

Use Case	Complex & potential functional annotation	Members	Current annotation
Catalytic activity entirely within a subunit	nuclear exosome (RNase complex) - (GO:0000176); function: 3'-5'-exoribonuclease activity (GO:0000175) - IDA; MAYBE? function: endoribonuclease activity (GO:0004521) - IDA, IMP The issue for us is that we found that, although the authors clearly demonstrated this function for DIS3, they did not actually demonstrate that DIS3 had this function WHILE part of the exosome (though the authors assume so). Also completely unclear weather this is specific for the cytoplasmic or nuclear exosome.	DIS3 (aka RRP44) RRP6 CSL4 RRP4 RRP40 SK16 (aka RRP41) RRP46 MTR3 RRP42 RRP43 RRP45 MPP6 LRP1	3'-5'-exoribonuclease activity (GO:0000175) - IDA, IMP; endoribonuclease activity (GO:0004521) - IDA, IMP 3'-5'-exoribonuclease activity (GO:0000175) -IDA molecular_function unknown molecular_function unknown other (manganese binding and RNA binding) molecular_function unknown molecular_function unknown molecular_function unknown molecular_function unknown other (poly(U) RNA binding) other (ds DNA binding, ds RNA binding)
Catalytic activity not demonstrated for single subunit, but some subunits proven to be dispensable	DNA-directed RNA polymerase II, core complex; function: DNA-directed RNA polymerase activity (GO:0003899) - IDA; MAYBE? DNA binding? RNA binding? One would think that this would be considered part of DNA-directed RNA polymerase activity (the same way that ATP binding is part of ATPase activity)	RP021 (aka RPB1) RPB2 RPB3 RPB4 RPB5 RPO26 (aka RPB6) RPB7 RPB8 RPB9 RPB10 RPB11 RPC10 (aka RPB12)	contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA Other (contributes_to DNA binding, contributes_to RNA binding) - IDA contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA Other (DNA binding, RNA binding) - IDA, IMP contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA molecular_function unknown contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA contributes_to DNA-directed RNA polymerase activity (GO:0003899) - IDA
Catalytic activity known to be distributed between subunits; no single polypeptide capable of activity on its own	ALL children of proton-transporting ATP synthase complex, catalytic core F(1) (GO:275) or just the "catalytic core" which doesn't form a functional complex by itself; function: hydrogen ion transporting ATP synthase activity, rotational mechanism (GO:46933) mitochondrial proton-transporting ATP synthase, catalytic core (GO:5754) mitochondrial proton-transporting ATP synthase, central stalk (GO:5756)	ATP1 ATP2 ATP3 ATP16 ATP15	contributes_to hydrogen ion transporting ATP synthase activity, rotational mechanism (IDA, IMP, ISS) contributes_to hydrogen ion transporting ATP synthase activity, rotational mechanism- IDA, IMP, ISS contributes_to hydrogen ion transporting ATP synthase activity, rotational mechanism (IDA, IMP, ISS) contributes_to hydrogen ion transporting ATP synthase activity, rotational mechanism- IDA, IMP, ISS contributes_to hydrogen ion transporting ATP synthase activity, rotational mechanism (IDA, IMP, ISS)
catalytic activity directly demonstrated for entire complex, but predicted for specific subunits	tRNA-intron endonuclease complex (GO:0000214); function: GO term: tRNA-intron endonuclease activity, Molecular Function (GO:0000213)	SEN2 SEN34 SEN15 SEN54	tRNA-intron endonuclease activity - IMP, IDA tRNA-intron endonuclease activity - IMP, IDA contributes_to: tRNA-intron endonuclease activity - IDA contributes_to: tRNA-intron endonuclease activity - IDA
catalytic activity optimal with both	ubiquitin ligase complex (GO:0000151); function: ubiquitin-protein ligase activity (GO:0004842)	SLX5 SLX8	contributes_to ubiquitin-protein ligase activity - IDA SLX5 (aka HEX3) and SLX8 together constitute a SUMO-targeted ubiquitin ligase complex. Both subunits together have the Ub ligase activity (PMID: 17848550 and 18032921), but alone have either weak (as reported in PMID: 17848550), or no activity (as reported in PMID: 18032921). The best paper to illustrate this would be PMID:18032921. I think here the 'contributes to' qualifier works well, perhaps better an ICM annotation. However, I think generally speaking that the ICM code might be better for multi-subunit complexes than for small complexes? contributes_to ubiquitin-protein ligase activity - IDA; (direct) ubiquitin-protein ligase activity IDA