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The Role of Natural Products in Revealing NRF2 Function

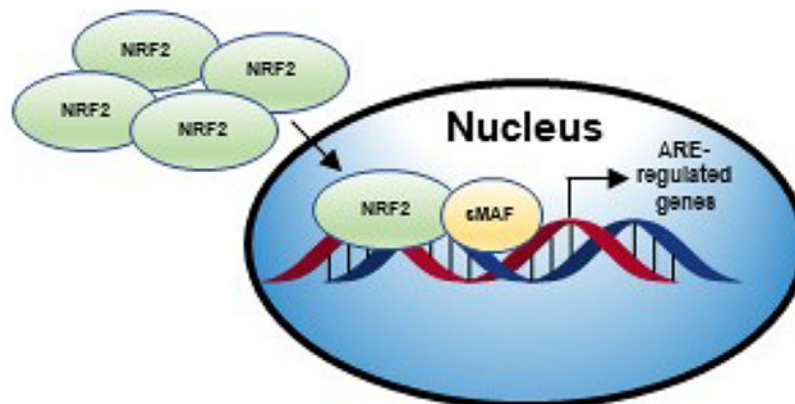
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Abstract

The transcription factor NRF2 is one of the body's major defense mechanisms, driving transcription of >300 antioxidant response element (ARE)-regulated genes that are involved in many critical cellular processes including redox regulation, proteostasis, xenobiotic detoxification, and primary metabolism. The transcription factor NRF2 and natural products have an intimately entwined history, as the discovery of NRF2 and much of its rich biology were revealed using natural products both intentionally and unintentionally. In addition, in the last decade a more sinister aspect of NRF2 biology has been revealed. NRF2 is normally present at very low cellular levels and only activated when needed, however, it has been recently revealed that chronic, high levels of NRF2 can lead to diseases such as diabetes and cancer, and may play a role in other diseases. Again, this "dark side" of NRF2 was revealed and studied largely using a natural product, the quassinoid, brusatol. In the present review, we provide an overview of NRF2 structure and function to orient the general reader, we will discuss the history of NRF2 and NRF2-activating compounds and the biology these have revealed, and we will delve into the dark side of NRF2 and contemporary issues related to the dark side biology and the role of natural products in dissecting this biology.

Graphical Abstract



NRF2 is a protective transcription factor that has been intentionally activated by many natural products for chemoprevention, but it has also been shown aberrant NRF2 activation can lead to disease and natural products have also been used to inhibit the NRF2 pathway.

1 Introduction

Natural products have long served as chemical matter for the discovery and/or development of clinical therapies¹⁻⁹. It has been posited that up to 40% of all new molecular entities submitted to the Food and Drug Administration (FDA) for approval are natural products, natural product-derived, or natural product inspired (containing a natural product pharmacophore) compounds. In the areas of cancer therapeutics and antibiotics, natural products make up 53% and 59%, respectively, of all FDA approved drugs⁴. But another important function of natural products has been in chemical biology, where natural products have served as potent and specific probes to dissect the physiologic and/or pathologic functions of biomolecules^{10, 11}. Although small, synthetic compounds have certainly been important, the evolutionary processes and principles that have shaped natural products to have exquisite and privileged architectures and related biological functions has facilitated the significant contributions made by these important chemical entities^{5, 8, 12}.

For many thousands of years, natural remedies for a variety of ailments have been employed¹³⁻¹⁷. Many of these traditional remedies remain without scientific explanation for their curative powers, but as natural products research has evolved so has the exploration of natural medicines and the organisms from which they are derived to both isolate active principles and to assign the mechanism(s) by which these active entities interact with their molecular target(s)¹⁸⁻²³. Isolation of active ingredients is often carried out by extracting compounds from the sample and using some form of biological readout to guide purification of the desired natural product²⁴⁻²⁷. The assignment of the mode of action of a given natural product, that has been isolated in a phenotypical screen, is often a bottleneck in this process, but has seen application of many exciting and novel approaches to the solving of this task²⁸. The assignment of a target(s) to natural products has often revealed new biology or even opened entirely new fields. This is certainly the case for the nuclear factor erythroid (NF-E2)-related factor 2 (NRF2) pathway²⁹⁻³⁷.

The NRF2 pathway, discussed in detail below, is the body's primary defense against oxidative stress and many environmentally and/or intentionally introduced xenobiotic agents. In the 1960s and 1970s, it was discovered that phase 2 metabolic enzymes could be activated by phenolic antioxidants that had been used as preservatives in food and that this activation could also be carried out using natural products from plants. Animal models demonstrated that this activation had chemopreventive properties, meaning animals exposed to phase 2 activating compounds were less likely to develop tumors. This led to the search for compounds that could activate this response more effectively and hence potentially protect users of these compounds from cancer³⁸⁻⁵⁴. One of the early natural product discoveries was the isothiocyanate, sulforaphane (discussed in detail below), which was found to be present in cruciferous vegetables and especially in the seeds and sprouts of broccoli^{55, 56}. The action of these anti-oxidant activating compounds ultimately led to the discovery of the anti-oxidant response element (ARE) that is found in the promoter region of the upregulated genes^{57, 58}. This in turn led to the discovery of the transcription factor, NRF2, that binds the ARE and regulates these genes. Finally, the regulation of the NRF2 pathway was revealed and with this the mechanism of activation of NRF2 by

chemopreventive agents was revealed. Thus, the observation of the action of the simple natural product sulforaphane led to the development of a large field of research that has expanded in many directions including the discovery of many other natural product activators and the discovery of some natural product pathway inhibitors. In addition, there have been and remain many clinical trials of NRF2 activating compounds initiated for a variety of indications and there is one NRF2 activator currently used in patients. The NRF2 field has now blossomed to >2000 publications per year with increasing growth every year (Fig. 1).

In this review article, we will provide a detailed discussion of the NRF2 pathway. Many readers with primary interest in natural products might not have knowledge of the NRF2 field, so we feel this will help to orient readers. We will then discuss the structure and function of NRF2 and its key regulatory protein, Kelch-like ECH-associated protein 1 (KEAP1). Presently, there are very little structural data regarding NRF2, which we will highlight, but there have been several studies of KEAP1 domain structure at high resolution and a full-length low-resolution structure that have revealed critical mechanistic details and explained the mechanisms by which some activating compounds may operate. Because a number of recent reviews have been written with emphasis on NRF2 pathway modulators, including an outstanding review on natural products in this context, we will avoid a detailed discussion of these compounds and instead direct readers to these reviews^{35, 59–66}. We will instead discuss NRF2-activating natural products or natural product-derived compounds based not as much on structural considerations but based on important principles of biology, biochemistry, or medicine they have revealed. In this context, we will focus primarily on compounds that regulate post-translational events, although we will discuss some post-translational modification modulators, transcriptional modulators, and translational modulators. We will not discuss epigenetic modulation as a mechanism to activate or deactivate NRF2 in any depth, but this is a rapidly growing field with important implications in the dark side of NRF2^{67–69}. In addition, recent work has indicated that dietary NRF2-modulating compounds can affect the gut microbiome, adding another layer of complexity to NRF2 research⁷⁰. We will also discuss the dark side of NRF2⁷¹. This is a more recent demonstration that the NRF2 pathway, like many stress-response pathways, can be hijacked by cells for nefarious purposes, allowing cells to survive the harsh conditions required for cancerous transformation, growth, and spread. Using the natural product, brusatol, it has been revealed that NRF2 inhibition might be a viable strategy to treat NRF2 addicted cancers either as a stand-alone therapy or an adjuvant to sensitize cancerous cells to first-line chemotherapies⁷². Moreover, brusatol has been used as a tool compound to reveal critical aspects of NRF2 biology as pertain to cancer and other diseases^{73, 74}.

2 The canonical NRF2 pathway

NRF2 is a basic leucine zipper (bZip) transcription factor from the Cap 'n' Collar (CNC) family^{29, 75, 76}. NRF2 is ubiquitously expressed in all cells, but under non-stressed, basal conditions, the level of NRF2 is kept low post translationally through the action of the ubiquitin proteasome system (UPS)^{77–81}. In a non-stress situation, the Nrf2-ECH homology 2 (Neh2) domain of NRF2 (see Section 3) is bound by two molecules of the adapter protein KEAP1. The Kelch domain of KEAP1 has a recognition site for ETGE and ETGE-like

motifs. The Neh2 domain of NRF2 has both an ETGE motif and a DLG motif. The ETGE motif binds one molecule of KEAP1 with high (8 nM) affinity and the DLG motif binds a second molecule of KEAP1 with lower affinity (500 nM)^{82–84}. The two KEAP1 molecules form a homodimer via their BTB domains, which also form the binding site for Cullin3 (CUL3), bringing NRF2 into proximity to the CUL3-Really interesting new gene (RING)-box 1 (RBX1) E3 ubiquitin ligase complex. The stoichiometry of binding between KEAP1 and CUL3 is not known, with differing views, however, the structure of the CUL3-KEAP1 BTB complex is 1:1⁸⁵. The 2:1 KEAP1:NRF2 binding arrangement is critical for the correct function of this regulatory complex. Between the ETGE and DLG motifs of NRF2 are seven lysine residues, which are the sites of ubiquitylations⁷⁷, so when both NRF2 motifs are bound to two KEAP1 molecules these lysines are correctly aligned and NRF2 is readily ubiquitylated. Polyubiquitylated NRF2 is then extracted from the KEAP1-CUL3-RBX1 complex through the action of the ATPase associated with various cellular activities (AAA+) chaperone, p97 and shuttled to the proteasome for degradation⁸⁶. This post-translational regulatory system ensures low levels of NRF2 under non-stressed conditions (Fig. 2).

When cells are exposed to oxidative or xenobiotic stress, the ubiquitylation of NRF2 is blocked, the levels of NRF2 rise, NRF2 translocates into the nucleus, and dimerizes with another bZip transcription factor, one of the small musculoaponeurotic fibrosarcoma (sMAF) proteins. This heterodimer binds AREs and ARE-regulated genes are activated to enhance cellular defense^{29, 33–35, 87}. Through elegant mechanistic studies, Talalay and co-workers showed there are ten classes of molecules that activate the NRF2-ARE axis: (i) oxidizable diphenols, phenylenediamines, and quinones; (ii) Michael acceptors; (iii) isothiocyanates; (iv) thio-carbamates; (v) trivalent arsenicals; (vi) dithiolethiones; (vii) hydroperoxides; (viii) vicinal dimercaptans; (ix) heavy metals; and (x) polyenes^{88–90}. However, most of the natural products that are used to intentionally activate NRF2 and the canonical NRF2 activators are electrophilic in nature (*i.e.* sulforaphane, bardoxolone (semi-synthetic), curcumin, cinnamaldehyde, withaferin A). KEAP1 contains a series of cysteines (27 in humans), and most prominently for the present review, cysteine151 that act as sensors^{79, 81, 91–93}. Cysteine151 has been shown to be surrounded by a collection of basic amino acids, bringing the pKa below 7 and increasing the nucleophilicity of this residue at physiologic pH^{94, 95}. When an electrophilic compound is adducted to this sensor residue, an incompletely defined structural rearrangement takes place. There are two primary, not mutually exclusive, models that have been put forth to explain the effects of electrophiles: the hinge and latch model^{82, 83} and the CUL3 dissociation model^{96–99}. In the hinge and latch model, electrophilic addition causes the lower affinity DLG-motif, the latch, to be released from KEAP1, while the ETGE motif, the hinge, remains attached. When the latch releases, the ubiquitylation of NRF2 is blocked, but NRF2 remains bound to the complex. In the CUL3 dissociation model, KEAP1 releases from CUL3, blocking ubiquitylation, but keeping KEAP1 bound to NRF2, blocking further NRF2 degradation. Both models then lead to inhibition of ubiquitylation of NRF2, an increase in the level of NRF2, nuclear translocation, dimerization with sMAF proteins, and subsequent transcriptional activation of ARE-containing NRF2 target genes (Fig. 2). Initially, it was thought NRF2 only regulated phase 2 metabolic enzymes, that is conjugating enzymes, however contemporary genetic experiments have revealed NRF2 controls many more (>300) genes including genes from

phase 1 metabolism, phase 2 metabolism, transporters, protein quality control, redox regulation, transcriptional regulation, iron metabolism, and autophagy^{33, 100}. It is interesting to note, that despite the historical use of the term phase 2 response, the assay used to define the response, the Prochaska assay (see below), measures the activity of NQO1, an enzyme of phase 1 metabolism.

3 The structure and function of NRF2 and KEAP1

NRF2 is a complex multi-domain protein that is likely predominantly intrinsically disordered in cells. For this reason, there are very little structural data on NRF2. Biochemical and genetic experiments have assigned function to seven (Neh1–7) regions of NRF2, leading to functional domains, but none of these have been shown to have stand-alone tertiary structure and thus are perhaps not domains in the traditional sense of the word. Several structures of KEAP1 domains have been solved and these have provided a great deal of mechanistic insight, but a full-length structure or a co-structure with the full CUL3-RBX1 E3 ligase complex or with other proteins in the pathway have not been solved. Although there are certainly possibilities to activate or inhibit the NRF2 pathway independent of directly targeting KEAP1 (activation) or NRF2 (possible inhibition), the present discussion of structure will be confined to NRF2 and KEAP1.

3.1 NRF2

NRF2 is a 67 kDa bZip CNC transcription factor. The NRF2 domains, Neh1–7 (NRF2-ECH homology 1–7), and currently assigned functions are shown in Figure 3A. There is very little structural data on NRF2, and NRF2 is likely predominantly intrinsically disordered in the unbound state. Certainly, the nuclear magnetic resonance (NMR) structure of the Neh1 domain (<https://www.rcsb.org>), which is α -helical with large unstructured regions (Fig. 3B), compared to other structural data of dimeric, DNA-bound bZip transcription factors (Fig. 3C) argues for this region being intrinsically disordered¹⁰¹. The lack of structural data has surely stymied efforts to find natural products that modulate NRF2 function through direct targeting.

Neh1, which lies near the C-terminus of NRF2 is the CNC-bZip domain. Although no structural data of the Neh1 domain bound to DNA exist, there is a monomeric NMR structure (Fig. 3B), showing an α -helical and disordered architecture, and there are a number of crystal structures for bZip transcription factors bound to DNA that are known and these are likely structurally similar to Neh1 when bound to sMAF proteins and ARE (Fig. 3C). In general, these DNA recognition elements contain a positively charged basic region that interacts with the negatively charged phosphate backbone of DNA and a series of leucines that form the hydrophobic dimerization domain, as implied by the name^{102–105}. In the case of NRF2, it forms a heterodimeric structure with another bZIP transcription factor, one of three sMAF proteins, MAFF, MAFG, or MAFK^{76, 87, 106, 107}. This heterodimeric structure then binds to an ARE with the consensus sequence 5'-TGA(G/C)NNNGC-3', which is found in the promoter region of more than 300 identified genes^{100, 108}. In addition to these functions, the nuclear localization sequence (NLS) and the nuclear export sequence are reported to be in the Neh1 domain^{109–111}.

The Neh2 domain is at the N-terminus of NRF2 and is the KEAP1 interacting domain^{83, 112, 113}. Two small peptides from this domain, one harboring the ETGE motif (Fig. 4A and B) and a second larger peptide harboring the DLG motif (Fig. 4C and D) bound to the KELCH domain of KEAP1 have been solved, but this is the extent of NRF2 x-ray crystallographic structural data (see below). The Neh2 domain contains the two essential KEAP1 recognition elements, the weak binding DLG motif and the tight binding ETGE motif that flank the seven critical lysines that are ubiquitylated by the CUL3 complex. Each of the two NRF2 recognition motifs binds to a single KEAP1 molecule and this weak-tight dual binding mode has been shown to be essential for the regulation of NRF2, with critical physiologic and pathologic implications (see Figure 3, above for regulatory considerations, and below for a more detailed discussion of physiologic and pathologic implications).

The Neh3 domain is at the extreme C-terminus of NRF2 (Fig. 3A). Deletion of this domain does not affect dimerization, DNA-binding or localization of NRF2, but it does block NRF2's transcriptional activity. Biochemical studies showed Neh3 interacts with chromo-ATPase/helicase DNA-binding protein (CHD6) and that this interaction is essential for expression of the NRF2 target gene NAD(P)H Quinone Dehydrogenase 1 (NQO1), arguing the Neh3 domain is a transactivation domain¹¹⁴.

The Neh4 and Neh5 domains play a dual role in NRF2 function (Fig. 3A). The initially assigned function was transcriptional activation^{115–117}. Deletion of either of these domains leads to a reduced expression of a number of NRF2 target genes, which was at least in part due to decreased binding to CREB (cAMP-response-element-binding protein)-binding protein (CBP) and Brahma-related gene 1 (BRG1)^{115, 118}. In addition, it was demonstrated that NRF2 can be ubiquitylated by the endoplasmic reticulum associated E3 ubiquitin ligase, HMG-CoA Reductase Degradation (HRD1), followed by proteasome-mediated degradation and that this interaction is mediated through the Neh4/5 domains, although the precise mechanism and structural details of this interaction remain to be defined¹¹⁹.

NRF2 has also been shown to be regulated by E3 ubiquitin ligases other than the KEAP1-CUL3-RBX1 complex and HRD1. The Neh6 domain, like Neh2 or described Neh4/5 above, comprises another degron^{82, 120–123}. The Neh6 domain can be phosphorylated by glycogen synthase kinase (GSK-3 β), which recruits the E3 ubiquitin ligase, β -transducin repeat-containing protein (β -TrCP), leading to the degradation of NRF2 (Fig. 7). This will be discussed in greater detail in Section 7 (see below).

The Neh7 domain was more recently described and early as well as some contemporary papers and figures do not show the Neh7 domain. However, biochemical and genetic data have shown that retinoic X receptor alpha (RXR α) is an NRF2 transcriptional repressor (see section 8.1 for further discussion). Biochemical experiments showed that the Neh7 domain of NRF2 directly interacts with RXR α , resulting in the negative regulation of NRF2 target genes (see Fig. 3A)¹²⁴.

3.2 KEAP1

As discussed in Section 2, the KEAP1-CUL3-RBX1 E3 ligase complex is the best studied and the most critical NRF2 negative regulator. KEAP1 is a member of the BTB-Kelch

family of proteins^{80, 125}. To date, only a low-resolution cryo-electron microscopy (cryo-EM) structure of the complete KEAP1 protein has been reported¹²⁶. However, several crystal structures of KEAP1 domains have been solved, including co-crystal structures with KEAP1-NRF2-ARE pathway activating molecules (Fig. 4, 5, and 6). In addition, co-crystal structures with NRF2 peptides comprising the ETGE and DLG motifs and with protein-protein interaction inhibitors (PPIs) have helped to discover and develop PPIs to activate the NRF2 pathway without the potential off-target actions of covalent activators (Fig. 4). Overall, KEAP1 has been shown to have three structural domains that will be discussed individually below (Fig. 5A). In addition, each of the domains has been assigned a function, but because no complete KEAP1 structure has been solved, some details of the mechanisms of modulation and domain communication remain incomplete.

KEAP1 is a cysteine-rich protein with 27 cysteines in the human KEAP1 protein^{80, 92, 125}. A great deal of effort both *in vitro* and *in vivo* has been put forth to understand the significance, or lack thereof, of these cysteines in sensing various cellular insults. This has led to what is called the cysteine code – the rules that dictate how KEAP1 senses xenobiotic agents^{79, 93}. In Figure 5A, the most important of these sensors are shown. As discussed, Cys151 is the major sensor for most of the molecules discussed in this review, it detects Michael acceptor containing molecules in addition to sensing nitric oxide and the thiocyanates. The mildly electrophilic sulfoxythiocarbamate alkyne derivative of sulforaphane revealed this compound modifies Cys273, Cys288, and Cys613. The cyclopentenone prostaglandins, alkenals, and nitro-oleic acid were shown to modify Cys288. Heavy metals were shown to be sensed by Cys226 and Cys613, which are close in space, allowing for chelation of the cations. Finally, Cys226, Cys622, and Cys624 have been shown to respond to H₂O₂¹²⁷. Interestingly, the cysteine sensors are located primarily outside of the KELCH domain, despite this domain being the primary sight of NRF2 binding, as discussed below.

Near the N-terminus of KEAP1 is the Broad complex, Tramtrack, and Bric-à-Brac (BTB) domain (residues 61 to 179; Fig. 5A, B and C)). The structure of the BTB domain has been solved, including in complex with a natural product-derived compound (bardoxolone, see below, Fig. 6B). The dimeric BTB domain is shown in Figure 5B⁹⁵ and the BTB domain bound to the N-terminus of CUL3 is shown in Figure 5C (<http://www.rcsb.org/structure/5NLB>). The BTB domain crystallized as a dimer mediated by helix 1 and a domain swapped β -sheet. The KEAP1 BTB domain is a protein-protein interaction domain that mediates formation of the KEAP1 homodimer and interaction with CUL3, however the structure of the CUL3-BTB domain is a 1:1 complex and this remains to be explained. In addition, the BTB domain contains Cys151 and a series of basic residues (His129, Lys131, Arg135, Lys150, and His154), which are near Cys151. The proximity of these basic amino acids decreases the pK_a of Cys151, leading to a more active (more nucleophilic or more oxidation prone) sensor. Although Cys151 is not the only reactive cysteine in KEAP1, most of the natural products that have been shown to activate NRF2 signaling have been shown to form a covalent adduct with this cysteine and mutation to serine or another non-reactive amino acid eliminates activation (Fig. 5A)⁷⁹.

Moving N-terminal to C-terminal, the intervening region (IVR) follows the BTB domain (residues 180 to 314; Fig. 5A). The IVR is also known as the BACK domain. There currently is not a structure of the KEAP1 IVR, but other homologous BACK domains have been solved^{92, 94}. Based on homology, the IVR is predicted to be an α -helical domain as the other BACK domains that have been solved are all highly extended α -helical domains. In addition to connecting the BTB and Kelch domains, the IVR contains Cys273 and Cys288, which have been shown to be important for stress modulation, but seem to play only a minor role, if any, in responding to covalently binding natural products⁹³. At the N-terminal side of the IVR is the 3-box motif, which connects the BTB and the IVR, likely mediating critical communication between the two. It has also been shown to facilitate the interaction between KEAP1 and CUL3¹²⁸.

Finally, the most C-terminal domain (residues 315 to 598; Fig. 4, 5A and D) is a β -propeller structure called the Kelch domain¹²⁹. As mentioned, a number of structures of this domain have been solved, including in complex with NRF2 peptides, which bind at the bottom of the “bowl-shaped” structure, engaging a series of positively charged residues (Fig. 4)^{83, 112, 113}. These peptide-Kelch co-crystal structures have provided critical guidance to the development of non-covalent NRF2 activating compounds^{130–132}. This will not be discussed extensively, as most of these PPIs are synthetic compounds, but the interested reader is directed towards a number of interesting publications on this matter, including an excellent recent analysis of the merits of each of the reported compounds and the traps that can befall the unwary when trying to discover compounds of this class, or really any class of inhibitor^{133, 134}. However, we will discuss a recent comparison between covalent and non-covalent natural product activators, the geopyxins, that were reported by our group¹³⁵.

4 KEAP1 targeting natural product NRF2 activators

The explosion of NRF2 research over the last decade or so has been quite remarkable (Fig. 1). The field had its beginning several decades prior to the discovery of the KEAP1-NRF2-ARE signaling axis, with the observation that small doses of polycyclic aromatic hydrocarbons protect against toxicity and carcinogenicity^{39, 40, 42}. It was later found in animal tests that phenolic antioxidants, such as the commonly used food preservative, 2(3)-*tert*-butyl-4-hydroxyanisole (BHA), and compounds naturally in foods, when fed to rats in high doses, could protect the animals from carcinogens^{43–54, 136–140}. These studies ultimately led to the field of chemoprevention, which was predicated on the intentional activation of phase 2 metabolic pathways, the so-called “phase 2 response”, to resist disease^{53, 54, 88, 90, 141, 142}. The pioneering work of Paul Talalay and his research group set out to understand the mechanistic underpinnings of this activation of metabolic enzymes. Using an assay that measured the level of NQO1, called the Prochaska bioassay^{143, 144}, Talalay and his team isolated 1-isothiocyanato-4R-(methyl-sulfinyl)butane – sulforaphane (SFN) from cruciferous vegetables, followed by many other natural products^{56, 145}. It is pertinent to mention that the activity of NRF2/phase 2 activating compounds is measured by a parameter called CD, which is a measure of the amount of compound required to double the activity of NQO1 in Hepa 1c1c7 cells. Talalay observed that the compounds that led to activation of phase 2 metabolism were electrophiles or redox active compounds, pointing towards the engagement of a cysteine residue¹⁴⁴.

Studies on chemoprevention also led to the search for the genetic element that regulated these phase 2 metabolic enzymes, ultimately revealing the ARE¹⁴⁶. This responsive element was shown to be present in the promoter of the glutathione S transferase alpha 1 (Gst-Ya) gene in rats and to be responsive to phenolic antioxidants^{57, 58}. This was followed by cloning of the ARE-responsive transcription factor, NRF2^{76, 147} and to the generation of an Nrf2 knockout mouse⁷⁵. Although the first report of an *Nrf2*^{-/-} mouse was from the Kan group, shortly after this report, the Yamamoto group reported their own knockout mouse and distributed it to many research groups around the world, having a huge impact on the NRF2 field, this remains one of the critical reagents used in the study of NRF2⁸⁷. The next critical breakthrough in the NRF2 field was the discovery that KEAP1 binds to NRF2 and acts as a negative regulator¹²⁵. This discovery led to a flurry of biochemical studies on KEAP1 demonstrating KEAP1-Cys151 is essential for sensing NRF2 activating compounds, supporting the observations of Talalay; KEAP1 is part of a CUL3 E3 ubiquitin ligase complex; and NRF2 is regulated post-translationally through ubiquitylation and degradation^{7977, 78, 99}.

4.1 Sulforaphane

Sulforaphane (SFN; 1-isothiocyanato-4-(methylsulfinyl)butane) is an isothiocyanate that is found in cruciferous vegetables such as broccoli, kale, and cabbage, with the highest concentration being found in broccoli sprouts. Normally, SFN is in the non-reactive glucoraphanin form until it is needed as a protective measure against herbivores, at which time it is hydrolyzed by Myrosinase (EC 3.2.1.147, thioglucoside glucohydrolase) to the aglycone¹⁴⁸. The aglycone (thiohydroximate-*O*-sulfonate) then undergoes a spontaneous thio-Lossen-type rearrangement to generate the reactive isothiocyanate at neutral or basic (physiological) pH or the nitrile, sulforaphane nitrile (5-(methylsulfinyl)pentanenitrile), will form at acidic pH (Fig. 7). In mammalian liver, glucoraphanin is reduced to glucoerucin, which is also a substrate of Myrosinase and can be converted to erucin ((4-isothiocyanatobutyl)(methyl)sulfane) or erucin nitrile (5-(methylthio)pentanenitrile). The erucin compounds are readily converted to SFN or SFN nitrile via oxidation of the sulfur atom. Pharmacokinetic studies of SFN and glucoraphanin have shown that SFN has much better bioavailability, which has influenced therapeutic preparations and dosing strategies^{148–158}. It is also interesting to note, that a series of epitionitriles have also been found to result from alkenyl glucosinolates (not shown in Fig. 7) and these also activate NRF2 in a KEAP1 dependent manner¹⁵⁹.

Sulforaphane has become the gold standard by which all other covalent NRF2 activators are measured and has been used in thousands of studies as represented by the many publications reporting its use (2047 publications listed in PubMed). SFN is the most potent unmodified natural product NRF2 activator that has been described (CD = 0.23 μ M) and it has been validated in many animal models using both wild-type animals and *Nrf2*^{-/-} animals, demonstrating the protective action of SFN is through the NRF2 pathway^{56, 149, 158, 160}. In addition to rodent models, SFN has been in many clinical trials for various indications. The initial clinical studies with SFN were conducted in Qidong, China, which had a high incidence of liver cancer due to aflatoxin exposure^{160, 161}. Presently, a search of clinical trials (clinicaltrials.gov) reveals trials for many indications including: schizophrenia, UV

skin damage, autism, lung cancer, prostate cancer, COPD, asthma, bladder cancer, osteoarthritis, melanoma, breast cancer, type 2 diabetes mellitus, and pancreatic cancer, validating pre-clinical studies^{162–177}. In addition, due to its protective role, SFN has been used as an adjuvant therapy to prevent side effects in a number of cancer drug trials¹⁷⁸.

As discussed above, NRF2 and SFN are intimately connected, as SFN has been used to dissect many of the critical features of NRF2 biology and biochemistry^{62, 160}. However, there have been conflicting studies about the mechanism by which SFN activates NRF2. There are studies that have shown SFN can react with Cys273 or 288 and other studies have shown SFN activity is dependent on Cys151^{79, 151, 179–186}. It was subsequently shown that this discrepancy was due to the different conditions used in the conflicting studies. Based on the current understanding of the cysteine code, SFN activates NRF2 by binding to Cys151 of KEAP1 at physiologically relevant conditions. However, as shown, Cys151 is in the BTB domain (Fig. 5A), thus the mechanism by which SFN adduction to Cys151 leads to blocked ubiquitylation of NRF2 and signaling remains uncertain. A recent co-crystal structure of the BTB domain with bardoxolone (Fig. 6B) argued against release of the DLG motif from the Kelch domain, arguing instead for KEAP1 dissociation from CUL3⁹⁵. However, given the size difference between SFN and bardoxolone, it is perhaps possible both mechanisms are operational depending on the identity of the adduct. There are certainly data supporting both models^{95, 97, 187–193}. Without a full structural characterization of KEAP1, KEAP1-CUL3, and KEAP1-NRF2, this remains an unresolved issue. Advances in cryo-electron microscopy may perhaps offer a solution to this.

4.2 Curcumin

Another important phytochemical is the polyphenol curcumin (Fig. 8A), isolated from *Curcuma longa*, which is what gives the spice turmeric its yellow color. Curcumin has long been used in Ayurveda to treat many diverse conditions and has even been the source of some scientific controversy leading to retraction of several papers reporting anti-cancer properties of curcumin. It has been shown that curcumin is a weak activator of NRF2 (maximum of 1.5-fold induction of an ARE-luciferase reporter in Beas-2B cells at 15 μ M)¹⁹⁴. In addition, curcumin has been reported to have poor pharmacological properties and has been shown to be active in many bio-assays, leading to it being referred to as a pan-assay interference (PAINS) compound^{195, 196}. However, there has been interest in optimizing curcumin's pharmacology and activity. This included work from our group that developed a synthetic derivative bis[2-hydroxybenzylidene]acetone (BHBA), which was shown to be more potent than curcumin at activating the KEAP1-NRF2-ARE axis in a variety of assays (Fig. 8B). It was shown to activate NRF2 in a KEAP1-Cys151 dependent manner, as expected for an electrophilic Michael acceptor containing compound. In addition, this derivative was shown to protect mice from lung cancer development when challenged with vinyl carbamate¹⁹⁴. Curcumin (Fig. 8A) and its synthetic derivatives (BHBA and F₁₀ in Fig. 8B and C) have been shown to be effective in treating or preventing other maladies, but so far, the poor pharmacology has prevented its use in the clinic^{178, 197–202}. In addition, like other NRF2 activating compounds of this sort, curcumin activates many pathways with a complex mode of action^{203–205}.

4.3 Cinnamaldehyde

Cinnamaldehyde (Fig. 8D) is the aromatic aldehyde that gives cinnamon its pleasant taste and odor. This simple diterpene has been investigated for both anti-inflammatory and chemopreventive properties^{206–208}. Our lab has carried out several investigations into the mode of action of cinnamaldehyde and its protective effects. We have shown that cinnamaldehyde can activate the NRF2 pathway and that this action can protect skin cells from photodamage²⁰⁹. We have also shown that this action can protect colon cells from genotoxic insults and azoxymethane/dextran sulfate-induced colon cancer formation^{210, 211}. We demonstrated cinnamaldehyde can protect mice from diabetes in a streptozotocin-induced murine type 1 diabetes model¹⁷⁷. These studies have been confirmed by others and expanded to include models of type 2 diabetes as well^{212–217}. In addition, and in line with the effects of other NRF2-inducing compounds, cinnamaldehyde offers neuroprotection and protection from kidney damage caused by chronic kidney disease^{218, 219}.

4.4 Bixin

Bixin (Fig. 8E) is an apocarotenoid derived from the seeds of the achiote tree (*Bixa orellana*) that is used as a spice in cooking and was demonstrated to induce the KEAP1-NRF2-ARE axis by adduction to KEAP1-Cys151 *in vitro*, although the chemical nature of the adduct is not yet known²²⁰. In these same studies, it was shown, in line with the data from cinnamaldehyde, that bixin protects SKH-1 mice from UV skin damage when applied directly to the skin. Moreover, using *Nrf2*^{+/+} and *Nrf2*^{-/-} animals, this was shown to be an *Nrf2* dependent process, as protection was only observed in the wild-type animals. Bixin was later shown to protect animals against ventilation induced lung injury (VILI) in a murine model. Animals treated by intraperitoneal injection of bixin showed normal lung morphology, decreased inflammation, and reduced oxidative DNA damage, all hallmarks of VILI²²¹. Again, using *Nrf2*^{+/+} and *Nrf2*^{-/-} mice, this response was shown to be *Nrf2*-dependent *in vivo*. Animal studies of cardiac injury caused by a high-fat diet demonstrated protection against cardiac dysfunction by inhibiting fibrosis, inflammation, and reactive oxygen induced damage. The reduction of inflammation was shown to be due to a decrease in the secretion of pro-inflammatory cytokines. These data were corroborated using an *in vitro* model of inflammation by treating cardiomyocytes with lipopolysaccharide to induce inflammation²²². This of course argues for bixin as a safe means to reduce ROS and inflammation in a variety of disease states, in agreement with other NRF2 inducing compounds. Finally, a series of studies *in vivo* showed bixin can protect animals from lung damage caused by particles, offering a potential prophylaxis for people living in areas with heavy air pollution^{223, 224}.

4.5 Withaferin A

Withaferin A is a steroidal lactone isolated from *Withania somnifera* (common name Ashwaganda or winter cherry), that has been used in Ayurveda for thousands of years and is reported to promote general well-being. This important compound was originally isolated in the 1960s and later shown to have a number of interesting activities including anti-cancer activity in a number of tumor lines, anti-inflammatory, immune-modulatory, anti-metastasis, and anti-angiogenesis^{225–229}. The discovery of the anti-cancer activity led to a flurry of

mode of action studies that indicated withaferin A can interact with a variety of pathways. As shown in Figure 9A, withaferin A contains both an A-ring and an E-ring Michael acceptor and a B-ring epoxide, all of which have the potential to interact with KEAP1 cysteines to activate NRF2 signaling. Several groups have reported activation of the NRF2 pathway by withaferin A and that it can be used to ameliorate a variety of effects in cellular and animal models of various disease states^{230–234}. Interestingly, recent studies on the prevention of acetaminophen induced hepatotoxicity in a mouse model and follow up *in vitro* mechanistic studies indicated withaferin A can induce Nrf2 in a Keap1-dependent and in a PTEN/PI3K/Akt-dependent manner as discussed in section 7 below²³⁵. However, many other modes of action have been assigned to withaferin A. Our work and others have shown that withaferin A and some of its derivatives can inhibit the 20S core particle of the proteasome, which would also be expected to activate NRF2. In addition, we found that withaferin A can inhibit p97 activity, which also can inhibit NRF2 degradation⁸⁶. Although withaferin A inhibited both p97 and the proteasome, a semi-synthetic-azido compound (Fig. 9B) was found to be selective for p97 and to still inhibit NRF2 degradation^{236–238}. Thus, it seems the action of withaferin A and perhaps other withanolides is quite complex. Despite this complicated pharmacology, withaferin A remains of interest and has been in clinical trials for the treatment of schizophrenia and schizoaffective disorder.

5 NRF2 activators in neurological disorders

Given the critical role of oxidative stress in a variety of neurodegenerative states, it is perhaps not surprising NRF2 has been shown to be at the heart of many neurological diseases, as has been mentioned above and is reflected in neuro related clinical trials using NRF2 activating compounds. In fact, at present the only FDA approved NRF2 activating compound in the clinic is a multiple sclerosis drug, dimethyl fumarate (Fig. 11G; section 5.2). The topic of Nrf2 in neurodegeneration has been reviewed quite recently and the interested reader is directed to these reviews^{36, 239, 240}. However, as will be discussed in the section on the GSK-3 β /NRF2/ β -TrCP axis and in other publications on the topic, a number of natural products have been shown to be important in the dissection of the role of NRF2 in neurophysiology^{241–253}. As shown in Figure 10, there are many other natural products that have been used in studies of neuropathology and physiology. Carnosic acid (Fig. 10A), sulfuretin (Fig. 10B), and methysticin (Fig. 10C) were each shown to prevent cell death in cellular and *in vivo* Alzheimer's disease (AD) models^{254–256}. Both resveratrol (Fig. 10D) and thymol (Fig. 10E) were also shown to protect neuronal function in an aging animal model and a high-fat diet animal model, respectively^{257, 258}. In addition, a number of recent papers have reported on the dual reactive oxygen species scavenging and NRF2 activating activity of a variety of natural compounds (Fig. 10F–O), and how these protect a neuronal cell line, however, the precise mechanistic details remain to be illuminated in many cases^{259–268}. These exciting results and the FDA approval of DMF offer hope for NRF2 modulating compounds in treating patients with neurological disorders.

6 KEAP1 targeting natural product-derived NRF2 activators

In addition to the many natural products that have been shown to activate the KEAP1-NRF2-ARE axis, there are compounds that are of natural origin but have been optimized through

medicinal chemistry efforts. We will focus our attention on two members of this class based on their important contributions to the development of NRF2 activating compounds as clinical candidates. The synthetic oleanane triterpenoids have been and are currently in numerous clinical trials, and the simple modified metabolite, dimethyl fumarate, is currently the only canonical NRF2 activator in the clinic. However, it is being constantly revealed that there are other clinical compounds that can activate the NRF2 pathway. In addition, it should be emphasized that the KEAP1-NRF2-ARE axis is not the sole target of these compounds, but that some of the important physiologic effects have been assigned to NRF2 using genetic and biochemical experiments.

6.1 Oleanane triterpenoids

Oleanolic acid (Fig. 11A) is found in many different plants and foods but is at very high levels in olive trees and most often isolated from olive pulp or leaves. It is perhaps this component of olive oil that is responsible for the salubrious benefits of the Mediterranean diet. In its parent form, oleanolic acid has modest anti-inflammatory activity. In an effort to optimize this anti-inflammatory potential, a series of synthetic oleanane triterpenoids were synthesized from oleanolic acid and evaluated for their ability to decrease NO synthesis^{269–273}. In the parent form, oleanolic acid is not an activator of the NRF2 pathway, but studies on the synthetic oleanolic acid derivatives, inspired by the Michael acceptors that are required for potent activity, revealed a series of cyano enones that are the most potent NRF2 activating compounds reported²⁷⁴. The introduction of a Michael acceptor in the A ring gave CD = 3.9 μM (Fig. 11B; see above for the definition of CD), indicating the importance of this modification. Surprisingly, the introduction of another Michael acceptor into the C ring further increased the potency (Fig. 11C; CD = 0.28 μM). Addition of an electron withdrawing group to the A ring Michael acceptor further enhanced activity. A cyano group at this position gives the well-known bardoxolone (CDDO (2-cyano-3,12-dioxolean-1,9-dien-28-oic acid)), which has a further order of magnitude improvement in the activity (Fig. 11D; CD = 0.0023 μM). Making the methyl ester of the acid (CDDO-Me) gives a more modest improvement of activity (Fig. 11D; CD = 0.0010 μM), but this substitution makes the compound orally bio-available. Other bardoxolone derivatives (*i.e.* Fig. 11E and F) have also been made, and those that have been most extensively studied or are in clinical trials are shown. Importantly, it was found that the NRF2 activating activity correlated well with the anti-inflammatory activity²⁷⁴. The initial synthetic efforts allowed for the development of a biotinylated probe that was used to pull down potential targets of bardoxolone that could be analyzed by LC-MS, which revealed >500 targets in addition to KEAP1²⁷⁵, indicating the promiscuous nature of these compounds.

Despite the many targets identified, or perhaps because of, bardoxolone and its derivatives have shown a great deal of pre-clinical success and are being evaluated in several clinical trials. Initially, these compounds were synthesized to treat malignant cells and have been evaluated both *in vitro* and *in vivo* to treat cancers of blood, breast, ovaries, prostate, lungs, pancreas, colon, skin, and brain. These compounds have been evaluated as both standalone therapies and as adjuvants, mainly in combination with immunotherapies^{276–356}. It must be pointed out that many of these studies attribute the activity of bardoxolone and its derivatives to an activity independent of NRF2 and at present this cannot be fully addressed. In addition,

it is interesting to note that not all of the derivatives behave equivalently³³². In addition to cancer treatment, CDDO and its derivatives have been used in chemoprevention, a more traditional role for an NRF2-activating compound^{281, 284, 287, 314, 353, 357–364}.

In addition to the complex role played by bardoxolone in cancer, it has also been studied in several other disease contexts. Most of these are related to inflammation, perhaps more directly implicating the actions of the KEAP1-NRF2-ARE signaling axis. These include neurodegenerative proteinopathies such as Parkinson's disease, Huntington's disease, Alzheimer's disease, and amyotrophic lateral sclerosis^{365–373}, diseases of the eyes^{369, 374–379}, the lungs^{376, 380–394}, the heart^{392, 395–398}, metabolic disorders^{399–401}, liver diseases^{402–407}, kidney disease^{408–413}, and autoimmune disorders^{332, 414–417}. It is interesting to note, that the bardoxolone derivative that is used in these studies is significant, as they have differential effects, again arguing for a much more complicated mode of action than simply activation of the KEAP1-NRF2-ARE axis. Despite the complexities and pleiotropic effects of bardoxolone and its derivatives, these remain an interesting class of compounds that are in clinical trials for a number of indications including: chronic kidney diseases, pulmonary hypertension, type 2 diabetes mellitus, liver disease, and diabetic nephropathy in the case of CDDO-Me. In addition, omaveloxolone (Fig. 11F) is currently under clinical investigation for a variety of indications, including Friedreich's ataxia, mitochondrial myopathies, immuno-oncology, and prevention of corneal endothelial cell loss following cataract surgery. As a final point, in 2013, CDDO-Me failed in phase 3 clinical trials due to cardio toxicity, there are a number of potential explanations for this⁴¹⁸, but it remains these are promising compounds and continue to be investigated. In addition, this setback does not dampen enthusiasm for the NRF2 pathway as a promising therapeutic target.

6.2 Dimethyl fumarate (Fumaderm; Tecfidera)

Fumarate is a primary metabolite of the citric acid cycle and an oncometabolite (a metabolite that activates a cancer promoting pathway) that is upregulated in a rare kidney cancer that has a fumarate dehydratase deficiency⁴¹⁹. Interestingly, a semisynthetic variant of fumarate, dimethylfumarate (DMF; Fig. 11G), is the only NRF2-modulating compound to enter the clinic. Originally, DMF had been approved in Europe to treat psoriasis and then in 2013, the US Food and Drug Administration (FDA) approved the use of DMF to treat relapsing multiple sclerosis (MS). Subsequent and/or concurrently with this event DMF, and the monomethyl variant (MMF), have been entered into several other clinical trials for pulmonary hypertension, brain cancer, lymphoma, psoriasis, rheumatoid arthritis, lupus erythematosus, and cutaneous T-cell lymphoma. The approval of DMF for MS has also spurred a flurry of other pre-clinical and mode of action studies on DMF. The preclinical studies have been on several indications with a seeming emphasis on neurodegenerative disorders, as discussed above. From the mode of action studies, it is clear that DMF and other fumarate derivatives, activate the NRF2 pathway and this can explain many of the benefits of DMF treatment, however, like many NRF2-activating compounds DMF does not have a straightforward mode of action and other, non-NRF2-mediated actions have been described. In all likelihood it is a combination of the NRF2-dependent and independent

actions that ultimately lead to disease treatment, however further work is needed to fully understand this drug^{420–422}.

7 A comparison between covalent and non-covalent activators – the geopyxins

As discussed extensively above in the section on electrophilic NRF2 activators, all the compounds in pre-clinical development, clinical assessment, or patient use have many potential targets and complex modes of action due to the nature of the reactive electrophilic moieties present. In addition, because these compounds likely modify many cysteines in the proteome, potentially leading to toxicity, there is growing interest in the discovery and development of non-covalent NRF2 activating compounds. This endeavor has produced many interesting studies and a flurry of structural studies including co-crystal structures of the ETGE and DLG motifs bound to the Kelch domain of KEAP1 (Fig. 4) that have guided the development of non-covalent protein-protein interaction inhibitors that block the interaction between, most likely, the DLG motif and the Kelch domain of KEAP1, mimicking the release of the latch in the hinge and latch model and leading to NRF2 activation. Nearly all these compounds have been synthetic compounds^{131, 423–427}. However, our lab recently published a study of the *ent*-kaurane diterpenoid, geopyxin A, and its derivatives (Fig. 12). We found among the geopyxins many with Michael acceptors required KEAP1-Cys151 for their activity (Fig. 12A as one example), but we also found geopyxin F (Fig. 12B), which is devoid of a Michael acceptor, requires KEAP1, but does not require Cys151. This compound was not as potent as the covalent compounds but increased the expression of NRF2 with kinetics distinct from the other, electrophilic NRF2 activators in the series. We also showed that geopyxin F increased the half-life of NRF2 to a much greater extent than the other geopyxins. We showed that this non-covalent variant was KEAP1 dependent, but, unlike the other geopyxin, was not dependent on Cys151. Finally, and importantly, we found that geopyxin F conferred greater cellular protection on cells challenged with toxicants than either SFN or the other geopyxin and that this activity depended on the NRF2 pathway¹³⁵. Presently, we are working to understand the mechanism by which geopyxin F activates NRF2. It seems, the most likely mechanism is by interacting with the Kelch domain of KEAP1, but we cannot rule out other mechanisms. In addition, given the modest activity of this compound, we are working to make more potent derivatives using a semi-synthetic strategy.

8 The GSK-3 β /NRF2/ β -TrCP signaling axis

NRF2 has recently been shown to be regulated by E3 ubiquitin ligases other than the KEAP1-CUL3-RBX1 complex and the Neh6 domain, like Neh4/5 described above, mediates one of these alternate (non-KEAP1-CUL3) degradative processes (Fig. 3A and 13; for a recent review see⁴²⁸). The Neh6 domain contains a series of phosphodegron sequences that enhance binding of β -transducin repeat-containing protein (β -TrCP), a substrate adaptor for the S-Phase Kinase Associated Protein 1 (Skp1)-Cullin 1 (Cul1)-(Rbx1/Roc1) ubiquitin ligase complex^{82, 120, 122}. The sequence at the N-terminus of the Neh6 domain was shown to be phosphorylated by glycogen synthase kinase-3 (GSK-3), leading to enhanced NRF2

degradation^{429–431}. This was shown to have important potential application in NRF2-driven cancers⁴³¹. In human lung A549 cells which contain a KEAP1 mutation leading to high NRF2 levels, GSK-3 activation by inhibition of the AKT/PKB (protein kinase-B) pathway led to a decrease of NRF2 levels and sensitized cells to first line chemotherapy¹²⁰.

In addition to the traditional electrophilic NRF2 activating compounds, such as sulforaphane, several other natural products have played a critical role in dissecting the details of the GSK-3 β /NRF2/ β -TrCP axis. An abbreviated overview of this axis is shown in Figure 13. It should be pointed out, this figure is not meant to indicate each of these comes from the same signaling event, but for the sake of clarity, details have been removed. In Figure 13, the labels A-D are associated with a given group of molecules, indicate a branch of the axis that has been modulated by natural products, and correspond with the labeling from Figure 14. This is not meant to be a comprehensive list but illustrates some of the elements of this axis that have been revealed. An important early discovery, prior to dissection of this axis, was the discovery that the natural product wortmannin (Fig. 14A) from the fungi *Penicillium funiculosum*, a phosphoinositide 3-kinase (PI3K) inhibitor could reverse the effects of the synthetic NRF2 activating compound, tert-butylhydroquinone, in IMR-32 neuroblastoma cells²⁴¹. More recent studies have looked at the relationship between PI3K and NRF2 using natural products in liver (shikonin) and neuro protection (desoxo-narchinol A and narchinol B), but the mechanistic details were a bit vague and these were not PI3K inhibitors, but somehow activated the axis^{252, 432}. It was also shown that a polysaccharide from *Abelmoschus esculentus* mitigated type 2 diabetes symptoms in a mouse model through a similar activation of the PI3K axis without mechanistic details⁴³³. Kaempferol was shown to have cardioprotective properties and this was thought to be due to NRF2 modulation through the PI3K/AKT/GSK-3 β axis⁴³⁴. A study using the protein kinase C (PKC) inhibitor, chelerythrine (Fig. 14B), showed inhibition of PKC could regulate NRF2 by deactivating GSK-3 β (Fig. 13B), which was used to show the M1 muscarinic receptor activates NRF2 through the PKC pathway²⁴⁵. The connection between PKC and NRF2 was further validated by showing sauchinone (Fig. 14B) can activate PKC δ , leading to GSK-3 β inhibition and NRF2 activation to protect the liver against acetaminophen toxicity⁴³⁵. NRF2 can also be positively regulated through activation of AMPK, which activates AKT and inhibits GSK-3 β (Fig. 13C). The compounds shown in Figure 14C have been shown to activate NRF2 through activation of AMPK. Three of these compounds, nectandrin B, esculentoside A, and pterostilbene were shown to confer hepatoprotection through NRF2 upregulation^{436–438}. Two other AMPK activating compounds, butin and emodin, were shown to protect animals in ischemia reperfusion models^{249, 439}. In Figure 14D, a series of compounds are shown that activate AKT/PKB, but do not necessarily contain mechanistic details or the details will be discussed separately here^{246, 251, 440–443}. Interestingly, the bioflavonoid, morin, was shown to inhibit the phosphatase PHLPP2, which is a negative regulator of AKT/PKB, leading to NRF2 activation (Fig. 14D) and conferring protection in an acetaminophen challenge model^{444–446}. Finally, the peptide melittin from the honeybee (*Apis mellifera*) was shown to protect against myocarditis by increasing the expression of HDAC2 and activation of the GSK-3 β /NRF2 axis⁴⁴⁷. The relationship between epigenetic modifiers and NRF2 is an expanding area of research, but is beyond the present discussion^{33, 448, 449}. Finally, it is worth mentioning that many of the compounds described in this

section likely have complex modes of action and many likely also activate NRF2 in a KEAP1-dependent manner. More rigorous investigations using KEAP1 knockout cells will solidify the conclusion that NRF2 activation by these compounds is through modulation of the GSK-3 β /NRF2/ β -TrCP signaling axis.

9 The dark side of NRF2 argues for the development of NRF2 inhibitors

After decades of chemopreventive research, data started to emerge indicating that persistent unregulated expression of NRF2 might have deleterious effects, the dark side of NRF2, which led to the discovery of the NRF2 pathway inhibitor, brusatol (see below)^{71, 72}. In 2008, our group demonstrated that NRF2 promotes cancer, a concept that has been further supported by recent work from our lab and other's demonstrating that once tumors have initiated, high levels of NRF2 promote tumor progression, metastasis, and chemoresistance. In addition, patients with high NRF2 levels in their tumor tissues have a higher risk of recurrence, increased incidence of chemoresistance, and overall poor prognosis⁴⁵⁰⁻⁴⁵⁴. Dysregulation of NRF2, resulting in high NRF2 expression, is common in many human cancers. Somatic NRF2/KEAP1 mutations that disrupt the NRF2-KEAP1 interaction and constitutively activate NRF2 are frequent in certain cancer types, particularly in lung cancer, where these mutations are present in up to one third of patients⁴⁵⁵⁻⁴⁵⁸. In fact, a recent genome-wide somatic point mutation saturation analysis of 21 tumor types, found that while only a few well-known cancer genes are significantly mutated across different tumor types, KEAP1 is significantly mutated in multiple cancer types, including lung, head and neck, and bladder (as a reference, classical cancer genes such as TP53, KRAS, BRAF and NRAS are also significantly mutated across four or more tumor types)⁴⁵⁹. Furthermore, in lung adenocarcinoma, KEAP1 is as frequently mutated (>30%) as the tumor suppressor gene TP53. In addition to the KEAP1 or NRF2 mutations that disrupt the NRF2-KEAP1 interaction, KEAP1 or CUL3 mutations that compromise KEAP1-CUL3 E3 ligase activity and result in high NRF2 expression have also been described⁴⁶⁰⁻⁴⁶³. High NRF2 expression can also be achieved by epigenetic silencing of KEAP1 through hypermethylation of its promoter⁴⁶⁴ or accumulation of oncometabolites that covalently modify KEAP1 and prevent NRF2 degradation⁴¹⁹. NRF2 is also upregulated at the transcriptional level by aberrant signaling of KRAS, BRAF, and MYC oncogenes^{74, 465}. An increasing number of studies have shown that high expression of NRF2 (through constitutive activation of NRF2) promotes cancer progression and resistance to treatment^{451, 466-468}. More recently, we reported our novel findings suggesting that activation of NRF2 accelerates metastasis of existing tumors in mice⁴⁶⁹. Even though the mechanism by which NRF2 upregulates metastasis-associated proteins has not been established, mechanisms by which constitutive activation of NRF2 contributes to tumor progression and resistance have been demonstrated, including increased detoxification of chemotherapeutic agents, maintenance of reducing conditions, metabolic reprogramming, increased proliferation, maintenance of cancer stem cells, suppression of apoptosis, induction of autophagy, upregulation of the proteasome, and modification of protein synthesis⁴⁷⁰⁻⁴⁷⁸. Furthermore, knockdown or deletion of NRF2 decreases NRF2-addicted cancer cell proliferation and viability *in vitro* and impedes tumor growth *in vivo*^{471, 476, 479}. This observation of the promotion of tumor development, growth, and metastasis by unregulated NRF2 led to the proposal of NRF2 as an oncogene and argues

for the discovery and development of NRF2 inhibitors^{67, 72, 480, 481}. A recent effort to define druggable targets in the NRF2 pathway has revealed potential new mechanisms of inhibiting NRF2 to combat NRF2 addicted cancers and especially chemo resistant cancers⁴⁸².

9.1 All-*trans* retinoic acid

The first NRF2 pathway inhibitor to be discovered was all-*trans* retinoic acid (ATRA; Fig. 15A) as well as other retinoic acid receptor α (RAR α) agonists⁴⁸³. Interestingly, there are conflicting reports of the effects of ATRA on the NRF2 pathway with claims of both activation and inhibition^{483–489}. This conflict has been shown for a number of NRF2 pathway inhibitors, perhaps arguing that careful control of doses and models is critical to accurately assess these reagents⁴⁹⁰. This discrepancy notwithstanding, ATRA is an important probe molecule that revealed the role of retinoic X receptor alpha (RXR α) in the NRF2 pathway. In particular, it showed RXR α can bind to the Neh7 domain of NRF2 in the nucleus and negatively regulate transcription of ARE-regulated genes¹²⁴. ATRA has also been shown to synergize with other cancer therapies, confirming the potential of an NRF2 inhibitor as either an adjuvant therapy or as a standalone cancer therapy^{485, 489}.

9.2 Brusatol

The first targeted attempt to discover an NRF2 inhibiting compound was carried out in our lab. Using an ARE-luciferase reporter cell line, we set out to discover compounds that decreased the level of the luciferase reporter from a series of natural product extracts. A plant extract derived from *Brucea javanica* showed the desired decrease in luciferase activity and the active principal was isolated using activity-guided fractionation, revealing the quassinoid, brusatol as a potent NRF2 pathway inhibitor, showing greater than 50% inhibition of luciferase activity at nM concentrations (Fig. 15B). Interestingly, the closely related compound, brucein C (Fig. 15C), did not show inhibition of NRF2 function. Bruceantin (Fig. 15D), however, was shown to be more potent than brusatol (data not shown). In each of the tested derivatives of brusatol, the only point of difference was the ester substitution on the C ring. Brusatol has proved to be an important probe molecule, allowing a detailed validation of the dark side of NRF2 hypothesis. Indeed, we went on to show that brusatol can sensitize NRF2-addicted^{491, 492} A549 lung cancer cells to the first line chemotherapeutic agents cisplatin and doxorubicin both *in vitro* and *in vivo*^{72, 73}. This critical observation argues for the continued development of NRF2 inhibitors. In addition, we have employed brusatol to dissect the contribution of NRF2 to cancer development, growth, and metastasis. Using either brusatol or SFN, we showed *in vivo* that treatment with SFN prevents tumor formation by upregulating the NRF2 pathway, but that after tumors have been initiated, SFN increased the rate of tumor growth and facilitated metastasis. In contrast, treatment with brusatol increased the formation of tumors, but brusatol treatment after tumors have formed led to a slowing of tumor growth and blocked metastasis⁷³. These critical studies argue for the importance of timing in the development of cancer treatment versus cancer prevention⁴⁹³.

Subsequent mode of action studies by our group confirmed what others have shown that brusatol, at least at higher concentrations, is a general translation inhibitor^{494–496}. The precise biochemical mechanism for this is not known, but we were able to show that brusatol

decreases the levels of short-lived proteins, such as NRF2, selectively over long-lived proteins, such as p97. This lack of a direct NRF2 targeting effect, however, does not lessen the importance of brusatol in the NRF2 field, as it has been used as an important probe in many studies of the dark side of NRF2, demonstrating NRF2-dependent effects. Therefore, brusatol remains the most potent NRF2 pathway inhibitor known^{497–503}. Indeed, much like the many natural product NRF2 activators, such as SFN and bardoxolone, the multiple effects of brusatol do not limit its usefulness and the importance of this probe in this new area of NRF2 research.

9.3 Halofuginone

Halofuginone (Fig. 15F) is a semi-synthetic derivative of the quinazolinone alkaloid, febrifugine from the Chinese herb *Dichroa febrifuga* (Fig. 15E). Febrifuginone was discovered by the Yamamoto lab in a high-throughput screen using an ARE-luciferase reporter cell line to look for compounds that decreased the luciferase signal. Further screening of compounds with scaffolds like febrifuginone revealed the semi-synthetic derivative halofuginone as a more potent and less toxic NRF2 pathway inhibitor. Halofuginone was shown to decrease the level of the NRF2 protein at sub- μ M levels. It was also shown to have selective cytotoxicity for NRF2 addicted cancer cell lines and to increase the efficacy of cisplatin *in vivo*, in an NRF2 dependent manner. Mode of action studies revealed halofuginone is an inhibitor of proline tRNA-synthetase, leading to a general inhibition of translation, similar to brusatol, and having greater effect on short-lived proteins⁵⁰⁴.

9.4 Wogonin

Wogonin (Fig. 15G) is a flavonoid isolated from the root of the Chinese skullcap (*Scutellaria baicalensis*) that has been shown to have anti-neoplastic activity against a variety of cancer cell lines. Initial reports on the relationship between wogonin and NRF2 were conducted in doxorubicin resistant MCF7 breast cancer cells. It was shown in these studies that increased NRF2 levels, and its downstream genes, correlated with resistance and that this could be mitigated by genetic knockdown of NRF2. Importantly, wogonin also decreased the level of NRF2 and imparted sensitivity to the cells⁵⁰⁵. In agreement with these studies, wogonin was shown to block multidrug resistance in a leukemia cell line and cisplatin resistance in head and neck cancers through NRF2 inhibition^{506, 507}. It was later shown that wogonin decreased NRF2 mRNA levels through the NF κ B pathway in drug resistant myelogenous leukemia cells, sensitizing the cells⁵⁰⁸. However, it is important to indicate that there are contradictory studies, indicating wogonin is an NRF2 activating compound and this conundrum remains without explanation^{509–512}.

10 Conclusions and future directions

The importance of natural products as drug discovery leads or as chemical biological tools has been revealed by many success stories in the clinic and a long list of publications. The importance of natural products is beautifully highlighted in the case of the NRF2-ARE cellular protective axis. The discovery of activation of phase 2 metabolic enzymes by natural products, the development of an assay to track down active principles, and the discovery of

SFN as an NRF2 activating chemopreventive compound are all successes of natural product chemistry. This simple isothiocyanate has been used in thousands of studies that have revealed many of the secrets of the NRF2 pathway, a success of chemical biology. These biochemical, physiological, and pathological discoveries have paved the way for a series of drug discovery campaigns that have led to clinical trials and an important drug, DMF, that is now used to treat relapsing MS. This is the first intentional NRF2 activating compound to reach the clinic, but there are many other clinical trials and compounds holding promise for future therapies. These compounds seemingly defy our current view of drugs, as we pursue more and more selective compounds, the canonical NRF2 activating compounds display complex modes of action and seem to engage many targets. Certainly, the effects of the most advanced compounds SFN, bardoxolone and its derivatives, and DMF are due to both NRF2 dependent and independent actions, likely determined by dose, by disease being treated, and by formulation.

In addition to the discovery of the importance of NRF2 in cellular protection, more contemporary studies have revealed a dark side of NRF2. In this context, the protective powers of NRF2 can be hijacked by malignant cells to allow them to survive the harsh conditions required for cancerous transformation, growth, and metastasis. Indeed, it has been proposed that NRF2 might even be an oncogene and its suppressor, KEAP1, a tumor suppressor gene. In this area, like the protective side of NRF2, natural products, in particular the quasinoid brusatol, have verified this hypothesis and have shown the importance of the search for NRF2 inhibitors as either standalone or adjuvant therapies to treat NRF2 addicted cancers or perhaps cancers that have chemoresistance due to increased expression of NRF2.

Despite the many thousands of papers that have been published on NRF2, there are several critical questions that remain open and are intimately connected. First, there are virtually no structural data on NRF2, limited structural data on KEAP1, and no structural data on the CUL3-RBX1-KEAP1-NRF2 complex. This, of course is a daunting task, but with the incredible advances being seen in the cryo-EM field, it is likely within reach. Better structural data will likely reveal many of the critical mechanistic details about regulation of the pathway that remain controversial. Second, the structural data coupled with advanced drug discovery efforts are needed to produce better and more selective probe molecules and possibly clinical leads. There is no denying the importance of the existing NRF2 modulating compounds, but the pleotropic effects of these compounds have added some confusion to the field. This is seen in the importance of use and timing of use of given drugs and possible indications. At which point should an NRF2 activator be used versus an NRF2 inhibitor? What effects seen with current compounds are truly NRF2 related and which are due to off-target or different target effects? Better probe molecules will also help to define another important area of active research: the crosstalk between NRF2 and other signaling pathways. Many important connections have been made in recent years, but some of these conclusions have been challenging to validate due to non-specificity of the NRF2 probes used.

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12 References

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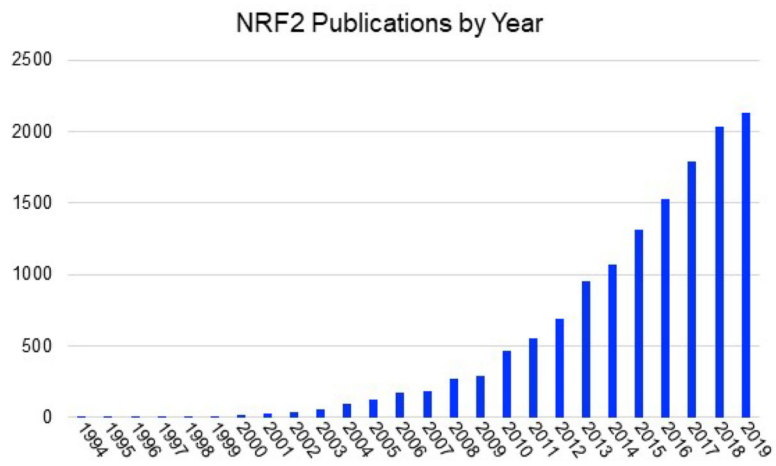


Figure 1. The NRF2 field is growing rapidly.

The graph shown lists the number of publications in pubmed by year.

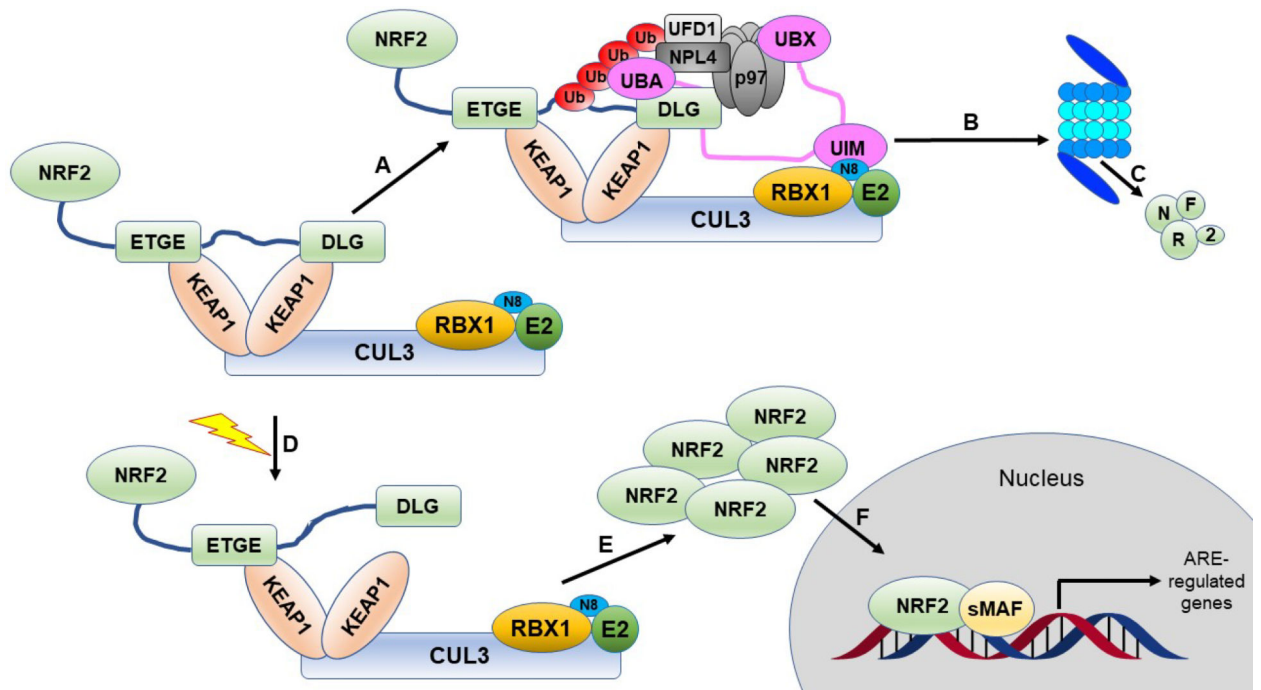


Figure 2. The canonical NRF2 pathway.

NRF2 is sequestered by the CUL3-RBX1 E3 ubiquitin ligase complex through the KEAP1 adapter protein, which binds the ETGE and DLG motifs of NRF2 in a 2:1 KEAP1:NRF2 ratio. **A)** Under basal, unstressed conditions, the CUL3 complex ubiquitylates NRF2 at one of the seven lysines residing between the ETGE and DLG motifs. **B)** Ubiquitylated NRF2 is then extracted from the CUL3 complex through the action of p97-UFD1-NPL4 mediated by UBXN7. **C)** Ubiquitylated NRF2 is transferred to the 26S proteasome, where it is destroyed. **D)** When cells are challenged with an oxidative or xenobiotic insult, one of the sensor cysteines of KEAP1 can become modified, which causes a structural rearrangement, releasing the DLG motif, and stopping subsequent ubiquitylation. Please see the text for alternate explanations and other models. **E)** The inhibited CUL3 complex blocks further NRF2 degradation, allowing NRF2 levels to rise in the cytosol. **F)** They then translocate to the nucleus, where they can bind to sMAF proteins and initiate ARE-regulated transcriptional programs.

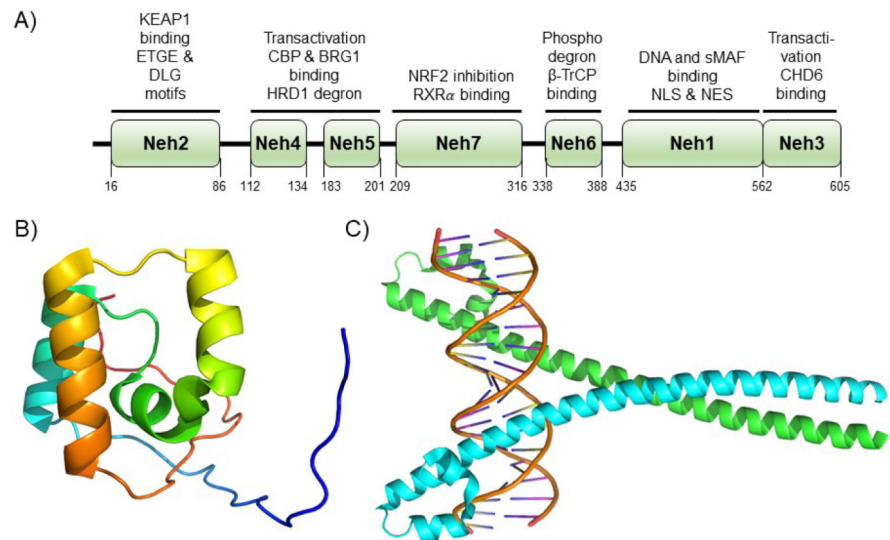


Figure 3. NRF2 domain architecture and structure.

A) NRF2 is comprised of seven domains termed Neh1–7 that have been defined according to biological function and homology to other protein domains. The numbering shown in the figure is for the human protein. Defined biological function of each of the domains is shown above the given domain and explained in greater detail in the text. **B)** The only structure of an unliganded domain of NRF2 is the NMR structure of the Neh1 domain shown (PDB ID 2LZ1). **C)** A crystal structure of the CNC bZip transcription factor MAFA as a potential model for the NRF2 Neh1 domain when bound to an obligate DNA-binding partner (PDB ID 4EOT). The high homology between bZip transcription factors argue this is a likely model for NRF2 in the active form, but to date, no structure has been solved.

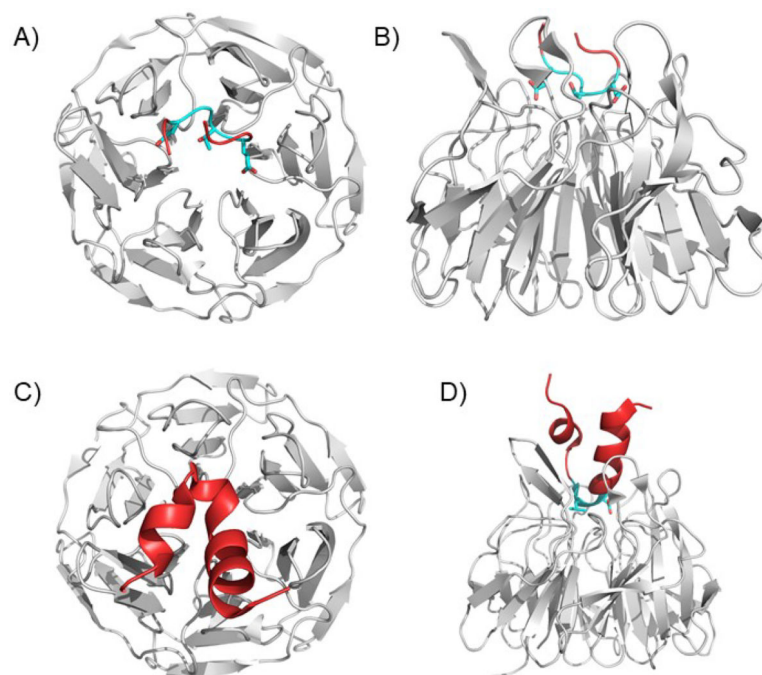


Figure 4. The KEAP1 Kelch domain bound to ETGE and DLG containing peptides. **A) and B)** The ETGE motif binds to a series of positively charged amino acids in the KEAP1 Kelch domain. The ETGE forms a loop in the binding pose. Two views are shown: from the top **A)** and the side **B)**. (PDB ID 5WFV). **C) and D)** The DLG containing peptide shows a pose like the ETGE, but shows fewer contacts, explaining the decreased affinity. The rest of the peptide forms an alpha-helical structure, but this is not known to be physiological or significant due to lack of larger structural data. Two views are shown: from the top **C)** and the side **D)**. (PDB ID 3WN7).

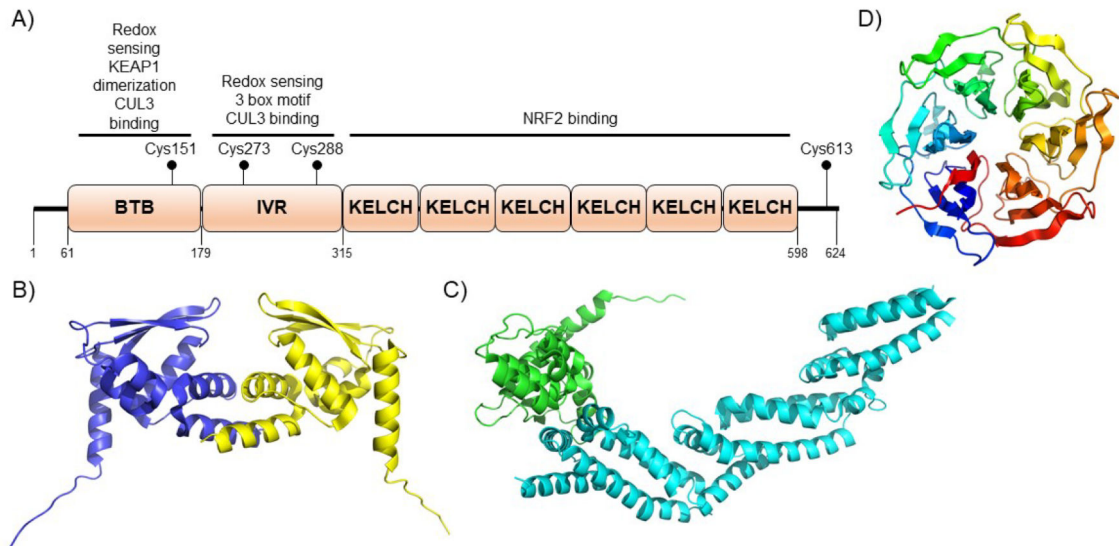


Figure 5. KEAP1 domain architecture and structure.

A) KEAP1 is comprised of three structural domains the BTB domain, the IVR domain, and the Kelch domain. The numbering shown is for the human protein. The assigned functions of each of the domains is shown above each domain. Human KEAP1 has 27 cysteines that can work as sensors. The most important cysteine sensors are also shown. For a detailed discussion of domain and cysteine function, see the text. **B)** The BTB domain of KEAP1 forms a functional dimer to bind to a single NRF2 protein. This dual binding mode is essential for physiologic function. (PDB ID 4CXI). **C)** The BTB domain bound to the N-terminus of CUL3. (PDB ID 5NLB). **D)** The unliganded Kelch domain of KEAP1. (PDB ID 5WFV).

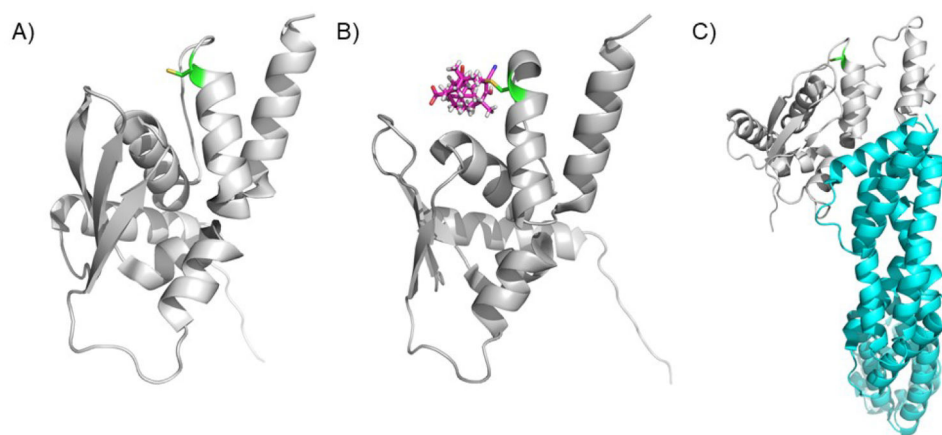


Figure 6. The KEAP1 BTB domain.

A) The apo BTB domain of KEAP1 showing Cys151 in green. **B)** The BTB domain of KEAP1 bound to the A ring of bardoxolone. This structure has been used to argue for dissociation of KEAP1 from the CUL3 complex upon activation by electrophiles. (PDB ID 4CXI). **C)** The KEAP1 BTB domain bound to CUL 3 with Cys150 highlighted in green. (PDB ID 4CXT). (PDB ID 5NLB).

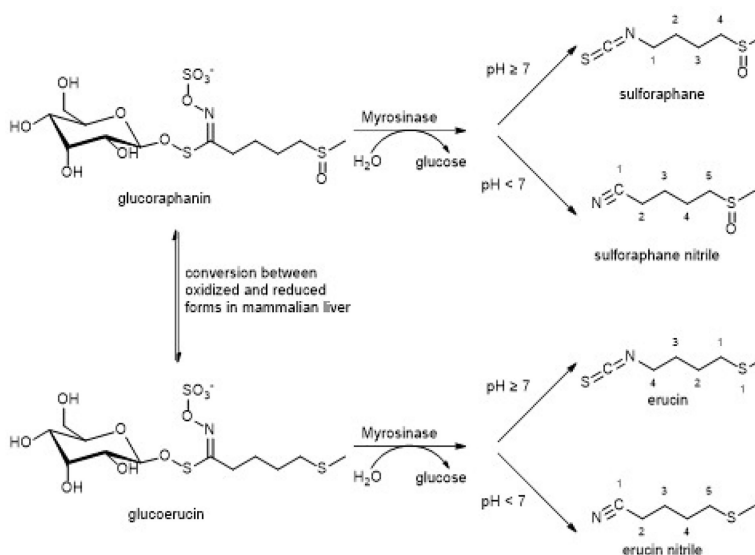


Figure 7. The conversion of glucoraphanin to sulforaphane by the plant enzyme Myrosinase. Normally, in cruciferous vegetables, sulforaphane is in the glycosylated form. It is thought that when plants are attacked by herbivores, the level of Myrosinase increases, releasing sulforaphane and deterring the herbivore. This has important implications in the use of sulforaphane as a drug, since glucoraphanin is poorly bio-available. In the liver of mammals, glucoraphanin is reduced to glucorauicin. Both of these forms are substrates for Myrosinase. Once the carbohydrate is hydrolyzed, the resulting product undergoes a spontaneous Lossen rearrangement to the final, NRF2 activating isothiocyanate.

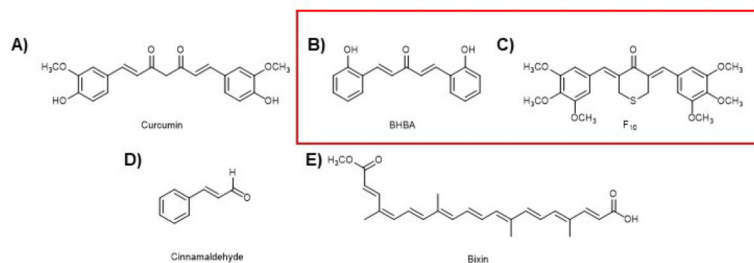


Figure 8. The NRF2 activators discussed in the text.

A) Curcumin from *Curcuma longa*. **B)** A curcumin derivative with more potent NRF2 activation and better pharmacological properties. **C)** A curcumin derivative with more potent NRF2 activation and better pharmacological properties. **D)** Cinnamaldehyde from *Cinnamomum verum*. **E)** Bixin from *Bixa orellana*. The red box is to differentiate natural product derived compounds from natural products.

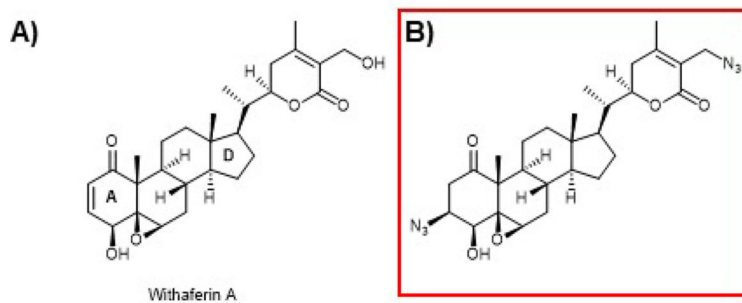


Figure 9. Withaferin A and a semi-synthetic derivative.

A) Withaferin A (from *Withania somnifera*) has been assigned many modes of action, but it is a known NRF2 activator as verified by our lab, however the precise mechanism by which it activates NRF2 is more complex than simple Cys151 adduction (See text for further discussion). **B)** A semi-synthetic withaferin A derivative that does not inhibit the proteasome but inhibits p97 and activates NRF2. The red box is to differentiate natural product derived compounds from natural products.

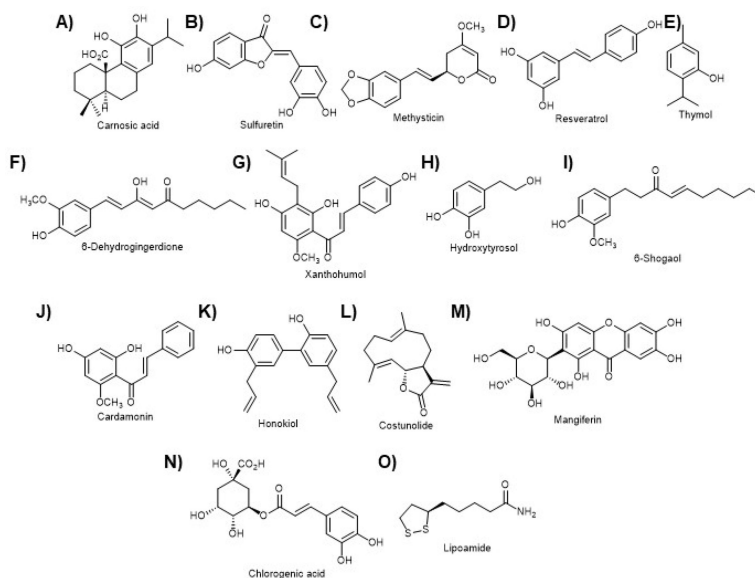


Figure 10. NRF2 activating compounds that have been used in neuroprotective studies. In addition to these, other compounds discussed in other sections shown in other figures have been used in neuroprotective studies. **A)** Carnosic acid from *Rosmarinus officinalis*. **B)** Sulfuretin from *Rhus verniciflua*. **C)** Methysticin from *Piper methysticum*. **D)** Resveratrol. **E)** Thymol from *Thymus vulgaris*. **F)** 6-Dehydrogingerdione from *Zingiber officinale*. **G)** Xanthohumol from *Humulus lupulus*. **H)** Hydroxytyrosol from *Olea europaea*. **I)** 6-Shogaol from *Zingiber officinale*. **J)** Cardamonin from *Alpinia katsumadae*. **K)** Honokiol from *Magnolia virginiana*. **L)** Costunolide from *Saussurea costus*. **M)** Mangiferin from *Mangifera indica*. **N)** Chlorogenic acid from coffee. **O)** Lipoamide. Please see the text for details.

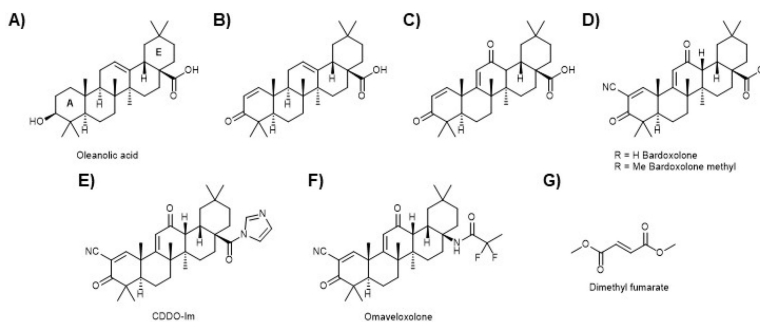


Figure 11. Natural product derived compounds.

A) Oleanolic acid is isolated in large quantity from olive (*Olea europaea*) waste and has been shown to have modest anti-inflammatory action but does not show NRF2 activation activity. **B)** Addition of a Michael acceptor to the A ring produced a μM NRF2 activating compound. **C)** Addition of a second Michael acceptor to the C ring led to an approximately order of magnitude increase in NRF2 activation activity, but it is not understood why. **D)** Electronic modulation of the A ring Michael acceptor gave another order of magnitude increase and the compound bardoxolone (CDDO), one of the most potent NRF2 activators known. Me Bardoxolone (more commonly CDDO-Me) only showed a modest increase in potency, but became orally bio-available, whereas bardoxolone must be injected. **E)** The imidazole variant has been in many studies but does not seem to be more efficacious. However, as discussed in the text, there are subtle differences between the activities of the various CDDO derivatives for yet undescribed reasons. **F)** Omaveloxolone is a recent iteration from Reata Pharmaceuticals that is in clinical trials for several indications (see text). **G)** Dimethyl fumarate is a synthetic derivative of a primary metabolite but is included since it is the only compound to be used in humans that uses NRF2 activation as its primary proposed mode of action.

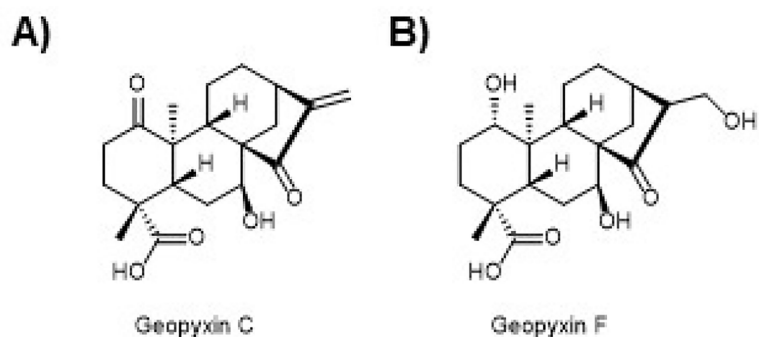


Figure 12. The geopyxins offer insight into the advantages of non-covalent NRF2 activation. **A)** A series of *ent*-kaurane diterpenoids were shown to activate NRF2. Geopyxin C from *Geopyxis* aff. *majalis*, a fungus occurring in the lichen *Pseudevernia intensa*, was shown to potently activate NRF2 in a KEAP1-Cys151 manner. **B)** Geopyxin F from *Geopyxis* sp. AZ0066 inhabiting the lichen *Pseudevernia intensa* was shown to be a modest activator of the NRF2 pathway. However, geopyxin F was shown to activate NRF2 in a KEAP1-dependent, but Cys151-independent manner. Moreover, geopyxin F showed greater protection of cells against toxicants and that this protection was NRF2-dependent.

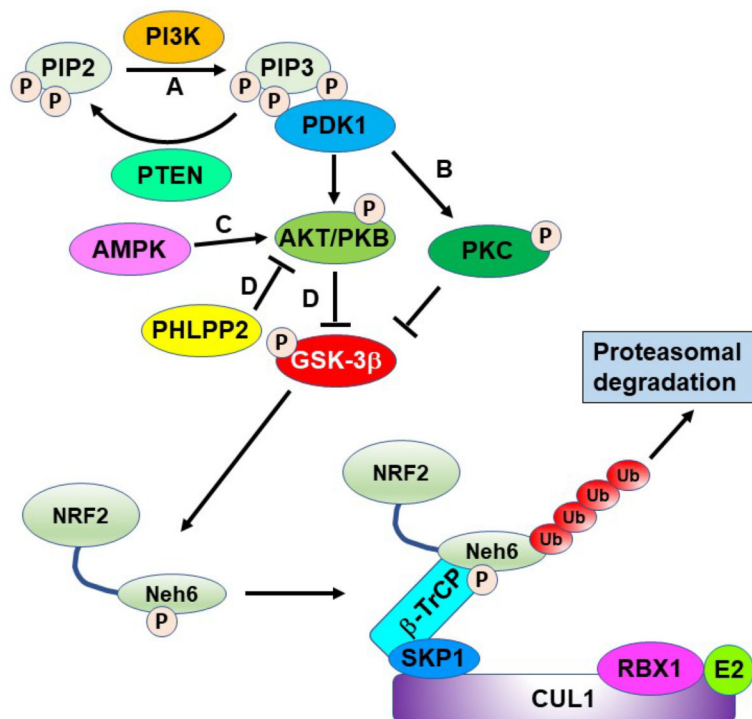


Figure 13. The GSK-3β/NRF2/β-TrCP regulatory axis. GSK-3β can phosphorylate the Neh6 domain of NRF2 making it an enhanced substrate for the CUL1/β-TrCP/RBX1 complex. GSK-3β is inhibited by Ser9 phosphorylation mediated by PKC or AKT/PKB, which are both activated by PDK1. AKT/PKB can also be activated by PDK1. AKT/PKB can also be activated by AMPK or inhibited by PHLPP2. PI3K converts PIP2 to PIP3, which activates PDK1. The action of PI3K can be reversed by PTEN. The letters A-D in the figure refer to sites of modulation by the compounds in Figure 14.

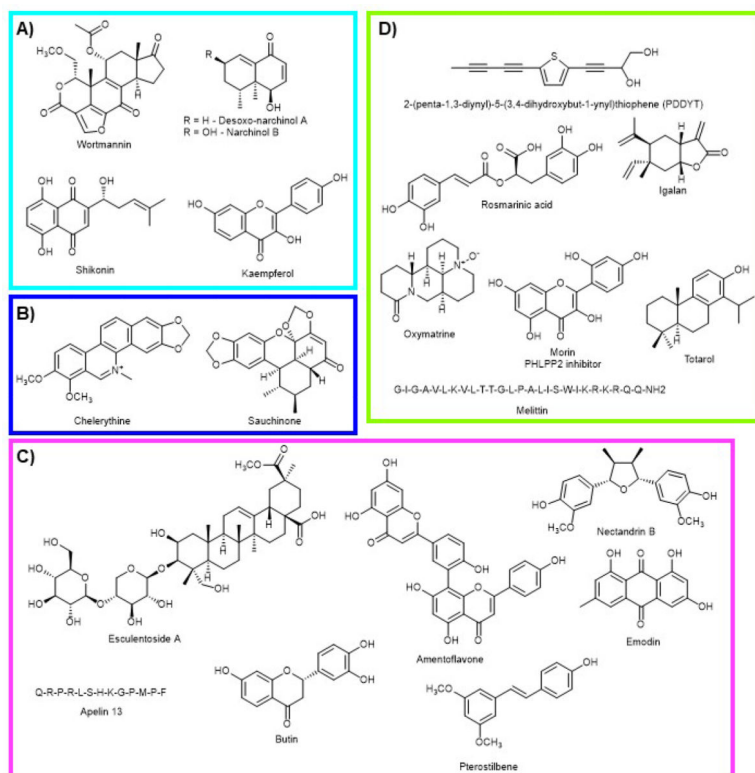


Figure 14. NRF2 modulating compounds that modulate the GSK-3 β /NRF2/ β -TrCP regulatory axis.

A) PI3K inhibitors that inhibit NRF2 by blocking PI3K. Wortmannin from *Penicillium funiculosum*. Despxo-narchinol A and narchinol B from *Nardostachys jatamansi*. Shikonin from *Lithospermum erythrorhizon*. Kaempferol from *Brassica oleracea* var. *viridis*. **B)** PKC modulators. Chelerythrine (*Chelidonium majus*) inhibits PKC and sauchinone (*Saururus chinensis*) activates PKC leading to inhibition of NRF2 and activation of NRF2, respectively. **C)** Compounds that activate AKT/PKB by increasing the activity of AMPK. Nectandrin B from *Myristica fragrans*. Emodin from *Rheum hybridum*. Esculentoside A from *Phytolacca esculenta*. Amentoflavone from *Ginkgo biloba*. Butin from *Vernonia anthelmintica*. Pterostilbene from blueberries. Apelin 13 from humans. **D)** Miscellaneous compounds that activate AKT/PKB by unknown mechanisms or through routes described in the text. 2-(penta-1,3-diyanyl)-5-(3,4-dihydroxybut-1-ynyl)thiophene (PDDYT) from *Echinops grijsii*. Rosmarinic acid from *Rosmarinus officinalis*. Igalan from *Inula helenium* L. Oxymatrine from *Sophora flavescens*. Morin from *Maclura pomifera*. Totarol from *Podocarpus totara*. Melittin from honeybee (*Apis mellifera*) venom.

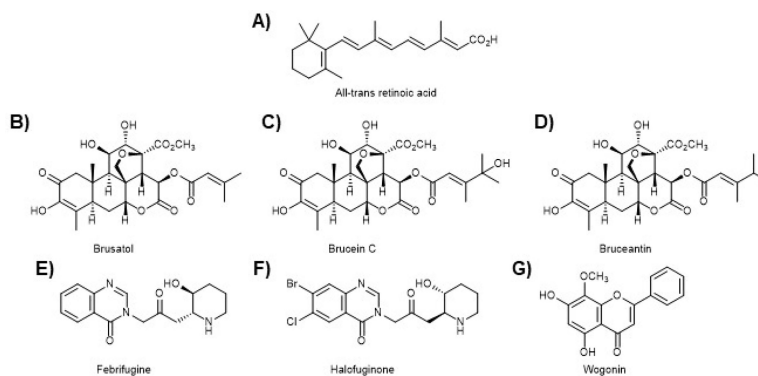


Figure 15. The dark side of NRF2 has led to a search for NRF2 inhibitors.

A) The first NRF2 pathway inhibitor to be revealed was all-*trans* retinoic acid (ATRA).

However, this was not without controversy as some groups reported ATRA to be an NRF2 activator. In any case, ATRA revealed RXR- α as a negative regulator of NRF2 transcription and defined the Neh7 domain as the site of RXR- α binding. **B)** Brusatol is a quassinoid that inhibits the synthesis of NRF2 and is the most potent NRF2 pathway inhibitor known.

Despite potential off-target effects, brusatol (*Brucia javanica*) has been used extensively to probe the NRF2 pathway and reveal the intricacies of the dark-side of NRF2. **C)** Brucein C (*Brucia javanica*) was found to be inactive in NRF2 pathway assays. **D)** Bruceantin (*Brucea antidysenterica*) has been shown to be more potent than brusatol at inhibiting NRF2

function. These three molecules, and others of the class, show interesting SAR related to the lipid ester. **E)** and **F)** Febrifugine (*Dichroa febrifuga*) and halofuginone, a semi-synthetic derivative of febrifugine, were shown to block prolyl-tRNA synthetase, thus blocking NRF2 synthesis and confirmed some of the studies conducted by brusatol, cementing the importance of the discovery and development of an NRF2 inhibitor. **G)** Wogonin (*Scutellaria baicalensis*) has been shown to decrease NRF2 mRNA levels and to reverse chemoresistance. However, conflicting studies have shown this to be an NRF2 activating compound.