

Table S1 | EMRinger analysis of selected maps above 5 Å resolution with atomic models. For the transmembrane-only scan of the TrpV1 Channel (EMDB 5778), residues 381-695 of each chain of the deposited model (PDB 3J5P) were used. For EMDB 2787, the two deposited half-models (PDB 4V19, 4V1A) were combined and run as a single model. The top scoring maps have scores above 3.0: the T20S proteasome, which used a crystallographic model with minimal refinement with MDFF¹, and the hepatitis B viral capsid, which was built *de novo* and refined using real space refinement in Phenix². Both maps are consistently better than 3.5 Å local resolution³, likely reflecting the underlying rigidity of the complexes. Recent mammalian ribosome structures^{4,5}, which are dynamic and have more variability in resolution, used masking to reconstruct the highest resolution regions. Refmac reciprocal-space refinement of *de novo* atomic models of these components results in EMRinger scores above 1.85⁶.

<i>EMDB ID</i>	<i>PDB ID</i>	<i>Resolution (Å)</i>	<i>Scannable Model Length</i>	<i>EMRinger Score</i>	<i>Description</i>	<i>Year</i>
5256	3IZX	3.1	2427	1.54	Cytoplasmic Polyhedrosis Virus ⁷	2012
5995	3J7H	3.2	2616	2.04	Beta-Galactosidase ⁸	2014
5160	3IYL	3.2	5708	2.18	Aquareovirus ⁹	2010
5623	3J9I	3.2	3439	3.05	T20S Proteasome ¹	2013
5778	3J5P	3.27	1484	0.56	TrpV1 Channel ¹⁰	2014
5778 (TM only)	3J5P	3.27	792	1.17	TrpV1 Channel ¹⁰	2014
5778 (Refined)	3J9J	3.27	876	2.58	TrpV1 Channel	2015
2513	4CIO	3.36	521	1.29	F420 reducing hydrogenase ¹¹	2013
2787	4V19, 4V1A	3.4	5326	1.85	Mammalian Mitochondrial Ribosome, Large Subunit ⁵	2014
2762	3J7Y	3.4	4806	2.09	Human Mitochondrial Ribosome Large	2014

					Subunit ⁴	
6035	3J7W	3.5	1267	0.96	Bacteriophage T7 capsid ¹²	2014
5764	3J4U	3.5	1757	1.95	Bordetella bacteriophage ¹³	2014
2278	3J2V	3.5	366	3.26	Hepatitis B Virus Core ²	2013
5925	3J6J	3.6	528	1.23	MAVS filament ²	2014
2764	3J80	3.75	3060	0.9	40S-eIF1-eIF1A preinitiation complex ¹⁴	2014
2773	4UY8	3.8	1976	0.36	TnaC stalled E.coli ribosome ¹⁵	2014
5830	3J63	3.8	915	1.05	ASC Pyrin Domain ¹⁶	2014
6000	3J7L	3.8	259	2.08	Brome Mosaic Virus ¹⁷	2014
2763	3J81	4	3225	0.54	Partial Yeast 48S preinitiation complex ¹⁴	2014
5600	3J3I	4.1	604	0.18	Penicillium Chrysogenum Virus ¹⁸	2014
2364	4BTG	4.4	898	-0.47	Bacteriophage phi procapsid ¹⁹	2013
2677	4UPC	4.5	235	-0.41	Human Gamma-secretase ²⁰	2014
2273	3ZIF	4.5	7430	0.13	Bovine Adenovirus 3 ²¹	2014
5678	3J40	4.5	1848	0.49	Bacteriophage epsilon15 ²²	2013
5645	3J3X	4.6	4528	-0.05	Mm Chaperonin, Training ²³	2013
5895	3J6E	4.7	4705	0.09	GMPCPP Microtubule ²⁴	2014
5646	3J3X	4.7	4528	0.55	Mm Chaperonin, Testing ²³	2013
2788	4V1W	4.7	2976	1.27	Horse spleen apoferritin ²⁵	2014
5391	3J1B	4.9	4816	0.2	apo rATcpn-alpha ²⁶	2013

6187	3J8X	5	737	-0.71	Empty Microtubule/Kinesin ²⁷	2014
6188	3J8Y	5	744	-0.16	ADP-AIF3 Microtubule/Kinesin ²⁷	2014
5896	3J6F	5	4706	0.06	GDP microtubule ²⁴	2014
5886	3J69	5	579	0.8	nanobody/poliovirus ²⁸	2014

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