THE CONCISE GUIDE TO PHARMACOLOGY 2021/22: Introduction and Other Protein Targets

Stephen P H Alexander1, Eamonn Kelly2, Alistair Mathie3, John A Peters4, Emma L Veale5, Jane F Armstrong6, Elena Faccenda6, Simon D Hardings6, Adam J Pawson6, Christopher Southan6, O’Peter Buneman7, John A Cidlowski8, Arthur Christophoulopous9, Anthony P Davenport10, Doriano Fabbro11, Michael Spedding12, Jörg Striessnig13, Jamie A Davies6, Katelin E. Ahlers-Dannen14, Mohammed Alqinyah15, Thiruma V. Arumugam16, Christopher Bodle17, Josephine Buo Dagner15, Bandana Chakravarti14, Shreoshi P. Choudhuri18, Kirk M. Druey19, Rory A. Fisher14, Kyle J. Gerber20, John R. Hepler21, Shelley B. Hooks15, Havish S. Kantheti22, Behirda Karaj23, Somayeh Layeghi-Ghaelsoukht24, Jae-Kyung Lee15, Zili Luo14, Kirill Martemyanov25, Luke D. Mascarenha22, Harrison McNabb26, Carolina Montañez-Miranda21, Osita Ogujoiofor22, Hoa Phan23, David L. Roman14, Vincent Shaw27, Benita Sjogren26, Christopher Sobey28, Mackenzie M. Spicer14, Katherine E. Squires21, Laurie Sutton29, Menbere Wendimu15, Thomas Wilkie22, Keqiang Xie25, Qian Zhang26, and Yalda Zolghadri22

1School of Life Sciences, University of Nottingham Medical School, Nottingham, NG7 2UH, UK, 2School of Physiology, Pharmacology and Neuroscience, University of Bristol, Bristol, BS8 1TD, UK, 3School of Engineering, Arts, Science and Technology, University of Suffolk, Ipswich, IP4 1QJ, UK, 4Neuroscience Division, Medical Education Institute, Ninewells Hospital and Medical School, University of Dundee, Dundee, DD1 9SY, UK, 5Medway School of Pharmacy, The Universities of Greenwich and Kent at Medway, Anson Building, Central Avenue, Chatham Maritime, Chatham, Kent, ME4 4TB, UK, 6Centre for Discovery Brain Sciences, University of Edinburgh, Edinburgh, EH9 9AD, UK, 7Laboratory for Foundations of Computer Science, School of Informatics, University of Edinburgh, Edinburgh, EH9 3JL, UK, 8National Institute of Environmental Health Sciences, National Institutes of Health, Department of Health and Human Services, Research Triangle Park, NC, 27709, USA, 9Monash Institute of Pharmaceutical Sciences and Department of Pharmacology, Monash University, Parkville Victoria 3052, Australia, 10Clinical Pharmacology Unit, University of Cambridge, Cambridge, CB2 0QQ, UK, 11PIQUR Therapeutics, Basel 4057, Switzerland, 12Spedding Research Solutions SARL, Le Vésinet 78110, France, 13Pharmacology and Toxicology, Institute of Pharmacy, University of Innsbruck, A-6020 Innsbruck, Austria, 14University of Iowa, Iowa City, USA, 15University of Georgia, Athens, USA, 16National University of Singapore, Singapore, Singapore, 17University of Pittsburgh, Iowa City, USA, 18University of Texas Southwestern Medical Center, Dallas, USA, 19National Institute of Health, Bethesda, USA, 20Tetracore, Inc., Athens, USA, 21Emory University, Athens, USA, 22University of Texas Southwestern, Dallas, USA, 23University of Michigan, East Lansing, USA, 24Cobel Darou, Shiraz, Iran, 25Scripps Research Institute, Jupiter, USA, 26Purdue University, West Lafayette, USA, 27Michigan State University, East Lansing, USA, 28La Trobe University, Clayton, Australia, 29University of Maryland, Jupiter, USA

Searchable database: http://www.guidetopharmacology.org/index.jsp
Full Contents of Concise Guide: http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full
Abstract
The Concise Guide to PHARMACOLOGY 2021/22 is the fifth in this series of biennial publications. The Concise Guide provides concise overviews, mostly in tabular format, of the key properties of nearly 1900 human drug targets with an emphasis on selective pharmacology (where available), plus links to the open access knowledgebase source of drug targets and their ligands (www.guidetopharmacology.org), which provides more detailed views of target and ligand properties. Although the Concise Guide constitutes over 500 pages, the material presented is substantially reduced compared to information and links presented on the website. It provides a permanent, citable, point-in-time record that will survive database updates. The full contents of this section can be found at http://onlinelibrary.wiley.com/doi/bph.15537. In addition to this overview, in which are identified ‘Other protein targets’ which fall outside of the subsequent categorisation, there are six areas of focus: G protein-coupled receptors, ion channels, nuclear hormone receptors, catalytic receptors, enzymes and transporters. These are presented with nomenclature guidance and summary information on the best available pharmacological tools, alongside key references and suggestions for further reading. The landscape format of the Concise Guide is designed to facilitate comparison of related targets from material contemporary to mid-2021, and supersedes data presented in the 2019/20, 2017/18, 2015/16 and 2013/14 Concise Guides and previous Guides to Receptors and Channels. It is produced in close conjunction with the Nomenclature and Standards Committee of the International Union of Basic and Clinical Pharmacology (NC-IUPHAR), therefore, providing official IUPHAR classification and nomenclature for human drug targets, where appropriate.

Conflict of interest
The authors state that there are no conflicts of interest to disclose.

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**Ion channels**

- Oxoglutarate receptor
- P2Y receptors
- Parathyroid hormone receptors
- Platelet-activating factor receptor
- Prokineticin receptors
- Prolactin-releasing peptide receptor
- Prostanoid receptors
- Proteinase-activated receptors
- Relaxin family peptide receptors
- Somatostatin receptors
- Succinate receptors
- Tachykinin receptors
- Thyrotropin-releasing hormone receptors
- Trace amine receptor
- Urotensin receptor
- Vasopressin and oxytocin receptors
- VIP and PACAP receptors

**Catalytic receptors**

- Volume regulated chloride channels
- Connexins and Pannexins
- Piezo channels
- Sodium leak channel, non-selective
- Oral channels

**Nuclear hormone receptors**

- 1A. Thyroid hormone receptors
- 1B. Retinoic acid receptors
- 1C. Peroxisome proliferator-activated receptors
- 1D. Rev-Erb receptors
- 1E. Retinoic acid-related orphan receptors
- 1H. Liver X receptor-like receptors
- 1I. Vitamin D receptor-like receptors
- 2A. Hepatocyte nuclear factor-4 receptors
- 2B. Retinoid X receptors
- 2C. Testicular receptors
- 2D. Tailless-like receptors
- 2E. COUP-TFI-like receptors
- 2F. CYP-like receptors
- 3B. Estrogen-related receptors
- 3C. 3-Ketosteroid receptors
- 3A. Estrogen receptors
- 3A. Steroid hormone receptors
- 3A. Fushi tarazu F1-like receptors
- 3G. Germ cell nuclear factor receptor
- 3H. DAX-like receptors
- 3I. Estrogen receptors
- 3J. 3C. Testosteroid receptors

**Receptor tyrosine kinases (RTKs)**

- ErbB (epidermal growth factor) receptor family
- Insulin receptor family
- Kit family
- FLT3 receptor family
- VEGF (vascular endothelial growth factor) receptor family
- FGF (fibroblast growth factor) receptor family
- PTK7/CK1 family
- Neurotrophin receptor
- TRK family
- ROR family
- MuSK family
- HGF (hepatocyte growth factor) receptor family
- TAM (TYRO3-, AXL- and MERTK) receptor family
- Tie family of angiopoietin receptors
- Ephrin receptor family
- RET family
- TYK2 family
- DDR (collagen receptor) family
- ROS receptors
- LMR family
- LTK family
- Leukocyte tyrosine kinase (LTK) receptor family
- STYK1 family
- Serine/threonine kinase (RSTK) family
- Serine/threonine kinases
- Serine/threonine kinase
- RSTK functional heteromers
- Tyrosine phosphatase (RTP) family
- Tumour necrosis factor (TNF) receptor family

**Enzymes**

- Acetylcholine turnover
- Adenosine turnover
- Amino acid hydroxylases
- L-Arginine turnover
- Protein arginine N-methyltransferases
- Arginase
- Arginine/glycine amidinotransferase
- Dimethylarginine dimethylaminohydrolases
- Nitric oxide synthases
- Carbonic anhydrases
- Carboxylases
- Carboxyyses
- Catecholamine turnover
- Ceramide turnover
| S331 | Serine palmitoyltransferase |
| S331 | Sphingoid lipid Δ4-desaturase |
| S332 | Sphingomyelin synthase |
| S332 | Sphingomyelin phosphodiesterase |
| S333 | Neutral sphingomyelinase coupling factors |
| S334 | Ceramide glucosyltransferase |
| S335 | Acid ceramidase |
| S335 | Alkaline ceramidas |
| S335 | Ceramide kinase |
| S336 | Chromatin modifying enzymes |
| S337 | Histone deacetylases (HDACs) |
| S338 | Cyclic nucleotide turnover/signalling |
| S338 | Adenylyl cyclases (ACs) |
| S339 | Exchange protein activated by cyclic AMP (EPACs) |
| S340 | S404 Kynurenine 3-monooxygenase |
| S341 | Phosphodiesterases, 3',5'-cyclic nucleotide (PDEs) |
| S342 | Cytochrome P450 |
| S342 | N-acylethanolamine turnover |
| S342 | S401 1.14.13.9 Kynurenine 3-monooxygenase |
| S343 | Serine palmitoyltransferase |
| S343 | Sphingoid lipid Δ4-desaturase |
| S343 | Sphingomyelin synthase |
| S344 | Sphingomyelin phosphodiesterase |
| S345 | Neutral sphingomyelinase coupling factors |
| S346 | Ceramide glucosyltransferase |
| S347 | Acid ceramidase |
| S348 | Alkaline ceramidas |
| S349 | Ceramide kinase |
| S350 | Chromatin modifying enzymes |
| S351 | Histone deacetylases (HDACs) |
| S352 | Cyclic nucleotide turnover/signalling |
| S352 | Adenylyl cyclases (ACs) |
| S353 | Exchange protein activated by cyclic AMP (EPACs) |
| S354 | Cytochrome P450 |
| S355 | N-acylethanolamine turnover |
| S355 | S401 1.14.13.9 Kynurenine 3-monooxygenase |
| S356 | Phosphodiesterases, 3',5'-cyclic nucleotide (PDEs) |
| S357 | Cytochrome P450 |
| S358 | N-acylethanolamine turnover |
| S358 | S401 1.14.13.9 Kynurenine 3-monooxygenase |
| S359 | Chromatin modifying enzymes |
| S360 | Histone deacetylases (HDACs) |
| S361 | Cyclic nucleotide turnover/signalling |
| S361 | Adenylyl cyclases (ACs) |
| S362 | Exchange protein activated by cyclic AMP (EPACs) |
| S363 | Cytochrome P450 |
| S364 | N-acylethanolamine turnover |
| S364 | S401 1.14.13.9 Kynurenine 3-monooxygenase |
| S365 | Phosphodiesterases, 3',5'-cyclic nucleotide (PDEs) |
| S366 | Cytochrome P450 |
| S367 | N-acylethanolamine turnover |
| S367 | S401 1.14.13.9 Kynurenine 3-monooxygenase |
| S368 | Chromatin modifying enzymes |
| S369 | Histone deacetylases (HDACs) |
| S370 | Cyclic nucleotide turnover/signalling |
| S370 | Adenylyl cyclases (ACs) |
| S371 | Exchange protein activated by cyclic AMP (EPACs) |
| S372 | Cytochrome P450 |
| S373 | N-acylethanolamine turnover |
| S373 | S401 1.14.13.9 Kynurenine 3-monooxygenase |

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Introduction

In order to allow clarity and consistency in pharmacology, there is a need for a comprehensive organisation and presentation of the targets of drugs. This is the philosophy of the IUPHAR/BPS Guide to PHARMACOLOGY presented on the online free access database (http://www.guidetopharmacology.org/). This database is supported by the British Pharmacological Society (BPS), the International Union of Basic and Clinical Pharmacology (IUPHAR), the University of Edinburgh and previously the Wellcome Trust. Data included in the Guide to PHARMACOLOGY are derived in large part from interactions with the subcommittees of the Nomenclature and Standards Committee of the International Union of Basic and Clinical Pharmacology (NC-IUPHAR). A major influence on the development of the database was Tony Harmar (1951-2014), who worked with a passion to establish the curators as a team of highly informed and informative individuals, with a focus on high-quality data input, ensuring a suitably validated dataset. The editors of the Concise Guide have compiled the individual records, of highly informed and informative individuals, with a focus on attempts to fit in within the general guidelines from NC-IUPHAR. This current edition, the Concise Guide to PHARMACOLOGY 2021/22, is the latest snapshot of the database in print form, following on from the Concise Guide to PHARMACOLOGY 2019/20. It contains data drawn from the online database as a rapid overview of the major pharmacological targets. Thus, there are many fewer targets presented in the Concise Guide compared to the online database. The priority for inclusion in the Concise Guide is the presence of quantitative pharmacological data for human proteins. This means that often orphan family members are not presented in the Concise Guide, although structural information is available on the online database. The organisation of the data is tabular.
(where appropriate) with a standardised format, where possible on a single page, intended to aid understanding of, and comparison within, a particular target group. The Concise Guide is intended as an initial resource, with links to additional reviews and resources for greater depth and information. Pharmacological and structural data focus primarily on human gene products, wherever possible, with links to HGNC gene nomenclature and UniProt IDs. In a few cases, where data from human proteins are limited, data from other species are indicated. Pharmacological tools listed are prioritised on the basis of selectivity and availability. That is, agents (agonists, antagonists, inhibitors, activators, etc.) are included where they are both available (by donation or from commercial sources, now or in the near future) AND the most selective. The Concise Guide is divided into seven sections, which comprise pharmacological targets of similar structure/function. These are G protein-coupled receptors, ion channels (combining previous records of ligand-gated, voltage-gated and other ion channels), catalytic receptors, nuclear hormone receptors, enzymes, transporters and other protein targets. We hope that the Concise Guide will provide for researchers, teachers and students a state-of-the-art source of accurate, curated information on the background to their work that they will use in the Introductions to their Research Papers or Reviews, or in supporting their teaching and studies. We recommend that any citations to information in the Concise Guide are presented in the following format:
Alexander SPH et al. (2021). The Concise Guide to PHARMACOLOGY 2021/22: Overview. Br J Pharmacol 178: S1–S26.
In this overview are listed protein targets of pharmacological interest, which are not G protein-coupled receptors, ion channels, nuclear hormone receptors, catalytic receptors, transporters or enzymes. For obvious reasons, we have included potential drug targets of the SARS-CoV-2 virus, despite the current limited pharmacological data.

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Conflict of interest
The authors state that there are no conflicts of interest to disclose.

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Family structure

- Abscisic acid receptor complex
- Adiponectin receptors
- Anti-infective targets
- Antimalarial targets
- Other anti-infective targets
- Atrial natriuretic peptides
- Bcl-2 family
- Bromodomain-containing proteins
- Butyrophilin and butyrophilin-like proteins
- CD molecules
- Chaperone proteins
- Lipid binding chaperones
- Chitinase-like proteins
- Chromatin-interacting transcriptional repressors
- methylation reader proteins
- Circadian clock proteins
- Claudins
- Cytoytic pore-forming proteins
- EF-hand domain containing proteins
- Fatty acid-binding proteins
- Guanine nucleotide exchange factors (GEFs)
- Heat shock proteins
- Hypoxia-inducible factors
- Immune checkpoint proteins
- Immunoglobulin C1-set
- Immunoglobulin C2-set
- Immunoglobulin like domain containing proteins
- Immunoglobulins
- Inhibitors of apoptosis (IAP) protein family
- Kelch-like proteins
- Kinesins
- Leucine-rich repeat proteins
- Lymphocyte antigens
- Mitochondrial-associated proteins
- Myosin binding proteins
- Neutrophils and Plexins
- Non-catalytic pattern recognition receptors
- Notch receptors
- Nuclear export proteins
- Pentraxins
- Regulators of G protein signaling (RGS) proteins
- Rho family
- Rho family
- Repulsive guidance molecules
- Reticulons and associated proteins
- Ribosomal factors
- Sialic acid binding Ig like lectins
- Sigma receptors
- Signal regulatory proteins
- Tetrascins
- Transcription factors
- Transcription factor regulators
- NF-kB regulators
- Transferrin
- Tubulins
- Tumour-associated antigens
- WD repeat-containing proteins
- Plasmodium multidrug resistance family
- SARS-CoV-2
- Structural proteins
- Polyproteins
- Proteases
- Nucleic acid turnover
- Other proteins

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Adiponectin receptors
Other protein targets → Adiponectin receptors

Overview: Adiponectin receptors (provisional nomenclature, ENSM0000000270960) respond to the 30 kDa complement-related protein hormone adiponectin (also known as ADIPOQ; adipocyte, C1q and collagen domain-containing protein; ACRP30, adipose most abundant gene transcript 1; apM-1; gelatin-binding protein: Q15848) originally cloned from adipocytes [69]. Although sequence data suggest 7TM domains, immunological evidence indicates that, contrary to typical 7TM topology, the carboxyl terminus is extracellular, while the amino terminus is intracellular [136]. Signalling through these receptors appears to avoid G proteins; modelling based on the crystal structures of the adiponectin receptors suggested ceramidase activity, which would make these the first in a new family of catalytic receptors [121].

Further reading on Adiponectin receptors
Fisman EZ et al. (2014) Adiponectin: a manifold therapeutic target for metabolic syndrome, diabetes, and coronary disease? Cardiovasc Diabetol 13: 103 [PMID:24957699]
Okada-Iwabu M et al. (2018) Structure and function analysis of adiponectin receptors toward development of novel antidiabetic agents promoting healthy longevity. Endocr J 65: 971-977 [PMID:30282888]
Ruan H et al. (2016) Adiponectin signaling and function in insulin target tissues. J Mol Cell Biol 8: 101-9 [PMID:26993044]
Wang Y et al. (2017) Cardiovascular Adiponectin Resistance: The Critical Role of Adiponectin Receptor Modification. Trends Endocrinol Metab 28: 519-530 [PMID:28473178]
Zhao L et al. (2014) Adiponectin and insulin cross talk: the microvascular connection. Trends Cardiovasc Med 24: 319-24 [PMID:25220977]

| Nomenclature | Adipo1 receptor | Adipo2 receptor |
|--------------|----------------|----------------|
| HGNC, UniProt | ADIPOR1, Q96A54 | ADIPOR2, Q86V24 |
| Rank order of potency | globular adiponectin (ADIPOQ, Q15848) > adiponectin (ADIPOQ, Q15848) | globular adiponectin (ADIPOQ, Q15848) = adiponectin (ADIPOQ, Q15848) |

Comments: T-Cadherin (CDH13, P55290) has also been suggested to be a receptor for (hexameric) adiponectin [47].
Aryl hydrocarbon receptor

Overview: The aryl hydrocarbon receptor, highly expressed in the liver and barrier organs, is resident in the cytoplasm bound to the chaperone heat shock protein hsp90. Upon agonist activation, the ligand:aryl hydrocarbon receptor complex migrates to the nucleus and binds the aryl hydrocarbon receptor nuclear translocator (ARNT, P27540, also known as HIF1β). The complex regulates transcription of selected genes through interaction with xenobiotic response elements (XRE). Among the genes regulated by the AHR/ARNT complex are cytochrome P450s, particularly CYP1A1, and the period circadian protein homolog 1 (PER1, O15534). The aryl hydrocarbon receptor is also capable of non-genomic signalling.

Further reading on Aryl hydrocarbon receptor

Bock KW. (2019) Aryl hydrocarbon receptor (AHR): From selected human target genes and crosstalk with transcription factors to multiple AHR functions. *Biochem Pharmacol* **168**: 65-70 [PMID:31228464]

Bock KW. (2020) Aryl hydrocarbon receptor (AHR) functions: Balancing opposing processes including inflammatory reactions. *Biochem Pharmacol* **178**: 114093 [PMID:32535308]

Esser C et al. (2015) The aryl hydrocarbon receptor in barrier organ physiology, immunology, and toxicology. *Pharmacol Rev* **67**: 259-79 [PMID:25657351]

Roman ÁC et al. (2018) The aryl hydrocarbon receptor in the crossroad of signalling networks with therapeutic value. *Pharmacol Ther* **185**: 50-63 [PMID:29258844]

Rothhammer V et al. (2019) The aryl hydrocarbon receptor: an environmental sensor integrating immune responses in health and disease. *Nat Rev Immunol* **19**: 184-197 [PMID:30718831]

Shi Y et al. (2020) The aryl hydrocarbon receptor: An environmental effector in the pathogenesis of fibrosis. *Pharmacol Res* **160**: 105180 [PMID:32877693]

Nomenclature

HGNC, UniProt

Aryl hydrocarbon receptor  
*AHRR, P35869*

Agonists

indolo[3,2-b]carbazole [12] – Mouse, tapinarof [110], indole-3-carbinol [12] – Mouse, TCDD ezutromid (pKd 7.3) [132]

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)  
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Aryl hydrocarbon receptor S9
Non-enzymatic BRD containing proteins

Other protein targets → Bromodomain-containing proteins → Non-enzymatic BRD containing proteins

Overview: Bromodomains bind proteins with acetylated lysine residues, such as histones, to regulate gene transcription. Listed herein are examples of bromodomain-containing proteins for which sufficient pharmacology exists.

Further reading on Non-enzymatic BRD containing proteins

Fujisawa T et al. (2017) Functions of bromodomain-containing proteins and their roles in homeostasis and cancer. Nat Rev Mol Cell Biol 18: 246-262 [PMID:28053347]
Miyantiopoulos V et al. (2019) From bench to bedside, via desktop. Recent advances in the application of cutting-edge in silico tools in the research of drugs targeting bromodomain modules. Biochim Biophys Acta 159: 40-51 [PMID:30414936]
Nicholas DA et al. (2017) BET bromodomain proteins and epigenetic regulation of inflammation: implications for type 2 diabetes and breast cancer. Cell Mol Life Sci 74: 231-243 [PMID:27491296]
Ramadoss M et al. (2018) Targeting the cancer epigenome: synergistic therapy with bromodomain inhibitors. Drug Discov Today 23: 76-89 [PMID:2984305]
Sprano F et al. (2020) Targeting BET bromodomain proteins in cancer: The example of lymphomas. Pharmacol Ther 215: 107631 [PMID:32693114]
Tang P et al. (2021) Targeting Bromodomain and Extraterminal Proteins for Drug Discovery: From Current Progress to Technological Development. J Med Chem 64: 2419-2435 [PMID:33616410]

Nomenclature|
|-----------------|-----------------|-----------------|-----------------|-----------------|
| Nomenclature | bromodomain adjacent to zinc finger domain 2A | bromodomain adjacent to zinc finger domain 2B | CREB binding protein | polybromo 1 |
| HGNC, UniProt | BAZ2A, Q9UIF9 | BAZ2B, Q9UIF8 | CREBBP, Q92793 | PBRM1, Q86U86 |
| Selective inhibitors | GSK2801 ($pK_d$ 6.6) [87] | GSK2801 (Binding) ($pK_d$ 6.9) [87] | I-CBP112 ($pK_d$ 6.8) [88] | PFI-3 (Binding) ($pK_d$ 7.3) [101] |
| Selective inhibitors | | | | PFI-3 (Binding) ($pK_d$ 7.1) [101] |

Searchable database: http://www.guidetopharmacology.org/index.jsp
Full Contents of ConciseGuide: http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full
CD molecules
Other protein targets → CD molecules

Overview: Cluster of differentiation refers to an attempt to catalogue systematically a series of over 300 cell-surface proteins associated with immunotyping. Many members of the group have identified functions as enzymes (for example, see CD73 ecto-5'-nucleotidase) or receptors (for example, see CD41 integrin, alpha 2b subunit). Many CDs are targeted for therapeutic gain using antibodies for the treatment of proliferative disorders. A full listing of all the Clusters of Differentiation proteins is not possible in the Guide to PHARMACOLOGY; listed herein are selected members of the family targeted for therapeutic gain.

Further reading on CD molecules
Bewersdorf JP et al. (2021) Immune checkpoint inhibition in myeloid malignancies: Moving beyond the PD-1/PD-L1 and CTLA-4 pathways. Blood Rev 45: 100709 [PMID:32487480]
Chi Z et al. (2021) Transcriptional and epigenetic regulation of PD-1 expression. Cell Mol Life Sci 78: 3239-3246 [PMID:3378533]
Gabius HJ et al. (2015) The glyciobiology of the CD system: a dictionary for translating marker designations into glycan/lectin structure and function. Trends Biochem Sci 40: 360-76
Huang MY et al. (2021) Combination therapy with PD-1/PD-L1 blockade in non-small cell lung cancer: strategies and mechanisms. Pharmacol Ther 219: 107694 [PMID:32980443]
Vosoughi T et al. (2019) CD markers variations in chronic lymphocytic leukemia: New insights into prognosis. J Cell Physiol 234: 19420-19439 [PMID:31049958]

| Nomenclature | CD2 | CD3e | CD6 | CD20 (membrane-spanning 4-domains, subfamily A, member 1) | CD33 |
|--------------|-----|------|-----|----------------------------------------------------------|------|
| Common abbreviation | – | – | – | – | SIGLEC3 |
| HGNC, UniProt | CD2, P06729 | CD3E, P07766 | CD6, P30203 | M54A1, P11836 | CD33, P20138 |
| Selective inhibitors | alefacept [23, 74] | – | – | ofatumumab (Binding) (pKd 9.9) [58], rituximab (Binding) (pKd 8.5) [113], birtumomab tiuxetan (Binding), obinutuzumab (Binding) [3, 90], tositumomab (Binding) | – |
| Antibodies | – | catumaxomab (Binding) [63], muromonab-CD3 (Binding) [32], otelixizumab (Binding) [14] | – | lintuzumab (Binding) (pKd ~10) [16], gemtuzumab ozogamicin (Binding) [10] | – |

Searchable database: http://www.guidetopharmacology.org/index.jsp
Full Contents of ConciseGuide: http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full
### Nomenclature

| CD52 | CD80 | CD86 | Cytotoxic T-lymphocyte-associated protein 4 (CD152) | Programmed cell death 1 (CD279) | CD300a |
|------|------|------|---------------------------------------------------|---------------------------------|--------|
|      |      |      | CTLA-4                                            | PD-1                            |        |
| CD52, P31358 | CD80, P33681 | CD86, P42081 | CTLL4, P16410                                      | PDCD1, Q15116                   | CD300A, Q9UCN4 |

### Endogenous ligands

| CD52 | CD80 | CD86 | Cytotoxic T-lymphocyte-associated protein 4 (CD152) | Programmed cell death 1 (CD279) | CD300a |
|------|------|------|---------------------------------------------------|---------------------------------|--------|
|      |      |      | CTLA-4                                            | PD-1                            |        |

### Selective inhibitors

| CD52 | CD80 | CD86 | Cytotoxic T-lymphocyte-associated protein 4 (CD152) | Programmed cell death 1 (CD279) | CD300a |
|------|------|------|---------------------------------------------------|---------------------------------|--------|
|      |      |      | CTLA-4                                            | PD-1                            |        |

### Antibodies

| CD52 | CD80 | CD86 | Cytotoxic T-lymphocyte-associated protein 4 (CD152) | Programmed cell death 1 (CD279) | CD300a |
|------|------|------|---------------------------------------------------|---------------------------------|--------|
|      |      |      | CTLA-4                                            | PD-1                            |        |

**Comments**: The endogenous ligands for human PD-1 are programmed death 1 ligand 1 (PD-L1 aka CD274 (CD274, Q9NZQ7)) and programmed death 1 ligand 2 (PD-L2; PDCD1LG2). These ligands are cell surface peptides, normally involved in immune system regulation. Expression of PD-1 by cancer cells induces immune tolerance and evasion of immune system attack. Anti-PD-1 monoclonal antibodies are used to induce immune checkpoint blockade as a therapeutic intervention in cancer, effectively re-establishing immune vigilance. Pembrolizumab was the first anti-PD-1 antibody to be approved by the US FDA.
Methyllysine reader proteins
Other protein targets → Chromatin-interacting transcriptional repressors → Methyllysine reader proteins

Overview: Methyllysine reader proteins bind to methylated proteins, such as histones, allowing regulation of gene expression.

Further reading on Methyllysine reader proteins
Daskalaki MG et al. (2018) Histone methylation and acetylation in macrophages as a mechanism for regulation of inflammatory responses. *J Cell Physiol* **233**: 6495-6507 [PMID:29574768]
Furuya K et al. (2019) Epigenetic interplays between DNA demethylation and histone methylation for protecting oncogenesis. *J Biochem* **165**: 297-299 [PMID:30605533]
Levy D. (2019) Lysine methylation signaling of non-histone proteins in the nucleus. *Cell Mol Life Sci* **76**: 2873-2883 [PMID:31123776]
Li J et al. (2019) Understanding histone H3 lysine 36 methylation and its deregulation in disease. *Cell Mol Life Sci* **76**: 2899-2916 [PMID:31147750]
Shafabakhsh R et al. (2019) Role of histone modification and DNA methylation in signaling pathways involved in diabetic retinopathy. *J Cell Physiol* **234**: 7839-7846 [PMID:30515789]

Nomenclature
HGNC, Uniprot
Selective agonists
L3MBTL histone methyl-lysine binding protein 3
L3MBTL3, Q96JM7
UNC1215 [50]

Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)
Full Contents of ConciseGuide: [http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full](http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full)
Fatty acid-binding proteins

Overview: Fatty acid-binding proteins are low molecular weight (100-130 aa) chaperones for long chain fatty acids, fatty acyl CoA esters, eicosanoids, retinols, retinoic acids and related metabolites and are usually regarded as being responsible for allowing the otherwise hydrophobic ligands to be mobile in aqueous media. These binding proteins may perform functions extracellularly (e.g., in plasma) or transport these agents; to the nucleus to interact with nuclear receptors (principally PPARs and retinoic acid receptors [99]) or for interaction with metabolic enzymes. Although sequence homology is limited, crystallographic studies suggest conserved 3D structures across the group of binding proteins.

Further reading on Fatty acid-binding proteins

Gajda AM et al. (2015) Enterocyte fatty acid-binding proteins (FABPs): different functions of liver and intestinal FABPs in the intestine. Prostaglandins Leukot Essent Fatty Acids 93: 9-16 [PMID:25458893]

Glatz JF. (2015) Lipids and lipid binding proteins: a perfect match. Prostaglandins Leukot Essent Fatty Acids 93: 45-9 [PMID:25154384]

Hotamisligil GS et al. (2015) Metabolic functions of FABPs—mechanisms and therapeutic implications. Nat Rev Endocrinol 11: 592-605 [PMID:26260145]

Matsumata M et al. (2016) Fatty acid binding proteins and the nervous system: Their impact on mental conditions. Neurosci Res 102: 47-55 [PMID:25205626]

Nguyen HC et al. (2020) Role of the Fatty Acid Binding Proteins in Cardiovascular Diseases: A Systematic Review. J Clin Med 9: [PMID:33105856]

Osumi T et al. (2016) Heart lipid droplets and lipid droplet-binding proteins: Biochemistry, physiology, and pathology. Exp Cell Res 340: 47-55 [PMID:25205626]

Searchable database: http://www.guidetopharmacology.org/index.jsp
Full Contents of ConciseGuide: http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full
### Nomenclature

| Fatty Acid-Binding Proteins | Retinol-Binding Proteins | Retinaldehyde-Binding Proteins |
|-----------------------------|--------------------------|--------------------------------|
| **HGNC, UniProt**           | **HGNC, UniProt**        | **HGNC, UniProt**              |
| FABP6, P51161               | RBP1, P09455             | RLBP1, P12271                  |
| FABP7, O15540               | RBP2, P50120             | CRABP1, P29762                 |
| PMP2, P02689                | RBP3, P10745             | CRABP2, P29373                 |
| FABP9, Q0Z7S8               | RBP4, P02753             |                               |
| FABP12, A6NFH5              | RBP5, P82980             |                               |
|                             | RBP7, Q96R05             |                               |

### Rank Order of Potency

- **Fatty Acid-Binding Proteins**
  - FABP6
  - FABP7
  - PMP2
  - FABP9
  - FABP12

- **Retinol-Binding Proteins**
  - RBP1
  - RBP2
  - RBP3
  - RBP4
  - RBP5
  - RBP7

- **Retinaldehyde-Binding Proteins**
  - RLBP1
  - CRABP1
  - CRABP2

### Inhibitors

- **Fatty Acid-Binding Proteins**
  - A1120 (pIC<sub>50</sub> 7.8) [128]

- **Retinol-Binding Proteins**
  - A1120 (pIC<sub>50</sub> 7.8) [128]

- **Retinaldehyde-Binding Proteins**
  - A1120 (pIC<sub>50</sub> 7.8) [128]

### Comments

- Although not tested at all FABPs, BMS309403 exhibits high affinity for FABP4 (pIC<sub>50</sub> 8.8) compared to FABP3 or FABP5 (pIC<sub>50</sub> < 6.6) [27, 118]. HTS01037 is reported to interfere with FABP4 action [42]. Ibuprofen displays some selectivity for FABP4 (pIC<sub>50</sub> 5.5) relative to FABP3 (pIC<sub>50</sub> 3.5) and FABP5 (pIC<sub>50</sub> 3.8) [68]. Fenofibric acid displays some selectivity for FABP5 (pIC<sub>50</sub> 5.5) relative to FABP3 (pIC<sub>50</sub> 4.5) and FABP4 (pIC<sub>50</sub> 4.6) [68]. Multiple pseudogenes for the FABPs have been identified in the human genome.

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Searchable database: [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

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**Notch receptors**

Other protein targets → Notch receptors

**Overview:** Aberrant Notch signalling is implicated in a number of human cancers [59, 80, 108, 126], and there is intense pharmaceutical activity being directed towards achieving clinically effective Notch pathway inhibition [24, 75].

**Further reading on Notch receptors**

Fabbro D et al. (2020) Notch Inhibition in Cancer: Challenges and Opportunities. *Chimia (Aarau)* **74**: 779-783 [PMID:33115560]

Moore G et al. (2020) Top Notch Targeting Strategies in Cancer: A Detailed Overview of Recent Insights and Current Perspectives. *Cells* **9**: [PMID:32575680]

Palmer WH et al. (2015) Ligand-Independent Mechanisms of Notch Activity. *Trends Cell Biol* **25**: 697-707 [PMID:26437585]

Previs RA et al. (2015) Molecular pathways: translational and therapeutic implications of the Notch signaling pathway in cancer. *Clin Cancer Res* **21**: 955-61 [PMID:25388163]

Takebe N et al. (2015) Targeting Notch, Hedgehog, and Wnt pathways in cancer stem cells: clinical update. *Nat Rev Clin Oncol* **12**: 445-64 [PMID:25850553]

**Nomenclature**

| Nomenclature | HGNC, UniProt | Inhibitors | Antibodies | Comments |
|--------------|---------------|------------|------------|----------|
| notch receptor 1 | *NOTCH1*, P46531 | IMR-1 (Binding) (pK<sub>d</sub> 5) [8] | brontictuzumab (Binding) (pK<sub>d</sub> 8.4) [30] | Various types of activating and inactivating NOTCH1 mutations have been reported to be associated with human diseases, for example: aortic valve disease [29, 73], Adams-Oliver syndrome 5 [114], T-cell acute lymphoblastic leukemia (T-ALL) [130], chronic lymphocytic leukemia (CLL) [89] and head and neck squamous cell carcinoma [1, 113]. |
| notch receptor 2 | *NOTCH2*, Q04721 | - | tarextumab (Binding) (pK<sub>d</sub> 10) [31] | - |
| notch receptor 3 | *NOTCH3*, Q9UM47 | - | tarextumab (Binding) (pK<sub>d</sub> 9.9) [31] | - |
| notch receptor 4 | *NOTCH4*, Q99466 | - | - | Notch receptor 4 is a potential therapeutic molecular target for triple-negative breast cancer [60, 77]. |

**Searchable database:** [http://www.guidetopharmacology.org/index.jsp](http://www.guidetopharmacology.org/index.jsp)

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Regulators of G protein Signaling (RGS) proteins

Overview: Regulator of G protein Signaling, or RGS, proteins serve an important regulatory role in signaling mediated by G protein-coupled receptors (GPCRs). They all share a common RGS domain that directly interacts with active, GTP-bound Gα subunits of heterotrimeric G proteins. RGS proteins stabilize the transition state for GTP hydrolysis on Gα and thus induce a conformational change in the Gα subunit that accelerates GTP hydrolysis, thereby effectively turning off signaling cascades mediated by GPCRs. This GTPase accelerating protein (GAP) activity is the canonical mechanism of action for RGS proteins, although many also possess additional functions and domains. RGS proteins are divided into four families, R4, R7, R12 and RZ, based on sequence homology, domain structure as well as specificity towards Gα subunits. For reviews on RGS proteins and their potential as therapeutic targets, see e.g. [5, 45, 79, 93, 105, 106, 107, 138, 140].

Further reading on Regulators of G protein Signaling (RGS) proteins

Alqinyah M et al. (2018) Regulating the regulators: Epigenetic, transcriptional, and post-translational regulation of RGS proteins. Cell Signal 42: 77-87 [PMID:29042285]
Fuentes N et al. (2021) RGS proteins, GRKs, and beta-arrestins modulate G protein-mediated signaling pathways in asthma. Pharmacol Ther 223: 107818 [PMID:33600853]
Neubig RR et al. (2002) Regulators of G-protein signalling as new central nervous system drug targets. Nat Rev Drug Discov 1: 187-97 [PMID:12120503]
Sethakorn N et al. (2010) Non-canonical functions of RGS proteins. Cell Signal 22: 1274-81 [PMID:20363320]
Sjögren B. (2017) The evolution of regulators of G protein signalling proteins as drug targets - 20 years in the making: IUPHAR Review 21. Br J Pharmacol 174: 427-437 [PMID:28098342]
Sjögren B et al. (2010) Thinking outside of the “RGS box”: new approaches to therapeutic targeting of regulators of G protein signaling. Mol Pharmacol 78: 550-7 [PMID:20664002]

RZ family

Overview: The RZ family of RGS proteins is less well characterized than the other families. It consists of, RGS17 (also known as RGSZ2), RGS19 (also known as GAIP) and RGS20 (with several splice variants including RGSZ1 and Ret-RGS). All members contain an N-terminal cysteine string motif [62] which is a site of palmitoylation and could serve functions in membrane targeting, protein stability or aid protein-protein interactions [2, 62]. However, the function in the case of RZ family RGS proteins is not yet fully understood. Members of the RZ family of RGS proteins are the only RGS proteins that have selective GAP activity for Gαz, a function that resulted in the name of the family [31, 71, 127, 134]. However, the members of the RZ family are able to also GAP Gαi/o members with varying selectivity.

Nomenclature

| Regulation of G-protein signaling 17 | Regulation of G-protein signaling 19 | Regulation of G-protein signaling 20 |
|-------------------------------------|-------------------------------------|-------------------------------------|
| Common abbreviation: RGS17          | Common abbreviation: RGS19          | Common abbreviation: RGS20          |
| HGNC, UniProt: RGS17/Q9UGC6         | HGNC, UniProt: RGS19/P49795          | HGNC, UniProt: RGS20/Q76081         |

Searchable database: http://www.guidetopharmacology.org/index.jsp
Full Contents of Concise Guide: http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full
R4 family

Overview: The R4 family of RGS proteins is the largest family of RGS proteins with 10 members. Each of the R4 family members contain only small N- and C-termini apart from the RGS domain. The N-terminal amphipathic helix present in most R4 family members serves an important function in membrane association and can directly bind phospholipids. In contrast to the RGS domain, which is well conserved among members of the R4 family of RGS proteins, the N- and C-termini vary, enabling specificity of non-GAP functions. Despite the non-complex structure of these proteins, several R4 family RGS proteins have been shown to possess additional functions apart from acting as GAPs at activated Gα subunits [11, 96].

Further reading on R4 family

Xie Z et al. (2016) R4 Regulator of G Protein Signaling (RGS) Proteins in Inflammation and Immunity. AAPS J 18: 294-304 [PMID:26597290]

| Nomenclature | regulator of G-protein signaling 1 | regulator of G-protein signaling 2 | regulator of G-protein signaling 3 | regulator of G-protein signaling 4 |
|--------------|-----------------------------------|-----------------------------------|-----------------------------------|-----------------------------------|
| Common abbreviation | RGS1 | RGS2 | RGS3 | RGS4 |
| HGNC, UniProt | RGST1, O08116 | RGST2, P41220 | RGST3, P49796 | RGST4, P49798 |
| Selective inhibitors | – | – | – | RGS4 inhibitor 11b (pIC50 7.8) [124], CCG-50014 (pIC50 7.5) [13, 124], RGS4 inhibitor 13 (pIC50 7.3) [124] |

| Nomenclature | regulator of G-protein signaling 5 | regulator of G-protein signaling 8 | regulator of G-protein signaling 13 | regulator of G-protein signaling 16 | regulator of G-protein signaling 18 | regulator of G-protein signaling 21 |
|--------------|-----------------------------------|-----------------------------------|-----------------------------------|-----------------------------------|-----------------------------------|-----------------------------------|
| Common abbreviation | RGS5 | RGS8 | RGS13 | RGS16 | RGS18 | RGS21 |
| HGNC, UniProt | RGSS, O15539 | RGSS, P57771 | RGSS, O14921 | RGSS, O15492 | RGSS, Q9NS28 | RGSS, Q2M5E4 |
**R7 family**

Other protein targets → Regulators of G protein Signaling (RGS) proteins → R7 family

**Overview:** The members of the R7 family of RGS proteins [6] are more complex structures than the R4 family and are closely related to the *C. elegans* homologues EGL-10 and EAT-16 that were identified in the early stage of RGS protein research [36, 55]. Apart from the RGS domain, several additional domains are present in these proteins that mediate protein-protein interactions, sub-cellular localization and protein stability. All R7 family members form obligatory dimers with Gβ5 through the G-γ-like (GGL) domain and the disheveled-EGL10-Pleckstrin homology (DEP) domain [109]. The DEP and DEP helical extension domain interact with R7 binding protein (R7BP) or RGS9 anchoring protein (R9AP; in retina) that serves as a plasma membrane anchoring mechanism [41, 51].

| Nomenclature | regulator of G-protein signaling 6 | regulator of G-protein signaling 7 | regulator of G-protein signaling 9 | regulator of G-protein signaling 11 |
|--------------|-----------------------------------|-----------------------------------|-----------------------------------|-----------------------------------|
| Common abbreviation | RGS6 | RGS7 | RGS9 | RGS11 |
| HGNC, UniProt | RG36, P49758 | RG37, P49802 | RG39, O75916 | RG37, O94810 |

**R12 family**

Other protein targets → Regulators of G protein Signaling (RGS) proteins → R12 family

**Overview:** The R12 family consisting of RGS10, 12 and 14. RGS12 and 14 are large proteins with additional domains that can participate in protein-protein interactions and other functions. In contrast, RGS10 is a small protein consisting of the RGS domain and small N- and C-termini, similar to members of the R4 family. However, the sequence homology the RGS10 RGS domain clearly places it in the R12 family [58]. The Ga<sub>10</sub>-Loco (GoLoco) motif in RGS12 and 14 has GDI activity (for Guanine nucleotide Dissociation Inhibitor) towards Ga<sub>11</sub>, Ga<sub>2</sub> and Ga<sub>13</sub> [S3, 105]. Through this activity RGS12 and RGS14 can inhibit G protein signaling both by accelerating GTP hydrolysis and by preventing G protein activation. Splice variants of RGS12 and RGS14 also contain membrane targeting and protein-protein interaction domains [97, 111, 112].

| Nomenclature | regulator of G-protein signaling 10 | regulator of G-protein signaling 12 | regulator of G-protein signaling 14 |
|--------------|-----------------------------------|-----------------------------------|-----------------------------------|
| Common abbreviation | RGS10 | RGS12 | RGS14 |
| HGNC, UniProt | RG510, O43665 | RG512, O14924 | RG514, O43566 |

Searchable database: http://www.guidetopharmacology.org/index.jsp
Full Contents of ConciseGuide: http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full
Sigma receptors
Other protein targets → Sigma receptors

**Overview:** Although termed ‘receptors’, the evidence for coupling through conventional signalling pathways is lacking. Initially described as a subtype of opioid receptors, there is only a modest pharmacological overlap and no structural convergence with the G protein-coupled receptors; the crystal structure of the sigma1 receptor [98] suggests a trimeric structure of a single short transmembrane domain traversing the endoplasmic reticulum membrane, with the bulk of the protein facing the cytosol. A wide range of compounds, ranging from psychoactive agents to antihistamines, have been observed to bind to these sites.

**Further reading on Sigma receptors**

Chu UB et al. (2016) Biochemical Pharmacology of the Sigma-1 Receptor. *Mol Pharmacol* 89: 142-53 [PMID:26560551]

Herrando-Grabulosa M et al. (2021) Sigma 1 receptor as a therapeutic target for amyotrophic lateral sclerosis. *Br J Pharmacol* 178: 1336-1352 [PMID:32761823]

Sambo DO et al. (2018) The sigma-1 receptor as a regulator of dopamine neurotransmission: A potential therapeutic target for methamphetamine addiction. *Pharmacol Ther* 186: 152-167 [PMID:29360540]

Schmidt HR et al. (2019) The Molecular Function of σ Receptors: Past, Present, and Future. *Trends Pharmacol Sci* 40: 636-654 [PMID:31387763]

Su TP et al. (2016) The Sigma-1 Receptor as a Pluripotent Modulator in Living Systems. *Trends Pharmacol Sci* 37: 262-278 [PMID:26869505]

Vavers E et al. (2019) Allosteric Modulators of Sigma-1 Receptor: A Review. *Front Pharmacol* 10: 223 [PMID:30941035]

| Nomenclature | sigma non-opioid intracellular receptor 1 | α2 |
|--------------|-------------------------------------|-----|
| HGNC, UniProt | SIGMAR1, Q99720 | TMEM97, Q5BJF2 |
| Agonists | – | 1,3-ditolylguanidine [61] – Guinea pig |
| Selective agonists | PRE-084 [117], (+)-SKF 10.047 | – |
| Antagonists | – | SM 21 (pIC50 7.2) [67] |
| Selective antagonists | NE-100 (pIC50 8.4) [81], BD-1047 (pIC50 7.4) [72] | – |
| Labelled ligands | [3H]pentazocine (Agonist) | [3H]-di-o-tolylguanidine (Agonist) |
| Comments | The sigma2 receptor has been reported to be TMEM97 [4], a 4TM protein partner of NPC1, the Niemann-Pick C1 protein, a 13TM cholesterol-binding protein. | The sigma2 receptor has recently been reported to be TMEM97 [4], a 4TM protein partner of NPC1, the Niemann-Pick C1 protein, a 13TM cholesterol-binding protein. |

**Comments:** (-)-pentazocine also shows activity at opioid receptors. The sigma2 receptor has recently been reported to be TMEM97 [4], a 4TM protein partner of NPC1, the Niemann-Pick C1 protein, a 13TM cholesterol-binding protein.

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Transthyretin
Other protein targets → Transthyretin

Overview: Transthyretin (TTR) is a homo-tetrameric protein which transports thyroxine in the plasma and cerebrospinal fluid and retinol (vitamin A) in the plasma. Many disease causing mutations in the protein have been reported, many of which cause complex dissociation and protein mis-assembly and deposition of toxic aggregates amyloid fibril formation [84]. These amyloidogenic mutants are linked to the development of pathological amyloidoses, including familial amyloid polyneuropathy (FAP) [7, 20], familial amyloid cardiomypathy (FAC) [49], amyloidotic vitreous opacities, carpal tunnel syndrome [76] and others. In old age, non-mutated TTR can also form pathological amyloid fibrils [131]. Pharmacological intervention to reduce or prevent TTR dissociation is being pursued as a therapeutic strategy. To date one small molecule kinetic stabilising molecule (tafamidis) has been approved for FAP, and is being evaluated in clinical trials for other TTR amyloidoses.

Further reading on Transthyretin
Adams D et al. (2019) Hereditary transthyretin amyloidosis: a model of medical progress for a fatal disease. Nat Rev Neurol 15: 387-404 [PMID:31209302]  
Bezerra F et al. (2020) Modulation of the Mechanisms Driving Transthyretin Amyloidosis. Front Mol Neurosci 13: 592644 [PMID:33362465]  
Dohrn MF et al. (2020) Targeting transthyretin - Mechanism-based treatment approaches and future perspectives in hereditary amyloidosis. J Neurochem [PMID:33155274]  
Galant NJ et al. (2017) Transthyretin amyloidosis: an under-recognized neuropathy and cardiomypathy. Clin Sci 131: 395-409 [PMID:28213611]  
Griffin JM et al. (2019) Transthyretin cardiac amyloidosis: A treatable form of heart failure with a preserved ejection fraction. Trends Cardiovasc Med [PMID:31889610]

Nomenclature
Common abbreviation
HGNC, UniProt
Inhibitors

transthyretin  
TTR  
TTR, P02766  
tafamidis (pKd 8.7) [15]

Comments: Excess production and accumulation of TTR causes hereditary transthyretin-mediated amyloidosis. Two novel drugs are now approved to combat this disease: inotersen (Tegsedi®) [52] and patisiran (Onpattro®) [46]. Both of these drugs act to reduce the amount of TTR protein (both wild type and mutant) produced in the liver, but by slightly different mechanisms. Inotersen is an antisense oligonucleotide inhibitor of TTR synthesis, whereas patisiran is a double-stranded small interfering RNA (which targets a conserved sequence in the 3’ UTR of mutant and wild-type TTR mRNA). Inotersen is administered subcutaneously, and patisiran is delivered by intravenous infusion in a lipid nanoparticle formulation.
Tubulins

Other protein targets → Tubulins

Overview: Tubulins are a family of intracellular proteins most commonly associated with microtubules, part of the cytoskeleton. They are exploited for therapeutic gain in cancer chemotherapy as targets for agents derived from a variety of natural products: taxanes, colchicine and vinca alkaloids. These are thought to act primarily through β-tubulin, thereby interfering with the normal processes of tubulin polymer formation and disassembly.

Further reading on Tubulins

Arnst KE et al. (2019) Current advances of tubulin inhibitors as dual acting small molecules for cancer therapy. *Med Res Rev* 39: 1398-1426 [PMID:30746734]

Boiarska Z et al. (2021) Microtubule-targeting agents and neurodegeneration. *Drug Discov Today* 26: 604-615 [PMID:33279455]

Eshun-Wilson L et al. (2019) Effects of α-tubulin acetylation on microtubule structure and stability. *Proc Natl Acad Sci USA* 116: 10366-10371 [PMID:31072936]

Gadadhar S et al. (2017) The tubulin code at a glance. *J Cell Sci* 130: 1347-1353 [PMID:28325758]

Magiera MM et al. (2018) Tubulin Posttranslational Modifications and Emerging Links to Human Disease. *Cell* 173: 1323-1327 [PMID:29856952]

Penna LS et al. (2017) Anti-mitotic agents: Are they emerging molecules for cancer treatment? *Pharmacol Ther* 173: 67-82 [PMID:28174095]

| Nomenclature | tubulin alpha 1a | tubulin alpha 4a | tubulin beta class I | tubulin beta 3 class III | tubulin beta 4B class IVb | tubulin beta 8 class VIII |
|--------------|------------------|------------------|-----------------------|--------------------------|----------------------------|--------------------------|
| HGNC, UniProt| TUBA1A, Q71U36   | TUBA4A, P68366   | TUBB, P07417           | TUBB3, Q13509             | TUBB4B, P68371             | TUBB8, Q3ZCM7             |
| Inhibitors   | –                | –                | vinblastine (pIC50 9), eribulin (pIC50 8.2) [78], paclitaxel (Mitotic cell cycle arrest in A431 cells) (pIC50 8.1) [83], colchicine (pIC50 8) [19], cabazitaxel, docetaxel, ixabepilone, vincristine | cabazitaxel, docetaxel, combretastatin A4 (pIC50 8.2) [20] | –                          | –                          |

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SARS-CoV-2

Coronaviruses are large, often spherical, enveloped, single-stranded positive-sense RNA viruses, ranging in size from 80–220 nm. Their genomes and protein structures are highly conserved. Three coronaviruses have emerged over the last 20 years as serious human pathogens: SARS-CoV was identified as the causative agent in an outbreak in 2002–2003, Middle East respiratory syndrome (MERS) CoV emerged in 2012 and the novel coronavirus SARS-CoV-2 emerged in 2019–2020. SARS-CoV-2 is the virus responsible for the infectious disease termed COVID-19 (WHO Technical Guidance 2020).

Further reading on Tubulins

Alexander SPH et al. (2020) A rational roadmap for SARS-CoV-2/COVID-19 pharmacotherapeutic research and development: IUPHAR Review 29. Br J Pharmacol, 177 (21): 4942-4966. [PMID:32358833]
Cannallire R et al. (2020) Targeting SARS-CoV-2 Proteases and Polymerase for COVID-19 Treatment: State of the Art and Future Opportunities. J Med Chem, [Epub ahead of print]. [PMID:33186944]
Cui J et al. (2019) Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol, 17 (3): 181-192. [PMID:30531947]

Structural proteins

Overview: The virus particle has four structural proteins. The envelope, membrane and spike proteins are on the viral surface, while the polybasic nucleoprotein enables the tight coiling of the viral RNA.

| Nomenclature | Envelope protein | Membrane glycoprotein | Nucleoprotein | Spike glycoprotein |
|--------------|-----------------|----------------------|---------------|------------------|
| Other names  | envelope small membrane protein, orf4 | Membrane protein | Nucleocapsid protein | Spike protein |
| UniProt      | P0DTC4          | P0DTC5               | P0DTC9        | P0DTC2           |
| Function     | By similarity to other coronavirus E proteins, SARS-CoV-2 E is predicted to constitute a single transmembrane (potentially homopentameric) ion channel with selectivity for monovalent cations over monovalent anions [85, 119, 133, 139] | The membrane glycoprotein (M) is usually regarded as the most abundant protein in the coronavirus envelope. By similarity with other coronavirus M proteins it is predicted to be essential for initiating assembly of the viral envelope components [94] | The coronavirus nucleocapsid phosphoprotein (N, or nucleoprotein) is highly basic and binds the viral RNA as a dimeric entity [23] into nucleocapsids which protect the viral genome, while also providing access for replication when required | The spike protein extends from the viral surface and binds to the host cell surface enzyme ACE2 to facilitate viral entry into the cell |

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Full Contents of ConciseGuide: [http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full](http://onlinelibrary.wiley.com/doi/10.1111/bph.15537/full)
Polyproteins

Overview: The viral RNA encodes two overlapping polyproteins which are cleaved autocatalytically by intrinsic proteases (see below).

| Nomenclature               | Replicase polyprotein 1a | Replicase polyprotein 1ab |
|----------------------------|--------------------------|---------------------------|
| Other names                | Polyprotein 1a           | Polyprotein 1ab           |
| UniProt                    | P0DTC1                   | P0DTD1                    |
| Function                   | The replicase polyprotein 1a (pp1a) encodes a set of 11 smaller proteins, including two proteases that are responsible for cleaving the polyprotein chain into its component parts | The replicase polyprotein 1ab (pp1ab) encodes a set of 16 smaller proteins (5 more than pp1a) |

Comment: The component proteins are non-structural and are involved in the transcription and replication of viral proteins and RNA.

Proteases

Overview: Other protein targets → SARS-CoV-2 → Proteases

| Nomenclature               | 3C-like (main) protease | Papain-like protease |
|----------------------------|-------------------------|----------------------|
| Other names                | 3c-like proteinase, SARS-CoV-2 Mpro, Chain A, 3c-like Proteinase, 3CL protease, Mpro, nsp5 | non-structural protein 3, NS3, nsp3, PL-PRO |
| UniProt                    | P0C6U8                  | P0DTC1               |
| EC number                  | 3.4.22.69              | 3.4.22.46            |
| Function                   | The 3C-like protease cleaves the two polyproteins encoded by the SARS-CoV-2 genome (pp1a and pp1ab) into a range of non-structural proteins (nsp1-11 from pp1a; nsp1-16 from pp1ab). As these component proteins play crucial roles in viral replication, the 3C-like protease is considered to be a good molecular target for drug development. Small molecule 3C-like protease inhibitors would be predicted to reduce viral replication [33, 85] | The papain-like protease is a domain within coronavirus Nsp3. Its proteolytic activity cleaves three sites in the viral replicase polyprotein (recognition consensus sequence LXGG↓XX) to release the three non-structural proteins Nsp1, Nsp2, and Nsp3 [40]. It has additional non-proteolytic functions as part of the multicomponent replicase-transcriptase complex [103] |
Nucleic acid turnover
Other protein targets $\rightarrow$ SARS-CoV-2 $\rightarrow$ Nucleic acid turnover

| Nomenclature | RNA-dependent RNA polymerase |
|--------------|------------------------------|
| Other names  | non-structural protein 12, nsp12 |
| UniProt      | P0DTD1 |
| Function     | The conservation of RdRP catalytic domain between different RNA viruses endows inhibitors that were designed against other viral pathogens with activity against the SARS coronaviruses. Viral RdRP is the molecular target of nucleotide-based broad-spectrum antiviral compounds like remdesivir, tenofovir and ribavirin [33, 129, 141] |

Other proteins
Other protein targets $\rightarrow$ SARS-CoV-2 $\rightarrow$ Other proteins

| Nomenclature | Protein 3a | Protein 7a | Protein 9b | Non-structural protein 6 | Non-structural protein 7b |
|--------------|------------|------------|------------|--------------------------|--------------------------|
| Other names  | Orf3a | Orf7a | Orf9b, Accessory protein 9b, ORF-9b | Nsp6 | Accessory protein 7b, nsp7b |
| UniProt      | P0DTC3 | P0DTC7 | P0DTC2 | P0DTD2 | P0DTD8 |
| Function     | Protein 3a is a transmembrane pore-forming viral protein (viroporin) with potassium ion channel activity | The main function of the SARS-CoV protein 7a appears to be disruption of the host cell cycle and induction of caspase-dependent apoptosis [120]. By homology SARS-CoV-2 protein 7a is likely to produce the same effect | SARS-CoV protein 9b is a virion-associated accessory protein [120] that acts to block the host's ability to mount an antiviral IFN-induced innate immune response [87]. By homology, 9b from SARS-CoV-2 would be predicted to exhibit a similar function | Coronavirus nsp6 proteins limit autophagosome expansion [21]. This mechanism may favour coronavirus infection by damaging autophagosome-mediated delivery of viral components to lysosomes for degradation | Protein 7b is a coronavirus accessory protein. Experimental evidence suggests that SARS-CoV 7b has some attenuating function [87]. By homology, SARS-CoV-2 7b is likely to have a similar function |

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