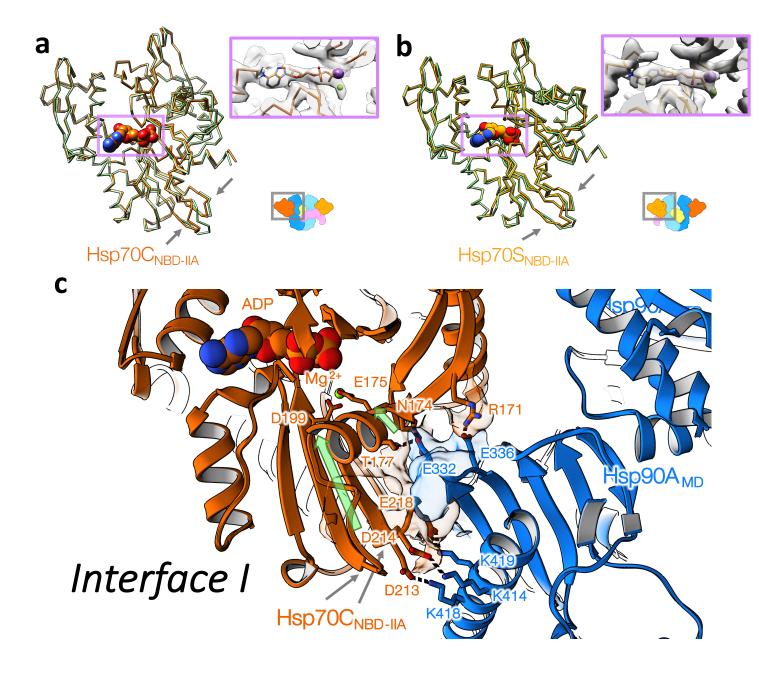
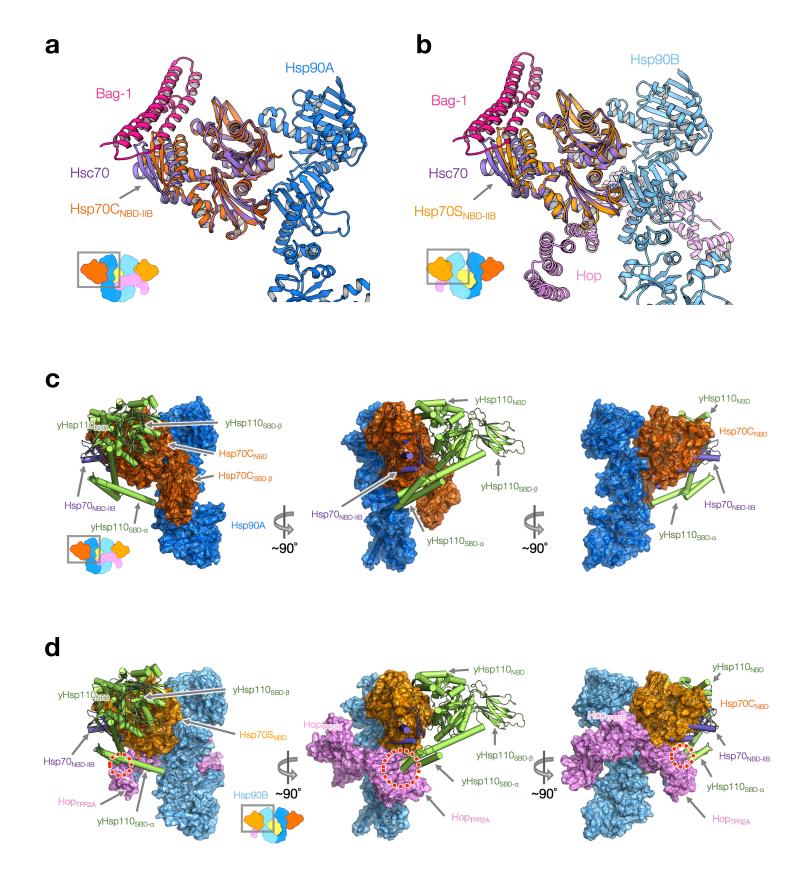
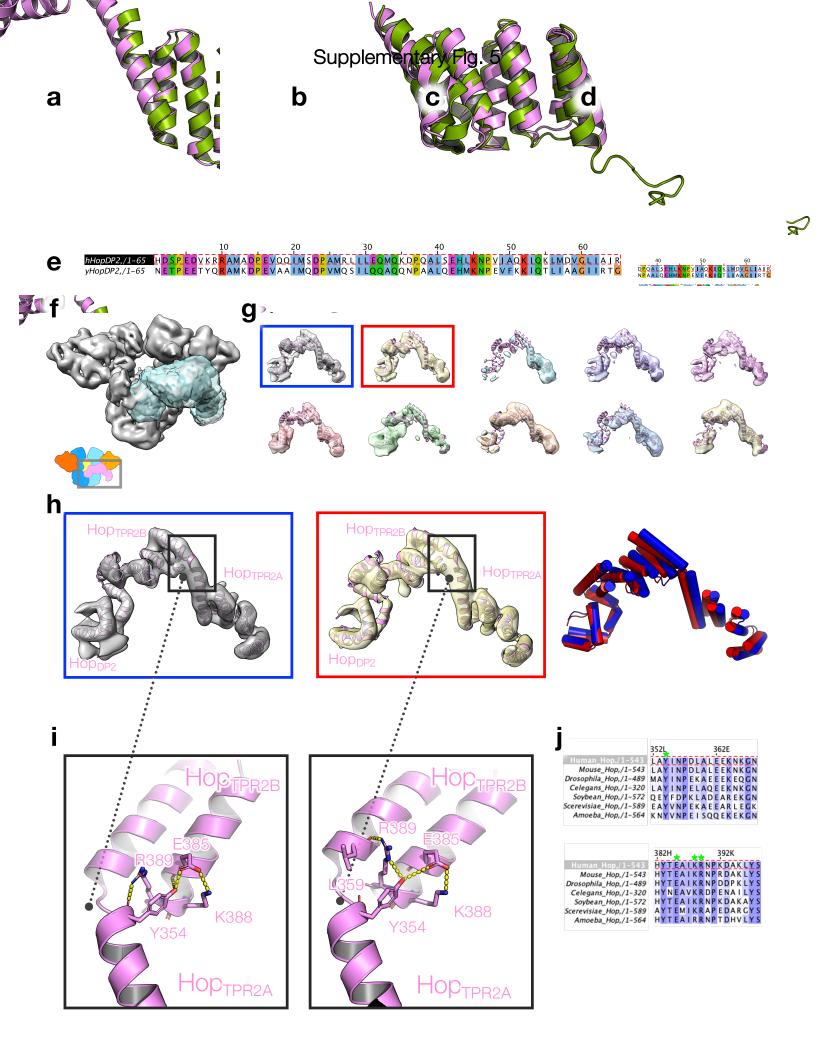


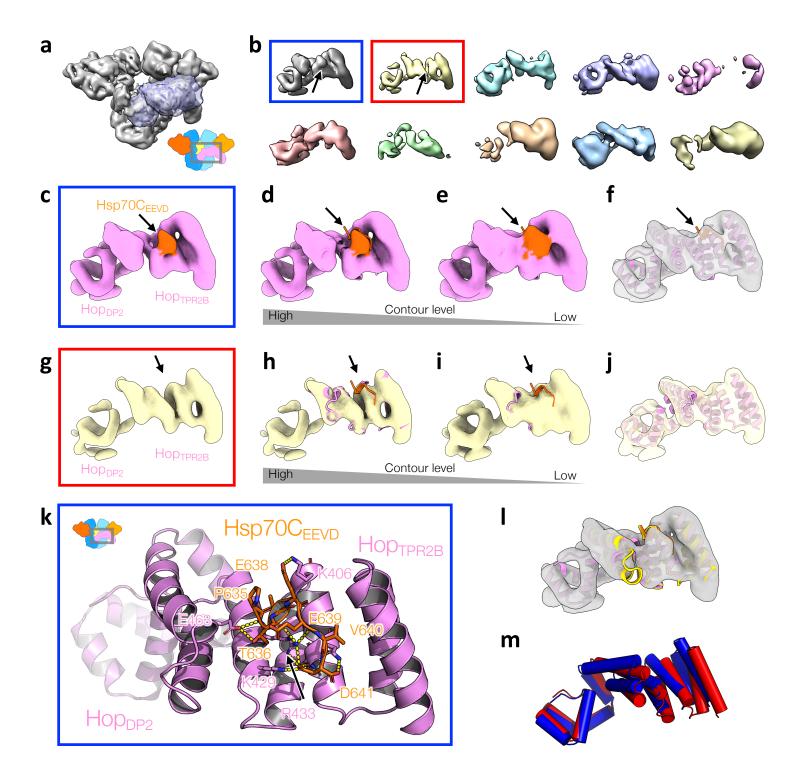
| | -61 | -51 | -41 | -31 | -21 | -11 | -1 | |
|------------------------------|--|-----------------------------------|-----------------------|----------------------------|------------------------------------|---------------------|---|-------------------|
| Hsp90α/1-732 Hsp90β/1-724 | -61 1 1 | | | | | | MPEETQTQC | <u>5</u> 9 - 4 |
| Hsp82/1-709 Grp94/1-650 | 1 | | | | | VQ | REEEAIQLDGASC | 2 15 |
| hTRAP1/1-704 HtpG/1-624 | 1 MAR ELRALLLWC | GR R L R P L L R A P A | LAAVPGGKP L | C P R R T T AQ L 0 | G P R R N P A W S L Q | AGRLFSTQTA | | s 77 - |
| Hsp90α/1-732 | 10Q 200 10 QPMEEEEVET F | 30M | 40N | 50S | 60R | | 80L | 5 86 |
| Hsp90β/1-724 Hsp82/1-709 | 5 VHHGEEEVETFA 1MASETFE | FQAEIAQLMSL | IINTFYSNKEI | FLRELISNA | SDALDKIRYES | LTDPSKLDSG | K E L K I D I I P N P Q E | E 81 |
| Grp94/1-650 hTRAP1/1-704 | 16 I R E L R E K S E K F A 78 T E S VQ G S T S K H E | FQAEVNRMMKL | IINSLYKNKEI | FLRELISNA | SDALDKIRLIS | LTDENALAGN | EELTVKIKCDKEK | < 92 |
| HtpG/1-624 | 1 MK GQ ET R (| FQSEVKQLLHL | M | FLRELISNA | <mark>S D A A D K L R</mark> F R A | LSNPDLYEGD | GELRVRVSFDKDK | |
| Hsp90α/1-732 | 90T 87 RTLTIVDTCICN | | | | | | 8V 157- T <mark>VITKHNDDE</mark> | E 158 |
| Hsp90β/1-724 Hsp82/1-709 | 82 R T L T L V D T G I G N 73 K V L E I R D S G I G N | ITKAELINNLGT | I A K S G T K A F M E | ALSAGAD | SMIGQFGVGF | YSLFLVADRV | 2 V I S K S N D D E | E 144 |
| | 152 GT I T I Q DT G I GN | ITQ E E L V S N L G T | IARSGSKAFLD | ALQNQAEAS | SKIIGQFGVGF | Y S A F M V A D R V | E <mark>V</mark> Y <mark>S R</mark> S A A – P G S L | L 227 |
| HtpG/1-624 | 74 R T L T I S D N G V G N 1655 | 175D | 184T | S L G S DQ A K D : 194Q | SQL <mark>IGQFGVGF</mark> 204K | 214I | T V R T R A A G E K P E N 224K | N 150 |
| Hsp90α/1-732 | 159 QYAWES SAGGS | TVRTD-TGEPM | GRGTKVILHLK | EDQTEYLEE | RRIKEIVKKHS | QFIGYPITLF | VEKERDKEVSDDE | E 234 |
| Hsp82/1-709 | 154 QYAWESSAGGS 145 QYIWESNAGGS | TVTLDEVNERI | G R G T I L R L F L K | DDQLEYLEE | KRIKEVIKRHS | EFVAYPIQLV | VTKEVEKEVPIPE | E 221 |
| hTRAP1/1-704 | 167 QHIWESDS-NE 228 GYQWLSDGSGVF | E I A E A S G V | RTGTKIIIHLK | SDCKEFSSE | ARVRDVVTKYS | NFVSFPLYLN | G | - 289 |
| HtpG/1-624 | 151 GV FWESAGEGEN 244E | | 264D | 274K | 284Y | 294K | 304I | - 218 |
| Hsp90α/1-732 | 235 AEEKEDKEEEKE 230 AEEEKGEKE | | IEDVGSDEEEE | KKDGDKKKK | KIKEKYIDQE | ELNKTKPIWT | | 311 |
| Hsp82/1-709 | 222 EEKKDE-EKKDE 237 | EEKKDEDDKKPK | LEEVDEEE | EKKPKTI | KKVKEEVOEIE | ELNKTKPLWT | RNPSDITOEEYNA | A 291 |
| hTRAP1/1-704 | 290 | | | | R | RMNTLQAIWM | M D P K D V R E W Q H E E | E 313 |
| 1100,1-024 | 314K | 324L 3 | | | 4N 362 | | | 210 |
| | 312 FYKSLTNDWEDH 304 FYKSLTNDWEDH | | | | | | | |
| | 292 FYKSISNDWEDP 267 FYKSFSKESDDP | | | | | | | |
| | 314 FYRYVAQAHDKP 249 FYKHIAHDFNDP | | | | | | | |
| | 392E | 402M | 412 | 422E | 431K | 441F | 451E 459 | |
| Hsp90β/1-724 | 387 GVVDSEDLPLNI 379 GVVDSEDLPLNI 367 GVVDSEDLPLNI | SREMLQQSKIL | KVIRKNIVKKC | LELFSELAE | DKENYKKFYE | AFSKNLKLGI | HEDSTNRRRLS | \$ 452 |
| Grp94/1-650 | 344 GVVDS EDLP LNI 349 GVVDS EDIP LNI 389 GVVDS EDIP LNI | SRETLQQHKLL | K V I R K K L V R K T | LDMIKKIAD | EKY-NDT FWK | EFGTNIKLGV | IEDHSNRTRLA | A 416 |
| | 323 GLIDSSDLPLN | | | | | | | |
| Hsn90a/1-732 | 469A 461 ELLRYYTSASG- | | | | 507F | | | 535 |
| Hsp90β/1-724 | 453 ELLRYHTSQSG- 441 KLLRYNSTKSV- | - DEMTSLSEYV | SRMKETQKSIY | YITGESKEQ | VANSAFVERVR | KRGFEVVYMT | EPIDEYCVQQLKE | 527 |
| Grp94/1-650 | 417 KLLRFQSSHHP- 466 KLLRYESSALP- | - S D I T <mark>S L</mark> DQ Y V | ERMKEKQDKIY | FMAGSSRKE | A E S <mark>S</mark> P F V E R L L | K K G Y E V I Y L T | EPVDEYCIQALPE | E 491 |
| HtpG/1-624 | 398 KLLRFASTHTDS | | | | | | | 474 |
| | 536 FEGKTLVSVTK | | EEEKKK-QEEK | | MKD-ILEKKV | | | |
| Hsp82/1-709 | 528 FDGKSLVSVTKE 516 FEGKTLVDITKE |) - FEL E <mark>E</mark> T | D | IKEYEPLTK | A L K E – I L G D Q V | EKVVVSYKL | D A <mark>P A </mark> A I R T G Q F G W | V 585 |
| hTRAP1/1-704 | 492 FDGKRFQNVAKE 542 FDKKKLISVETE | D I V V D H Y K E E K F | EDRSPAAECLS | EKETEELMAN | W M R N - V L G S R V | TNVKVTLRLD | T H <mark>P A</mark> MV T V L EMGA | A 617 |
| HtpG/1–624 | 475 FDGKPFQSVSKN 611E | DESLEKL 618A | | EKALTPFIDI 635E | | | DT <mark>PAIVST</mark> DADEN 564I 674S | |
| Hsp90α/1-732 | 607 TANMER I MK | AQALR DNS | TMGYMAAKKHL | EINPDHSII | ET LRQKA- EAD | KNDKSVKDLV | LLYETALLSSG | F 676 |
| Hsp82/1-709 | 586 SANMERI MK 558 SGNMERI MK | AQALR DSS | M S S Y M S S K K T F | EISPKSPIII | KELKKRVDEGG | AQDKTVKDLT | K L L Y E T A L L T S G F | F 656 |
| hTRAP1/1-704 | 618 ARHFLRMQQLAK 547 STQMAKLFA | TQEER | AQ L L Q P T L | EINPRHALII | K | - EPGLAQLLV | DQ IYENAMIAAG- | - 681 |
| nip0/1-024 | 684H | 694L | 704T | 714E | 724D | COLAR FOLWY | | |
| | 677 SLEDPOTHANR | | | | | | | 732 724 |
| Hsp82/1-709 Grp94/1-650 | 657 SLDEPTSFASR | NRLISLGLNID | EDEETETAPEA | S T A A P V | EEVPADTEMEE | V D | | 709 650 |
| hTRAP1/1-704 | 682 LVDDPRAMVGRI 607 TLEDPNLFIRRM | NELLVKALERH | | | | | | 704 624 |
| | | | | | | | | |

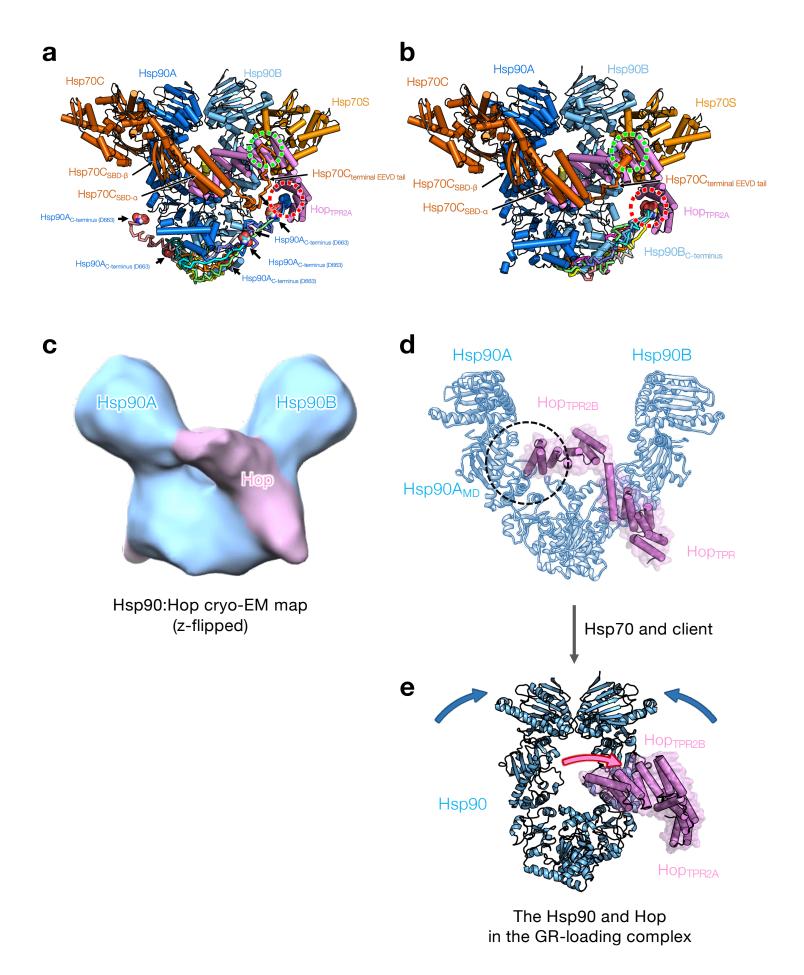
| b | | | | | | | | |
|---|--|---|---|---|---|--|--|---|
| | | -51 -4 | 41 -3 | 31 -2 | -11 | -1 | 10D | 20V |
| | Hsp70/1-641 | 1 | | | | MAK MAK | AAAIGIDLGTTY | SCVGVFQHGK 25 |
| | Hsc70/1-646 SSA1/1-642 | 1 | | | | MSK | GPAVGIDLGTTY | SCVGVFQHGK 25 SCVAHFANDR 23 |
| | BiP/1-654 | 1 | | MK L S | LVAAMLLLLSA | ARAEEEDKKEDV | GTVVGIDLGTTY | SCVGVFKNGR 49 |
| | Mortalin/1-679 | 1 M I SASRAAAAR L | VGAAASRGPT | | | | | |
| | DnaK/1-638 | 1 | | | | M | GKII <mark>GIDLGTT</mark> N | SCVAIMDGTT 23 |
| | | 30A | 40S | 49R | 59V | 69D 79 | G 89H | 99D |
| | Hsp70/1-641 | 26 VELLANDOGNET | | | | | | |
| | Hsc70/1-646 SSA1/1-642 | 26 VEIIANDQGNRT 24 VDIIANDQGNRT | | | | | | |
| | BiP/1-654 | 50 VEIIANDQGNRI | TPSYVAFTPE | GERLIGDAAK | NQLTSNPENTV | FDAKRLIGRTWN | DP S VQQ D I K F L P | FKVVEKKTKP 126 |
| | Mortalin/1-679 DnaK/1-638 | 75 AKVLENAEGART 24 PRVLENAEGDRT | | | | | | |
| | Dilak/1-038 | | | | | | | |
| | | 109- | 118E | 128K | 138P | 148A | | 168N |
| | | 102 K V V S Y K - G E T K 102 K V Q V E Y K - G E T K | | | | | | |
| | SSA1/1-642 | 100 Q I Q V E F K - G E T K | NFTPEQISSM | V L G K M K E T A E | S Y L G A K V N D A V | VTVPAYFNDSQR | QATKDAGTIAGL | NVLRIINEPT 175 |
| | | 127 Y I Q V D I G G G Q T K 152 A - W V E A H G K | | | | | | |
| | | 101 A - WVE VKGQ | | | | | | |
| | | 178A 188 | | | | | 234D | 244E |
| | Hsp70/1-641 | 178 AAAIAYGLDRTG | | 1 | ** * | FEVKATACDTHI | | 1 |
| | Hsc70/1–646 | 178 AAAIAYGLDKKV | GAERNVLIFD | LGGGTFDVSI | LT EDG | FEVKSTAGDTHL | GGEDFDNRMVNH | FIAEFKRKHK 250 |
| | | 176 AAAIAYGLDKKG 204 AAAIAYGLDKRE | | | | | | |
| | | 225 AAALAYGLDK SE | | | | | | |
| | | 174 AAALAYGLDKGT | | | | | | |
| | | 254S | 264R | 274L | 284 | 290G 300/ | A 310F | 320A |
| | Hsp70/1-641 | 251 KDI SQNKRAVRR | LRTACERAKR | TLSSSTOASL | EDSLFE | GIDFYTSITRAR | FEELCSDLFRST | LEPVEKALRD 323 |
| | | 251 KDISENKRAVRR | | | | | | |
| | | 248 K D L S T NQ R A L R R 276 K D V R K D N R A V Q K | | | | | | |
| | Mortalin/1-679 | 296 VDLTKDNMALQR | VREAAEKAKC | ELSSSVQTDI | N L P Y L T M D S S G | P K H L NMK L T R A Q | FEGIVTDLIRRT | IAPCQKAMQD 372 |
| | DnaK/1-638 | 250 IDLRNDPLAMQR | LKEAAEKAKI | E L S S AQQT DV | N L P Y I T A D A T G | P K HM N I K <mark>V T R A</mark> K | | IEPLKVALQD 326 |
| | | 330Q | 340S | 350L | 360N | 370A | 1 1- | 0D |
| | | 324 AKLDKAQIHDLV | LVGGSTRIPK | VOKILODEEN | | EAVAVCAAVOAA | | |
| | HSC/0/1-040 | 224 AKIDKSOLHDIV | LVCCSTRIPK | | | | | |
| | SSA1/1-642 | 324 AKLDKSQIHDIV 321 AKLDKSQVDEIV | | IQKLLQDFFN | GKELNKSINPD | EAVAYGAAVQAA | ILSGDKSENVQD | LLLLDVTPLS 400 |
| | BiP/1-654 | 321 AKLDKSQVDEIV 349 SDLKKSDIDEIV | L V G G S T R I P K L V G G S T R I P K | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN | GK E L NK S I NP D GK E P NR S I NP D GK E P SR G I NP D | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG | I L S G D K S E N V Q D I L T G D E S S K T Q D V L S G D Q D T G D | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 |
| | BiP/1-654 Mortalin/1-679 | 321 AK LDK SQVDEIV 349 SDLKK SDIDEIV 373 AEV SK SDIGEVI | L V G G S T R I P K L V G G S T R I P K L V G G M T R M P K | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- | GK E L NK S I NP D GK EP NR S I NP D GK EP SR G I NP D GR AP SK AV NP D | EAVAY GAAVQAA EAVAY GAAVQAA EAVAY GAAVQAG EAVAI GAA I QGG | I L S G D K S E N VQ D I L T G D E S S K T Q D V L S G D Q D - - T G D V L A G D - - - - V T D | L L L D V T P L S 400 L L L D V A P L S 397 L V L L D V C P L T 423 V L L D V T P L S 444 |
| | BiP/1-654 Mortalin/1-679 | 321 AKLDK SQVDEIV 349 SDLKKSDIDEIV 373 AEVSKSDIGEVI 327 AGLSVSDIDDVI | L V G G S T R I P K L V G G S T R I P K L V G G M T R M P K L V G G Q T R M P M | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- | GK E L NK S I NP D GK E P NR S I NP D GK E P S R G I NP D GR A P S K A V NP D GK E P R K D V NP D | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAVQGG | I L S G D K S E N V Q D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V T D V L T G D V K D | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 398 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEVSK SDIGEVI 327 AGL SV SDIDDVI 410M | LVGGSTRIPK LVGGSTRIPK LVGGMTRMPK LVGGQTRMPM 4201 | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T | GK E L NK S I NP D GK E P NR S I NP D GK E P S R G I NP D GR A P S K A V NP D GK E P R K D V NP D 440i | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAVQGG 450T | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V T D V L T G D V K D 460E | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 398 470G |
| | BIP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 | 321 AK L DK SQVDE I V 349 S D L K K S D I D E I V 373 A E V S K S D I G E V I 327 AG L S V S D I D D V I 410M 401 L G L E T A G G V M T V | LVGGSTRIPK LVGGSTRIPK LVGGMTRMPK LVGGQTRMPM 4201 LIKRNSTIPT LIKRNTTIPT | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T KQTQJFTTYS KQTQJFTTYS | GK E L NK S I NP D GK EP NR S I NP D GK EP SR G I NP D GR AP SKAVNP D GK EP RK DV NP D 4400 DNQP GV L I QVY DNQP GV L I QVY | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAVQGG 450T EGERAMTKDNNL EGERAMTKDNNL | I L S G D K S E N V Q D I L T G D E S S K T Q D V L S G D Q D T G D V L T G D V K D V L T G D V K D 460E L G R F E L S G I P P A L G K F E L T G I P P A | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 398 470G PRCVPQIEVT 477 PRCVPQIEVT 477 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 | 321 AK L DK SQVDE IV 349 S DL KK S D I DE IV 373 A EV SK S D I G EV I 327 AG L S V S D I DD V I 410M 401 L G L ET AG G VM T K 398 L G I ET AG G VM T K | LVGGSTRIPK LVGGSTRIPK LVGGMTRMPK LVGGQTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIPRNSTIPT | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T KQTQIFTTYS KQTQIFTTYS KKSEIFSTYA | GK E L NK S I NP D GK EP NR S I NP D GK EP SR G I NP D GR AP SK AV NP D GK EP RK DV NP D 4401 DNQP GV L I QVY DNQP GV L I QVY | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVA I GAAIQGG EAVA I GAAVQGG 450T EGERAMTKDNNL EGERAMTKDNNL | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L T G D V K D' 460E L G R F E L S G I P P A L G K F E L S G I P P A | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 474 |
| | BIP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BIP/1-654 | 321 AK L DK SQVDE I V 349 S D L K K S D I D E I V 373 A E V S K S D I G E V I 327 AG L S V S D I D D V I 410M 401 L G L E T A G G V M T V | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPK LVGGQTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIPRNTIPT LIPRNTVVPT | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T KQTQIFTTYS KQTQIFTTYS KKSEIFSTYA KKSQIFSTAS | GK E L NK S I NP D GK EP NR S I NP D GR AP S KAVNP D GK EP RK DV NP D 4401 DNQP GV L I QVY DNQP GV L I QVY DNQP GV L I QVY DNQP GV L I QVY | EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG 450T EGERAMTKDNNL EGERAKTKDNNL EGERAKTKDNNL | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V T D V L T G D V K D 460E L G F F E L S G I P P A L G K F E L S G I P P A L G T F D L T G I P P A | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 474 PRGVPQIEVT 500 |
| I | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEV SK SDIGEV I 327 AGL SV SDIDDV I 410M 401 LGLETAGGVMTA 401 LGIETAGGVMTV 398 LGIETAGGVMTK 424 LGIETVGGVMTK | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPK LVGGQTRMPM 4201 LIKRNSTIPT LIKRNTTIPT LIPRNSTIPT LIPRNSTIPT LIPRNSTIPT | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T KQTQJFTTYS KKSTQJFTTYS KKSEIFSTYA KKSQVFSTAA | GK E L NK S I NP D GK E P NR S I NP D GR A P S K A V NP D GK E P R K D V NP D 4401 DNQ P G V L I Q V Y DNQ P G V L I Q V Y DNQ P G V L I Q V Y DNQ P T V T I K V Y D Q T Q V E I K V C | EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG 450T EGERAMTKDNNL EGERAKTKDNNL EGERAKTKDNNL EGERPLTKDNHL QGEREMAGDNKL | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V T D V L T G D V K D 460E L G R F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G T F D L T G I P P A | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLDVTPLS 444 VLLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 474 PRGVPQIEVT 500 PRGVPQIEVT 521 |
| I | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 | 321 AK L DK SQVDE IV 349 SDLKKSDIDE IV 373 AEVSKSDIGEVI 327 AGLSVSDIDDVI 410M 401 LGLETAGGVMTA 401 LGIETAGGVMTV 398 LGIETAGGVMTK 424 LGIETVGGVMTK 445 LGIETLGGVFTK 399 LGIETMGGVMT | LVGGSTRIPK LVGGSTRIPK LVGGSTRIPK LVGGQTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIPRNSTIPT LIPRNSTVVPT LINRNTTIPT LIAKNTTIPT | IQK LLQDFFN VQK LVT DYFN IQQLVK EFFN VQQT VQDLF- VQKK VA EFF- 430T KQTQIFTTYS KK TQIFTTYS KK SEIFSTYA KK SQIFSTAS KK SQVFSTAA KH SQVFSTAE | GK E L NK S I NP D GK E P NR S I NP D GK E P SR G I NP D GK E P RK DV NP D GK E P RK DV NP D DNQ P GV L I QV Y DNQ P GV L I QV Y DNQ P GV L I QV Y DNQ P T VT I K VY DGQ T Q V E I K VC DNQ S AV T I HV L | EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG 450T EGERAMTKDNNL EGERAKTKDNNL EGERAKTKDNNL EGERPLTKDNHL QGEREMAGDNKL | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V T D V L T G D V K D 460E L G R F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G T F D L T G I P P A | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLDVTPLS 444 VLLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 474 PRGVPQIEVT 500 PRGVPQIEVT 521 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEV SK SDIGEV I 327 AGL SV SDIDDV I 410M 401 LGLETAGGYMTA 401 LGIETAGGYMTA 402 LGIET VGGVMTK 445 LGIET VGGVMTK 445 LGIET LGGVFTK 399 LGIETMGGVMT 480I 478 FDIDANGILNVT | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPK 4201 LIKRNSTIPT LIKRNTTIPT LIPRNTVVPT LINRNTTIPT LIAKNTTIPT 490A ATDKSJGKAN | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T KQTQIFTTYS KQTQIFTTYS KKSEIFSTYA KKSQIFSTAS KKSQVFSTAE 500K KITJTNDKGR | GK E L NK S I NP D GK E P NR S I NP D GR A P S K A V NP D GK E P R K D V NP D QF A P S K A V NP D QF QF V L I QVY DNQ P G V L I QVY D Q T Q V E I K V C D NQ S A VT I H V L S10L S7 L SKEELERMVQ | EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAQGG 450T EGERAMTKDNNL EGERAKTKDNNL EGERAKTKDNNL EGERAKTKDNNL QGEREMAGDNKL QGEREMAGDNKL QGERKRAADNKS 20Q 530E EAEKYKAEDEVQ | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V K D 460E L G R F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G T F D L T G I P P A L G Q F T L I G I P P A L G Q F N L D G I N P A S40N R E R V S A K N A L E S | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLDVCPLT 423 VLLDVTPLS 444 VLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 474 PRGVPQIEVT 521 PRGMPQIEVT 521 PRGMPQIEVT 521 S50K VAENMKSAVE 554 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEVSK SDIGEVI 327 AGL SV SDIDDVI 410M 401 LGLETAGGVMTA 401 LGI ETAGGVMTK 424 LGI ET VGGVMTK 424 LGI ET VGGVMTK 424 LGI ET LGGVFTK 399 LGI ET MGGVMT 480I 478 FDIDANGILNVT 478 FDIDANGILNVT | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPK 4201 LIKRNSTIPT LIKRNSTIPT LIPRNSTIPT LIPRNSTIPT LINRNTTIPT LIAKNTTIPT 490A ATDKSTGKAN AVDKSTGKEN | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQCVQDLF- VQKKVAEFF- 430T KQTQIFTTYS KKSEIFSTYA KKSQIFSTAS KKSQVFSTAA KHSQVFSTAE 500K KITITNDKGR | GK E L NK S I NP D GK EP NR S I NP D GK EP SR G I NP D GR AP SK AV NP D GK EP RK DV NP D DNQ P GV L I QVY DNQ F QV E I KVC DNQ S AVT I HV L S10L SZ L SK EE L ER MVQ L SK ED I ER MVQ | EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAVQAG EAVAIGAAIQGG EAVAIGAAVQGG 450T EGERAMTKDNNL EGERAMTKDNNL EGERAKTKDNNL EGERPLTKDNHL QGEREMAGDNKL QGERKRAADNKS 20Q 530E EAEKYKAEDEVQ EAEKYKAEDEVQ | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V K D 460E L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G T F D L T G I P P A L G Q F T L I G I P P A L G Q F N L D G I N P A S40N R E R V S A K N A L E S R D K V S S K N S L E S | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLDVTPLS 444 VLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 500 PRGVPQIEVT 500 PRGVPQIEVT 521 PRGMPQIEVT 475 550K YAFNMKSAVE 554 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-644 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEV SK SDIGEV I 327 AGL SV SDIDDV I 410M 401 LGLETAGGYMTA 401 LGIETAGGYMTA 402 LGIET VGGVMTK 445 LGIET VGGVMTK 445 LGIET LGGVFTK 399 LGIETMGGVMT 480I 478 FDIDANGILNVT | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIPRNSTIPT LIPRNTVVPT LINRNTTIPT LIAKNTTIPT A90A ATDKSTGKAN AVDKSTGKAN | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- VQKKVAEFF- KQTQIFTTYS KKSQIFSTAS KKSQIFSTAS KKSQVFSTAA KHSQVFSTAE 500K KITITNDKGR KITITNDKGR | GK E L NK S I NP D GK E P NR S I NP D GK E P S R G I NP D GK E P S R G I NP D GK E P R K D V NP D GK E P R K D V NP D Q Q P C V L I Q V Y D NQ P C V L I Q V Y D NQ P C V L I Q V Y D NQ P C V L I Q V Y D NQ P C V L I Q V Y D NQ P C V L I Q V Y D NQ P C V L I Q V Y D NQ P C V L I Q V Y S I Q C V L I Q V Y D NQ P C V L I Q V Y S I Q C V V S I Q C V Y S I | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG 450T EGERAMTKDNNL EGERAMTKDNNL EGERAMTKDNNL EGERAKTKDNNL GGER KRADNKS 20Q 530E EAEKYKAEDEVQ EAEKYKAEDEVQ EAEKYKAEDEKQ | I L S G D K S E N V Q D I L T G D E S K T Q D V L S G D Q D T G D V L S G D Q D V K D V L T G D V K D 460E L G R F E L S G I P P A L G K F E L S G I P A L G K F E L S G I P | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLDVTPLS 444 VLLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 474 PRGVPQIEVT 521 PRGVPQIEVT 521 PRGMPQIEVT 475 550K VAFNMKSATVE 554 IAYSLKNTIS 551 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsc70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsc70/1-641 Hsc70/1-644 SSA1/1-642 BiP/1-654 | 321 AK L DK SQ V DE I V 349 S D LK K S D I DE I V 373 A E V SK S D I G E V I 327 AG L S V S D I DD V I 410M 401 LG L E T AGG V M T V 398 LG I E T AGG V M T V 398 LG I E T AGG V M T K 445 LG I E T L GG V F T K 399 LG I E T M GG V M T T 480I 478 FD I DANG I L N V T 478 FD I DANG I L N V T 575 FD V D S NG I L N V S 501 F E I D V NG I L N V S 501 F E I D V NG I L N V S | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPK 4201 LIKRNSTIPT LIKRNSTIPT LIPRNSTIPT LIPRNTVVPT LINRNTTIPT 490A ATDKSTGKAN AVDKSTGKEN AVEKGTGKSN AEDKGTGNKN | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQQTVQDLF- VQKKVAEFF- 430T KQTQIFTTYS KKSEIFSTA KKSQIFSTAS KKSQVFSTAA KHSQVFSTAE 500K KITITNDKGR KITITNDKGR KITITNDKGR KITITNDQNR | GK E L NK S I NP D GK E P NR S I NP D GK E P S R G I NP D GR A P S K A V NP D GK E P RK D V NP D DNQ P GV L I QVY DNQ P T VT I K VY DGQ T Q V E I K VC DNQ S A VT I HV L S10L SI S K E E I E RMVQ L S K E D I E RMVQ L S K E D I E RMVA L T P E E I E RMVN L S K D I E NMVK | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG EAVAIGAAVQGG EAVAIGAAVQGG EGERAMTKDNNL EGERAMTKDNNL EGERAMTKDNNL EGERAKTKDNNL EGERAKTKDNNL QGERKAADNKS 20Q 530E EAEKYKAEDEVQ EAEKYKAEDEVQ EAEKYKAEDEKQ EAEKFAEEDEKE DAEKFAEEDEKE DAEKFAEEDEKE | I L S G D K S EN VQ D I L T G D E S S K T Q D V L S G D Q D T G D V L A G D V K D 460E L G K F E L T G I P P A L G K F E L S G I P P A L G K F L S G K N S L E S S Q R I A S K N Q L E S K E R V E A V N M A E G K E R V E A V N M A E G | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLDVCPLT 423 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 398 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 <u>\$50K</u> <u>YAENMKSAVE</u> 554 YAENMKATVE 551 YAYSLKNQIG 577 I IHDTETKME 597 |
| | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsc70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsc70/1-641 Hsc70/1-644 SSA1/1-642 BiP/1-654 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEVSK SDIGEVI 327 AGL SV SDIDDVI 410M 401 LGLETAGGVMTA 401 LGIETAGGVMTV 398 LGIETAGGVMTV 424 LGIETVGGVMTK 424 LGIETVGGVMTK 425 LGIETLGGVFTK 399 LGIETMGGVMT 480I 478 FDIDANGILNVT 480I 478 FDIDANGILNVS 501 FEIDVNGILNVS 501 | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIPRNSTIPT LINRNTTIPT LINRNTTIPT LAKNTTIPT 490A ATDKSTGKAN AVDKSTGKSN AEDKGTGRKN AKDKGTGREQ AKDKNSGKEQ | I Q K L L Q D F F N VQ K L V T D Y F N I Q L V K E F F N VQ T VQ D L F - VQ K K V A E F F - VQ K K V A E F F - VQ K K S E I F S T Y A K K S Q I F S T A S K K S Q V F S T A E SOOK K T T T T N D K G R K T T T N D K G R | GK E L NK S I N P D GK E P NR S I N P D GK E P S R G I N P D GK E P S R G I N P D GK E P R K D V N P D GK E P R K D V N P D D Q P G V L I Q V Y D N Q P G V L I Q V Y D N Q P G V L I Q V Y D N Q P G V L I Q V Y D N Q P G V L I Q V Y D N Q P G V L I Q V Y D N Q P G V L I Q V Y D N Q F G V L I Q V Y D N Q F G V L I Q V Y D N Q F G V L I Q V Y D N Q F G V L I Q V Y D N Q F G V L I Q V Y D N Q F G V L I Q V Y D N Q F G V L I Q V Y D Q G T Q V E I K V Z D N Q S A V T I H V L S I D L S K E D I E K M V Q L S K E D I E K M V N L S K D D I E N M V K L N E D E I Q K M V R | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG EAVAIGAAVQGG EAVAIGAAVQGG EGERAMTKDNNL EGERAMTKDNNL EGERAMTKDNNL EGERAMTKDNNL EGERAKTKDNNL EGERAMTKDNNL EGERAMTKDNNL 200 GERKRAADNKS 200 S30E EAEKYKAEDEVQ EAEKYKAEDEVQ EAEKYKAEDEKE DAEKFKEEDKKL NAEKYAEEDRKK DAEANAEADRKF | I L S G D K S E N V Q D I L T G D E S K T Q D V L S G D Q D T G D V L S G D Q D V K D 460E L G K F E L S G I P P A L G K F E L S G I P A S K K N S K N S L E S S K R I A S K N S K N S L E S K E R V A K N M A E G E E L V Q T R N Q G D H | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLDVTPLS 444 VLLLDVTPLS 444 VLLLDVTPLS 498 470G PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 <u>\$50K</u> <u>YAFNMKSAVE</u> 554 IAYSLKNTIS 551 YAYSLKNQIG 577 IHDTETKME 597 LHSTRKQVE 551 |
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E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A S G K I S K N S L E S K E R V S A K N Q L E S K E R V E A V N M A E G G L Y Q G A G G P | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 444 VLLLDVTPLS 444 VLLLDVTPLS 447 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 <u>550K</u> <u>YAFNMKSAVE 554</u> IAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 COMPGGFC 627 LHSTRKQVE 551 <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> <u>623G</u> 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| 1 | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-641 Hsc70/1-641 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 349 SDLKK SDIGEVI 327 AEV SK SDIGEVI 327 AGL SV SDIDDVI 410M 401 LGLETAGGYMTA 401 LGIETAGGYMTA 401 LGIETAGGYMTK 445 LGIETVGGVMTK 445 LGIETVGGVMTK 445 LGIETLGGVFTK 399 LGIETMGGVMTT 480I 478 FDIDANGILNVT 478 FDIDANGILNVT 501 FEIDVDSILNVT 505 D-EGLKGKISEA 555 D-EGLKGKISEA 555 D-EGLKGKISEA 555 P-EGLKGKISEA 558 E-GRAGKLSSE 598 EFKDQLPAD 552 EAGDKLPAD | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIKRNTTIPT LIPRNSTIPT LIPRNSTIPT LIPRNSTIPT LIAKNTTIPT LAKNTIPT LAKNTTIPT LAKNTTIPT LAKNTIPT LAKNTIPT LAKNTIPT LAKNTIPT LAKNTIPT LAKNTIPT LAKNTIPT | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQCTVQDLF- VQKKVAEFF- VQKKVAEFF- KQTQIFTTYS KKSQIFSTAS KKSQIFSTAS KKSQVFSTAE SOOK KITITNDKGR KITIKAS- SOG SOOK | GK E L NK S I NP D GK E P NR S I NP D GK E P SR G I NP D GK E P SR G I NP D GK E P RK DV NP D D QP GV L I QVY DNQ P GV L I QVY DNQ F GV L I QVY SI D Q F GV L I QVY SI D Q F GV L I QVY SI D Q SA VT I HVL SI D L SK E D I E KMVQ L SK E D I E KMV SK D D I E NMVK L SK D D I E NMVK L SK D D I E NMVK L SK E G I E KMV SK D D I E NMVK L SK E G I E KMV L | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG EAVAIGAAVQGG EAVAIGAAVQGG EAGAAVQGG EAGAAVQGG EGERAMTKDNNL EGERAMTKDNL EGERAMTCDNL EGERAMTKDNL | I L S G D K S EN VQ D I L T G D E S K T Q D V L S G D Q D T G D V L S G D Q D T O D V L T G D V K D 460E L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A S G K I S K N S L E S K E R V S A K N Q L E S K E R V E A V N M A E G G L Y Q G A G G P | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLLDVCPLT 423 VLLLDVTPLS 444 VLLLDVTPLS 444 VLLLDVTPLS 444 VLLLDVTPLS 447 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 <u>550K</u> <u>YAFNMKSAVE 554</u> IAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNTIS 551 YAYSLKNCIG 577 IIHDTETKME 597 LLHSTRKQVE 551 <u>623G</u> <u>GPGGFG-623</u> PGGPGFFG 625 ED647 SGSSGTG668 |
| I | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-644 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-641 Hsc70/1-641 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEV SK SDIGEV I 327 AGL SV SDIDDV I 410M 401 LGLETAGGVMTA 401 LGIETAGGVMTK 401 LGIETAGGVMTK 424 LGIETVGGVMTK 424 LGIETVGGVMTK 425 LGIETLGGVFTK 399 LGIETMGGVMTT 480I 478 FDIDANGILNVT 478 FDIDANGILNVT 478 FDIDANGILNVS 575 FDVDSNGILNVS 501 FEIDVNGILNVS 501 FEIDVNGILNVS 505 D - EGLKGKISEA 555 D - EGLKGKISEA 555 D - EKLQGKINDE 522 E - AG - DKLEQA 552 E - AGC - DKLEQA 553 F - F KDQLPA 554 - AGC - F KDQLPA 555 D - E CL KG S G 628 GAP P A - P E A E G | LVGGSTRIPK LVGGSTRIPK LVGGSTRIPK 4201 LIKRNSTIPT LIKRNSTIPT LIKRNTTIPT LIPRNSTIPT LIPRNTVVPT LIPRNTVVPT LINRNTTIPT 490A ATDKSTGKAN AVDKSTGKEN A | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQCTVQDLF- VQKKVAEFF- VQKKVAEFF- KQTQIFTTYS KKSQIFSTAS KKSQIFSTAS KKSQVFSTAE SOOK KITITNDKGR KITIKAS- SOG SOOK | GK E L NK S I NP D GK E P NR S I NP D GK E P SR G I NP D GK E P SR G I NP D GK E P RK DV NP D D QP GV L I QVY DNQ P GV L I QVY DNQ F GV L I QVY SI D Q F GV L I QVY SI D Q F GV L I QVY SI D Q SA VT I HVL SI D L SK E D I E KMVQ L SK E D I E KMV SK D D I E NMVK L SK D D I E NMVK L SK D D I E NMVK L SK E G I E KMV SK D D I E NMVK L SK E G I E KMV L | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG EAVAIGAAVQGG EAVAIGAAVQGG EAGAAVQGG EAGAAVQGG EGERAMTKDNNL EGERAMTKDNL EGERAMTCDNL EGERAMTKDNL | I L S G D K S EN VQ D I L T G D E S K T Q D V L S G D Q D T G D V L S G D Q D T O D V L T G D V K D 460E L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A S G K I S K N S L E S K E R V S A K N Q L E S K E R V E A V N M A E G G L Y Q G A G G P | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLDVCPLT 423 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 447 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 S50K YAFNMKSAVE 554 YAFNMKSAVE 554 YAFNMKATVE 554 YAFNMKATVE 554 IAYSLKNQIG 577 I HDTETKME 597 LHSTRKQVE 551 - 623G GPGGFG-623 PGGMPGGFPG 627 AGCAPGGFPG 627 AGCAPGFPG 625 ED647 SGSSGTG668 GADASAN619 641 646 642 |
| 1 | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-644 SSA1/1-638 Hsp70/1-644 Hsc70/1-644 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-644 BiP/1-654 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 349 SDLKK SDIGEVI 327 AEVSK SDIGEVI 327 AGL SV SDIDDVI 410M 401 LGLETAGGYMTA 401 LGIETAGGYMTK 401 LGIETAGGYMTK 401 LGIETAGGYMTK 401 LGIETAGGYMTK 403 LGIETAGGYMTK 404 LGIETVGGVMTK 405 LGIETLGGVFTK 399 LGIETMGGVMTT 480I 478 FDIDANGILNVS 476 FDIDANGILNVS 501 FEIDVNGILNVS 501 FEIDVNGILNVS 501 FEIDVNGILNVS 505 D-EGLKGKISEA 555 D-EGLKGKISEA 555 D-EKLQGKINDE 552 E-AG-DKLEQA 578 DKEKLGGKLSSE 598 EFKDQLPAD 522 EAGCPKGGSGSG 626 GAPPAPEAEG 648 TAE | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPM 4201 LIKRNTIPT LIKRNTIPT LIKRNTIPT LIPRNTVVPT LIPRNTVVPT LIPRNTVVPT LINRNTIPT 490A ATDKSTGKEN AVDKSTGKEN AVDKSTGKEN AVDKSTGKEN AVDKSTGKEN AVDKSTGKEN AVDKSTGKEN AVDKSTGKEN AKDKNSGKEQ S69K DKKKVLDKCQ DKQKILDKCN CKQC CKQC CCC CCC CCC CCC CCC CCC CCC C | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQCTVQDLF- VQKKVAEFF- VQKKVAEFF- KQTQIFTTYS KKSQIFSTAS KKSQIFSTAS KKSQVFSTAE SOOK KITITNDKGR KITIKAS- SOG SOOK | GK E L NK S I NP D GK E P NR S I NP D GK E P SR G I NP D GK E P SR G I NP D GK E P RK DV NP D D QP GV L I QVY DNQ P GV L I QVY DNQ F GV L I QVY SI D Q F GV L I QVY SI D Q F GV L I QVY SI D Q SA VT I HVL SI D L SK E D I E KMVQ L SK E D I E KMV SK D D I E NMVK L SK D D I E NMVK L SK D D I E NMVK L SK E G I E KMV SK D D I E NMVK L SK E G I E KMV L | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG EAVAIGAAVQGG EAVAIGAAVQGG EAGAAVQGG EAGAAVQGG EGERAMTKDNNL EGERAMTKDNL EGERAMTCDNL EGERAMTKDNL | I L S G D K S EN VQ D I L T G D E S K T Q D V L S G D Q D T G D V L S G D Q D T O D V L T G D V K D 460E L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A S G K I S K N S L E S K E R V S A K N Q L E S K E R V E A V N M A E G G L Y Q G A G G P | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLDVCPLT 423 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 444 YLLLDVTPLS 444 YLLLDVTPLS 444 YA70 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 S50K YAFNMKSAVE 554 IAYSLKNTIS 551 IAYSLKNTIS 551 IAYSLKNTIS 551 IAYSLKNQIG 577 IIHDTETKME 597 LLHSTRKQVE 551 - 623G GPGGFG-623 PGGMPGGFPG 627 AGGAPGGFPG 625 EED 647 SGSSGTG 668 GADASAN 619 641 646 642 654 |
| I | BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-646 SSA1/1-642 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-644 BiP/1-654 Mortalin/1-679 DnaK/1-638 Hsp70/1-641 Hsc70/1-645 SSA1/1-642 BiP/1-654 Mortalin/1-679 | 321 AK L DK SQVDE IV 349 SDLKK SDIDE IV 373 AEV SK SDIGEV I 327 AGL SV SDIDDV I 410M 401 LGLETAGGVMTA 401 LGIETAGGVMTK 401 LGIETAGGVMTK 424 LGIETVGGVMTK 424 LGIETVGGVMTK 425 LGIETLGGVFTK 399 LGIETMGGVMTT 480I 478 FDIDANGILNVT 478 FDIDANGILNVT 478 FDIDANGILNVS 575 FDVDSNGILNVS 501 FEIDVNGILNVS 501 FEIDVNGILNVS 505 D - EGLKGKISEA 555 D - EGLKGKISEA 555 D - EKLQGKINDE 522 E - AG - DKLEQA 552 E - AGC - DKLEQA 553 F - F KDQLPA 554 - AGC - F KDQLPA 555 D - E CL KG S G 628 GAP P A - P E A E G | LVGGSTRIPK LVGGSTRIPK LVGGVTRMPM 4201 LIKRNSTIPT LIKRNSTIPT LIKRNTTIPT LIPRNSTVVPT LINRNTTIPT LIAKNTTIPT LAKNTTIPT | IQKLLQDFFN VQKLVTDYFN IQQLVKEFFN VQCTVQDLF- VQKKVAEFF- VQKKVAEFF- KQTQIFTTYS KKSQIFSTAS KKSQIFSTAS KKSQVFSTAE SOOK KITITNDKGR KITIKAS- SOG SOOK | GK E L NK S I NP D GK E P NR S I NP D GK E P SR G I NP D GK E P SR G I NP D GK E P RK DV NP D D QP GV L I QVY DNQ P GV L I QVY DNQ F GV L I QVY SI D Q F GV L I QVY SI D Q F GV L I QVY SI D Q SA VT I HVL SI D L SK E D I E KMVQ L SK E D I E KMV SK D D I E NMVK L SK D D I E NMVK L SK D D I E NMVK L SK E G I E KMV SK D D I E NMVK L SK E G I E KMV L | EAVAYGAAVQAA EAVAYGAAVQAA EAVAYGAAVQAG EAVAIGAAIQGG EAVAIGAAIQGG EAVAIGAAVQGG EAVAIGAAVQGG EAVAIGAAVQGG EAGAAVQGG EAGAAVQGG EGERAMTKDNNL EGERAMTKDNL EGERAMTCDNL EGERAMTKDNL | I L S G D K S EN VQ D I L T G D E S K T Q D V L S G D Q D T G D V L S G D Q D T O D V L T G D V K D 460E L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A L G K F E L S G I P P A S G K I S K N S L E S K E R V S A K N Q L E S K E R V E A V N M A E G G L Y Q G A G G P | LLLLDVTPLS 400 LLLLDVAPLS 397 LVLDVCPLT 423 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 444 VLLDVTPLS 447 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 477 PRGVPQIEVT 475 S50K YAFNMKSAVE 554 YAFNMKSAVE 554 YAFNMKATVE 554 YAFNMKATVE 554 IAYSLKNQIG 577 I HDTETKME 597 LHSTRKQVE 551 - 623G GPGGFG-623 PGGMPGGFPG 627 AGCAPGGFPG 627 AGCAPGFPG 625 ED647 SGSSGTG668 GADASAN619 641 646 642 |

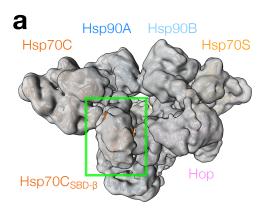


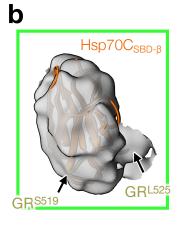


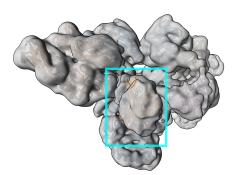




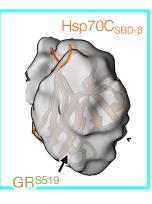




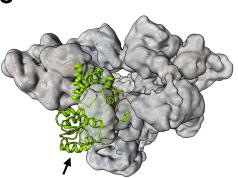




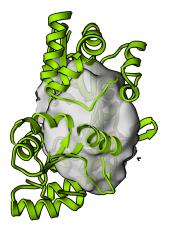
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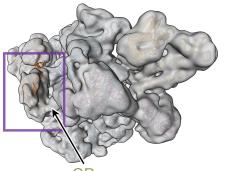


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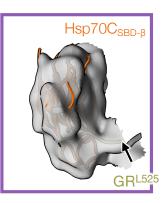


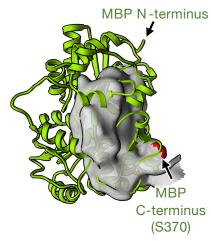
Maltose-binding protein (MBP)

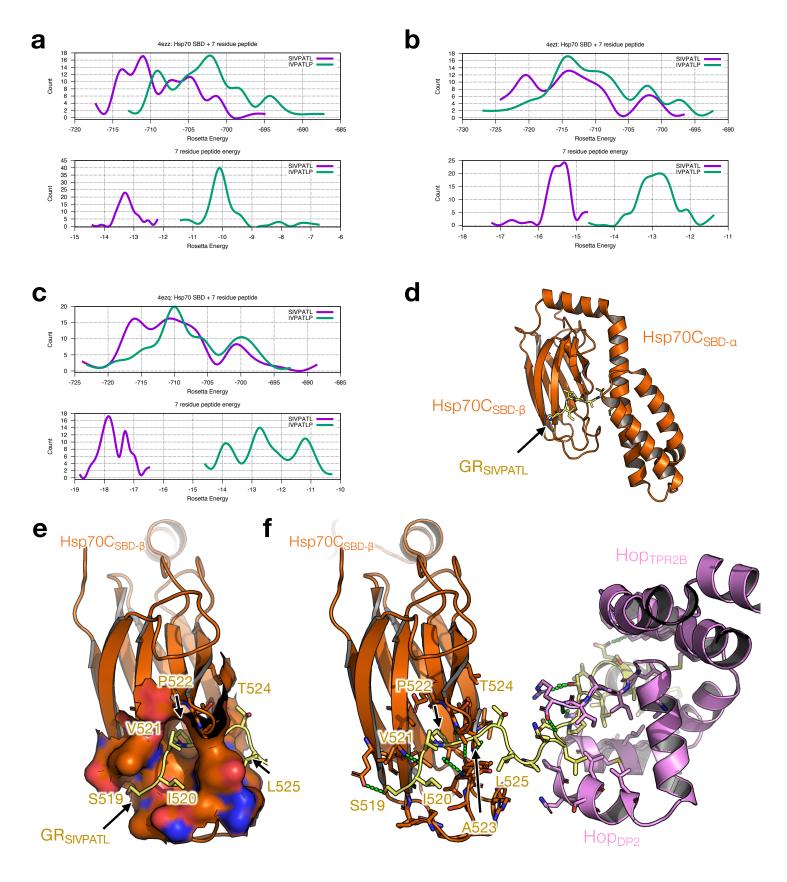




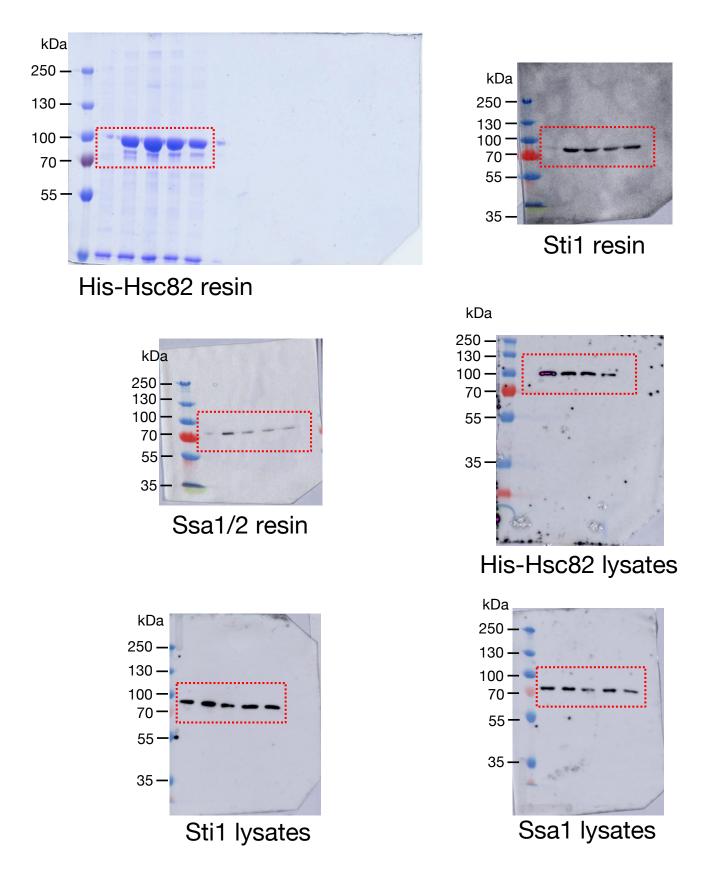
GRpre-Helix 1 strand

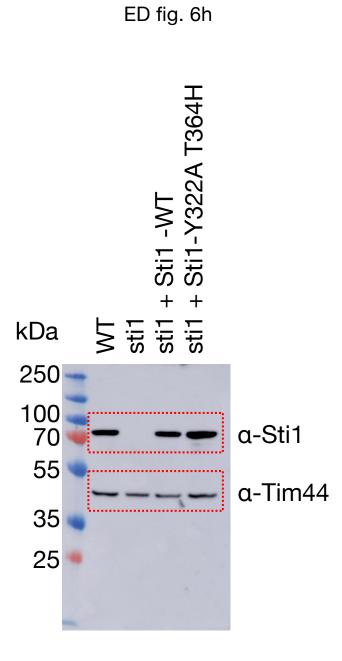


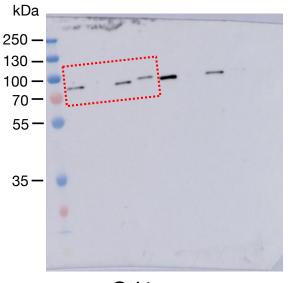




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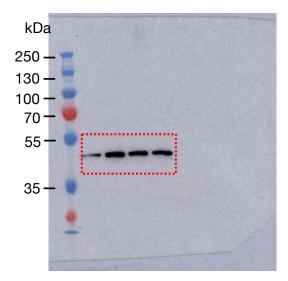












a-Tim44