Phyre^2

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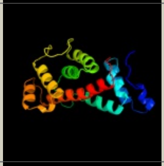
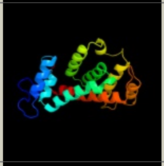
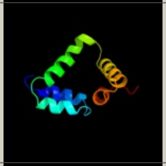
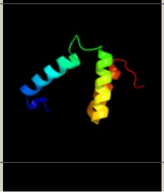
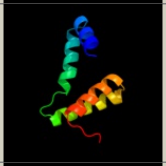
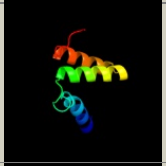
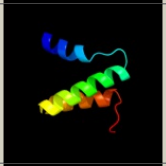
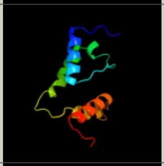
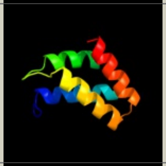
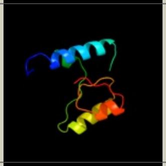
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pfxa1	Alignment		99.9	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
2	c3c1lB_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative antioxidant defense protein mlr4105; **PDBTitle:** crystal structure of an antioxidant defense protein (mlr4105) from2 mesorhizobium loti maff303099 at 2.00 a resolution
3	d2oyoa1	Alignment		99.8	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
4	d2prra1	Alignment		99.8	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
5	c3lvyB_	Alignment		99.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
6	d2o4da1	Alignment		99.1	18	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
7	d2ouwa1	Alignment		99.0	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
8	d2gmya1	Alignment		98.8	18	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**Atu0492-like
9	c2qeuA_	Alignment		97.6	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
10	d2cwqa1	Alignment		97.5	16	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like
11	c3beyC_	Alignment		96.9	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
						PDB header:lyase

12	c3d7iB_	Alignment		96.8	12	**Chain:** B: **PDB Molecule:**carboxymuconolactone decarboxylase family protein; **PDBTitle:** crystal structure of carboxymuconolactone decarboxylase family protein2 possibly involved in oxygen detoxification (1591455) from3 methanococcus jannaschii at 1.75 a resolution
13	c1p8cD_	Alignment		96.8	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
14	d1vkea_	Alignment		95.7	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
15	d1vkeb_	Alignment		95.3	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
16	d2q0ta1	Alignment		94.3	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
17	d2af7a1	Alignment		79.5	19	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
18	c2r8rB_	Alignment		54.4	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
19	d1knca_	Alignment		38.8	14	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**AhpD
20	c1ckxA_	Alignment		31.6	38	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**cystic fibrosis transmembrane conductance **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
21	c3ntsB_	Alignment	not modelled	21.6	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**vsdc; **PDBTitle:** catalytic domain of vsdc from aeromonas hydrophila
22	c2dgxA_	Alignment	not modelled	17.6	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rna recognition motif in kiaa04302 protein
23	c3k1tA_	Alignment	not modelled	17.1	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamate--cysteine ligase gsha; **PDBTitle:** crystal structure of putative gamma-glutamylcysteine synthetase2 (yp_546622.1) from methylobacillus flagellatus kt at 1.90 a3 resolution
24	c1ckwA_	Alignment	not modelled	16.7	31	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein (cystic fibrosis transmembrane **PDBTitle:** cystic fibrosis transmembrane conductance regulator:2 solution structures of peptides based on the phe508 region,3 the most common site of disease-causing delta-f508 mutation
25	d1hw8c2	Alignment	not modelled	16.2	24	**Fold:**Substrate-binding domain of HMG-CoA reductase **Superfamily:**Substrate-binding domain of HMG-CoA reductase **Family:**Substrate-binding domain of HMG-CoA reductase
26	c3c18B_	Alignment	not modelled	15.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
27	c2pehA_	Alignment	not modelled	14.3	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**splicing factor 45; **PDBTitle:** crystal structure of the uhm domain of human spf45 in complex with2 sf3b155-ulm5
28	c1ponB_	Alignment	not modelled	12.3	38	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr

29	c3btpA_	Alignment	not modelled	11.1	35	**PDB header:**dna binding protein, chaperone **Chain:** A: **PDB Molecule:**single-strand dna-binding protein; **PDBTitle:** crystal structure of agrobacterium tumefaciens vire2 in complex with2 its chaperone vire1: a novel fold and implications for dna binding
30	d1zk8a2	Alignment	not modelled	11.1	12	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
31	d1sbxa_	Alignment	not modelled	10.5	25	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Dachshund-homology domain
32	c3f4mA_	Alignment	not modelled	10.1	18	**PDB header:**immune system **Chain:** A: **PDB Molecule:**tumor necrosis factor, alpha-induced protein 8- **PDBTitle:** crystal structure of tipe2
33	c3kx6C_	Alignment	not modelled	9.8	35	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
34	c2qb0D_	Alignment	not modelled	9.4	23	**PDB header:**hydrolase regulator **Chain:** D: **PDB Molecule:**telsam domain - lysozyme chimera; **PDBTitle:** structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
35	c2eapA_	Alignment	not modelled	9.4	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**lymphocyte cytosolic protein 2; **PDBTitle:** solution structure of the n-terminal sam-domain of human2 lymphocyte cytosolic protein 2
36	c1zzaA_	Alignment	not modelled	9.3	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**stannin; **PDBTitle:** solution nmr structure of the membrane protein stannin
37	d1rz4a1	Alignment	not modelled	9.1	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
38	c1rue4_	Alignment	not modelled	8.9	33	**PDB header:**virus **Chain:** 4: **PDB Molecule:**rhinovirus 14; **PDBTitle:** rhinovirus 14 site directed mutant n1219a complexed with2 antiviral compound win 52035
39	c3jvfC_	Alignment	not modelled	8.6	24	**PDB header:**signaling protein / cytokine **Chain:** C: **PDB Molecule:**interleukin-17 receptor a; **PDBTitle:** crystal structure of an interleukin-17 receptor complex
40	d1wj7a1	Alignment	not modelled	8.4	36	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
41	d1zpya1	Alignment	not modelled	8.3	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**half-ferritin
42	d1jmsa4	Alignment	not modelled	8.2	27	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
43	d2ce7a2	Alignment	not modelled	8.2	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
44	c3thfA_	Alignment	not modelled	8.2	27	**PDB header:**actin-binding protein/protein binding **Chain:** A: **PDB Molecule:**protein shroom; **PDBTitle:** crystal structure of the sd2 domain from drosophila shroom
45	c1dgi4_	Alignment	not modelled	8.2	39	**PDB header:**virus/viral protein, receptor **Chain:** 4: **PDB Molecule:**vp4; **PDB Fragment:**poliovirus fragments vp1,vp2,vp3,vp4; **PDBTitle:**
46	c1bev4_	Alignment	not modelled	8.2	36	**PDB header:**virus **Chain:** 4: **PDB Molecule:**bovine enterovirus coat proteins vp1 to vp4; **PDBTitle:** bovine enterovirus vg-5-27
47	c3pgwP_	Alignment	not modelled	8.1	15	**PDB header:**splicing/dna/rna **Chain:** P: **PDB Molecule:**u1-a; **PDBTitle:** crystal structure of human u1 snrnp
48	c3vbhD_	Alignment	not modelled	7.8	27	**PDB header:**virus **Chain:** D: **PDB Molecule:**genome polyprotein, capsid protein vp4; **PDBTitle:** crystal structure of formaldehyde treated human enterovirus 71 (space2 group r32)
49	d1jmxa2	Alignment	not modelled	7.8	31	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
50	c3odnA_	Alignment	not modelled	7.7	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dally-like protein; **PDBTitle:** the crystal structure of drosophila dally-like protein core domain
51	c3eq5G_	Alignment	not modelled	7.6	24	**PDB header:**signaling protein **Chain:** G: **PDB Molecule:**ski-like protein; **PDBTitle:** crystal structure of fragment 137 to 238 of the human ski-like protein
52	d1sxja1	Alignment	not modelled	7.3	31	**Fold:**post-AAA+ oligomerization domain-like **Superfamily:**post-AAA+ oligomerization domain-like **Family:**DNA polymerase III clamp loader subunits, C-terminal domain
53	d2vana2	Alignment	not modelled	7.3	9	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
54	c1jew4_	Alignment	not modelled	7.2	39	**PDB header:**virus/receptor **Chain:** 4: **PDB Molecule:**coxsackievirus capsid, coat protein vp4; **PDB Fragment:**residues 21-140; **PDBTitle:** cryo-em structure of coxsackievirus b3(m strain) with its2 cellular receptor, coxsackievirus and adenovirus receptor3 (car).

55	c1hwjB_	Alignment	not modelled	7.2	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hmg-coa reductase; **PDBTitle:** complex of the catalytic portion of human hmg-coa reductase2 with cerivastatin
56	c3kf9D_	Alignment	not modelled	7.1	31	**PDB header:**cell cycle/calcium-binding protein **Chain:** D: **PDB Molecule:**myosin light chain kinase 2, skeletal/cardiac muscle; **PDBTitle:** crystal structure of the sdcen/skmlck complex
57	c2bbnB_	Alignment	not modelled	7.1	31	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase; **PDBTitle:** solution structure of a calmodulin-target peptide complex2 by multidimensional nmr
58	c2bbmB_	Alignment	not modelled	7.1	31	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase; **PDBTitle:** solution structure of a calmodulin-target peptide complex2 by multidimensional nmr
59	c3kf9B_	Alignment	not modelled	7.0	31	**PDB header:**cell cycle/calcium-binding protein **Chain:** B: **PDB Molecule:**myosin light chain kinase 2, skeletal/cardiac muscle; **PDBTitle:** crystal structure of the sdcen/skmlck complex
60	c1us7B_	Alignment	not modelled	6.6	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**hsp90 co-chaperone cdc37; **PDBTitle:** complex of hsp90 and p50
61	d1us7b_	Alignment	not modelled	6.6	21	**Fold:**Hsp90 co-chaperone CDC37 **Superfamily:**Hsp90 co-chaperone CDC37 **Family:**Hsp90 co-chaperone CDC37
62	d1ussa_	Alignment	not modelled	6.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
63	c2ee7A_	Alignment	not modelled	6.4	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**sperm flagellar protein 1; **PDBTitle:** solution structure of the ch domain from human sperm2 flagellar protein 1
64	c1g2yC_	Alignment	not modelled	6.4	25	**PDB header:**transcription **Chain:** C: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
65	c2la3A_	Alignment	not modelled	6.3	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the nmr structure of the protein np_344798.1 reveals a cca-adding2 enzyme head domain
66	c1g2yB_	Alignment	not modelled	6.3	25	**PDB header:**transcription **Chain:** B: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
67	c1g2yD_	Alignment	not modelled	6.3	25	**PDB header:**transcription **Chain:** D: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
68	c2ihmA_	Alignment	not modelled	6.1	36	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** polymerase mu in ternary complex with gapped 11mer dna2 duplex and bound incoming nucleotide
69	d2bcqa3	Alignment	not modelled	6.1	18	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
70	c1g2yA_	Alignment	not modelled	6.1	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** hnf-1alpha dimerization domain, with selenomethionine2 substitued at leu 12
71	d1g2ya_	Alignment	not modelled	6.1	25	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
72	d2fmpa3	Alignment	not modelled	6.0	9	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
73	c2jmfA_	Alignment	not modelled	6.0	45	**PDB header:**ligase/signaling protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase suppressor of deltex; **PDBTitle:** solution structure of the su(dx) ww4- notch py peptide2 complex
74	d2jmfa1	Alignment	not modelled	6.0	57	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
75	d1id3b_	Alignment	not modelled	5.9	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
76	c3c2qA_	Alignment	not modelled	5.9	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
77	c2kneB_	Alignment	not modelled	5.8	18	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**atpase, ca++ transporting, plasma membrane 4; **PDBTitle:** calmodulin wraps around its binding domain in the plasma2 membrane ca2+ pump anchored by a novel 18-1 motif
78	d1hrti_	Alignment	not modelled	5.8	32	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
79	c3ty8A_	Alignment	not modelled	5.8	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide 2',3'-cyclic phosphate phosphodiesterase / **PDBTitle:** crystal structure of c. thermocellum pnkp ligase domain apo form
80	c2krcA_	Alignment	not modelled	5.7	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit delta;

						PDBTitle: solution structure of the n-terminal domain of bacillus2 subtilis delta subunit of rna polymerase
81	c2zt9E_	Alignment	not modelled	5.7	27	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**cytochrome b6-f complex subunit 6; **PDBTitle:** crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
82	c2xpnA_	Alignment	not modelled	5.7	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**iws1; **PDBTitle:** crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form i
83	c3h6pD_	Alignment	not modelled	5.7	32	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**esat-6-like protein esxr; **PDBTitle:** crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
84	d4htci_	Alignment	not modelled	5.7	32	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
85	d1ojqa_	Alignment	not modelled	5.6	27	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**ADP-ribosylating toxins
86	c1kdhA_	Alignment	not modelled	5.6	27	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
87	c1f93H_	Alignment	not modelled	5.5	25	**PDB header:**transcription **Chain:** H: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
88	c3i3nA_	Alignment	not modelled	5.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**kelch-like protein 11; **PDBTitle:** crystal structure of the btb-back domains of human klhl11
89	d1danl3	Alignment	not modelled	5.4	58	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
90	d1afwa2	Alignment	not modelled	5.4	26	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
91	d1f93f_	Alignment	not modelled	5.4	25	**Fold:**Dimerisation interlock **Superfamily:**Dimerization cofactor of HNF-1 alpha **Family:**Dimerization cofactor of HNF-1 alpha
92	c1f93F_	Alignment	not modelled	5.4	25	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
93	d1jb0j_	Alignment	not modelled	5.4	63	**Fold:**Single transmembrane helix **Superfamily:**Subunit IX of photosystem I reaction centre, PsaJ **Family:**Subunit IX of photosystem I reaction centre, PsaJ
94	d1iooa_	Alignment	not modelled	5.4	16	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
95	d1bgfa_	Alignment	not modelled	5.3	27	**Fold:**Transcription factor STAT-4 N-domain **Superfamily:**Transcription factor STAT-4 N-domain **Family:**Transcription factor STAT-4 N-domain
96	c1f93G_	Alignment	not modelled	5.3	25	**PDB header:**transcription **Chain:** G: **PDB Molecule:**hepatocyte nuclear factor 1-alpha; **PDBTitle:** crystal structure of a complex between the dimerization2 domain of hnf-1 alpha and the coactivator dcoh
97	d1jqra_	Alignment	not modelled	5.3	20	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
98	c3ol4B_	Alignment	not modelled	5.3	46	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
99	d2huga1	Alignment	not modelled	5.3	56	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo domain