

Supplementary Information

Amphipathic environments for determining the structure of membrane proteins by single-particle electron cryo-microscopy

Christel Le Bon^{1,2}, Baptiste Michon^{1,2}, Jean-Luc Popot^{1,2}, Manuela Zoonens^{1,2*}

¹Université de Paris, Laboratoire de Biologie Physico-Chimique des Protéines Membranaires, CNRS, UMR 7099, F-75005 Paris, France

²Institut de Biologie Physico-Chimique, Fondation Edmond de Rothschild pour le développement de la recherche Scientifique, F-75005 Paris, France

*Correspondence should be addressed to Manuela Zoonens
(manuela.zoonens@ibpc.fr)

Keywords: amphipols, detergents, integral membrane protein complexes, lipids, nanodiscs, structural biology

Running title: Trends in the use of amphipathic environments for determining the structure of membrane proteins by cryo-EM.

Surfactants used for vitrification	Surfactants used for solubilization		
	<i>Maltosides</i>	<i>MNGs</i>	<i>Digitonin</i>
Maltosides	(Griebel et al., 2017; Gopalasingam et al., 2019; Maity et al., 2019; Caspy et al., 2020; Jamali et al., 2020; Kieuvongngam et al., 2020; Perez-Boerema et al., 2020; Wang et al., 2020g)	(Lü et al., 2017; Winkler et al., 2017; Tucker et al., 2019)	
MNGs	(Oshima et al., 2016; Koehl et al., 2018; Bai et al., 2019a; Bai et al., 2019b; Parey et al., 2019; Tang et al., 2019; Timcenko et al., 2019; Tsai et al., 2019; Burendei et al., 2020; Mou et al., 2020; Su et al., 2020; Zhang et al., 2020i; Zhang et al., 2020g)	(Huynh et al., 2016; Liang et al., 2017; Hughes et al., 2018; Jin et al., 2020)	
Digitonin	(Qian et al., 2017; Duan et al., 2018a; Duan et al., 2018c; Gong et al., 2018a; Gong et al., 2018c; Kang et al., 2018; Oosterheert et al., 2018; Qi et al., 2018a; Qi et al., 2018b; Su et al., 2018; Sui et al., 2018; Lee et al., 2019b; Liu et al., 2019c; Qi et al., 2019a; Qi et al., 2019b; Yin et al., 2019a; Cannac et al., 2020; Clark et al., 2020; Huang et al., 2020a; Liu et al., 2020a; Peng et al., 2020; Shaye et al., 2020; Zhang et al., 2020b; Zhu et al., 2020)	(Zhang et al., 2016; Johnson et al., 2017; Lee et al., 2017a; Liu et al., 2017; Zhang et al., 2017; Baradaran et al., 2018; Butterwick et al., 2018; Fay et al., 2018; Johnson et al., 2018; Kefauver et al., 2018; Paknejad et al., 2018; Zhang et al., 2018a; Zhang et al., 2018b; Zhang et al., 2018d; Zhang et al., 2018e; Chew et al., 2019; Lee et al., 2019a; Liu et al., 2019a; Tao et al., 2019; Sun, 2020; Wang et al., 2020c; Wang et al., 2020d; Wu et al., 2020)	
GDN	(She et al., 2018; Hiraizumi et al., 2019; Koehl et al., 2019; Liu et al., 2019b; Nakagawa, 2019; Poweleit et al., 2019; She et al., 2019; Shen et al., 2019a; Zhao et al., 2019c; Chi et al., 2020; Demura et al., 2020; Gao et al., 2020; Jiang et al., 2020; Li et al., 2020c; Li et al., 2020e; Papasergi-Scott et al., 2020; Qi et al., 2020b; Ren et al., 2020; Tsutsumi et al., 2020; Yan et al., 2020; Zhang et al., 2020d)	(Itskanov et al., 2019; Tucker et al., 2019; Yan et al., 2019; Deng et al., 2020a; Deng et al., 2020b; Diederichs et al., 2020; Drożdżyk et al., 2020; Kim et al., 2020c; Li et al., 2020d; Purushotham et al., 2020; Qi et al., 2020a; Wang et al., 2020e; Xie et al., 2020a; Xie et al., 2020b)	(Singh et al., 2018a; Araiso et al., 2019; McGoldrick et al., 2019; Singh et al., 2019; Walter et al., 2019; Zhao et al., 2019b)
CYMAL-7	(Vinothkumar et al., 2014; Zhu et al., 2016; Blaza et al., 2018)		
Amphipathic polymers	(Cao et al., 2013; Liao et al., 2013; Mazhab-Jafari et al., 2016; Shen et al., 2016; Zubcevic et al., 2016; Hirschi et al., 2017; Schoebel et al., 2017; Duan et al., 2018b; Hulse et al., 2018; Huynh et al., 2018; McGoldrick et al., 2018; Myers et al., 2018; Singh et al., 2018b; Vinayagam et al., 2018; Yoo et al., 2018; Zhang et al., 2018c; Zubcevic et al., 2018; Suga et al., 2019; Wang et al., 2019a; Zubcevic et al., 2019a; Zubcevic et al., 2019b; Hou et al., 2020; Johnson et al., 2020; Kuhlen et al., 2020; Long et al., 2020; Owji et al., 2020; Sauer et al., 2020; Vinayagam et al., 2020; Weaver et al., 2020)	(Paulsen et al., 2015; Chen et al., 2016; Fitzpatrick et al., 2017; Li et al., 2017; Wilkes et al., 2017; Zhou et al., 2017; Diver et al., 2019; Letts et al., 2019; Theßeling et al., 2019; Maeda et al., 2020; McDowell et al., 2020)	(Lu et al., 2014; Bai et al., 2015; Lee et al., 2017b; Yin et al., 2019c; Maldonado et al., 2020)
MSP-based nanodiscs	(Gao et al., 2016; Matthies et al., 2016; Shen et al., 2016; Chen et al., 2017; Dang et al., 2017; Jin et al., 2017; Mi et al., 2017; Taylor et al., 2017; Autzen et al., 2018; Jackson et al., 2018; Jojoa-Cruz et al., 2018; Manolaridis et al., 2018; Matthies et al., 2018; McGoldrick et al., 2018; Rheinberger et al., 2018; Roh et al., 2018; Srivastava et al., 2018; Wild et al., 2018; Yoo et al., 2018; Celia et al., 2019; Dang et al., 2019; Feng et al., 2019; Hofmann et al., 2019; Kalienkova et al., 2019; Kern et al., 2019; Khelashvili et al., 2019; Kim et al., 2019; Koehl et al., 2019; Li et al., 2019; Liu et al., 2019b; Rasmussen et al., 2019; Safarian et al., 2019; Saotome et al., 2019; Wang et al., 2019b; Zhou et al., 2019a; Zubcevic et al., 2019b; Arkhipova et al., 2020; Billesbølle et al., 2020;	(Hughes et al., 2019; Laverty et al., 2019; Pumroy et al., 2019; Diederichs et al., 2020; Maeda et al., 2020; Nakane et al., 2020; Wang et al., 2020k; Yin et al., 2020; Zheng et al., 2020)	(Alvadia et al., 2019; Falzone et al., 2019; Guan et al., 2020; Suo et al., 2020)

	Burendei et al., 2020; Fan et al., 2020a; Flores et al., 2020; Glavier et al., 2020; Huang et al., 2020c; Kishikawa et al., 2020; Kumar et al., 2020b; Kumar et al., 2020a; Lee et al., 2020b; Li et al., 2020a; Liu et al., 2020b; Luo et al., 2020; Orlando et al., 2020; Pleiner et al., 2020; Qian et al., 2020; Reid et al., 2020; Roh et al., 2020; Sauer et al., 2020; Shimada et al., 2020; Staus et al., 2020; Tan et al., 2020; Wang et al., 2020i; Wang et al., 2020j)
Saposin-based nanodiscs	(Kintzer et al., 2018; Nguyen et al., 2018; Gharpure et al., 2019; Nagamura et al., 2019; Du et al., 2020; Kim et al., 2020a)
Peptidiscs	(Angiulli et al., 2020; Zeytuni et al., 2020)
Mixed detergents	(Kato et al., 2019a; Krishna Kumar et al., 2019; Qi et al., 2019c; Kim et al., 2020b; Yuan et al., 2020)
Others ^a	(Yao et al., 2020)
Same as for purification	(Du et al., 2015; Hite et al., 2015; Bokori-Brown et al., 2016; Iadanza et al., 2016; Meyerson et al., 2016; Oldham et al., 2016; Wei et al., 2016; Whicher et al., 2016; Guo et al., 2017a; Hite et al., 2017a; Hite et al., 2017b; Klusch et al., 2017; Park et al., 2017; Su et al., 2017; Sun et al., 2017; Tao et al., 2017; Wang et al., 2017; Agip et al., 2018; Deng et al., 2018; Du et al., 2018; Garaeva et al., 2018; García-Nafria et al., 2018b; Kim et al., 2018; Lee et al., 2018; Nguyen et al., 2018; Noreng et al., 2018; Parey et al., 2018; Park et al., 2018; Phulera et al., 2018; Pi et al., 2018; Sousa et al., 2018; Sui et al., 2018; Walsh et al., 2018; Wiseman et al., 2018; Xin et al., 2018; Yoder et al., 2018; Yu et al., 2018; Zhu et al., 2018; Zubcevic et al., 2018; Bushell et al., 2019; Chen et al., 2019; Chernyatina et al., 2019; Garaeva et al., 2019; Gharpure et al., 2019; Gopalasingam et al., 2019; Kalienkova et al., 2019; Kato et al., 2019b; Laughlin et al., 2019; Klusch et al., 2017; Lunelli et al., 2020; McCarthy et al., 2019; Miller et al., 2019; Murphy et al., 2019; Parey et al., 2019; Pi et al., 2019; Reddy et al., 2019; Savva et al., 2019; Schuller et al., 2019; Shang et al., 2019; Shen et al., 2019b; Su et al., 2019; Toporik et al., 2019; Zhang et al., 2019; Abbas et al., 2020; Akita et al., 2020; Cao et al., 2020; Coleman et al., 2020; Johnson et al., 2020; Kato et al., 2020; Li et al., 2020b; Lunelli et al., 2020; Mukherjee et al., 2020; Niu et al., 2020; Pan et al., 2020; Rempel et al., 2020; Sauer et al., 2020; Soufari et al., 2020; Sun et al., 2020a; Toporik et al., 2020; Van der Verren et al., 2020; Xu et al., 2020; Zhang et al., 2020a; Zhang et al., 2020c)
	(Zhao et al., 2019a; Chen et al., 2020a; Duan et al., 2020; Hilger et al., 2020; Hua et al., 2020; Huang et al., 2020b; Liu et al., 2020c; Sun et al., 2020b; Yang et al., 2020a)
	(Fiedorczuk et al., 2016)
	(Dang et al., 2017; James et al., 2017; Zhou et al., 2017; Alam et al., 2018; Draper-Joyce et al., 2018; García-Nafria et al., 2018a; Jojoa-Cruz et al., 2018; Kuhlen et al., 2018; Lauber et al., 2018; Liang et al., 2018a; Liang et al., 2018b; Wang et al., 2018; Dosey et al., 2019; Gao et al., 2019; Kampjut et al., 2019; Nguyen et al., 2019; Yu et al., 2019; Chang et al., 2020; Chou et al., 2020; Deme et al., 2020; Dong et al., 2020; Fan et al., 2020b; Fukuhara et al., 2020; Guardia et al., 2020; Kampjut et al., 2020; Kobayashi et al., 2020; Kuhlen et al., 2020; Lee et al., 2020a; Liang et al., 2020a; Liang et al., 2020b; Maeda et al., 2020; Mao et al., 2020; Oh et al., 2020; Park et al., 2020; Pinke et al., 2020; Qiao et al., 2020; Santiveri et al., 2020; Schrecker et al., 2020; Vinayagam et al., 2020; Wang et al., 2020a; Wang et al., 2020b; Wang et al., 2020f; Yang et al., 2020b; Yang et al., 2020c; Zhang et al., 2020f; Zhang et al., 2020h; Zhao et al., 2020a; Zhao et al., 2020b)
	(Sun et al., 2015; Wu et al., 2015; Gong et al., 2016; Voorhees et al., 2016; Wu et al., 2016b; Wu et al., 2016a; Guo et al., 2017b; Martin et al., 2017; Paulino et al., 2017; Shen et al., 2017; Twomey et al., 2017; Yan et al., 2017; Guo et al., 2017b; Bai et al., 2018; Deneka et al., 2018; Fan et al., 2018; Gong et al., 2018b; Kasuya et al., 2018; Pan et al., 2018; Shen et al., 2018; Singh et al., 2018a; Wu et al., 2018; Yin et al., 2018; Alvadia et al., 2019; Choi et al., 2019; Clairfeuille et al., 2019; Ding et al., 2019; Feng et al., 2019; Gu et al., 2019; Martin et al., 2019; Ramírez et al., 2019; Rathore et al., 2019; Tao et al., 2019; Wu et al., 2019; Yan et al., 2019; Yin et al., 2019b; Yin et al., 2019c; Zhao et al., 2019b; Zhou et al., 2019b; Bai et al., 2020; Chen et al., 2020b; Flygaard et al., 2020; Gérard et al., 2020; Hartley et al., 2020; Kater et al., 2020; McGilvray et al., 2020; Nakamura et al., 2020; Noreng et al., 2020; Qu et al., 2020; Sobti et al., 2020; Wang et al., 2020h; Zhang et al., 2020e; Zhou et al., 2020)

Table S1. References to studies in which the target membrane protein was initially solubilized and purified in either maltosides, neopentyl glycols or digitonin, sorted out according to the surfactant used for vitrification. Note that, in most cases, the latest steps of purification were used to substitute one surfactant with the other.

^a "Others" refers to liposomes (Yao et al., 2020) and Brij-35 (Fiedorczuk et al., 2016).

References

- Abbas YM, Wu D, Bueler SA, Robinson CV and Rubinstein JL (2020) Structure of V-ATPase from the mammalian brain. *Science* **367**, 1240–1246.
- Agip A-NA, Blaza JN, Bridges HR, Visconti C, Rawson S, Muench SP and Hirst J (2018) Cryo-EM structures of complex I from mouse heart mitochondria in two biochemically defined states. *Nature Structural & Molecular Biology* **25**, 548–556.
- Akita F, Nagao R, Kato K, Nakajima Y, Yokono M, Ueno Y, Suzuki T, Dohmae N, Shen J-R, Akimoto S and Miyazaki N (2020) Structure of a cyanobacterial photosystem I surrounded by octadecameric IsiA antenna proteins. *Communications Biology* **3**, 232.
- Alam A, Küng R, Kowal J, McLeod RA, Tremp N, Broude EV, Roninson IB, Stahlberg H and Locher KP (2018) Structure of a zosuquidar and UIC2-bound human-mouse chimeric ABCB1. *Proceedings of the National Academy of Sciences* **115**, e1973–1982.
- Alvadia C, Lim NK, Clerico Mosina V, Oostergetel GT, Dutzler R and Paulino C (2019) Cryo-EM structures and functional characterization of the murine lipid scramblase TMEM16F. *eLife* **8**, e44365.
- Angiulli G, Dhupar HS, Suzuki H, Wason IS, Duong Van Hoa F and Walz T (2020) New approach for membrane protein reconstitution into peptidiscs and basis for their adaptability to different proteins. *eLife* **9**, e53530.
- Araiso Y, Tsutsumi A, Qiu J, Imai K, Shiota T, Song J, Lindau C, Wenz L-S, Sakaue H, Yunoki K, Kawano S, Suzuki J, Wischnewski M, Schütze C, Ariyama H, Ando T, Becker T, Lithgow T, Wiedemann N, Pfanner N, Kikkawa M and Endo T (2019) Structure of the mitochondrial import gate reveals distinct preprotein paths. *Nature* **575**, 395–401.
- Arkhipova V, Guskov A and Slotboom DJ (2020) Structural ensemble of a glutamate transporter homologue in lipid nanodisc environment. *Nature Communications* **11**, 998.
- Autzen HE, Myasnikov AG, Campbell MG, Asarnow D, Julius D and Cheng Y (2018) Structure of the human TRPM4 ion channel in a lipid nanodisc. *Science* **359**, 228–232.
- Bai L, Kovach A, You Q, Hsu H-C, Zhao G and Li H (2019a) Autoinhibition and activation mechanisms of the eukaryotic lipid flippase Drs2p-Cdc50p. *Nature Communications* **10**, 4142.
- Bai L, Kovach A, You Q, Kenny A and Li H (2019b) Structure of the eukaryotic protein O-mannosyltransferase Pmt1-Pmt2 complex. *Nature Structural & Molecular Biology* **26**, 704–711.
- Bai L, Wang T, Zhao G, Kovach A and Li H (2018) The atomic structure of a eukaryotic oligosaccharyltransferase complex. *Nature* **555**, 328–333.
- Bai L, You Q, Feng X, Kovach A and Li H (2020) Structure of the ER membrane complex, a transmembrane-domain insertase. *Nature* **584**, 475–478.
- Bai X, Yan C, Yang G, Lu P, Ma D, Sun L, Zhou R, Scheres SHW and Shi Y (2015) An atomic structure of human γ-secretase. *Nature* **525**, 212–217.
- Baradaran R, Wang C, Siliciano AF and Long SB (2018) Cryo-EM structures of fungal and metazoan mitochondrial calcium uniporters. *Nature* **559**, 580–584.
- Billesbølle CB, Azumaya CM, Kretsch RC, Powers AS, Gonon S, Schneider S, Arvedson T, Dror RO, Cheng Y and Manglik A (2020) Structure of hepcidin-bound ferroportin reveals iron homeostatic mechanisms. *Nature* **586**, 807–811.

Blaza JN, Vinothkumar KR and Hirst J (2018) Structure of the Deactive State of Mammalian Respiratory Complex I. *Structure* **26**, 312-319.e3.

Bokori-Brown M, Martin TG, Naylor CE, Basak AK, Titball RW and Savva CG (2016) Cryo-EM structure of lysenin pore elucidates membrane insertion by an aerolysin family protein. *Nature Communications* **7**, 11293.

Burendei B, Shinozaki R, Watanabe M, Terada T, Tani K, Fujiyoshi Y and Oshima A (2020) Cryo-EM structures of undocked innexin-6 hemichannels in phospholipids. *Science Advances* **6**, eaax3157.

Bushell SR, Pike ACW, Falzone ME, Rorsman NJG, Ta CM, Corey RA, Newport TD, Christianson JC, Scofano LF, Shintre CA, Tessitore A, Chu A, Wang Q, Shrestha L, Mukhopadhyay SMM, Love JD, Burgess-Brown NA, Sitsapesan R, Stansfeld PJ, Huisken JT, Tammaro P, Accardi A and Carpenter EP (2019) The structural basis of lipid scrambling and inactivation in the endoplasmic reticulum scramblase TMEM16K. *Nature Communications* **10**, 3956.

Butterwick JA, Del Marmol J, Kim KH, Kahlson MA, Rogow JA, Walz T and Ruta V (2018) Cryo-EM structure of the insect olfactory receptor Orco. *Nature* **560**, 447–452.

Cannac F, Qi C, Falschlunger J, Hausmann G, Basler K and Korkhov VM (2020) Cryo-EM structure of the Hedgehog release protein Dispatched. *Science Advances* **6**, eaay7928.

Cao E, Liao M, Cheng Y and Julius D (2013) TRPV1 structures in distinct conformations reveal activation mechanisms. *Nature* **504**, 113–118.

Cao P, Cao D, Si L, Su X, Tian L, Chang W, Liu Z, Zhang X and Li M (2020) Structural basis for energy and electron transfer of the photosystem I-IsiA-flavodoxin supercomplex. *Nature Plants* **6**, 167–176.

Caspy I, Borovikova-Sheinker A, Klaiman D, Shkolnisky Y and Nelson N (2020) The structure of a triple complex of plant photosystem I with ferredoxin and plastocyanin. *Nature Plants* **6**, 1300–1305.

Celia H, Botos I, Ni X, Fox T, De Val N, Lloubes R, Jiang J and Buchanan SK (2019) Cryo-EM structure of the bacterial Ton motor subcomplex ExbB-ExbD provides information on structure and stoichiometry. *Communications Biology* **2**, 358.

Chang R, Zhang X, Qiao A, Dai A, Belousoff MJ, Tan Q, Shao L, Zhong L, Lin G, Liang Y-L, Ma L, Han S, Yang D, Danev R, Wang M-W, Wootten D, Wu B and Sexton PM (2020) Cryo-electron microscopy structure of the glucagon receptor with a dual-agonist peptide. *The Journal of Biological Chemistry* **295**, 9313–9325.

Chen G, Wang X, Ge Y, Ma L, Chen Q, Liu H, Du Y, Ye RD, Hu H and Ren R (2020a) Cryo-EM structure of activated bile acids receptor TGR5 in complex with stimulatory G protein. *Signal Transduction and Targeted Therapy* **5**, 142.

Chen M, Perez-Boerema A, Zhang L, Li Y, Yang M, Li S and Amunts A (2020b) Distinct structural modulation of photosystem I and lipid environment stabilizes its tetrameric assembly. *Nature Plants* **6**, 314–320.

Chen Q, She J, Zeng W, Guo J, Xu H, Bai X-C and Jiang Y (2017) Structure of mammalian endolysosomal TRPML1 channel in nanodiscs. *Nature* **550**, 415–418.

Chen Q, Zeng W, She J, Bai X-C and Jiang Y (2019) Structural and functional characterization of an otopetrin family proton channel. *eLife* **8**, e46710.

Chen Y, Clarke OB, Kim J, Stowe S, Kim Y-K, Assur Z, Cavalier M, Godoy-Ruiz R, von Alpen DC, Manzini C, Blaner WS, Frank J, Quadro L, Weber DJ, Shapiro L, Hendrickson WA and Mancia F (2016) Structure of the STRA6 receptor for retinol uptake. *Science* **353**.

Chernyatina AA and Low HH (2019) Core architecture of a bacterial type II secretion system. *Nature Communications* **10**, 5437.

Chew TA, Orlando BJ, Zhang J, Latorraca NR, Wang A, Hollingsworth SA, Chen D-H, Dror RO, Liao M and Feng L (2019) Structure and mechanism of the cation-chloride cotransporter NKCC1. *Nature* **572**, 488–492.

Chi X, Jin X, Chen Y, Lu X, Tu X, Li X, Zhang Y, Lei J, Huang J, Huang Z, Zhou Q and Pan X (2020) Structural insights into the gating mechanism of human SLC26A9 mediated by its C-terminal sequence. *Cell Discovery* **6**, 55.

Choi W, Clemente N, Sun W, Du J and Lü W (2019) The structures and gating mechanism of human calcium homeostasis modulator 2. *Nature* **576**, 163–167.

Chou T-H, Tajima N, Romero-Hernandez A and Furukawa H (2020) Structural Basis of Functional Transitions in Mammalian NMDA Receptors. *Cell* **182**, 357-371.e13.

Clairfeuille T, Cloake A, Infield DT, Llongueras JP, Arthur CP, Li ZR, Jian Y, Martin-Eauclaire M-F, Bougis PE, Ciferri C, Ahern CA, Bosmans F, Hackos DH, Rohou A and Payandeh J (2019) Structural basis of α-scorpion toxin action on Nav channels. *Science* **363**, eaav8573.

Clark MD, Contreras GF, Shen R and Perozo E (2020) Electromechanical coupling in the hyperpolarization-activated K⁺ channel KAT1. *Nature* **583**, 145–149.

Coleman JA, Navratna V, Antermite D, Yang D, Bull JA and Gouaux E (2020) Chemical and structural investigation of the paroxetine-human serotonin transporter complex. *eLife* **9**, e56427.

Dang S, Feng S, Tien J, Peters CJ, Bulkley D, Lolicato M, Zhao J, Zuberbühler K, Ye W, Qi L, Chen T, Craik CS, Jan YN, Minor DL, Cheng Y and Jan LY (2017) Cryo-EM structures of the TMEM16A calcium-activated chloride channel. *Nature* **552**, 426–429.

Dang S, van Goor MK, Asarnow D, Wang Y, Julius D, Cheng Y and van der Wijst J (2019) Structural insight into TRPV5 channel function and modulation. *Proceedings of the National Academy of Sciences of the United States of America* **116**, 8869–8878.

Deme JC, Johnson S, Vickery O, Aron A, Monkhouse H, Griffiths T, James RH, Berks BC, Coulton JW, Stansfeld PJ and Lea SM (2020) Structures of the stator complex that drives rotation of the bacterial flagellum. *Nature Microbiology* **5**, 1553–1564.

Demura K, Kusakizako T, Shihoya W, Hiraizumi M, Nomura K, Shimada H, Yamashita K, Nishizawa T, Taruno A and Nureki O (2020) Cryo-EM structures of calcium homeostasis modulator channels in diverse oligomeric assemblies. *Science Advances* **6**, eaba8105.

Deneka D, Sawicka M, Lam AKM, Paulino C and Dutzler R (2018) Structure of a volume-regulated anion channel of the LRRC8 family. *Nature* **558**, 254–259.

Deng Z, He Z, Maksaev G, Bitter RM, Rau M, Fitzpatrick JAJ and Yuan P (2020a) Cryo-EM structures of the ATP release channel pannexin 1. *Nature Structural & Molecular Biology* **27**, 373–381.

Deng Z, Maksaev G, Schlegel AM, Zhang J, Rau M, Fitzpatrick JAJ, Haswell ES and Yuan P (2020b) Structural mechanism for gating of a eukaryotic mechanosensitive channel of small conductance. *Nature Communications* **11**, 3690.

Deng Z, Paknejad N, Maksaev G, Sala-Rabanal M, Nichols CG, Hite RK and Yuan P (2018) Cryo-EM and X-ray structures of TRPV4 reveal insight into ion permeation and gating mechanisms. *Nature Structural & Molecular Biology* **25**, 252–260.

- Diederichs KA, Ni X, Rollauer SE, Botos I, Tan X, King MS, Kunji ERS, Jiang J and Buchanan SK (2020) Structural insight into mitochondrial β -barrel outer membrane protein biogenesis. *Nature Communications* **11**, 3290.
- Ding D, Wang M, Wu J-X, Kang Y and Chen L (2019) The Structural Basis for the Binding of Repaglinide to the Pancreatic KATP Channel. *Cell Reports* **27**, 1848-1857.e4.
- Diver MM, Cheng Y and Julius D (2019) Structural insights into TRPM8 inhibition and desensitization. *Science* **365**, 1434–1440.
- Dong M, Deganutti G, Piper SJ, Liang Y-L, Khoshouei M, Belousoff MJ, Harikumar KG, Reynolds CA, Glukhova A, Furness SGB, Christopoulos A, Danev R, Wootten D, Sexton PM and Miller LJ (2020) Structure and dynamics of the active Gs-coupled human secretin receptor. *Nature Communications* **11**, 4137.
- Dosey TL, Wang Z, Fan G, Zhang Z, Serysheva II, Chiu W and Wensel TG (2019) Structures of TRPV2 in distinct conformations provide insight into role of the pore turret. *Nature Structural & Molecular Biology* **26**, 40–49.
- Draper-Joyce CJ, Khoshouei M, Thal DM, Liang Y-L, Nguyen ATN, Furness SGB, Venugopal H, Baltos J-A, Plitzko JM, Danev R, Baumeister W, May LT, Wootten D, Sexton PM, Glukhova A and Christopoulos A (2018) Structure of the adenosine-bound human adenosine A 1 receptor–G i complex. *Nature* **558**, 559–563.
- Drożdżyk K, Sawicka M, Bahamonde-Santos M-I, Jonas Z, Deneka D, Albrecht C and Dutzler R (2020) Cryo-EM structures and functional properties of CALHM channels of the human placenta. *eLife* **9**, e55853.
- Du D, Neuberger A, Orr MW, Newman CE, Hsu P-C, Samsudin F, Szewczak-Harris A, Ramos LM, Debela M, Khalid S, Storz G and Luisi BF (2020) Interactions of a Bacterial RND Transporter with a Transmembrane Small Protein in a Lipid Environment. *Structure* **28**, 625-634.e6.
- Du J, Lü W, Wu S, Cheng Y and Gouaux E (2015) Glycine receptor mechanism illuminated by electron cryo-microscopy. *Nature* **526**, 224–229.
- Du M, Yuan Z, Yu H, Henderson N, Sarowar S, Zhao G, Werneburg GT, Thanassi DG and Li H (2018) Handover mechanism of the growing pilus by the bacterial outer-membrane usher FimD. *Nature* **562**, 444–447.
- Duan J, Li J, Zeng B, Chen G-L, Peng X, Zhang Y, Wang J, Clapham DE, Li Z and Zhang J (2018a) Structure of the mouse TRPC4 ion channel. *Nature Communications* **9**, 3102.
- Duan J, Li Z, Li J, Hulse RE, Santa-Cruz A, Valinsky WC, Abiria SA, Krapivinsky G, Zhang J and Clapham DE (2018b) Structure of the mammalian TRPM7, a magnesium channel required during embryonic development. *Proceedings of the National Academy of Sciences* **115**, e8201-8210.
- Duan J, Li Z, Li J, Santa-Cruz A, Sanchez-Martinez S, Zhang J and Clapham DE (2018c) Structure of full-length human TRPM4. *Proceedings of the National Academy of Sciences of the United States of America* **115**, 2377–2382.
- Duan J, Shen D-D, Zhou XE, Bi P, Liu Q-F, Tan Y-X, Zhuang Y-W, Zhang H-B, Xu P-Y, Huang S-J, Ma S-S, He X-H, Melcher K, Zhang Y, Xu HE and Jiang Y (2020) Cryo-EM structure of an activated VIP1 receptor-G protein complex revealed by a NanoBiT tethering strategy. *Nature Communications* **11**, 4121.
- Falzone ME, Rheinberger J, Lee B-C, Peyear T, Sasset L, Raczkowski AM, Eng ET, Di Lorenzo A, Andersen OS, Nimigean CM and Accardi A (2019) Structural basis of Ca²⁺-dependent activation and lipid transport by a TMEM16 scramblase. *eLife* **8**, e43229.

- Fan C, Choi W, Sun W, Du J and Lü W (2018) Structure of the human lipid-gated cation channel TRPC3. *eLife* **7**, e36852.
- Fan C, Sukomon N, Flood E, Rheinberger J, Allen TW and Nimigean CM (2020a) Ball-and-chain inactivation in a calcium-gated potassium channel. *Nature* **580**, 288–293.
- Fan M, Zhang J, Tsai C-W, Orlando BJ, Rodriguez M, Xu Y, Liao M, Tsai M-F and Feng L (2020b) Structure and mechanism of the mitochondrial Ca²⁺ uniporter holocomplex. *Nature* **582**, 129–133.
- Fay JF, Aleksandrov LA, Jensen TJ, Cui LL, Kousouros JN, He L, Aleksandrov AA, Gingerich DS, Riordan JR and Chen JZ (2018) Cryo-EM Visualization of an Active High Open Probability CFTR Anion Channel. *Biochemistry* **57**, 6234–6246.
- Feng S, Dang S, Han TW, Ye W, Jin P, Cheng T, Li J, Jan YN, Jan LY and Cheng Y (2019) Cryo-EM Studies of TMEM16F Calcium-Activated Ion Channel Suggest Features Important for Lipid Scrambling. *Cell Reports* **28**, 567–579.e4.
- Fiedorczuk K, Letts JA, Degliesposti G, Kaszuba K, Skehel M and Sazanov LA (2016) Atomic structure of the entire mammalian mitochondrial complex I. *Nature* **538**, 406–410.
- Fitzpatrick AWP, Llabrés S, Neuberger A, Blaza JN, Bai X-C, Okada U, Murakami S, Veen HW van, Zachariae U, Scheres SHW, Luisi BF and Du D (2017) Structure of the MacAB–TolC ABC-type tripartite multidrug efflux pump. *Nature Microbiology* **2**, 17070.
- Flores JA, Haddad BG, Dolan KA, Myers JB, Yoshioka CC, Copperman J, Zuckerman DM and Reichow SL (2020) Connexin-46/50 in a dynamic lipid environment resolved by CryoEM at 1.9 Å. *Nature Communications* **11**, 4331.
- Flygaard RK, Mühléip A, Tobiasson V and Amunts A (2020) Type III ATP synthase is a symmetry-deviated dimer that induces membrane curvature through tetramerization. *Nature Communications* **11**, 5342.
- Fukuhara S, Kobayashi K, Kusakizako T, Iida W, Kato M, Shihoya W and Nureki O (2020) Structure of the human secretin receptor coupled to an engineered heterotrimeric G protein. *Biochemical and Biophysical Research Communications* **533**, 861–866.
- Gao S, Valinsky WC, On NC, Houlihan PR, Qu Q, Liu L, Pan X, Clapham DE and Yan N (2020) Employing NaChBac for cryo-EM analysis of toxin action on voltage-gated Na⁺ channels in nanodisc. *Proceedings of the National Academy of Sciences of the United States of America* **117**, 14187–14193.
- Gao Y, Cao E, Julius D and Cheng Y (2016) TRPV1 structures in nanodiscs reveal mechanisms of ligand and lipid action. *Nature* **534**, 347–351.
- Gao Y, Hu H, Ramachandran S, Erickson JW, Cerione RA and Skiniotis G (2019) Structures of the Rhodopsin-Transducin Complex: Insights into G-Protein Activation. *Molecular Cell* **75**, 781–790.e3.
- Garaeva AA, Guskov A, Slotboom DJ and Paulino C (2019) A one-gate elevator mechanism for the human neutral amino acid transporter ASCT2. *Nature Communications* **10**, 3427.
- Garaeva AA, Oostergetel GT, Gati C, Guskov A, Paulino C and Slotboom DJ (2018) Cryo-EM structure of the human neutral amino acid transporter ASCT2. *Nature Structural & Molecular Biology* **25**, 515–521.
- García-Nafria J, Lee Y, Bai X, Carpenter B and Tate CG (2018a) Cryo-EM structure of the adenosine A2A receptor coupled to an engineered heterotrimeric G protein. *eLife* **7**, e35946.

García-Nafría J, Nehmé R, Edwards PC and Tate CG (2018b) Cryo-EM structure of the serotonin 5-HT1B receptor coupled to heterotrimeric Go. *Nature* **558**, 620–623.

Gérard SF, Hall BS, Zaki AM, Corfield KA, Mayerhofer PU, Costa C, Whelligan DK, Biggin PC, Simmonds RE and Higgins MK (2020) Structure of the Inhibited State of the Sec Translocon. *Molecular Cell* **79**, 406–415.e7.

Gharpure A, Teng J, Zhuang Y, Noviello CM, Walsh RM, Cabuco R, Howard RJ, Zaveri NT, Lindahl E and Hibbs RE (2019) Agonist Selectivity and Ion Permeation in the $\alpha 3\beta 4$ Ganglionic Nicotinic Receptor. *Neuron* **104**, 501–511.e6.

Glavier M, Puwanendran D, Salvador D, Decossas M, Phan G, Garnier C, Frezza E, Cece Q, Schoehn G, Picard M, Taveau J-C, Daury L, Broutin I and Lambert O (2020) Antibiotic export by MexB multidrug efflux transporter is allosterically controlled by a MexA-OprM chaperone-like complex. *Nature Communications* **11**, 4948.

Gong D, Chi X, Ren K, Huang G, Zhou G, Yan N, Lei J and Zhou Q (2018a) Structure of the human plasma membrane Ca²⁺-ATPase 1 in complex with its obligatory subunit neuroplastin. *Nature Communications* **9**, 3623.

Gong H, Li J, Xu A, Tang Y, Ji W, Gao R, Wang S, Yu L, Tian C, Li J, Yen H-Y, Man Lam S, Shui G, Yang X, Sun Y, Li X, Jia M, Yang C, Jiang B, Lou Z, Robinson CV, Wong L-L, Guddat LW, Sun F, Wang Q and Rao Z (2018b) An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. *Science* **362**.

Gong X, Qian H, Cao P, Zhao X, Zhou Q, Lei J and Yan N (2018c) Structural basis for the recognition of Sonic Hedgehog by human Patched1. *Science* **361**.

Gong X, Qian H, Zhou X, Wu J, Wan T, Cao P, Huang W, Zhao X, Wang X, Wang P, Shi Y, Gao GF, Zhou Q and Yan N (2016) Structural Insights into the Niemann-Pick C1 (NPC1)-Mediated Cholesterol Transfer and Ebola Infection. *Cell* **165**, 1467–1478.

Gopalasingam CC, Johnson RM, Chiduza GN, Tosha T, Yamamoto M, Shiro Y, Antonyuk SV, Muench SP and Hasnain SS (2019) Dimeric structures of quinol-dependent nitric oxide reductases (qNORs) revealed by cryo-electron microscopy. *Science Advances* **5**, eaax1803.

Griebel M, Pike ACW, Shintre CA, Venturi E, El-Ajouz S, Tessitore A, Shrestha L, Mukhopadhyay S, Mahajan P, Chalk R, Burgess-Brown NA, Sitsapesan R, Huiskonen JT and Carpenter EP (2017) Structure of the polycystic kidney disease TRP channel Polycystin-2 (PC2). *Nature Structural & Molecular Biology* **24**, 114–122.

Gu J, Zhang L, Zong S, Guo R, Liu T, Yi J, Wang P, Zhuo W and Yang M (2019) Cryo-EM structure of the mammalian ATP synthase tetramer bound with inhibitory protein IF1. *Science* **364**, 1068–1075.

Guan C, Niu Y, Chen S-C, Kang Y, Wu J-X, Nishi K, Chang CCY, Chang T-Y, Luo T and Chen L (2020) Structural insights into the inhibition mechanism of human sterol O-acyltransferase 1 by a competitive inhibitor. *Nature Communications* **11**, 2478.

Guardia CM, Tan X-F, Lian T, Rana MS, Zhou W, Christenson ET, Lowry AJ, Faraldo-Gómez JD, Bonifacino JS, Jiang J and Banerjee A (2020) Structure of Human ATG9A, the Only Transmembrane Protein of the Core Autophagy Machinery. *Cell Reports* **31**, 107837.

Guo J, She J, Zeng W, Chen Q, Bai X-C and Jiang Y (2017a) Structures of the calcium-activated, non-selective cation channel TRPM4. *Nature* **552**, 205–209.

Guo YR and MacKinnon R (2017b) Structure-based membrane dome mechanism for Piezo mechanosensitivity. *eLife* **6**, e33660.

- Hartley AM, Meunier B, Pinotsis N and Maréchal A (2020) Rcf2 revealed in cryo-EM structures of hypoxic isoforms of mature mitochondrial III-IV supercomplexes. *Proceedings of the National Academy of Sciences of the United States of America* **117**, 9329–9337.
- Hilger D, Kumar KK, Hu H, Pedersen MF, O'Brien ES, Giehm L, Jennings C, Eskici G, Inoue A, Lerch M, Mathiesen JM, Skiniotis G and Kobilka BK (2020) Structural insights into differences in G protein activation by family A and family B GPCRs. *Science* **369**, eaba3373.
- Hiraizumi M, Yamashita K, Nishizawa T and Nureki O (2019) Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. *Science* **365**, 1149–1155.
- Hirschi M, Herzik Jr MA, Wie J, Suo Y, Borschel WF, Ren D, Lander GC and Lee S-Y (2017) Cryo-electron microscopy structure of the lysosomal calcium-permeable channel TRPML3. *Nature* **550**, 411–414.
- Hite RK and MacKinnon R (2017a) Structural Titration of Slo2.2, a Na⁺-Dependent K⁺ Channel. *Cell* **168**, 390-399.e11.
- Hite RK, Tao X and MacKinnon R (2017b) Structural basis for gating the high-conductance Ca²⁺-activated K⁺ channel. *Nature* **541**, 52–57.
- Hite RK, Yuan P, Li Z, Hsuing Y, Walz T and MacKinnon R (2015) Cryo-electron microscopy structure of the Slo2.2 Na⁺-activated K⁺ channel. *Nature* **527**, 198–203.
- Hofmann S, Januliene D, Mehdipour AR, Thomas C, Stefan E, Brüchert S, Kuhn BT, Geertsma ER, Hummer G, Tampé R and Moeller A (2019) Conformation space of a heterodimeric ABC exporter under turnover conditions. *Nature* **571**, 580–583.
- Hou X, Outhwaite IR, Pedi L and Long SB (2020) Cryo-EM structure of the calcium release-activated calcium channel Orai in an open conformation. *eLife* **9**, e62772.
- Hua T, Li X, Wu L, Iliopoulos-Tsoutsouvas C, Wang Y, Wu M, Shen L, Johnston CA, Nikas SP, Song F, Song X, Yuan S, Sun Q, Wu Y, Jiang S, Grim TW, Benchama O, Stahl EL, Zvonok N, Zhao S, Bohn LM, Makriyannis A and Liu Z-J (2020) Activation and Signaling Mechanism Revealed by Cannabinoid Receptor-Gi Complex Structures. *Cell* **180**, 655-665.e18.
- Huang C-S, Yu X, Fordstrom P, Choi K, Chung BC, Roh S-H, Chiu W, Zhou M, Min X and Wang Z (2020a) Cryo-EM structures of NPC1L1 reveal mechanisms of cholesterol transport and ezetimibe inhibition. *Science Advances* **6**, eabb1989.
- Huang W, Masureel M, Qu Q, Janetko J, Inoue A, Kato HE, Robertson MJ, Nguyen KC, Glenn JS, Skiniotis G and Kobilka BK (2020b) Structure of the neuropeptidyl receptor 1 in complex with β-arrestin 1. *Nature* **579**, 303–308.
- Huang Y, Wang X, Lv G, Razavi AM, Huysmans GHM, Weinstein H, Bracken C, Eliezer D and Boudker O (2020c) Use of paramagnetic 19F NMR to monitor domain movement in a glutamate transporter homolog. *Nature Chemical Biology* **16**, 1006–1012.
- Hughes TE, Del Rosario JS, Kapoor A, Yazici AT, Yudin Y, Fluck EC, Filizola M, Rohacs T and Moiseenkova-Bell VY (2019) Structure-based characterization of novel TRPV5 inhibitors. *eLife* **8**, e49572.
- Hughes TET, Lodowski DT, Huynh KW, Yazici A, Del Rosario J, Kapoor A, Basak S, Samanta A, Han X, Chakrapani S, Zhou ZH, Filizola M, Rohacs T, Han S and Moiseenkova-Bell VY (2018) Structural basis of TRPV5 channel inhibition by econazole revealed by cryo-EM. *Nature Structural & Molecular Biology* **25**, 53–60.
- Hulse RE, Li Z, Huang RK, Zhang J and Clapham DE (2018) Cryo-EM structure of the polycystin 2-I1 ion channel. *eLife* **7**, e36931.

Huynh KW, Cohen MR, Jiang J, Samanta A, Lodowski DT, Zhou ZH and Moiseenkova-Bell VY (2016) Structure of the full-length TRPV2 channel by cryo-EM. *Nature Communications* **7**, 11130.

Huynh KW, Jiang J, Abuladze N, Tsirulnikov K, Kao L, Shao X, Newman D, Azimov R, Pushkin A, Zhou ZH and Kurtz I (2018) CryoEM structure of the human SLC4A4 sodium-coupled acid-base transporter NBCe1. *Nature Communications* **9**, 900.

Iadanza MG, Higgins AJ, Schiffri B, Calabrese AN, Brockwell DJ, Ashcroft AE, Radford SE and Ranson NA (2016) Lateral opening in the intact β-barrel assembly machinery captured by cryo-EM. *Nature Communications* **7**, 12865.

Itskanov S and Park E (2019) Structure of the posttranslational Sec protein-translocation channel complex from yeast. *Science* **363**, 84–87.

Jackson SM, Manolaridis I, Kowal J, Zechner M, Taylor NMI, Bause M, Bauer S, Bartholomaeus R, Bernhardt G, Koenig B, Buschauer A, Stahlberg H, Altmann K-H and Locher KP (2018) Structural basis of small-molecule inhibition of human multidrug transporter ABCG2. *Nature Structural & Molecular Biology* **25**, 333–340.

Jamali MAM, Gopalasingam CC, Johnson RM, Tosha T, Muramoto K, Muench SP, Antonyuk SV, Shiro Y and Hasnain SS (2020) The active form of quinol-dependent nitric oxide reductase from Neisseria meningitidis is a dimer. *IUCrJ* **7**, 404–415.

James ZM, Borst AJ, Haitin Y, Frenz B, DiMaio F, Zagotta WN and Veesler D (2017) CryoEM structure of a prokaryotic cyclic nucleotide-gated ion channel. *Proceedings of the National Academy of Sciences of the United States of America* **114**, 4430–4435.

Jiang D, Shi H, Tonggu L, Gamal El-Din TM, Lenaeus MJ, Zhao Y, Yoshioka C, Zheng N and Catterall WA (2020) Structure of the Cardiac Sodium Channel. *Cell* **180**, 122-134.e10.

Jin P, Bulkley D, Guo Y, Zhang W, Guo Z, Huynh W, Wu S, Meltzer S, Cheng T, Jan LY, Jan Y-N and Cheng Y (2017) Electron cryo-microscopy structure of the mechanotransduction channel NOMPC. *Nature* **547**, 118-122.

Jin Q, Zhang B, Zheng X, Li N, Xu L, Xie Y, Song F, Bhat EA, Chen Y, Gao N, Guo J, Zhang X and Ye S (2020) Cryo-EM structures of human pannexin 1 channel. *Cell Research* **30**, 449–451.

Johnson S, Fong YH, Deme JC, Furlong EJ, Kuhlen L and Lea SM (2020) Symmetry mismatch in the MS-ring of the bacterial flagellar rotor explains the structural coordination of secretion and rotation. *Nature Microbiology* **5**, 966–975.

Johnson ZL and Chen J (2018) ATP Binding Enables Substrate Release from Multidrug Resistance Protein 1. *Cell* **172**, 81-89.e10.

Johnson ZL and Chen J (2017) Structural Basis of Substrate Recognition by the Multidrug Resistance Protein MRP1. *Cell* **168**, 1075-1085.e9.

Jojoa-Cruz S, Saotome K, Murthy SE, Tsui CCA, Sansom MS, Patapoutian A and Ward AB (2018) Cryo-EM structure of the mechanically activated ion channel OSCA1.2. *eLife* **7**, e41845.

Kalienkova V, Clerico Mosina V, Bryner L, Oostergetel GT, Dutzler R and Paulino C (2019) Stepwise activation mechanism of the scramblase nhTMEM16 revealed by cryo-EM. *eLife* **8**, e44364.

Kampjut D and Sazanov LA (2019) Structure and mechanism of mitochondrial proton-translocating transhydrogenase. *Nature* **573**, 291–295.

Kampjut D and Sazanov LA (2020) The coupling mechanism of mammalian respiratory complex I. *Science* **370**, eabc4209.

- Kang Y, Kuybeda O, de Waal PW, Mukherjee S, Van Eps N, Dutka P, Zhou XE, Bartesaghi A, Erramilli S, Morizumi T, Gu X, Yin Y, Liu P, Jiang Y, Meng X, Zhao G, Melcher K, Ernst OP, Kossiakoff AA, Subramaniam S and Xu HE (2018) Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. *Nature* **558**, 553–558.
- Kasuya G, Nakane T, Yokoyama T, Jia Y, Inoue M, Watanabe K, Nakamura R, Nishizawa T, Kusakizako T, Tsutsumi A, Yanagisawa H, Dohmae N, Hattori M, Ichijo H, Yan Z, Kikkawa M, Shirouzu M, Ishitani R and Nureki O (2018) Cryo-EM structures of the human volume-regulated anion channel LRRC8. *Nature Structural & Molecular Biology* **25**, 797–804.
- Kater L, Wagener N, Berninghausen O, Becker T, Neupert W and Beckmann R (2020) Structure of the Bcs1 AAA-ATPase suggests an airlock-like translocation mechanism for folded proteins. *Nature Structural & Molecular Biology* **27**, 142–149.
- Kato HE, Zhang Y, Hu H, Suomivuori C-M, Kadji FMN, Aoki J, Krishna Kumar K, Fonseca R, Hilger D, Huang W, Latorraca NR, Inoue A, Dror RO, Kobilka BK and Skiniotis G (2019a) Conformational transitions of a neurotensin receptor 1-Gi1 complex. *Nature* **572**, 80–85.
- Kato K, Nagao R, Jiang T-Y, Ueno Y, Yokono M, Chan SK, Watanabe M, Ikeuchi M, Shen J-R, Akimoto S, Miyazaki N and Akita F (2019b) Structure of a cyanobacterial photosystem I tetramer revealed by cryo-electron microscopy. *Nature Communications* **10**, 4929.
- Kato K, Shinoda T, Nagao R, Akimoto S, Suzuki T, Dohmae N, Chen M, Allakhverdiev SI, Shen J-R, Akita F, Miyazaki N and Tomo T (2020) Structural basis for the adaptation and function of chlorophyll f in photosystem I. *Nature Communications* **11**, 238.
- Kefauver JM, Saotome K, Dubin AE, Pallesen J, Cottrell CA, Cahalan SM, Qiu Z, Hong G, Crowley CS, Whitwam T, Lee W-H, Ward AB and Patapoutian A (2018) Structure of the human volume regulated anion channel. *eLife* **7**, e38461.
- Kern DM, Oh S, Hite RK and Brohawn SG (2019) Cryo-EM structures of the DCPIB-inhibited volume-regulated anion channel LRRC8A in lipid nanodiscs. *eLife* **8**, e42636.
- Khelashvili G, Falzone ME, Cheng X, Lee B-C, Accardi A and Weinstein H (2019) Dynamic modulation of the lipid translocation groove generates a conductive ion channel in Ca²⁺-bound nhTMEM16. *Nature Communications* **10**, 1–15.
- Kieuvongngam V, Olinares PDB, Palillo A, Oldham ML, Chait BT and Chen J (2020) Structural basis of substrate recognition by a polypeptide processing and secretion transporter. *eLife* **9**, e51492.
- Kim J, Tan YZ, Wicht KJ, Erramilli SK, Dhingra SK, Okombo J, Vendome J, Hagenah LM, Giacometti SI, Warren AL, Nosol K, Roepe PD, Potter CS, Carragher B, Kossiakoff AA, Quick M, Fidock DA and Mancia F (2019) Structure and drug resistance of the Plasmodium falciparum transporter PfCRT. *Nature* **576**, 315–320.
- Kim JJ, Gharpure A, Teng J, Zhuang Y, Howard RJ, Zhu S, Noviello CM, Walsh RM, Lindahl E and Hibbs RE (2020a) Shared structural mechanisms of general anaesthetics and benzodiazepines. *Nature* **585**, 303–308.
- Kim K, Che T, Panova O, DiBerto JF, Lyu J, Krumm BE, Wacker D, Robertson MJ, Seven AB, Nichols DE, Shoichet BK, Skiniotis G and Roth BL (2020b) Structure of a Hallucinogen-Activated Gq-Coupled 5-HT2A Serotonin Receptor. *Cell* **182**, 1574–1588.e19.
- Kim Y and Chen J (2018) Molecular structure of human P-glycoprotein in the ATP-bound, outward-facing conformation. *Science* **359**, 915–919.
- Kim Y, Jeong E, Jeong J-H, Kim Y and Cho Y (2020c) Structural Basis for Activation of the Heterodimeric GABAB Receptor. *Journal of Molecular Biology* **432**, 5966–5984.

Kintzer AF, Green EM, Dominik PK, Bridges M, Armache J-P, Deneka D, Kim SS, Hubbell W, Kossiakoff AA, Cheng Y and Stroud RM (2018) Structural basis for activation of voltage sensor domains in an ion channel TPC1. *Proceedings of the National Academy of Sciences of the United States of America* **115**, E9095–E9104.

Kishikawa J-I, Nakanishi A, Furuta A, Kato T, Namba K, Tamakoshi M, Mitsuoka K and Yokoyama K (2020) Mechanical inhibition of isolated Vo from V/A-ATPase for proton conductance. *eLife* **9**, e56862.

Klusch N, Murphy BJ, Mills DJ, Yildiz Ö and Kühlbrandt W (2017) Structural basis of proton translocation and force generation in mitochondrial ATP synthase. *eLife* **6**, e33274.

Kobayashi K, Shihoya W, Nishizawa T, Kadji FMN, Aoki J, Inoue A and Nureki O (2020) Cryo-EM structure of the human PAC1 receptor coupled to an engineered heterotrimeric G protein. *Nature Structural & Molecular Biology* **27**, 274–280.

Koehl A, Hu H, Feng D, Sun B, Zhang Y, Robertson MJ, Chu M, Kobilka TS, Laeremans T, Steyaert J, Tarrasch J, Dutta S, Fonseca R, Weis WI, Mathiesen JM, Skiniotis G and Kobilka BK (2019) Structural insights into the activation of metabotropic glutamate receptors. *Nature* **566**, 79–84.

Koehl A, Hu H, Maeda S, Zhang Y, Qu Q, Paggi JM, Latorraca NR, Hilger D, Dawson R, Matile H, Schertler GFX, Granier S, Weis WI, Dror RO, Manglik A, Skiniotis G and Kobilka BK (2018) Structure of the μ -opioid receptor-Gi protein complex. *Nature* **558**, 547–552.

Krishna Kumar K, Shalev-Benami M, Robertson MJ, Hu H, Banister SD, Hollingsworth SA, Latorraca NR, Kato HE, Hilger D, Maeda S, Weis WI, Farrens DL, Dror RO, Malhotra SV, Kobilka BK and Skiniotis G (2019) Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. *Cell* **176**, 448–458.e12.

Kuhlen L, Abrusci P, Johnson S, Gault J, Deme J, Caesar J, Dietsche T, Mebrhatu MT, Ganief T, Macek B, Wagner S, Robinson CV and Lea SM (2018) Structure of the core of the type III secretion system export apparatus. *Nature Structural & Molecular Biology* **25**, 583–590.

Kuhlen L, Johnson S, Zeitler A, Bäurle S, Deme JC, Caesar JJE, Debo R, Fisher J, Wagner S and Lea SM (2020) The substrate specificity switch FlhB assembles onto the export gate to regulate type three secretion. *Nature Communications* **11**, 1296.

Kumar A, Basak S, Rao S, Gicheru Y, Mayer ML, Sansom MSP and Chakrapani S (2020a) Mechanisms of activation and desensitization of full-length glycine receptor in lipid nanodiscs. *Nature Communications* **11**, 3752.

Kumar P, Wang Y, Zhang Z, Zhao Z, Cymes GD, Tajkhорشید E and Grosman C (2020b) Cryo-EM structures of a lipid-sensitive pentameric ligand-gated ion channel embedded in a phosphatidylcholine-only bilayer. *Proceedings of the National Academy of Sciences of the United States of America* **117**, 1788–1798.

Lauber F, Deme JC, Lea SM and Berks BC (2018) Type 9 secretion system structures reveal a new protein transport mechanism. *Nature* **564**, 77–82.

Laughlin TG, Bayne AN, Trempe J-F, Savage DF and Davies KM (2019) Structure of the complex I-like molecule NDH of oxygenic photosynthesis. *Nature* **566**, 411–414.

Laverty D, Desai R, Uchański T, Masiulis S, Stec WJ, Malinauskas T, Zivanov J, Pardon E, Steyaert J, Miller KW and Aricescu AR (2019) Cryo-EM structure of the human $\alpha 1\beta 3\gamma 2$ GABAA receptor in a lipid bilayer. *Nature* **565**, 516–520.

Lee C-H and MacKinnon R (2018) Activation mechanism of a human SK-calmodulin channel complex elucidated by cryo-EM structures. *Science* **360**, 508–513.

- Lee C-H and MacKinnon R (2017a) Structures of the Human HCN1 Hyperpolarization-Activated Channel. *Cell* **168**, 111-120.e11.
- Lee C-H and MacKinnon R (2019a) Voltage Sensor Movements during Hyperpolarization in the HCN Channel. *Cell* **179**, 1582-1589.e7.
- Lee H-J, Jeong H, Hyun J, Ryu B, Park K, Lim H-H, Yoo J and Woo J-S (2020a) Cryo-EM structure of human Cx31.3/GJC3 connexin hemichannel. *Science Advances* **6**, eaba4996.
- Lee KPK, Chen J and MacKinnon R (2017b) Molecular structure of human KATP in complex with ATP and ADP. *eLife* **6**, e32481.
- Lee Y, Warne T, Nehmé R, Pandey S, Dwivedi-Agnihotri H, Chaturvedi M, Edwards PC, García-Nafría J, Leslie AGW, Shukla AK and Tate CG (2020b) Molecular basis of β-arrestin coupling to formoterol-bound β1-adrenoceptor. *Nature* **583**, 862–866.
- Lee Y, Wiriyasermkul P, Jin C, Quan L, Ohgaki R, Okuda S, Kusakizako T, Nishizawa T, Oda K, Ishitani R, Yokoyama T, Nakane T, Shirouzu M, Endou H, Nagamori S, Kanai Y and Nureki O (2019b) Cryo-EM structure of the human L-type amino acid transporter 1 in complex with glycoprotein CD98hc. *Nature Structural & Molecular Biology* **26**, 510–517.
- Letts JA, Fiedorczuk K, Degliesposti G, Skehel M and Sazanov LA (2019) Structures of Respiratory Supercomplex I+III₂ Reveal Functional and Conformational Crosstalk. *Molecular Cell* **75**, 1131–1146.e6.
- Li B, Rietmeijer RA and Brohawn SG (2020a) Structural basis for pH gating of the two-pore domain K⁺ channel TASK2. *Nature* **586**, 457–462.
- Li B, Zhang K, Nie Y, Wang X, Zhao Y, Zhang XC and Wu X-L (2020b) Structure of the *Dietzia* Mrp complex reveals molecular mechanism of this giant bacterial sodium proton pump. *Proceedings of the National Academy of Sciences of the United States of America* **117**, 31166–31176.
- Li F, Eriksen J, Finer-Moore J, Chang R, Nguyen P, Bowen A, Myasnikov A, Yu Z, Bulkley D, Cheng Y, Edwards RH and Stroud RM (2020c) Ion transport and regulation in a synaptic vesicle glutamate transporter. *Science* **368**, 893–897.
- Li M, Zhou X, Wang S, Michailidis I, Gong Y, Su D, Li H, Li X and Yang J (2017) Structure of a eukaryotic cyclic-nucleotide-gated channel. *Nature* **542**, 60–65.
- Li S, Yang F, Sun D, Zhang Y, Zhang M, Liu S, Zhou P, Shi C, Zhang L and Tian C (2020d) Cryo-EM structure of the hyperpolarization-activated inwardly rectifying potassium channel KAT1 from Arabidopsis. *Cell Research* **30**, 1049–1052.
- Li X, Zhang Q, Guo P, Fu J, Mei L, Lv D, Wang J, Lai D, Ye S, Yang H and Guo J (2020e) Molecular basis for ligand activation of the human KCNQ2 channel. *Cell Research* **31**, 52–61.
- Li Y, Orlando BJ and Liao M (2019) Structural basis of lipopolysaccharide extraction by the LptB2FGC complex. *Nature* **567**, 486–490.
- Liang Y-L, Belousov MJ, Fletcher MM, Zhang X, Khoshouei M, Deganutti G, Koole C, Furness SGB, Miller LJ, Hay DL, Christopoulos A, Reynolds CA, Danev R, Wootten D and Sexton PM (2020a) Structure and Dynamics of Adrenomedullin Receptors AM1 and AM2 Reveal Key Mechanisms in the Control of Receptor Phenotype by Receptor Activity-Modifying Proteins. *ACS pharmacology & translational science* **3**, 263–284.
- Liang Y-L, Belousov MJ, Zhao P, Koole C, Fletcher MM, Truong TT, Julita V, Christopoulos G, Xu HE, Zhang Y, Khoshouei M, Christopoulos A, Danev R, Sexton PM and Wootten D (2020b) Toward a Structural Understanding of Class B GPCR Peptide Binding and Activation. *Molecular Cell* **77**, 656–668.e5.

- Liang Y-L, Khoshouei M, Deganutti G, Glukhova A, Koole C, Peat TS, Radjainia M, Plitzko JM, Baumeister W, Miller LJ, Hay DL, Christopoulos A, Reynolds CA, Wootten D and Sexton PM (2018a) Cryo-EM structure of the active, Gs-protein complexed, human CGRP receptor. *Nature* **561**, 492–497.
- Liang Y-L, Khoshouei M, Glukhova A, Furness SGB, Zhao P, Clydesdale L, Koole C, Truong TT, Thal DM, Lei S, Radjainia M, Danev R, Baumeister W, Wang M-W, Miller LJ, Christopoulos A, Sexton PM and Wootten D (2018b) Phase-plate cryo-EM structure of a biased agonist-bound human GLP-1 receptor-Gs complex. *Nature* **555**, 121–125.
- Liang Y-L, Khoshouei M, Radjainia M, Zhang Y, Glukhova A, Tarrasch J, Thal DM, Furness SGB, Christopoulos G, Coudrat T, Danev R, Baumeister W, Miller LJ, Christopoulos A, Kobilka BK, Wootten D, Skiniotis G and Sexton PM (2017) Phase-plate cryo-EM structure of a class B GPCR-G-protein complex. *Nature* **546**, 118–123.
- Liao M, Cao E, Julius D and Cheng Y (2013) Structure of the TRPV1 ion channel determined by electron cryo-microscopy. *Nature* **504**, 107–112.
- Liu C, Ma J, Wang J, Wang H and Zhang L (2020a) Cryo-EM Structure of a Bacterial Lipid Transporter YebT. *Journal of Molecular Biology* **432**, 1008–1019.
- Liu F, Zhang Z, Csandy L, Gadsby DC and Chen J (2017) Molecular Structure of the Human CFTR Ion Channel. *Cell* **169**, 85–95.e8.
- Liu F, Zhang Z, Levit A, Levring J, Touhara KK, Shoichet BK and Chen J (2019a) Structural identification of a hotspot on CFTR for potentiation. *Science* **364**, 1184–1188.
- Liu J, Wan F, Jin Q, Li X, Bhat EA, Guo J, Lei M, Guan F, Wu J and Ye S (2020b) Cryo-EM structures of human calcium homeostasis modulator 5. *Cell Discovery* **6**, 81.
- Liu K, Wu L, Yuan S, Wu M, Xu Y, Sun Q, Li S, Zhao S, Hua T and Liu Z-J (2020c) Structural basis of CXC chemokine receptor 2 activation and signalling. *Nature* **585**, 135–140.
- Liu S, Chang S, Han B, Xu L, Zhang M, Zhao C, Yang W, Wang F, Li J, Delpire E, Ye S, Bai X-C and Guo J (2019b) Cryo-EM structures of the human cation-chloride cotransporter KCC1. *Science* **366**, 505–508.
- Liu X, Zeng J, Huang K and Wang J (2019c) Structure of the mannose transporter of the bacterial phosphotransferase system. *Cell Research* **29**, 680–682.
- Long T, Qi X, Hassan A, Liang Q, De Brabander JK and Li X (2020) Structural basis for itraconazole-mediated NPC1 inhibition. *Nature Communications* **11**, 152.
- Lu P, Bai X, Ma D, Xie T, Yan C, Sun L, Yang G, Zhao Y, Zhou R, Scheres SHW and Shi Y (2014) Three-dimensional structure of human γ -secretase. *Nature* **512**, 166–170.
- Lü W, Du J, Goehring A and Gouaux E (2017) Cryo-EM structures of the triheteromeric NMDA receptor and its allosteric modulation. *Science* **355**, eaal3729.
- Lunelli M, Kamprad A, Brger J, Mielke T, Spahn CMT and Kolbe M (2020) Cryo-EM structure of the Shigella type III needle complex. *PLoS pathogens* **16**, e1008263.
- Luo M, Zhou W, Patel H, Srivastava AP, Symersky J, Bonar MM, Faraldo-Gmez JD, Liao M and Mueller DM (2020) Bedaquiline inhibits the yeast and human mitochondrial ATP synthases. *Communications Biology* **3**, 452.
- Maeda S, Yamamoto H, Kinch LN, Garza CM, Takahashi S, Otomo C, Grishin NV, Forli S, Mizushima N and Otomo T (2020) Structure, lipid scrambling activity and role in autophagosome formation of ATG9A. *Nature Structural & Molecular Biology* **27**, 1194–1201.

Maity K, Heumann JM, McGrath AP, Kopcho NJ, Hsu P-K, Lee C-W, Mapes JH, Garza D, Krishnan S, Morgan GP, Hendargo KJ, Klose T, Rees SD, Medrano-Soto A, Saier MH, Piñeros M, Komives EA, Schroeder JI, Chang G and Stowell MHB (2019) Cryo-EM structure of OSCA1.2 from *Oryza sativa* elucidates the mechanical basis of potential membrane hyperosmolality gating. *Proceedings of the National Academy of Sciences of the United States of America* **116**, 14309–14318.

Maldonado M, Padavannil A, Zhou L, Guo F and Letts JA (2020) Atomic structure of a mitochondrial complex I intermediate from vascular plants. *eLife* **9**, e56664.

Manolaridis I, Jackson SM, Taylor NMI, Kowal J, Stahlberg H and Locher KP (2018) Cryo-EM structures of a human ABCG2 mutant trapped in ATP-bound and substrate-bound states. *Nature* **563**, 426–430.

Mao C, Shen C, Li C, Shen D-D, Xu C, Zhang S, Zhou R, Shen Q, Chen L-N, Jiang Z, Liu J and Zhang Y (2020) Cryo-EM structures of inactive and active GABAB receptor. *Cell Research* **30**, 564–573.

Martin GM, Kandasamy B, DiMaio F, Yoshioka C and Shyng S-L (2017) Anti-diabetic drug binding site in a mammalian KATP channel revealed by Cryo-EM. *eLife* **6**, e31054.

Martin GM, Sung MW, Yang Z, Innes LM, Kandasamy B, David LL, Yoshioka C and Shyng S-L (2019) Mechanism of pharmacochaperoning in a mammalian KATP channel revealed by cryo-EM. *eLife* **8**, e46417.

Matthies D, Bae C, Toombes GE, Fox T, Bartesaghi A, Subramaniam S and Swartz KJ (2018) Single-particle cryo-EM structure of a voltage-activated potassium channel in lipid nanodiscs. *eLife* **7**, e37558.

Matthies D, Dalmas O, Borgnia MJ, Dominik PK, Merk A, Rao P, Reddy BG, Islam S, Bartesaghi A, Perozo E and Subramaniam S (2016) Cryo-EM Structures of the Magnesium Channel CorA Reveal Symmetry Break upon Gating. *Cell* **164**, 747–756.

Mazhab-Jafari MT, Rohou A, Schmidt C, Bueler SA, Benlekbir S, Robinson CV and Rubinstein JL (2016) Atomic model for the membrane-embedded VO motor of a eukaryotic V-ATPase. *Nature* **539**, 118–122.

McCarthy AE, Yoshioka C and Mansoor SE (2019) Full-Length P2X7 Structures Reveal How Palmitoylation Prevents Channel Desensitization. *Cell* **179**, 659–670.e13.

McDowell MA, Heimes M, Fiorentino F, Mehmood S, Farkas Á, Coy-Vergara J, Wu D, Bolla JR, Schmid V, Heinze R, Wild K, Flemming D, Pfeffer S, Schwappach B, Robinson CV and Sinning I (2020) Structural Basis of Tail-Anchored Membrane Protein Biogenesis by the GET Insertase Complex. *Molecular Cell* **80**, 72–86.e7.

McGilvray PT, Anghel SA, Sundaram A, Zhong F, Trnka MJ, Fuller JR, Hu H, Burlingame AL and Keenan RJ (2020) An ER translocon for multi-pass membrane protein biogenesis. *eLife* **9**, e56889.

McGoldrick LL, Singh AK, Demirkhanyan L, Lin T-Y, Casner RG, Zakharian E and Sobolevsky AI (2019) Structure of the thermo-sensitive TRP channel TRP1 from the alga *Chlamydomonas reinhardtii*. *Nature Communications* **10**, 4180.

McGoldrick LL, Singh AK, Saotome K, Yelshanskaya MV, Twomey EC, Grassucci RA and Sobolevsky AI (2018) Opening of the human epithelial calcium channel TRPV6. *Nature* **553**, 233–237.

Meyerson JR, Chittori S, Merk A, Rao P, Han TH, Serpe M, Mayer ML and Subramaniam S (2016) Structural basis of kainate subtype glutamate receptor desensitization. *Nature* **537**, 567–571.

- Mi W, Li Y, Yoon SH, Ernst RK, Walz T and Liao M (2017) Structural basis of MsbA-mediated lipopolysaccharide transport. *Nature* **549**, 233–237.
- Miller AN, Vaisey G and Long SB (2019) Molecular mechanisms of gating in the calcium-activated chloride channel bestrophin K. J. Swartz & R. Aldrich, eds. *eLife* **8**, e43231.
- Mou L, Ke M, Song M, Shan Y, Xiao Q, Liu Q, Li J, Sun K, Pu L, Guo L, Geng J, Wu J and Deng D (2020) Structural basis for gating mechanism of Pannexin 1 channel. *Cell Research* **30**, 452–454.
- Mukherjee S, Erramilli SK, Ammirati M, Alvarez FJD, Fennell KF, Purdy MD, Skrobek BM, Radziwon K, Coukos J, Kang Y, Dutka P, Gao X, Qiu X, Yeager M, Eric Xu H, Han S and Kossiakoff AA (2020) Synthetic antibodies against BRIL as universal fiducial marks for single-particle cryoEM structure determination of membrane proteins. *Nature Communications* **11**, 1598.
- Murphy BJ, Klusch N, Langer J, Mills DJ, Yildiz Ö and Kühlbrandt W (2019) Rotary substates of mitochondrial ATP synthase reveal the basis of flexible F₁-F₀ coupling. *Science* **364**, eaaw9128.
- Myers JB, Haddad BG, O'Neill SE, Chorev DS, Yoshioka CC, Robinson CV, Zuckerman DM and Reichow SL (2018) Structure of native lens connexin 46/50 intercellular channels by cryo-EM. *Nature* **564**, 372.
- Nagamura R, Fukuda M, Kawamoto A, Matoba K, Dohmae N, Ishitani R, Takagi J and Nureki O (2019) Structural basis for oligomerization of the prokaryotic peptide transporter PepTSo2. *Acta Crystallographica. Section F, Structural Biology Communications* **75**, 348–358.
- Nakagawa T (2019) Structures of the AMPA receptor in complex with its auxiliary subunit cornichon. *Science* **366**, 1259–1263.
- Nakamura R, Numata T, Kasuya G, Yokoyama T, Nishizawa T, Kusakizako T, Kato T, Hagino T, Dohmae N, Inoue M, Watanabe K, Ichijo H, Kikkawa M, Shirouzu M, Jentsch TJ, Ishitani R, Okada Y and Nureki O (2020) Cryo-EM structure of the volume-regulated anion channel LRRC8D isoform identifies features important for substrate permeation. *Communications Biology* **3**, 240.
- Nakane T, Kotecha A, Sente A, McMullan G, Masiulis S, Brown PMGE, Grigoras IT, Malinauskaitė L, Malinauskas T, Miehling J, Uchański T, Yu L, Karia D, Pechnikova EV, de Jong E, Keizer J, Bischoff M, McCormack J, Tiemeijer P, Hardwick SW, Chirgadze DY, Murshudov G, Aricescu AR and Scheres SHW (2020) Single-particle cryo-EM at atomic resolution. *Nature* **587**, 152–156.
- Nguyen AH, Thomsen ARB, Cahill TJ, Huang R, Huang L-Y, Marcink T, Clarke OB, Heissel S, Masoudi A, Ben-Hail D, Samaan F, Dandey VP, Tan YZ, Hong C, Mahoney JP, Triest S, Little J, Chen X, Sunahara R, Steyaert J, Molina H, Yu Z, des Georges A and Lefkowitz RJ (2019) Structure of an endosomal signaling GPCR-G protein-β-arrestin megacomplex. *Nature Structural & Molecular Biology* **26**, 1123–1131.
- Nguyen NX, Armache J-P, Lee C, Yang Y, Zeng W, Mootha VK, Cheng Y, Bai X-C and Jiang Y (2018) Cryo-EM structure of a fungal mitochondrial calcium uniporter. *Nature* **559**, 570–574.
- Niu Y, Tao X, Touhara KK and MacKinnon R (2020) Cryo-EM analysis of PIP2 regulation in mammalian GIRK channels. *eLife* **9**, e60552.
- Noreng S, Bharadwaj A, Posert R, Yoshioka C and Baconguis I (2018) Structure of the human epithelial sodium channel by cryo-electron microscopy. *eLife* **7**, e39340.
- Noreng S, Posert R, Bharadwaj A, Houser A and Baconguis I (2020) Molecular principles of assembly, activation, and inhibition in epithelial sodium channel. *eLife* **9**, e59038.

Oh S, Paknejad N and Hite RK (2020) Gating and selectivity mechanisms for the lysosomal K⁺ channel TMEM175. *eLife* **9**, e53430.

Oldham ML, Grigorieff N and Chen J (2016) Structure of the transporter associated with antigen processing trapped by herpes simplex virus. *eLife* **5**, e21829.

Oosterheert W, van Bezouwen LS, Rodenburg RNP, Granneman J, Förster F, Mattevi A and Gros P (2018) Cryo-EM structures of human STEAP4 reveal mechanism of iron(III) reduction. *Nature Communications* **9**, 4337.

Orlando BJ and Liao M (2020) ABCG2 transports anticancer drugs via a closed-to-open switch. *Nature Communications* **11**, 2264.

Oshima A, Tani K and Fujiyoshi Y (2016) Atomic structure of the innexin-6 gap junction channel determined by cryo-EM. *Nature Communications* **7**, 13681.

Owji AP, Zhao Q, Ji C, Kittredge A, Hopiauori A, Fu Z, Ward N, Clarke OB, Shen Y, Zhang Y, Hendrickson WA and Yang T (2020) Structural and functional characterization of the bestrophin-2 anion channel. *Nature Structural & Molecular Biology* **27**, 382–391.

Paknejad N and Hite RK (2018) Structural basis for the regulation of inositol trisphosphate receptors by Ca²⁺ and IP3. *Nature Structural & Molecular Biology* **25**, 660–668.

Pan X, Cao D, Xie F, Xu F, Su X, Mi H, Zhang X and Li M (2020) Structural basis for electron transport mechanism of complex I-like photosynthetic NAD(P)H dehydrogenase. *Nature Communications* **11**, 610.

Pan X, Ma J, Su X, Cao P, Chang W, Liu Z, Zhang X and Li M (2018) Structure of the maize photosystem I supercomplex with light-harvesting complexes I and II. *Science* **360**, 1109–1113.

Papasergi-Scott MM, Robertson MJ, Seven AB, Panova O, Mathiesen JM and Skiniotis G (2020) Structures of metabotropic GABAB receptor. *Nature* **584**, 310–314.

Parey K, Brandt U, Xie H, Mills DJ, Siegmund K, Vonck J, Kühlbrandt W and Zickermann V (2018) Cryo-EM structure of respiratory complex I at work. *eLife* **7**, e39213.

Parey K, Haapanen O, Sharma V, Köfeler H, Züllig T, Prinz S, Siegmund K, Wittig I, Mills DJ, Vonck J, Kühlbrandt W and Zickermann V (2019) High-resolution cryo-EM structures of respiratory complex I: Mechanism, assembly, and disease. *Science Advances* **5**, eaax9484.

Park E, Campbell EB and MacKinnon R (2017) Structure of a CLC chloride ion channel by cryo-electron microscopy. *Nature* **541**, 500–505.

Park E and MacKinnon R (2018) Structure of the CLC-1 chloride channel from Homo sapiens. *eLife* **7**, e36629.

Park J, Fu Z, Frangaj A, Liu J, Mosyak L, Shen T, Slavkovich VN, Ray KM, Taura J, Cao B, Geng Y, Zuo H, Kou Y, Grassucci R, Chen S, Liu Z, Lin X, Williams JP, Rice WJ, Eng ET, Huang RK, Soni RK, Kloss B, Yu Z, Javitch JA, Hendrickson WA, Slesinger PA, Quick M, Graziano J, Yu H, Fiehn O, Clarke OB, Frank J and Fan QR (2020) Structure of human GABAB receptor in an inactive state. *Nature* **584**, 304–309.

Paulino C, Kalienkova V, Lam AKM, Neldner Y and Dutzler R (2017) Activation mechanism of the calcium-activated chloride channel TMEM16A revealed by cryo-EM. *Nature* **552**, 421–425.

Paulsen CE, Armache J-P, Gao Y, Cheng Y and Julius D (2015) Structure of the TRPA1 ion channel suggests regulatory mechanisms. *Nature* **520**, 511–517.

- Peng W, Casey AK, Fernandez J, Carpinone EM, Servage KA, Chen Z, Li Y, Tomchick DR, Starai VJ and Orth K (2020) A distinct inhibitory mechanism of the V-ATPase by Vibrio VopQ revealed by cryo-EM. *Nature Structural & Molecular Biology* **27**, 589–597.
- Perez-Boerema A, Klaiman D, Caspy I, Netzer-EI SY, Amunts A and Nelson N (2020) Structure of a minimal photosystem I from the green alga Dunaliella salina. *Nature Plants* **6**, 321–327.
- Phulera S, Zhu H, Yu J, Claxton DP, Yoder N, Yoshioka C and Gouaux E (2018) Cryo-EM structure of the benzodiazepine-sensitive $\alpha 1\beta 1\gamma 2S$ tri-heteromeric GABA_A receptor in complex with GABA. *eLife* **7**, e39383.
- Pi X, Tian L, Dai H-E, Qin X, Cheng L, Kuang T, Sui S-F and Shen J-R (2018) Unique organization of photosystem I-light-harvesting supercomplex revealed by cryo-EM from a red alga. *Proceedings of the National Academy of Sciences of the United States of America* **115**, 4423–4428.
- Pi X, Zhao S, Wang W, Liu D, Xu C, Han G, Kuang T, Sui S-F and Shen J-R (2019) The pigment-protein network of a diatom photosystem II-light-harvesting antenna supercomplex. *Science* **365**, eaax4406.
- Pinke G, Zhou L and Sazanov LA (2020) Cryo-EM structure of the entire mammalian F-type ATP synthase. *Nature Structural & Molecular Biology* **27**, 1077–1085.
- Pleiner T, Tomaleri GP, Januszyk K, Inglis AJ, Hazu M and Voorhees RM (2020) Structural basis for membrane insertion by the human ER membrane protein complex. *Science* **369**, 433–436.
- Powelet N, Czudnochowski N, Nakagawa R, Trinidad DD, Murphy KC, Sasetti CM and Rosenberg OS (2019) The structure of the endogenous ESX-3 secretion system. *eLife* **8**, e52983.
- Pumroy RA, Samanta A, Liu Y, Hughes TE, Zhao S, Yudin Y, Rohacs T, Han S and Moiseenkova-Bell VY (2019) Molecular mechanism of TRPV2 channel modulation by cannabidiol. *eLife* **8**, e48792.
- Purushotham P, Ho R and Zimmer J (2020) Architecture of a catalytically active homotrimeric plant cellulose synthase complex. *Science* **369**, 1089–1094.
- Qi C, Di Minin G, Vercellino I, Wutz A and Korkhov VM (2019a) Structural basis of sterol recognition by human hedgehog receptor PTCH1. *Science Advances* **5**, eaaw6490.
- Qi C, Sorrentino S, Medalia O and Korkhov VM (2019b) The structure of a membrane adenylyl cyclase bound to an activated stimulatory G protein. *Science* **364**, 389–394.
- Qi L, Wang Q, Guan Z, Wu Y, Shen C, Hong S, Cao J, Zhang X, Yan C and Yin P (2020a) Cryo-EM structure of the human mitochondrial translocase TIM22 complex. *Cell Research* (doi: 10.1038/s41422-020-00400-w).
- Qi X, Friedberg L, De Bose-Boyd R, Long T and Li X (2020b) Sterols in an intramolecular channel of Smoothened mediate Hedgehog signaling. *Nature Chemical Biology* **16**, 1368–1375.
- Qi X, Liu H, Thompson B, McDonald J, Zhang C and Li X (2019c) Cryo-EM structure of oxysterol-bound human Smoothened coupled to a heterotrimeric Gi. *Nature* **571**, 279–283.
- Qi X, Schmiege P, Coutavas E and Li X (2018a) Two Patched molecules engage distinct sites on Hedgehog yielding a signaling-competent complex. *Science* **362**, eaas8843.
- Qi X, Schmiege P, Coutavas E, Wang J and Li X (2018b) Structures of human Patched and its complex with native palmitoylated sonic hedgehog. *Nature* **560**, 128–132.
- Qian H, Wu X, Du X, Yao X, Zhao X, Lee J, Yang H and Yan N (2020) Structural Basis of Low-pH-Dependent Lysosomal Cholesterol Egress by NPC1 and NPC2. *Cell* **182**, 98–111.e18.

Qian H, Zhao X, Cao P, Lei J, Yan N and Gong X (2017) Structure of the Human Lipid Exporter ABCA1. *Cell* **169**, 1228-1239.e10.

Qiao A, Han S, Li X, Li Z, Zhao P, Dai A, Chang R, Tai L, Tan Q, Chu X, Ma L, Thorsen TS, Reedtz-Runge S, Yang D, Wang M-W, Sexton PM, Wootten D, Sun F, Zhao Q and Wu B (2020) Structural basis of Gs and Gi recognition by the human glucagon receptor. *Science* **367**, 1346–1352.

Qu R, Dong L, Zhang J, Yu X, Wang L and Zhu S (2020) Cryo-EM structure of human heptameric Pannexin 1 channel. *Cell Research* **30**, 446–448.

Ramírez AS, Kowal J and Locher KP (2019) Cryo-electron microscopy structures of human oligosaccharyltransferase complexes OST-A and OST-B. *Science* **366**, 1372–1375.

Rasmussen T, Flegler VJ, Rasmussen A and Böttcher B (2019) Structure of the Mechanosensitive Channel MscS Embedded in the Membrane Bilayer. *Journal of Molecular Biology* **431**, 3081–3090.

Rathore S, Berndtsson J, Marin-Buera L, Conrad J, Carroni M, Brzezinski P and Ott M (2019) Cryo-EM structure of the yeast respiratory supercomplex. *Nature Structural & Molecular Biology* **26**, 50–57.

Reddy B, Bavi N, Lu A, Park Y and Perozo E (2019) Molecular basis of force-from-lipids gating in the mechanosensitive channel MscS. *eLife* **8**, e50486.

Reid MS, Kern DM and Brohawn SG (2020) Cryo-EM structure of the potassium-chloride cotransporter KCC4 in lipid nanodiscs. *eLife* **9**, e52505.

Rempel S, Gati C, Nijland M, Thangaratnarajah C, Karyolaimos A, de Gier JW, Guskov A and Slotboom DJ (2020) A mycobacterial ABC transporter mediates the uptake of hydrophilic compounds. *Nature* **580**, 409–412.

Ren Y, Wen T, Xi Z, Li S, Lu J, Zhang X, Yang X and Shen Y (2020) Cryo-EM structure of the calcium homeostasis modulator 1 channel. *Science Advances* **6**, eaba8161.

Rheinberger J, Gao X, Schmidpeter PA and Nimigean CM (2018) Ligand discrimination and gating in cyclic nucleotide-gated ion channels from apo and partial agonist-bound cryo-EM structures. *eLife* **7**, e39775.

Roh S-H, Shekhar M, Pintilie G, Chipot C, Wilkens S, Singharoy A and Chiu W (2020) Cryo-EM and MD infer water-mediated proton transport and autoinhibition mechanisms of Vo complex. *Science Advances* **6**, eabb9605.

Roh S-H, Stam NJ, Hryc CF, Couoh-Cardel S, Pintilie G, Chiu W and Wilkens S (2018) The 3.5-Å CryoEM Structure of Nanodisc-Reconstituted Yeast Vacuolar ATPase Vo Proton Channel. *Molecular Cell* **69**, 993-1004.e3.

Safarian S, Hahn A, Mills DJ, Radloff M, Eisinger ML, Nikolaev A, Meier-Credo J, Melin F, Miyoshi H, Gennis RB, Sakamoto J, Langer JD, Hellwig P, Kühlbrandt W and Michel H (2019) Active site rearrangement and structural divergence in prokaryotic respiratory oxidases. *Science* **366**, 100–104.

Santiveri M, Roa-Eguiara A, Kühne C, Wadhwa N, Hu H, Berg HC, Erhardt M and Taylor NMI (2020) Structure and Function of Stator Units of the Bacterial Flagellar Motor. *Cell* **183**, 244-257.e16.

Saotome K, Teng B, Tsui CCA, Lee W-H, Tu Y-H, Kaplan JP, Sansom MSP, Liman ER and Ward AB (2019) Structures of the otopetrin proton channels Otop1 and Otop3. *Nature Structural & Molecular Biology* **26**, 518–525.

- Sauer DB, Trebesch N, Marden JJ, Cocco N, Song J, Koide A, Koide S, Tajkhorshid E and Wang D-N (2020) Structural basis for the reaction cycle of DASS dicarboxylate transporters. *eLife* **9**, e61350.
- Savva CG, Clark AR, Naylor CE, Popoff MR, Moss DS, Basak AK, Titball RW and Bokori-Brown M (2019) The pore structure of Clostridium perfringens epsilon toxin. *Nature Communications* **10**, 2641.
- Schoebel S, Mi W, Stein A, Ovchinnikov S, Pavlovicz R, DiMaio F, Baker D, Chambers MG, Su H, Li D, Rapoport TA and Liao M (2017) Cryo-EM structure of the protein-conducting ERAD channel Hrd1 in complex with Hrd3. *Nature* **548**, 352–355.
- Schrecker M, Korobenko J and Hite RK (2020) Cryo-EM structure of the lysosomal chloride-proton exchanger CLC-7 in complex with OSTM1. *eLife* **9**, e59555.
- Schuller JM, Birrell JA, Tanaka H, Konuma T, Wulffhorst H, Cox N, Schuller SK, Thiemann J, Lubitz W, Sétif P, Ikegami T, Engel BD, Kurisu G and Nowaczyk MM (2019) Structural adaptations of photosynthetic complex I enable ferredoxin-dependent electron transfer. *Science* **363**, 257–260.
- Shang G, Zhang C, Chen ZJ, Bai X-C and Zhang X (2019) Cryo-EM structures of STING reveal its mechanism of activation by cyclic GMP-AMP. *Nature* **567**, 389–393.
- Shaye H, Ishchenko A, Lam JH, Han GW, Xue L, Rondard P, Pin J-P, Katritch V, Gati C and Cherezov V (2020) Structural basis of the activation of a metabotropic GABA receptor. *Nature* **584**, 298–303.
- She J, Guo J, Chen Q, Zeng W, Jiang Y and Bai X-C (2018) Structural insights into the voltage and phospholipid activation of the mammalian TPC1 channel. *Nature* **556**, 130–134.
- She J, Zeng W, Guo J, Chen Q, Bai X-C and Jiang Y (2019) Structural mechanisms of phospholipid activation of the human TPC2 channel. *eLife* **8**, e45222.
- Shen H, Li Z, Jiang Y, Pan X, Wu J, Cristofori-Armstrong B, Smith JJ, Chin YKY, Lei J, Zhou Q, King GF and Yan N (2018) Structural basis for the modulation of voltage-gated sodium channels by animal toxins. *Science* **362**, eaau2596.
- Shen H, Liu D, Wu K, Lei J and Yan N (2019a) Structures of human Nav1.7 channel in complex with auxiliary subunits and animal toxins. *Science* **363**, 1303–1308.
- Shen H, Zhou Q, Pan X, Li Z, Wu J and Yan N (2017) Structure of a eukaryotic voltage-gated sodium channel at near-atomic resolution. *Science* **355**, eaal4326.
- Shen L, Huang Z, Chang S, Wang W, Wang J, Kuang T, Han G, Shen J-R and Zhang X (2019b) Structure of a C2S2M2N2-type PSII-LHCII supercomplex from the green alga Chlamydomonas reinhardtii. *Proceedings of the National Academy of Sciences of the United States of America* **116**, 21246–21255.
- Shen PS, Yang X, DeCaen PG, Liu X, Bulkley D, Clapham DE and Cao E (2016) The Structure of the Polycystic Kidney Disease Channel PKD2 in Lipid Nanodiscs. *Cell* **167**, 763–773.e11.
- Shimada H, Kusakizako T, Dung Nguyen TH, Nishizawa T, Hino T, Tominaga M and Nureki O (2020) The structure of lipid nanodisc-reconstituted TRPV3 reveals the gating mechanism. *Nature Structural & Molecular Biology* **27**, 645–652.
- Singh AK, McGoldrick LL, Demirkhanyan L, Leslie M, Zakharian E and Sobolevsky AI (2019) Structural basis of temperature sensation by the TRP channel TRPV3. *Nature Structural & Molecular Biology* **26**, 994–998.

- Singh AK, McGoldrick LL and Sobolevsky AI (2018a) Structure and gating mechanism of the transient receptor potential channel TRPV3. *Nature Structural & Molecular Biology* **25**, 805-813.
- Singh AK, Saotome K, McGoldrick LL and Sobolevsky AI (2018b) Structural bases of TRP channel TRPV6 allosteric modulation by 2-APB. *Nature Communications* **9**, 2465.
- Sobti M, Walshe JL, Wu D, Ishmukhametov R, Zeng YC, Robinson CV, Berry RM and Stewart AG (2020) Cryo-EM structures provide insight into how *E. coli* F1Fo ATP synthase accommodates symmetry mismatch. *Nature Communications* **11**, 2615.
- Soufari H, Parrot C, Kuhn L, Waltz F and Hashem Y (2020) Specific features and assembly of the plant mitochondrial complex I revealed by cryo-EM. *Nature Communications* **11**, 5195.
- Sousa JS, Calisto F, Langer JD, Mills DJ, Refojo PN, Teixeira M, Kühlbrandt W, Vonck J and Pereira MM (2018) Structural basis for energy transduction by respiratory alternative complex III. *Nature Communications* **9**, 1728.
- Srivastava AP, Luo M, Zhou W, Symersky J, Bai D, Chambers MG, Faraldo-Gómez JD, Liao M and Mueller DM (2018) High-resolution cryo-EM analysis of the yeast ATP synthase in a lipid membrane. *Science* **360**, eaas9699.
- Staus DP, Hu H, Robertson MJ, Kleinhenz ALW, Wingler LM, Capel WD, Latorraca NR, Lefkowitz RJ and Skiniotis G (2020) Structure of the M2 muscarinic receptor-β-arrestin complex in a lipid nanodisc. *Nature* **579**, 297–302.
- Su M, Zhu L, Zhang Y, Paknejad N, Dey R, Huang J, Lee M-Y, Williams D, Jordan KD, Eng ET, Ernst OP, Meyerson JR, Hite RK, Walz T, Liu W and Huang X-Y (2020) Structural Basis of the Activation of Heterotrimeric Gs-Protein by Isoproterenol-Bound β1-Adrenergic Receptor. *Molecular Cell* **80**, 59-71.e4.
- Su Q, Hu F, Ge X, Lei J, Yu S, Wang T, Zhou Q, Mei C and Shi Y (2018) Structure of the human PKD1-PKD2 complex. *Science* **361**, eaat9819.
- Su X, Ma J, Pan X, Zhao X, Chang W, Liu Z, Zhang X and Li M (2019) Antenna arrangement and energy transfer pathways of a green algal photosystem-I-LHCI supercomplex. *Nature Plants* **5**, 273–281.
- Su X, Ma J, Wei X, Cao P, Zhu D, Chang W, Liu Z, Zhang X and Li M (2017) Structure and assembly mechanism of plant C2S2M2-type PSII-LHCII supercomplex. *Science* **357**, 815–820.
- Suga M, Ozawa S-I, Yoshida-Motomura K, Akita F, Miyazaki N and Takahashi Y (2019) Structure of the green algal photosystem I supercomplex with a decameric light-harvesting complex I. *Nature Plants* **5**, 626–636.
- Sui X, Arlt H, Brock KP, Lai ZW, DiMaio F, Marks DS, Liao M, Farese RV and Walther TC (2018) Cryo-electron microscopy structure of the lipid droplet-formation protein seipin. *The Journal of Cell Biology* **217**, 4080–4091.
- Sun D, Liu S, Li S, Zhang M, Yang F, Wen M, Shi P, Wang T, Pan M, Chang S, Zhang X, Zhang L, Tian C and Liu L (2020a) Structural insights into human acid-sensing ion channel 1a inhibition by snake toxin mambalgin1. *eLife* **9**, e57096.
- Sun J (2020) Structures of mouse DUOX1-DUOXA1 provide mechanistic insights into enzyme activation and regulation. *Nature Structural & Molecular Biology* **27**, 1086–1093.
- Sun J and MacKinnon R (2017) Cryo-EM Structure of a KCNQ1/CaM Complex Reveals Insights into Congenital Long QT Syndrome. *Cell* **169**, 1042-1050.e9.

- Sun L, Zhao L, Yang G, Yan C, Zhou R, Zhou X, Xie T, Zhao Y, Wu S, Li X and Shi Y (2015) Structural basis of human γ -secretase assembly. *Proceedings of the National Academy of Sciences* **112**, 6003–6008.
- Sun W, Chen L-N, Zhou Q, Zhao L-H, Yang D, Zhang H, Cong Z, Shen D-D, Zhao F, Zhou F, Cai X, Chen Y, Zhou Y, Gadgaard S, van der Velden WJC, Zhao S, Jiang Y, Rosenkilde MM, Xu HE, Zhang Y and Wang M-W (2020b) A unique hormonal recognition feature of the human glucagon-like peptide-2 receptor. *Cell Research* **30**, 1098–1108.
- Suo Y, Wang Z, Zubcevic L, Hsu AL, He Q, Borgnia MJ, Ji R-R and Lee S-Y (2020) Structural Insights into Electrophile Irritant Sensing by the Human TRPA1 Channel. *Neuron* **105**, 882-894.e5.
- Tan YZ, Rodrigues J, Keener JE, Zheng RB, Brunton R, Kloss B, Giacometti SI, Rosário AL, Zhang L, Niederweis M, Clarke OB, Lowary TL, Marty MT, Archer M, Potter CS, Carragher B and Mancia F (2020) Cryo-EM structure of arabinosyltransferase EmbB from *Mycobacterium smegmatis*. *Nature Communications* **11**, 3396.
- Tang X, Chang S, Luo Q, Zhang Z, Qiao W, Xu C, Zhang C, Niu Y, Yang W, Wang T, Zhang Z, Zhu X, Wei X, Dong C, Zhang X and Dong H (2019) Cryo-EM structures of lipopolysaccharide transporter LptB2FGC in lipopolysaccharide or AMP-PNP-bound states reveal its transport mechanism. *Nature Communications* **10**, 4175.
- Tao X, Hite RK and MacKinnon R (2017) Cryo-EM structure of the open high-conductance Ca²⁺-activated K⁺ channel. *Nature* **541**, 46–51.
- Tao X and MacKinnon R (2019) Molecular structures of the human Slo1 K⁺ channel in complex with β 4. *eLife* **8**, e51409.
- Taylor NMI, Manolaridis I, Jackson SM, Kowal J, Stahlberg H and Locher KP (2017) Structure of the human multidrug transporter ABCG2. *Nature* **546**, 504–509.
- Theßeling A, Rasmussen T, Burschel S, Wohlwend D, Kägi J, Müller R, Böttcher B and Friedrich T (2019) Homologous bd oxidases share the same architecture but differ in mechanism. *Nature Communications* **10**, 5138.
- Timcenko M, Lyons JA, Januliene D, Ulstrup JJ, Dieudonné T, Montigny C, Ash M-R, Karlsen JL, Boesen T, Kühlbrandt W, Lenoir G, Moeller A and Nissen P (2019) Structure and autoregulation of a P4-ATPase lipid flippase. *Nature* **571**, 366–370.
- Toporik H, Khmelnitskiy A, Dobson Z, Riddle R, Williams D, Lin S, Jankowiak R and Mazor Y (2020) The structure of a red-shifted photosystem I reveals a red site in the core antenna. *Nature Communications* **11**, 5279.
- Toporik H, Li J, Williams D, Chiu P-L and Mazor Y (2019) The structure of the stress-induced photosystem I-IsiA antenna supercomplex. *Nature Structural & Molecular Biology* **26**, 443–449.
- Tsai C-J, Marino J, Adaixo R, Pamula F, Muehle J, Maeda S, Flock T, Taylor NM, Mohammed I, Matile H, Dawson RJ, Deupi X, Stahlberg H and Schertler G (2019) Cryo-EM structure of the rhodopsin-Gai- β complex reveals binding of the rhodopsin C-terminal tail to the g β subunit. *eLife* **8**, e46041.
- Tsutsumi N, Mukherjee S, Waghray D, Janda CY, Jude KM, Miao Y, Burg JS, Aduri NG, Kossiakoff AA, Gati C and Garcia KC (2020) Structure of human Frizzled5 by fiducial-assisted cryo-EM supports a heterodimeric mechanism of canonical Wnt signaling. *eLife* **9**, e58464.
- Tucker K and Park E (2019) Cryo-EM structure of the mitochondrial protein-import channel TOM complex at near-atomic resolution. *Nature Structural & Molecular Biology* **26**, 1158–1166.

Twomey EC, Yelshanskaya MV, Grassucci RA, Frank J and Sobolevsky AI (2017) Channel opening and gating mechanism in AMPA-subtype glutamate receptors. *Nature* **549**, 60–65.

Van der Verren SE, Van Gerven N, Jonckheere W, Hambley R, Singh P, Kilgour J, Jordan M, Wallace EJ, Jayasinghe L and Remaut H (2020) A dual-constriction biological nanopore resolves homonucleotide sequences with high fidelity. *Nature Biotechnology* **38**, 1415–1420.

Vinayagam D, Mager T, Apelbaum A, Bothe A, Merino F, Hofnagel O, Gatsogiannis C and Raunser S (2018) Electron cryo-microscopy structure of the canonical TRPC4 ion channel. *eLife* **7**, e36615.

Vinayagam D, Quentin D, Yu-Strzelczyk J, Sitsel O, Merino F, Stabrin M, Hofnagel O, Yu M, Ledeboer MW, Nagel G, Malojcic G and Raunser S (2020) Structural basis of TRPC4 regulation by calmodulin and pharmacological agents. *eLife* **9**, e60603.

Vinothkumar KR, Zhu J and Hirst J (2014) Architecture of mammalian respiratory complex I. *Nature* **515**, 80–84.

Voorhees RM and Hegde RS (2016) Structure of the Sec61 channel opened by a signal sequence. *Science* **351**, 88–91.

Walsh RM, Roh S-H, Gharpure A, Morales-Perez CL, Teng J and Hibbs RE (2018) Structural principles of distinct assemblies of the human $\alpha 4\beta 2$ nicotinic receptor. *Nature* **557**, 261–265.

Walter JD, Sawicka M and Dutzler R (2019) Cryo-EM structures and functional characterization of murine Slc26a9 reveal mechanism of uncoupled chloride transport. *eLife* **8**, e46986.

Wang C, Cao C, Wang N, Wang X, Wang X and Zhang XC (2020a) Cryo-electron microscopy structure of human ABCB6 transporter. *Protein Science: A Publication of the Protein Society* **29**, 2363–2374.

Wang J, Song X, Zhang D, Chen X, Li X, Sun Y, Li C, Song Y, Ding Y, Ren R, Harrington EH, Hu LA, Zhong W, Xu C, Huang X, Wang H-W and Ma Y (2020b) Cryo-EM structures of PAC1 receptor reveal ligand binding mechanism. *Cell Research* **30**, 436–445.

Wang K, Preisler SS, Zhang L, Cui Y, Missel JW, Grønberg C, Gotfryd K, Lindahl E, Andersson M, Calloe K, Egea PF, Klaerke DA, Pusch M, Pedersen PA, Zhou ZH and Gourdon P (2019a) Structure of the human CIC-1 chloride channel. *PLOS Biology* **17**, e3000218.

Wang L, Fu T-M, Zhou Y, Xia S, Greka A and Wu H (2018) Structures and gating mechanism of human TRPM2. *Science* **362**, eaav4809.

Wang L, Hou W-T, Chen L, Jiang Y-L, Xu D, Sun L, Zhou C-Z and Chen Y (2020c) Cryo-EM structure of human bile salts exporter ABCB11. *Cell Research* **30**, 623–625.

Wang L, Johnson ZL, Wasserman MR, Levring J, Chen J and Liu S (2020d) Characterization of the kinetic cycle of an ABC transporter by single-molecule and cryo-EM analyses. *eLife* **9**, e56451.

Wang L, Qian H, Nian Y, Han Y, Ren Z, Zhang H, Hu L, Prasad BVV, Laganowsky A, Yan N and Zhou M (2020e) Structure and mechanism of human diacylglycerol O-acyltransferase 1. *Nature* **581**, 329–332.

Wang L, Wu D, Robinson CV, Wu H and Fu T-M (2020f) Structures of a Complete Human V-ATPase Reveal Mechanisms of Its Assembly. *Molecular Cell* **80**, 501-511.e3.

Wang Q, Corey RA, Hedger G, Aryal P, Grieben M, Nasrallah C, Baronina A, Pike ACW, Shi J, Carpenter EP and Sansom MSP (2020g) Lipid Interactions of a Ciliary Membrane TRP Channel: Simulation and Structural Studies of Polycystin-2. *Structure (London, England: 1993)* **28**, 169–184.e5.

- Wang W, Chen X, Zhang L, Yi J, Ma Q, Yin J, Zhuo W, Gu J and Yang M (2020h) Atomic structure of human TOM core complex. *Cell Discovery* **6**, 67.
- Wang W and MacKinnon R (2017) Cryo-EM Structure of the Open Human Ether-à-go-go-Related K⁺ Channel hERG. *Cell* **169**, 422-430.e10.
- Wang X and Boudker O (2020i) Large domain movements through the lipid bilayer mediate substrate release and inhibition of glutamate transporters. *eLife* **9**, e58417.
- Wang Y, Han Y, She J, Nguyen NX, Mootha VK, Bai X-C and Jiang Y (2020j) Structural insights into the Ca²⁺-dependent gating of the human mitochondrial calcium uniporter. *eLife* **9**, e60513.
- Wang Y, Nguyen NX, She J, Zeng W, Yang Y, Bai X-C and Jiang Y (2019b) Structural Mechanism of EMRE-Dependent Gating of the Human Mitochondrial Calcium Uniporter. *Cell* **177**, 1252-1261.e13.
- Wang Z, Hu W and Zheng H (2020k) Pathogenic siderophore ABC importer YbtPQ adopts a surprising fold of exporter. *Science Advances* **6**, eaay7997.
- Wasilko DJ, Johnson ZL, Ammirati M, Che Y, Griffor MC, Han S and Wu H (2020) Structural basis for chemokine receptor CCR6 activation by the endogenous protein ligand CCL20. *Nature Communications* **11**, 3031.
- Weaver SJ, Ortega DR, Sazinsky MH, Dalia TN, Dalia AB and Jensen GJ (2020) CryoEM structure of the type IVa pilus secretin required for natural competence in *Vibrio cholerae*. *Nature Communications* **11**, 5080.
- Wei X, Su X, Cao P, Liu X, Chang W, Li M, Zhang X and Liu Z (2016) Structure of spinach photosystem II-LHCII supercomplex at 3.2 Å resolution. *Nature* **534**, 69–74.
- Whicher JR and MacKinnon R (2016) Structure of the voltage-gated K⁺ channel Eag1 reveals an alternative voltage sensing mechanism. *Science* **353**, 664–669.
- Wild R, Kowal J, Eyring J, Ngwa EM, Aebi M and Locher KP (2018) Structure of the yeast oligosaccharyltransferase complex gives insight into eukaryotic N-glycosylation. *Science* **359**, 545–550.
- Wilkes M, Madej MG, Kreuter L, Rhinow D, Heinz V, De Sanctis S, Ruppel S, Richter RM, Joos F, Grieben M, Pike ACW, Huiskonen JT, Carpenter EP, Kühlbrandt W, Witzgall R and Ziegler C (2017) Molecular insights into lipid-assisted Ca²⁺ regulation of the TRP channel Polycystin-2. *Nature Structural & Molecular Biology* **24**, 123–130.
- Winkler PA, Huang Y, Sun W, Du J and Lü W (2017) Electron cryo-microscopy structure of a human TRPM4 channel. *Nature* **552**, 200–204.
- Wiseman B, Nitharwal RG, Fedotovskaya O, Schäfer J, Guo H, Kuang Q, Benlekbir S, Sjöstrand D, Ädelroth P, Rubinstein JL, Brzezinski P and Högbom M (2018) Structure of a functional obligate complex III2IV2 respiratory supercomplex from *Mycobacterium smegmatis*. *Nature Structural & Molecular Biology* **25**, 1128–1136.
- Wu J, Yan Z, Li Z, Qian X, Lu S, Dong M, Zhou Q and Yan N (2016a) Structure of the voltage-gated calcium channel Ca(v)1.1 at 3.6 Å resolution. *Nature* **537**, 191–196.
- Wu J, Yan Z, Li Z, Yan C, Lu S, Dong M and Yan N (2015) Structure of the voltage-gated calcium channel Cav1.1 complex. *Science* **350**, aad2395.
- Wu J-X, Ding D, Wang M, Kang Y, Zeng X and Chen L (2018) Ligand binding and conformational changes of SUR1 subunit in pancreatic ATP-sensitive potassium channels. *Protein & Cell* **9**, 553–567.

- Wu M, Gu J, Guo R, Huang Y and Yang M (2016b) Structure of Mammalian Respiratory Supercomplex I1III2IV1. *Cell* **167**, 1598–1609.e10.
- Wu X, Cabanos C and Rapoport TA (2019) Structure of the post-translational protein translocation machinery of the ER membrane. *Nature* **566**, 136–139.
- Wu X, Siggel M, Ovchinnikov S, Mi W, Svetlov V, Nudler E, Liao M, Hummer G and Rapoport TA (2020) Structural basis of ER-associated protein degradation mediated by the Hrd1 ubiquitin ligase complex. *Science* **368**, eaaz2449.
- Xie J, Ke M, Xu L, Lin S, Huang J, Zhang J, Yang F, Wu J and Yan Z (2020a) Structure of the human sodium leak channel NALCN in complex with FAM155A. *Nature Communications* **11**, 5831.
- Xie Y, Chang S, Zhao C, Wang F, Liu S, Wang J, Delpire E, Ye S and Guo J (2020b) Structures and an activation mechanism of human potassium-chloride cotransporters. *Science Advances* **6**, eabc5883.
- Xin Y, Shi Y, Niu T, Wang Q, Niu W, Huang X, Ding W, Yang L, Blankenship RE, Xu X and Sun F (2018) Cryo-EM structure of the RC-LH core complex from an early branching photosynthetic prokaryote. *Nature Communications* **9**, 1568.
- Xu X, Shi H, Gong X, Chen P, Gao Y, Zhang X and Xiang S (2020) Structural insights into sodium transport by the oxaloacetate decarboxylase sodium pump J. D. Faraldo-Gómez, K. J. Swartz, & L. Guan, eds. *eLife* **9**, e53853.
- Yan R, Li Y, Shi Y, Zhou J, Lei J, Huang J and Zhou Q (2020) Cryo-EM structure of the human heteromeric amino acid transporter b0₊AT-rBAT. *Science Advances* **6**, eaay6379.
- Yan R, Zhao X, Lei J and Zhou Q (2019) Structure of the human LAT1-4F2hc heteromeric amino acid transporter complex. *Nature* **568**, 127–130.
- Yan Z, Zhou Q, Wang L, Wu J, Zhao Y, Huang G, Peng W, Shen H, Lei J and Yan N (2017) Structure of the Nav1.4-β1 Complex from Electric Eel. *Cell* **170**, 470–482.e11.
- Yang F, Mao C, Guo L, Lin J, Ming Q, Xiao P, Wu X, Shen Q, Guo S, Shen D-D, Lu R, Zhang L, Huang S, Ping Y, Zhang C, Ma C, Zhang K, Liang X, Shen Y, Nan F, Yi F, Luca VC, Zhou J, Jiang C, Sun J-P, Xie X, Yu X and Zhang Y (2020a) Structural basis of GPBAR activation and bile acid recognition. *Nature* **587**, 499–504.
- Yang W, Wang Y, Guo J, He L, Zhou Y, Zheng H, Liu Z, Zhu P and Zhang XC (2020b) Cryo-electron microscopy structure of CLHM1 ion channel from *Caenorhabditis elegans*. *Protein Science: A Publication of the Protein Society* **29**, 1803–1815.
- Yang X, Wang Q and Cao E (2020c) Structure of the human cation-chloride cotransporter NKCC1 determined by single-particle electron cryo-microscopy. *Nature Communications* **11**, 1016.
- Yao X, Fan X and Yan N (2020) Cryo-EM analysis of a membrane protein embedded in the liposome. *Proceedings of the National Academy of Sciences* **117**, 18497–18503.
- Yin J, Chen K-YM, Clark MJ, Hijazi M, Kumari P, Bai X-C, Sunahara RK, Barth P and Rosenbaum DM (2020) Structure of a D2 dopamine receptor-G-protein complex in a lipid membrane. *Nature* **584**, 125–129.
- Yin W, Li Z, Jin M, Yin Y-L, de Waal PW, Pal K, Yin Y, Gao X, He Y, Gao J, Wang X, Zhang Y, Zhou H, Melcher K, Jiang Y, Cong Y, Edward Zhou X, Yu X and Eric Xu H (2019a) A complex structure of arrestin-2 bound to a G protein-coupled receptor. *Cell Research* **29**, 971–983.
- Yin Y, Le SC, Hsu AL, Borgnia MJ, Yang H and Lee S-Y (2019b) Structural basis of cooling agent and lipid sensing by the cold-activated TRPM8 channel. *Science* **363**, eaav9334.

- Yin Y, Wu M, Hsu AL, Borschel WF, Borgnia MJ, Lander GC and Lee S-Y (2019c) Visualizing structural transitions of ligand-dependent gating of the TRPM2 channel. *Nature Communications* **10**, 1–14.
- Yin Y, Wu M, Zubcevic L, Borschel WF, Lander GC and Lee S-Y (2018) Structure of the cold- and menthol-sensing ion channel TRPM8. *Science* **359**, 237–241.
- Yoder N, Yoshioka C and Gouaux E (2018) Gating mechanisms of acid-sensing ion channels. *Nature* **555**, 397–401.
- Yoo J, Wu M, Yin Y, Herzik MA, Lander GC and Lee S-Y (2018) Cryo-EM structure of a mitochondrial calcium uniporter. *Science* **361**, 506–511.
- Yu H, Wu C-H, Schut GJ, Haja DK, Zhao G, Peters JW, Adams MWW and Li H (2018) Structure of an Ancient Respiratory System. *Cell* **173**, 1636–1649.e16.
- Yu X, Plotnikova O, Bonin PD, Subashi TA, McLellan TJ, Dumiao D, Che Y, Dong YY, Carpenter EP, West GM, Qiu X, Culp JS and Han S (2019) Cryo-EM structures of the human glutamine transporter SLC1A5 (ASCT2) in the outward-facing conformation. *eLife* **8**, e48120.
- Yuan D, Liu Z, Kaindl J, Maeda S, Zhao J, Sun X, Xu J, Gmeiner P, Wang H-W and Kobilka BK (2020) Activation of the α 2B adrenoceptor by the sedative sympatholytic dexmedetomidine. *Nature Chemical Biology* **16**, 507–512.
- Zeytuni N, Dickey SW, Hu J, Chou HT, Worrall LJ, Alexander J a. N, Carlson ML, Nosella M, Duong F, Yu Z, Otto M and Strynadka NCJ (2020) Structural insight into the Staphylococcus aureus ATP-driven exporter of virulent peptide toxins. *Science Advances* **6**.
- Zhang B, Jin Q, Xu L, Li N, Meng Y, Chang S, Zheng X, Wang J, Chen Y, Neculai D, Gao N, Zhang X, Yang F, Guo J and Ye S (2020a) Cooperative transport mechanism of human monocarboxylate transporter 2. *Nature Communications* **11**, 2429.
- Zhang C, Shang G, Gui X, Zhang X, Bai X-C and Chen ZJ (2019) Structural basis of STING binding with and phosphorylation by TBK1. *Nature* **567**, 394–398.
- Zhang C, Shuai J, Ran Z, Zhao J, Wu Z, Liao R, Wu J, Ma W and Lei M (2020b) Structural insights into NDH-1 mediated cyclic electron transfer. *Nature Communications* **11**, 888.
- Zhang H, Pan Y, Hu L, Hudson MA, Hofstetter KS, Xu Z, Rong M, Wang Z, Prasad BVV, Lockless SW, Chiu W and Zhou M (2020c) TrkA undergoes a tetramer-to-dimer conversion to open TrkH which enables changes in membrane potential. *Nature Communications* **11**, 547.
- Zhang J-B, Chang S, Xu P, Miao M, Wu H, Zhang Y, Zhang T, Wang H, Zhang J, Xie C, Song N, Luo C, Zhang X and Zhu S (2018a) Structural Basis of the Proton Sensitivity of Human GluN1-GluN2A NMDA Receptors. *Cell Reports* **25**, 3582–3590.e4.
- Zhang L, Zhao Y, Gao Y, Wu L, Gao R, Zhang Q, Wang Y, Wu C, Wu F, Gurcha SS, Veerapen N, Batt SM, Zhao W, Qin L, Yang X, Wang M, Zhu Y, Zhang B, Bi L, Zhang X, Yang H, Guddat LW, Xu W, Wang Q, Li J, Besra GS and Rao Z (2020d) Structures of cell wall arabinosyltransferases with the anti-tuberculosis drug ethambutol. *Science* **368**, 1211–1219.
- Zhang M, Wang D, Kang Y, Wu J-X, Yao F, Pan C, Yan Z, Song C and Chen L (2018b) Structure of the mechanosensitive OSCA channels. *Nature Structural & Molecular Biology* **25**, 850–858.
- Zhang S, Liu Y, Zhang B, Zhou J, Li T, Liu Z, Li Y and Yang M (2020e) Molecular insights into the human CLC-7/Ostm1 transporter. *Science Advances* **6**, eabb4747.
- Zhang X, Belousoff MJ, Zhao P, Kooistra AJ, Truong TT, Ang SY, Underwood CR, Egebjerg T, Šenel P, Stewart GD, Liang Y-L, Glukhova A, Venugopal H, Christopoulos A, Furness SGB, Miller LJ,

- Reedtz-Runge S, Langmead CJ, Gloriam DE, Danev R, Sexton PM and Wootten D (2020f) Differential GLP-1R Binding and Activation by Peptide and Non-peptide Agonists. *Molecular Cell* **80**, 485-500.e7.
- Zhang Y, Bulkley DP, Xin Y, Roberts KJ, Asarnow DE, Sharma A, Myers BR, Cho W, Cheng Y and Beachy PA (2018c) Structural Basis for Cholesterol Transport-like Activity of the Hedgehog Receptor Patched. *Cell* **175**, 1352-1364.e14.
- Zhang Y, Inoue M, Tsutsumi A, Watanabe S, Nishizawa T, Nagata K, Kikkawa M and Inaba K (2020g) Cryo-EM structures of SERCA2b reveal the mechanism of regulation by the luminal extension tail. *Science Advances* **6**, eabb0147.
- Zhang Y, Ou X, Wang X, Sun D, Zhou X, Wu X, Li Q and Li L (2020h) Structure of the mitochondrial TIM22 complex from yeast. *Cell Research* (doi: 10.1038/s41422-020-00399-0).
- Zhang Y, Yang F, Ling S, Lv P, Zhou Y, Fang W, Sun W, Zhang L, Shi P and Tian C (2020i) Single-particle cryo-EM structural studies of the β2AR-Gs complex bound with a full agonist formoterol. *Cell Discovery* **6**, 45.
- Zhang Z and Chen J (2016) Atomic Structure of the Cystic Fibrosis Transmembrane Conductance Regulator. *Cell* **167**, 1586-1597.e9.
- Zhang Z, Liu F and Chen J (2017) Conformational Changes of CFTR upon Phosphorylation and ATP Binding. *Cell* **170**, 483-491.e8.
- Zhang Z, Liu F and Chen J (2018d) Molecular structure of the ATP-bound, phosphorylated human CFTR. *Proceedings of the National Academy of Sciences of the United States of America* **115**, 12757–12762.
- Zhang Z, Tóth B, Szollosi A, Chen J and Csanády L (2018e) Structure of a TRPM2 channel in complex with Ca²⁺ explains unique gating regulation. *eLife* **7**, e36409.
- Zhao J, Lin King JV, Paulsen CE, Cheng Y and Julius D (2020a) Irritant-evoked activation and calcium modulation of the TRPA1 receptor. *Nature* **585**, 141–145.
- Zhao L-H, Ma S, Sutkeviciute I, Shen D-D, Zhou XE, de Waal PW, Li C-Y, Kang Y, Clark LJ, Jean-Alphonse FG, White AD, Yang D, Dai A, Cai X, Chen J, Li C, Jiang Y, Watanabe T, Gardella TJ, Melcher K, Wang M-W, Vilardaga J-P, Xu HE and Zhang Y (2019a) Structure and dynamics of the active human parathyroid hormone receptor-1. *Science* **364**, 148–153.
- Zhao P, Liang Y-L, Belousov MJ, Deganutti G, Fletcher MM, Willard FS, Bell MG, Christe ME, Sloop KW, Inoue A, Truong TT, Clydesdale L, Furness SGB, Christopoulos A, Wang M-W, Miller LJ, Reynolds CA, Danev R, Sexton PM and Wootten D (2020b) Activation of the GLP-1 receptor by a non-peptidic agonist. *Nature* **577**, 432–436.
- Zhao Y, Huang G, Wu J, Wu Q, Gao S, Yan Z, Lei J and Yan N (2019b) Molecular Basis for Ligand Modulation of a Mammalian Voltage-Gated Ca²⁺ Channel. *Cell* **177**, 1495-1506.e12.
- Zhao Y, Huang G, Wu Q, Wu K, Li R, Lei J, Pan X and Yan N (2019c) Cryo-EM structures of apo and antagonist-bound human Cav3.1. *Nature* **576**, 492–497.
- Zheng X, Fu Z, Su D, Zhang Y, Li M, Pan Y, Li H, Li S, Grassucci RA, Ren Z, Hu Z, Li X, Zhou M, Li G, Frank J and Yang J (2020) Mechanism of ligand activation of a eukaryotic cyclic nucleotide-gated channel. *Nature Structural & Molecular Biology* **27**, 625–634.
- Zhou L and Sazanov LA (2019a) Structure and conformational plasticity of the intact *Thermus thermophilus* V/A-type ATPase. *Science* **365**, eaaw9144.

- Zhou R, Yang G, Guo X, Zhou Q, Lei J and Shi Y (2019b) Recognition of the amyloid precursor protein by human γ -secretase. *Science* **363**, eaaw0930.
- Zhou X, Li M, Su D, Jia Q, Li H, Li X and Yang J (2017) Cryo-EM structures of the human endolysosomal TRPML3 channel in three distinct states. *Nature Structural and Molecular Biology* **24**, 1146–1154.
- Zhou Y, Liao L, Wang C, Li J, Chi P, Xiao Q, Liu Q, Guo L, Sun L and Deng D (2020) Cryo-EM structure of the human concentrative nucleoside transporter CNT3. *PLoS biology* **18**, e3000790.
- Zhu G, Zeng H, Zhang S, Juli J, Pang X, Hoffmann J, Zhang Y, Morgner N, Zhu Y, Peng G, Michel H and Sun F (2020) A 3.3 Å-Resolution Structure of Hyperthermophilic Respiratory Complex III Reveals the Mechanism of Its Thermal Stability. *Angewandte Chemie (International Ed. in English)* **59**, 343–351.
- Zhu J, Vinothkumar KR and Hirst J (2016) Structure of mammalian respiratory complex I. *Nature* **536**, 354–358.
- Zhu S, Noviello CM, Teng J, Walsh RM, Kim JJ and Hibbs RE (2018) Structure of a human synaptic GABA_A receptor. *Nature* **559**, 67–72.
- Zubcevic L, Borschel WF, Hsu AL, Borgnia MJ and Lee S-Y (2019a) Regulatory switch at the cytoplasmic interface controls TRPV channel gating. *eLife* **8**, e47746.
- Zubcevic L, Herzik MA, Chung BC, Liu Z, Lander GC and Lee S-Y (2016) Cryo-electron microscopy structure of the TRPV2 ion channel. *Nature Structural & Molecular Biology* **23**, 180–186.
- Zubcevic L, Herzik MA, Wu M, Borschel WF, Hirschi M, Song AS, Lander GC and Lee S-Y (2018) Conformational ensemble of the human TRPV3 ion channel. *Nature Communications* **9**, 1–12.
- Zubcevic L, Hsu AL, Borgnia MJ and Lee S-Y (2019b) Symmetry transitions during gating of the TRPV2 ion channel in lipid membranes K. J. Swartz, R. Aldrich, R. K. Hite, & R. Dutzler, eds. *eLife* **8**, e45779.