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 et al. | 2.3 Å Resolution Cryo-Em Structure of Human P97 and Mechanism of Allosteric Inhibition | EMD-3295       | 2.3            | (Banerjee et al., 2016)                        |
| 3jcs  | 2016         | 26S alpha ribosomal RNA                     | Shalev-Benami et al. | 2.8- Å Cryo-EM Structure of the Large Ribosomal Subunit from the Eukaryotic Parasite Leishmania. | EMD-6583       | 2.8            | (Shalev-Benami et al., 2016)                   |
| 5iqr  | 2016         | 70S ribosome-ReLA complex                   | Brown et al.    | Ribosome-dependent activation of stringent control.                               | EMD-8107       | 3.0            | (Brown et al., 2016)                          |
| 3jct  | 2016         | Pre60S ribosome                             | Wu et al.       | Diverse roles of assembly factors revealed by structures of late nuclear pre-60S ribosomes | EMD-6616       | 3.1            | (Wu et al., 2016)                             |
| 3izx  | 2011         | Structural protein VP3                      | Yu et al.       | 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 et al., 2011)                             |
| 3j6b  | 2014         | Large ribosomal subunit                     | Amunts et al.   | Structure of the yeast mitochondrial large ribosomal subunit.                    | EMD-2566       | 3.2            | (Amunts et al., 2014)                         |
| 3j79  | 2014         | 80S ribosome                               | Wong et al.     | Cryo-EM structure of the Plasmodium falciparum 80S ribosome bound to the anti-protozoan drug emetine. | EMD-2661       | 3.2            | (Wong et al., 2014)                           |
| 3jcu  | 2016         | Photosystem II                             | Wei et al.      | Structure of spinach photosystem II-LHCII supercomplex at 3.2 Å resolution        | EMD-6617       | 3.2            | (Wei et al., 2016)                            |
| 3ji9  | 2015         | 20S proteasome                             | Li et al.       | Electron counting and beam-induced motion correction enable near-atomic-resolution single-particle cryo-EM. | EMD-5623       | 3.3            | (Li et al., 2013b)                            |
| 3jak  | 2015         | Microtubules                               | Zhang et al.    | Mechanistic Origin of Microtubule Dynamic Instability and Its Modulation by EB Proteins. | EMD-6348       | 3.3            | (Zhang et al., 2015)                          |
| 5an9  | 2015         | 60S Ribosome                               | Weis et al.     | Mechanism of Eif6 Release from the Nascent 60S Ribosomal Subunit                  | EMD-3147       | 3.3            | (Weis et al., 2015)                           |
| Code  | Deposit date | Protein/substructure                              | Authors             | Publication Title                                                                                   | Main EMD entry | Resolution (Å) |
|-------|--------------|--------------------------------------------------|---------------------|----------------------------------------------------------------------------------------------------|----------------|---------------|
| 3j7q  | 2014         | Sec61-ribosome complex                           | Voorhees et al.     | Structure of the Mammalian ribosome-sec61 complex to 3.4 Å resolution.                             | EMD-2650       | 3.4           |
| 3j7y  | 2014         | Large ribosome                                   | Brown et al.        | Structure of the large ribosomal subunit from human mitochondria.                                 | EMD-2762       | 3.4           |
| 4v19  | 2014         | Mitoribosome                                     | Greber et al.       | The Complete Structure of the Large Subunit of the Mammalian Mitochondrial Ribosome                | EMD-2787       | 3.4           |
| 5flm  | 2015         | Pol II elongation complex                        | Bernecky et al.     | Structure of Transcribing Mammalian RNA Polymerase II                                             | EMD-3218       | 3.4           |
| 5lkh  | 2016         | TcdA1                                            | Gatsogiannis et al. | Membrane insertion of a Tc toxin in near-atomic detail.                                            | EMD-4068       | 3.5           |
| 3j26  | 2012         | Virophage                                        | Zhang et al.        | Structure of Sputnik, a virophage, at 3.5- Å resolution.                                          | EMD-5495       | 3.5           |
| 3j9g  | 2015         | VipA                                             | Kudryashev et al.   | Structure of the Type VI Secretion System Contractile Sheath.                                    | EMD-2699       | 3.5           |
| 5a0q  | 2015         | 20S Proteasome                                   | Da Fonseca et al.   | Cryo-Em Reveals the Conformation of a Substrate Analogue in the Human 20S Proteasome Core.        | EMD-2981       | 3.5           |
| 5aj0  | 2015         | Native polysomes                                 | Behrmann et al.     | Structural Snapshots of Actively Translating Human Ribosomes                                      | EMD-2875       | 3.5           |
| 5gjr  | 2016         | 26S proteasome                                   | Huang et al.        | An atomic structure of the human 26S proteasome                                                    | EMD-9511       | 3.5           |
| 3iyn  | 2010         | Adenovirus type 5                                | Liu et al.          | Atomic structure of human adenovirus by cryo-EM reveals interactions among protein networks        | EMD-5172       | 3.6           |
| 3j92  | 2014         | Ribosome quality control complex                 | Shao et al.         | Structure and Assembly Pathway of the Ribosome Quality Control Complex.                          | EMD-2832       | 3.6           |
| 3ja1  | 2015         | 70S-P-tRNA-E-tRNA complex                        | Li et al.           | Activation of GTP hydrolysis in mRNA-tRNA translocation by elongation factor G.                   | EMD-6315       | 3.6           |
| 3ja7  | 2015         | Portal protein gp20                              | Sun et al.          | Cryo-EM structure of the bacteriophage T4 portal protein assembly at near-atomic resolution.       | EMD-6324       | 3.6           |
| 3jb9  | 2015         | Spliceosome                                      | Yan et al.          | Structure of a yeast spliceosome at 3.6- Å resolution                                             | EMD-6413       | 3.6           |
| 4ui9  | 2015         | Anaphase-promoting complex subunit 1             | Chang et al.        | Atomic Structure of the Apc and its Mechanism of Protein Ubiquitination                           | EMD-2924       | 3.6           |
| Code  | Deposit date | Protein/substructure                      | Authors          | Publication Title                                                                 | Main EMD entry | Resolution (Å) | Authors/Reference                      |
|-------|--------------|-------------------------------------------|------------------|-----------------------------------------------------------------------------------|----------------|----------------|----------------------------------------|
| 5aj3  | 2015         | 28S mitoribosome                          | Greber et al.    | Ribosome. The Complete Structure of the 55S Mammalian Mitochondrial Ribosome.     | EMD-2913       | 3.6            | (Greber et al., 2015)                  |
| 5fmg  | 2015         | 20S proteasome                            | Li et al.        | Structure and Function Based Design of Plasmodium-Selective Proteasome Inhibitors | EMD-3231       | 3.6            | (Li et al., 2016)                      |
| 5kcr  | 2016         | 70S ribosome                              | Arenz et al.     | Structures of the orthosomycin antibiotics avilamycin and evernimicin in complex with the bacterial 70S ribosome. | EMD-8237       | 3.6            | (Arenz et al., 2016)                  |
| 3jai  | 2015         | 80S ribosome-nascent chain complex        | Brown et al.     | Structural basis for stop codon recognition in eukaryotes.                       | EMD-3040       | 3.7            | (Brown et al., 2015)                  |
| 5gad  | 2015         | Ribosome-nascent chain complex             | Jomaa et al.     | Structures of the E. coli translating ribosome with SRP and its receptor and with the translocon. | EMD-8000       | 3.7            | (Jomaa et al., 2016)                  |
| 5gan  | 2015         | Spliceosome                               | Nguyen et al.    | Cryo-EM structure of the yeast U4/U6.U5 tri-snRNP at 3.7 Å resolution.            | EMD-8012       | 3.7            | (Nguyen et al., 2016)                 |
| 3j8h  | 2014         | Ryanodine receptor 1                      | Yan et al.       | Structure of the rabbit ryanodine receptor RyR1 at near-atomic resolution.        | EMD-2807       | 3.8            | (Yan et al., 2015b)                   |
| 3ja8  | 2015         | Minichromosome maintenance complex2       | Li et al.        | Structure of the eukaryotic MCM complex at 3.8 Å                                 | EMD-6338       | 3.8            | (Li et al., 2015a)                    |
| 3jcm  | 2015         | Spliceosome                               | Wan et al.       | The 3.8 Å structure of the U4/U6.U5 tri-snRNP: Insights into spliceosome assembly and catalysis | EMD-6561       | 3.8            | (Wan et al., 2016)                    |
| 4v7q  | 2010         | Rotavirus particle                        | Settembre et al. | Atomic model of an infectious rotavirus particle.                                | EMD-5199       | 3.8            | (Settembre et al., 2011)             |
| 5imq  | 2016         | Ribosome-eF4 complex                      | Kumar et al.     | Structure of the GTP Form of Elongation Factor 4 (EF4) Bound to the Ribosome       | EMD-6584       | 3.8            | (Kumar et al., 2016)                  |
| 5ipk  | 2016         | Adeno-associated virus-2                  | Drouin et al.    | 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 et al., 2016)                |
| 3j9q  | 2015         | Pyocin                                    | Ge et al.        | Atomic structures of a bactericidal contractile nanotube in its pre- and postcontraction states. | EMD-6270       | 3.5            | (Ge et al., 2015)                     |
| 3j9w  | 2015         | MitM-ribosome complex                      | Sohmen et al.    | Structure of the Bacillus subtilis 70S ribosome reveals the basis for species-specific stalling. | EMD-6306       | 3.9            | (Sohmen et al., 2015)                |
| 5fj8  | 2015         | RNA polymerase III elongation complex     | Hoffmann et al.  | Molecular Structures of Unbound and Transcribing RNA Polymerase III.              | EMD-3178       | 3.9            | (Hoffmann et al., 2015)              |
| Code  | Deposit date | Protein/substructure                      | Authors                | Publication Title                                                                                                                                                                                                 | Main EMD entry | Resolution (Å) |
|-------|--------------|-------------------------------------------|------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|----------------|
| 5jzh  | 2016         | Aerolysin                                 | Iacovache et al.       | Cryo-EM structure of aerolysin variants reveals a novel protein fold and the pore-formation process.                                                                                                          | EMD-8185       | 3.9            |
| N/A   | 2016         | 26S proteasome                            | Schweitzer et al.      | 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            |
| 3j81  | 2014         | 48S preinitiation complex                 | Hussain et al.         | Structural changes enable start codon recognition by the eukaryotic translation initiation complex.                                                                                                                                                                        | EMD-2763       | 4.0            |
| 3jc1  | 2015         | IST1NTD-CHMP1B assembly                   | McCullough et al.      | Structure and membrane remodeling activity of ESCRT-III helical polymers.                                                                                                                                       | EMD-6461       | 4.0            | (McCullough et al., 2014) |
| 5kyh  | 2016         | Iho670 filament                           | Braun et al.           | Archaeal flagellin combines a bacterial type IV pilin domain with an Ig-like domain.                                                                                                                            | EMD-8298       | 4.0            | (Braun et al., 2016) |
| 5iv5  | 2016         | T4 baseplate-tail tube complex            | Taylor et al.          | Atomic structure of bacteriophage T4 baseplate and its function in triggering sheath contraction.                                                                                                               | EMD-3374       | 4.1            | (Taylor et al., 2016) |
| 3j94  | 2015         | SNARE complex                             | Zhao et al.            | Mechanistic insights into the recycling machine of the SNARE complex.                                                                                                                                          | EMD-6204       | 4.2            | (Zhao et al., 2015b) |
| 4v8y  | 2013         | 80S-eIF5B-Met-tnRNAMet eukaryotic translation complex | Fernandez et al.      | Molecular architecture of the 80S-eIF5B-Met-tnRNAMet Eukaryotic Translation Initiation Complex.                                                                                                              | EMD-2421       | 4.3            | (Fernandez et al., 2013) |
| 5gaf  | 2015         | SRP-ribosome nascent chain complex        | Jomaa et al.           | Structures of the E. coli translating ribosome with SRP and its receptor and with the translocon.                                                                                                               | EMD-8002       | 4.3            | (Jomaa et al., 2016) |
| 5fwy  | 2016         | Pol II transcription initiation complex   | Plaschka et al.        | Transcription Initiation Complex Structures Elucidate DNA Opening.                                                                                                                                              | EMD-3378       | 4.4            | (Plaschka et al., 2016) |
| 4btg  | 2013         | Bacteriophage phi6 P1247 procapsid        | Nemecek et al.         | Subunit Folds and Maturation Pathway of dsRNA Virus Capsid.                                                                                                                                                   | EMD-2364       | 4.4            | (Nemecek et al., 2013) |
| 3j31  | 2013         | Sulfolobus Turreted Virus                 | Veesler et al.         | Atomic structure of the 75 mDa extremophile Sulfolobus turreted icosahedral virus determined by CryoEM and X-ray crystallography.                                                                                 | EMD-5584       | 4.5            | (Veesler et al., 2013) |
| 3j32  | 2013         | Hemocyanin isoform 1                      | Zhang et al.           | Cryo-EM structure of a molluscan hemocyanin suggests its allosteric mechanism.                                                                                                                                  | EMD-5586       | 4.5            | (Zhang et al., 2013b) |
| 3zif  | 2013         | Adenovirus type 3                         | Cheng et al.           | Cryo-Em Structures of Two Bovine Adenovirus Type 3 Intermediates.                                                                                                                                              | EMD-2273       | 4.5            | (Cheng et al., 2014) |
| 3jcn  | 2015         | 70S ribosomes-IF2 complex                 | Sprink et al.          | Structures of ribosome bound initiation factor 2 reveal the mechanism of subunit association.                                                                                                                  | EMD-3285       | 4.6            | (Sprink et al., 2016) |
| Code  | Deposit date | Protein/substructure                             | Authors               | Publication Title                                                                 | Main EMD entry | Resolution (Å) | Reference              |
|-------|--------------|-------------------------------------------------|-----------------------|-----------------------------------------------------------------------------------|----------------|----------------|------------------------|
| 4bml  | 2013         | Syn5 marine virus                               | Gipson *et al.*       | Proruding Knob-Like Proteins Violate Local Symmetries in an Icosahedral Marine Virus. | EMD-5954       | 4.7            | (Gipson *et al.*, 2014) |
| 3jav  | 2015         | Inositol 1,4,5-trisphosphate receptor type 1    | Fan *et al.*          | Gating machinery of InsP3R channels revealed by electron cryomicroscopy.          | EMD-6369       | 4.7            | (Fan *et al.*, 2015)   |
| 3jc7  | 2015         | CMG complex                                     | Yuan *et al.*         | Structure of the eukaryotic replicative CMG helicase suggests a pumpjack motion for translocation. | EMD-6536       | 4.8            | (Yuan *et al.*, 2016)  |
| 3j03  | 2011         | Group II chaperonin                             | Zhang *et al.*        | Mechanism of folding chamber closure in a group II chaperonin.                     | EMD-5138       | 4.8            | (Zhang *et al.*, 2010a) |
| 3j8e  | 2014         | Ryanodine receptor 1-calstabin complex           | Zalk *et al.*         | Structure of a mammalian ryanodine receptor.                                      | EMD-6106       | 4.8            | (Zalk *et al.*, 2015)  |
| 3jac  | 2015         | Piezo-type mechanosensitive ion channel component 1 | Ge *et al.*           | Architecture of the mammalian mechanosensitive Piezo1 channel                     | EMD-6343       | 4.8            | (Efremov *et al.*, 2015) |
| 3jco  | 2016         | 26S proteasome                                  | Luan *et al.*         | Structure of an endogenous yeast 26S proteasome reveals two major conformational states. | EMD-6574       | 4.8            | (Luan *et al.*, 2016)  |
| 5g5l  | 2016         | RNA polymerase I-Rrn3 complex                    | Engel *et al.*        | RNA Polymerase I-Rrn3 Complex at 4.8 Å Resolution                                  | EMD-3439       | 4.8            | (Engel *et al.*, 2013) |
| 3j1b  | 2012         | rATcpn-alpha                                    | Zhang *et al.*        | Flexible interwoven termini determine the thermal stability of thermosomes.        | EMD-5391       | 4.9            | (Zhang *et al.*, 2013a) |
| 4ce4  | 2013         | Mitochondrial ribosome 39S large subunit         | Greber *et al.*       | Architecture of the Large Subunit of the Mammalian Mitochondrial Ribosome.        | EMD-2490       | 4.9            | (Greber *et al.*, 2014b) |
| 4uq8  | 2014         | NADH ubiquinone oxidoreductase                   | Vinothkumar *et al.*  | Architecture of mammalian respiratory complex I.                                  | EMD-2676       | 5.0            | (Vinothkumar *et al.*, 2014) |
| 3j8G  | 2014         | EngA-50S subunit complex                         | Zhang *et al.*        | Structural insights into the function of a unique tandem GTPase EngA in bacterial ribosome assembly | EMD-6149       | 5.0            | (Zhang *et al.*, 2014) |
| 4v7e  | 2013         | 80S ribosome                                    | Armache *et al.*      | Localization of eukaryote-specific ribosomal proteins in a 5.5-A cryo-EM map of the 80S eukaryotic ribosome. | EMD-1780       | 5.5            | (Armache *et al.*, 2010) |
| 4v8m  | 2012         | 80S ribosome                                    | Hashem *et al.*       | High-resolution cryo-electron microscopy structure of the Trypanosoma brucei ribosome. | EMD-2239       | 5.6            | (Hashem *et al.*, 2013) |
| 5kne  | 2016         | Heat shock protein 104                          | Yokom *et al.*        | Spiral architecture of the Hsp104 disaggregase reveals the basis for polypeptide translocation. | EMD-8267       | 5.6            | (Yokom *et al.*, 2016) |
| 5k0y  | 2016         | m48S late-stage initiation complex              | Simonetti *et al.*    | eIF3 peripheral subunits rearrangement after mRNA binding and start-codon recognition. | EMD-8190       | 5.8            | (Simonetti *et al.*, 2016) |
| Code  | Deposit date | Protein/substructure | Authors                  | Publication Title                                                                 | Main EMD entry | Resolution (Å) | Reference                              |
|-------|--------------|----------------------|--------------------------|-----------------------------------------------------------------------------------|----------------|----------------|----------------------------------------|
| 5flc  | 2015         | mTOR complex I       | Aylett et al.            | Architecture of human mTor complex 1                                              | EMD-3213       | 5.9            | (Aylett et al., 2016)                  |
| 4aod  | 2012         | Acetylcholine binding protein | Saur et al.          | Acetylcholine-binding protein in the hemolymph of the planorbid snail Biomphalaria glabrata is a pentagonal dodecahedron (60 subunits) | EMD-2055       | 6.0            | (Saur et al., 2012)                   |
| 4cct  | 2012         | Dengue virus         | Kostyuchenko et al.     | Immature and mature Dengue serotype 1 virus structures provide insight into the maturation process. | EMD-2142       | 6.0            | (Kostyuchenko et al., 2013)            |
| 4c2i  | 2013         | Dengue virus with Fab fragment | Fibriansah et al.     | A potent anti-Dengue human antibody preferentially recognizes the conformation of E protein monomers assembled on the virus surface. | EMD-2442       | 6.0            | (Fibriansah et al., 2014)              |
| 5a5t  | 2015         | eIF3 octamer core    | Des Georges et al.      | Structure of mammalian Eif3 in the context of the 43S preinitiation complex.      | EMD-3056       | 6.0            | (des Georges A. et al., 2015)          |
| 3j6y  | 2014         | 80S ribosome         | Koh et al.              | Taura syndrome virus IRES initiates translation by binding its tRNA-mRNA-like structural element in the ribosomal decoding center. | EMD-5943       | 6.1            | (Koh et al., 2014)                    |
| 5fvm  | 2016         | Tor1-Lst8 complex    | Baretic et al.          | Tor Forms a Dimer Through an N-Terminal Helical Solenoid with a Complex Topology   | EMD-3329       | 6.1            | (Baretic et al., 2016)                 |
| 3z1l  | 2010         | Group II chaperonin  | Douglas et al.          | Dual action of ATP hydrolysis couples lid closure to substrate release into the group II chaperonin chamber. | EMD-5248       | 6.2            | (Douglas et al., 2011)                 |
| N/A   | 2014         | Microtubule          | Alushin et al.          | High-resolution microtubule structures reveal the structural transitions in alpha beta-tubulin upon GTP hydrolysis. | EMD-5899       | 6.3            | (Alushin et al., 2014)                 |
| 2y9j  | 2011         | Needle complex       | Schraidt & Marlovits    | Three-Dimensional Model of Salmonella’S Needle Complex at Subnanometer Resolution. | EMD-1874       | 6.4            | (Schraidt & Marlovits2011)            |
| 4uer  | 2014         | 40S-eIF1-eIF1A-eIF3J initiation complex | Aylett et al.  | Structure of a Yeast 40S-Eif1-Eif1A-Eif3J Initiation Complex                      | EMD-2845       | 6.5            | (Aylett et al., 2015)                  |
| 5jyg  | 2016         | Magnetosome-associated MamK filament | Bergeron et al.     | Structure of the Magnetosome-associated actin-like MamK filament at sub-nanometer resolution. | EMD-8180       | 6.5            | (Bergeron et al., 2016)               |
| 3j15  | 2012         | 70S ribosome         | Becker et al.           | Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. | EMD-2009       | 6.6            | (Becker et al., 2012)                 |
| 5fmw  | 2015         | C9                   | Dudkina et al.          | Structure of the Poly-C9 Component of the Complement Membrane Attack Complex        | EMD-3235       | 6.7            | (Dudkina et al., 2016)                |
| Code | Deposit date | Protein/substructure | Authors | Publication Title | Main EMD entry | Resolution (Å) |
|------|--------------|----------------------|---------|-------------------|----------------|---------------|
| 4v4l | 2010         | Apoptosome           | Yuan et al. | Structure of the Drosophila apoptosome at 6.9 Å resolution | EMD-5235 | 6.9 (Yuan et al., 2011) |
| 511m | 2016         | V ATPase             | Schep et al. | Unpublished | EMD-8070 | - |
| 3iyk | 2010         | Bluetongue virus     | Zhang et al. | Bluetongue virus coat protein VP2 contains sialic acid-binding domains, and VP5 resembles enveloped virus fusion proteins. | EMD-5147 | 7.0 (Zhang et al., 2010b) |
| 3jcr | 2016         | U4/U6.U5 tri-snRNP   | Agafonov et al. | Molecular architecture of the human U4/U6.U5 tri-snRNP. | EMD-6581 | 7.0 (Agafonov et al., 2016) |
| 4v6m | 2011         | SecYEG complex       | Frauenfeld et al. | Cryo-EM structure of the ribosome-SecYE complex in the membrane environment. | EMD-1858 | 7.1 (Frauenfeld et al., 2011) |
| 5jpq | 2016         | Ribo-nucleoprotein complex | Kornprobst et al. | Architecture of the 90S Pre-ribosome: A Structural View on the Birth of the Eukaryotic Ribosome. | EMD-8143 | 7.3 (Kornprobst et al., 2016) |
| 5kk2 | 2016         | GluA2 AMPA receptor - TARP complex | Zhao et al. | Architecture of fully occupied GluA2 AMPA receptor-TARP complex elucidated by cryo-EM. | EMD-8256 | 7.3 (Zhao et al., 2016) |
| 4v8l | 2012         | Fatty acid synthase 1 | Boehringer et al. | 7.5- A Cryo-Em Structure of the Mycobacterial Fatty Acid Synthase. | EMD-2238 | 7.5 (Boehringer et al., 2013) |
| 4cr2 | 2014         | 26S Proteasome       | Unverdorben et al. | Deep Classification of a Large Cryo-Em Dataset Defines the Conformational Landscape of the 26S Proteasome. | EMD-2594 | 7.7 (Unverdorben et al., 2014) |
| 5a9e | 2015         | Rous-Sarcoma Virus Gag particles | Schur et al. | 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 et al., 2015) |
| 4v1n | 2014         | cITC                 | Plaschka et al. | Architecture of the RNA Polymerase II-Mediator Core Initiation Complex. | EMD-2785 | 7.8 (Plaschka et al., 2015) |
| 3j02 | 2011         | group II chaperonin  | Zhang et al. | Cryo-EM structure of a group II chaperonin in the prehydrolysis ATP-bound state leading to lid closure. | EMD-5258 | 8.0 (Zhang et al., 2011) |
| 4v8t | 2012         | 60S ribosomal subunit-Arx1 and Rei1complex | Greber et al. | Cryo-Em Structures of Arx1 and Maturation Factors Rei1 and Jji1 Bound to the 60S Ribosomal Subunit | EMD-2169 | 8.1 (Greber et al., 2012) |
| 4v93 | 2014         | Hemoglobin           | Chen et al. | Structural Basis for Cooperative Oxygen Binding and Bracelet-Assisted Assembly of Lumbricus Terrestris Hemoglobin. | EMD-2627 | 8.1 (Chen et al., 2015) |
| 4bip | 2013         | Coxsackievirus       | Seitsonen et al. | Structural analysis of coxsackievirus A7 reveals conformational changes associated with uncoating. | EMD-2028 | 8.2 (Seitsonen et al., 2012) |
| 3j9v | 2015         | V-ATPase             | Zhao et al. | Electron cryomicroscopy observation of rotational states in a eukaryotic V-ATPase. | EMD-6286 | 8.3 (Zhao et al., 2015a) |
| Code   | Deposit date | Protein/substructure          | Authors                  | Publication Title                                                                 | Main EMD entry | Resolution (Å) | Reference                                |
|--------|--------------|-------------------------------|--------------------------|-----------------------------------------------------------------------------------|----------------|----------------|------------------------------------------|
| 4v6k   | 2011         | 70S-TC complex                | Agirrezabala et al.      | Structural insights into cognate versus near-cognate discrimination during decoding.| EMD-1849       | 8.3            | (Agirrezabala et al., 2011)             |
| 3j1e   | 2012         | rATcpn-beta                   | Zhang et al.             | Flexible interwoven termini determine the thermal stability of thermosomes.        | EMD-5395       | 8.3            | (Zhang et al., 2013a)                   |
| 2ynj   | 2012         | GroEL                         | Bartesaghi et al.        | Protein Secondary Structure Determination by Constrained Single-Particle Cryo-Electron Tomography | EMD-2221       | 8.4            | (Bartesaghi et al., 2012)              |
| 3zbi   | 2012         | traN/traO/traF complex         | Rivera-Calzada et al.    | Structure of a Bacterial Type Iv Secretion Core Complex at Subnanometre Resolution.| EMD-2233       | 8.5            | (Rivera-Calzada et al., 2013)          |
| 5fur   | 2016         | TFIID-TFIIA complex           | Louder et al.            | Structure of Promoter-Bound TFIID and Model of Human Pre-Initiation Complex Assembly.| EMD-3305       | 8.7            | (Louder et al., 2016)                  |
| 3j34   | 2013         | HIV-1 capsid                  | Zhao et al.              | Mature HIV-1 capsid structure by cryo-electron microscopy and all-atom molecular dynamics. | EMD-5582       | 8.6            | (Zhao et al., 2013)                    |
| 4v7f   | 2013         | 5S ribonucleoprotein particle | Leidig et al.            | 60S ribosome biogenesis requires rotation of the 5S ribonucleoprotein particle.    | EMD-2528       | 8.7            | (Leidig et al., 2014)                  |
| 4v6i   | 2010         | 80S ribosome- Ssh1 complex    | Becker et al.            | Structure of monomeric yeast and mammalian Sec61 complexes interacting with the translating ribosome. | EMD-1669       | 8.8            | (Becker et al., 2009)                  |
| 3j0s   | 2011         | Actin, cytoplasmic 1          | Galkin et al.            | Remodeling of actin filaments by ADF/cofilin proteins.                            | EMD-5354       | 9.0            | (Galkin et al., 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 et al.             | 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 et al., 2015)                    |
| 4v4n   | 2013         | 70S ribosome-SecYEbeta complex | Park et al.             | Structure of the SecY channel during initiation of protein translocation.          | EMD-5691       | 9.0            | (Park et al., 2014)                    |
| 3j3r   | 2013         | MecA-ClpC                     | Liu et al.               | Structural dynamics of the MecA-ClpC complex: a type II AAA+ protein unfolding machine | EMD-5610       | 9.4            | (Liu et al., 2013)                     |
| 3j2t   | 2012         | Apoptosome                    | Yuan et al.              | Structure of an apoptosome-procaspase-9 CARD complex                               | EMD-5186       | 9.5            | (Yuan et al., 2010)                    |
| 5fl8   | 2015         | Pre-60S ribosomal particle    | Barrio-Garcia et al.     | Architecture of the Rix1-Real checkpoint machinery during pre-60S-ribosome remodeling. | EMD-3199       | 9.5            | (Barrio-Garcia et al., 2016)           |
| Code | Deposit date | Protein/substructure | Authors | Publication Title | Main EMD entry | Resolution (Å) |
|------|--------------|----------------------|---------|-------------------|----------------|----------------|
| 4v6v | 2013         | 70S-Tet(O)           | Li et al. | Mechanism of tetracycline resistance by ribosomal protection protein Tet(O). | EMD-5562 | 9.8 | (Li et al., 2013a) |
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