INNOSC Theranostics
and Pharmacological Sciences

ORIGINAL RESEARCH ARTICLE

# *In silico* evaluation of heat shock proteins reveals an interplay with polyamines as a survival strategy for the *Plasmodium falciparum*

## Supplementary Files

**Supplementary S1. Bioinformatics databases and tools used in this study**

| Bioinfomatics tool | Website address | Tool use |
|---|---|---|
| PlasmoDB | https://plasmodb.org/plasmo/app | Sequence retrieval of *Plasmodium falciparum* 3D7 HSPs |
| NCBI | https://www.ncbi.nlm.nih.gov/ | Sequence retrieval of *Escherichia coli* and *Saccharomyces cerevisiae* |
| Bioedit | bioedit.software.informer.com | Global alignment |
| Phyre2 | http://www.sbg.bio.ic.ac.uk/phyre2 | Prediction of 3D structures |
| PyMol | http://pymol.org/academic | Viewing structures |
| PDBSum | https://www.ebi.ac.uk/thornton-srv/databases/cgi-bin/pdbsum/GetPage.pl?pdbcode=index.html | Structure validation |
| SiteMap | https://www.schrodinger.com/products/sitemap | Identification of binding sites of the HSPs |
| PubChem | https://pubchem.ncbi.nlm.nih.gov/ | Retrieval of ligands (Putrescine, Spermidine, and Spermine) |
| QM Conformer and Tautomer Predictor | https://forum.knime.com/t/qm-conformer-tautomer-predictor/26153 | To find the lowest energy tautomers or conformers for the ligands |
| OPLS4 | https://www.schrodinger.com/products/opls4 | Molecular Docking |
| Desmond Molecular Dynamics System | https://www.schrodinger.com/products/desmond | Molecular Dynamics Simulations |

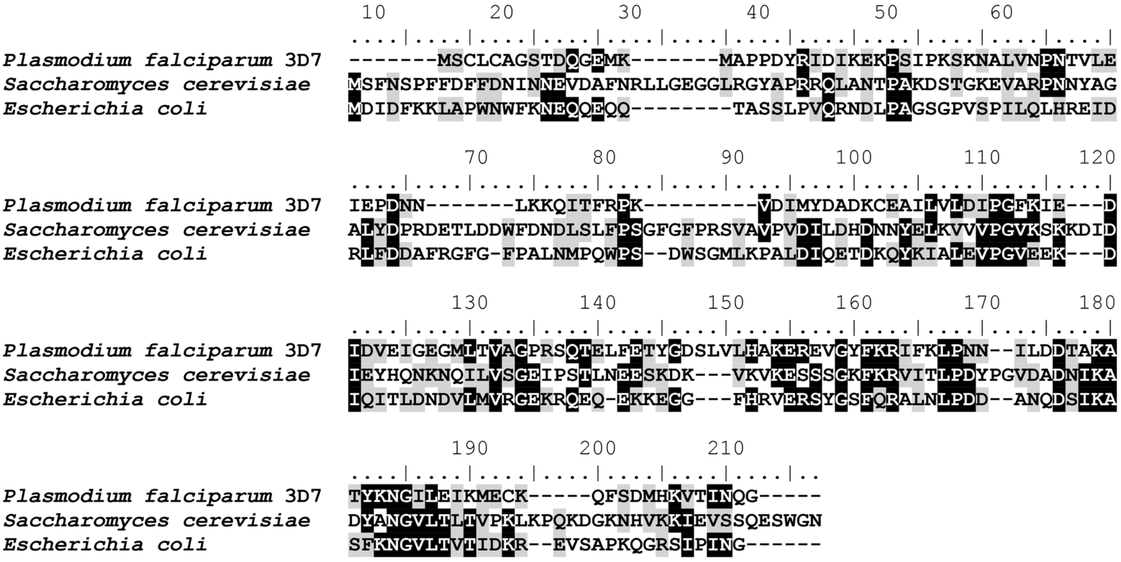
**Supplementary S2. Number of $Na^+$ or $Cl^-$ counterions used assigned to each system for neutralization during molecular docking**

| Protein | Counterions |
|---|---|
| HSP20 | 3 $Na^+$ |
| HSP40 | 5 $Na^+$ |
| HSP60 | 0 |
| HSP70 | 7 $Na^+$ |
| HSP90 | 10 $Na^+$ |
| HSP20-Put | 1 $Na^+$ |
| HSP20-Spd | 0 |
| HSP20-Spn | 1 $Cl^-$ |
| HSP40-Put | 3 $Na^+$ |
| HSP40-Spd | 2 $Na^+$ |
| HSP40-Spn | 1 $Na^+$ |
| HSP60-Put | 2 $Cl^-$ |
| HSP60-Spd | 3 $Cl^-$ |
| HSP60-Spn | 4 $Cl^-$ |
| HSP70-Put | 5 $Na^+$ |
| HSP70-Spd | 4 $Na^+$ |
| HSP70-Spn | 3 $Na^+$ |
| HSP90-Put | 8 $Na^+$ |
| HSP90-Spd | 7 $Na^+$ |
| HSP90-Spn | 6 $Na^+$ |

**Supplementary S3. Genomic characterization of *Plasmodium falciparum* 3D7 strain major heat shock proteins**

| Protein | Accession # | Genomic locus | Gene ID | Exons | Introns |
|---|---|---|---|---|---|
| HSP20 | XP_001349359.1 | Chromosome: 8; NC_004329.3 | 2655428 | 3 | 2 |
| HSP40 | XP_001349799.1 | Chromosome: 13; NC_004331.3 | 814015 | 1 | - |
| HSP60 | CZT98408.1 | Chromosome: 10; NC_037281.1 | 810311 | 2 | 1 |
| HSP70 | XP_001349336.1 | Chromosome: 8; NC_004329.3 | 2655254 | 1 | - |
| HSP90 | XP_001348998.1 | Chromosome: 7; NC_004328.3 | 2655065 | 2 | 1 |

**Supplementary 4. Multiple sequence alignment of *Plasmodium falciparum* HSP 20, 40, 60, 70, and 90 with *Saccharomyces cerevisiae* and *Escherichia coli.***



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                                     10        20        30        40        50        60
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        -------MSCLCAGSTDQGEMK-------MAPPDYRIDIKEKPSIPKSKNALVNPNTVLE
Saccharomyces cerevisiae         MSFNSPFFDFFDNINNEVDAFNRLLGEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
Escherichia coli                 MDIDFKKLAPWNWFKNEQQEQQ--------TASSLPVQRNDLPAGSGPVSPILQLHREID

                                     70        80        90       100       110       120
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        IEPDNN-------LKKQITFRPK---------VDIMYDADKCEAILVLDIPGFKIE---D
Saccharomyces cerevisiae         ALYDPRDETLDDWFDNDLSLFPSGFGFPRSVAVPVDILDHDNNYELKVVVPGVKSKKDID
Escherichia coli                 RLFDDAFRGFG-FPALNMPQWPS--DWSGMLKPALDIQETDKQYKIALEVPGVEEK---D

                                    130       140       150       160       170       180
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        IDVEIGEGMLTVAGPRSQTELFETYGDSLVLHAKEREVGYFKRIFKLPNN--ILDDTAKA
Saccharomyces cerevisiae         IEYHQNKNQILVSGEIPSTLNEESKDK---VKVKESSSGKFKRVITLPDYPGVDADNIKA
Escherichia coli                 IQITLDNDVLMVRGEKRQEQ-EKKEGG---FHRVERSYGSFQRALNLPDD--ANQDSIKA

                                    190       200       210
                                 ....|....|....|....|....|....|....|..
Plasmodium falciparum 3D7        TYKNGILEIKMECK-----QFSDMHKVTINQG-----
Saccharomyces cerevisiae         DYANGVLTLTVPKLKPQKDGKNHVKKIEVSSQESWGN
Escherichia coli                 SFKNGVLTVTIDKR--EVSAPKQGRSIPING------
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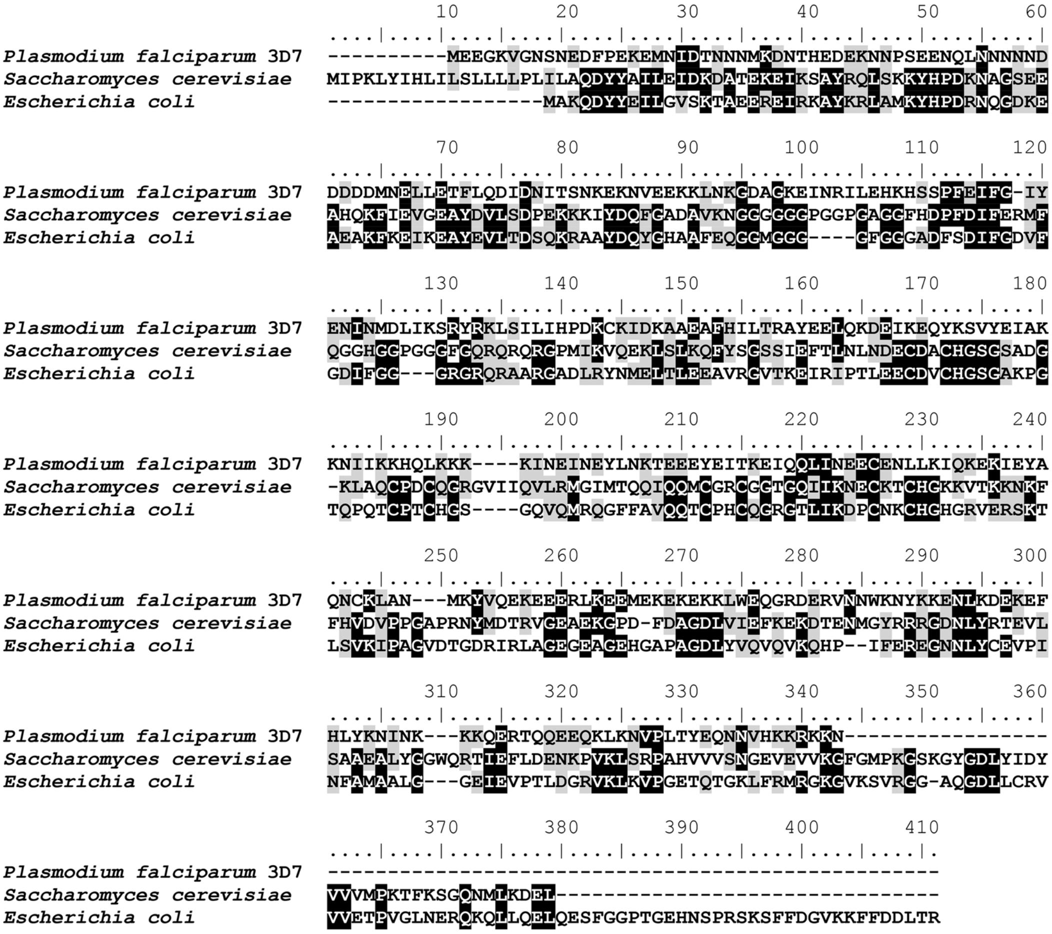
Multiple sequence alignment of HSP20 in *P. falciparum* 3D7, *S. cerevisiae,* and *E. coli* indicating identical (black), similar (grey), and nonidentical (white) residues.



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                                     10        20        30        40        50        60
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        ----------MEEGKVGNSNEDFPEKEMNIDTNNNMKDNTHEDEKNNPSEENQLNNNNND
Saccharomyces cerevisiae         MIPKLYIHLILSLLLLPLILAQDYYAILEIDKDATEKEIKSAYRQLSKKYHPDKNAGSEE
Escherichia coli                 ------------------MAKQDYYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKE

                                     70        80        90       100       110       120
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        DDDDMNELLETFLQDIDNITSNKEKNVEEKKLNKGDAGKEINRILEHKHSSPFEIFG-IY
Saccharomyces cerevisiae         AHQKFIEVGEAYDVLSDPEKKKIYDQFGADAVKNGGGGGGPGGPGAGGFHDPFDIFERMF
Escherichia coli                 AEAKFKEIKEAYEVLTDSQKRAAYDQYGHAAFEQGGMGGG----GFGGGADFSDIFGDVF

                                    130       140       150       160       170       180
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        ENINMDLIKSRYRKLSILIHPDKCKIDKAAEAFHILTRAYEELQKDEIKEQYKSVYEIAK
Saccharomyces cerevisiae         QGGHGGPGGGFGQRQRQRGPMIKVQEKLSLKQFYSGSSIEFTLNLNDECDACHGSGSADG
Escherichia coli                 GDIFGG---GRGRQRAARGADLRYNMELTLEEAVRGVTKEIRIPTLEECDVCHGSGAKPG

                                    190       200       210       220       230       240
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        KNIIKKHQLKKK----KINEINEYLNKTEEEYEITKEIQQLINEECENLLKIQKEKIEYA
Saccharomyces cerevisiae         -KLAQCPDCQGRGVIIQVLRMGIMTQQIQQMCGRCGGTGQIIKNECKTCHGKKVTKKNKF
Escherichia coli                 TQPQTCPTCHGS----GQVQMRQGFFAVQQTCPHCQGRGTLIKDPCNKCHGHGRVERSKT

                                    250       260       270       280       290       300
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        QNCKLAN---MKYVQEKEEERLKEEMEKEKEKKLWEQGRDERVNNWKNYKKENLKDEKEF
Saccharomyces cerevisiae         FHVDVPPGAPRNYMDTRVGEAEKGPD-FDAGDLVIEFKEKDTENMGYRRRGDNLYRTEVL
Escherichia coli                 LSVKIPAGVDTGDRIRLAGEGEAGEHGAPAGDLYVQVQVKQHP--IFEREGNNLYCEVPI

                                    310       320       330       340       350       360
                                 ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7        HLYKNINK---KKQERTQQEEQKLKNVPLTYEQNNVHKKRKKN-----------------
Saccharomyces cerevisiae         SAAEALYGGWQRTIEFLDENKPVKLSRPAHVVVSNGEVEVVKGFGMPKGSKGYGDLYIDY
Escherichia coli                 NFAMAALG---GEIEVPTLDGRVKLKVPGETQTGKLFRMRGKGVKSVRGG-AQGDLLCRV

                                    370       380       390       400       410
                                 ....|....|....|....|....|....|....|....|....|.
Plasmodium falciparum 3D7        ---------------------------------------------------
Saccharomyces cerevisiae         VVVMPKTFKSGQNMLKDEL--------------------------------
Escherichia coli                 VVETPVGLNERQKQLLQELQESFGGPTGEHNSPRSKSFFDGVKKFFDDLTR
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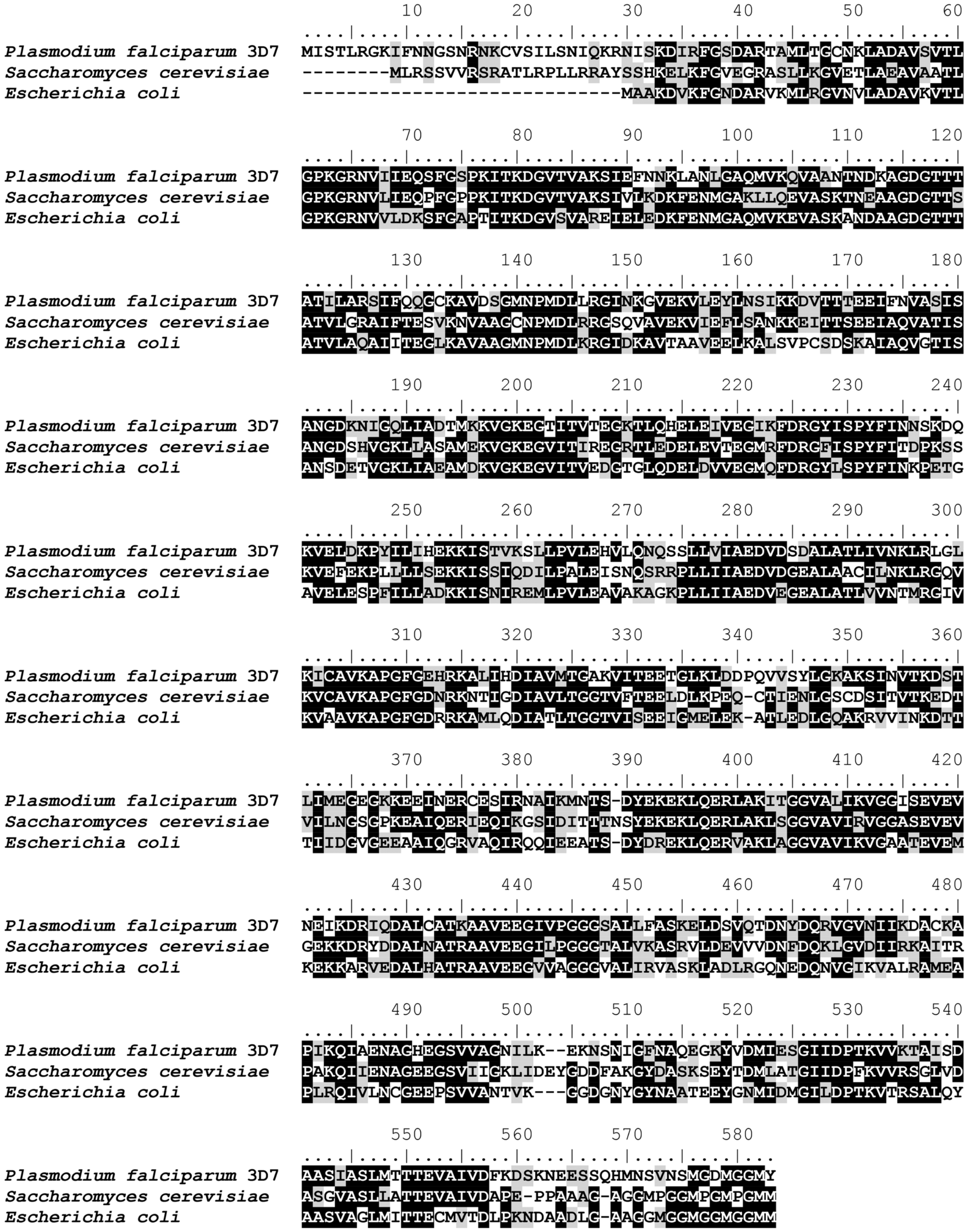
Multiple sequence alignment of HSP40 in *P. falciparum* 3D7, *S. cerevisiae,* and *E. coli* indicating identical (black), similar (grey), and nonidentical (white) residues.



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                                     10        20        30        40        50        60
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   MISTLRGKIFNNGSNRNKCVSILSNIQKRNISKDIRFGSDARTAMLTGCNKLADAVSVTL
Saccharomyces cerevisiae    --------MLRSSVVRSRATLRPLLRRAYSSHKELKFGVEGRASLLKGVETLAEAVAATL
Escherichia coli            -----------------------------MAAKDVKFGNDARVKMLRGVNVLADAVKVTL

                                     70        80        90       100       110       120
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   GPKGRNVIIEQSFGSPKITKDGVTVAKSIEFNNKLANLGAQMVKQVAANTNDKAGDGTTT
Saccharomyces cerevisiae    GPKGRNVLIEQPFGPPKITKDGVTVAKSIVLKDKFENMGAKLLQEVASKTNEAAGDGTTS
Escherichia coli            GPKGRNVVLDKSFGAPTITKDGVSVAREIELEDKFENMGAQMVKEVASKANDAAGDGTTT

                                    130       140       150       160       170       180
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   ATILARSIFQQGCKAVDSGMNPMDLLRGINKGVEKVLEYLNSIKKDVTTTEEIFNVASIS
Saccharomyces cerevisiae    ATVLGRAIFTESVKNVAAGCNPMDLRRGSQVAVEKVIEFLSANKKEITTSEEIAQVATIS
Escherichia coli            ATVLAQAIITEGLKAVAAGMNPMDLKRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTIS

                                    190       200       210       220       230       240
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   ANGDKNIGQLIADTMKKVGKEGTITVTEGKTLQHELEIVEGIKFDRGYISPYFINNSKDQ
Saccharomyces cerevisiae    ANGDSHVGKLLASAMEKVGKEGVITIREGRTLEDELEVTEGMRFDRGFISPYFITDPKSS
Escherichia coli            ANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDELDVVEGMQFDRGYLSPYFINKPETG

                                    250       260       270       280       290       300
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   KVELDKPYILIHEKKISTVKSLLPVLEHVLQNQSSLLVIAEDVDSDALATLIVNKLRLGL
Saccharomyces cerevisiae    KVEFEKPLLLLSEKKISSIQDILPALEISNQSRRPLLIIAEDVDGEALAACILNKLRGQV
Escherichia coli            AVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATLVVNTMRGIV

                                    310       320       330       340       350       360
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   KICAVKAPGFGEHRKALIHDIAVMTGAKVITEETGLKLDDPQVVSYLGKAKSINVTKDST
Saccharomyces cerevisiae    KVCAVKAPGFGDNRKNTIGDIAVLTGGTVFTEELDLKPEQ-CTIENLGSCDSITVTKEDT
Escherichia coli            KVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEK-ATLEDLGQAKRVVINKDTT

                                    370       380       390       400       410       420
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   LIMEGEGKKEEINERCESIRNAIKMNTS-DYEKEKLQERLAKITGGVALIKVGGISEVEV
Saccharomyces cerevisiae    VILNGSGPKEAIQERIEQIKGSIDITTTNSYEKEKLQERLAKLSGGVAVIRVGGASEVEV
Escherichia coli            TIIDGVGEEAAIQGRVAQIRQQIEEATS-DYDREKLQERVAKLAGGVAVIKVGAATEVEM

                                    430       440       450       460       470       480
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   NEIKDRIQDALCATKAAVEEGIVPGGGSALLFASKELDSVQTDNYDQRVGVNIIKDACKA
Saccharomyces cerevisiae    GEKKDRYDDALNATRAAVEEGILPGGGTALVKASRVLDEVVVDNFDQKLGVDIIRKAITR
Escherichia coli            KEKKARVEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVGIKVALRAMEA

                                    490       500       510       520       530       540
                            ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7   PIKQIAENAGHEGSVVAGNILK--EKNSNIGFNAQEGKYVDMIESGIIDPTKVVKTAISD
Saccharomyces cerevisiae    PAKQIIENAGEEGSVIIGKLIDEYGDDFAKGYDASKSEYTDMLATGIIDPFKVVRSGLVD
Escherichia coli            PLRQIVLNCGEEPSVVANTVK---GGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQY

                                    550       560       570       580
                            ....|....|....|....|....|....|....|....|...
Plasmodium falciparum 3D7   AASIASLMTTTEVAIVDFKDSKNEESSQHMNSVNSMGDMGGMY
Saccharomyces cerevisiae    ASGVASLLATTEVAIVDAPE-PPAAAG-AGGMPGGMPGMPGMM
Escherichia coli            AASVAGLMITTECMVTDLPKNDAADLG-AAGGMGGMGGMGGMM
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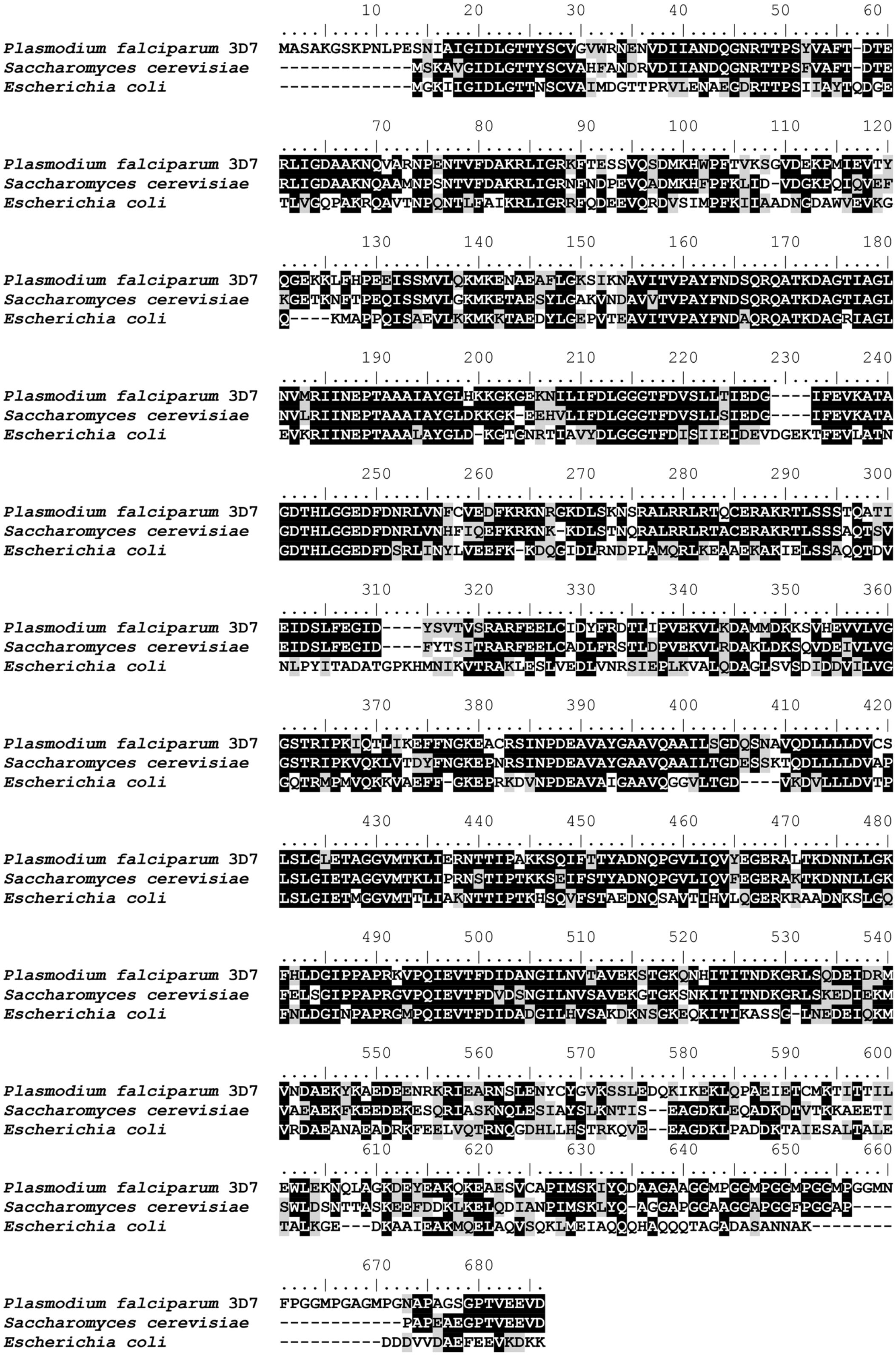
Multiple sequence alignment of HSP60 in *P. falciparum* 3D7, *S. cerevisiae,* and *E. coli* indicating identical (black), similar (grey), and nonidentical (white) residues.



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                                      10        20        30        40        50        60
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     MASAKGSKPNLPESNIAIGIDLGTTYSCVGVWRNENVDIIANDQGNRTTPSYVAFT-DTE
Saccharomyces cerevisiae      -------------MSKAVGIDLGTTYSCVAHFANDRVDIIANDQGNRTTPSFVAFT-DTE
Escherichia coli              -------------MGKIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTTPSIIAYTQDGE

                                      70        80        90       100       110       120
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     RLIGDAAKNQVARNPENTVFDAKRLIGRKFTESSVQSDMKHWPFTVKSGVDEKPMIEVTY
Saccharomyces cerevisiae      RLIGDAAKNQAAMNPSNTVFDAKRLIGRNFNDPEVQADMKHFPFKLID-VDGKPQIQVEF
Escherichia coli              TLVGQPAKRQAVTNPQNTLFAIKRLIGRRFQDEEVQRDVSIMPFKIIAADNGDAWVEVKG

                                     130       140       150       160       170       180
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     QGEKKLFHPEEISSMVLQKMKENAEAFLGKSIKNAVITVPAYFNDSQRQATKDAGTIAGL
Saccharomyces cerevisiae      KGETKNFTPEQISSMVLGKMKETAESYLGAKVNDAVVTVPAYFNDSQRQATKDAGTIAGL
Escherichia coli              Q----KMAPPQISAEVLKKMKKTAEDYLGEPVTEAVITVPAYFNDAQRQATKDAGRIAGL

                                     190       200       210       220       230       240
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     NVMRIINEPTAAAIAYGLHKKGKGEKNILIFDLGGGTFDVSLLTIEDG----IFEVKATA
Saccharomyces cerevisiae      NVLRIINEPTAAAIAYGLDKKGK-EEHVLIFDLGGGTFDVSLLSIEDG----IFEVKATA
Escherichia coli              EVKRIINEPTAAALAYGLD-KGTGNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATN

                                     250       260       270       280       290       300
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     GDTHLGGEDFDNRLVNFCVEDFKRKNRGKDLSKNSRALRRLRTQCERAKRTLSSSTQATI
Saccharomyces cerevisiae      GDTHLGGEDFDNRLVNHFIQEFKRKNK-KDLSTNQRALRRLRTACERAKRTLSSSAQTSV
Escherichia coli              GDTHLGGEDFDSRLINYLVEEFK-KDQGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTDV

                                     310       320       330       340       350       360
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     EIDSLFEGID----YSVTVSRARFEELCIDYFRDTLIPVEKVLKDAMMDKKSVHEVVLVG
Saccharomyces cerevisiae      EIDSLFEGID----FYTSITRARFEELCADLFRSTLDPVEKVLRDAKLDKSQVDEIVLVG
Escherichia coli              NLPYITADATGPKHMNIKVTRAKLESLVEDLVNRSIEPLKVALQDAGLSVSDIDDVILVG

                                     370       380       390       400       410       420
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     GSTRIPKIQTLIKEFFNGKEACRSINPDEAVAYGAAVQAAILSGDQSNAVQDLLLLDVCS
Saccharomyces cerevisiae      GSTRIPKVQKLVTDYFNGKEPNRSINPDEAVAYGAAVQAAILTGDESSKTQDLLLLDVAP
Escherichia coli              GQTRMPMVQKKVAEFF-GKEPRKDVNPDEAVAIGAAVQGGVLTGD----VKDVLLLDVTP

                                     430       440       450       460       470       480
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     LSLGLETAGGVMTKLIERNTTIPAKKSQIFTTYADNQPGVLIQVYEGERALTKDNNLLGK
Saccharomyces cerevisiae      LSLGIETAGGVMTKLIPRNSTIPTKKSEIFSTYADNQPGVLIQVFEGERAKTKDNNLLGK
Escherichia coli              LSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQ

                                     490       500       510       520       530       540
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     FHLDGIPPAPRKVPQIEVTFDIDANGILNVTAVEKSTGKQNHITITNDKGRLSQDEIDRM
Saccharomyces cerevisiae      FELSGIPPAPRGVPQIEVTFDVDSNGILNVSAVEKGTGKSNKITITNDKGRLSKEDIEKM
Escherichia coli              FNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSG-LNEDEIQKM

                                     550       560       570       580       590       600
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     VNDAEKYKAEDEENRKRIEARNSLENYCYGVKSSLEDQKIKEKLQPAEIETCMKTITTIL
Saccharomyces cerevisiae      VAEAEKFKEEDEKESQRIASKNQLESIAYSLKNTIS--EAGDKLEQADKDTVTKKAEETI
Escherichia coli              VRDAEANAEADRKFEELVQTRNQGDHLLHSTRKQVE--EAGDKLPADDKTAIESALTALE
                                     610       620       630       640       650       660
                              ....|....|....|....|....|....|....|....|....|....|....|....|
Plasmodium falciparum 3D7     EWLEKNQLAGKDEYEAKQKEAESVCAPIMSKIYQDAAGAAGGMPGGMPGGMPGGMPGGMN
Saccharomyces cerevisiae      SWLDSNTTASKEEFDDKLKELQDIANPIMSKLYQ-AGGAPGGAAGGAPGGFPGGAP----
Escherichia coli              TALKGE---DKAAIEAKMQELAQVSQKLMEIAQQQHAQQQTAGADASANNAK--------

                                     670       680
                              ....|....|....|....|....|.
Plasmodium falciparum 3D7     FPGGMPGAGMPGNAPAGSGPTVEEVD
Saccharomyces cerevisiae      ------------PAPEAEGPTVEEVD
Escherichia coli              ----------DDDVVDAEFEEVKDKK
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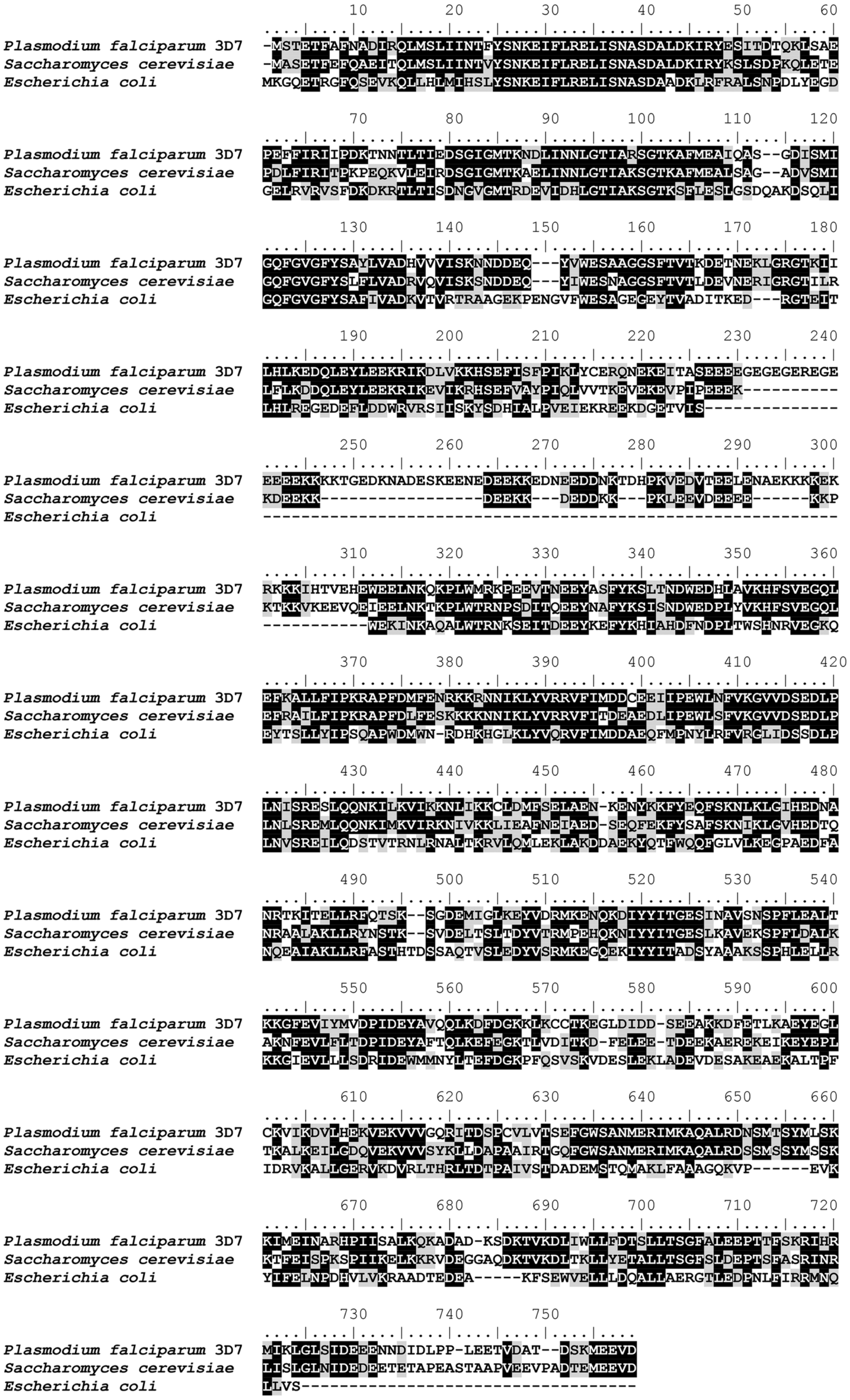
Multiple sequence alignment of HSP70 in *P. falciparum* 3D7, *S. cerevisiae,* and *E. coli* indicating identical (black), similar (grey), and nonidentical (white) residues.



Multiple sequence alignment of HSP90 in *P. falciparum* 3D7, *S. cerevisiae,* and *E. coli* indicating identical (black), similar (grey), and nonidentical (white) residues.

**Supplementary S5. SiteScore, docking score, and volume of *Plasmodium falciparum* 3D7 selected heat shock proteins obtained for the identified active sites obtained from SiteMap**

| Protein | Site | SiteScore | DScore | Volume |
|---|---|---|---|---|
| HSP20 | 1 | 1.028 | 0.990 | 543.098 |
| | 2 | 0.888 | 0.758 | 149.419 |
| | 3 | 0.772 | 0.774 | 151.049 |
| | 4 | 0.672 | 0.595 | 130.297 |
| HSP40 | 1 | 1.051 | 1.033 | 2112.623 |
| | 2 | 0.970 | 0.896 | 251.934 |
| | 3 | 0.863 | 0.868 | 115.977 |
| | 4 | 0.796 | 0.658 | 118.549 |
| | 5 | 0.712 | 0.518 | 86.951 |
| HSP60 | 1 | 1.156 | 1.014 | 268.998 |
| | 2 | 1.069 | 0.958 | 243.873 |
| | 3 | 1.018 | 0.978 | 1547.659 |
| | 4 | 0.988 | 0.954 | 321.605 |
| | 5 | 0.978 | 0.928 | 148.519 |
| HSP70 | 1 | 1.123 | 0.866 | 502.066 |
| | 2 | 1.067 | 0.940 | 1224.982 |
| | 3 | 1.059 | 0.877 | 273.028 |
| | 4 | 0.976 | 1.027 | 267.454 |
| | 5 | 0.966 | 0.953 | 377.300 |
| HSP90 | 1 | 1.092 | 0.898 | 488.775 |
| | 2 | 1.025 | 0.932 | 242.887 |
| | 3 | 1.024 | 1.035 | 196.496 |
| | 4 | 1.023 | 0.925 | 453.446 |
| | 5 | 0.874 | 0.879 | 203.999 |