Phyre2

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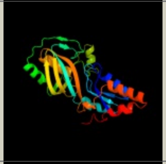
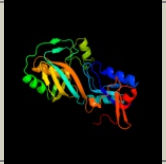
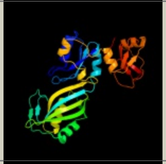
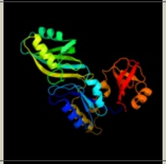
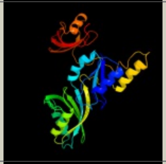
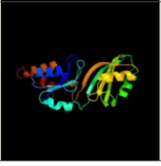
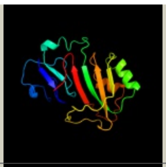
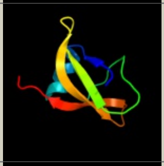
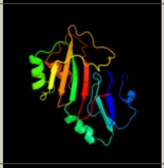
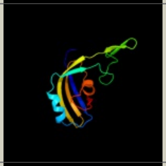
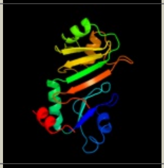
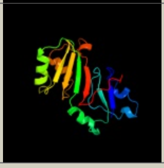
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1k8wA_	Alignment		100.0	100	**PDB header:**lyase/rna **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** crystal structure of the e. coli pseudouridine synthase2 trub bound to a t stem-loop rna
2	d1k8wa5	Alignment		100.0	100	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
3	d1r3ea2	Alignment		100.0	33	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
4	c1sgvA_	Alignment		100.0	32	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** structure of trna psi55 pseudouridine synthase (trub)
5	c2ey4A_	Alignment		100.0	29	**PDB header:**isomerase/biosynthetic protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of a cbf5-nop10-gar1 complex
6	c3uaiA_	Alignment		100.0	28	**PDB header:**isomerase/chaperone **Chain:** A: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
7	c2apoA_	Alignment		100.0	31	**PDB header:**isomerase/rna binding protein **Chain:** A: **PDB Molecule:**probable trna pseudouridine synthase b; **PDBTitle:** crystal structure of the methanococcus jannaschii cbf52 nop10 complex
8	d2ey4a2	Alignment		100.0	32	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
9	d1sgva2	Alignment		100.0	37	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
10	c1ze2B_	Alignment		100.0	29	**PDB header:**lyase/rna **Chain:** B: **PDB Molecule:**trna pseudouridine synthase b; **PDBTitle:** conformational change of pseudouridine 55 synthase upon its2 association with rna substrate
11	d2apoa2	Alignment		100.0	32	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB

12	c2omlA_	Alignment		99.2	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
13	d1k8wa3	Alignment		99.1	100	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
14	c2olwB_	Alignment		98.9	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribosomal large subunit pseudouridine synthase e; **PDBTitle:** crystal structure of e. coli pseudouridine synthase rlue
15	c2v9kA_	Alignment		98.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein flj32312; **PDBTitle:** crystal structure of human pus10, a novel pseudouridine2 synthase.
16	d1vioa1	Alignment		98.2	23	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
17	c2gmlA_	Alignment		98.1	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of catalytic domain of e.coli rluf
18	c3dh3C_	Alignment		98.1	18	**PDB header:**isomerase/rna **Chain:** C: **PDB Molecule:**ribosomal large subunit pseudouridine synthase f; **PDBTitle:** crystal structure of rluf in complex with a 22 nucleotide2 rna substrate
19	d1kska4	Alignment		98.0	19	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
20	c1vioA_	Alignment		97.7	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridylate synthase
21	d1v9ka_	Alignment	not modelled	97.5	20	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
22	c3zv0D_	Alignment	not modelled	97.5	19	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**h/aca ribonucleoprotein complex subunit 4; **PDBTitle:** structure of the shq1p-cbf5p complex
23	c2i82D_	Alignment	not modelled	97.4	17	**PDB header:**lyase/rna **Chain:** D: **PDB Molecule:**ribosomal large subunit pseudouridine synthase a; **PDBTitle:** crystal structure of pseudouridine synthase rlua: indirect2 sequence readout through protein-induced rna structure
24	c1kskA_	Alignment	not modelled	97.3	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal small subunit pseudouridine synthase a; **PDBTitle:** structure of rsua
25	c1qyuA_	Alignment	not modelled	97.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** structure of the catalytic domain of 23s rrna pseudouridine2 synthase rlud
26	d1v9fa_	Alignment	not modelled	97.3	23	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase RsuA/RluD
27	c1v9fA_	Alignment	not modelled	97.3	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ribosomal large subunit pseudouridine synthase d; **PDBTitle:** crystal structure of catalytic domain of pseudouridine2 synthase rlud from escherichia coli
						Fold:PUA domain-like

28	d2apoa1	Alignment	not modelled	95.5	23	**Superfamily:**PUA domain-like **Family:**PUA domain
29	d1r3ea1	Alignment	not modelled	93.5	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
30	d2ey4a1	Alignment	not modelled	93.1	13	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
31	d1sgva1	Alignment	not modelled	90.2	18	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
32	c1q7hA_	Alignment	not modelled	75.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of a conserved pua domain protein from thermoplasma2 acidophilum
33	c3d79A_	Alignment	not modelled	74.1	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0734; **PDBTitle:** crystal structure of hypothetical protein ph0734.1 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
34	d1iq8a3	Alignment	not modelled	73.3	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
35	d2as0a1	Alignment	not modelled	68.7	21	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
36	c1sb7A_	Alignment	not modelled	67.7	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**trna pseudouridine synthase d; **PDBTitle:** crystal structure of the e.coli pseudouridine synthase trud
37	d1szwa_	Alignment	not modelled	67.5	10	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**tRNA pseudouridine synthase TruD
38	d2b78a1	Alignment	not modelled	59.6	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical RNA methyltransferase domain (HRMD)
39	c2b78A_	Alignment	not modelled	57.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein smu.776; **PDBTitle:** a putative sam-dependent methyltransferase from2 streptococcus mutans
40	d1q7ha1	Alignment	not modelled	54.4	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
41	c3r90E_	Alignment	not modelled	50.6	11	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**malignant t cell-amplified sequence 1; **PDBTitle:** crystal structure of malignant t cell-amplified sequence 1 protein
42	c1zs7A_	Alignment	not modelled	44.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ape0525; **PDBTitle:** the structure of gene product ape0525 from aeropyrum pernix
43	c2gagC_	Alignment	not modelled	37.2	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**heterotetrameric sarcosine oxidase gamma-subunit; **PDBTitle:** heteroteterameric sarcosine: structure of a diflavin metaloenzyme at2 1.85 a resolution
44	c2frxD_	Alignment	not modelled	35.0	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypothetical protein yebu; **PDBTitle:** crystal structure of yebu, a m5c rna methyltransferase from e.coli
45	c3m4xA_	Alignment	not modelled	34.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
46	c2xzmW_	Alignment	not modelled	34.4	23	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**40s ribosomal protein s4; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
47	c2hjgA_	Alignment	not modelled	29.6	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein enga; **PDBTitle:** the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp
48	d2a2pa1	Alignment	not modelled	28.4	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
49	d2jn9a1	Alignment	not modelled	28.2	9	**Fold:**Split barrel-like **Superfamily:**YkvR-like **Family:**YkvR-like
50	d1o7qa_	Alignment	not modelled	24.8	21	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**alpha-1,3-galactosyltransferase-like
51	d2cx1a1	Alignment	not modelled	22.1	20	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
52	d1lzia_	Alignment	not modelled	21.7	15	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**alpha-1,3-galactosyltransferase-like
53	d2gx8a1	Alignment	not modelled	21.5	17	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
54	c1z2zB_	Alignment	not modelled	18.9	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**probable trna pseudouridine synthase d; **PDBTitle:** crystal structure of the putative trna pseudouridine2

						synthase d (trud) from methanosarcina mazei, northeast3 structural genomics target mar1
55	d1mkya3	Alignment	not modelled	18.9	3	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Probable GTPase Der, C-terminal domain **Family:**Probable GTPase Der, C-terminal domain
56	c2gx8B_	Alignment	not modelled	18.3	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**nif3-related protein; **PDBTitle:** the crystal stucture of bacillus cereus protein related to nif3
57	d1k7ia2	Alignment	not modelled	16.6	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
58	c3czxA_	Alignment	not modelled	15.3	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
59	d1g9ka2	Alignment	not modelled	14.5	39	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
60	c1mkyA_	Alignment	not modelled	14.3	3	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**probable gtp-binding protein enga; **PDBTitle:** structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains
61	c3m6wA_	Alignment	not modelled	13.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
62	c3or5A_	Alignment	not modelled	13.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein, thioredoxin family **PDBTitle:** crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum tls
63	c3eykA_	Alignment	not modelled	13.2	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha1 chain; **PDBTitle:** structure of influenza haemagglutinin in complex with an2 inhibitor of membrane fusion
64	c3cmiA_	Alignment	not modelled	11.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxiredoxin hyr1; **PDBTitle:** crystal structure of glutathione-dependent phospholipid peroxidase2 hyr1 from the yeast saccharomyces cerevisiae
65	c1iq8B_	Alignment	not modelled	11.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**archaeosine trna-guanine transglycosylase; **PDBTitle:** crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
66	c2nydB_	Alignment	not modelled	11.5	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**upf0135 protein sa1388; **PDBTitle:** crystal structure of staphylococcus aureus hypothetical protein sa1388
67	d1sata2	Alignment	not modelled	11.3	33	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Serralysin-like metalloprotease, catalytic (N-terminal) domain
68	d3saka_	Alignment	not modelled	11.1	29	**Fold:**p53 tetramerization domain **Superfamily:**p53 tetramerization domain **Family:**p53 tetramerization domain
69	c2owlA_	Alignment	not modelled	10.0	12	**PDB header:**recombination **Chain:** A: **PDB Molecule:**recombination-associated protein rdgc; **PDBTitle:** crystal structure of e. coli rdgc
70	c3ne8A_	Alignment	not modelled	10.0	50	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
71	d1muga_	Alignment	not modelled	9.1	19	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Mug-like
72	c3kbgA_	Alignment	not modelled	9.0	15	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s4e; **PDBTitle:** crystal structure of the 30s ribosomal protein s4e from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar28.
73	c2d07A_	Alignment	not modelled	8.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**g/t mismatch-specific thymine dna glycosylase; **PDBTitle:** crystal structure of sumo-3-modified thymine-dna glycosylase
74	d1jwqa_	Alignment	not modelled	8.3	50	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
75	d2gy9i1	Alignment	not modelled	8.3	18	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
76	c1yp3C_	Alignment	not modelled	7.7	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucose-1-phosphate adenylyltransferase small **PDBTitle:** crystal structure of potato tuber adp-glucose2 pyrophosphorylase in complex with atp
77	c2xs4A_	Alignment	not modelled	7.4	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
78	d1xova2	Alignment	not modelled	7.3	29	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like

79	c1pk1B_	Alignment	not modelled	7.3	12	**PDB header:**transcription repression **Chain:** B: **PDB Molecule:**sex comb on midleg cg9495-pa; **PDBTitle:** hetero sam domain structure of ph and scm.
80	d1hv5a_	Alignment	not modelled	7.3	26	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
81	c1mszA_	Alignment	not modelled	7.3	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
82	d1msza_	Alignment	not modelled	7.3	21	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
83	c2vn1A_	Alignment	not modelled	7.1	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase; **PDBTitle:** crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506
84	d1cgla_	Alignment	not modelled	7.0	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
85	c3lfmA_	Alignment	not modelled	7.0	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein fto; **PDBTitle:** crystal structure of the fat mass and obesity associated (fto) protein2 reveals basis for its substrate specificity
86	d1bqqm_	Alignment	not modelled	7.0	32	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
87	d1g0da2	Alignment	not modelled	6.8	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
88	d1nmpa_	Alignment	not modelled	6.7	6	**Fold:**NIF3 (NGG1p interacting factor 3)-like **Superfamily:**NIF3 (NGG1p interacting factor 3)-like **Family:**NIF3 (NGG1p interacting factor 3)-like
89	d2fg9a1	Alignment	not modelled	6.6	19	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
90	d1s1qa_	Alignment	not modelled	6.6	18	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UEV domain
91	c3eytA_	Alignment	not modelled	6.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spoa0173; **PDBTitle:** crystal structure of thioredoxin-like superfamily protein spoa0173
92	c2e1cA_	Alignment	not modelled	6.4	16	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ph1519; **PDBTitle:** structure of putative hth-type transcriptional regulator ph1519/dna2 complex
93	d2ovxa1	Alignment	not modelled	6.2	22	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
94	d2b5xa1	Alignment	not modelled	6.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
95	c2obiA_	Alignment	not modelled	6.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phospholipid hydroperoxide glutathione **PDBTitle:** crystal structure of the selenocysteine to cysteine mutant2 of human phospholipid hydroperoxide glutathione peroxidase3 (gpx4)
96	d1nkva_	Alignment	not modelled	6.0	8	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Hypothetical Protein YjhP
97	d1r9ha_	Alignment	not modelled	5.8	16	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
98	c2l4bA_	Alignment	not modelled	5.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of a putative acyl carrier protein from anaplasma2 phagocytophilum. seattle structural genomics center for infectious3 disease target anpha.01018.a
99	c3iz6D_	Alignment	not modelled	5.7	14	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**40s ribosomal protein s4 (s4e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome