



STRUCTURAL BIOLOGY  
COMMUNICATIONS

Volume 73 (2017)

Supporting information for article:

**Cryo-electron microscopy and X-ray crystallography: complementary approaches to structural biology and drug discovery**

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**Table S1** Extraction from the Protein Data Bank of the objects (>500 kDa) resolved at less than 10 Å since 2010, assuming that most of them were obtained by cryo-electron microscopy

Code	Deposit date	Protein/substructure	Authors	Publication Title	Main EMD entry	Resolution (Å)	Reference
5ftj	2016	Translational endoplasmic reticulum ATPase	Banerjee <i>et al.</i>	2.3 Å Resolution Cryo-Em Structure of Human P97 and Mechanism of Allosteric Inhibition	EMD-3295	2.3	(Banerjee <i>et al.</i> , 2016)
3jcs	2016	26S alpha ribosomal RNA	Shalev-Benami <i>et al.</i>	2.8- Å Cryo-EM Structure of the Large Ribosomal Subunit from the Eukaryotic Parasite Leishmania.	EMD-6583	2.8	(Shalev-Benami <i>et al.</i> , 2016)
5iqr	2016	70S ribosome-ReIA complex	Brown <i>et al.</i>	Ribosome-dependent activation of stringent control.	EMD-8107	3.0	(Brown <i>et al.</i> , 2016)
3jet	2016	Pre60S ribosome	Wu <i>et al.</i>	Diverse roles of assembly factors revealed by structures of late nuclear pre-60S ribosomes	EMD-6616	3.1	(Wu <i>et al.</i> , 2016)
3izx	2011	Structural protein VP3	Yu <i>et al.</i>	Atomic Model of CPV Reveals the Mechanism Used by This Single-Shelled Virus to Economically Carry Out Functions Conserved in Multishelled Reoviruses.	EMD-5256	3.1	(Yu <i>et al.</i> , 2011)
3j6b	2014	Large ribosomal subunit	Amunts <i>et al.</i>	Structure of the yeast mitochondrial large ribosomal subunit.	EMD-2566	3.2	(Amunts <i>et al.</i> , 2014)
3j79	2014	80S ribosome	Wong <i>et al.</i>	Cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to the anti-protozoan drug emetine.	EMD-2661	3.2	(Wong <i>et al.</i> , 2014)
3jcu	2016	Photosystem II	Wei <i>et al.</i>	Structure of spinach photosystem II-LHCII supercomplex at 3.2 Å resolution	EMD-6617	3.2	(Wei <i>et al.</i> , 2016)
3j9i	2015	20S proteasome	Li <i>et al.</i>	Electron counting and beam-induced motion correction enable near-atomic-resolution single-particle cryo-EM.	EMD-5623	3.3	(Li <i>et al.</i> , 2013b)
3jak	2015	Microtubules	Zhang <i>et al.</i>	Mechanistic Origin of Microtubule Dynamic Instability and Its Modulation by EB Proteins.	EMD-6348	3.3	(Zhang <i>et al.</i> , 2015)
5an9	2015	60S Ribosome	Weis <i>et al.</i>	Mechanism of Eif6 Release from the Nascent 60S Ribosomal Subunit	EMD-3147	3.3	(Weis <i>et al.</i> , 2015)

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3j7q	2014	Sec61-ribosome complex	Voorhees <i>et al.</i>	Structure of the Mammalian ribosome-sec61 complex to 3.4 Å resolution.	EMD-2650	3.4	(Voorhees <i>et al.</i> , 2014)
3j7y	2014	Large ribosome	Brown <i>et al.</i>	Structure of the large ribosomal subunit from human mitochondria.	EMD-2762	3.4	(Brown <i>et al.</i> , 2014)
4v19	2014	Mitoribosome	Greber <i>et al.</i>	The Complete Structure of the Large Subunit of the Mammalian Mitochondrial Ribosome	EMD-2787	3.4	(Greber <i>et al.</i> , 2014a)
5flm	2015	Pol II elongation complex	Bernecky <i>et al.</i>	Structure of Transcribing Mammalian RNA Polymerase II	EMD-3218	3.4	(Bernecky <i>et al.</i> , 2016)
5lkh	2016	TcdA1	Gatsogiannis <i>et al.</i>	Membrane insertion of a Tc toxin in near-atomic detail.	EMD-4068	3.5	(Gatsogiannis <i>et al.</i> , 2016)
3j26	2012	Virophage	Zhang <i>et al.</i>	Structure of Sputnik, a virophage, at 3.5- Å resolution.	EMD-5495	3.5	(Zhang <i>et al.</i> , 2012)
3j9g	2015	VipA	Kudryashev <i>et al.</i>	Structure of the Type VI Secretion System Contractile Sheath.	EMD-2699	3.5	(Kudryashev <i>et al.</i> , 2015)
5a0q	2015	20S Proteasome	Da Fonseca <i>et al.</i>	Cryo-Em Reveals the Conformation of a Substrate Analogue in the Human 20S Proteasome Core.	EMD-2981	3.5	(da Fonseca & Morris 2015)
5aj0	2015	Native polysomes	Behrmann <i>et al.</i>	Structural Snapshots of Actively Translating Human Ribosomes	EMD-2875	3.5	(Behrmann <i>et al.</i> , 2015)
5gjr	2016	26S proteasome	Huang <i>et al.</i>	An atomic structure of the human 26S proteasome	EMD-9511	3.5	(Huang <i>et al.</i> , 2016)
3iyn	2010	Adenovirus type 5	Liu <i>et al.</i>	Atomic structure of human adenovirus by cryo-EM reveals interactions among protein networks	EMD-5172	3.6	(Liu <i>et al.</i> , 2010)
3j92	2014	Ribosome quality control complex.	Shao <i>et al.</i>	Structure and Assembly Pathway of the Ribosome Quality Control Complex.	EMD-2832	3.6	(Shao <i>et al.</i> , 2015)
3jal	2015	70S-P-tRNA-E-tRNA complex	Li <i>et al.</i>	Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G.	EMD-6315	3.6	(Li <i>et al.</i> , 2015b)
3ja7	2015	Portal protein gp20	Sun <i>et al.</i>	Cryo-EM structure of the bacteriophage T4 portal protein assembly at near-atomic resolution.	EMD-6324	3.6	(Sun <i>et al.</i> , 2015)
3jb9	2015	Spliceosome	Yan <i>et al.</i>	Structure of a yeast spliceosome at 3.6- Å resolution	EMD-6413	3.6	(Yan <i>et al.</i> , 2015a)
4ui9	2015	Anaphase-promoting complex subunit 1	Chang <i>et al.</i>	Atomic Structure of the Apc and its Mechanism of Protein Ubiquitination	EMD-2924	3.6	(Chang <i>et al.</i> , 2015)

Code	Deposit date	Protein/substructure	Authors	Publication Title	Main EMD entry	Resolution (Å)	
5aj3	2015	28S mitoribosome	Greber <i>et al.</i>	Ribosome. The Complete Structure of the 55S Mammalian Mitochondrial Ribosome.	EMD-2913	3.6	(Greber <i>et al.</i> , 2015)
5fmg	2015	20S proteasome	Li <i>et al.</i>	Structure and Function Based Design of Plasmodium-Selective Proteasome Inhibitors	EMD-3231	3.6	(Li <i>et al.</i> , 2016)
5kcr	2016	70S ribosome	Arenz <i>et al.</i>	Structures of the orthosomycin antibiotics avilamycin and evernimicin in complex with the bacterial 70S ribosome.	EMD-8237	3.6	(Arenz <i>et al.</i> , 2016)
3jai	2015	80S ribosome-nascent chain complex	Brown <i>et al.</i>	Structural basis for stop codon recognition in eukaryotes.	EMD-3040	3.7	(Brown <i>et al.</i> , 2015)
5gad	2015	Ribosome-nascent chain complex	Jomaa <i>et al.</i>	Structures of the <i>E. coli</i> translating ribosome with SRP and its receptor and with the translocon.	EMD-8000	3.7	(Jomaa <i>et al.</i> , 2016)
5gan	2015	Spliceosome	Nguyen <i>et al.</i>	Cryo-EM structure of the yeast U4/U6.U5 tri-snRNP at 3.7 Å resolution.	EMD-8012	3.7	(Nguyen <i>et al.</i> , 2016)
3j8h	2014	Ryanodine receptor 1	Yan <i>et al.</i>	Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution.	EMD-2807	3.8	(Yan <i>et al.</i> , 2015b)
3ja8	2015	Minichromosome maintenance complex2	Li <i>et al.</i>	Structure of the eukaryotic MCM complex at 3.8 Å	EMD-6338	3.8	(Li <i>et al.</i> , 2015a)
3jcm	2015	Spliceosome	Wan <i>et al.</i>	The 3.8 Å structure of the U4/U6.U5 tri-snRNP: Insights into spliceosome assembly and catalysis	EMD-6561	3.8	(Wan <i>et al.</i> , 2016)
4v7q	2010	Rotavirus particle	Settembre <i>et al.</i>	Atomic model of an infectious rotavirus particle.	EMD-5199	3.8	(Settembre <i>et al.</i> , 2011)
5imq	2016	Ribosome-eF4 complex	Kumar <i>et al.</i>	Structure of the GTP Form of Elongation Factor 4 (EF4) Bound to the Ribosome	EMD-6584	3.8	(Kumar <i>et al.</i> , 2016)
5ipk	2016	Adeno-associated virus-2	Drouin <i>et al.</i>	Cryo-electron microscopy reconstruction and stability studies of Wild-Type and R432A Variant of AAV2 Reveals Capsid Structural Stability is a Major Factor in Genome Packaging.	EMD-8100	3.7	(Drouin <i>et al.</i> , 2016)
3j9q	2015	Pyocin	Ge <i>et al.</i>	Atomic structures of a bactericidal contractile nanotube in its pre- and postcontraction states.	EMD-6270	3.5	(Ge <i>et al.</i> , 2015)
3j9w	2015	MifM-ribosome complex	Sohmen <i>et al.</i>	Structure of the <i>Bacillus subtilis</i> 70S ribosome reveals the basis for species-specific stalling.	EMD-6306	3.9	(Sohmen <i>et al.</i> , 2015)
5fj8	2015	RNA polymerase III elongation complex	Hoffmann <i>et al.</i>	Molecular Structures of Unbound and Transcribing RNA Polymerase III.	EMD-3178	3.9	(Hoffmann <i>et al.</i> , 2015)

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5jzh	2016	Aerolysin	Iacovache <i>et al.</i>	Cryo-EM structure of aerolysin variants reveals a novel protein fold and the pore-formation process.	EMD-8185	3.9	(Iacovache <i>et al.</i> , 2016)
N/A	2016	26S proteasome	Schweitzer <i>et al.</i>	Structure of the human 26S proteasome at a resolution of 3.9 Å	EMD-4002	3.9	[10]
3jan	2015	SRP-ribosome complex	Voorhees & Hegde	Structures of the scanning and engaged states of the mammalian SRP-ribosome complex.	EMD-3045	3.9	(Voorhees & Hegde 2015)
3j81	2014	48S preinitiation complex	Hussain <i>et al.</i>	Structural changes enable start codon recognition by the eukaryotic translation initiation complex.	EMD-2763	4.0	(Hussain <i>et al.</i> , 2014)
3jc1	2015	IST1 <sub>NTD</sub> -CHMP1B assembly	McCullough <i>et al.</i>	Structure and membrane remodeling activity of ESCRT-III helical polymers.	EMD-6461	4.0	(McCullough <i>et al.</i> , 2015)
5kyh	2016	Iho670 filament	Braun <i>et al.</i>	Archaeal flagellin combines a bacterial type IV pilin domain with an Ig-like domain.	EMD-8298	4.0	(Braun <i>et al.</i> , 2016)
5iv5	2016	T4 baseplate-tail tube complex	Taylor <i>et al.</i>	Atomic structure of bacteriophage T4 baseplate and its function in triggering sheath contraction.	EMD-3374	4.1	(Taylor <i>et al.</i> , 2016)
3j94	2015	SNARE complex	Zhao <i>et al.</i>	Mechanistic insights into the recycling machine of the SNARE complex.	EMD-6204	4.2	(Zhao <i>et al.</i> , 2015b)
4v8y	2013	80S-eIF5B-Met-itRNAMet eukaryotic translation complex	Fernandez <i>et al.</i>	Molecular architecture of the 80S-eIF5B-Met-itRNAMet Eukaryotic Translation Initiation Complex.	EMD-2421	4.3	(Fernandez <i>et al.</i> , 2013)
5gaf	2015	SRP-ribosome nascent chain complex	Jomaa <i>et al.</i>	Structures of the <i>E. coli</i> translating ribosome with SRP and its receptor and with the translocon.	EMD-8002	4.3	(Jomaa <i>et al.</i> , 2016)
5fyw	2016	Pol II transcription initiation complex	Plaschka <i>et al.</i>	Transcription Initiation Complex Structures Elucidate DNA Opening	EMD-3378	4.4	(Plaschka <i>et al.</i> , 2016)
4btg	2013	Bacteriophage phi6 P1247 procapsid	Nemecek <i>et al.</i>	Subunit Folds and Maturation Pathway of dsRNA Virus Capsid.	EMD-2364	4.4	(Nemecek <i>et al.</i> , 2013)
3j31	2013	Sulfolobus Turreted Virus	Veesler <i>et al.</i>	Atomic structure of the 75 mDa extremophile Sulfolobus turreted icosahedral virus determined by CryoEM and X-ray crystallography.	EMD-5584	4.5	(Veesler <i>et al.</i> , 2013)
3j32	2013	Hemocyanin isoform 1	Zhang <i>et al.</i>	Cryo-EM structure of a molluscan hemocyanin suggests its allosteric mechanism.	EMD-5586	4.5	(Zhang <i>et al.</i> , 2013b)
3zif	2013	Adenovirus type 3	Cheng <i>et al.</i>	Cryo-Em Structures of Two Bovine Adenovirus Type 3 Intermediates	EMD-2273	4.5	(Cheng <i>et al.</i> , 2014)
3jcn	2015	70S ribosomes-IF2 complex	Sprink <i>et al.</i>	Structures of ribosome bound initiation factor 2 reveal the mechanism of subunit association.	EMD-3285	4.6	(Sprink <i>et al.</i> , 2016)

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4bml	2013	Syn5 marine virus	Gipson <i>et al.</i>	Protruding Knob-Like Proteins Violate Local Symmetries in an Icosahedral Marine Virus.	EMD-5954	4.7	(Gipson <i>et al.</i> , 2014)
3jav	2015	Inositol 1,4,5-trisphosphate receptor type 1	Fan <i>et al.</i>	Gating machinery of InsP3R channels revealed by electron cryomicroscopy.	EMD-6369	4.7	(Fan <i>et al.</i> , 2015)
3jc7	2015	CMG complex	Yuan <i>et al.</i>	Structure of the eukaryotic replicative CMG helicase suggests a pumpjack motion for translocation.	EMD-6536	4.8	(Yuan <i>et al.</i> , 2016)
3j03	2011	Group II chaperonin	Zhang <i>et al.</i>	Mechanism of folding chamber closure in a group II chaperonin.	EMD-5138	4.8	(Zhang <i>et al.</i> , 2010a)
3j8e	2014	Ryanodine receptor 1-calstabin complex	Zalk <i>et al.</i>	Structure of a mammalian ryanodine receptor.	EMD-6106	4.8	(Zalk <i>et al.</i> , 2015)
3jac	2015	Piezo-type mechanosensitive ion channel component 1	Ge <i>et al.</i>	Architecture of the mammalian mechanosensitive Piezo1 channel	EMD-6343	4.8	(Efremov <i>et al.</i> , 2015)
3jco	2016	26S proteasome	Luan <i>et al.</i>	Structure of an endogenous yeast 26S proteasome reveals two major conformational states.	EMD-6574	4.8	(Luan <i>et al.</i> , 2016)
5g5l	2016	RNA polymerase I-Rrn3 complex	Engel <i>et al.</i>	RNA Polymerase I-Rrn3 Complex at 4.8 Å Resolution	EMD-3439	4.8	(Engel <i>et al.</i> , 2013)
3j1b	2012	rATcpn-alpha	Zhang <i>et al.</i>	Flexible interwoven termini determine the thermal stability of thermosomes.	EMD-5391	4.9	(Zhang <i>et al.</i> , 2013a)
4ce4	2013	Mitochondrial ribosome 39S large subunit	Greber <i>et al.</i>	Architecture of the Large Subunit of the Mammalian Mitochondrial Ribosome.	EMD-2490	4.9	(Greber <i>et al.</i> , 2014b)
4uq8	2014	NADH ubiquinone oxidoreductase	Vinothkumar <i>et al.</i>	Architecture of mammalian respiratory complex I.	EMD-2676	5.0	(Vinothkumar <i>et al.</i> , 2014)
3J8G	2014	EngA-50S subunit complex	Zhang <i>et al.</i>	Structural insights into the function of a unique tandem GTPase EngA in bacterial ribosome assembly	EMD-6149	5.0	(Zhang <i>et al.</i> , 2014)
4v7e	2013	80S ribosome	Armache <i>et al.</i>	Localization of eukaryote-specific ribosomal proteins in a 5.5-A cryo-EM map of the 80S eukaryotic ribosome.	EMD-1780	5.5	(Armache <i>et al.</i> , 2010)
4v8m	2012	80S ribosome	Hashem <i>et al.</i>	High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome.	EMD-2239	5.6	(Hashem <i>et al.</i> , 2013)
5kne	2016	Heat shock protein 104	Yokom <i>et al.</i>	Spiral architecture of the Hsp104 disaggregase reveals the basis for polypeptide translocation.	EMD-8267	5.6	(Yokom <i>et al.</i> , 2016)
5k0y	2016	m48S late-stage initiation complex	Simonetti <i>et al.</i>	eIF3 peripheral subunits rearrangement after mRNA binding and start-codon recognition.	EMD-8190	5.8	(Simonetti <i>et al.</i> , 2016)

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5flc	2015	mTOR complex I	Aylett <i>et al.</i>	Architecture of human mTor complex 1	EMD-3213	5.9	(Aylett <i>et al.</i> , 2016)
4aod	2012	Acetylcholine binding protein	Saur <i>et al.</i>	Acetylcholine-binding protein in the hemolymph of the planorbid snail <i>Biomphalaria glabrata</i> is a pentagonal dodecahedron (60 subunits)	EMD-2055	6.0	(Saur <i>et al.</i> , 2012)
4cct	2012	Dengue virus	Kostyuchenko <i>et al.</i>	Immature and mature Dengue serotype 1 virus structures provide insight into the maturation process.	EMD-2142	6.0	(Kostyuchenko <i>et al.</i> , 2013)
4c2i	2013	Dengue virus with Fab fragment	Fibriansah <i>et al.</i>	A potent anti-Dengue human antibody preferentially recognizes the conformation of E protein monomers assembled on the virus surface.	EMD-2442	6.0	(Fibriansah <i>et al.</i> , 2014)
5a5t	2015	eIF3 octamer core	Des Georges <i>et al.</i>	Structure of mammalian Eif3 in the context of the 43S preinitiation complex.	EMD-3056	6.0	(des Georges A. <i>et al.</i> , 2015)
3j6y	2014	80S ribosome	Koh <i>et al.</i>	Taura syndrome virus IRES initiates translation by binding its tRNA-mRNA-like structural element in the ribosomal decoding center.	EMD-5943	6.1	(Koh <i>et al.</i> , 2014)
5fvm	2016	Tor1-Lst8 complex	Baretic <i>et al.</i>	Tor Forms a Dimer Through an N-Terminal Helical Solenoid with a Complex Topology	EMD-3329	6.1	(Baretic <i>et al.</i> , 2016)
3izl	2010	Group II chaperonin	Douglas <i>et al.</i>	Dual action of ATP hydrolysis couples lid closure to substrate release into the group II chaperonin chamber.	EMD-5248	6.2	(Douglas <i>et al.</i> , 2011)
N/A	2014	Microtubule	Alushin <i>et al.</i>	High-resolution microtubule structures reveal the structural transitions in alpha beta-tubulin upon GTP hydrolysis.	EMD-5899	6.3	(Alushin <i>et al.</i> , 2014)
2y9j	2011	Needle complex	Schraadt & Marlovits	Three-Dimensional Model of <i>Salmonella</i> 'S Needle Complex at Subnanometer Resolution.	EMD-1874	6.4	(Schraadt & Marlovits 2011)
4uer	2014	40S-eIF1-eIF1A-eIF3-eIF3j initiation complex	Aylett <i>et al.</i>	Structure of a Yeast 40S-Eif1-Eif1A-Eif3-Eif3J Initiation Complex	EMD-2845	6.5	(Aylett <i>et al.</i> , 2015)
5jyg	2016	Magnetosome-associated MamK filament	Bergeron <i>et al.</i>	Structure of the Magnetosome-associated actin-like MamK filament at sub-nanometer resolution.	EMD-8180	6.5	(Bergeron <i>et al.</i> , 2016)
3j15	2012	70S ribosome	Becker <i>et al.</i>	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea.	EMD-2009	6.6	(Becker <i>et al.</i> , 2012)
5fmw	2015	C9	Dudkina <i>et al.</i>	Structure of the Poly-C9 Component of the Complement Membrane Attack Complex	EMD-3235	6.7	(Dudkina <i>et al.</i> , 2016)

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4v4l	2010	Apoptosome	Yuan <i>et al.</i>	Structure of the Drosophila apoptosome at 6.9 Å resolution	EMD-5235	6.9	(Yuan <i>et al.</i> , 2011)
5i1m	2016	V ATPase	Schep <i>et al.</i>	Unpublished	EMD-8070	7.0	-
3iyk	2010	Bluetongue virus	Zhang <i>et al.</i>	Bluetongue virus coat protein VP2 contains sialic acid-binding domains, and VP5 resembles enveloped virus fusion proteins.	EMD-5147	7.0	(Zhang <i>et al.</i> , 2010b)
3jcr	2016	U4/U6.U5 tri-snRNP	Agafonov <i>et al.</i>	Molecular architecture of the human U4/U6.U5 tri-snRNP.	EMD-6581	7.0	(Agafonov <i>et al.</i> , 2016)
4v6m	2011	SecYEG complex	Frauenfeld <i>et al.</i>	Cryo-EM structure of the ribosome-SecYE complex in the membrane environment.	EMD-1858	7.1	(Frauenfeld <i>et al.</i> , 2011)
5jpq	2016	Ribo-nucleoprotein complex	Kornprobst <i>et al.</i>	Architecture of the 90S Pre-ribosome: A Structural View on the Birth of the Eukaryotic Ribosome.	EMD-8143	7.3	(Kornprobst <i>et al.</i> , 2016)
5kk2	2016	GluA2 AMPA receptor - TARP complex	Zhao <i>et al.</i>	Architecture of fully occupied GluA2 AMPA receptor-TARP complex elucidated by cryo-EM.	EMD-8256	7.3	(Zhao <i>et al.</i> , 2016)
4v8l	2012	Fatty acid synthase 1	Boehringer <i>et al.</i>	7.5- Å Cryo-Em Structure of the Mycobacterial Fatty Acid Synthase.	EMD-2238	7.5	(Boehringer <i>et al.</i> , 2013)
4cr2	2014	26S Proteasome	Unverdorben <i>et al.</i>	Deep Classification of a Large Cryo-Em Dataset Defines the Conformational Landscape of the 26S Proteasome.	EMD-2594	7.7	(Unverdorben <i>et al.</i> , 2014)
5a9e	2015	Rous-Sarcoma Virus Gag particles	Schur <i>et al.</i>	The Structure of Immature-Like Rous Sarcoma Virus Gag Particles Reveals a Structural Role for the P10 Domain in Assembly.	EMD-3101	7.7	(Schur <i>et al.</i> , 2015)
4v1n	2014	cITC	Plaschka <i>et al.</i>	Architecture of the RNA Polymerase II-Mediator Core Initiation Complex.	EMD-2785	7.8	(Plaschka <i>et al.</i> , 2015)
3j02	2011	group II chaperonin	Zhang <i>et al.</i>	Cryo-EM structure of a group II chaperonin in the prehydrolysis ATP-bound state leading to lid closure.	EMD-5258	8.0	(Zhang <i>et al.</i> , 2011)
4v8t	2012	60S ribosomal subunit-Arx1 and Rei1 complex	Greber <i>et al.</i>	Cryo-Em Structures of Arx1 and Maturation Factors Rei1 and Jjj1 Bound to the 60S Ribosomal Subunit	EMD-2169	8.1	(Greber <i>et al.</i> , 2012)
4v93	2014	Hemoglobin	Chen <i>et al.</i>	Structural Basis for Cooperative Oxygen Binding and Bracelet-Assisted Assembly of <i>Lumbricus Terrestris</i> Hemoglobin	EMD-2627	8.1	(Chen <i>et al.</i> , 2015)
4bip	2013	Coxsackievirus	Seitsonen <i>et al.</i>	Structural analysis of coxsackievirus A7 reveals conformational changes associated with uncoating.	EMD-2028	8.2	(Seitsonen <i>et al.</i> , 2012)
3j9v	2015	V-ATPase	Zhao <i>et al.</i>	Electron cryomicroscopy observation of rotational states in a eukaryotic V-ATPase.	EMD-6286	8.3	(Zhao <i>et al.</i> , 2015a)

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4v6k	2011	70S-TC complex	Agirrezabala <i>et al.</i>	Structural insights into cognate versus near-cognate discrimination during decoding.	EMD-1849	8.3	(Agirrezabala <i>et al.</i> , 2011)
3j1e	2012	rATcpn-beta	Zhang <i>et al.</i>	Flexible interwoven termini determine the thermal stability of thermosomes.	EMD-5395	8.3	(Zhang <i>et al.</i> , 2013a)
2ynj	2012	GroEL	Bartesaghi <i>et al.</i>	Protein Secondary Structure Determination by Constrained Single-Particle Cryo-Electron Tomography	EMD-2221	8.4	(Bartesaghi <i>et al.</i> , 2012)
3zbi	2012	traN/traO/traF complex	Rivera-Calzada <i>et al.</i>	Structure of a Bacterial Type Iv Secretion Core Complex at Subnanometre Resolution.	EMD-2233	8.5	(Rivera-Calzada <i>et al.</i> , 2013)
5fur	2016	TFIID-TFIIA complex	Louder <i>et al.</i>	Structure of Promoter-Bound TFIID and Model of Human Pre-Initiation Complex Assembly.	EMD-3305	8.7	(Louder <i>et al.</i> , 2016)
3j34	2013	HIV-1 capsid	Zhao <i>et al.</i>	Mature HIV-1 capsid structure by cryo-electron microscopy and all-atom molecular dynamics.	EMD-5582	8.6	(Zhao <i>et al.</i> , 2013)
4v7f	2013	5S ribonucleoprotein particle	Leidig <i>et al.</i>	60S ribosome biogenesis requires rotation of the 5S ribonucleoprotein particle.	EMD-2528	8.7	(Leidig <i>et al.</i> , 2014)
4v6i	2010	80S ribosome- Ssh1	Becker <i>et al.</i>	Structure of monomeric yeast and mammalian Sec61 complexes interacting with the translating ribosome.	EMD-1669	8.8	(Becker <i>et al.</i> , 2009)
3j0s	2011	Actin, cytoplasmic 1	Galkin <i>et al.</i>	Remodeling of actin filaments by ADF/cofilin proteins.	EMD-5354	9.0	(Galkin <i>et al.</i> , 2011)
4bed	2013	Hemocyanin KLH1	Gatsogiannis & Markl	Keyhole Limpet Hemocyanin: 9-A Cryoem Structure and Molecular Model of the Klh1 Didecamer Reveal the Interfaces and Intricate Topology of the 160 Functional Units.	EMD-1569	9.1	(Gatsogiannis & Markl2009)
4d67	2014	80S ribosome termination complex	Muhs <i>et al.</i>	Cryo-Em Structures of Ribosomal 80S Complexes with Termination Factors and Cricket Paralysis Virus Ires Reveal the Ires in the Translocated State	EMD-2813	8.9	(Muhs <i>et al.</i> , 2015)
4v4n	2013	70S ribosome-SecYEbeta complex	Park <i>et al.</i>	Structure of the SecY channel during initiation of protein translocation.	EMD-5691	9.0	(Park <i>et al.</i> , 2014)
3j3r	2013	MecA-ClpC	Liu <i>et al.</i>	Structural dynamics of the MecA-ClpC complex: a type II AAA+ protein unfolding machine	EMD-5610	9.4	(Liu <i>et al.</i> , 2013)
3j2t	2012	Apoptosome	Yuan <i>et al.</i>	Structure of an apoptosome-procaspase-9 CARD complex	EMD-5186	9.5	(Yuan <i>et al.</i> , 2010)
5fl8	2015	Pre-60S ribosomal particle	Barrio-Garcia <i>et al.</i>	Architecture of the Rix1-Rea1 checkpoint machinery during pre-60S-ribosome remodeling.	EMD-3199	9.5	(Barrio-Garcia <i>et al.</i> , 2016)

Code	Deposit date	Protein/substructure	Authors	Publication Title	Main EMD entry	Resolution (Å)	
4v6v	2013	70S-Tet(O)	Li <i>et al.</i>	Mechanism of tetracycline resistance by ribosomal protection protein Tet(O).	EMD-5562	9.8	(Li <i>et al.</i> , 2013a)

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