Phyre^2

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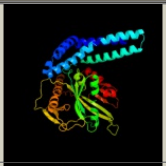
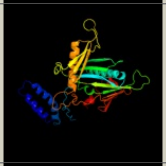
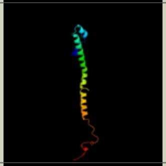
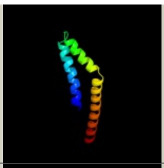
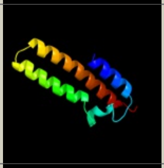
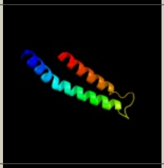
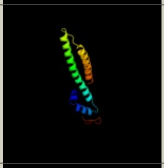
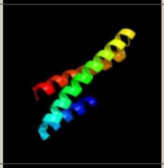
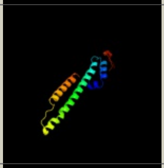
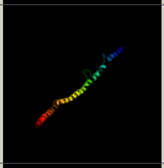
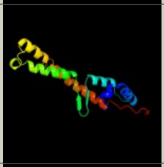
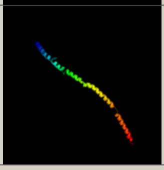
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gqea_	Alignment		100.0	97	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
2	c2ihr1_	Alignment		100.0	46	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
3	c3d5cX_	Alignment		100.0	34	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
4	d1rq0a_	Alignment		100.0	39	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
5	d2b3tb1	Alignment		100.0	43	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
6	c1zbtA_	Alignment		100.0	30	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
7	c2jvaA_	Alignment		99.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase domain protein; **PDBTitle:** nmr solution structure of peptidyl-trna hydrolase domain protein from2 pseudomonas syringae pv. tomato. northeast structural genomics3 consortium target psr211
8	c2jy9A_	Alignment		99.8	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative trna hydrolase domain; **PDBTitle:** nmr structure of putative trna hydrolase domain from2 salmonella typhimurium. northeast structural genomics3 consortium target str220
9	d1j26a_	Alignment		99.8	25	**Fold:**dsRBD-like **Superfamily:**Peptidyl-tRNA hydrolase domain-like **Family:**Peptidyl-tRNA hydrolase domain
10	c3errB_	Alignment		91.6	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**fusion protein of microtubule binding domain from **PDBTitle:** microtubule binding domain from mouse cytoplasmic dynein as2 a fusion with seryl-trna synthetase
11	c1wpaA_	Alignment		90.3	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** 1.5 angstrom crystal structure of human occludin fragment2 413-522

12	c1xawA_	Alignment		89.7	17	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**occludin; **PDBTitle:** crystal structure of the cytoplasmic distal c-terminal2 domain of occludin
13	d1fpoa2	Alignment		85.8	11	**Fold:**Open three-helical up-and-down bundle **Superfamily:**HSC20 (HSCB), C-terminal oligomerisation domain **Family:**HSC20 (HSCB), C-terminal oligomerisation domain
14	c3layF_	Alignment		60.9	22	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
15	c2dq3A_	Alignment		56.2	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of aq_298
16	c3uo2A_	Alignment		49.6	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**j-type co-chaperone jac1, mitochondrial; **PDBTitle:** jac1 co-chaperone from saccharomyces cerevisiae
17	c2dq0A_	Alignment		46.2	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
18	c1deqO_	Alignment		45.6	11	**PDB header:** **PDB COMPND:**
19	d1seta1	Alignment		45.2	20	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Seryl-tRNA synthetase (SerRS)
20	c3dtpA_	Alignment		43.7	14	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
21	c3ghgK_	Alignment	not modelled	41.7	13	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
22	c2wmoA_	Alignment	not modelled	39.2	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dedicator of cytokinesis protein 9; **PDBTitle:** structure of the complex between dock9 and cdc42.
23	c2e1mA_	Alignment	not modelled	38.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
24	c2jyaA_	Alignment	not modelled	37.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1810; **PDBTitle:** nmr solution structure of protein atu1810 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr23,3 ontario centre for structural proteomics target atc1776
25	c3lssA_	Alignment	not modelled	34.4	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** trypanosoma brucei seryl-trna synthetase in complex with atp
26	c1f8sA_	Alignment	not modelled	33.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
27	c3s2xB_	Alignment	not modelled	32.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
						PDB header:transport protein

28	c3fhnA_	Alignment	not modelled	32.1	19	**Chain:** A: **PDB Molecule:**protein transport protein tip20; **PDBTitle:** structure of tip20p
29	c2yrvA_	Alignment	not modelled	30.3	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**at-rich interactive domain-containing protein 4a; **PDBTitle:** solution structure of the rbb1nt domain of human2 rb(retinoblastoma)-binding protein 1
30	c1s1hI_	Alignment	not modelled	30.2	15	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**40s ribosomal protein s16; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
31	c1wleB_	Alignment	not modelled	29.1	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
32	c3qo8A_	Alignment	not modelled	29.0	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**seryl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of seryl-trna synthetase from candida albicans
33	d1cuna2	Alignment	not modelled	28.8	11	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
34	c2chpC_	Alignment	not modelled	28.1	19	**PDB header:**dna-binding protein **Chain:** C: **PDB Molecule:**metalloregulation dna-binding stress protein; **PDBTitle:** crystal structure of the dodecameric ferritin mrga from2 b.subtilis 168
35	d1tjoa_	Alignment	not modelled	26.3	18	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
36	c1sryB_	Alignment	not modelled	25.0	15	**PDB header:**ligase(synthetase) **Chain:** B: **PDB Molecule:**seryl-trna synthetase; **PDBTitle:** refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
37	d2spca_	Alignment	not modelled	24.7	18	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
38	d1mqva_	Alignment	not modelled	24.3	8	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
39	c1ei3E_	Alignment	not modelled	23.6	15	**PDB header:** **PDB COMPND:**
40	c2gl2B_	Alignment	not modelled	23.5	7	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
41	d1ivsa1	Alignment	not modelled	23.4	15	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
42	d1nj1a3	Alignment	not modelled	23.1	17	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
43	d1s05a_	Alignment	not modelled	22.2	12	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
44	c3iq1A_	Alignment	not modelled	21.1	15	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**dps family protein; **PDBTitle:** crystal structure of dps protein from vibrio cholerae o1, a member of2 a broad superfamily of ferritin-like diiron-carboxylate proteins
45	c3gitA_	Alignment	not modelled	19.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
46	c2c41K_	Alignment	not modelled	19.8	10	**PDB header:**iron-binding/oxidation protein **Chain:** K: **PDB Molecule:**dps family dna-binding stress response protein; **PDBTitle:** x-ray structure of dps from thermosynechococcus elongatus
47	c2r6cG_	Alignment	not modelled	19.7	12	**PDB header:**replication **Chain:** G: **PDB Molecule:**dnag primase, helicase binding domain; **PDBTitle:** crystal form bh2
48	c2cazF_	Alignment	not modelled	19.4	60	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**protein srn2; **PDBTitle:** escrt-i core
49	c3ojaB_	Alignment	not modelled	18.8	16	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
50	c1s35A_	Alignment	not modelled	18.5	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spectrin beta chain, erythrocyte; **PDBTitle:** crystal structure of repeats 8 and 9 of human erythroid2 spectrin
51	c1ei3C_	Alignment	not modelled	18.2	9	**PDB header:** **PDB COMPND:**
52	c2c5iT_	Alignment	not modelled	18.2	19	**PDB header:**protein transport **Chain:** T: **PDB Molecule:**t-snare affecting a late golgi compartment **PDBTitle:** n-terminal domain of tlg1 complexed with n-terminus of2 vps51 in distorted conformation

53	d1gqaa_	Alignment	not modelled	18.0	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
54	d1s35a1	Alignment	not modelled	17.5	15	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
55	c2vvlD_	Alignment	not modelled	17.4	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**monoamine oxidase n; **PDBTitle:** the structure of mao-n-d3, a variant of monoamine oxidase2 from aspergillus niger.
56	c2qbvA_	Alignment	not modelled	16.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**chorismate mutase; **PDBTitle:** crystal structure of intracellular chorismate mutase from2 mycobacterium tuberculosis
57	d2gy9i1	Alignment	not modelled	16.6	38	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
58	c3kwoA_	Alignment	not modelled	16.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative bacterioferritin; **PDBTitle:** crystal structure of putative bacterioferritin from2 campylobacter jejuni
59	d2vqei1	Alignment	not modelled	16.2	28	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
60	d2pc6a2	Alignment	not modelled	15.9	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
61	c2d5kC_	Alignment	not modelled	15.8	12	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**dps family protein; **PDBTitle:** crystal structure of dps from staphylococcus aureus
62	c3ci9B_	Alignment	not modelled	15.8	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
63	d1fafa_	Alignment	not modelled	15.7	18	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
64	d1m0da_	Alignment	not modelled	15.7	33	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
65	c3h0gA_	Alignment	not modelled	15.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb1; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
66	d1ji4a_	Alignment	not modelled	15.3	17	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
67	d1cpqa_	Alignment	not modelled	15.2	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
68	c3m3wA_	Alignment	not modelled	15.2	11	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**protein kinase c and casein kinase ii substrate protein 3; **PDBTitle:** crystal strcuture of mouse pacsin3 bar domain mutant
69	c3pdgA_	Alignment	not modelled	15.1	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
70	c1gk4A_	Alignment	not modelled	15.1	10	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
71	d1ji5a_	Alignment	not modelled	14.8	16	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
72	d1u5pa2	Alignment	not modelled	14.7	20	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
73	c2pc6C_	Alignment	not modelled	14.7	19	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
74	d1ru3a_	Alignment	not modelled	14.6	19	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
75	d2fgca2	Alignment	not modelled	14.6	28	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
76	d1p7hl1	Alignment	not modelled	14.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
77	c2k6lA_	Alignment	not modelled	14.5	44	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the solution structure of xacb0070 from xanthonomas2 axonopodis pv citri reveals this new protein is a member of3 the rhh family of transcriptional repressors
78	d1nj8a3	Alignment	not modelled	14.5	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
79	c3bbnI	Alignment	not modelled	14.4	19	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein s9;

79	c3bbnI_	Alignment	not modelled	14.4	19	**PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
80	c2c6rA_	Alignment	not modelled	14.3	14	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**dna-binding stress response protein, dps family; **PDBTitle:** fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
81	c3bboH_	Alignment	not modelled	14.0	26	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**ribosomal protein l5; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
82	c2z9fC_	Alignment	not modelled	13.9	37	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**cellulose synthase operon protein d; **PDBTitle:** crystal structure of axcesd protein from acetobacter xylinum
83	d2j8wa1	Alignment	not modelled	13.6	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
84	c2xzml_	Alignment	not modelled	13.5	23	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**rps16e; **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
85	d2f1fa1	Alignment	not modelled	13.1	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
86	d1oaoc_	Alignment	not modelled	13.1	19	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Acetyl-CoA synthase
87	c2f7nA_	Alignment	not modelled	13.0	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding stress response protein, dps family; **PDBTitle:** structure of d. radiodurans dps-1
88	c2zkqi_	Alignment	not modelled	12.8	29	**PDB header:**ribosomal protein/rna **Chain:** I: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
89	d2f66c1	Alignment	not modelled	12.7	47	**Fold:**Long alpha-hairpin **Superfamily:**Endosomal sorting complex assembly domain **Family:**VPS37 C-terminal domain-like
90	d2gu3a1	Alignment	not modelled	12.1	21	**Fold:**Cystatin-like **Superfamily:**Cystatin/monellin **Family:**PepSY-like
91	c2lf0A_	Alignment	not modelled	12.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yibl; **PDBTitle:** solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scatting, nesg4 target sfr339/ocsp target sf3636
92	d1utya_	Alignment	not modelled	11.8	15	**Fold:**BTV NS2-like ssRNA-binding domain **Superfamily:**BTV NS2-like ssRNA-binding domain **Family:**BTV NS2-like ssRNA-binding domain
93	c1utyA_	Alignment	not modelled	11.8	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 2; **PDBTitle:** crystal structure of the rna binding domain of bluetongue2 virus non-structural protein 2(ns2)
94	c2jzxA_	Alignment	not modelled	11.4	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**poly(rc)-binding protein 2; **PDBTitle:** pcbp2 kh1-kh2 domains
95	d1u5pa1	Alignment	not modelled	11.4	16	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat
96	c3pdyB_	Alignment	not modelled	11.2	11	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin; **PDBTitle:** structure of the third and fourth spectrin repeats of the plakin2 domain of plectin
97	d2g5ca1	Alignment	not modelled	11.1	19	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**TyrA dimerization domain-like
98	d1e85a_	Alignment	not modelled	11.1	7	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like
99	c2obaE_	Alignment	not modelled	10.9	24	**PDB header:**lyase **Chain:** E: **PDB Molecule:**probable 6-pyruvoyl tetrahydrobiopterin synthase; **PDBTitle:** pseudomonas aeruginosa 6-pyruvoyl tetrahydrobiopterin synthase