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Biflavonoid as potential 3-chymotrypsin-like protease (3CLpro) inhibitor of SARS-Coronavirus

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ABSTRACT

3CL protease is one of the key proteins expressed by SARS-Coronavirus-2 cell, the potential to be targeted in the discovery of antivirus during this COVID-19 pandemic. This protein regulates the proteolysis of viral polypeptide essential in forming RNA virus. 3CL protease (3CLpro) was commonly targeted in the previous SARS-Coronavirus including bat and MERS, hence, by blocking this protein activity, the coronavirus should be eradicated. This study aims to review the potency of biflavonoid as the SARS-Coronavirus-2 3CLpro inhibitor. The review was initiated by describing the chemical structure of biflavonoid and followed by listing its natural source. Instead, the synthetic pathway of biflavonoid was also elaborated. The 3CLpro structure and its function were also illustrated followed by the list of its 3D-crystal structure available in a protein data bank. Lastly, the pharmacophores of biflavonoid have been identified as a protease inhibitor, was also discussed. This review hopefully will help researchers to obtain packed information about biflavonoid which could lead to the study in designing and discovering a novel SARS-Coronavirus-2 drug by targetting the 3CLpro enzyme.

Contents

1. Introduction

The Covid-19 pandemic has extended for almost 10 months since its outbreak in January 2020 [1]. The present statistic (by 24 October 2020) shows 43 M cases, 29 M recovered and 1.15 M death across the world. The United States of America is the country with the highest cases reported at 8.5 M approximately [2]. Meanwhile, the cases in Indonesia are still increasing. There are approximately 393,000 cases with 318,000 treated and 13,500 death [3]. This situation has made very huge impacts on all aspects of life including the economy, politics,

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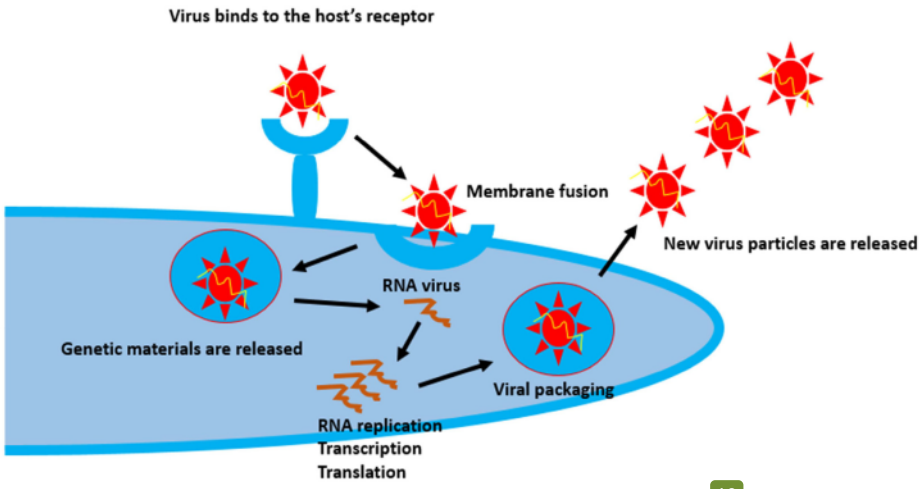


Fig. 1. The life cycle of coronaviruses is initiated by the binding of the viral cell through its protein spike (S) to the host cell's receptor namely angiotensin-converting enzyme 2 (ACE2). Upon membrane fusion (endocytosis), the virus is coated by the endosome. The following endosomal break down releases RNA from the virus into the host cell. The incoming viral genome is translated to produce two large precursor polyproteins 1a (pp1a) and 1ab (pp1ab) which are cleaved by proteases into small products. A series of subgenomic mRNA are transcripted and finally translated into viral proteins. The viral protein along with RNA is packed into virion in the ER and Golgi and then transported via vesicles and released out of the cell [9].

social, culture, health, and education. For example, United Nations Industrial Development Organization (UNIDO) reported that since April 2020, the high-income countries (30 countries) have a 18% average economic losses, whereas upper-middle-income countries (13 countries) suffer a 24% average losses. The lower-middle-income countries (6 countries) are hit by a 22% average loss, confirming the economic crisis unleashed by the pandemic, regardless of the income level [4]. The SARS-Coronavirus-2 viral vector is still a topic for debate. However, either bats or snakes are predicted as the first virus transmitting species to human [5].

Like some other coronaviruses, SARS-Coronavirus-2 is also a family of coronaviridae, which is genomically composed by the structural as well as non-structural proteins. This is an RNA virus in which on one hand, the structural protein contains S protein (spike), M protein (membrane), E protein (envelope), and N protein (nucleocapsid) [6]. On the other hand, the non-structural protein (ORF) is an open reading frame (ORF) consisting of NSP1-16 [7]. Upon entry into the host cell, the incoming viral genome is translated to produce two large precursor polyproteins 1a (pp1a) and 1ab (pp1ab) that are processed by ORF 1a-encoded viral proteinases, papain-like proteinase (PLpro), and 3C-like proteinase (3CLpro) into 16 mature non-structural proteins (NSP1–NSP16, numbered according to their order from the N-terminus to the C-terminus of the ORF 1 polyproteins). Many of the NSPs perform essential functions in viral RNA replication and transcription [8]. The virus life cycle is illustrated in Fig. 1.

One of the common studied NSPs is NSP5, in which chymotrypsin-like protease (3CLpro) is one kind of this non-structural protein [10]. 3CLpro cleaves the polyprotein into viral RNA which is then replicated and packed in the new mature virus. Therefore, by interfering with this proteolytic step, the viral RNA replication will be interrupted leading to the prevention of new viruses for further expansion. 3CLpro is one of the interesting protein targets in combating coronavirus by competitive inhibition with the peptide substrate [11].

Reviews on natural product compounds potential for SARS-Coronavirus have been published by targeting diverse proteins. These includes tanshinones, diarylheptanoids and geranylated flavonoids targeting PLpro [12], quercetine (reverse transcriptase) [13], aloeemodin and hesperitin (3CLpro) [14], apigenin (viral internal ribosome entry) [15], isatisindigotica (protease) [16], amentoflavone (biflavonoid; protease) [17], kaempferol (3a ion channel) [18], glycyrrhizin (protease) [19], tetradrine (viral S and N) [20], silvestrol (cap-dependent viral mRNA translation) [21,22], etc.

Biflavonoid is currently attractive to be proposed as the serine protease inhibitor due to the suitability of its chemical structure with the active site of the protease [23]. Serine proteases are characterized by a distinctive structure, consisting of two beta-barrel domains that converge at the catalytic active site. These enzymes can be further categorized based on their substrate specificity as either trypsin-like, chymotrypsin-like, or elastase-like. Therefore, the dimer form of biflavonoid is such a good inhibitor model that would fully occupy the two beta-barrel domain (main site and prime site) [24].

In this review, we will focus on the biflavonoid as the interesting compound, which is potential for the 3CLpro inhibitor of SARS-Coronavirus-2. The review will start by defining the chemical structure of biflavonoid and its sources from both natural products as well as synthesis. The following section would elaborate the 3CLpro structure and its function as the interesting protein target for biflavonoid. The review also summarizes the existing SARS-Coronavirus-2 3CLpro 3D crystal structure in the protein data bank. Last but not least, the current study on the biflavonoid as a diverse protease inhibitor will be carried out to give the insight mechanism on how the biflavonoid can act as a potential SARS-Coronavirus-2 antiviral agent.

2. Chemical structure

Biflavonoid is a natural product compound bearing a dimer of two sets of flavonoid, linked by either C–C or C-O bond [25,26]. The flavonoid itself is chemically constructed by a 15-C skeleton, which is divided into two aromatic rings (Ring A and Ring B) and connected by a heterocyclic ring having α, β- unsaturated carbonyl chain [27]. In addition to flavonoid being the major form of such compound class, there are two kind of analogs which enrich the flavonoid structural diversity. They are isoflavonoid (derived from 3-phenylchromen-4-one (3-phenyl-1,4-benzopyrone) and neoflavonoid (derived from 4-phenylcoumarine (4-phenyl-1,2-benzopyrone). Other sub-groups of flavonoid including flavan, flavanone, flavanonol, anthocyanidin,

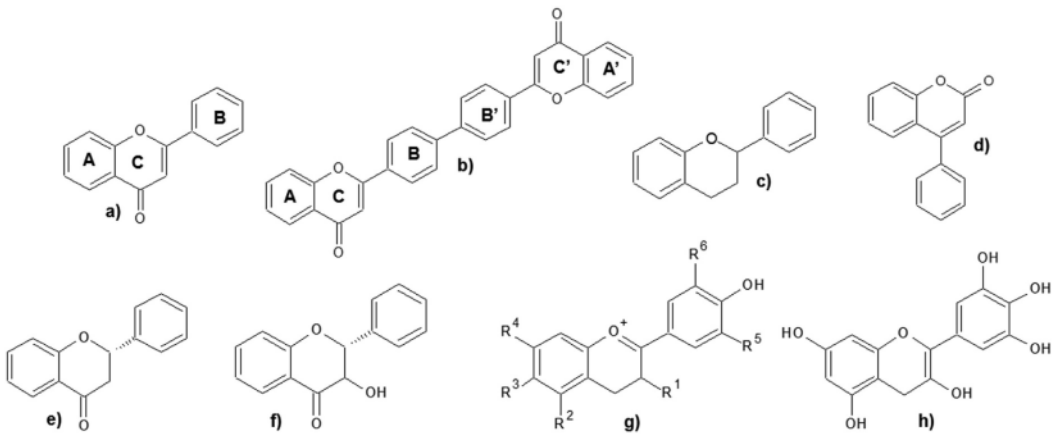


Fig. 2. The structures of a) flavonoid, b) biflavonoid, c) isoflavonoid, d) neoflavonoid, e) flavanone, f) flavanonol, g) anthocyanidin and h) anthoxantin which are naturally occurred in plants.

and anthoxantin are also widely distributed among natural resources [28]. Fig. 2 illustrates the structure of flavonoid and their analogs.

The aromatic rings are often decorated by poly-hydroxy group. Therefore, this compound's class are frequently called polyphenolic compounds. The presence of OH group has also given chance for the flavonoid to be biosynthetically formed in a glycoside. The sugar moiety in the glycosidic form makes the flavonoid more soluble in water than organic solvents due to the polar character of the sugar [29,30].

Spectroscopically, alike to the polyphenolic flavonoid, the yellowish biflavonoid absorbs UV light at 500–600 nm. The colorimetric reaction namely bathochromic shift (redshift) occurs when it reacts with an alkaline solution to prolong the maximum wavelength (650 nm). Similarly, polyvalent ion such as Al^{3+} may shift the wavelength into a hypsochromic shift (blue shift) with a lower wavelength (450 nm) [31]. Using the fourier transform infrared (FTIR) spectroscopy, the carbonyl of chromone group stretching vibration is transmitted at 1600 cm^{-1}. Meanwhile, the vinyl aromatic group appears at 3600 cm^{-1} as a bending vibration [32]. The proton of biflavonoid is indicated as multiplet signals around 6–8 ppm which often overlap in *trans/ cis* configuration protons of α, β- unsaturated carbonyl chain as confirmed by nuclear magnetic resonance (NMR) spectroscopy. In conjunction, the carbon signal of the carbonyl chromone group is indicated at 160 ppm, whereas the vinylic aromatic carbon appears at 150 ppm. Using a mass spectroscopy, the origin of the flavonoid skeleton could be the most stable mass/ion (base peak) during the fragmentation due to the electron impact bombardment [33].

3. Natural sources

A naturally occurring biflavonoid is distributed in various plant species. The first isolated natural biflavonoid was from *Ochna squarrosa* Linn. (Ochnaceae) [34] and later was from *Lonicera japonica* (Caprifoliaceae) [35]. *Torreya nucifera* was also identified as the natural source producing four biflavonoids [36]. Amentoflavone is another kind of biflavonoid isolated from abroad family of plants such as selaginellaceae, cupressaceae, euphorbiaceae, podocarpaceae, and calophyllaceae [37]. It was reported that at least 127 biflavonoids are distributed among plants, but the most occurrences are *Gingko biloba*, *Lobelia chinensis*, *Polygala sibirica*, *Ranunculus ternatus*, *Selaginella pulvinata*, and *Selagenella tamariscina* [37].

A more recent study had identified the biflavonoid I3′ II8-binaringenin in drupes of *Schinus terebinthifolius*, which was indicated by UHPLC-MS [38]. Five biflavonoids were lately found in *Ceratodon purpureus* presenting a diastereomeric form in the second biflavonoid [39]. In the same year, three biflavonoid types were also discovered in *Selaginella doederleinii* including the amentoflavone type, robustaflavone type, and hinokiflavone type [40]. From the zingiberaceae family, new biflavonoids with flavanone-chalcone type can be found in fingerroot (*Boesenbergia rotunda*) [41]. The pure biflavonoid with aglycones morelloflavone (Mo) type, volkensiflavone (Vo) type, as well as the morelloflavone's glycoside fukugiside (Fu) type was characterized in *Garcinia madruno* [42]. The genus of garcinia again shows its source of biflavonoid by the discovery of seven compounds including volkensiflavone, fukugetin, fukugeside, GB 1a, GB 1a glucoside, GB 2a, and GB 2a glucoside from *Garcinia xanthochymus* fruits [43]. Fig. 3 illustrates the chemical structure of hinokiflavone, ochnaflavone, amentoflavone, morelloflavone, and volkensiflavone. For more data, Table 1 tabulates the various studies reporting biflavonid found in a natural source in the last three years.

4. Synthetic sources

Instead of natural sources, biflavonoid is also produced via a synthetic pathway. This usually aims to derivatize the biflavonoid lead compound into a modified diverse functional group that could be responsible for its biological activity. Besides, the synthetic pathway could be more reproducible than isolating the biflavonoid from its genuine natural sources. This will proportionally reduce the cost of production as well as increase the yields [74,75].

Biflavonoid is synthetically formed by two units (monomer) of flavonoid undergoing the Ullmann coupling reaction [76]. This reaction forms a diaryl ether link between two units of flavonoid, which is conditioned by mixing them with an alkaline carbonate solution, *N*, *N*-dimethylacetamide, and dry toluene solvent under nitrogen exposure, followed by heating the mixture above 100 °C for several hours [77]. The total synthesis of biflavonoid is initiated by reacting *ortho*-hydroxy acetophenone with benzaldehyde under Claissen Smith condensation to form chalcone as the intermediate compound [78]. The next step is the synthesis of flavone (monomer) by iodinating the chalcone using DMSO as the solvent [79]. The detailed total synthesis of biflavonoid is schemed out in Scheme 1.

An interesting biflavonoid was constructed according to the naringenin monomer by reacting to the available phloroglucinol and 4-hydroxy- or 4-methoxybenzaldehyde. Naringenin is the flavanone-skeleton structure attached by three hydroxy groups at the 4′, 5, and

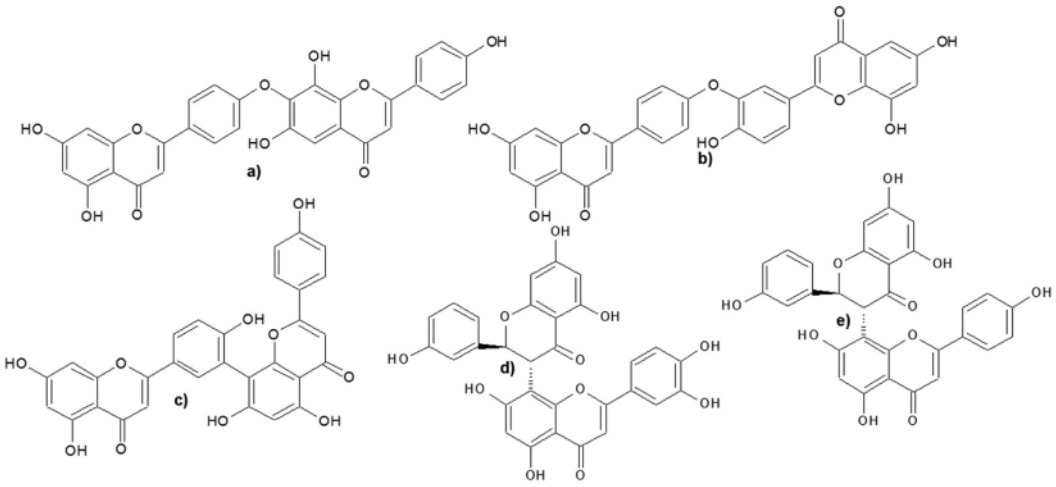


Fig. 3. The chemical structures of earlier biflavonoid found in plants: a) hinokiflavone, b) ochnaflavone, c) amentoflavone, d) morelloflavone, and e) volkensiflavone.

7 carbons. The product was confirmed as 3′,3‴-binaringenin, and four related biflavonoids with a considerably good yield (15–35%) [81].

Biflavonoid was also prepared electrochemically by reacting to flavonol isorhamnetin, $LiClO_4$, and amine in acetonitrile solvent. The mixture was electrolyzed in a diaphragm cell at anodic current density of 5 mA/cm^2 for 3.5 h. Platinum-plated with a working surface of 2 cm^2 was used as the anode. Once the electrolysis was completed, about 90% of the acetonitrile was distilled from the anode compartment. Further purification using chromatography column was applied and followed by recrystallization to obtain the biflavonoid product with a good yield (60–70%) [82].

A step-economical preparation of a very rare biflavonoid has been performed by combining the methylated biaurone undergoing a modular and divergent synthesis strategy. The divergent synthesis was carried out by using bialdehyde as the building block such as isophthalaldehyde, terephthalaldehyde, and benzene-1,3,5-tricarbaldehyde to produce the chalcone intermediate under Claissen Smith condensation. The following reaction was oxidative cyclization to obtain the biflavonoid as the targeted compound. Interestingly, instead of biflavonoid, the divergent method is also applied in the production of triflavonoid [83].

The synthesis of biflavonoid was further explored by applying the Suzuki-Miyaura cross-coupling reaction followed by alcohol methylation for the synthesis of rare 'hybrid' derivatives. These derivatives belong to different sub-classes of monomers. The second biflavonoid was constructed as homodimeric compounds in which a methylenedioxy group acts as the linker between the two flavonoid monomers. This reaction facilitates the probing of uncharted regions of biologically interesting chemical space [84].

The first stereodivergent synthesis of biflavanone was conducted by exclusively controlling the temperature to produce a stereoselective product. The scaffold of 2,2′-biflavanones was attached by diverse substitution at the phenyl ring and conditioned by SmI_2/Methanol/THF, confirmed by a highly selected good yield for both stereoisomers of the expected compounds. On one hand, the (R*,R*)-stereoisomer was only formed when the temperature was controlled at −40 °C. On the other hand, the reaction generated the (R*,S*)-isomer when the mixture was refluxed [85]. The control of regioselective reaction was performed using aromatic prenyltransferase from *Aspergillus terreus* (AtaPT). Prenylation was applied to produce biflavonoids 1–3 dimerized connected by a diphenyl linkage at the hydrogen bond involving C5″–OH group. This OH is chemically less accessible than other OH groups in the ring. The AtaPT was used as the substrate that successfully yielded the different regio and chemoselective products. This study would be recommended for developing green synthetic reactions for such prenylated biflavonoids [86].

5. 3-Chymotrypsine-like protease

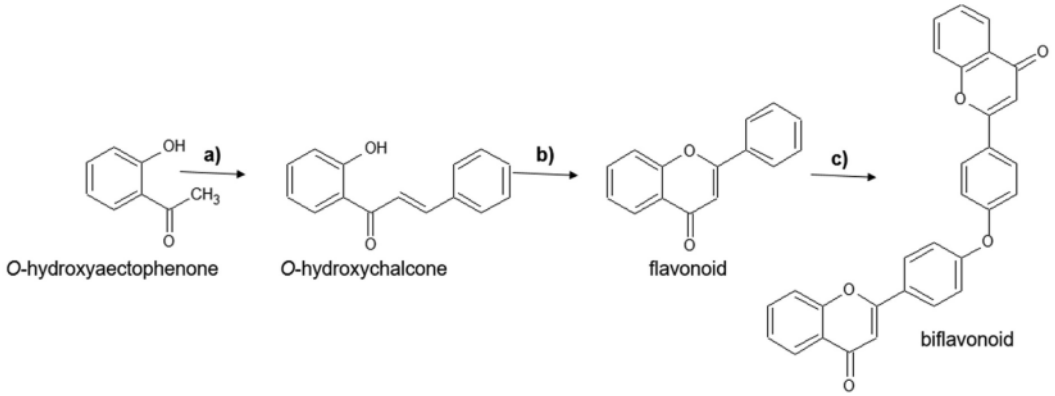
The extensive process of proteolysis releases the functional polypeptides which are mainly achieved by the main proteinase and are also frequently named 3C-like proteinase (3CLpro). This indicates a similar cleavage site with the early picornavirus of 3C proteinases (3Cpro), although further studies showed that the similarity is limited by two families of the protease. 3CLpro cleaves at least 11 conserved amino acid residues includes GLN---(SER, ALA, GLY) sequences (the cleavage site is indicated by ---) [87]. This process is initiated by the autocleavage of its enzyme from two polypeptides (polypeptide A and polypeptide B). There are three non-canonical 3CLpro cleavage sites at the P2 position employing PHE, MET, or VAL residues in SARS-Coronavirus polyproteins. The cleavage site of 3CLpro SARS-Coronavirus is illustrated in Fig. 4 [10,88].

The availability of experimentally determined three-dimensional (3D) structures of the SARS-Coronavirus-2 3CLpro has greatly aided in the design of anti-SARS-Coronavirus-2 drug [91]. Recently, the sudden increase in the number of crystal structures of 3CLpro is deposited in the protein data bank (PDB) [92]. Most of the earlier crystal structures are devoid of inhibitor. Thus, it could not explain the particular binding site of 3CLpro properly [93]. Therefore, many efforts conducted to understand the structure and function of 3CLpro relied mainly on the models developed based on the crystal structures of other betacoronavirus such as SARS-Coronavirus, MERS, Bat Corona, etc [94].

To date, there are more than 100 3D structures of SARS-Coronavirus-2 3CLpro deposited in the protein data bank (PDB) (www.rcsb.org). In general, the crystal structures of 3CLpro reveal the presence of three structural domains in each monomer, in which domains I (position 8–101), II (position 102–184), and III (position 201–303) have a chymotrypsin-like characteristic fold with a catalytic cysteine (CYS145) and histidine (HIS41). This is linked to a third C-terminal domain by a long loop (position 185–200) by orienting the

Table 1
Biflavonoids from natural resources have been reported in the last three years.

No	Biflavonoid	Plants	References
1	dihydrodaphnodorin B	*Fumana procumbens*	[44]
2	daphnodorin B	*Fumana procumbens*	[44]
3	volkesiflavone	*Garcinia gardneriana*	[45]
4	[illegible]lloflavone	*Garcinia gardneriana, Garcinia madruno*	[45]
5	7,7″-di-*O*-methylchamaejasmin	*Ormocarpum kirkii*	[46]
6	campylospermone A	*Ormocarpum kirkii*	[46]
7	a dimeric chromene [diphysin	[illegible]ocarpum kirkii	[46]
8	amentoflavone 7″-*O*-*β*-*d*-glucopyranoside	*Ginkgo Biloba*	[47]
9	bilobetin	*Ginkgo Biloba*	[47]
10	isoginkgetin	*Ginkgo Biloba*	[47]
11	sciadopitysin	*Ginkgo Biloba*	[48]
12	agathisflavone	*Schinus terebinthifolius; Anacardium occidentale*	[49,50]
13	tetrahydroamentoflavone	*Schinus terebinthifolius*	[49]
14	uncinatabiflavone C 7-methyl ether	*Selaginella uncinata*	[50]
15	7, 4′, 7‴, 4‴-tetra-*O*-methyl amentoflavone	*Cephalotaxus harringtonia*	[51]
16	7, 4′, 7″-tri-*O*-methyl amentoflavone	*Cephalotaxus harringtonia*	[51]
17	sequoiaflavone	*Cephalotaxus harringtonia; Ouratea ferruginea*	[51,52]
18	amentoflavone monomethoxy derivatives	*Cunninghamia lanceolata*	[53]
19	dihydrochalcone flavanone	*Sophora flavescens*	[54]
20	2′,3′-dihydroochnaflavone	*Ochna mauritiana*	[55]
21	dulcisbiflavonoid B	*Garcinia dulcis*	[56]
22	dulcisbiflavonoid C	*Garcinia dulcis*	[56]
23	umcephabiflovin A	*Cephalotaxus oliveri*	[57]
24	umcephabiflovin B	*Cephalotaxus oliveri*	[57]
25	S-taiwanhomoflavone-B	*Cephalotaxus oliveri*	[57]
26	5, 6, 6′-trihydroxy-[1,1′-biphenyl]-3,3′-dicarboxylic acid	*Mesua ferrea*	[58]
27	fukugiside	*Garcinia madruno*	[59]
28	neochamaejasmin B	*Stellera chamaejasme*	[60]
29	oliveriflavone A, B, and C	*Cephalotaxus oliveri*	[61]
30	rhusflavanone	*Mesua ferrea*	[62]
31	mesuaferrone B	*Mesua ferrea*	[62]
35	sinodiflavonoids A	*Sinopodophyllum emodi*	[63]
36	sinodiflavonoids B	*Sinopodophyllum emodi*	[63]
37	oxytrodiflavanone A	*Oxytropis chiliophylla*	[64]
38	oxytrochalcoflavanones A	*Oxytropis chiliophylla*	[64]
39	oxytrochalcoflavanones B	*Oxytropis chiliophylla*	[64]
40	hinokiflavone	*Selaginella sinensis*	[65]
41	isocampylospermone A	*Ochna Serrulata*	[66]
42	campylospermone A	*Ochna Serrulata*	[66]
43	c[illegible]ssuflavone	*Cupressus sempervirens*	[67]
44	(8-hydroxy-3′-*β*-*D*-galactosyl-isoflavone)-2′-8″-(4‴-hydroxy-flavone)-biflavone	*Solanum nigrum*	[68]
45	2′,3′,5-trihydroxy-5″-methoxy-3″-*O*- α-glucosyl-3–4‴-*O*-biflavone	*Solanum nigrum*	[68]
46	7′-*O*-methyl hinokiflavone	*Selaginella tamariscina*	[69]
47	(2*R*,3*S*)-volkensiflavone-7-*O*-*β*-acetylglucopyranoside	*Allanblackia floribunda*	[70]
48	(2*S*,3*S*)-[illegible]morelloflavone-7-*O*-β-acetylglucopyranoside	*Allanblackia floribunda*	[70]
49	(*S*)-2″*R*,3″*R*- and (*R*)-2″*S*,3″*S*-dihydro-3″-hydroxyamentoflavone-7- methyl ether	*Cardiocrinum giganteum*	[71]
50	(*S*)-2″*R*,3″*R*- and (*R*)-2″*S*,3″*S*-dihydro-3″-hydroxyamentoflavone	*Cardiocrinum giganteum*	[71]
51	4,4′,7-tri-*O*-methylisocampylospermone A	*Ochna serrulata*	[72]
52	4‴-de-*O*-methylafzelone A	*Ochna serrulata*	[72]
53	serrulone A	*Ochna serrulata*	[72]
54	sumaflavone	*Juniperus phoenicea*	[73]



Scheme 1. Total synthesis of biflavonoid. Reagents and conditions: a) benzaldehyde, KOH, MeOH, rt, overnight, 70–87%; b) I_2, DMSO, 100 °C, overnight, 75–86%; and c) Ullmann modified coupling reaction, 8–58% [80].

3CLpro Cleavage Site	P6	P5	P4	P3	P2	P1	P1′	P2′	P3′	P4′	P5′	Relative Kcal/Km
nsp4/5	T	S	A	V	L	Q	S	G	F	R	K	100%
nsp5/6	S	G	V	T	F	Q	G	K	F	K	K	41%
nsp6/7	K	V	A	T	V	Q	S	K	M	S	D	3%
nsp7/8	N	R	A	T	L	Q	A	I	A	S	E	5%
nsp8/9	S	A	V	K	L	Q	N	N	E	L	S	2%
nsp9/10	A	T	V	R	L	Q	A	G	N	A	T	22%
nsp10-12	R	E	P	L	M	Q	S	A	D	A	S	0,2%
nsp12/13	P	H	T	V	L	Q	A	V	G	A	C	8%
nsp13/14	N	V	A	T	L	Q	A	E	N	V	T	9%
nsp14/15	T	F	T	R	L	Q	S	L	E	N	V	28%
nsp16/15	F	Y	P	K	L	Q	A	S	Q	A	W	27%

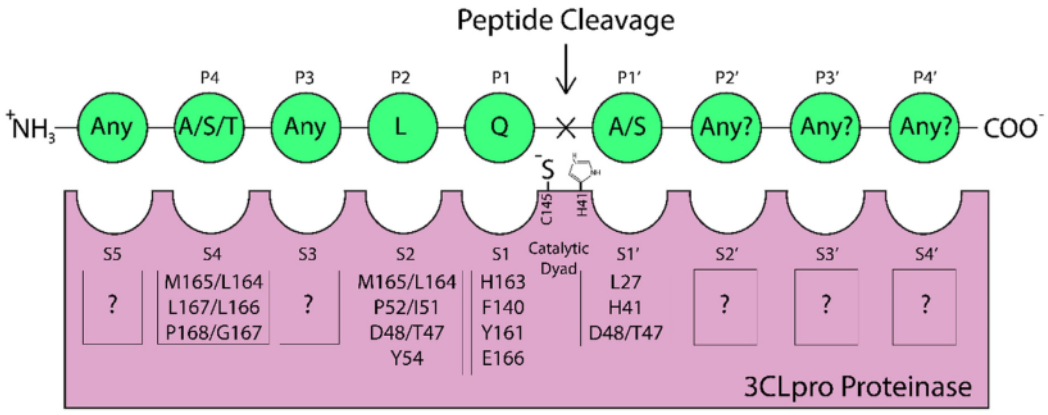


Fig. 4. The 3CLpro cleavage sites of SARS Coronavirus which recognize 11 sequences of peptide substrate with their respective Kcal/Km. These Kcal/Km values reflect the canonical recognition which is supported by the recognition sites of a series of other coronavirus 3C proteases [89,90].

N-terminal residues that are essential for the dimerization [95-98]. Domain I and domain II are decorated in antiparallel β-barrel structure, whereas domain III is composed of five α-helices arranged in a globular cluster. The helical domains of the two monomers form a dimer through H-bond interactions from the end to end of the N-terminal residues and the key residues from the individual monomers. The catalytic activity is suggested to be contributed by the salt bridge between the N-terminal SER1 of one monomer and GLU166 of the other monomer [97,99]. Table 2 presents the 115 3D-structures of 3CLpro available in the protein data bank.

SARS-Coronavirus-2 3CL pro in complex with a novel inhibitor 5,6,7-trihydroxy-2-phenyl-4H-chromen-4-one solved its 3D-crystal structure in 2.20 Å solution. This flavonoid inhibitor binds the active site of the protease through the hydrogen bond interaction between *ortho*-hydroxyphenyl (ring A) of the ligand with GLY143, and the carbonyl group of ring C with GLU166. The non-bonding interaction was also observed between the phenyl of ring with HIS41 and CYS44. Fig. 5 illustrates the interaction between 5,6,7-trihydroxy-2-phenyl-4 H-chromen-4-one and the active site of SARS-Coronavirus-2 3CLpro (PDB ID 6M2N) [100].

Two peptidomimetic-based inhibitors are complexed with SARS-Coronavirus-2 in different monomer of trimer with 2.15 Å of the crystal resolution (PDB 6WTT) [101]. (1*S*,2*S*)-2-({*N*-[(benzyloxy) carbonyl]-*L*-leucyl}amino)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propane-1-sulfonic acid binds the active site in monomer A by interacting it with CYS145, GLU166, GLN189, HIS164, and PHE140 at the respective atoms of O (OH), O (C = O), H (NH-amide), H (NH-amide) and H (NH-pyrrolidinone) (Fig. 6). Monomer B demonstrates the same binding mode as monomer A, whereas monomer C is bound by ~ 2 ~ -[(benzyloxy)carbonyl]-*N*-[(1*R*,2*S*)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]-1-(trimethyl-lambda ~ 4 ~ -sulfanyl)propan-2-yl]-*L*-leucinamide. In monomer C, the ligand interacts with GLU166, HIS164, HIS41, and GLN189 at the respective atoms of O (C = O), N (NH-amide) and N- (NH-pyrrolidinone), O (OH), and N (NH-amide).

A class of imidazole-4-carboxamide compound was also complexed to SARS-Coronavirus-2 3CLpro and the 3D crystal structure was resolved at 1.46 Å (PDB ID 6W79; Fig. 7a) [102]. This inhibitor binds the active site of the protease by interacting it with the residues GLY143 and GLU166 at atom O (C=O-amide) and also the next O (C=O-amide), respectively. The hydrophobic interaction was also performed via the interaction between ASN142- O (C=O-amide), THR26-H-CH-imidazole), CYS145-imidazole ring, and LEU141-ASN142-pyridine.

An inhibitor which was a repurposed drug from antineoplastic, was complexed with SARS-Coronavirus-2 3CLpro in 1.60 Å of 3D-crystal resolution (PDB ID 7BUY; Fig. 7b) [103]. Interestingly, this inhibitor binds covalently (distance 1.8 Å) at its O (C=O) to CYS145 which is one of the catalytic site residues. This inhibitor's name is carmofur,

Table 2
The list of 3CLpro 3D-crystal structure available in protein data bank.

PDB ID	Co-crystallized Ligand	Resolution (Å)	Reference
6M2N	5,6,7-trihydroxy-2-phenyl-4H-chromen-4-one	2.20	[100]
6M2Q	–	1.70	[100]
6WQF	–	2.30	[105]
6XB1	1-ethyl-pyrrolidine-2,5-dione	1.80	[106]
6XB0	dimethyl sulfoxide	1.80	[106]
6XB2	1-ethyl-pyrrolidine-2,5-dione, dimethyl sulfoxide	2.10	[106]
6L00 and 6LNY	(2~{S})-4-methyl-~{N}-[(2~{S})-1-oxidanylidene-3-[(3~{S})-2-oxidanylidenepyrrolidin-3-yl]propan-2-yl]-2-[[(~{E})-3-phenylprop-2-enoyl]amino]pentanamide	1.94 and 2.25	[107]
7JFQ	1,2-ethanediol, formic acid	1.55	[108]
6XKF	1,2-ethanediol, chloride ion	1.80	[109]
6XKH	1,2-ethanediol, acetate ion, formic acid	1.28	[110]
6XOA	1,2-ethanediol	2.10	[111]
6LNQ	*N*-[(2*S*)-3-methyl-1-[[(2*S*)-4-methyl-1-oxidanylidene-1-[[(2*S*)-1-oxidanylidene-3-[(3*S*)-2-oxidanylidenepyrrolidin-3-yl]propan-2-yl]amino]pentan-2-yl]amino]-1-oxidanylidene-butan-2-yl]-1H-indole-2-carboxamide	2.24	[107]
7JUN	–	2.30	[112]
7JR3	–	1.55	[113]
7JR4	–	1.55	[114]
6XHU	–	1.80	[115]
6XQT	(1*R*,2*S*,5*S*)-3-[*N*-({1-[(*tert*-butylsulfonyl)methyl]cyclohexyl}carbamoyl)-3-methyl-*L*-valyl]-*N*-{(1*S*)-1-[(1*R*)-2-(cyclopropylamino)-1-hydroxy-2-oxoethyl]pentyl}-6,6-dimethyl-3-azabicyclo[3.1.0]hexane-2-carboxamide	2.30	[116]
6XQS	(1*S*,3a*R*,6a*S*)-2-[(2*S*)-2-({(2*S*)-2-cyclohexyl-2-[(pyrazin-2-ylcarbonyl)amino]acetyl}amino)-3,3-dimethylbutanoyl]-*N*-[(2*R*,3*S*)-1-(cyclopropylamino)-2-hydroxy-1-oxohexan-3-yl]octahydrocyclopenta[c]pyrrole-1-carboxamide	1.90	[116]
6XQU	boceprevir (bound form)	2.20	[116]
6W2A	[4,4-*bis*(fluoranyl)cyclohexyl]methyl ~{*N*}-[(2~{*S*})-1-[[(1~{*R*},2~{*S*})-1-[*bis*(oxidanyl)-oxidanylidene-$l^{5}-sulfanyl]-1-oxidanyl-3-[(3~{*S*})-2-oxidanylidenepyrrolidin-3-yl]propan-2-yl]amino]-4-methyl-1-oxidanylidene-pentan-2-yl]carbamate, (1*S*,2*S*)-2-[(*N*-{[(4,4-difluorocyclohexyl)methoxy]carbonyl}-*L*-leucyl)amino]-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propane-1-sulfonic acid	1.65	[117]
6WTK	*N* ~ 2 ~ -[(benzyloxy)carbonyl]-*N*-{(2*S*)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propan-2-yl}-*L*-leucinamide	2.00	[118]
6WTM	–	1.85	[118]
6WTJ	(1*S*,2*S*)-2-({*N*-[(benzyloxy)carbonyl]-*L*-leucyl}amino)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propane-1-sulfonic acid	1.90	[118]
6 W63 and 6 W79	*N*-(4-*tert*-butylphenyl)-*N*-[(1R)-2-(cyclohexylamino)-2-oxo-1-(pyridin-3-yl)ethyl]-1H-imidazole-4-carboxamide	2.10	[102]
6WCO	N-(4-*tert*-butylphenyl)-N-[(1R)-2-(cyclopentylamino)-2-oxo-1-(pyridin-3-yl)ethyl]-1H-imidazole-4-carboxamide	1.48	[102]
6XBH	–	1.60	[119]
6XBG	–	1.45	[120]
6XFN	–	1.70	[121]
7JU7	Masitinib	1.60	[122]
3SZN	ethyl (4*R*)-4-({*N*-[(benzyloxy)carbonyl]-l-phenylalanyl}amino)-5-[(3*S*)-2-oxopyrrolidin-3-yl]pentanoate	1.69	[123]
3SNE	2-(*N*-morpholino)-ethanesulfonic acid	2.60	[124]
3SNA, 3SNB, and 3SNC	–	3.05, 2.40 and 2.58	[124]
6XBI	–	1.70	[125]
6XHO	ethyl (2*E*,4*S*)-4-{[*N*-(4-methoxy-1H-indole-2-carbonyl)-*L*-leucyl]amino}-5-[(3*S*)-2-oxopyrrolidin-3-yl]pent-2-enoate	1.45	[126]
6XHN	(1*S*)-3-{[*N*-(4-methoxy-1H-indole-2-carbonyl)-*L*-leucyl]amino}-2-oxo-4-[(3*S*)-2-oxopyrrolidin-3-yl]butyl 2-cyanobenzoate	1.38	[126]
6XHL and 6XHM	(2*S*)-1-({(2*S*)-4-hydroxy-3-oxo-1-[(3*S*)-2-oxopyrrolidin-3-yl]butan-2-yl}amino)-4-methyl-1-oxopentan-2-yl]-4-methoxy-1H-indole-2-carboxamide	1.47 and 1.41	[126]
6XA4	–	1.65	[127]
6Y2E	–	1.75	[128]
6Y2G, 6Y2F	~{*tert*}-butyl~{*N*}-[1-[(2~{*S*})-3-cyclopropyl-1-oxidanylidene-1-[[(2~{*S*},3~{*R*})-3-oxidanyl-4-oxidanylidene-1-[(3~{*S*})-2-oxidanylidenepyrrolidin-3-yl]-4-[(phenylmethyl)amino]butan-2-yl]amino]propan-2-yl]-2-oxidanylidene-pyridin-3-yl]carbamate	2.20, and 1.95	[128]
7JKV	*N*-[(2*S*)-1-({(1*S*,2*S*)-1-(1,3-benzothiazol-2-yl)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propan-2-yl}amino)-4-methyl-1-oxopentan-2-yl]-4-methoxy-1H-indole-2-carboxamide	1.25	[129]
5RHF	1-acetyl-*N*-methyl-*N*-phenylpiperidine-4-carboxamide	1.76	[104]
5RHE	1-acetyl-*N*-(6-methoxypyridin-3-yl)piperidine-4-carboxamide	1.56	[104]
5RGG	4-methyl-*N*-phenylpiperazine-1-carboxamide	2.26	[104]
5RG1	N-alpha-acetyl-*N*-(3-bromoprop-2-yn-1-yl)-*L*-tyrosinamide	1.57	[104]
5RGH	5-fluoro-1-[(5-methyl-1,3,4-thiadiazol-2-yl)methyl]-1,2,3,6-tetrahydropyridine	1.70	[104]
5RGR	*N*,1-dimethyl-*N*-(pr[illegible]2-yl)-1H-pyrazolo[3,4-d]pyrimidin-4-amine	1.41	[104]
5RG3	*N* ~ 2 ~ -acetyl-*N* ~ 1 ~ -prop-2-en-1-yl-*L*-aspartamide	1.58	[104]
5RG2	*N* ~ 2 ~ -acetyl-*N*-prop-2-en-1-yl-*D*-allothreoninamide	1.63	[104]
5RGS	(2*R*)-4-(phenylmethyl)morpholin-2-yl]methanol	1.72	[104]
5RGK	2-fluoro-*N*-[2-(pyridin-4-yl)ethyl]benzamide	1.43	[104]
5RGJ	(5*S*)-7-(pyr[illegible]2-yl)-2-oxa-7-azaspiro[4.4]nonane	1.34	[104]
5RGM	*N*-acetyl-4,5,6,7-tetrahydro-1-benzothiophene-2-carbohydrazide	2.04	[104]
5RGM	*N*-acetyl-4,5,6,7-tetrahydro-1-benzothiophene-2-carbohydrazide	2.04	[104]
5RG0	1,1′-(piperazine-1,4-diyl)di(ethan-1-one)	1.72	[104]
5RGN	1-{4-[(4-methylphenyl)sulfonyl]piperazin-1-yl}ethan-1-one	1.86	[104]
5RGQ	5-fluoro-2-methylphenyl)methanesulfonamide	2.15	[104]
5RGP	1-{4-[(2,4-dimethylphenyl)sulfonyl]piperazin-1-yl}ethan-1-one	2.07	[104]
5R8T	–	1.27	[104]
5RGZ	*N*-(3-cyanophenyl)-*N*-(pyridin-3-yl)acetamide	1.52	[104]
5RHA	1-{4-[(thiophen-2-yl)methyl]piperazin-1-yl}ethan-1-one	1.51	[104]

(*continued on next page*)

Table 2 (*continued*)

PDB ID	Co-crystallized Ligand	Resolution (Å)	Reference
5RH3	(1*R*)-2-(3-chlorophenyl)-*N*-(4-methylpyridin-3-yl)propanamide	1.69	[104]
5RH4	(2*R*)-2-(6-chloro-9H-carbazol-2-yl)propanoic acid	1.34	[104]
5RGU	*N*-(3-{[(2*R*)-4-oxoazetidin-2-yl]oxy}phenyl)-2-(pyrimidin-5-yl)acetamide	2.11	[104]
5RH6	*N*-[(1*R*)-2-ethyl-6-methylphenyl]amino}-2-oxo-1-(pyridin-3-yl)ethyl]-*N*-[6-(propan-2-yl)pyridin-3-yl]propanamide	1.60	[104]
5RGT	(1*R*)-2-(*tert*-butylamino)-2-oxo-1-(pyridin-3-yl)ethyl]-*N*-(5-*tert*-butyl-1,2-oxazol-3-yl)propanamide	2.22	[104]
5RH5	(5-*tert*-butyl-1,2-oxazol-3-yl)-*N*-[(1*R*)-2-[(4-methoxy-2-methylphenyl)amino]-2-oxo-1-(pyridin-3-yl)ethyl]propanamide	1.72	[104]
5RGW	2-(5-cyanopyridin-3-yl)-*N*-(pyridin-3-yl)acetamide	1.43	[104]
5RH8	2-(cyanomethoxy)-*N*-[(1,2-thiazol-4-yl)methyl]benzamide	1.81	[104]
5RGV	2-(isoquinolin-4-yl)-*N*-phenylacetamide	1.82	[104]
5RH7	(*tert*-butyl-1H-pyrazol-3-yl)-*N*-[(1R)-2-[(2-ethyl-6-methylphenyl)amino]-2-oxo-1-(pyridin-3-yl)ethyl]propanamide	1.71	[104]
5RGY	*N*-(6-ethoxypyridin-2-yl)-2-(naphthalen-2-yl)acetamide	1.976	[104]
5RGX	2-(3-cyanophenyl)-*N*-(4-methylpyridin-3-yl)acetamide	1.69	[104]
5RH9	4-[(1*S*)-1-methoxyethyl]phenyl}-*N*-[(1*R*)-2-[(4-methoxy-2-methylphenyl)amino]-2-oxo-1-(pyridin-3-yl)ethyl]propanamide	1.91	[104]
5RH0	5-methylthiophen-2-yl)-*N*-pyridin-3-ylurea	1.92	[104]
5RH2	2-(3-chlorophenyl)-*N*-(4-methylpyridin-3-yl)acetamide	1.83	[104]
5RH1	2-(5-chlorothiophen-2-yl)-*N*-(pyridin-3-yl)acetamide	1.96	[104]
5REA	(azepan-1-yl)(2H-1,3-benzodioxol-5-yl)methanone	1.63	[104]
5REB	1-[(thiophen-3-yl)methyl]piperidin-4-ol	1.68	[104]
5REC	2-{[(1H-benzimidazol-2-yl)amino]methyl}phenol	1.73	[104]
5REE	(2*R*,3*R*)-1-benzyl-2-methylpiperidin-3-ol	1.77	[104]
7JVZ	–	2.50	[130]
7JVQ	–	2.05	[131]
7BRR	(1*S*,2*S*)-2-({*N*-[(benzyloxy)carbonyl]-L-leucyl}amino)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propane-1-sulfonic acid	1.40	[132]
7BRO		2.00	[133]
7BRP	(1*R*,2*S*,5*S*)-*n*-[(1*S*)-3-amino-1-(cyclobutylmethyl)-2,3-dioxopropyl]-3-[(2*S*)-2-{[(*tert*-butylamino)carbonyl]amino}-3,3-dimethylbutanoyl]-6,6-dimethyl-3-azabicyclo[3.1.0]hexane-2-carboxamide	1.80	[134]
7C2Q		1.93	[135]
7C8T	*N*-[(benzyloxy)carbonyl]-*O*-(*tert*-butyl)-l-threonyl-3-cyclohexyl-*N*-[(1*S*)-2-hydroxy-1-{[(3*S*)-2-oxopyrrolidin-3-yl]methyl}ethyl]-l-alaninamide	2.05	[136]
7C8R	Ethyl (4*R*)-4-[[(2*S*)-4-methyl-2-[[(2*S*,3*R*)-3-[(2-methylpropan-2-yl)oxy]-2-(phenylmethoxycarbonylamino)butanoyl]amino]pentanoyl]amino]-5-[(3*S*)-2-oxidanylidenepyrrolidin-3-yl]pentanoate	2.30	[136]
6XCH		2.20	[137]
6L70	(1*S*,2*S*)-2-({*N*-[(benzyloxy)carbonyl]-L-leucyl}amino)-1-hydroxy-3-[(3*S*)-2-oxopyrrolidin-3-yl]propane-1-sulfonic acid	1.56	[138]
6FV1	(2~{*S*})-4-methyl-~{*N*}-[(2~{*S*},3~{*R*})-3-[(3~{*S*})-2-oxidanyl-4-oxidanylidene-1-[(3~{*S*})-2-oxidanylidenepyrrolidin-3-yl]-4-[(phenylmethyl)amino]butan-2-yl]-2-[[(~{*E*})-3-phenylprop-2-enoyl]amino]pentanamide	2.30	[139]
6FV2	(*S*)-*N*-benzyl-3-((*S*)-2-cinnamamido-3-phenylpropanamido)-2-oxo-4-((*S*)-2-oxopyrrolidin-3-yl)butanamide	2.95	[139]
7D31	(3~{*S*},3~{a}~{*S*},6~{a}~{*R*})-2-[3-[3,5-bis(fluoranyl)phenyl]propanoyl]-~{*N*}-[(2~{*S*})-1-oxidanylidene-3-[(3~{*S*})-2-oxidanylidenepyrrolidin-3-yl]propan-2-yl]-3,3~{a},4,5,6,6~{a}-hexahydro-1~{H}-cyclopenta[c]pyrrole-3-carboxamide	2.00	[140]
7D1O	(1*R*,2*S*,5*S*)-3-[*N*-({1-[(*tert*-butylsulfonyl)methyl]cyclohexyl}carbamoyl)-3-methyl-*L*-valyl]-*N*-{(1*S*)-1-[(1*R*)-2-(cyclopropylamino)-1-hydroxy-2-oxoethyl]pentyl}-6,6-dimethyl-3-azabicyclo[3.1.0]hexane-2-carboxamide	1.78	[141]
7C7P	(1*S*,3a*R*,6a*S*)-2-[(2*S*)-2-{(2*S*)-2-cyclohexyl-2-[(pyrazin-2-ylcarbonyl)amino]acetyl}amino)-3,3-dimethylbutanoyl]-*N*-[(2*R*,3*S*)-1-(cyclopropylamino)-2-hydroxy-1-oxohexan-3-yl]octahydrocyclopenta[c]pyrrole-1-carboxamide (3~{*S*},3~{a}~{*S*},6~{a}~{*R*})-~{*N*}-[(2~{*R*},3~{*S*})-1-(cyclopropylamino)-2-oxidanyl-1-oxidanylidene-hexan-3-yl]-2-methanoyl-3,3~{a},4,5,6,6~{a}-hexahydro-1~{H}-cyclopenta[c]pyrrole-3-carboxamide	1.74	[142]
7COM	boceprevir (bound form)	2.25	[143]
6ZRU	boceprevir (bound form)	2.10	[144]
6ZRT	(1*S*,3a*R*,6a*S*)-2-[(2*S*)-2-{(2*S*)-2-cyclohexyl-2-[(pyrazin-2-ylcarbonyl)amino]acetyl}amino)-3,3-dimethylbutanoyl]-*N*-[(2*R*,3*S*)-1-(cyclopropylamino)-2-hydroxy-1-oxohexan-3-yl]octahydrocyclopenta[c]pyrrole-1-carboxamide	2.10	[145]
6MOK	–	5.10	[146]
6LZE	~{*N*}-[(2~{*S*})-3-cyclohexyl-1-oxidanylidene-1-[[(2~{*S*})-1-oxidanylidene-3-[(3~{*S*})-2-oxidanylidenepyrrolidin-3-yl]propan-2-yl]amino]propan-2-yl]-1~{H}-indole-2-carboxamide	1.50	[147]
7C6S	boceprevir (bound form)	1.60	[148]
7CX9	3-iodanyl-1~{H}-indazole-7-carbaldehyde	1.73	[149]

bearing hexylcarbamide acid structure, in which the fatty acid tail occupies the hydrophobic S2 sub-site. A study reported that carmofur inhibits viral replication in cells (EC_{50} = 24.30 μM) and is a promising lead compound to develop a new antiviral treatment for SARS-Coronavirus-2.

A more diverse inhibitor's structure was observed from the 3D-crystal structure with PDB ID 5RGG which was resolved at 2.26 Å of resolution [104]; Fig. 7c). The inhibitor is a carboxamide derivative namely 4-methyl-*N*-phenylpiperazine-1-carboxamide, binds at HIS80 via H-bond interaction. Instead of H-bond, HIS80 was also interacting with the inhibitor via hydrophobic interaction which was co-bound with LYS90. This experiment could give an insight into understanding that even a small molecule is able to bind the protease. However, the potency of such inhibitor could be low due to the larger cavities which need an extending occupation.

6. Biflavonoid as the protease –Inhibitor

There are a few studies of biflavonoid-class compounds reporting their activities as protease inhibitors. Amentoflavone from *Torreya nucifera* was the early biflavonoid studied in its inhibitory activity against SARS-Coronavirus 3CLpro by showing IC_{50} 8.3 μM. The results were compared to three types of flavonoid (apigenin, luteolin, and quercetin) which showed less inhibition and therefore, the structure–activity relationships were generated to confirm that the more potent activity of biflavonoid appeared to be associated with the presence of benzene ring moiety at C-3′ position of flavones, as biflavone affected 3CLpro inhibitory activity [36].

Based on Ryu et al. findings, a QSAR study of biflavonoid and its analogs was carried out to generate a QSAR model defining the increasing value of the dipole moment along the X-axis that may be

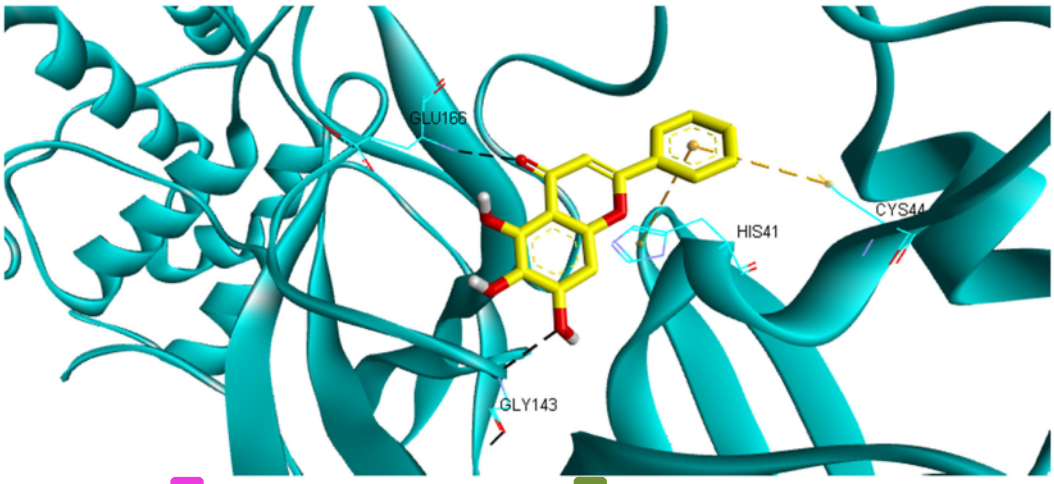


Fig. 5. The interaction between 5,6,7-trihydroxy-2-phenyl-4H-chromen-4-one and the active site of SARS-Coronavirus-2 (PDB ID 6M2N). The 3CLpro is presented in a blue ribbon model whereas the inhibitor is in a stick model (yellow = C, white = H, and red = O). The H-bond and hydrophobic interactions are presented in black and yellow dot lines, respectively. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

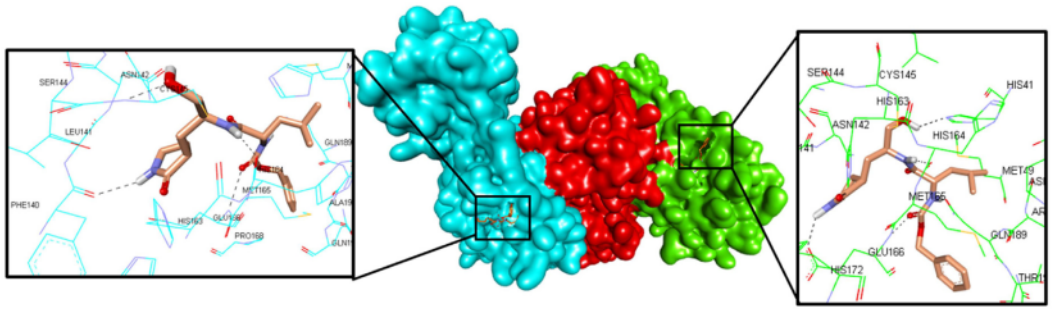


Fig. 6. The trimer structure of 3CLpro as indicated by blue (monomer A), red (monomer B), and green (monomer C) surface models. Inset is the ligand complex to the active site of the enzyme (presented by blue stick and green stick, for monomer A and monomer C, respectively), presented in a stick model (orange = C, white = H, blue = N and red = O). The H-bond is presented in black dot lines, respectively. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

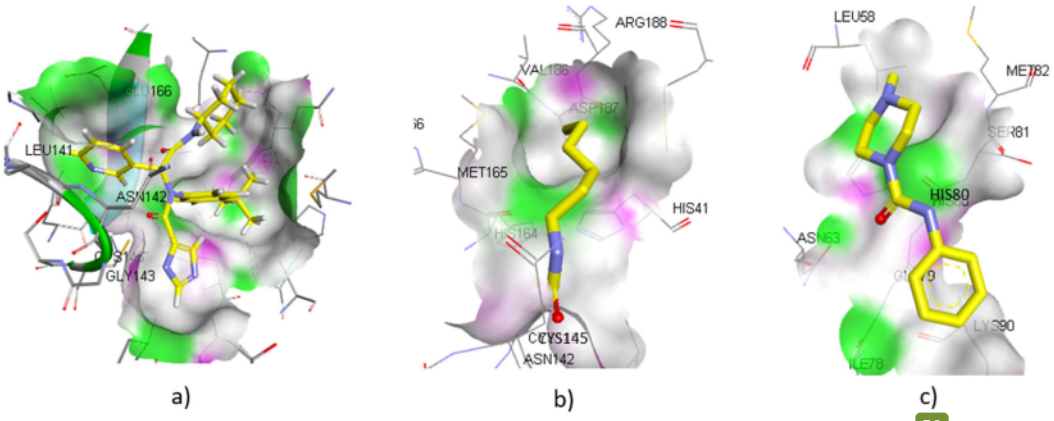


Fig. 7. The presentation of a) imidazole-4-carboxamide, b) carmofur, and c) 4-methyl-*N*-phenylpiperazine-1-carboxamide bound into the active site of SARS-Coronavirus-2 3CLpro. The protein is visualized in the surface model with the green area = hydrogen bond acceptor residues, white area = neutral residues, and magenta area = hydrogen bond donor residues. The ligands are presented in a stick form with yellow = C, white = H, blue = N, and red = O. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

conducive to the activity. Therefore, the steric character of this part may be favorable for its activity. Compounds having higher dipole moment due to the much bulky aryl groups, therefore, have a higher activity than the compound having less bulky aryl group [23].

The antiproteolytic activity of biflavonoid was determined early on morelloflavone-4‴-*O*-*β*-*D*-glycosyl, (±)-fukugiside, and morelloflavone. These biflavonoids were isolated from the fruit epocarp of *Garcinia brasiliensis* which were further semi synthesized into three moreflavone derivatives i.e. morelloflavone-7,4′,7″,3‴,4′‴- penta-*O*-acetyl, morelloflavone-7,4′,7″,3‴,4‴-penta-*O*-methyl, and morelloflavone-7,4′,7″,3‴,4‴-penta-[-butanoyl. High inhibitory activity was demonstrated by this biflavonioid against r-CPB2.8 and r-CPB3 isoforms which are papain-like protease of *Leismania mexicana* with IC_{50} 0.42–1.01 μM for the four most active compounds. Interestingly, there was no cytotoxic activity towards the normal cell lines as observed from the *in vitro* study [150].

Further study was pursued by the same research group in evaluating those biflavonoid activities against the cysteine protease (papain and cruzain) and serine protease of *Trypanozoma cruzii*. All biflavonoid compounds demonstrated excellent inhibitions toward all protease enzymes (IC_{50} 0.02–106 μM). However, morelloflavone-7,4′,7″,4‴′- penta-*O*-acetyl showed the best activity which might be due to the carbonyl group in the structure. This functional group could favor a higher nucleophilic attack by serine and cysteine proteases. This is in accordance with morelloflavone-7,4′,7″,3‴,4‴-penta-*O*-methyl (IC_{50} = 15.4 ± 0.7 μM for papain), in which the compound having no carbonyl group in structure was less active in the inhibition process. This was confirmed by the structure–activity relationships (SARs) study which had been performed using flexible docking simulations [151].

A study by Assis et al. reported that fukugetin, a biflavone originated from *Garcinia brasiliensis*, demonstrated partial competitive and hyperbolic-mix type inhibitions against the major cysteine protease of *Trypanosoma cruzii* (cruzain and papain), respectively. The potency of such biflavone was expressed in a slowly reversible type of inhibition with Ki 1.1 and 13.4 μM for cruzain and papain, respectively, describing that the biflavone has 12 times faster inhibition toward cruzain than papain in inhibiting the enzymes. The molecular docking study predicted that this activity is due to the chemical interaction between biflavone at ring C with S3 pocket, whereas the ring C' binds at S2 pocket through hydrogen bonds as well as the hydrophobic interactions [152].

Virtual screening was performed to identify the hits of the tryptase inhibitor followed by *in vitro* experiments to identify the lead compounds. Tryptase is a class of serine protease enzyme released as the allergic response such as skin inflammation and asthma from the mast cells. Out of the 98,000 compounds screened, 2.28% of the library (2503 compounds) were selected as the hits. Interestingly, biflavonoids were one of the most frequently represented in the 200 compounds with the strongest tryptase binding energy. Using fluorescence resonane energy transfer (FRET)-based assay, these 200 compounds were further *in vitro* screened to afford the lead compound, and then the biflavonoid podocorpus flavone A blocks the tryptase activity by 61.6.%. The docking study suggested that the biflavonoid is favorably binding at the S4 of tryptase [153].

Biflavonoid was also reported to down-regulate the expression of matrix metalloproteinase-1 (MMP-1) from human skin fibroblasts. MMP is a zymogen (zinc-dependent peptidase) that degrades the extracellular matrix to perform angiogenesis, inflammation, cell migration, and tissue remodeling. The high expression of this enzyme is often associated with cancer and wound diabetic foot ulcers. 2′,8″-biapigenin, sumaflavone, taiwaniaflavone, amentoflavone, and robustaflavone which were isolated from *Selaginella tamariscina* showed significant MMP-1 inhibitory activity in primary human dermal fibroblasts after UV irradiation. The IC_{50} values of sumaflavone, amentoflavone, and retinoic acid (used as the positive control) were 0.78, 1.8, and 10 μM, respectively [154].

7. Perspectives

Two main protein targets in the coronaviral genome are classified into structural and non-structural proteins. Structural protein which is composed of the membrane, envelope and nucleocapsid is formed in the inner viral cell, whereas the spike protein is located in the outer cell [155,156]. It might be difficult to control the activity of such structural protein because they control the virus's life during the viral cell assembly which could be too fast to control. Most likely, the host will be suddenly infected by the virus while there is no time to block the activity of the S protein during viral-host attachment as well as its endocytosis. Therefore, in designing the protein inhibitor for coronavirus, the non-structural protein could be more favorable than the structural protein due to its role in controlling the polypeptide proteolytic, reverse transcription, RNA replication as well as protein translation, which might take more time than the viral assembly.

Among the 16 non-structural proteins, NSP5 is the most attractive target while the others are still elusive [157]. The NSP5 main protease (3CLpro) is the most common targeted protein in coronavirus because it is formed in the host and acts during cleavage and post-translational polyprotein synthesis. Thus, it is relatively easier to control their activities. Two classes of the compound are reported to have these protein activities, including peptide and non-peptide compound. Naturally, the protease has a peptide substrate due to its function to hydrolyze the peptide bond upon proteolysis. Therefore, for a competitive inhibitor, a compound having a peptide-like structure should be suitable to block the enzyme-substrate binding. There are notable peptide (like) compounds demonstrating low micromolar activity towards the protease such as lopinavir and ritonavir [158].

Although peptide is the suitable structure designed for the protease inhibitor, however, the physic-chemical properties of this class of compound often make it fails under clinical trials. The peptide has a number of flexible bonds which makes it energetically unstable either during preparation or the pharmacokinetic stage. The structure is mimicking protein, therefore, it is sensitive towards denaturation and hydrolysis during preparation. At the pharmacokinetic stage especially during absorption, the peptide is less absorbed due to its isoelectric character which makes it very polar in aqueous biological fluids. Thus, it is hard to penetrate the intestinal membrane lipid bilayer [159]. This causes the peptide to become unsuitable for oral preparation which requires the absorption process.

Another alternative is formulated in the parenteral preparation. However, this is costly and not applicable to be administered by the patient. Therefore, the peptide is practically used as the model only and then should be further modified to the more rigid character to improve the stability. One effort has been conducted to formulate the drug delivery system to improve bioavailability such as using liposome technology. However, the use of organic solvents in the liposome dosage form could make it toxic [160,161].

Non-peptide or often called as small molecule inhibitors currently takes more attention used as the molecule target for protease inhibitors. The presence of aromatic rings could make the compound energetically more stable than the peptide due to its rigid character [162]. The rigid character causes less entropy of the compound and thus stabilizes the compound-enzyme affinity upon binding [163]. The non-peptide inhibitor can still be divided into natural and synthetic compounds. Natural compound is a unique structure due to the presence of chiral carbon which could make the ligand–protein binding more specific. A class of biflavonoid showed the *in vitro* competitive inhibition in low micromolar activities towards the protease which agreed with the docking explanation. Amentoflavone is the

early biflavonoid found active against 3CLpro of SARS-Coronavirus underlining the potency of 21 compounds to be this protease inhibitor. It was postulated that the presence of benzene ring moiety is at position C-3′ of flavones, as biflavone affected 3CLpro inhibitory activity. The synthetic (semi-synthetic) biflavonoids are the further strategy to get the product being more feasible to be developed as a protease inhibitor. Compounds bearing more carbonyl groups 4 seem promising to be the protease inhibitor as it is designed to favor a higher nucleophilic attack by serine 10 cysteine proteases using molecular docking. The complex of 5,6,7-trihydroxy-2-phenyl-4H-chromen-4-one with SARS-Coronavirus-2 3CLpro (PDB ID 6M2N) is one of the proofs that flavonoid is such an important feature for 3CLpro pharmacophore and so does the biflavonoid which could cover more space to interact with the 3CLpro.

3CLpro is still the most recommended protein target in the discovery of anti-SARS coronaviral agents. The availability of crystal structure and its high conserved binding site make the structure-based drug design becomes applicable [164,165]. The structure-based drug design can also be combined with ligand-based drug design since the structure information of the compounds either in peptide or non-peptide has been reported as the protease inhibitors. The non-peptide compound such as biflavonoid provides more promising candidate to enter either pre- or clinical stage due to its more stable physicchemical properties during preparation as well as pharmacokinetics.

8. Conclusion

In conclusion, our review strongly recommends that biflavonoid, either from the natural product or its synthetic is very potential to be used as of SARS-Coronavirus-2 3CLpro inhibitor. Its dimer and big structure are more suitable for a 3CLpro binding site composing two beta barrels than the corresponding flavones. To the best of our knowledge, this is the first review to describe the potential inhibit 31 effects of biflavonoid against SARS-Coronavirus-2 3CLpro. Thus, we believe that this compound may be a good candidate for development as a natural therapeutic drug against SARS-Coronavirus-2 infection.

CRediT authorship contribution statement

Yustina Hartini: Writing. **Bakti Saputra:** Writing. **Bryan Wahono:** Writing. **Zerlinda Auw:** Writing. **Friska Indayani:** Writing. **Lintang Adelya:** Writing. **Gabriel Namba:** Writing. **Maywan Hariono:** Conceptualization, Editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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