Species-specific evolution of immune receptor tyrosine based activation motif-containing CEACAM1-related immune receptors in the dog

Table 5: Titles of top-5 similar paper recommendations by SciBERT