Phyre2

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Description	P77735
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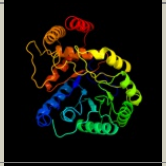
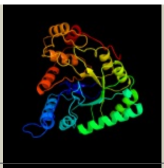
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lqaa_	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
2	d3eaua1	Alignment		100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
3	c3lutA_	Alignment		100.0	31	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel subunit beta-2; **PDBTitle:** a structural model for the full-length shaker potassium channel kv1.2
4	d1pyfa_	Alignment		100.0	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
5	c3erpA_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of idp01002, a putative oxidoreductase from and essential2 gene of salmonella typhimurium
6	d1pz1a_	Alignment		100.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
7	c3n2tA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the glycerol dehydrogenase akr11b4 from gluconobacter2 oxydans
8	c3n6qF_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**yghz aldo-keto reductase; **PDBTitle:** crystal structure of yghz from e. coli
9	d1ur3m_	Alignment		100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
10	d1gvea_	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
11	c2bp1C_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aflatoxin b1 aldehyde reductase member 2; **PDBTitle:** structure of the aflatoxin aldehyde reductase in complex2 with nadph

12	c1ynpA_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** aldo-keto reductase akr11c1 from bacillus halodurans (apo form)
13	d1q5ma_	Alignment		100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
14	d1j96a_	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
15	c3h7uA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c9
16	d1afsa_	Alignment		100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
17	d1us0a_	Alignment		100.0	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
18	c3up8B_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative 2,5-diketo-d-gluconic acid reductase b; **PDBTitle:** crystal structure of a putative 2,5-diketo-d-gluconic acid reductase b
19	c3f7jB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**yvgn protein; **PDBTitle:** b.subtilis yvgn
20	d1frba_	Alignment		100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
21	d1qwka_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
22	d1s1pa_	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
23	d1mi3a_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
24	c3h7rA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase; **PDBTitle:** crystal structure of the plant stress-response enzyme akr4c8
25	d1hqta_	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
26	d1ah4a_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
27	c3buvB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxo-5-beta-steroid 4-dehydrogenase; **PDBTitle:** crystal structure of human delta(4)-3-ketosteroid 5-beta-reductase in2 complex with nadp and hepes. resolution: 1.35 a.
28	c1zgdB_	Alignment	not modelled	100.0	23	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**chalcone reductase; **PDBTitle:** chalcone reductase complexed with nadp+ at 1.7 angstrom2 resolution
29	c2wztA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldo-keto reductase;

29	c2wzlA_	Alignment	not modelled	100.0	20	**PDBTitle:** crystal structure of a mycobacterium aldo-keto reductase in2 its apo and liganded form
30	d1c9wa_	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
31	d1mzra_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
32	d2alra_	Alignment	not modelled	100.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
33	d1vp5a_	Alignment	not modelled	100.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
34	c2bgsA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldose reductase; **PDBTitle:** holo aldose reductase from barley
35	d1hw6a_	Alignment	not modelled	100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
36	c3o0kB_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
37	c3b3dA_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative morphine dehydrogenase; **PDBTitle:** b.subtilis ytbe
38	c1vbjB_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**prostaglandin f synthase; **PDBTitle:** the crystal structure of prostaglandin f synthase from2 trypanosoma brucei
39	c3krbB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldose reductase; **PDBTitle:** structure of aldose reductase from giardia lamblia at 1.75a resolution
40	c3ln3A_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of putative reductase (np_038806.2) from2 mus musculus at 1.18 a resolution
41	c2ekcA_	Alignment	not modelled	81.6	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
42	c3g8rA_	Alignment	not modelled	69.2	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
43	c3ktcB_	Alignment	not modelled	64.3	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
44	d1vpqa_	Alignment	not modelled	57.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**TM1631-like **Family:**TM1631-like
45	d3bofa2	Alignment	not modelled	55.5	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Homocysteine S-methyltransferase **Family:**Homocysteine S-methyltransferase
46	c3oqbF_	Alignment	not modelled	49.2	14	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
47	d1qopa_	Alignment	not modelled	46.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
48	c3noeA_	Alignment	not modelled	46.4	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
49	c3hf3A_	Alignment	not modelled	46.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chromate reductase; **PDBTitle:** old yellow enzyme from thermus scotoductus sa-01
50	c1xuzA_	Alignment	not modelled	44.7	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
51	d1uwka_	Alignment	not modelled	44.4	21	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
52	d1ujpa_	Alignment	not modelled	43.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
53	c3ng3A_	Alignment	not modelled	43.1	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
54	d1jpma1	Alignment	not modelled	41.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like

55	d1olta_	Alignment	not modelled	41.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
56	c2fknC_	Alignment	not modelled	36.0	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**urocanate hydratase; **PDBTitle:** crystal structure of urocanase from bacillus subtilis
57	d1o0ya_	Alignment	not modelled	35.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
58	c3navB_	Alignment	not modelled	35.5	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
59	c2h90A_	Alignment	not modelled	33.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
60	c3ju2A_	Alignment	not modelled	31.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
61	c3ewbX_	Alignment	not modelled	30.4	11	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
62	c2vwtA_	Alignment	not modelled	30.3	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
63	d1p1xa_	Alignment	not modelled	28.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
64	c2kzhA_	Alignment	not modelled	28.2	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tryptophan biosynthesis protein trpcf; **PDBTitle:** three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
65	c3lerA_	Alignment	not modelled	28.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
66	c1vliA_	Alignment	not modelled	26.6	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
67	c3ik4A_	Alignment	not modelled	25.9	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from herpetosiphon aurantiacus
68	c3eegB_	Alignment	not modelled	24.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
69	c3ox4D_	Alignment	not modelled	22.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**alcohol dehydrogenase 2; **PDBTitle:** structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
70	d2nlya1	Alignment	not modelled	20.9	9	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
71	d1xcfa_	Alignment	not modelled	20.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
72	c3bolB_	Alignment	not modelled	20.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5-methyltetrahydrofolate s-homocysteine **PDBTitle:** cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
73	c1ydoC_	Alignment	not modelled	19.6	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
74	d1g5ta_	Alignment	not modelled	19.4	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
75	d1jfla1	Alignment	not modelled	19.4	10	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
76	d1dxea_	Alignment	not modelled	19.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
77	d1g64b_	Alignment	not modelled	18.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
78	d1dwka1	Alignment	not modelled	18.3	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
79	c3f6wE_	Alignment	not modelled	17.8	9	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
						Fold:EF Hand-like

80	d1wlza1	Alignment	not modelled	17.6	26	**Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
81	c1wlzD_	Alignment	not modelled	17.6	26	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cap-binding protein complex interacting protein **PDBTitle:** crystal structure of djbp fragment which was obtained by2 limited proteolysis
82	c2xecD_	Alignment	not modelled	17.3	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
83	c3sdoB_	Alignment	not modelled	16.9	6	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase; **PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
84	d1vlja_	Alignment	not modelled	16.6	14	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
85	c2v5jB_	Alignment	not modelled	16.1	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
86	c3l8mA_	Alignment	not modelled	16.0	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable thiamine pyrophosphokinase; **PDBTitle:** crystal structure of a probable thiamine pyrophosphokinase2 from staphylococcus saprophyticus subsp. saprophyticus.3 northeast structural genomics consortium target id syr86
87	c2nqlB_	Alignment	not modelled	16.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**isomerase/lactonizing enzyme; **PDBTitle:** crystal structure of a member of the enolase superfamily from2 agrobacterium tumefaciens
88	c3hl0B_	Alignment	not modelled	15.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**maleylacetate reductase; **PDBTitle:** crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
89	d1vcva1	Alignment	not modelled	15.6	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
90	c2q04C_	Alignment	not modelled	15.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**acetoin utilization protein; **PDBTitle:** crystal structure of acetoin utilization protein (zp_00540088.1) from2 exiguobacterium sibiricum 255-15 at 2.33 a resolution
91	d1ub3a_	Alignment	not modelled	15.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
92	c3ezyB_	Alignment	not modelled	15.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
93	c3d0cB_	Alignment	not modelled	14.7	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
94	d1x87a_	Alignment	not modelled	14.3	19	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
95	d1rrma_	Alignment	not modelled	14.1	10	**Fold:**Dehydroquinate synthase-like **Superfamily:**Dehydroquinate synthase-like **Family:**Iron-containing alcohol dehydrogenase
96	c3b7hA_	Alignment	not modelled	13.6	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
97	c2gruB_	Alignment	not modelled	13.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-deoxy-scyllo-inosose synthase; **PDBTitle:** crystal structure of 2-deoxy-scyllo-inosose synthase2 complexed with carbaglucose-6-phosphate, nad+ and co2+
98	c2ph5A_	Alignment	not modelled	12.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
99	c3c5yD_	Alignment	not modelled	12.0	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution