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| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|1|c5tkyA\_.1.pdb|1|54|30|597|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|2|c5e84B\_.2.pdb|1|70|29|598|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|3|c3d2fC\_.3.pdb|1|28|33|607|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|4|c2khoA\_.4.pdb|1|52|35|600|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|5|c3c7nB\_.5.pdb|1|68|33|550|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|6|c5obuA\_.6.pdb|1|52|33|550|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|7|c2v7yA\_.7.pdb|1|59|32|553|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-8|4e3289581f5387b1|8|c5mb9B\_.8.pdb|1|29|33|512|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|9|c4j8fA\_.9.pdb|1|67|33|407|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-8|4e3289581f5387b1|10|c6gfaA\_.10.pdb|1|37|35|396|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|11|c3iucC\_.11.pdb|1|75|31|402|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-8|4e3289581f5387b1|12|c1hpmA\_.12.pdb|1|69|33|400|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-8|4e3289581f5387b1|13|c4gniA\_.13.pdb|1|32|33|400|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|14|c2v7zA\_.14.pdb|1|68|33|401|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-8|4e3289581f5387b1|15|c4kboA\_.15.pdb|1|55|34|400|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|16|c1dkgD\_.16.pdb|1|53|35|400|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-8|4e3289581f5387b1|17|c4rtfD\_.17.pdb|1|54|35|399|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|18|c4czeA\_.18.pdb|1|23|33|396|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|19|c1jcgA\_.19.pdb|1|23|32|396|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-8|4e3289581f5387b1|20|c7bvzA\_.20.pdb|1|19|31|399|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|1|c3d2fC\_.1.pdb|1|30|26|750|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|2|c5tkyA\_.2.pdb|1|27|24|737|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-6|cec422646656506a|3|c5e84B\_.3.pdb|1|29|26|739|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|4|c2khoA\_.4.pdb|1|25|28|740|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|5|c3c7nB\_.5.pdb|1|31|25|546|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|6|c5mb9B\_.6.pdb|1|21|28|546|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|7|c5obuA\_.7.pdb|1|25|25|592|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|8|c4j8fA\_.8.pdb|1|32|24|454|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-6|cec422646656506a|9|c2v7yA\_.9.pdb|1|27|26|586|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-6|cec422646656506a|10|c4gniA\_.10.pdb|1|25|28|421|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|11|c6gfaA\_.11.pdb|1|34|28|417|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|12|c4kboA\_.12.pdb|1|28|27|421|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|13|c1hpmA\_.13.pdb|1|35|27|421|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-6|cec422646656506a|14|c2v7zA\_.14.pdb|1|36|24|422|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-6|cec422646656506a|15|c3iucC\_.15.pdb|1|35|18|422|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-6|cec422646656506a|16|c1dkgD\_.16.pdb|1|31|28|421|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-6|cec422646656506a|17|c4rtfD\_.17.pdb|1|29|28|420|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|18|c4czeA\_.18.pdb|1|20|26|417|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|19|c1jcgA\_.19.pdb|1|19|26|420|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-6|cec422646656506a|20|c7bvzA\_.20.pdb|1|19|25|420|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|1|c3d2fC\_.1.pdb|1|28|8|626|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|2|c5e84B\_.2.pdb|1|64|3|615|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|3|c5tkyA\_.3.pdb|1|59|8|613|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|4|c2khoA\_.4.pdb|1|51|9|617|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|5|c3c7nB\_.5.pdb|1|82|6|553|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|6|c5obuA\_.6.pdb|1|50|6|553|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|7|c2v7yA\_.7.pdb|1|54|6|540|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|8|c5mb9B\_.8.pdb|1|27|9|499|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|9|c4j8fA\_.9.pdb|1|80|5|394|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-23|bdcb2ef1c492539b|10|c6gfaA\_.10.pdb|1|36|9|383|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|11|c3iucC\_.11.pdb|1|67|1|388|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-23|bdcb2ef1c492539b|12|c1hpmA\_.12.pdb|1|82|7|387|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-23|bdcb2ef1c492539b|13|c2v7zA\_.13.pdb|1|82|6|388|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|14|c4gniA\_.14.pdb|1|31|9|388|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|15|c4kboA\_.15.pdb|1|52|8|387|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|16|c1dkgD\_.16.pdb|1|50|8|387|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-23|bdcb2ef1c492539b|17|c4rtfD\_.17.pdb|1|48|8|386|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|18|c4czeA\_.18.pdb|1|21|10|383|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|19|c1jcgA\_.19.pdb|1|26|6|383|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-23|bdcb2ef1c492539b|20|c7bvzA\_.20.pdb|1|20|8|386|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|1|c5tkyA\_.1.pdb|1|29|26|574|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|2|c3c7nB\_.2.pdb|1|34|28|574|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|3|c3d2fC\_.3.pdb|1|18|28|574|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|4|c5e84B\_.4.pdb|1|30|28|574|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|5|c5obuA\_.5.pdb|1|29|25|574|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|6|c2khoA\_.6.pdb|1|30|28|574|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|7|c2v7yA\_.7.pdb|1|32|28|574|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|8|c5mb9B\_.8.pdb|1|22|26|525|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|9|c4j8fA\_.9.pdb|1|31|25|416|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-13|f525e7fefcb700c7|10|c4gniA\_.10.pdb|1|23|26|412|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|11|c6gfaA\_.11.pdb|1|24|28|408|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|12|c4kboA\_.12.pdb|1|27|28|412|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|13|c3iucC\_.13.pdb|1|29|26|413|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-13|f525e7fefcb700c7|14|c1hpmA\_.14.pdb|1|32|28|412|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-13|f525e7fefcb700c7|15|c1dkgD\_.15.pdb|1|27|28|412|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-13|f525e7fefcb700c7|16|c2v7zA\_.16.pdb|1|32|28|413|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|17|c4rtfD\_.17.pdb|1|27|28|411|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|18|c4czeA\_.18.pdb|1|16|29|408|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|19|c1jcgA\_.19.pdb|1|19|26|408|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-13|f525e7fefcb700c7|20|c7bvzA\_.20.pdb|1|15|23|411|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|1|c3d2fC\_.1.pdb|1|28|7|625|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|2|c5e84B\_.2.pdb|1|65|3|615|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|3|c5tkyA\_.3.pdb|1|59|9|613|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|4|c2khoA\_.4.pdb|1|51|9|617|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|5|c3c7nB\_.5.pdb|1|83|6|553|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|6|c5obuA\_.6.pdb|1|50|6|553|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|7|c2v7yA\_.7.pdb|1|55|6|540|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|8|c5mb9B\_.8.pdb|1|27|9|499|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|9|c4j8fA\_.9.pdb|1|80|5|394|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-2|6d2303f69914daf7|10|c6gfaA\_.10.pdb|1|37|9|383|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|11|c1hpmA\_.11.pdb|1|83|7|387|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-2|6d2303f69914daf7|12|c4gniA\_.12.pdb|1|31|9|388|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|13|c3iucC\_.13.pdb|1|67|1|389|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-2|6d2303f69914daf7|14|c2v7zA\_.14.pdb|1|82|5|388|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-2|6d2303f69914daf7|15|c4kboA\_.15.pdb|1|53|8|387|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|16|c1dkgD\_.16.pdb|1|51|9|387|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-2|6d2303f69914daf7|17|c4rtfD\_.17.pdb|1|49|8|386|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|18|c4czeA\_.18.pdb|1|22|10|383|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|19|c1jcgA\_.19.pdb|1|24|6|393|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-2|6d2303f69914daf7|20|c7bvzA\_.20.pdb|1|20|8|386|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|1|c3d2fC\_.1.pdb|1|26|65|673|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|2|c2khoA\_.2.pdb|1|56|67|665|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|3|c5e84B\_.3.pdb|1|51|63|663|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|4|c5tkyA\_.4.pdb|1|44|65|661|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|5|c3c7nB\_.5.pdb|1|54|66|602|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|6|c2v7yA\_.6.pdb|1|64|64|592|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|7|c5obuA\_.7.pdb|1|54|64|602|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|8|c5mb9B\_.8.pdb|1|28|65|549|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|9|c4j8fA\_.9.pdb|1|51|62|447|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-21|e4546891f3a9d6a4|10|c4kboA\_.10.pdb|1|55|67|441|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|11|c1dkgD\_.11.pdb|1|56|66|441|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-21|e4546891f3a9d6a4|12|c6gfaA\_.12.pdb|1|36|67|437|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|13|c4gniA\_.13.pdb|1|32|65|441|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|14|c3iucC\_.14.pdb|1|53|62|443|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-21|e4546891f3a9d6a4|15|c1hpmA\_.15.pdb|1|52|66|441|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-21|e4546891f3a9d6a4|16|c2v7zA\_.16.pdb|1|52|66|442|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|17|c4rtfD\_.17.pdb|1|61|66|440|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|18|c4czeA\_.18.pdb|1|24|65|437|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|19|c1jcgA\_.19.pdb|1|25|64|437|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-21|e4546891f3a9d6a4|20|c7bvzA\_.20.pdb|1|22|65|440|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|1|c3d2fC\_.1.pdb|1|29|35|651|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|2|c5e84B\_.2.pdb|1|73|31|641|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|3|c5tkyA\_.3.pdb|1|56|37|639|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|4|c2khoA\_.4.pdb|1|52|37|643|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|5|c3c7nB\_.5.pdb|1|68|35|578|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|6|c5obuA\_.6.pdb|1|53|35|578|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|7|c2v7yA\_.7.pdb|1|60|34|565|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|8|c5mb9B\_.8.pdb|1|29|37|524|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|9|c4j8fA\_.9.pdb|1|68|35|419|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-3|25ee3211af6d0c15|10|c6gfaA\_.10.pdb|1|37|37|408|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|11|c3iucC\_.11.pdb|1|78|33|414|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-3|25ee3211af6d0c15|12|c4gniA\_.12.pdb|1|32|37|413|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|13|c1hpmA\_.13.pdb|1|69|35|412|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-3|25ee3211af6d0c15|14|c4kboA\_.14.pdb|1|57|36|412|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|15|c2v7zA\_.15.pdb|1|68|33|413|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|16|c1dkgD\_.16.pdb|1|54|37|412|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-3|25ee3211af6d0c15|17|c4rtfD\_.17.pdb|1|55|37|411|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|18|c1jcgA\_.18.pdb|1|26|34|408|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|19|c4czeA\_.19.pdb|1|24|35|408|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-3|25ee3211af6d0c15|20|c7bvzA\_.20.pdb|1|20|36|411|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|1|c3d2fC\_.1.pdb|1|40|2|702|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|2|c5e84B\_.2.pdb|1|31|1|692|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|3|c5tkyA\_.3.pdb|1|31|3|690|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|4|c2khoA\_.4.pdb|1|28|3|694|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|5|c3c7nB\_.5.pdb|1|31|2|548|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|6|c2v7yA\_.6.pdb|1|29|1|540|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|7|c5mb9B\_.7.pdb|1|23|3|497|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|8|c5obuA\_.8.pdb|1|27|3|543|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|9|c4j8fA\_.9.pdb|1|37|2|399|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-18|2c57c0f3899644ce|10|c6gfaA\_.10.pdb|1|44|3|377|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|11|c4kboA\_.11.pdb|1|35|2|381|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|12|c4gniA\_.12.pdb|1|27|3|381|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|13|c1dkgD\_.13.pdb|1|34|3|381|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-18|2c57c0f3899644ce|14|c1hpmA\_.14.pdb|1|39|2|381|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-18|2c57c0f3899644ce|15|c3iucC\_.15.pdb|1|36|2|382|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-18|2c57c0f3899644ce|16|c2v7zA\_.16.pdb|1|39|2|382|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|17|c4rtfD\_.17.pdb|1|34|3|380|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|18|c4czeA\_.18.pdb|1|15|2|377|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|19|c1jcgA\_.19.pdb|1|19|1|388|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-18|2c57c0f3899644ce|20|c7bvzA\_.20.pdb|1|16|2|380|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|1|c3d2fC\_.1.pdb|1|28|41|656|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|2|c5e84B\_.2.pdb|1|68|39|646|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|3|c5tkyA\_.3.pdb|1|56|43|644|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|4|c2khoA\_.4.pdb|1|50|43|648|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|5|c3c7nB\_.5.pdb|1|66|41|585|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|6|c5obuA\_.6.pdb|1|52|41|585|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|7|c2v7yA\_.7.pdb|1|61|40|572|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-10|ff733559c10eb320|8|c5mb9B\_.8.pdb|1|28|43|531|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|9|c4j8fA\_.9.pdb|1|67|41|426|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-10|ff733559c10eb320|10|c6gfaA\_.10.pdb|1|38|43|415|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|11|c3iucC\_.11.pdb|1|73|39|420|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-10|ff733559c10eb320|12|c1hpmA\_.12.pdb|1|68|41|419|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-10|ff733559c10eb320|13|c4gniA\_.13.pdb|1|31|43|420|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|14|c2v7zA\_.14.pdb|1|68|41|420|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-10|ff733559c10eb320|15|c4kboA\_.15.pdb|1|56|42|419|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|16|c1dkgD\_.16.pdb|1|51|43|419|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-10|ff733559c10eb320|17|c4rtfD\_.17.pdb|1|54|42|418|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|18|c4czeA\_.18.pdb|1|23|41|415|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|19|c1jcgA\_.19.pdb|1|25|40|415|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-10|ff733559c10eb320|20|c7bvzA\_.20.pdb|1|22|42|418|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|1|c3d2fC\_.1.pdb|1|28|10|631|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|2|c5e84B\_.2.pdb|1|64|6|618|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|3|c5tkyA\_.3.pdb|1|59|11|616|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|4|c2khoA\_.4.pdb|1|50|12|618|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|5|c3c7nB\_.5.pdb|1|78|9|556|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|6|c5obuA\_.6.pdb|1|50|10|556|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|7|c2v7yA\_.7.pdb|1|56|10|543|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-11|795d63830c2f0824|8|c5mb9B\_.8.pdb|1|28|9|501|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|9|c4j8fA\_.9.pdb|1|77|7|397|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-11|795d63830c2f0824|10|c6gfaA\_.10.pdb|1|36|12|386|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|11|c3iucC\_.11.pdb|1|66|4|391|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-11|795d63830c2f0824|12|c1hpmA\_.12.pdb|1|79|10|390|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-11|795d63830c2f0824|13|c4gniA\_.13.pdb|1|31|10|391|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|14|c2v7zA\_.14.pdb|1|77|9|391|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-11|795d63830c2f0824|15|c4kboA\_.15.pdb|1|55|12|390|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|16|c1dkgD\_.16.pdb|1|50|11|390|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-11|795d63830c2f0824|17|c4rtfD\_.17.pdb|1|49|11|389|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|18|c4czeA\_.18.pdb|1|22|13|386|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|19|c1jcgA\_.19.pdb|1|26|10|386|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-11|795d63830c2f0824|20|c7bvzA\_.20.pdb|1|21|7|389|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|1|c3d2fC\_.1.pdb|1|41|2|705|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|2|c5e84B\_.2.pdb|1|32|1|694|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|3|c5tkyA\_.3.pdb|1|31|3|692|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|4|c2khoA\_.4.pdb|1|28|3|695|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|5|c3c7nB\_.5.pdb|1|31|2|550|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|6|c2v7yA\_.6.pdb|1|29|1|539|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|7|c5mb9B\_.7.pdb|1|23|3|499|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|8|c5obuA\_.8.pdb|1|28|3|545|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|9|c4j8fA\_.9.pdb|1|36|2|413|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-17|06cbd9b3e6074c55|10|c6gfaA\_.10.pdb|1|44|3|377|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|11|c4gniA\_.11.pdb|1|27|3|381|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|12|c4kboA\_.12.pdb|1|35|2|381|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|13|c1hpmA\_.13.pdb|1|39|2|381|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-17|06cbd9b3e6074c55|14|c3iucC\_.14.pdb|1|37|1|383|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-17|06cbd9b3e6074c55|15|c2v7zA\_.15.pdb|1|39|2|382|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|16|c1dkgD\_.16.pdb|1|34|3|381|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-17|06cbd9b3e6074c55|17|c4rtfD\_.17.pdb|1|34|3|380|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|18|c1jcgA\_.18.pdb|1|21|1|387|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|19|c4czeA\_.19.pdb|1|15|2|377|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-17|06cbd9b3e6074c55|20|c7bvzA\_.20.pdb|1|16|2|380|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|1|c2khoA\_.1.pdb|1|62|49|642|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|2|c3d2fC\_.2.pdb|1|28|49|654|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|3|c5e84B\_.3.pdb|1|50|49|644|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|4|c5tkyA\_.4.pdb|1|49|47|644|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|5|c3c7nB\_.5.pdb|1|53|49|583|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|6|c5obuA\_.6.pdb|1|56|46|583|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|7|c2v7yA\_.7.pdb|1|66|49|570|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-5|239f8c9c9181825c|8|c5mb9B\_.8.pdb|1|27|47|530|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|9|c4j8fA\_.9.pdb|1|51|45|428|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-5|239f8c9c9181825c|10|c4kboA\_.10.pdb|1|71|49|422|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|11|c1dkgD\_.11.pdb|1|65|48|422|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-5|239f8c9c9181825c|12|c6gfaA\_.12.pdb|1|38|49|418|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|13|c4gniA\_.13.pdb|1|29|47|423|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|14|c3iucC\_.14.pdb|1|54|40|424|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-5|239f8c9c9181825c|15|c1hpmA\_.15.pdb|1|52|49|422|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-5|239f8c9c9181825c|16|c2v7zA\_.16.pdb|1|51|45|423|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-5|239f8c9c9181825c|17|c4rtfD\_.17.pdb|1|60|48|421|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|18|c4czeA\_.18.pdb|1|22|50|418|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|19|c1jcgA\_.19.pdb|1|24|47|418|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-5|239f8c9c9181825c|20|c7bvzA\_.20.pdb|1|20|44|421|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|1|c3d2fC\_.1.pdb|1|36|2|651|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|2|c5e84B\_.2.pdb|1|29|1|640|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|3|c5tkyA\_.3.pdb|1|29|3|638|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|4|c2khoA\_.4.pdb|1|25|3|642|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|5|c3c7nB\_.5.pdb|1|32|3|578|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|6|c2v7yA\_.6.pdb|1|28|1|537|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|7|c5obuA\_.7.pdb|1|27|3|578|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|8|c5mb9B\_.8.pdb|1|22|3|494|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|9|c4j8fA\_.9.pdb|1|36|1|402|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|10|c6gfaA\_.10.pdb|1|47|3|377|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|11|c4kboA\_.11.pdb|1|33|2|381|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|12|c4gniA\_.12.pdb|1|25|3|381|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|13|c3iucC\_.13.pdb|1|36|1|383|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-7|96ff8d2d40212f11|14|c1dkgD\_.14.pdb|1|31|3|381|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-7|96ff8d2d40212f11|15|c1hpmA\_.15.pdb|1|38|2|381|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-7|96ff8d2d40212f11|16|c2v7zA\_.16.pdb|1|38|2|382|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|17|c4rtfD\_.17.pdb|1|31|3|380|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|18|c4czeA\_.18.pdb|1|16|2|377|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|19|c1jcgA\_.19.pdb|1|19|1|387|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-7|96ff8d2d40212f11|20|c7bvzA\_.20.pdb|1|18|2|380|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|1|c2khoA\_.1.pdb|1|63|59|650|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|2|c3d2fC\_.2.pdb|1|28|57|664|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|3|c5tkyA\_.3.pdb|1|50|57|648|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|4|c5e84B\_.4.pdb|1|51|57|650|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|5|c3c7nB\_.5.pdb|1|53|57|593|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|6|c2v7yA\_.6.pdb|1|66|57|583|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|7|c5obuA\_.7.pdb|1|57|56|593|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|8|c5mb9B\_.8.pdb|1|27|57|540|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|9|c4j8fA\_.9.pdb|1|51|55|438|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-1|5369a0fb25cf80ea|10|c4kboA\_.10.pdb|1|71|58|432|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|11|c1dkgD\_.11.pdb|1|65|58|432|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-1|5369a0fb25cf80ea|12|c6gfaA\_.12.pdb|1|38|59|428|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|13|c4gniA\_.13.pdb|1|30|57|432|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|14|c3iucC\_.14.pdb|1|54|57|434|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-1|5369a0fb25cf80ea|15|c1hpmA\_.15.pdb|1|52|58|432|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-1|5369a0fb25cf80ea|16|c2v7zA\_.16.pdb|1|51|51|433|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|17|c4rtfD\_.17.pdb|1|60|58|431|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|18|c4czeA\_.18.pdb|1|22|60|428|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|19|c1jcgA\_.19.pdb|1|24|57|431|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-1|5369a0fb25cf80ea|20|c7bvzA\_.20.pdb|1|20|54|431|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|1|c3d2fC\_.1.pdb|1|28|36|656|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|2|c5e84B\_.2.pdb|1|73|34|642|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|3|c5tkyA\_.3.pdb|1|55|37|640|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|4|c2khoA\_.4.pdb|1|52|38|644|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|5|c3c7nB\_.5.pdb|1|69|36|579|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|6|c5obuA\_.6.pdb|1|54|36|579|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|7|c2v7yA\_.7.pdb|1|60|35|566|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|8|c5mb9B\_.8.pdb|1|28|38|525|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|9|c4j8fA\_.9.pdb|1|67|33|420|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-19|a2e9c90dc2fec722|10|c3iucC\_.10.pdb|1|75|31|414|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-19|a2e9c90dc2fec722|11|c6gfaA\_.11.pdb|1|36|38|409|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|12|c4gniA\_.12.pdb|1|31|38|413|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|13|c1hpmA\_.13.pdb|1|69|36|413|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-19|a2e9c90dc2fec722|14|c2v7zA\_.14.pdb|1|68|36|414|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|15|c4kboA\_.15.pdb|1|56|37|413|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|16|c1dkgD\_.16.pdb|1|54|38|413|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-19|a2e9c90dc2fec722|17|c4rtfD\_.17.pdb|1|54|37|412|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|18|c1jcgA\_.18.pdb|1|24|35|412|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|19|c4czeA\_.19.pdb|1|23|36|409|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-19|a2e9c90dc2fec722|20|c7bvzA\_.20.pdb|1|20|37|412|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|1|c3d2fC\_.1.pdb|1|28|8|626|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|2|c5e84B\_.2.pdb|1|64|3|615|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|3|c5tkyA\_.3.pdb|1|60|8|613|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|4|c2khoA\_.4.pdb|1|50|9|617|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|5|c3c7nB\_.5.pdb|1|83|6|553|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|6|c5obuA\_.6.pdb|1|50|6|553|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|7|c2v7yA\_.7.pdb|1|54|6|540|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|8|c5mb9B\_.8.pdb|1|26|9|499|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|9|c4j8fA\_.9.pdb|1|80|5|394|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-16|e59c5086baf1ba3d|10|c6gfaA\_.10.pdb|1|37|9|383|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|11|c3iucC\_.11.pdb|1|67|1|388|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-16|e59c5086baf1ba3d|12|c1hpmA\_.12.pdb|1|84|7|387|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-16|e59c5086baf1ba3d|13|c2v7zA\_.13.pdb|1|83|6|388|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|14|c4gniA\_.14.pdb|1|30|9|387|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|15|c4kboA\_.15.pdb|1|53|8|387|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|16|c1dkgD\_.16.pdb|1|50|8|387|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-16|e59c5086baf1ba3d|17|c4rtfD\_.17.pdb|1|49|8|386|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|18|c4czeA\_.18.pdb|1|21|10|383|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|19|c1jcgA\_.19.pdb|1|26|6|383|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-16|e59c5086baf1ba3d|20|c7bvzA\_.20.pdb|1|21|8|386|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|1|c3d2fC\_.1.pdb|1|27|6|624|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|2|c5e84B\_.2.pdb|1|65|2|614|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|3|c5tkyA\_.3.pdb|1|60|8|612|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|4|c2khoA\_.4.pdb|1|51|8|616|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|5|c3c7nB\_.5.pdb|1|82|5|552|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|6|c5obuA\_.6.pdb|1|51|5|552|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|7|c2v7yA\_.7.pdb|1|55|6|542|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|8|c5mb9B\_.8.pdb|1|27|5|498|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|9|c4j8fA\_.9.pdb|1|80|4|393|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|10|c6gfaA\_.10.pdb|1|38|8|382|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|11|c1hpmA\_.11.pdb|1|82|6|386|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-9|d50e9ecca5f69dc1|12|c4gniA\_.12.pdb|1|31|8|386|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|13|c2v7zA\_.13.pdb|1|81|4|387|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|14|c3iucC\_.14.pdb|1|68|4|387|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|15|c4kboA\_.15.pdb|1|54|7|386|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|16|c1dkgD\_.16.pdb|1|51|7|386|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|17|c4rtfD\_.17.pdb|1|49|7|385|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|18|c4czeA\_.18.pdb|1|21|6|382|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|19|c1jcgA\_.19.pdb|1|24|6|382|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-9|d50e9ecca5f69dc1|20|c7bvzA\_.20.pdb|1|19|4|385|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|1|c3d2fC\_.1.pdb|1|28|10|627|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|2|c5e84B\_.2.pdb|1|65|5|617|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|3|c5tkyA\_.3.pdb|1|60|11|615|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|4|c2khoA\_.4.pdb|1|51|11|619|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|5|c3c7nB\_.5.pdb|1|84|8|555|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|6|c5obuA\_.6.pdb|1|50|9|555|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|7|c2v7yA\_.7.pdb|1|55|8|545|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-15|50fa879da6b92f30|8|c5mb9B\_.8.pdb|1|27|8|501|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|9|c4j8fA\_.9.pdb|1|81|8|396|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-15|50fa879da6b92f30|10|c6gfaA\_.10.pdb|1|38|11|385|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|11|c1hpmA\_.11.pdb|1|84|9|389|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-15|50fa879da6b92f30|12|c3iucC\_.12.pdb|1|68|8|390|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-15|50fa879da6b92f30|13|c2v7zA\_.13.pdb|1|83|8|390|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-15|50fa879da6b92f30|14|c4gniA\_.14.pdb|1|30|11|390|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|15|c4kboA\_.15.pdb|1|54|10|389|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|16|c1dkgD\_.16.pdb|1|51|11|389|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-15|50fa879da6b92f30|17|c4rtfD\_.17.pdb|1|50|10|388|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|18|c4czeA\_.18.pdb|1|21|12|385|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|19|c1jcgA\_.19.pdb|1|24|8|389|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-15|50fa879da6b92f30|20|c7bvzA\_.20.pdb|1|20|6|388|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|1|c3d2fC\_.1.pdb|1|29|8|622|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|2|c5e84B\_.2.pdb|1|64|3|615|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|3|c5tkyA\_.3.pdb|1|59|9|613|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|4|c2khoA\_.4.pdb|1|50|9|617|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|5|c3c7nB\_.5.pdb|1|82|6|553|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|6|c5obuA\_.6.pdb|1|50|6|553|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|7|c2v7yA\_.7.pdb|1|54|6|543|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|8|c5mb9B\_.8.pdb|1|27|9|499|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|9|c4j8fA\_.9.pdb|1|79|5|394|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-22|f1892e3c83e344dc|10|c6gfaA\_.10.pdb|1|37|9|383|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|11|c3iucC\_.11.pdb|1|67|1|388|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-22|f1892e3c83e344dc|12|c1hpmA\_.12.pdb|1|82|7|387|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-22|f1892e3c83e344dc|13|c4gniA\_.13.pdb|1|30|9|388|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|14|c2v7zA\_.14.pdb|1|82|6|388|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|15|c4kboA\_.15.pdb|1|53|8|387|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|16|c1dkgD\_.16.pdb|1|49|9|387|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-22|f1892e3c83e344dc|17|c4rtfD\_.17.pdb|1|49|8|386|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|18|c4czeA\_.18.pdb|1|20|10|383|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|19|c1jcgA\_.19.pdb|1|24|6|383|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-22|f1892e3c83e344dc|20|c7bvzA\_.20.pdb|1|20|8|386|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|1|c3d2fC\_.1.pdb|1|28|7|625|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|2|c5e84B\_.2.pdb|1|64|3|615|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|3|c5tkyA\_.3.pdb|1|59|8|614|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-4|fea22737d4540347|4|c2khoA\_.4.pdb|1|51|9|617|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|5|c3c7nB\_.5.pdb|1|82|6|553|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|6|c5obuA\_.6.pdb|1|50|6|553|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|7|c2v7yA\_.7.pdb|1|55|7|540|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-4|fea22737d4540347|8|c5mb9B\_.8.pdb|1|27|9|499|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|9|c4j8fA\_.9.pdb|1|80|5|394|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-4|fea22737d4540347|10|c6gfaA\_.10.pdb|1|37|9|383|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|11|c1hpmA\_.11.pdb|1|83|7|387|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-4|fea22737d4540347|12|c3iucC\_.12.pdb|1|67|1|388|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-4|fea22737d4540347|13|c4gniA\_.13.pdb|1|31|9|388|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|14|c2v7zA\_.14.pdb|1|82|6|388|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-4|fea22737d4540347|15|c4kboA\_.15.pdb|1|53|8|387|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|16|c1dkgD\_.16.pdb|1|50|9|387|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-4|fea22737d4540347|17|c4rtfD\_.17.pdb|1|50|8|386|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|18|c4czeA\_.18.pdb|1|20|10|383|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|19|c1jcgA\_.19.pdb|1|23|9|393|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-4|fea22737d4540347|20|c7bvzA\_.20.pdb|1|20|4|386|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|1|c3d2fC\_.1.pdb|1|27|57|664|2.30|PDB header: chaperone| Chain: C: PDB Molecule: heat shock protein homolog sse1;| PDBTitle: crystal structure of a complex of sse1p and hsp70| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|2|c2khoA\_.2.pdb|1|56|57|655|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|3|c5e84B\_.3.pdb|1|51|57|653|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|4|c5tkyA\_.4.pdb|1|45|55|651|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|5|c3c7nB\_.5.pdb|1|54|56|592|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|6|c5obuA\_.6.pdb|1|55|54|592|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|7|c2v7yA\_.7.pdb|1|64|56|579|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|8|c5mb9B\_.8.pdb|1|28|55|539|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|9|c4j8fA\_.9.pdb|1|51|52|437|2.70|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b, hsc70-interacting protein;| PDBTitle: crystal structure of a fusion protein containing the nbd of hsp70 and2 the middle domain of hip| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-14|07e4268cbf8c1950|10|c4kboA\_.10.pdb|1|54|57|431|2.80|PDB header: signaling protein| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: crystal structure of the human mortalin (grp75) atpase domain in the2 apo form| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|11|c1dkgD\_.11.pdb|1|55|56|431|2.80|PDB header: complex (hsp24/hsp70)| Chain: D: PDB Molecule: molecular chaperone dnak;| PDBTitle: crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak| | | | | | | | | | | | | | | | | | |  |
| SlHsp70-14|07e4268cbf8c1950|12|c6gfaA\_.12.pdb|1|33|57|427|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 105 kda;| PDBTitle: structure of nucleotide binding domain of hsp110, atp and mg2+2 complexed| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|13|c4gniA\_.13.pdb|1|32|57|431|1.80|PDB header: chaperone| Chain: A: PDB Molecule: putative heat shock protein;| PDBTitle: structure of the ssz1 atpase bound to atp and magnesium| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|14|c3iucC\_.14.pdb|1|52|52|432|2.40|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| | | | | | | | | | | | | | | | | |  |  |
| SlHsp70-14|07e4268cbf8c1950|15|c1hpmA\_.15.pdb|1|52|56|431|1.70|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| | | | | | | | | | | | | | | | | | | |
| SlHsp70-14|07e4268cbf8c1950|16|c2v7zA\_.16.pdb|1|52|56|432|3.50|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| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|17|c4rtfD\_.17.pdb|1|60|56|430|2.77|PDB header: chaperone| Chain: D: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of molecular chaperone dnak from mycobacterium2 tuberculosis h37rv| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|18|c4czeA\_.18.pdb|1|26|58|427|2.00|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: c. crescentus mreb, double filament, empty| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|19|c1jcgA\_.19.pdb|1|27|56|427|3.10|PDB header: structural protein| Chain: A: PDB Molecule: rod shape-determining protein mreb;| PDBTitle: mreb from thermotoga maritima, amppnp| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-14|07e4268cbf8c1950|20|c7bvzA\_.20.pdb|1|20|52|430|2.30|PDB header: protein fibril| Chain: A: PDB Molecule: cell shape determining protein mreb;| PDBTitle: crystal structure of mreb5 of spiroplasma citri bound to adp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|1|c5gjjA\_.1.pdb|0.999|49|95|177|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a;| PDBTitle: glutathionylated hhsp70 sbd| | | | | | | | |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|2|c1u00A\_.2.pdb|0.999|22|95|171|1.95|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein hsca;| PDBTitle: hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|3|c3dpqE\_.3.pdb|0.999|37|95|176|2.60|PDB header: chaperone, peptide binding protein| Chain: E: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the substrate binding domain of e.2 coli dnak in complex with a long pyrrhocoricin-derived3 inhibitor peptide (form b)| | | | | | | | | | | | | | | | | | | |
| SlHsp70-12|6f0355d388d6ae42|4|c2op6A\_.4.pdb|0.998|41|95|177|1.85|PDB header: peptide binding protein| Chain: A: PDB Molecule: heat shock 70 kda protein d;| PDBTitle: peptide-binding domain of heat shock 70 kda protein d precursor from2 c.elegans| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|5|d1u00a2.5.pdb|0.998|21|95|176|1.95|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein hsca;| PDBTitle: hsca substrate binding domain complexed with the iscu2 recognition peptide elppvkihc| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|6|c5e85A\_.6.pdb|0.998|45|95|177|2.57|PDB header: chaperone| Chain: A: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: isolated sbd of bip| | | | | | | | |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|7|c1bprA\_.7.pdb|0.998|37|95|176|UNK|PDB header: molecular chaperone| Chain: A: PDB Molecule: dnak;| PDBTitle: nmr structure of the substrate binding domain of dnak,2 minimized average structure| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|8|c6zhiB\_.8.pdb|0.998|47|95|177|3.25|PDB header: chaperone| Chain: B: PDB Molecule: heat shock protein 70;| PDBTitle: structure of the plasmodium falciparum hsp70-x substrate binding2 domain in complex with hydrophobic peptide| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|9|c3dqgC\_.9.pdb|0.998|38|95|174|1.72|PDB header: chaperone| Chain: C: PDB Molecule: heat shock 70 kda protein f;| PDBTitle: peptide-binding domain of heat shock 70 kda protein f, mitochondrial2 precursor, from caenorhabditis elegans.| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|10|d1yuwa1.10.pdb|0.998|52|95|177|2.60|PDB header: chaperone| Chain: A: PDB Molecule: heat shock cognate 71 kda protein;| PDBTitle: crystal structure of bovine hsc70(aa1-554)e213a/d214a mutant| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|11|c3n8eA\_.11.pdb|0.998|43|95|171|2.80|PDB header: chaperone| Chain: A: PDB Molecule: stress-70 protein, mitochondrial;| PDBTitle: substrate binding domain of the human heat shock 70kda protein 92 (mortalin)| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|12|c4po2A\_.12.pdb|0.998|49|95|177|2.00|PDB header: chaperone| Chain: A: PDB Molecule: heat shock 70 kda protein 1a/1b;| PDBTitle: crystal structure of the stress-inducible human heat shock protein2 hsp70 substrate-binding domain in complex with peptide substrate| | | | | | | | | | | | | | | | | | | |
| SlHsp70-12|6f0355d388d6ae42|13|d1dkza2.13.pdb|0.998|37|95|176|2.00|PDB header: complex (molecular chaperone/peptide)| Chain: A: PDB Molecule: substrate binding domain of dnak;| PDBTitle: the substrate binding domain of dnak in complex with a substrate2 peptide, determined from type 1 native crystals| | | | | | | | | | | | | | | | | | | |
| SlHsp70-12|6f0355d388d6ae42|14|c5obuA\_.14.pdb|0.994|39|95|171|2.00|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: mycoplasma genitalium dnak deletion mutant lacking sbdalpha in complex2 with amppnp.| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|15|c3c7nB\_.15.pdb|0.994|52|95|176|3.12|PDB header: chaperone/chaperone| Chain: B: PDB Molecule: heat shock cognate;| PDBTitle: structure of the hsp110:hsc70 nucleotide exchange complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|16|c2v7yA\_.16.pdb|0.993|42|95|171|2.37|PDB header: chaperone| Chain: A: PDB Molecule: chaperone protein dnak;| PDBTitle: crystal structure of the molecular chaperone dnak from2 geobacillus kaustophilus hta426 in post-atp hydrolysis3 state| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|17|c5tkyA\_.17.pdb|0.993|30|95|177|2.60|PDB header: chaperone| Chain: A: PDB Molecule: putative uncharacterized protein;| PDBTitle: crystal structure of the co-translational hsp70 chaperone ssb in the2 atp-bound, open conformation| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|18|c2khoA\_.18.pdb|0.992|39|95|171|UNK|PDB header: chaperone| Chain: A: PDB Molecule: heat shock protein 70;| PDBTitle: nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone (1-605)2 complexed with adp and substrate| | | | | | | | | | | | | | | |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|19|c5e84B\_.19.pdb|0.988|39|103|177|2.99|PDB header: chaperone| Chain: B: PDB Molecule: 78 kda glucose-regulated protein;| PDBTitle: atp-bound state of bip| | | | | | | | |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-12|6f0355d388d6ae42|20|c5mb9B\_.20.pdb|0.979|9|104|161|3.20|PDB header: chaperone| Chain: B: PDB Molecule: putative heat shock protein;| PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair| | | | | | | | | | | | | | | |  |  |  |  |
| # Job Description|Job ID|Rank|Template/Model|Confidence|Sequence ID|Qstart|Qend|Resolution|Template Info |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|1|c5nnrD\_.1.pdb|1|13|3|573|3.10|PDB header: transferase| Chain: D: PDB Molecule: n-terminal acetyltransferase-like protein;| PDBTitle: structure of naa15/naa10 bound to hypk-thb| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|2|c6c95A\_.2.pdb|1|11|3|573|3.15|PDB header: transferase| Chain: A: PDB Molecule: n-alpha-acetyltransferase 15, nata auxiliary subunit;| PDBTitle: the human nata (naa10/naa15) amino-terminal acetyltransferase complex2 bound to hypk| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|3|c4kvmA\_.3.pdb|1|11|4|573|2.60|PDB header: transferase/transferase inhibitor| Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1;| PDBTitle: the nata (naa10p/naa15p) amino-terminal acetyltransferase complex2 bound to a bisubstrate analog| | | | | | | | | | | | | | | | | | | |
| SlHsp70-20|2b0aeb2f6bc5dde2|4|c4hnxA\_.4.pdb|1|10|2|573|2.34|PDB header: transferase| Chain: A: PDB Molecule: n-terminal acetyltransferase a complex subunit nat1;| PDBTitle: the nata acetyltransferase complex bound to ppgpp| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|5|c4uzyA\_.5.pdb|1|10|5|563|2.48|PDB header: motor protein| Chain: A: PDB Molecule: flagellar associated protein;| PDBTitle: crystal structure of the chlamydomonas ift70 and ift52 complex| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|6|c6yj6A\_.6.pdb|1|11|5|573|3.10|PDB header: transcription| Chain: A: PDB Molecule: transcription factor tau 131 kda subunit;| PDBTitle: structure of the tfiiic subcomplex taua| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|7|c4bujF\_.7.pdb|1|11|2|573|3.70|PDB header: hydrolase| Chain: F: PDB Molecule: superkiller protein 3;| PDBTitle: crystal structure of the s. cerevisiae ski2-3-8 complex| | | | | | | | | |  |  |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|8|d1w3ba\_.8.pdb|1|19|5|507|2.85|PDB header: transferase| Chain: A: PDB Molecule: udp-n-acetylglucosamine--peptide| PDBTitle: the superhelical tpr domain of o-linked glcnac transferase2 reveals structural similarities to importin alpha.| | | | | | | | | | | | | | | | |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|9|c6q6hK\_.9.pdb|1|10|3|579|3.20|PDB header: cell cycle| Chain: K: PDB Molecule: cell division cycle protein 16 homolog;| PDBTitle: cryo-em structure of the apc/c-cdc20-cdk2-cyclina2-cks2 complex, the2 d2 box class| | | | | | | | | | | | | | |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|10|c7kdtA\_.10.pdb|1|19|2|513|3.05|PDB header: viral protein| Chain: A: PDB Molecule: mitochondrial import receptor subunit tom70;| PDBTitle: human tom70 in complex with sars cov2 orf9b| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|11|c4ui9K\_.11.pdb|1|10|3|523|3.60|PDB header: cell cycle| Chain: K: PDB Molecule: cell division cycle protein 16 homolog;| PDBTitle: atomic structure of the human anaphase-promoting complex| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|12|c5dseA\_.12.pdb|1|12|1|523|2.90|PDB header: protein binding| Chain: A: PDB Molecule: tetratricopeptide repeat protein 7b;| PDBTitle: crystal structure of the ttc7b/hyccin complex| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|13|c6tedQ\_.13.pdb|1|11|2|567|3.10|PDB header: transcription| Chain: Q: PDB Molecule: rna polymerase-associated protein ctr9 homolog;| PDBTitle: structure of complete, activated transcription complex pol ii-dsif-2 paf-spt6 uncovers allosteric elongation activation by rtf1| | | | | | | | | | | | | | | | | | | |
| SlHsp70-20|2b0aeb2f6bc5dde2|14|c2xpiA\_.14.pdb|1|8|3|523|2.60|PDB header: cell cycle| Chain: A: PDB Molecule: anaphase-promoting complex subunit cut9;| PDBTitle: crystal structure of apc/c hetero-tetramer cut9-hcn1| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|15|c5aioA\_.15.pdb|1|11|5|520|3.15|PDB header: transcription| Chain: A: PDB Molecule: transcription factor tau 131 kda subunit;| PDBTitle: crystal structure of t131 n-terminal tpr array| | | | | | | | | | |  |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|16|c2gw1A\_.16.pdb|1|20|1|559|3.00|PDB header: protein transport| Chain: A: PDB Molecule: mitochondrial precursor proteins import receptor;| PDBTitle: crystal structure of the yeast tom70| | | | | | | | | | | |  |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|17|c6af0A\_.17.pdb|1|11|2|573|2.88|PDB header: transcription| Chain: A: PDB Molecule: ctr9 protein;| PDBTitle: structure of ctr9, paf1 and cdc73 ternary complex from myceliophthora2 thermophila| | | | | | | | | | | | |  |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|18|c3fp4A\_.18.pdb|1|16|1|513|2.14|PDB header: transport protein| Chain: A: PDB Molecule: tpr repeat-containing protein yhr117w;| PDBTitle: crystal structure of tom71 complexed with ssa1 c-terminal2 fragment| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|19|c5ganJ\_.19.pdb|1|10|2|569|3.60|PDB header: transcription| Chain: J: PDB Molecule: pre-mrna-splicing factor 6;| PDBTitle: the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom| | | | | | | | | | | | | |  |  |  |  |  |  |
| SlHsp70-20|2b0aeb2f6bc5dde2|20|c2y4tA\_.20.pdb|1|21|2|573|3.00|PDB header: chaperone| Chain: A: PDB Molecule: dnaj homolog subfamily c member 3;| PDBTitle: crystal structure of the human co-chaperone p58(ipk)| | | | | | | | | | | |  |  |  |  |  |  |  |  |