Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0ADG1
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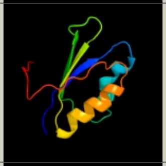
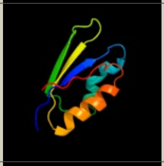
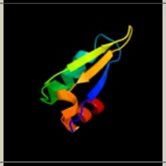
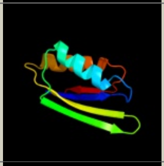
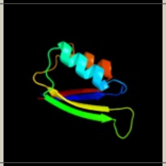
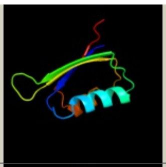
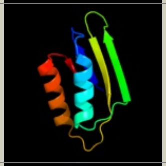
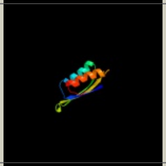
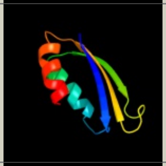
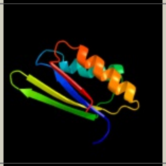
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pc6C_	Alignment		100.0	20	**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
2	c2fgcA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
3	c2f1fA_	Alignment		100.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
4	d2fgca2	Alignment		100.0	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
5	d2pc6a2	Alignment		99.9	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
6	d2f1fa1	Alignment		99.9	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
7	d2f06a2	Alignment		99.7	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
8	d1sc6a3	Alignment		99.4	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
9	d1ygya3	Alignment		99.3	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
10	c2f06B_	Alignment		99.3	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
11	c3ibwA_	Alignment		99.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a

12	c1ygyA_	Alignment		98.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
13	d1u8sa2	Alignment		98.2	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
14	c1y7pB_	Alignment		98.0	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
15	d1zpva1	Alignment		97.9	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
16	d2qmwa2	Alignment		97.8	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
17	c2nyiB_	Alignment		97.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
18	d1u8sa1	Alignment		97.7	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
19	c1ybaC_	Alignment		97.7	7	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
20	c3n0vD_	Alignment		97.6	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
21	c1u8sB_	Alignment	not modelled	97.6	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
22	c3o1lB_	Alignment	not modelled	97.5	3	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
23	c3louB_	Alignment	not modelled	97.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
24	c3mwbA_	Alignment	not modelled	97.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
25	c2qmwA_	Alignment	not modelled	97.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
26	c3k5pA_	Alignment	not modelled	97.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
27	c2qmxB_	Alignment	not modelled	97.3	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
						PDB header:isomerase

28	c3luyA_	Alignment	not modelled	97.3	14	**Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
29	c3nrbD_	Alignment	not modelled	97.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
30	d1phza1	Alignment	not modelled	97.2	10	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
31	d2f06a1	Alignment	not modelled	97.2	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
32	c3obiC_	Alignment	not modelled	96.9	8	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
33	c3mtjA_	Alignment	not modelled	96.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
34	c2dtjA_	Alignment	not modelled	95.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
35	d2hmfa3	Alignment	not modelled	95.2	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
36	d2cdqa2	Alignment	not modelled	94.1	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
37	d2hmfa2	Alignment	not modelled	94.0	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
38	c2re1A_	Alignment	not modelled	93.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
39	d2nzca1	Alignment	not modelled	92.4	9	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
40	c2zhoB_	Alignment	not modelled	92.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
41	c3mahA_	Alignment	not modelled	92.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
42	c3mgjA_	Alignment	not modelled	90.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
43	c2dgbA_	Alignment	not modelled	89.2	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
44	c3l76B_	Alignment	not modelled	89.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
45	d2cdqa3	Alignment	not modelled	88.0	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
46	c2zw2B_	Alignment	not modelled	86.5	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
47	d2j0wa2	Alignment	not modelled	86.4	21	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
48	c1rwuA_	Alignment	not modelled	86.3	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
49	d1rwua_	Alignment	not modelled	86.3	20	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
50	c3c1nA_	Alignment	not modelled	84.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
51	c2phmA_	Alignment	not modelled	84.4	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
52	c3ab4K_	Alignment	not modelled	83.9	12	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
53	d1gtda_	Alignment	not modelled	83.4	19	**Fold:**PurS-like **Superfamily:**PurS-like

						Family: PurS subunit of FGAM synthetase
54	d1vq3a_	Alignment	not modelled	82.9	11	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
55	c1tdjA_	Alignment	not modelled	80.9	17	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
56	c2cdqB_	Alignment	not modelled	78.1	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
57	c2rjzA_	Alignment	not modelled	76.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pilo protein; **PDBTitle:** crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
58	d2j0wa3	Alignment	not modelled	66.3	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
59	c3p96A_	Alignment	not modelled	65.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
60	c2jsxA_	Alignment	not modelled	62.9	4	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd
61	d1t4aa_	Alignment	not modelled	56.0	14	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
62	c2yx5A_	Alignment	not modelled	51.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
63	d1tdja2	Alignment	not modelled	42.9	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
64	d2joqa1	Alignment	not modelled	42.7	14	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**HP0495-like
65	d1kona_	Alignment	not modelled	29.9	16	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
66	c3ftbA_	Alignment	not modelled	28.9	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** the crystal structure of the histidinol-phosphate2 aminotransferase from clostridium acetobutylicum
67	d1nhkl_	Alignment	not modelled	23.9	13	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
68	c3cg4A_	Alignment	not modelled	23.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey-like); **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
69	c2j0wA_	Alignment	not modelled	21.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
70	d2hoxa1	Alignment	not modelled	19.8	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
71	d1ehwa_	Alignment	not modelled	19.4	27	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
72	c3js9A_	Alignment	not modelled	19.1	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside diphosphate kinase family protein; **PDBTitle:** crystal structure of nucleoside diphosphate kinase family protein from2 babesia bovis
73	d2c7pa1	Alignment	not modelled	19.0	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**C5 cytosine-specific DNA methylase, DCM
74	c2hurF_	Alignment	not modelled	17.8	13	**PDB header:**signaling protein,transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** escherichia coli nucleoside diphosphate kinase
75	c3hdvB_	Alignment	not modelled	16.3	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
76	d1mw7a_	Alignment	not modelled	16.1	11	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
77	d1dcta_	Alignment	not modelled	15.8	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**C5 cytosine-specific DNA methylase, DCM
78	d2b3tb1	Alignment	not modelled	15.7	13	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
79	d1w7wa_	Alignment	not modelled	15.6	12	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK

						Family: Nucleoside diphosphate kinase, NDK
80	d1p4xa2	Alignment	not modelled	15.2	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
81	d1qkka_	Alignment	not modelled	15.1	15	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
82	d3bbba1	Alignment	not modelled	15.0	15	**Fold:**Ferredoxin-like **Superfamily:**Nucleoside diphosphate kinase, NDK **Family:**Nucleoside diphosphate kinase, NDK
83	d1lc5a_	Alignment	not modelled	14.1	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
84	c1zbtA_	Alignment	not modelled	13.8	11	**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
85	d3ctaa1	Alignment	not modelled	13.6	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
86	d2a9pa1	Alignment	not modelled	13.5	8	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	d1rq0a_	Alignment	not modelled	13.2	9	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
88	c1w7wF_	Alignment	not modelled	13.1	12	**PDB header:**transferase **Chain:** F: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** structure and mutational analysis of a plant mitochondrial2 nucleoside diphosphate kinase: identification of residues3 involved in serine phosphorylation and oligomerization.
89	c3me5A_	Alignment	not modelled	13.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytosine-specific methyltransferase; **PDBTitle:** crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 301
90	c3d5cX_	Alignment	not modelled	12.3	13	**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.
91	c3eodA_	Alignment	not modelled	12.2	4	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
92	c2l69A_	Alignment	not modelled	12.2	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
93	c3q89H_	Alignment	not modelled	12.1	16	**PDB header:**transferase **Chain:** H: **PDB Molecule:**nucleoside diphosphate kinase; **PDBTitle:** crystal structure of staphylococcus aureus nucleoside diphosphate2 kinase complexed with cdp
94	c3o2sB_	Alignment	not modelled	12.0	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72 complex
95	c3o2qB_	Alignment	not modelled	11.7	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
96	d1y7pa2	Alignment	not modelled	11.5	6	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**AF1403 N-terminal domain-like
97	d1wxma1	Alignment	not modelled	11.1	7	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
98	d1mvoa_	Alignment	not modelled	11.0	9	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
99	c3fdfA_	Alignment	not modelled	10.7	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fr253; **PDBTitle:** crystal structure of the serine phosphatase of rna2 polymerase ii ctd (ssu72 superfamily) from drosophila3 melanogaster. orthorhombic crystal form. northeast4 structural genomics consortium target fr253.