Phyre^{2}

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Description	P45753
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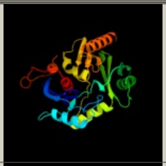
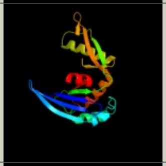
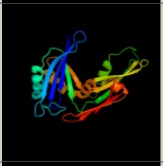
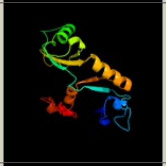
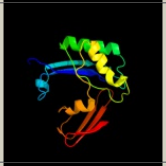
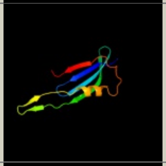
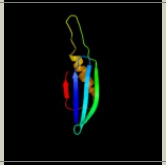
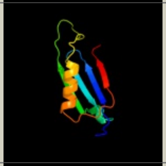
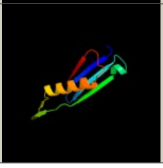
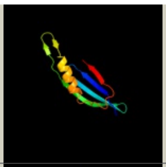
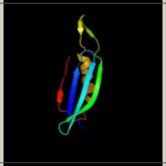
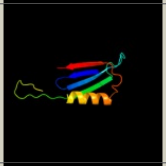
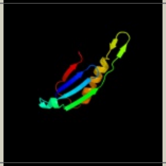
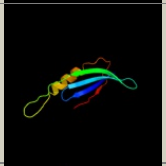
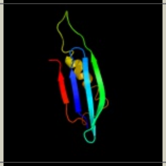
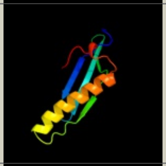
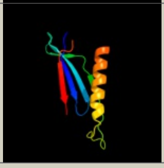
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ychA_	Alignment		100.0	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
2	d1e4ft1	Alignment		99.7	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
3	d2bh1a2	Alignment		99.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Cyto-EpsL domain
4	c1e4gT_	Alignment		99.6	9	**PDB header:**bacterial cell division **Chain:** T: **PDB Molecule:**cell division protein ftsa; **PDBTitle:** ftsa (atp-bound form) from thermotoga maritima
5	c1yf5L_	Alignment		99.4	16	**PDB header:**transport protein **Chain:** L: **PDB Molecule:**general secretion pathway protein l; **PDBTitle:** cyto-epsl: the cytoplasmic domain of epsl, an inner membrane component2 of the type ii secretion system of vibrio cholerae
6	c3h1qB_	Alignment		99.1	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
7	d2p3ra1	Alignment		96.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
8	c3ezwD_	Alignment		96.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
9	c3ifrB_	Alignment		96.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
10	c3g25B_	Alignment		96.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
11	c3flcX_	Alignment		96.6	10	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol

12	c2zf5O_	Alignment		96.5	8	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
13	c3h6eB_	Alignment		96.5	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
14	c2nlxA_	Alignment		96.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
15	c3i8bA_	Alignment		96.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
16	c2d4wA_	Alignment		96.4	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
17	c3gbtA_	Alignment		96.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
18	c1glbG_	Alignment		96.1	14	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
19	c3gg4B_	Alignment		96.1	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
20	c3hz6A_	Alignment		96.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
21	c2dpnB_	Alignment	not modelled	95.8	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
22	c2w40C_	Alignment	not modelled	94.9	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
23	c2cgkB_	Alignment	not modelled	94.7	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-rhamnulose kinase; **PDBTitle:** crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
24	c3jvpA_	Alignment	not modelled	94.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
25	c1xupO_	Alignment	not modelled	94.5	10	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
26	d1u6za2	Alignment	not modelled	93.8	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
27	d1t6ca1	Alignment	not modelled	93.6	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ppx/GppA phosphatase
28	d2aa4a1	Alignment	not modelled	93.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
						Fold: Ribonuclease H-like motif

29	d1r59o1	Alignment	not modelled	93.0	11	**Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
30	d2ap1a2	Alignment	not modelled	92.9	8	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
31	d1woqa1	Alignment	not modelled	92.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
32	d1q18a1	Alignment	not modelled	92.2	6	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
33	d1z6ra2	Alignment	not modelled	92.1	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
34	c3htvA_	Alignment	not modelled	91.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-allose kinase; **PDBTitle:** crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
35	d2hoea3	Alignment	not modelled	91.5	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
36	c3iucC_	Alignment	not modelled	91.1	8	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock 70kda protein 5 (glucose-regulated **PDBTitle:** crystal structure of the human 70kda heat shock protein 52 (bip/grp78) atpase domain in complex with adp
37	c2q2rA_	Alignment	not modelled	90.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
38	d1z05a3	Alignment	not modelled	90.8	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
39	c2ap1A_	Alignment	not modelled	89.7	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
40	d2ewsa1	Alignment	not modelled	89.2	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
41	d1zc6a1	Alignment	not modelled	88.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
42	c3r8eA_	Alignment	not modelled	87.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical sugar kinase; **PDBTitle:** crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
43	c1z6rC_	Alignment	not modelled	85.3	11	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
44	c1zc6A_	Alignment	not modelled	84.4	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable n-acetylglucosamine kinase; **PDBTitle:** crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
45	c1z05A_	Alignment	not modelled	83.3	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
46	d1huxa_	Alignment	not modelled	80.8	7	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
47	c3hi0B_	Alignment	not modelled	79.5	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
48	c1woqB_	Alignment	not modelled	79.4	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inorganic polyphosphate/atp-glucomannokinase; **PDBTitle:** crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
49	c1t6dB_	Alignment	not modelled	79.0	3	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
50	c2e2pA_	Alignment	not modelled	78.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
51	c3mdqA_	Alignment	not modelled	77.8	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
52	c2qm1D_	Alignment	not modelled	77.0	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
53	c2floA_	Alignment	not modelled	76.4	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
						PDB header:transferase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase;

54	c2aa4B_	Alignment	not modelled	74.6	14	**PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
55	d2gupa1	Alignment	not modelled	72.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
56	d1sz2a1	Alignment	not modelled	71.6	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
57	d1jcea1	Alignment	not modelled	71.2	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
58	c2hoeA_	Alignment	not modelled	68.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylglucosamine kinase; **PDBTitle:** crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
59	c2ch5D_	Alignment	not modelled	68.7	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
60	c3cerD_	Alignment	not modelled	68.6	11	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein; **PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
61	c1jcgA_	Alignment	not modelled	67.7	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**rod shape-determining protein mreb; **PDBTitle:** mreb from thermotoga maritima, amppnp
62	c2khoA_	Alignment	not modelled	66.0	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein 70; **PDBTitle:** nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
63	d1hjra_	Alignment	not modelled	60.6	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
64	c2gupA_	Alignment	not modelled	60.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rok family protein; **PDBTitle:** structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
65	c3mcpA_	Alignment	not modelled	58.4	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
66	c3eo3B_	Alignment	not modelled	57.5	6	**PDB header:**isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
67	d1bdga1	Alignment	not modelled	56.7	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
68	c1mwmA_	Alignment	not modelled	56.6	0	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**parm; **PDBTitle:** parm from plasmid r1 adp form
69	d1cdwa2	Alignment	not modelled	54.1	19	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
70	d1qnaa2	Alignment	not modelled	53.7	18	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
71	c3vgkB_	Alignment	not modelled	49.7	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
72	d1nbwa2	Alignment	not modelled	49.2	5	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
73	d2d0oa2	Alignment	not modelled	48.6	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ATPase domain of dehydratase reactivase alpha subunit
74	c1nbwA_	Alignment	not modelled	48.0	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycerol dehydratase reactivase alpha subunit; **PDBTitle:** glycerol dehydratase reactivase
75	c1xc3A_	Alignment	not modelled	47.3	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
76	c2v7zA_	Alignment	not modelled	45.8	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock cognate 71 kda protein; **PDBTitle:** crystal structure of the 70-kda heat shock cognate protein2 from rattus norvegicus in post-atp hydrolysis state
77	d2ch5a2	Alignment	not modelled	45.7	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
78	c1hpmA_	Alignment	not modelled	43.5	16	**PDB header:**hydrolase (acting on acid anhydrides) **Chain:** A: **PDB Molecule:**44k atpase fragment (n-terminal) of 7o kd heat- **PDBTitle:** how potassium affects the activity of the molecular2 chaperone hsc70. ii. potassium binds specifically in the3 atpase active site
79	c1bdgA_	Alignment	not modelled	41.2	10	**PDB header:**hexokinase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** hexokinase from schistosoma mansoni complexed with

						glucose
80	d1czan3	Alignment	not modelled	40.2	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
81	d1mp9a1	Alignment	not modelled	37.0	16	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
82	d2fsja2	Alignment	not modelled	36.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Ta0583-like
83	d1nh2a2	Alignment	not modelled	33.6	18	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
84	d1bg3a3	Alignment	not modelled	32.7	7	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
85	d1xc3a1	Alignment	not modelled	32.4	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
86	d2f9wa2	Alignment	not modelled	29.8	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**CoaX-like
87	c2fsnB_	Alignment	not modelled	28.2	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
88	c3d2fC_	Alignment	not modelled	27.7	9	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**heat shock protein homolog sse1; **PDBTitle:** crystal structure of a complex of sse1p and hsp70
89	d1cdwa1	Alignment	not modelled	26.6	21	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
90	d1aisa2	Alignment	not modelled	26.0	19	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
91	d1mp9a2	Alignment	not modelled	24.7	21	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
92	d1czan1	Alignment	not modelled	23.9	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
93	d2e8aa1	Alignment	not modelled	23.7	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
94	d1dkgd1	Alignment	not modelled	23.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
95	d1aisa1	Alignment	not modelled	23.1	12	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
96	c2d0oA_	Alignment	not modelled	23.0	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**diol dehydratase-reactivating factor large **PDBTitle:** strcuture of diol dehydratase-reactivating factor complexed2 with adp and mg2+
97	d1nh2a1	Alignment	not modelled	22.1	19	**Fold:**TBP-like **Superfamily:**TATA-box binding protein-like **Family:**TATA-box binding protein (TBP), C-terminal domain
98	d2zgya1	Alignment	not modelled	21.7	0	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
99	c3lm2B_	Alignment	not modelled	21.7	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution