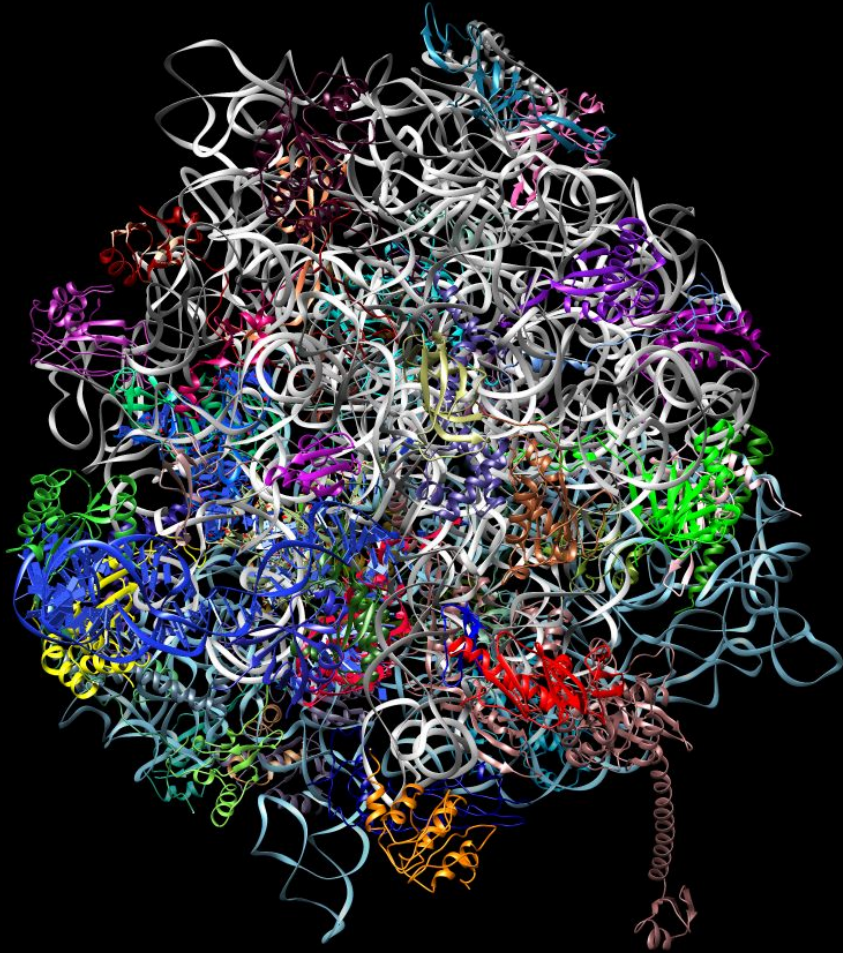




The Ribosome

Structural biology

Arola Altimir
Emma Bigas
Irene Calderón
Joana Oliver

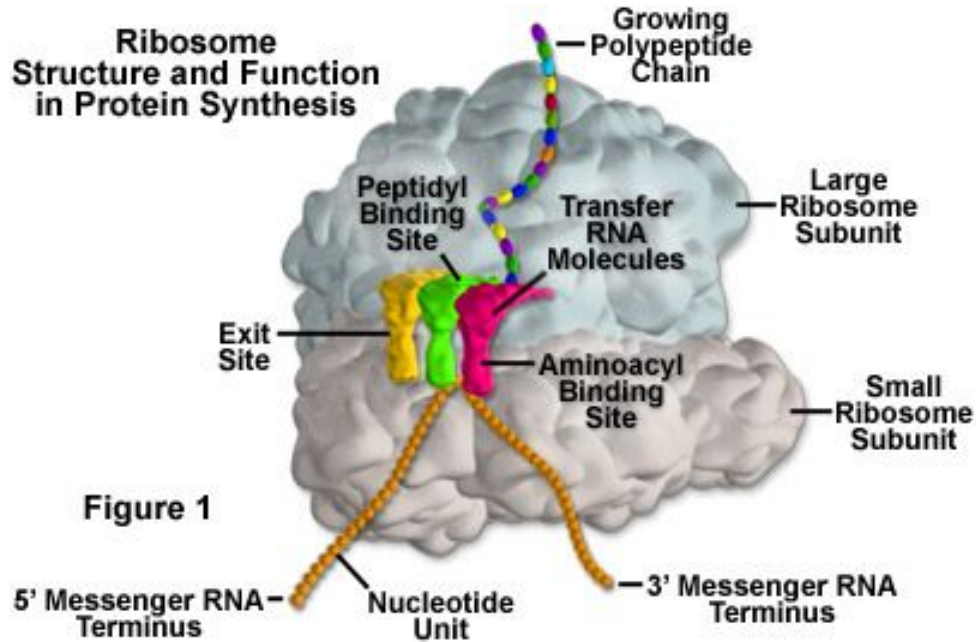
Index

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 - Subunit 30S
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 - Biological importance
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- Protein GTPase ERA
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 - Conservation
- Conclusions
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- PEM questions

INTRODUCTION



Ribosome function



- Protein biosynthesis
- Universally conserved
- Located: cytoplasm or endoplasmic reticulum
- Ligands: mRNA and tRNA

Prokaryote vs. Eukaryote

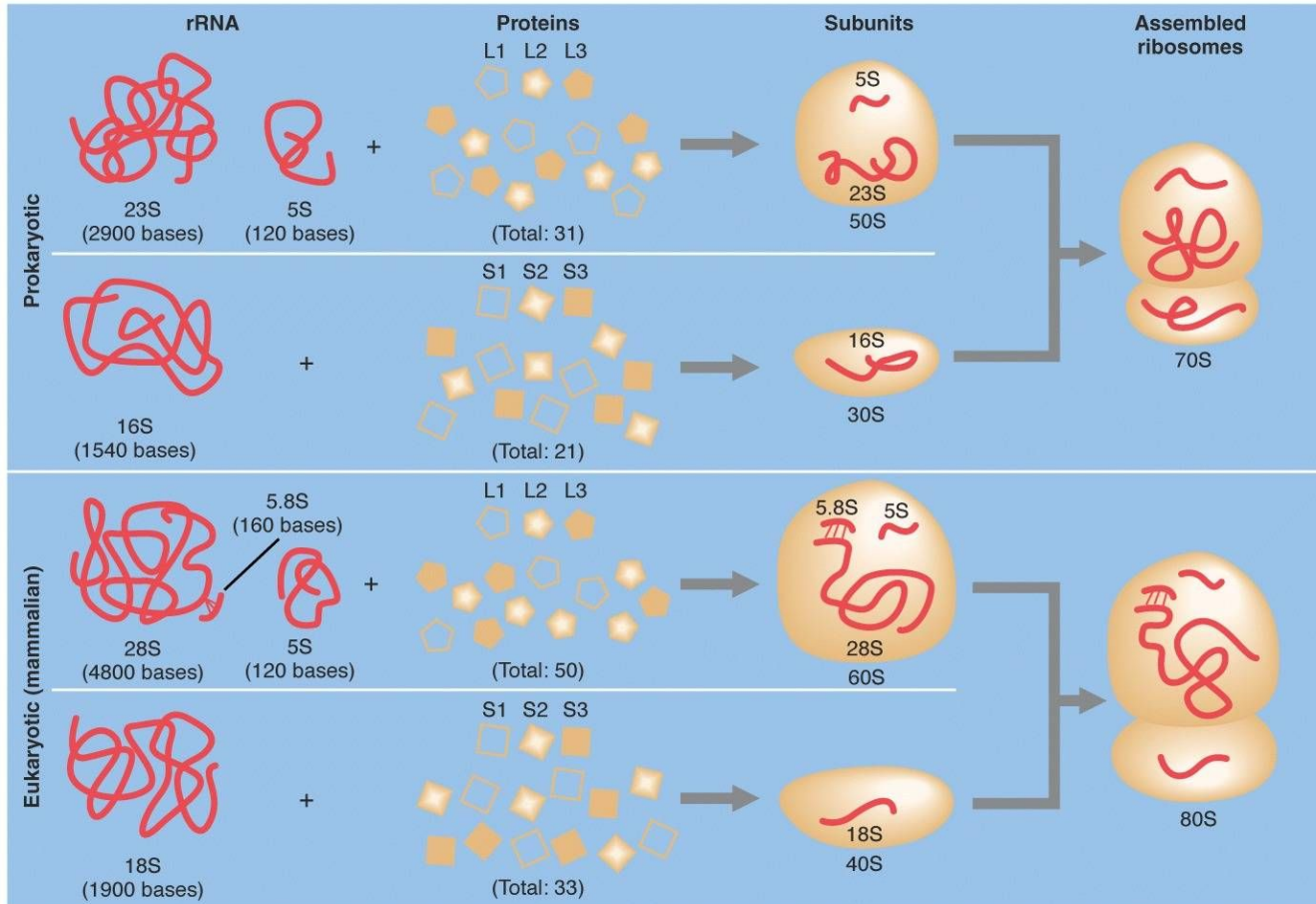


Figure © 2004 by Griffiths et al. ; text © 2010 by Steven M. Carr

Small subunit 30S



16S

S12

S3

S13

S4

S14

S5

S15

S6

S16

S7

S17

S8

S18

S9

S19

S10

S20

S11

Small subunit 30S



16S

S12

S3

S13

S4

S14

S5

S15

S6

S16

S7

S17

S8

S18

S9

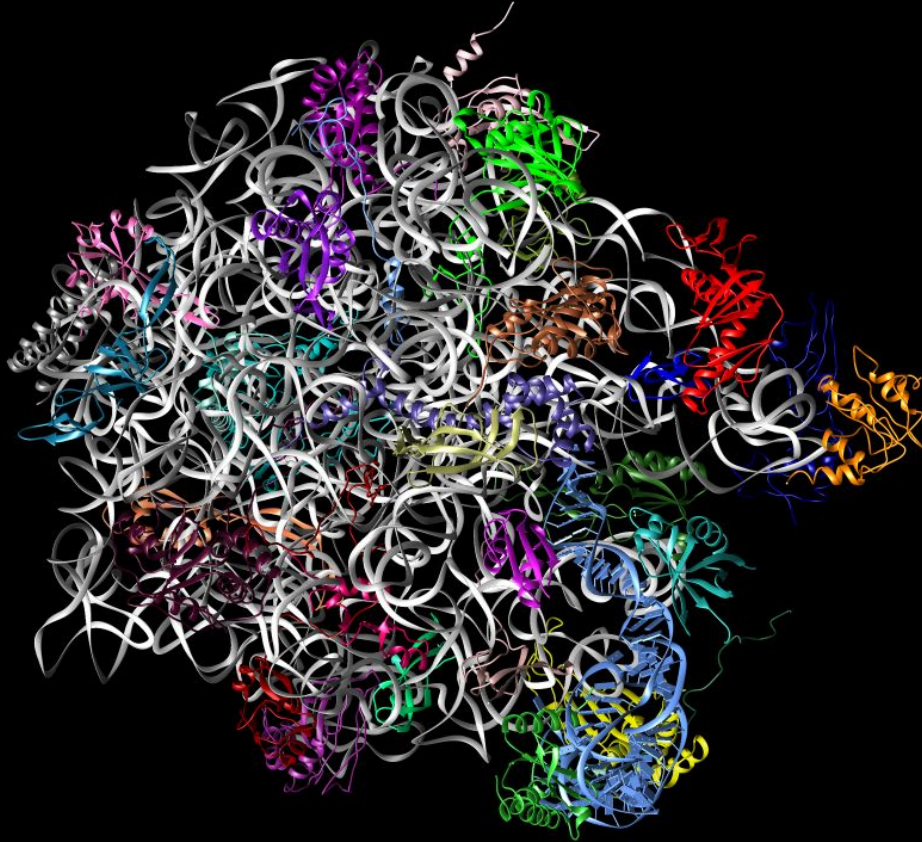
S19

S10

S20

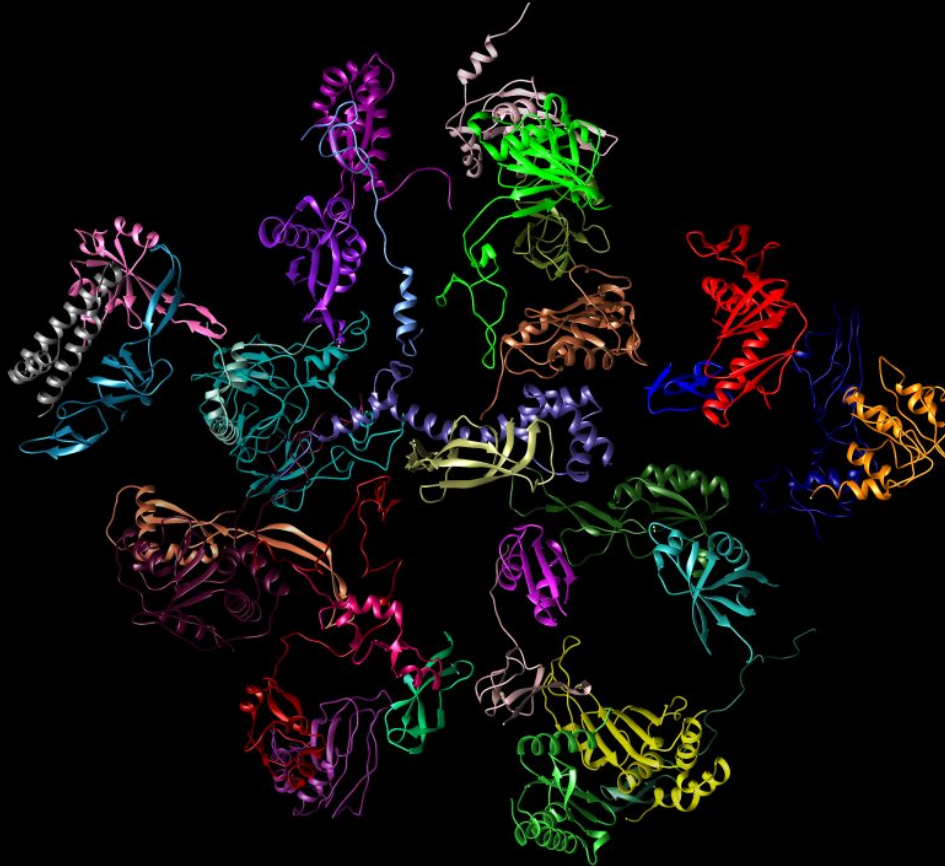
S11

Large subunit 50S

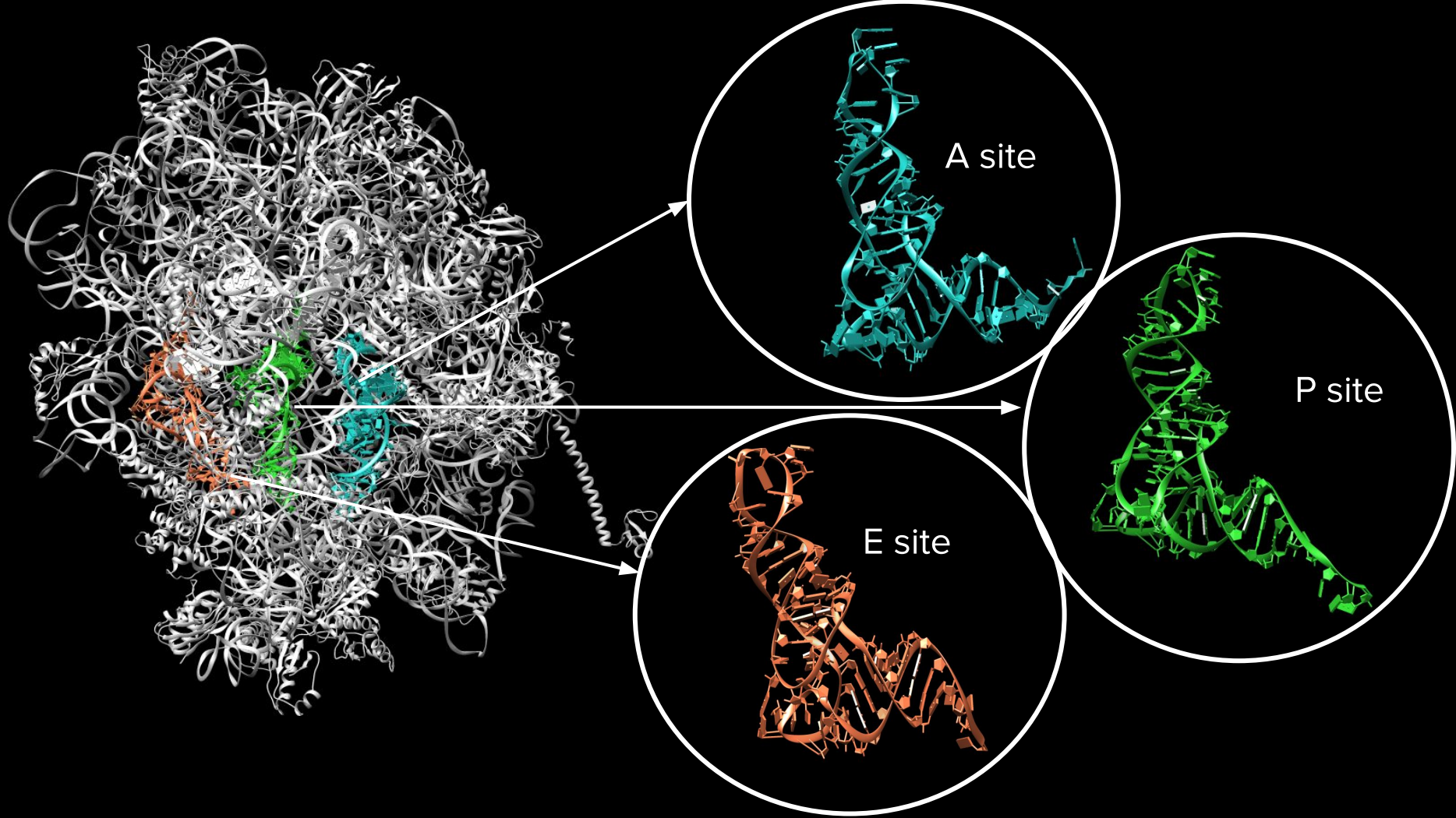


23S	L13	L25
5S	L14	L26
L1	L15	L27
L2	L16	L28
L3	L17	L29
L4	L18	L30
L5	L19	L31
L6	L20	
L8	L21	
L9	L22	
L10	L23	
L11	L24	

Large subunit 50S

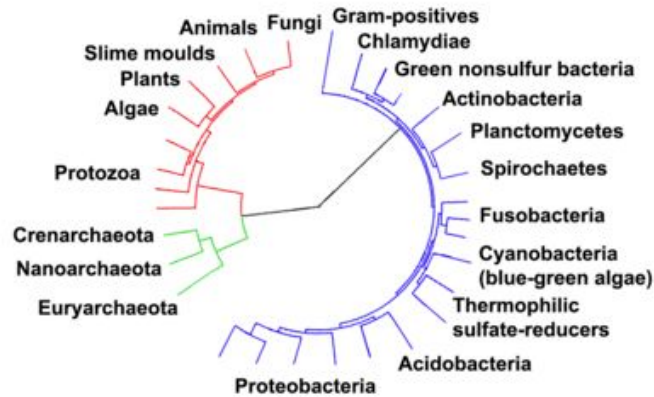


23S	L13	L25
5S	L14	L26
L1	L15	L27
L2	L16	L28
L3	L17	L29
L4	L18	L30
L5	L19	L31
L6	L20	
L8	L21	
L9	L22	
L10	L23	
L11	L24	

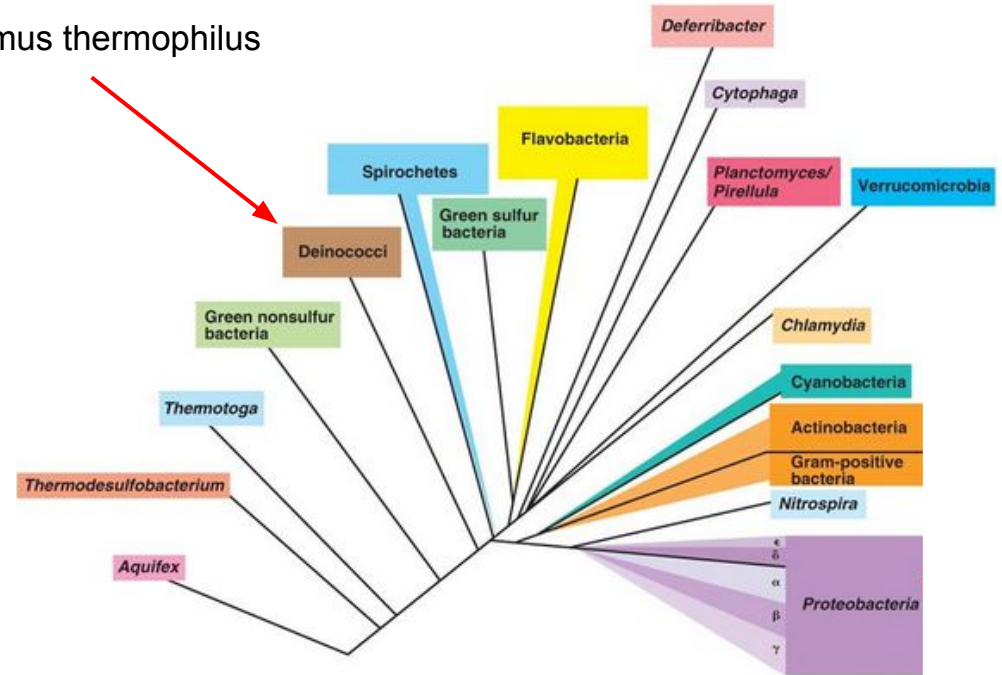


Phylogeny

Thermus thermophilus



Ciccarelli FD; et al. (2006). "Toward automatic reconstruction of a highly resolved tree of life". *Science*. **311** (5765): 1283–7.



Escherichia coli

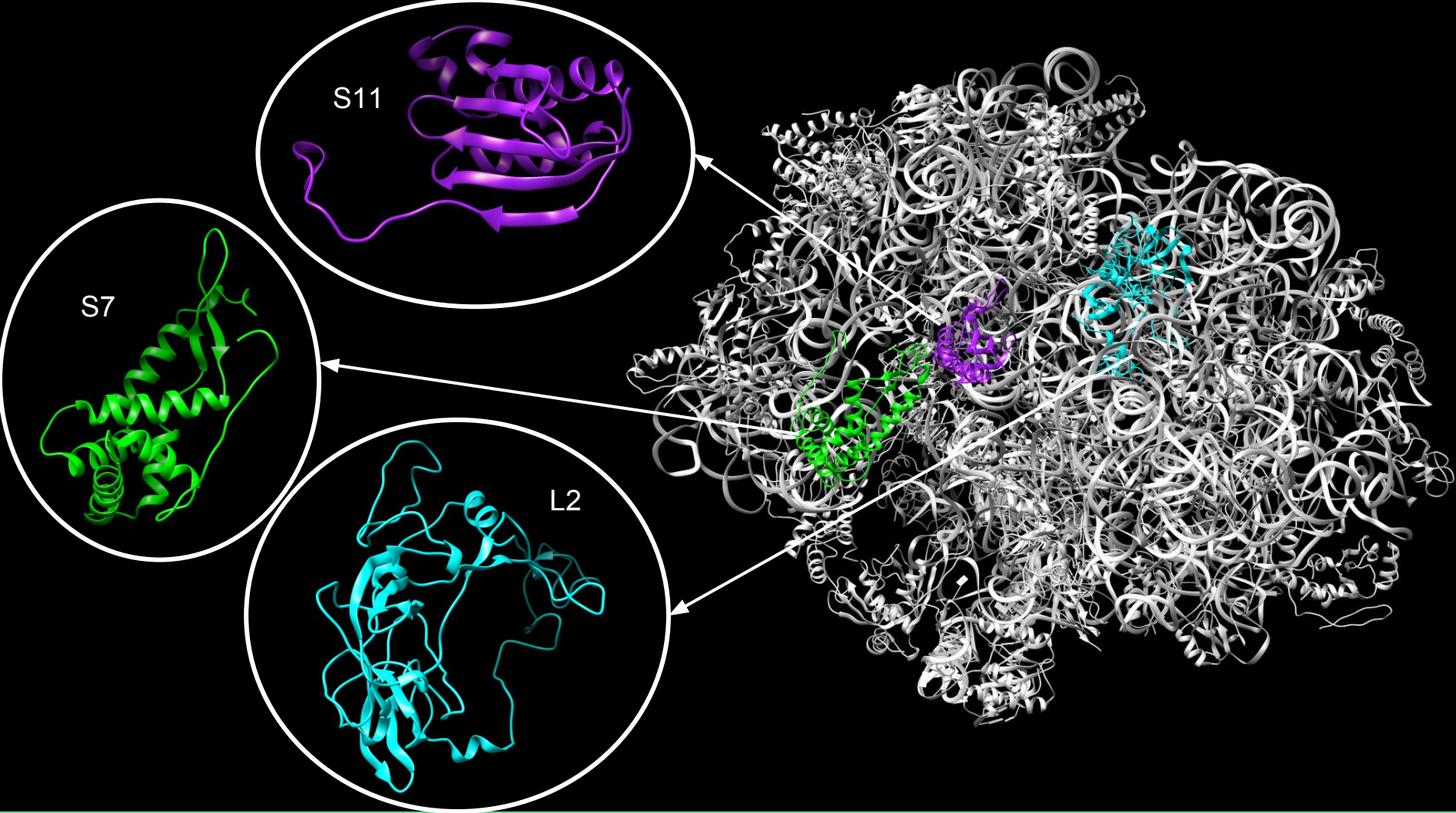
Homologous proteins

TABLE 1 Concordance between the universally conserved ribosomal proteins from the three kingdoms of life.

Small Subunit				Large Subunit			
Bacteria: <i>E. coli</i> *	Archaea <i>H. ma</i> *	Low Eukarya: <i>Yeast</i> *	High Eukarya: <i>Rat</i> *	Bacteria: <i>E. coli</i> *	Archaea <i>H. ma</i> *	Low Eukarya: <i>Yeast</i>	High Eukarya: <i>Rat</i> *
S2	S2	S0	Sa	L1	L1	L1	L10a
S3	S3	S3	S3	L2	L2	L2	L8
S4	S4	S9	S9	L3	L3	L3	L3
S5	S5	S4	S2	L4	L4	L4	L4
S7	S7	S5	S5	L5	L5	L11	L11
S8	S8	S22	S15a	L6	L6	L9	L9
S9	S9	S9	S16	L10	L10	P0(A0)	P0
S10	S10	S20	S20	L11	L11	L12	L12
S11	S11	S14	S14	L12	L12	P1/P2	P1/P2
S12	S12	S28	S23	L13	L13	L16	L13a
S13	S13	S18	S18	L14	L14	L23	L23
S14	S14	S29	S29	L15	L15	L28	L27a
S15	S15	S13	S13	L16	L10e	L10	L10
S17	S17	S18	S11	L18	L18	L5	L5
S19	S19	S15	S15	L22	L22	L17	L17
				L23	L23	L25	L23a
				L24	L24	L26	L26
				L29	L29	L35	L35
				L30	L30	L7	L7

**E. coli*, *Escherichia coli*; *H. ma.* = *Haloarcula marismortui*; *Sc. cer.* = *Saccharomyces cerevisiae*; *Rat* = *Rattus norvegicus*.

Table1. Wilson D, Nierhaus K. Ribosomal Proteins in the Spotlight. *Critical Reviews in Biochemistry and Molecular Biology*. 2005;40(5):243-267



L2/L8



Classification

CATH

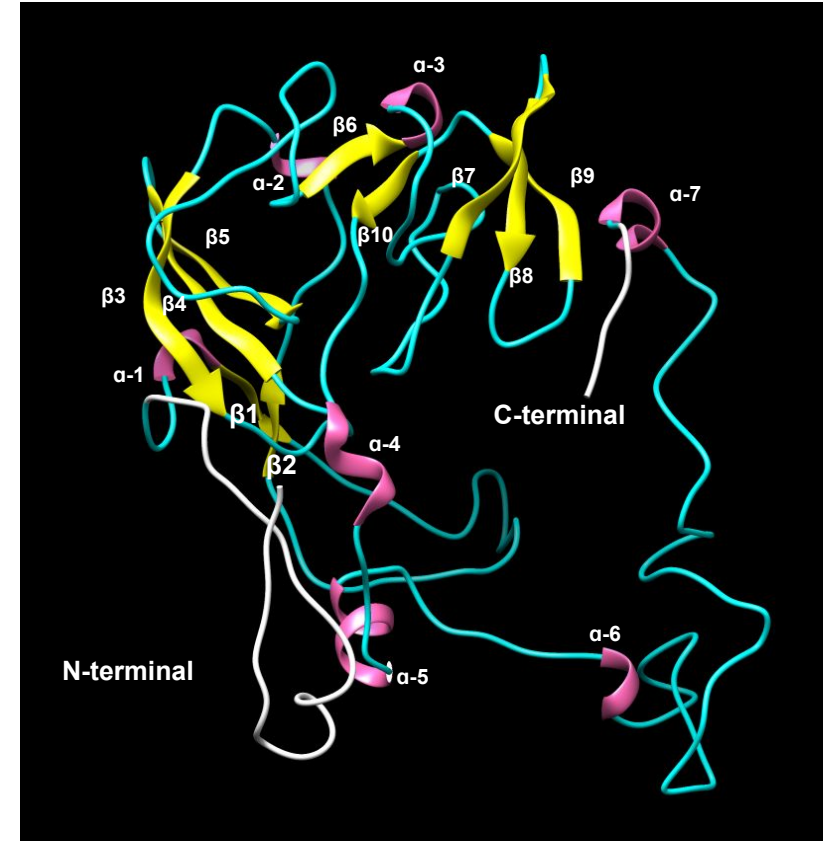
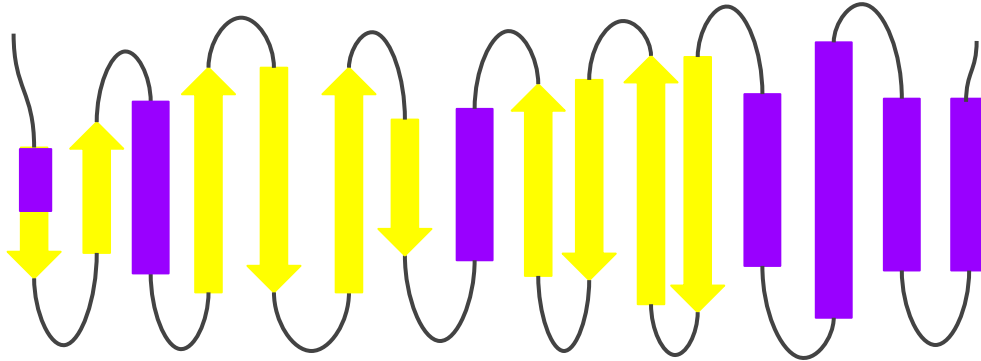
Class	Mainly Beta
Architecture	Beta barrel
Topology	OB Fold (Dihydrolipoamide Acetyltransferase, E2P)
Homologous Superfamily	Nucleic acid-binding proteins

SCOP

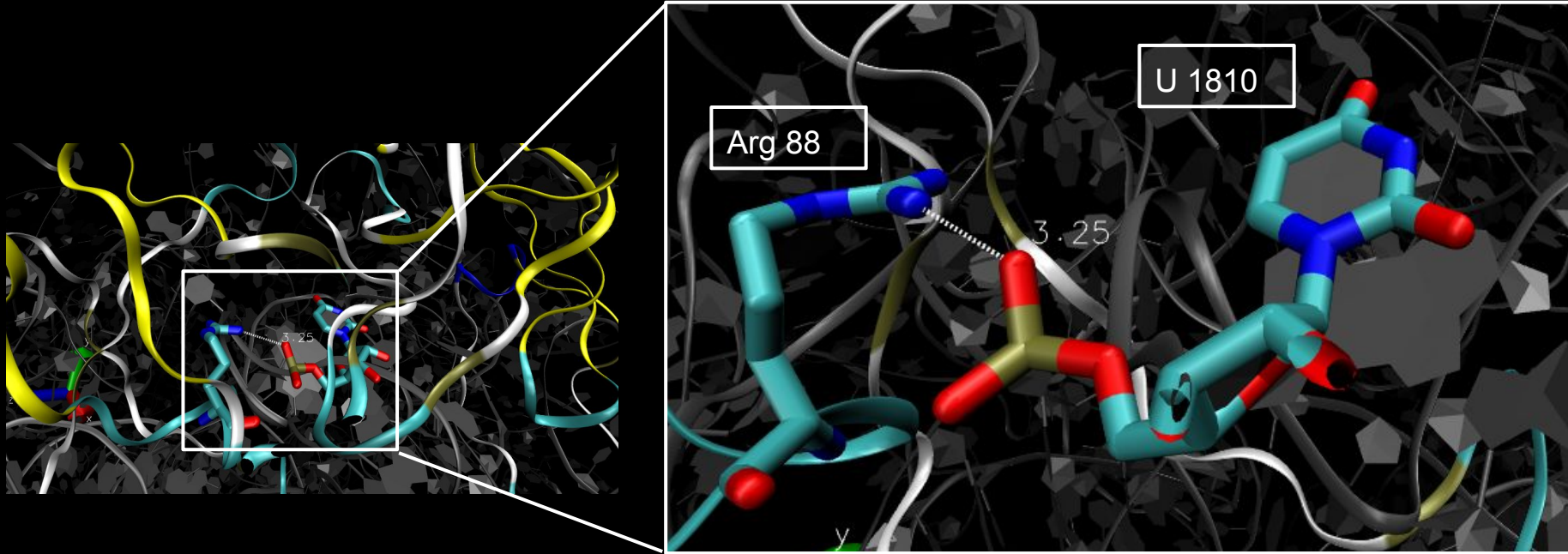
Class	All beta proteins
Fold	SH3-like barrel
Superfamily	Translation proteins SH3-like domain
Family	Ribosomal protein L2
Protein	Ribosomal protein L2

Biological importance

- Required for the association of 30S and 50S ribosome subunits
- Involved in tRNA binding to both A and P sites.
- Involvement in catalysis of peptide synthesis.



L2-23S rRNA interactions



Sequence conservation

Homo
 Mus
 Xenopus
 Danio
 Drosophila
 Saccharomyces
 Deinococcus
 Thermophilus
 ECOLI

-----MGRVIRGQRKGAGSVFRAHVVKHRK--GAAR-
 -----MGRVIRGQRKGAGSVFRAHVVKHRK--GAAR-
 -----MGRVIRGQRKGAGSVFKAHVVKHRK--GAAK-
 -----MGRVIRGQRKGAGSVFKAHVVKHRK--GAAK-
 -----MGRVIRGQRKGAGSVFKAHVVKHRK--GAAK-
 -----MGRVIRNQRKGAGSIFTSHTLRQ--GAAK-
 MAVKKYRPYPYPSRRQMTTADFSGLTKKRPEKALTEALPKTGRRNNRGRITSRFIGGGHKKR
 MAVKKFKPYTPSRRFMTVADFSEITKTEPEKSLVKPLKKTGRRNNQGRITVFRFGGGHKKR
 MAVVKCKPTSPGRRHVVKVNPELHKGKPFAPLLEKNSKSGRRNNNGRITTRHIGGGHKKO
 : . * . * . : * . * . :

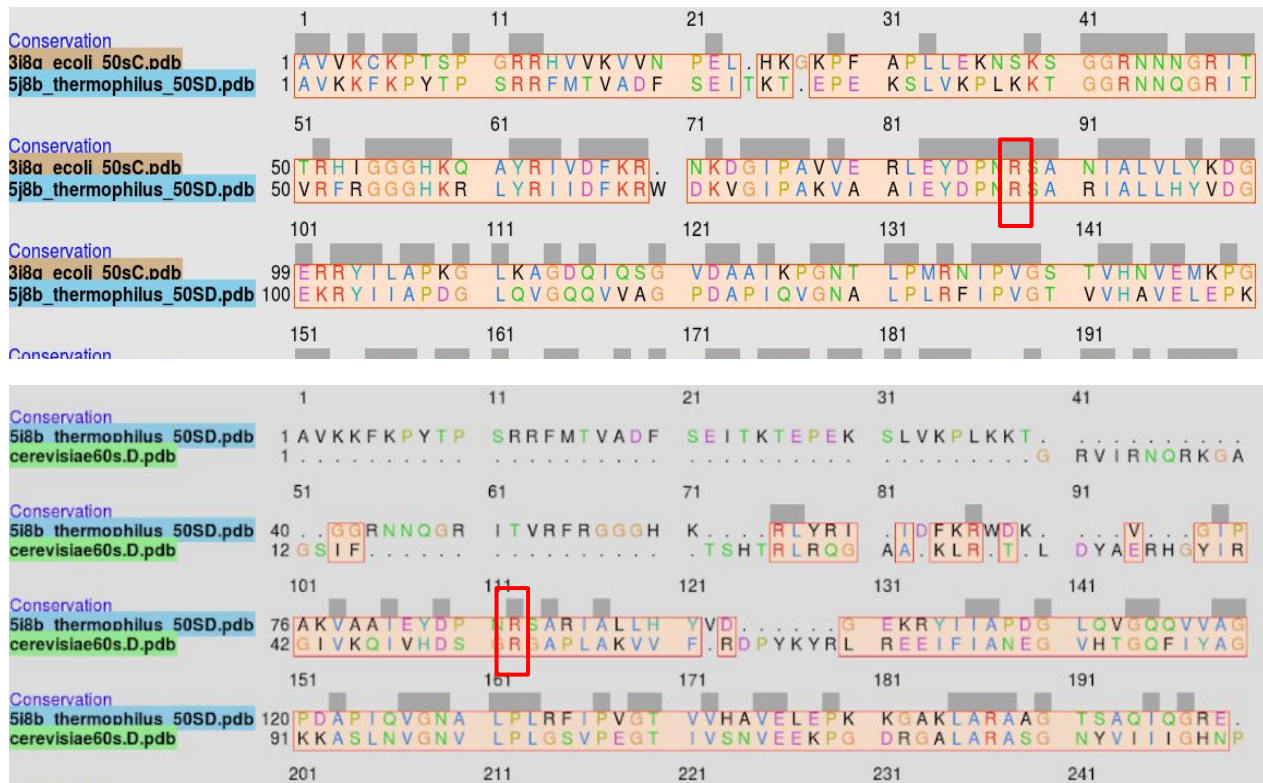
Homo
 Mus
 Xenopus
 Danio
 Drosophila
 Saccharomyces
 Deinococcus
 Thermophilus
 ECOLI

-LRVDFAE-RHGYIKGIVKDIHDPRLAPLAKVFRDPYRFKKRTELFAAEGIHGQ
 -LRVDFAE-RHGYIKGIVKDIHDPRLAPLAKVFRDPYRFKKRTELFAAEGIHGQ
 -LRVIDFAE-RNGYIKGIVKDIHDPRLAPLAKVAFRDPYRFKKRTELFVAEIGHGQ
 -LRVIDFAE-RHGYIKGIVKDIHDPRLAPLAKVMFRDPYRFKKRTELFAAEGIHGQ
 -LRSLDAE-RSGYIRGVVKDIHDPRLAPLAVVHFRDPYRYKIRKELFIAPEGMHGQ
 -LRSLDAE-RHGYIRGIVKQIVHDSRLAPLAKVFRDPYKYRLREEFIANEGVHTGQ
 LYRIIDFKRRDKSGVNAKVAIEYDRLARIALLHYAD----GEKRYILAPEGLTVGA
 LYRIIDFKRWDKVGIPAKVAIEYDRLARIALLHYVD----GEKRYIAPDGLQVGG
 AYRIIDFKR-NKDGIPAVVERLEYDRLARIALLVLYKD----GERRYILAPKGLKAGD
 * : : . : . * : : * * : : * : . . : : * . * : *

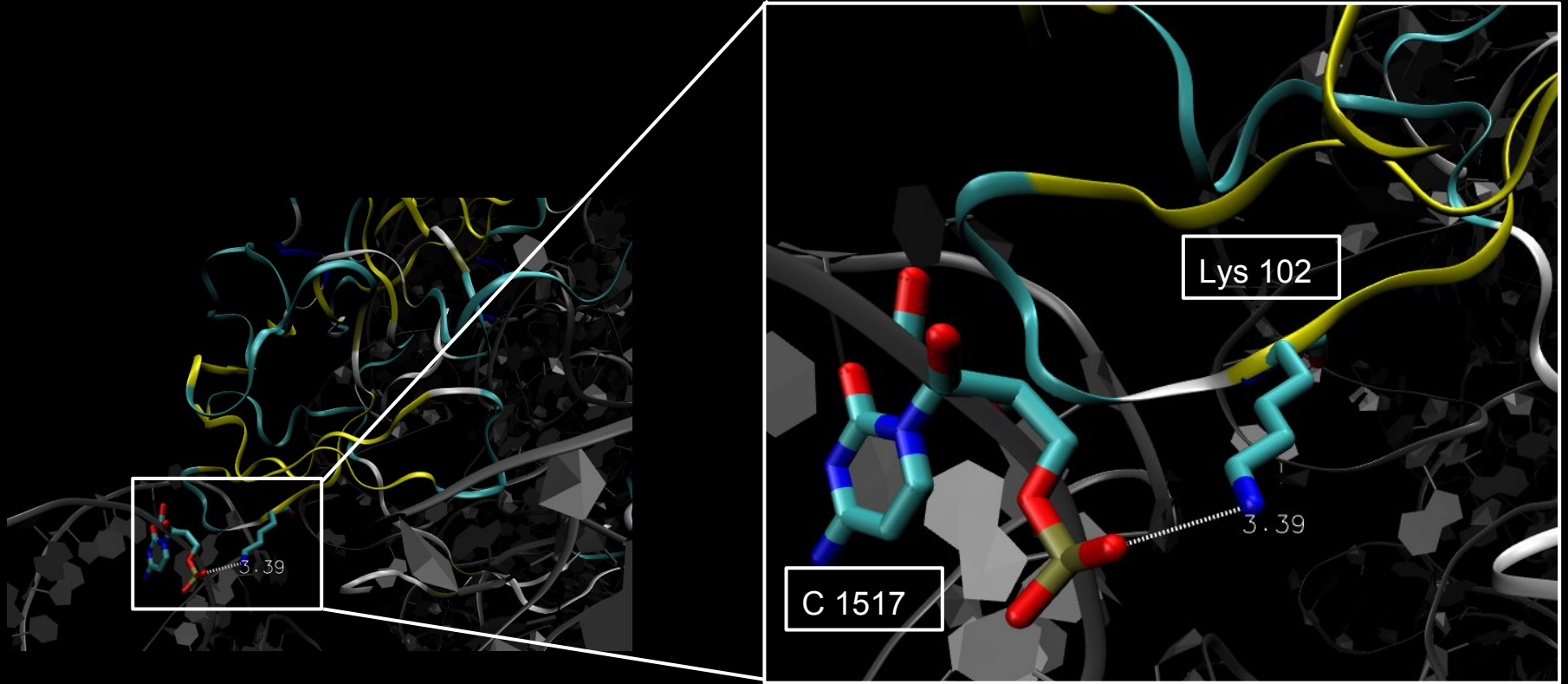
Homo
 Mus
 Xenopus
 Danio
 Drosophila
 Saccharomyces
 Deinococcus
 Thermophilus
 ECOLI

FVYCGKKAQLNIGN/LPVGTMPEGTIVCCLEEKPGDRGKLARASGNVATVISHNPETKKT
 FVYCGKKAQLNIGN/LPVGTMPEGTIVCCLEEKPGDRGKLARASGNVATVISHNPETKKT
 FVYCGKKAQLNIGN/LPVGTMPEGTIVCCLEEKPGDRGKLARASGNVATVISHNPETKKT
 FVYCGKKAQLNIGN/LPVGTMPEGTIVCCLEEKPGDRGKLARASGNVATVISHNPETKKS
 FVYCGKATLQIGN/MPLSQMPEGTIICNLEEKTDGDRGLARTSGNVATVIAHNQDTKKT
 FIYAGKKAQLNIGN/LPLGSVPEGTIVSNVEEKPGDRGALARASGNVYIIIGHNPENKT
 TVNAGPEAEPLGNALPLRFVPGVAVHAEELVPGKGAQLARASGTVSQVQGGK--ESDYV
 QVAGPADLPIQGNALPLRFIPVGTVVHAELEPKKGAQLARASGSAQIQIVR--EGDYV
 QIQSGVDAAIKPGNTLPMRNIPVGTSTVHNEMKPGKGGQLARASGTVYQIVR--DGAYV
 : . * : * : : * : : : * : . . * : : * : : :

Structural conservation



L2-23S rRNA interactions



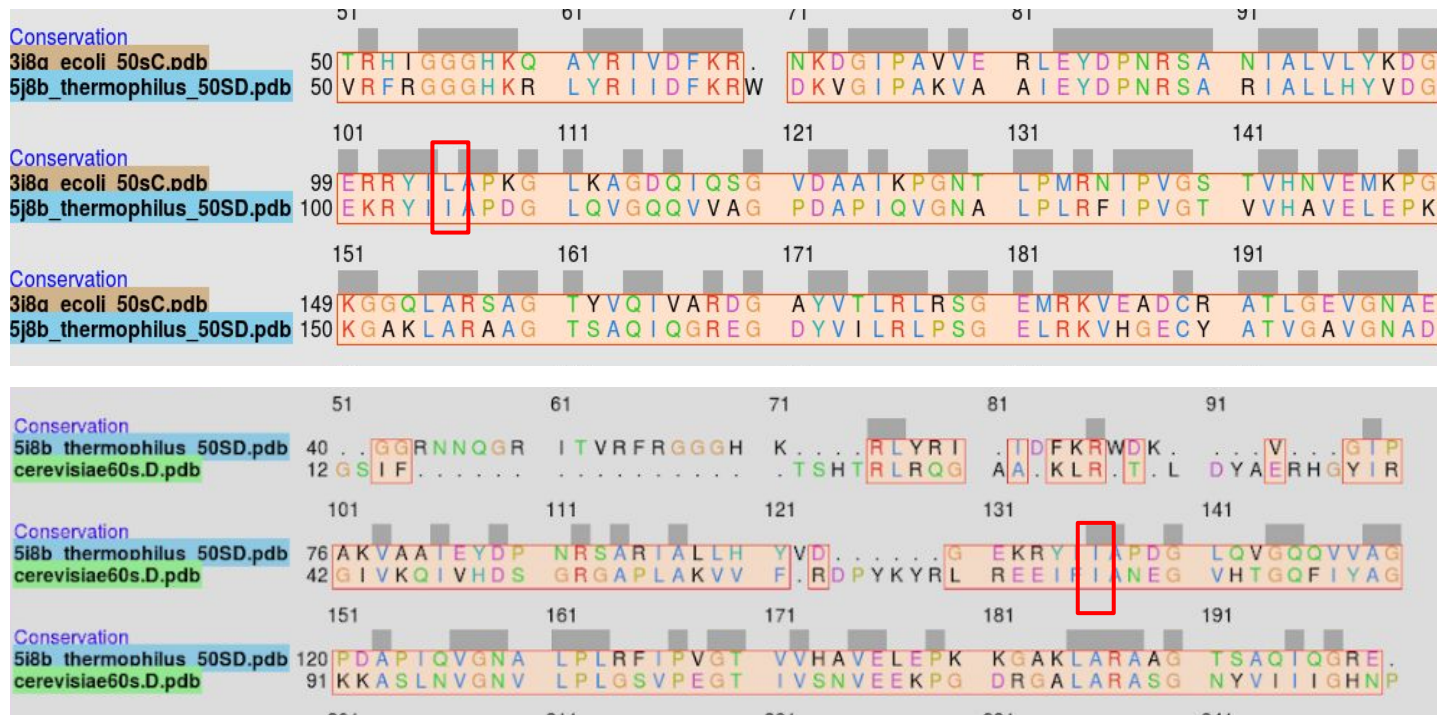
Sequence conservation

Homo -----MGRVIRGQRKGAGSVFRAHVKKHRK--GAAR-
 Mus -----MGRVIRGQRKGAGSVFRAHVKKHRK--GAAR-
 Xenopus -----MGRVIRGQRKGAGSVFKAHVKKHRK--GAAK-
 Danio -----MGRVIRGQRKGAGSVFKAHVKKHRK--GAAK-
 Drosophila -----MGRVIRAQRKGAGSVFKAHVKKRK--GAAK-
 Saccharomyces -----MGRVIRNQRKGAGSIFTSHTRLRQ--GAAK-
 Deinococcus MAVKKYRPYTPSRRQMTTADFSLTKKRPEKALTEALPKTGGRNNRGRITSRFIGGCHKR
 Thermophilus MAVKKFKPYTPSRRFMTVADFSEITKTEPKSLVKPLKKTGGRNNQGRITVFRFGGCHKR
 ECOLI MAVVKCKPTSPGRRHVVKVNPENLHKGKPFAPLLEKNSKSGGRNNNGRITTRHIGGCHKQ

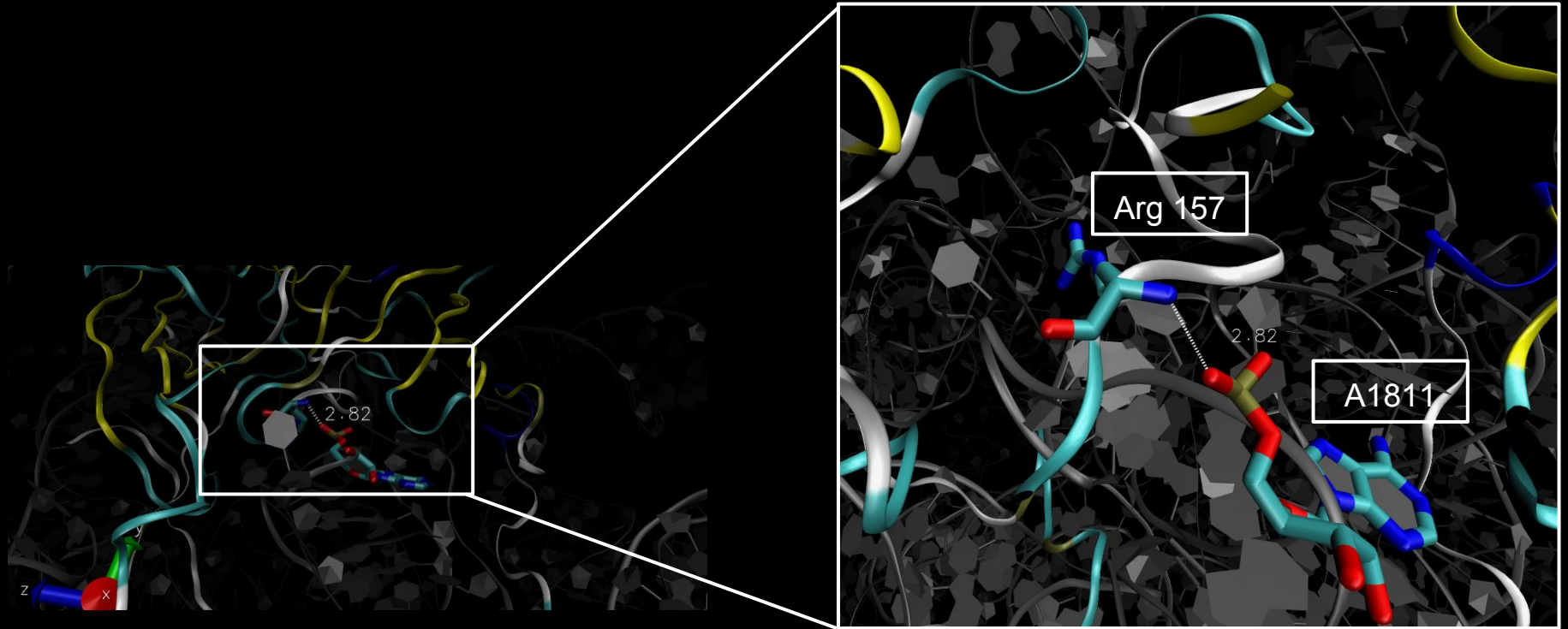
Homo	-LRVDFAE-RHGYIKGIVKDIIDPCRGAPLAKVVFDPYRFFKKRTELFI	IAEGIIHTGQ
Mus	-LRVDFAE-RHGYIKGIVKDIIDPCRGAPLAKVVFDPYRFFKKRTELFI	IAEGIIHTGQ
Xenopus	-LRVIDFAE-RNGYIKGIVKDIIDPCRGAPLAKVAFRDPYRFFKKRTELFI	IAEGIIHTGQ
Danio	-LRVIDFAE-RHGYIKGIVKDIIDPCRGAPLAKVFRDPYRFFKKRTELFI	IAEGIIHTGQ
Drosophila	-LRSLDFAE-RHGYIRGVVKDIIDPCRGAPLAVVHFRDPYRYKIRKELFI	IAPEGMHTGQ
Saccharomyces	-LRLTDFAE-RHGYIRGIVKQIVHDSRGAPLAKVVFDPYKYRLREEIFI	IANEGVHTGQ
Deinococcus	LYRIIDFKRRDQSGVNAKVAEIEYDPNRSARIALHLYAD----	GEKRYLIAPEGLTVGA
Thermophilus	LYRIIDFKRWKVGIPAKVAEIEYDPNRSARIALHLYVD----	GEKRYLIAPDGLQVGG
ECOLI	AYRIIDFKR-NKDGIPAVVERLEYDPNRSANIALVLYKD----	GERRYLIAPKGLKAGD
	* * * * *	* * * * *

Homo	FVYCGKKAQLNIGNVLPVGTMP	EGTIVCCLEEKPGDRGKLARASG	NYATVISHNPETKKT
Mus	FVYCGKKAQLNIGNVLPVGTMP	EGTIVCCLEEKPGDRGKLARASG	NYATVISHNPETKKT
Xenopus	FVYCGKKAQLNIGNVLPVGTMP	EGTIVCCLEEKPGDRGKLARASG	NYATVISHNPETKKT
Danio	FIYCGKKAQLNIGNVLPVGTMP	EGTIVCCLEEKPGDRGKLARASG	NYATVISHNPETKKS
Drosophila	FVYCGRKATLQIGNVMPLSQM	PEGTIICNLEEKTDGRGLARTSG	NYATVIAHNQDTKTS
Saccharomyces	FIYAGKKASLNVGNVPLGSP	EGTIVSNVEEKPGDRGALARASG	NYVIIIGHNPDENKT
Deinococcus	TVNAGPEAEPLGNALPLRFV	PGAVVHALELVPKGGAQLARASG	TSVQVQKG - - ESDYV
Thermophilus	QVVAGPDAPIQVGNALPLRF	IPVGTVVHAVELEPKKGAKLARASG	TSAQIQGR - - EGDYV
ECOLI	QIQSGVDAAIKPNLPMRNIP	GVSTVHNVMKPGKGGQLARASG	TSYVQIVAR - - DGAYV
	* * * * *	* * * * *	* * * * *

Structural conservation



L2-23S rRNA interactions



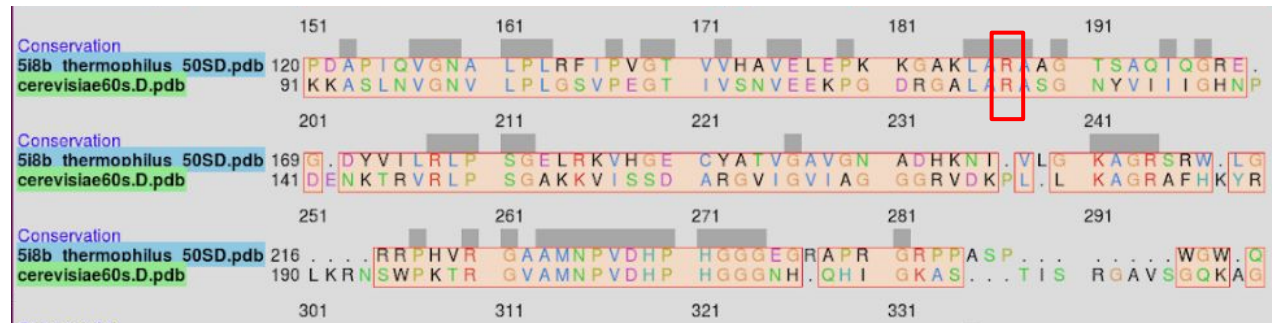
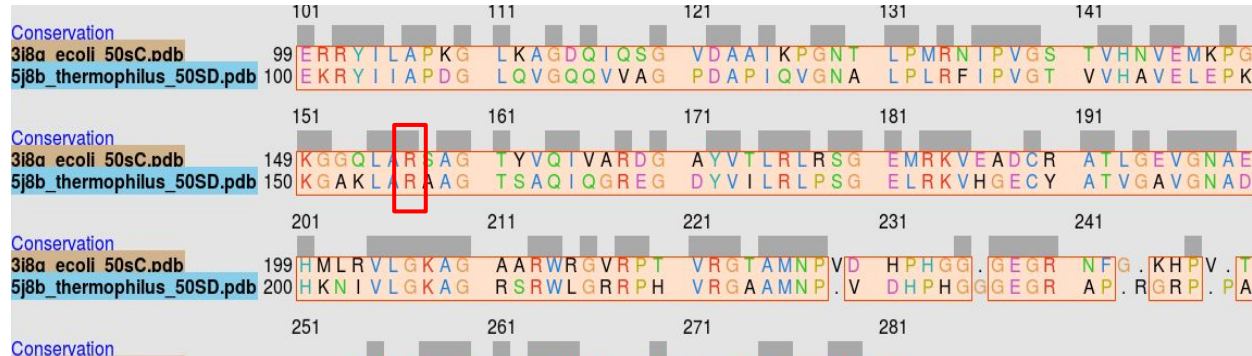
Sequence conservation

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Mus	-----MGRVIRGQRKGAGSVFRAHVKHRK--GAAR-
Xenopus	-----MGRVIRGQRKGAGSVFKAHVKHRK--GAAK-
Danio	-----MGRVIRGQRKGAGSVFKAHVKHRK--GAAK-
Drosophila	-----MGRVIRAQRKGAGSVFKAHVKKRK--GAAK-
Saccharomyces	-----MGRVIRNQRKGAGSIFTSHTRLRQ--GAAK-
Deinococcus	MAVKKYRPTYPSRRQMTADFSGLTKKRPEKALTEALPKTGGRNNRGRITSRFIGGGHKKR
Thermophilus	MAVKKFKPYTPSRRFMTVADFSEITKTEPEKSLVKPLKKTGGRNNQGRITVFRGGGHHKR
ECOLI	MAVVKCKPTSPGRRHVVKVNPVPELHKGKPFAPLLEKNSKSGGRNNNGRITTRHIGGGHKKQ

Homo	-LRVDFAE-RHGYIKGIVKDIIHDPGRGAPLAKVVFRDPYRFKKRTELFIAAEGIHTGQ
Mus	-LRVDFAE-RHGYIKGIVKDIIHDPGRGAPLAKVVFRDPYRFKKRTELFIAAEGIHTGQ
Xenopus	-LRVIDFAE-RNGYIKGIVKDIIHDPGRGAPLAKVAFRDPYRFKKRTELFVAAEGIHTGQ
Danio	-LRVIDFAE-RHGYIKGIVKDIIHDPGRGAPLAKVMFRDPYRFKKRTELFIAAEGIHTGQ
Drosophila	-LRVIDFAE-RSGYIRGVVDIIHDPGRGAPLAVVHFRDPYRYKIRKELFIAPEGMHTGQ
Saccharomyces	-LRVIDFAE-RHGYIRGIVKQIVHDSGRGAPLAKVVFRDPYKYRLREEIFIANEGVHTGQ
Deinococcus	LYRIIDFKRRDKSGVNAKVAIEYDPNRSARIALHLYAD-----GEKRYILAPEGLTVGA
Thermophilus	LYRIIDFKRWDKVGIPAKVAIEYDPNRSARIALHLYVD-----GEKRYIIAPDGLQVGG
ECOLI	AYRIIDFKR-NKDGIPAVVERLEYDPNRSANIALVLYKD-----GERRYILAPKGLKAGD
	* : * . : . : . : * : * : * : * : * : * : * : * : * : * : * : *

Homo	FVYCGKKAQLNIGNVLPVGTMPGCTIVCCLEEKPGDRGKLRLSGNYATVISHNPETKKT
Mus	FVYCGKKAQLNIGNVLPVGTMPGCTIVCCLEEKPGDRGKLRLSGNYATVISHNPETKKT
Xenopus	FVYCGKKAQLNIGNVLPVGTMPGCTIVCCVEEKPGDRGKLRLSGNYATVISHNPETKKT
Danio	FIYCGKKAQLNIGNVLPVGTMPGCTIVCCLEEKPGDRGKLRLSGNYATVISHNPETKKS
Drosophila	FVYCGRKATLQIGNVPLSQMPGCTIICNLEEKTGDRGRLRLSGNYATVIAHNQDTKKT
Saccharomyces	FIYAGKKASLNIGNVPLGVSMPGCTIVSNVEEKPGDRGALRLSGNYVIIIGHNPDENKT
Deinococcus	TVNAGPEAEPKLGNALPLRFVPGVAVVHALELVPGKGAQLRLAGTSVQVQGGK--ESDYV
Thermophilus	QVVAGPDAPIQVGNALPLRFVPGTVVHAVELEPKKGAKLRLAGTSAIQGR--EGDYV
ECOLI	QIQSGVDAAIKPGNTLPMRNIPVGVSTVHNVMKPGKGGQLRLAGTYVQIVAR--DGAYV
	: . * . * : * * . : * * : : * . . . * * : * . : : :

Structural conservation



Sequence conservation in bacteria

CLUSTAL 2.1 multiple sequence alignment

```
Thermophilus -AVKKFKPYTPSRRFMTVADFSEITK-----TEPEKSLVKPLKKTGGRN-
Deinococcus --VKKYRPYTPSRRQMTTADFSGLTK-----KRPEKALTEALPKTGGRN-
Aquifex      MGVRLKLPVTNGTRHAVLYDFEEIEKLVKRGKEWVLLKKNQVEPEKSLLKWWHRAKGRSR
Ecoli        -AVVKCKPTSPGRRHVVKVVNPELHK-----GKPFAPLLEKNSKSGGRN-
Salmonella   MAVVKCKPTSPGRRHVVKVVNPELHK-----GKPFAPLVEKNSKSGGRN-
Haemophilus  MAIVKCKPTSAGRRHVVKIVNPELHK-----GKPYAPLLDTKSKTGGRN-
              : * : * : . * . : * . * . : : **.
```

```
Thermophilus NQGRITVFRGGGHHKRLRYIIDFKRWDKVGIPAKVAAIEYDPNRSARIALHLYVDGEKRY
Deinococcus  NRGRITSRFIGGGHKKRLRYIIDFKRRDKSGVNAKVAAIEYDPNRSARIALHLYADGEKRY
Aquifex      QRGNITARHRRGGGHHKRLRYIIDFKR-DKSLVPAKVVSIEYDPNRSARICLLHYADGEKRY
Ecoli        NNGRITTRHIGGGHKKQAYRIVDFKR-NKDGI PAVVERLEYDPNRSANIALVLYKDGERRY
Salmonella   NNGRITTRHIGGGHKKQAYRIVDFKR-NKDGI PAVVERLEYDPNRSANIALVLYKDGERRY
Haemophilus  NYGRITTRHIGGGHKKQHYRLIDFKR-NKLDI PAVVERLEYDPNRSANIALVLYKDGERRY
              : *.** *. *****: **::*** :* : * * :**** ***.*. : * **.*:
```

```
Thermophilus I IAPDGLQVGQQVV-----AG-PDAPIQVGNALPLRFIPVGTVVHAVELEPKKGAKL
Deinococcus  I IAPDGLTVGATVN-----AG-PEAEPLGNALPLRFVPVGAHVHLELVPGKGAKL
Aquifex      I IAPDGLKVGDTVMSISWEDAEAGKPLPEIKPGNAMPLKYIPEGTIVHNIEFIPGKGQI
Ecoli        I IAPKGLKAGDQIQ-----SG-VDAAIKPGNTLPMRNIPVGSTVHNVMKPGKGGQI
Salmonella   I IAPKGLKAGDQIQ-----SG-VDAAIKAGNTLPMRNIPVGSTVHNVMKPGKGGQI
Haemophilus  I IAPKGLSVGDQIQ-----AG-INSPIKVGNSLPMRNIPVGSTVHNVELKPGKGGQI
              : *.** *. : : * . : **::*** :* * : * * : * * : * * : *
```

Arg 88

Bacterial and eukaryotic conservation

Lys 102

Discordance in *E.coli* → two groups in bacteria (Lys and Ile)

Sequence conservation in bacteria

Arg 157

Bacterial and eukaryotic conservation

Thermophilus	ARAAGTSAQIQGREG--DYVILRLPSGELRKVHGECYATVGAVGNADHKNIIVLGKAGRSR
Deinococcus	ARSAGTSVQVQGKES--DYVIVRLPSGELRRVHSECYATIGAVGNAEHKNIIVLGKAGRSR
Aquifex	ARAAGTWAQVLGRSTRKGYVLRMPSGEVRMIHERCMATVGRVGLAEHELVLKGKAGRAR
Ecoli	ARSAGTYVQIVARDG--AYVTLRLRSGEMRKVEADCRATLGEVGNAEHMLRVLGKAGAAR
Salmonella	ARSAGTYVQIVARDG--AYVTLRLRSGEMRKVEADCRATLGEVGNAEHMLRVLGKAGAAR
Haemophilus	ARSAGAYVQIIAREG--NYVTLRLRSGEMRKVLAECVATIGEVGNSEHMLRVLGKAGANR
	:: .*: :. . ** :*: **:* : * **:* ** ::* ***** *

Thermophilus	WLGRRPHVRGAAMNPVDHPHGGGEGRAPRGRPPASPWGWQTKGLKTRKRRKPSSRFIIAR
Deinococcus	WLGRKPHQRGSAMNPVDHPHGGGEGRTGAGRVPVTPWGKPTKGLKTRRKRKTSDFIVT-
Aquifex	WLGWRPHTRGATAMNPVDHPHGGGEGRT-RGKHPESPWGWKTGKYKTRRGKKYSQDFIVTR
Ecoli	WRGVRPTVRGTAMNPVDHPHGGGEGRN-FGKHPVTPWGVQTKGKKTRSNKR-TDKFIVRR
Salmonella	WRGVRPTVRGTAMNPVDHPHGGGEGRN-FGKHPVTPWGVQTKGKKTRSNKR-TDKFIVRR
Haemophilus	WRGIRPTVRGTAMNPVDHPHGGGEGRN-FGKHPVTPWGVQTKGKKTRHNKR-TDKYIVRR
	* * :* **:***** **:* :*** *** ** : : :. :. :. :

Thermophilus	RKK---
Deinococcus	-----
Aquifex	RDGRPL
Ecoli	RS---
Salmonella	RSK---
Haemophilus	RGK---

Sequence conservation

Homo	-----MGRVIRGQRKGAGSVFRAHVKKHRK--GAAR-
Mus	-----MGRVIRGQRKGAGSVFRAHVKKHRK--GAAR-
Xenopus	-----MGRVIRGQRKGAGSVFKAHVKKHRK--GAAR-
Danio	-----MGRVIRGQRKGAGSVFKAHVKKHRK--GAAR-
Drosophila	-----MGRVIRGQRKGAGSVFKAHVKKHRK--GAAR-
Saccharomyces	-----MGRVIRNQRKGAGSIFTSHTRLRQ--GAAR-
Deinococcus	MAVKKYRPYTPSRQMTTADFSLTKKRPEKALTEALPKTGGRNNRGRITSRFIGGGHKKR
Thermophilus	MAVKKFKPYTPSRRFMTVADFSEITKTEPEKSLVKPLKKTGGRNNQGRITVRFRRGGHKKR
ECOLI	MAVVKCKPTSPGRRHVVKVNPVPELHKGKPFAPLLEKNSKSGGRNNGRITTRHIGGGHKKQ
Homo	-LRVDFAE-RHGYIKGIVKDIIDPCRGAPLAKVVFDRDPYRFKKRTELFIAAEGIHTGQ
Mus	-LRVDFAE-RHGYIKGIVKDIIDPCRGAPLAKVVFDRDPYRFKKRTELFIAAEGIHTGQ
Xenopus	-LRVIDFAE-RNGYIKGIVKDIIDPCRGAPLAKVAFDRDPYRFKKRTELFVAAEGIHTGQ
Danio	-LRVIDFAE-RHGYIKGIVKDIIDPCRGAPLAKVMFRDPYRFKKRTELFIAAEGIHTGQ
Drosophila	-LRSLDFAE-RSGYIRGVVKDIIDPCRGAPLAVVHFRDPYRYKIRKELFIAPEGMHTGQ
Saccharomyces	-LRLTLDYAE-RHGYIRGIVKQIVHDSRGAPLAKVVFDRDPYKYRLREEIFIANEGVHTGQ
Deinococcus	LYRIIDFKRRDKSGVNAKVAIEYDPNRSARIALHLYAD----GEKRYILAPEGLTVGA
Thermophilus	LYRIIDFKRWKVGIPAKVAAIEYDPNRSARIALHLYVD----GEKRYIIPDGLQVQV
ECOLI	AYRIIDFKR-NKDGIPAVVERLEYDPNRSANIALVLYKD----GERRYILAPKGLKAGQ
Homo	FVYCGKKAQLNIGNVLPGVTMPEGTIVCCLEEKPGDRGKLARASGNATVISHNPETKKT
Mus	FVYCGKKAQLNIGNVLPGVTMPEGTIVCCLEEKPGDRGKLARASGNATVISHNPETKKT
Xenopus	FVYCGKKAQLNIGNVLPGVTMPEGTIVCCVEEKPGDRGKLARASGNATVISHNPETKKT
Danio	FIYCGKKAQLNIGNVLPGVTMPEGTIVCCLEEKPGDRGKLARASGNATVISHNPETKKS
Drosophila	FVYCGRKATLQIGNVMPLSQMPEGTIIICNLEEKTDGRGLARTSGNYATVIAHNQDTKKT
Saccharomyces	FIYAGKKASLNGNVLPLGVSPEGTIVSNVEEKPGDRGALARASGNVYIIIGHNPDENKT
Deinococcus	TVNAGPEAEPKLGNALPLRFVPMGAVVHALELVPKGGAQLARSAGTSVQVQGK--ESDYV
Thermophilus	QVVAGPDAPIQVGNALPLRFIPVGTVVHAVELEPKKGAKLARAAGTSAQIQGR--EGDYV
ECOLI	QIQSGVDAAIKPNLTPMRNIPVGSTVHNVMKPKGGQLARSAGTYVQIVAR--DGAYV

RNA binding domain

Complete conservation

23s RNA binding sites

Determinant residues for the OB fold

Sequence conservation

Homo	RVKLP	SGSKKVISSANRAVVG	VVAGGGRIDKPILKAGRAYHKYKAKRNCWPRVRGVAMNP
Mus	RVKLP	SGSKKVISSANRAVVG	VVAGGGRIDKPILKAGRAYHKYKAKRNCWPRVRGVAMNP
Xenopus	RVKLP	SGSKKVISSANRAIVG	VVAGGGRIDKPILKAGRAYHKYKAKRNCWPRVRGVAMNP
Danio	RVKLP	SGSKKVISSANRAVVG	VVAGGGRIDKPILKAGRAYHKYKAKRNCWPRVRGVAMNP
Drosophila	RVKLP	SGAKKVVP	SANRAMVGIVAGGGRIDKPILKAGRAYHKYKVKRNSWPKVRGVAMNP
Saccharomyces	RVRLP	SGAKKVISSDARGVIC	VIAGGGRVDKPLLKAGRAFHKYRLKRNSWPKTRGVAMNP
Deinococcus	IVRLP	SGELRRVHSECYATIG	AVGNAEHKNIVLGKAGRS--RWLGRK---PHQRGSAMNP
Thermophilus	ILRLP	SGELRKVHSECYATVG	AVGNADHKNIIVLGKAGRS--RWLGRR---PHVRGAAMNP
ECOLI	TLRLP	SGEMRKVEADCRATLG	EVGNAEHMLRVLGKAGAA--RWRGVR---PTVRGTAMNP
	:	:* **	: : . : * : . . . : : *** : : : * ** ****

Homo	VEHPF	GGG-NHQHIGKPSTIRRDAPAGRKVGLIAARRTGRLRGTKTVQEKEN
Mus	VEHPF	GGG-NHQHIGKPSTIRRDAPAGRKVGLIAARRTGRLRGTKTVQEKEN
Xenopus	VEHPF	GGG-NHQHIGKPSTIRRDAPAGRKVGLIAARRTGRLRGTKTVQEKEN
Danio	VEHPF	GGG-NHQHIGKPSTIRRDAPAGRKVGLIAARRTGRLRGTKTVQDKEN
Drosophila	VEHPH	GGG-NHQHIGKASTVKRGTSAGRKVGLIAARRTGRIIRGGKGDSDK-
Saccharomyces	VDHPH	GGG-NHQHIGKASTISRGAVSGQKAGLIAARRTGLLRGSQKTQD---
Deinococcus	VDHPH	GGGEGRTGAGRVPVTPWGKPTKGLKTRRKRKTSDFRIVTRRK----
Thermophilus	VDHPH	GGGEGRAPRGRPPASPWGQTKGLKTRKRRKPSSRFIARRKK----
ECOLI	VDHPH	GGGEGRN-FGKHPVTPWGVQTKGKKTRSNKR-TDKFIVRRRSK----
	*	***.*** : : * : . . . : : : : : :

RNA binding domain

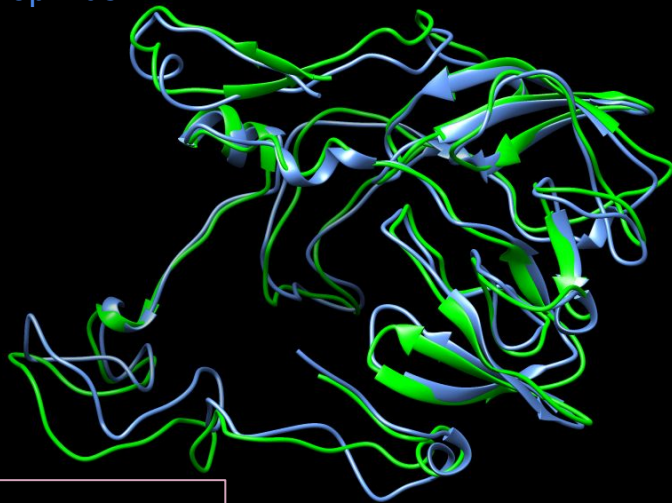
Complete conservation

His 229 important for
peptidyl-transferase
activity

Structural conservation

Bacteria/Bacteria

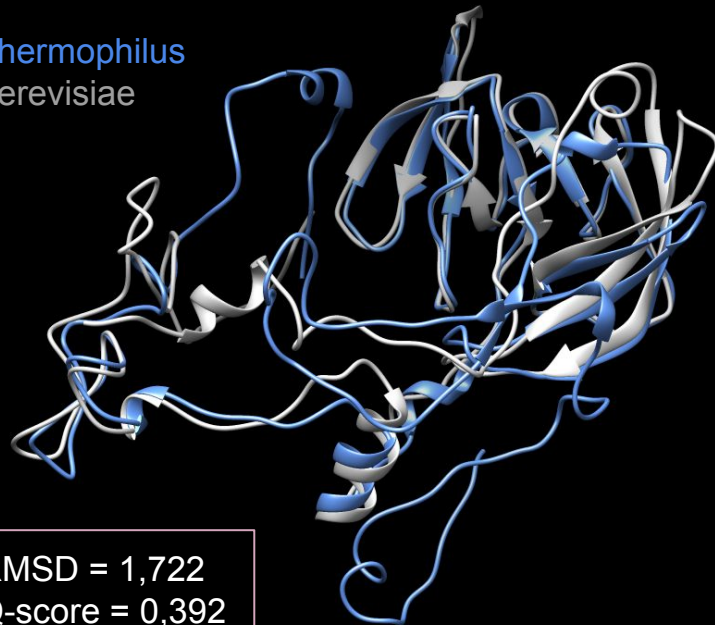
T. thermophilus
E. coli



RMSD = 1,553
Q-score = 0,737
% id. = 55,72%

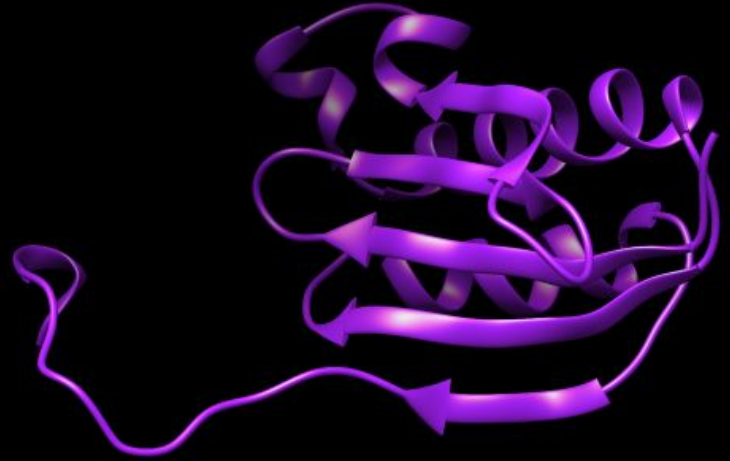
Bacteria/Eukaryote

T. thermophilus
S. cerevisiae



RMSD = 1,722
Q-score = 0,392
% id. = 25,79%

S11/S14



Classification

CATH

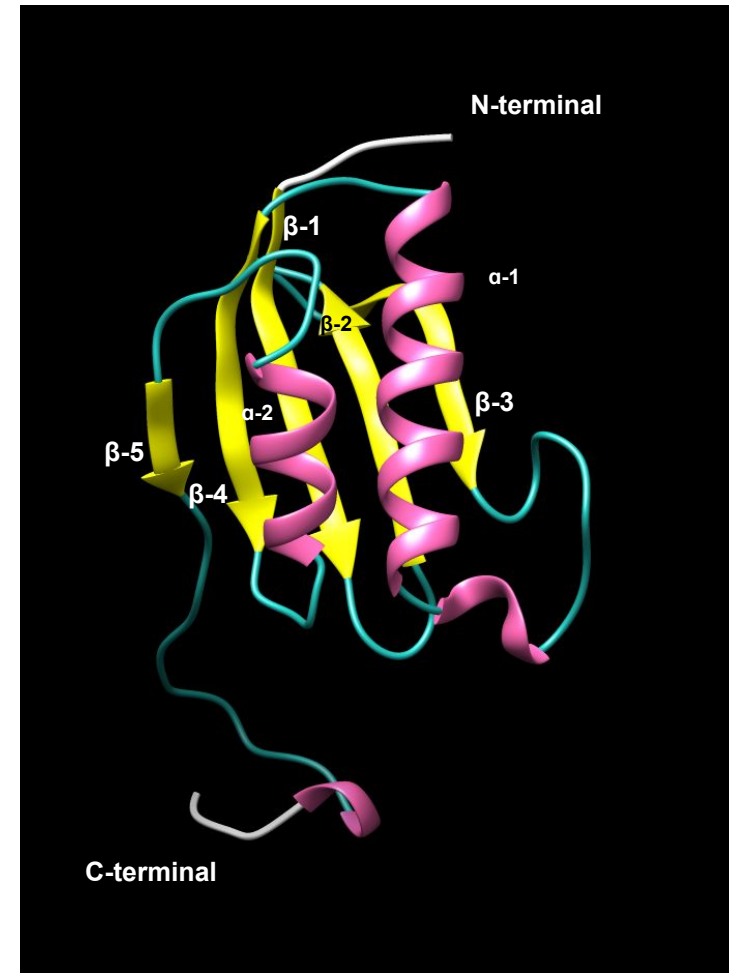
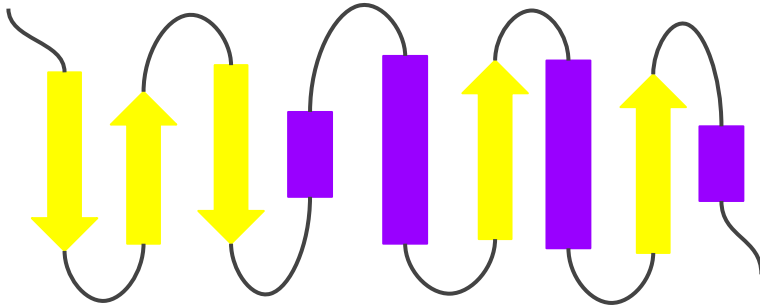
Class	Alpha Beta
Architecture	2-Layer Sandwich
Topology	Nucleotidyltransferase; domain 5
Homologous Superfamily	Ribosomal protein S11

SCOP

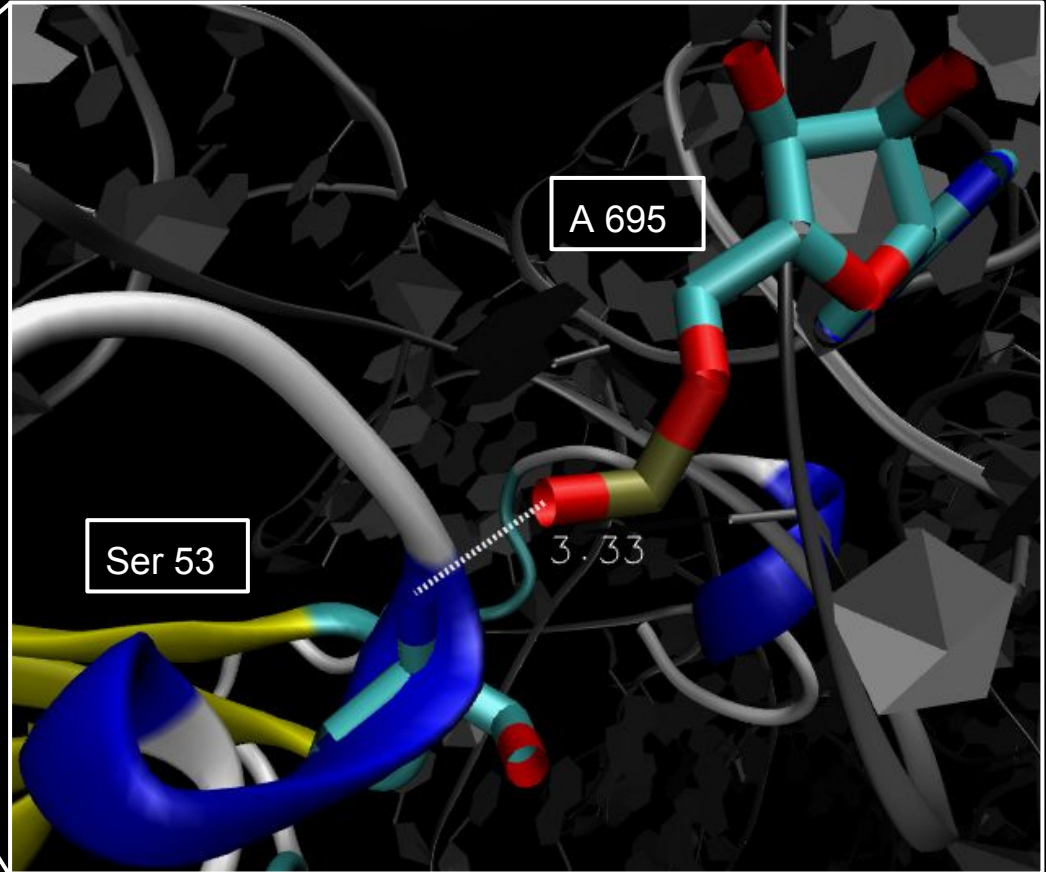
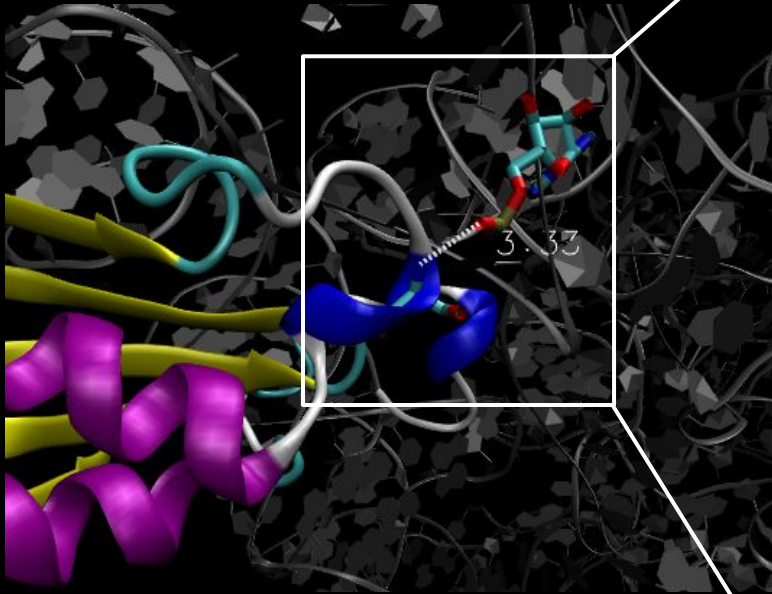
Class	Alpha and beta protein
Fold	Ribonuclease H-like motif
Superfamily	Translational machinery components
Family	Ribosomal protein L18 and S11
Protein	Ribosomal protein S11

Biological importance

- Selection of the correct tRNA
- Interacts with 16S rRNA:
 - Generate the platform of 30S
 - Forms a bridge with the 50S ribosomal subunit



S11-16S rRNA interactions



Sequence conservation

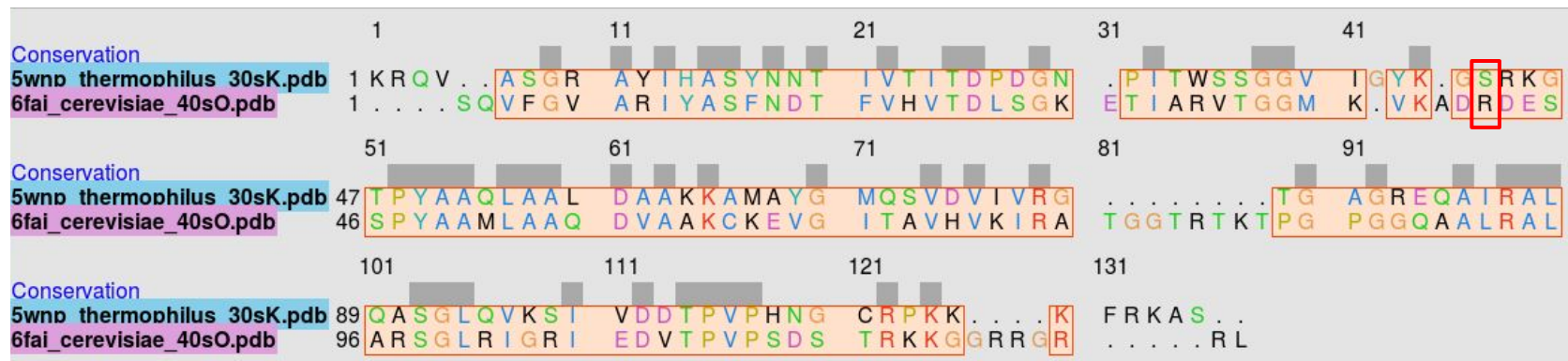
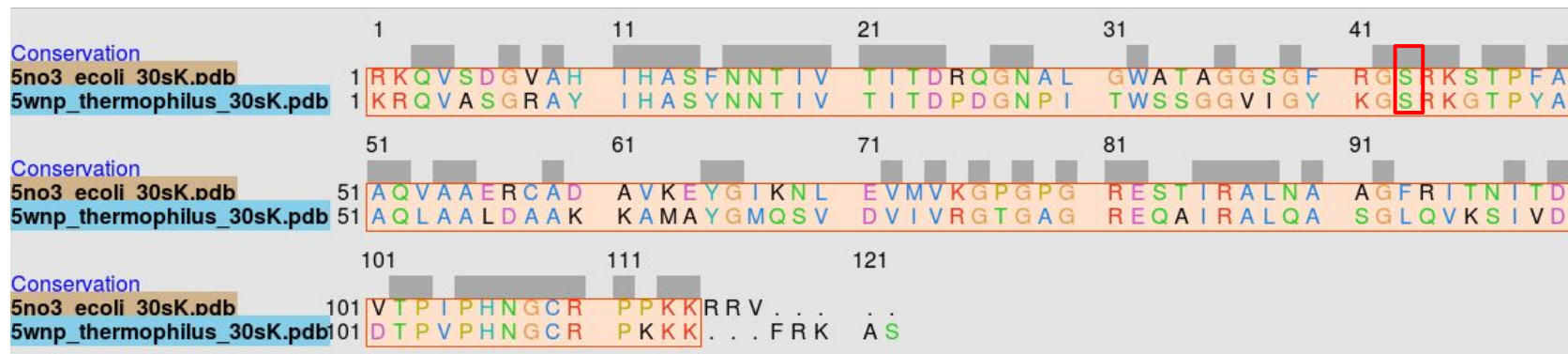
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CLUSTAL 2.1 multiple sequence alignment

Mus      MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Xenopus  MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Homo     MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Danio    MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Saccharomyces -----MSNVVQARDNSQVFGVARIYASFNDTFVHVTDLSGKETIARVTGGM
Deinococcus -----MAK-PTKGKAPRRSRRNISAGRAYVHASYNNTIVTITDLDGNSVAWSSGGTI
Thermus   -----MAKKPSK----KKVKRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVI
Escherichia -----MAKAPIR--ARKRVRKQVSDGVAHIHASFNNITIVTITDRQGNALGWATAGGS
          :      .      *      .      .:***:*:*:*  **:  .*:      *

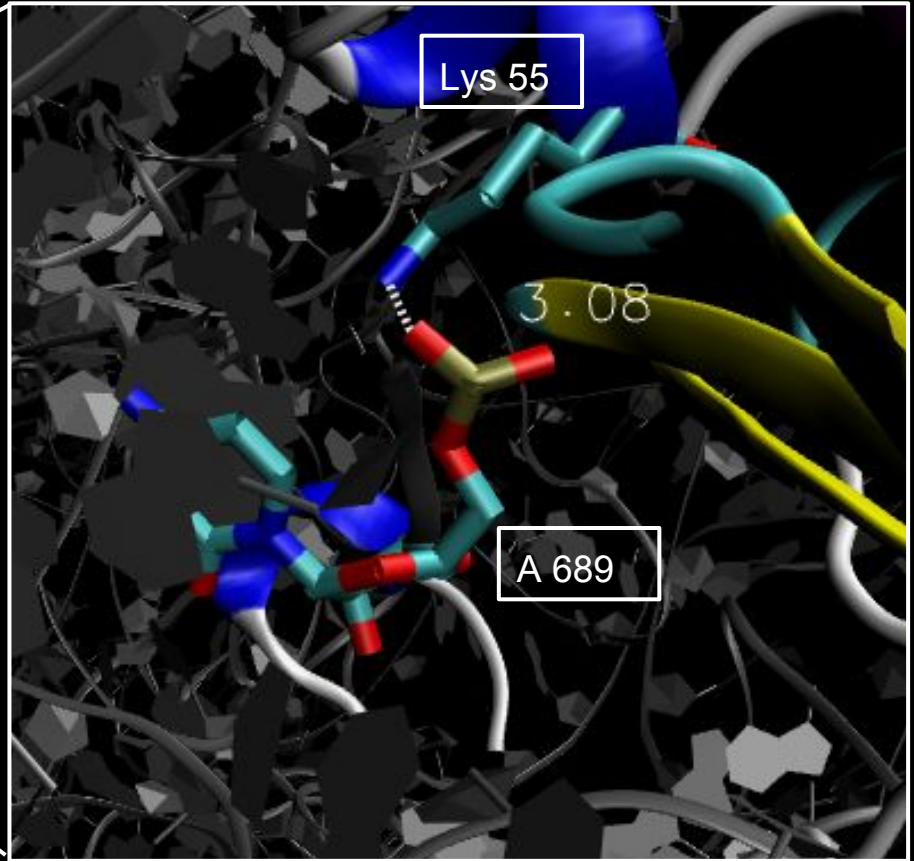
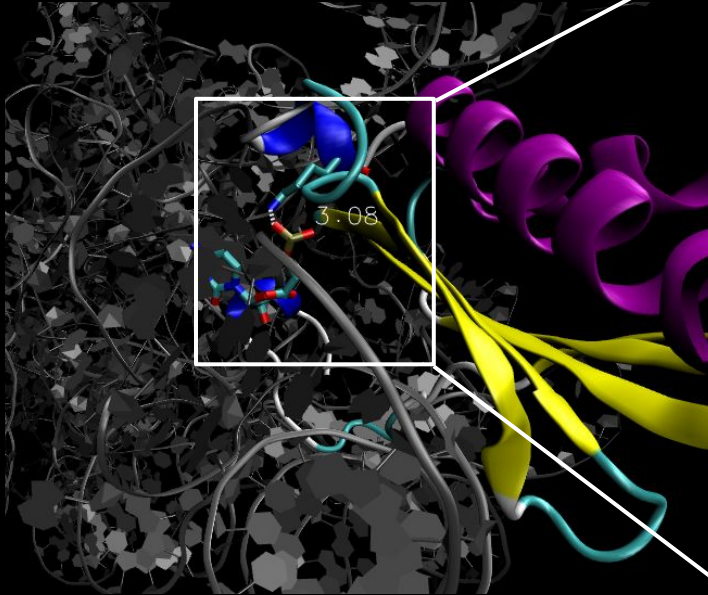
Mus      KVKADRDDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Xenopus  KVKADRDDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Homo     KVKADRDDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Danio    KVKADRDDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Saccharomyces KVKADRDDESSPYAAMLAADVAA-KCKEVGITAVHVKIRATGGTRTKTPGGGQAALRAL
Deinococcus  GYKCSK-KGTPYAAQLAAADAVKKAQTSFGMAAVDVIVRGSG-----SGREQAIRAI
Thermus   GYKCSR-KGTPYAAQLAALDAAKKAMA-YGMQSVDVIVRGTG-----AGREQAIRAL
Escherichia GFRCSR-KSTPFAAQVAERCAD-AVKEYGIKNLEVMVKGPG-----PGRESTIRAL
          :... :*:***:**  .      *:  :.. :...*      .* : :***:

Mus      ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Xenopus  ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Homo     ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Danio    ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Saccharomyces ARSGLRIGRIEDVTPVPSDSTRKGGRRGRRL
Deinococcus  QASGIEVRSIMDDSPVPHNGCRPKKKFRA---
Thermus   QASGLQVKSIVDDTPVPHNGCRPKKKFRKAS-
Escherichia NAAGFRITNITDVTPIPHNGCRPPKKRRV---
          :*:.:  * * :*: * . *      *
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Structural conservation



S11-16S rRNA interactions



Sequence conservation

CLUSTAL 2.1 multiple sequence alignment

```

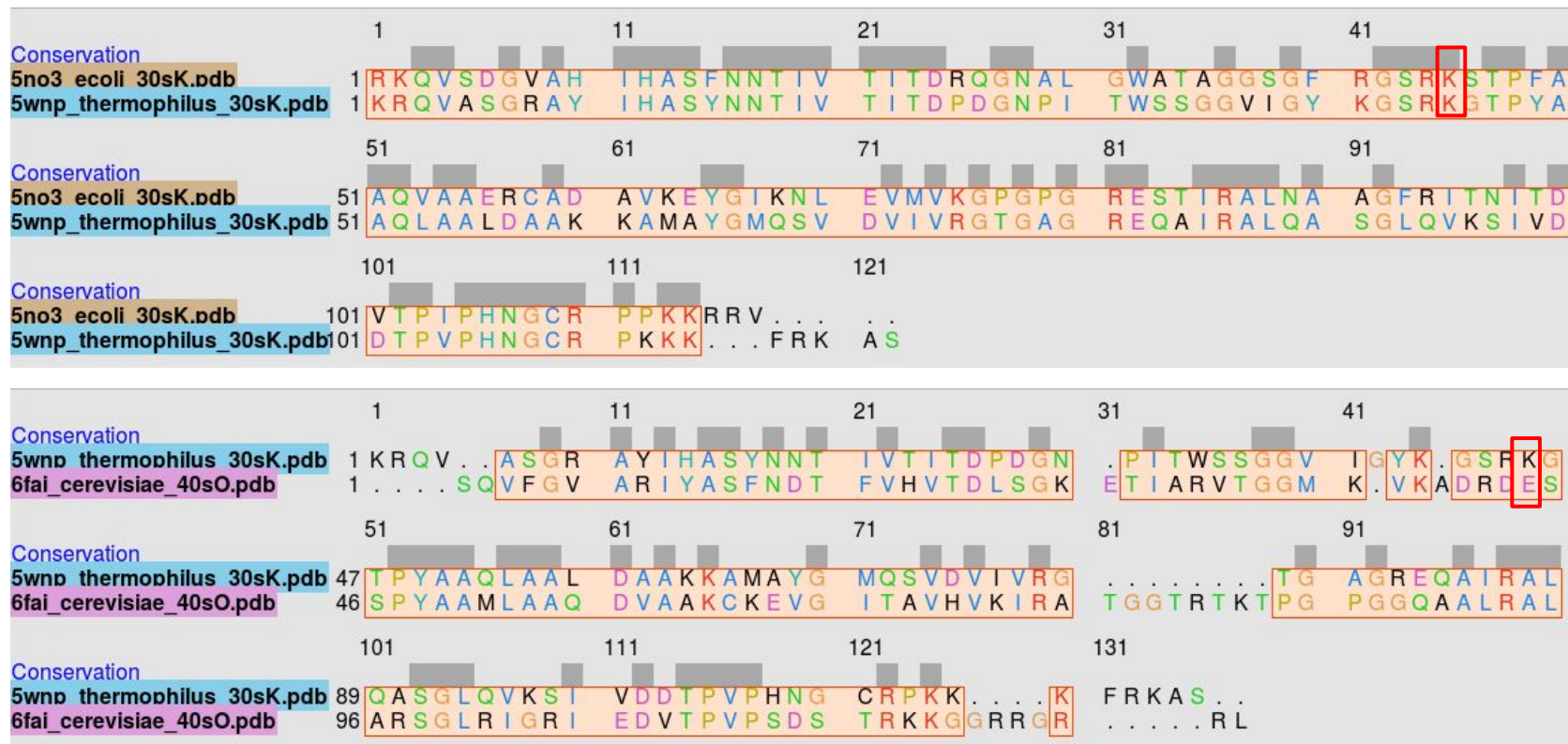
Mus      MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Xenopus MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Homo     MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Danio    MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Saccharomyces -----MSNVVQARDNSQVFGVARIYASFNDTFVHVTDLSGKETIARVTGGM
Deinococcus -----MAK-PTKGKAPRRSRRNISAGRAYVHASYNNTIVTITDLDGNSVAWSSGGTI
Thermus  -----MAKKPSK----KKVKRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVI
Escherichia -----MAKAPIR--ARKVRVKQVSDGVAHIHASFNNITVITIDRQNALGAWATAGS

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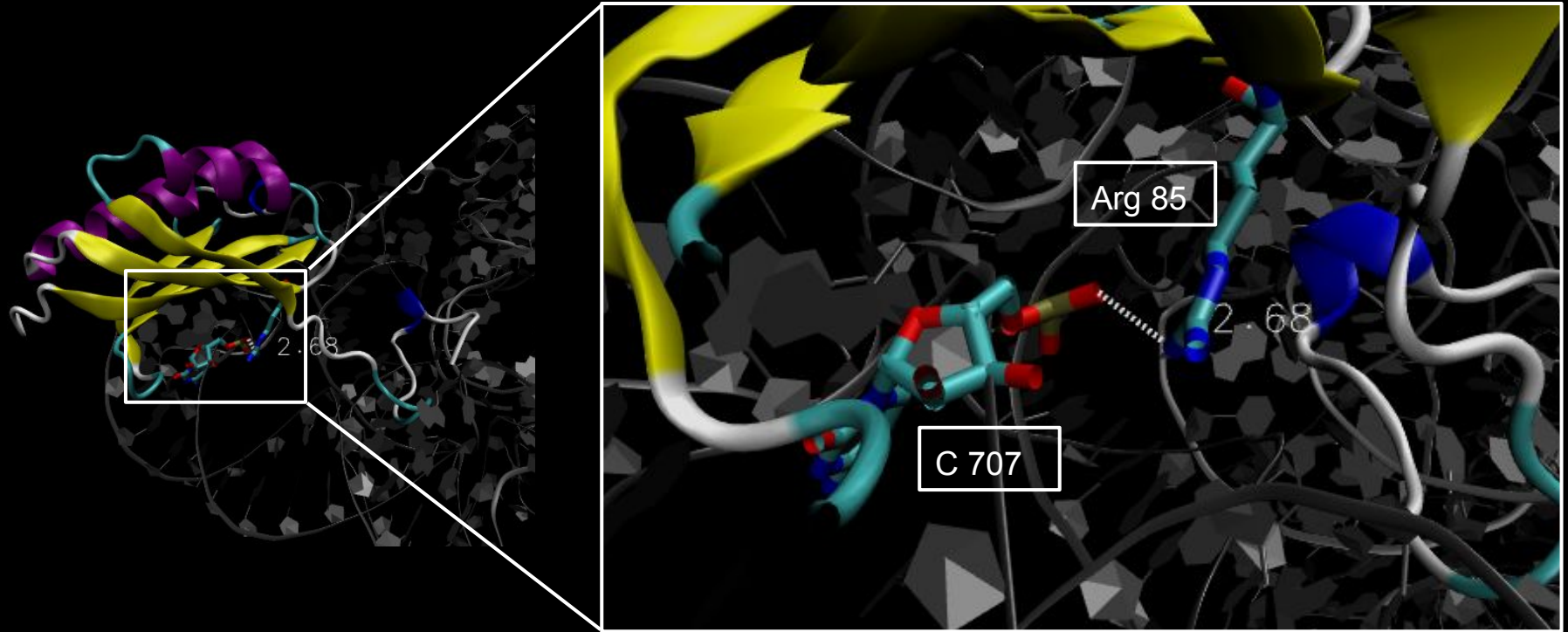
Mus	KVKADRD	ESSPYAAMLAQQDVAQ-	RCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Xenopus	KVKADRD	ESSPYAAMLAQQDVAQ-	RCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Homo	KVKADRD	ESSPYAAMLAQQDVAQ-	RCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Danio	KVKADRD	ESSPYAAMLAQQDVAQ-	KCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Saccharomyces	KVKADRDESSPYAAMLAQQDVAA-	KCKEVGITAVHVKIRATGGTRTKTTPGGGQAALRAL	
Deinococcus	GYKGSK-KGTPYAAQLAAADVKAQT	SFGMAAVDVIVRGS-----SGREQAIRAI	
Thermus	GYKGR-KGTPYAAQLAALDAKKAMA-	YGMQSVDIVRGTG-----AGREQAIRAI	
Escherichia	GFRGSR-KSTPFAAQVAAERCAD-	AVKEYGIKNLEVMVKGPG-----PGRESTIRAL	

Mus	ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Xenopus	ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Homo	ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Danio	ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Saccharomyces	ARSGLRIGRIEDVTPVPDSTRKKGGRRGRRL
Deinococcus	QASGIEVRSIMDDSPVPHNGCRPKKKFRA---
Thermus	QASGLQVKSIVDTPVPVPHNGCRPKKKFRKAS-
Escherichia	NAAGFRITNITDVPTPIPHNGCRPPKKRRV---
	:*: *: *: *: *: *: *

Structural conservation



S11-16S rRNA interactions



Sequence conservation

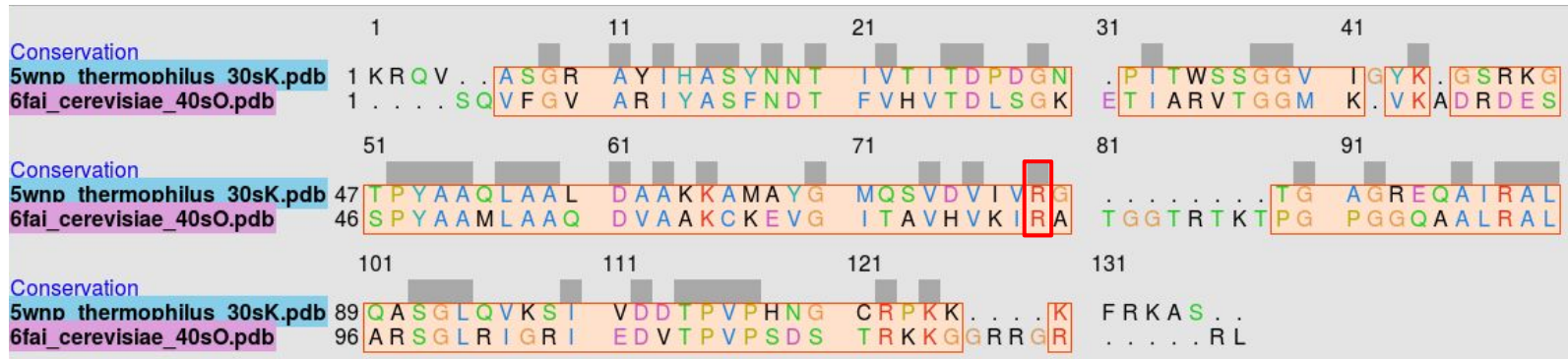
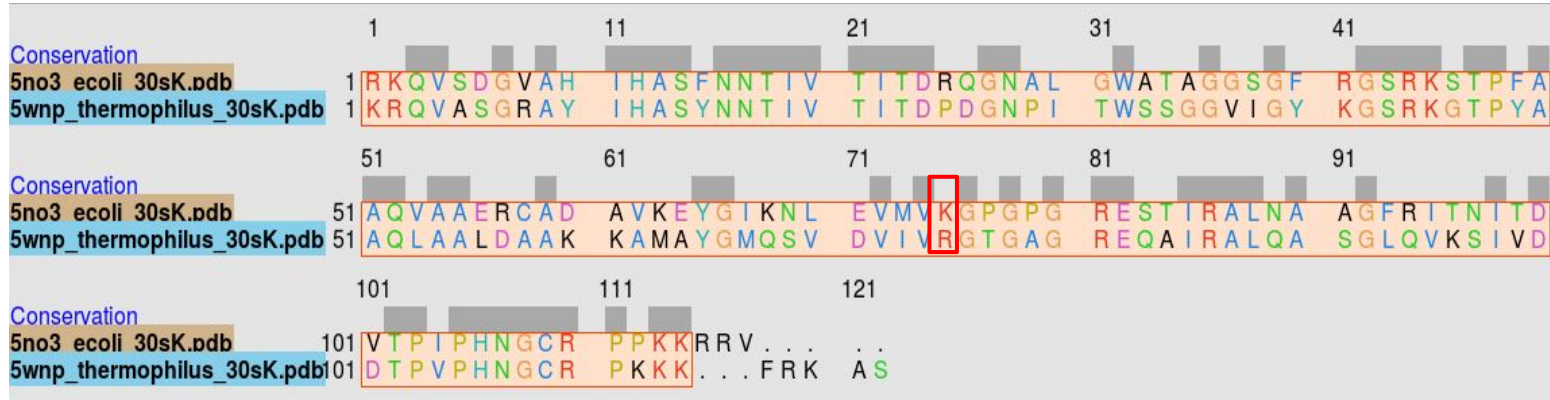
```
CLUSTAL 2.1 multiple sequence alignment

Mus      MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Xenopus  MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Homo     MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Danio    MAPRKGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Saccharomyces -----MSNVVQARDNSQVFGVARIYASFNDTFVHVTDLSGKETIARVTGGM
Deinococcus -----MAK-PTKGKAPRRSRNISAGRAYVHASYNNTIVTITDLGNSVAWSSGGTI
Thermus   -----MAKKPSK----KVKRQVASGRAYIHASYNNTIVTITDPGPNITWSSGGVI
Escherichia -----MAKAPIR--ARKRVRKQVSDGVAHIHASFNNITIVTITDRQGNALGWATAGGS
              :      .      *      .      .      .      .      .      .      .      .      .      .

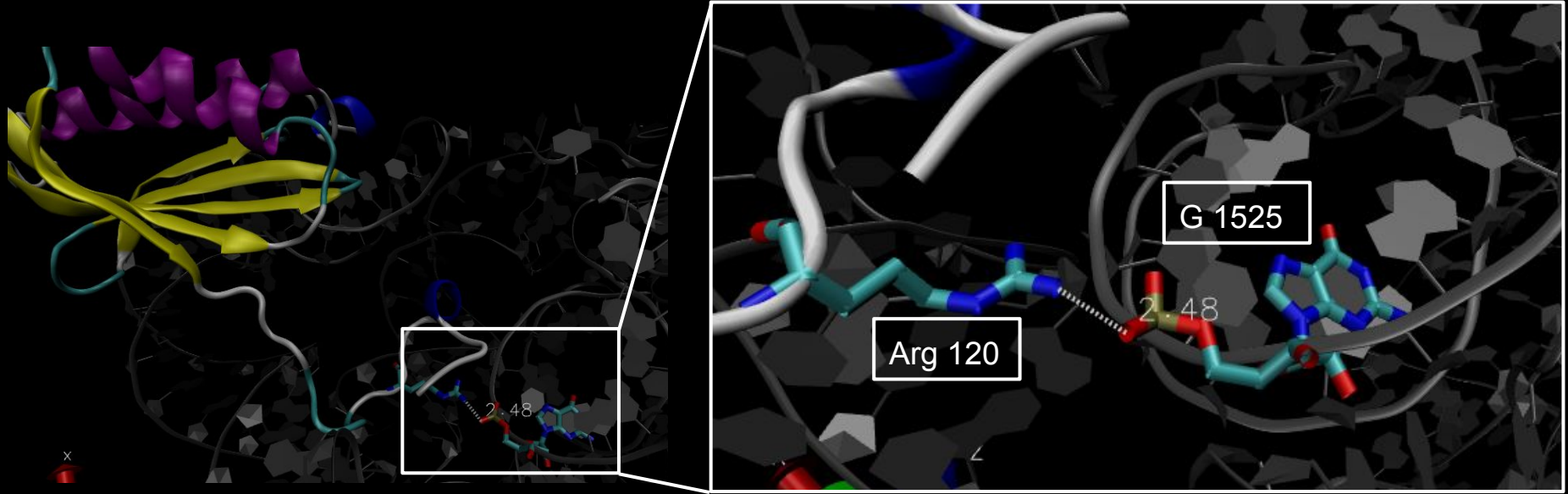
Mus      KVKADRDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Xenopus  KVKADRDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Homo     KVKADRDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Danio    KVKADRDESSPYAAMLAADVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSALRAL
Saccharomyces KVKADRDESSPYAAMLAADVAQ-KCKEVGITAVHVKIRATGGTRTKTPGPGGQAALRAL
Deinococcus  GYKGSK-KGTPYAAQLAAADAVKKAQTSFGMAAVDVIVRGSG-----SGREQAIRAI
Thermus   GYKGSR-KGTPYAAQLAALDAKKAMA-YGMQSVDDVIVRGTG-----AGREQAIRAL
Escherichia GFRGSR-KSTPFAAQVAAERCAD-AVKEYGIKNLEVMVKGPG-----PGRESTIRAL
              :...: :.:*:*:*:*:*      .      *:*      :.: :...*      .* : :*:

Mus      ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Xenopus  ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Homo     ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Danio    ARSGMKIGRIEDVTPIPSDSTRKGGRRGRRL
Saccharomyces ARSLRIGRIEDVTPVPSDSTRKGGRRGRRL
Deinococcus  QASGIEVRSIMDDSPVPHNGCRPKKKFRA---
Thermus   QASGLQVKSIVDDTPVPHNGCRPKKKFRKAS-
Escherichia NAAGFRITNITDVTPIPHNGCRPPKKRRV---
              :*:.:  * * :*: * :. *      *
```

Structural conservation



S11-16S rRNA interactions



Sequence conservation

CLUSTAL 2.1 multiple sequence alignment

```

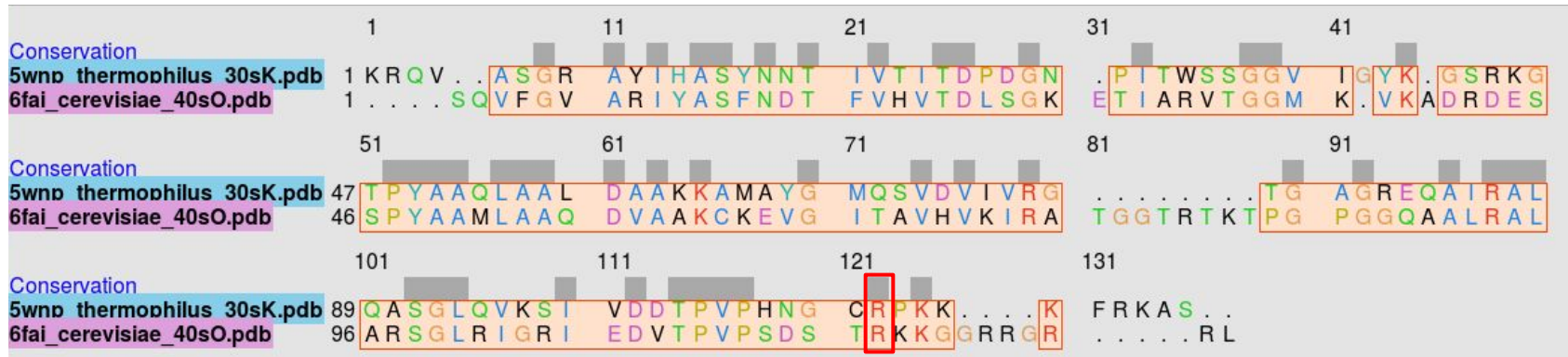
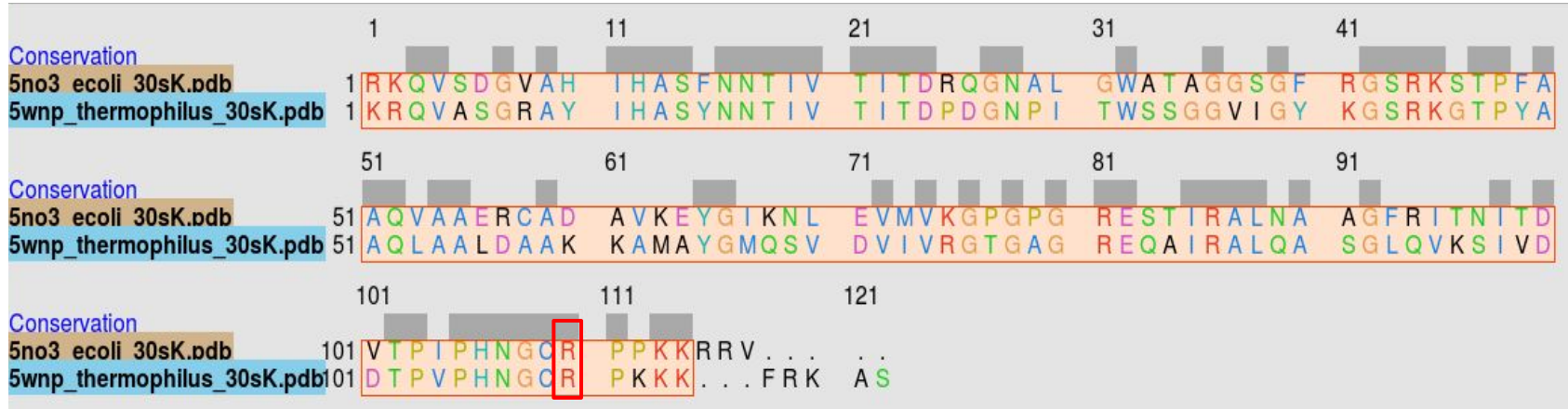
Mus      MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Xenopus MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Homo     MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Danio    MAPRKGGKEKKEEQVISLGPQVAEGENVFGVCHIFASFNDTFVHVTDLSGKETICRVTTGGM
Saccharomyces -----MSNVVQARDNSQVFGVARIYASFNDTFVHVTDLSGKETIARVTTGGM
Deinococcus -----MAK-PTKGKAPRRSRRNISAGRAYVHASYNNTIVTITDLDGNSVAWSSGGTI
Thermus  -----MAKKPSK----KKVKRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVI
Escherichia -----MAKAPIR---ARKVRVKQVSDGVAHIHASFNNITVITIDRQNALGAWATAGS

```

Mus	KVKADRDDESSPYAAMLAQQDVAQ-RCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Xenopus	KVKADRDDESSPYAAMLAQQDVAQ-RCKELGITALHKLRLATGGNRTKTTPGPGAQSALRAL
Homo	KVKADRDDESSPYAAMLAQQDVAQ-RCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Danio	KVKADRDDESSPYAAMLAQQDVAQ-KCKELGITALHIKLRATGGNRTKTTPGPGAQSALRAL
Saccharomyces	KVKADRDDESSPYAAMLAQQDVAA-KCKEVGITAVHVKIRATGGTRTKTTPGGGQAALRAL
Deinococcus	GKYGSK-KGTPYAAQLAADAVKKAQTSFGMAAVDVIVRGS-----SGREQAIRAI
Thermus	GKYGSR-KGTPYAAQLAALDAKKAMA-YGMQSVDDVVRGTG-----AGREQAIRAI
Escherichia	GFRGRS-KSTPFAAQVAIERCAD-AVKEYGIKNLEVMVKGPG-----PGRESTIRAL
	.::.:.*:*:**.*.* *: *: *::**:

Mus	ARSGMKIGRIEDVTPIPSDSTRKKGRRGRRL
Xenopus	ARSGMKIGRIEDVTPIPSDSTRKKGRRGRRL
Homo	ARSGMKIGRIEDVTPIPSDSTRKKGRRGRRL
Danio	ARSGMKIGRIEDVTPIPSDSTRKKGRRGRRL
Saccharomyces	ARSLRIGRIEDVTPVPSDSTRKKGRRGRRL
Deinococcus	QASGIEVRSIMDDSPVPHNGCRPKKKFRA---
Thermus	QASGLQVKSIVDDTPVPHNGCRPKKKFKRAS-
Escherichia	NAAGFRITNITDVTPIPHNGCRPPKKRRV---
	::***:***:***:***:***:***:

Structural conservation



Sequence conservation in bacteria

CLUSTAL 2.1 multiple sequence alignment

```

Ecoli      -----RKQVSDGVAHIHASFNNITIVTITDRQGNALGWATAGGSGFRGSRKST
Salmonella MAKAPV-CARKRVRKQVSDGVAHIHASFNNITIVTITDRQGNALGWATAGGSGFRGSRKST
Haemophilus MAKTPV-RARKRVKKQVVDGVRHIHASFNNITIVTITDRQGNALAWATAGGSGFRGSRKST
Aquifex    MAKK-----KKKQKRQVTKAIVHIHTTFNNTIVNVTDTQGNTIAWASGGTVGFKGTRKST
Deinococcus MAKPTKKGAPRRSRRNISAGRAYVHASYNNTIVTITDLDGNSVAWSSGGTIGYKGSKKGT
Thermophilus -----KRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVIGYKGSRKGT
          :::: .  :::::*****:** :*: :*: *::* *:::*.
    
```

```

Ecoli      PFAAQVAAERCADAVKE-YGIKNLEVMVKGP GPGRESTIRALNAAGFRITNITDVTPIPH
Salmonella PFAAQVAAERCADAVKE-YGIKNLEVMVKGP GPGRESTIRALNAAGFRITNITDVTPIPH
Haemophilus PFAAQVAAERCAEIVKE-FGLKNLEVMVKGP GPGRESTIRALNAAGFRITNITDVTPIPH
Aquifex    PYAAQLAAQKAMKEAKE-HGVQEVEIWKGP GAGRESAVRAVFASGVKVTAIRDVTPIPH
Deinococcus PYAAQLAAADAVKKAQTSFGMAAVDVIVRGSGSGREQAIRAIQASGIEVRSIMDDSPVPH
Thermophilus PYAAQLAALDAKKAMA-YGMQSV DVIVRG TGAGREQAIRALQASGLQVKSIVDDTPVPH
          *:***:** . . . . *: :*: :*: *::* *::: * * :*:**
    
```

```

Ecoli      NGCRPPKKRRV--
Salmonella NGCRPPKKRRV--
Haemophilus NGCRPPKKRRV--
Aquifex    NGCRPPARRRV--
Deinococcus NGCRPKKKFRA--
Thermophilus NGCRPKKKFRKAS
          ***** : * |
    
```

Ser 53

Bacterial conservation
Asp in eukaryotes

Lys 55

Bacterial conservation
Glu in eukaryotes

Arg 85

Discordance in *E.coli* →
two groups in bacteria
(Lys and Arg)

Arg 120

Bacterial and eukaryotic
conservation


```
CLUSTAL 2.1 multiple sequence alignment
```

Mus
Xenopus
Homo
Danio
Saccharomyces
Deinococcus
Thermus
Escherichia

KVKAADRESSPYAAMLAQQDVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSAALRAL
KVKAADRESSPYAAMLAQQDVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSAALRAL
KVKAADRESSPYAAMLAQQDVAQ-RCKELGITALHIKLRATGGNRTKTPGPGAQSAALRAL
KVKAADRESSPYAAMLAQQDVAQ-KCKELGITALHIKLRATGGNRTKTPGPGAQSAALRAL
KVKAADRESSPYAAMLAQQDVAQ-KCKEVGITAVHVKIRATGGTRTKTPGGGGAAALRAL
GYKGSK-KGTPYAAQLAAADAVKKAQTSFGMAAVDVIVRGSG-----SGREQAIRAI
GYKGSR-KGTPYAAQLAALDAAKKAMA-YGMQSVDDIVRGTG-----AGREQAIRAI
GFGSR-KSTPFAAQVAAERCAD-AVKEYGIKNLEVMVKGP-----PGRESTIRAI

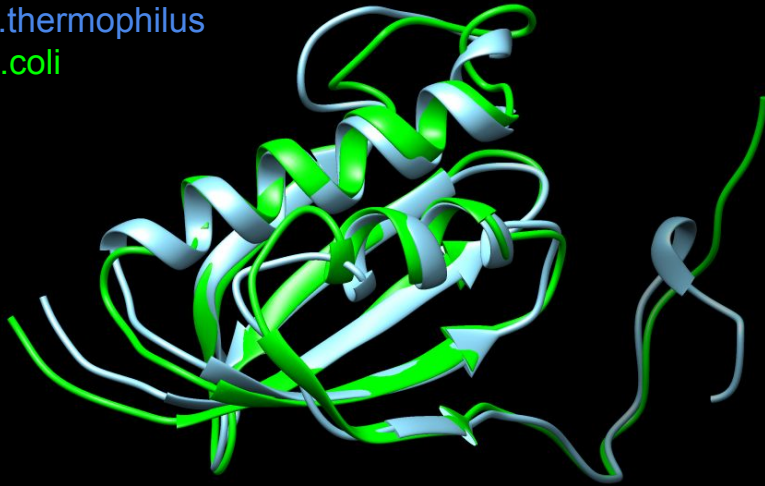
.....
: : : : * * * * * : : : : * * * * * : : : : * * * * *

Carboxy terminal tail

Structural conservation

Bacteria/Bacteria

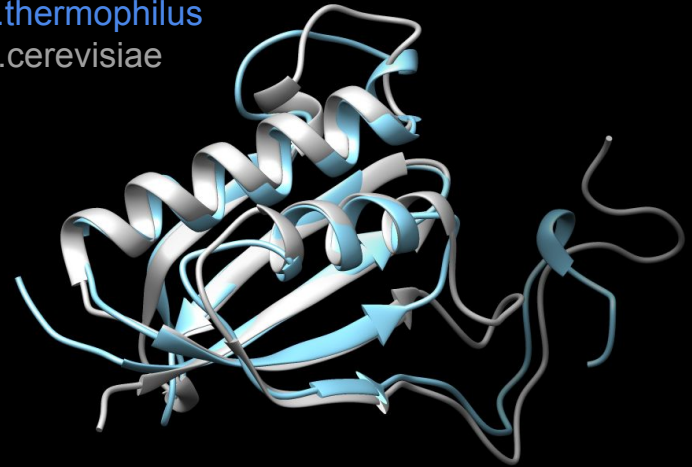
T.thermophilus
E.coli



RMSD = 1,316
Q-score = 0,783
%id. = 52,99%

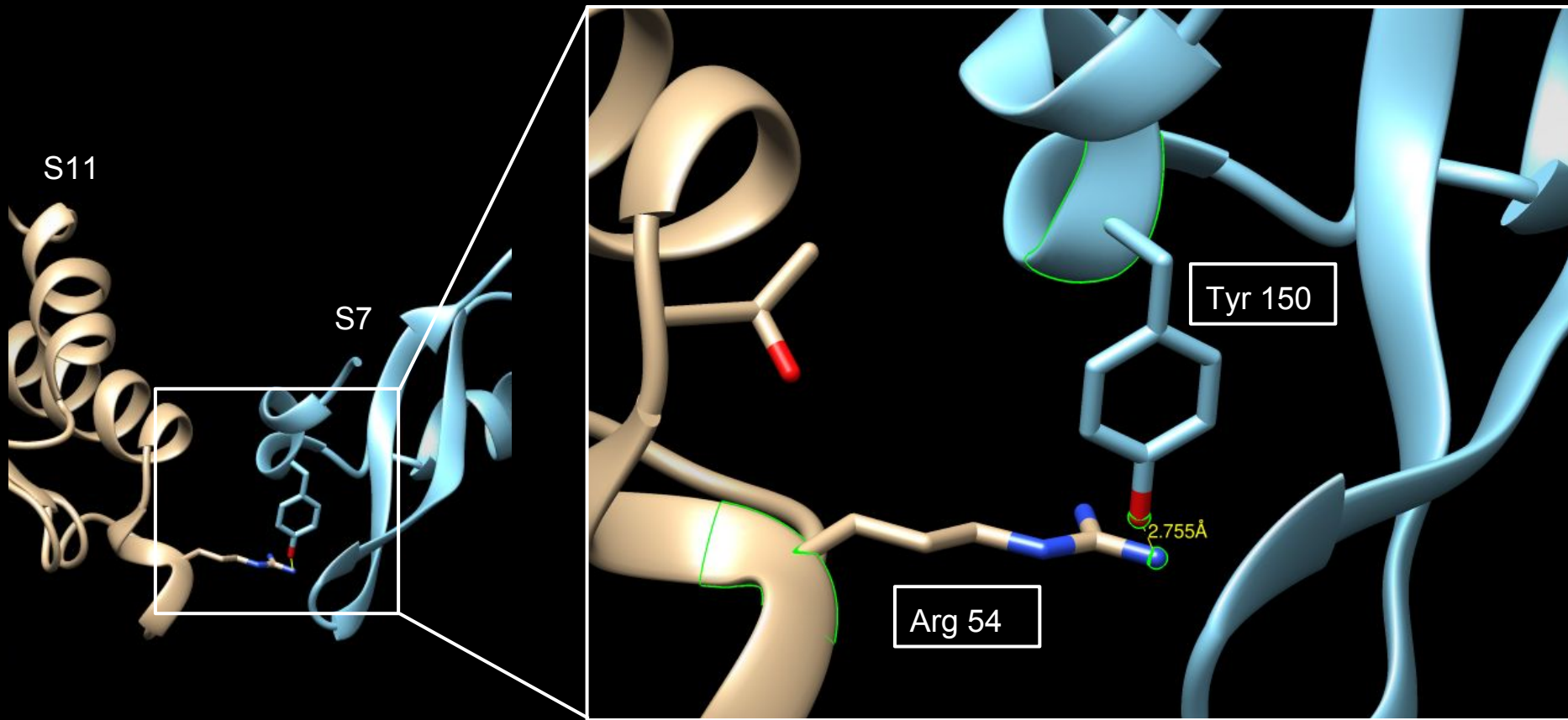
Bacteria/Eukaryote

T.thermophilus
S.cerevisiae



RMSD = 1,327
Q-score = 0,657
% id. = 38,66%

S11-S7 interactions



S7/S5



Classification

CATH

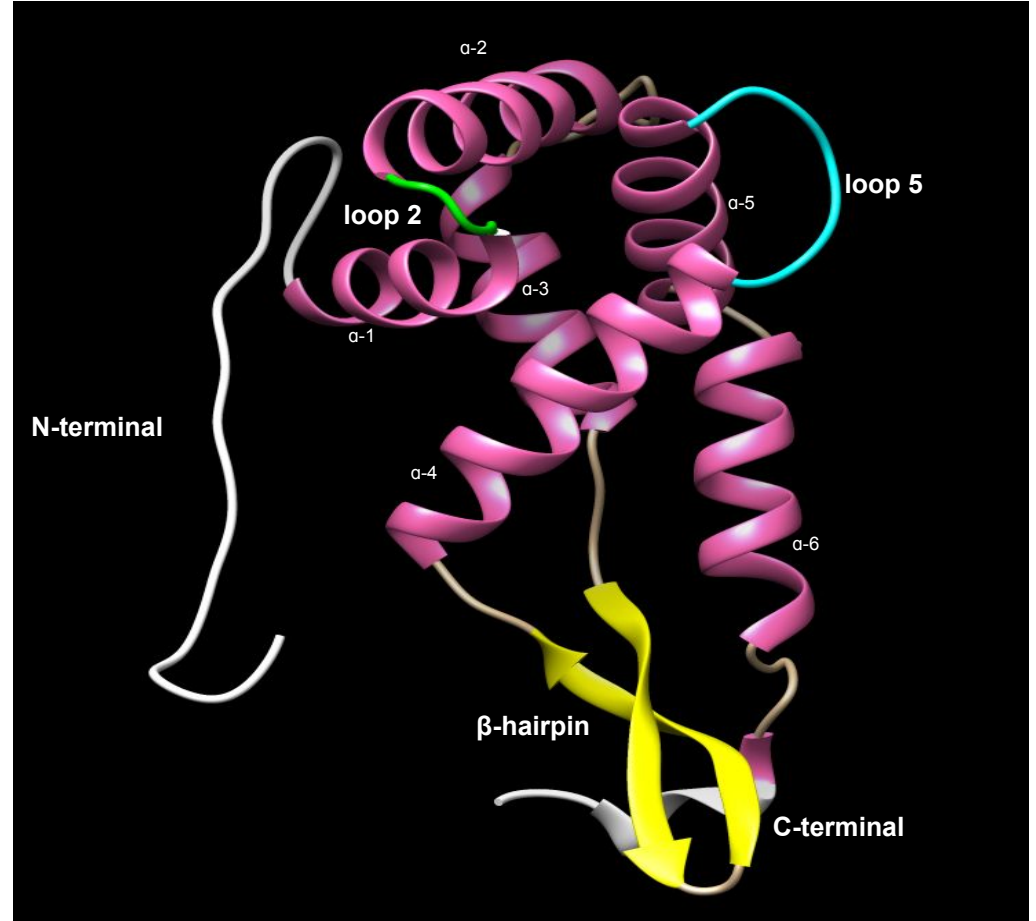
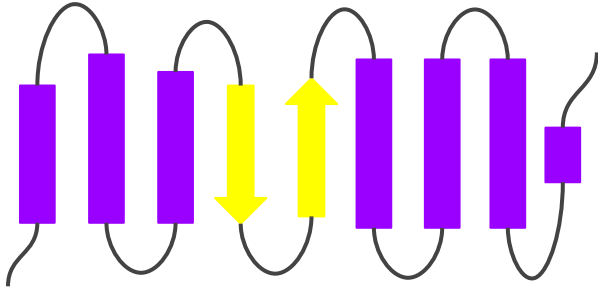
Class	Mainly Alpha
Architecture	Orthogonal Bundle
Topology	Ribosomal Protein S7
Homologous Superfamily	Ribosomal Protein S7 domain

SCOP

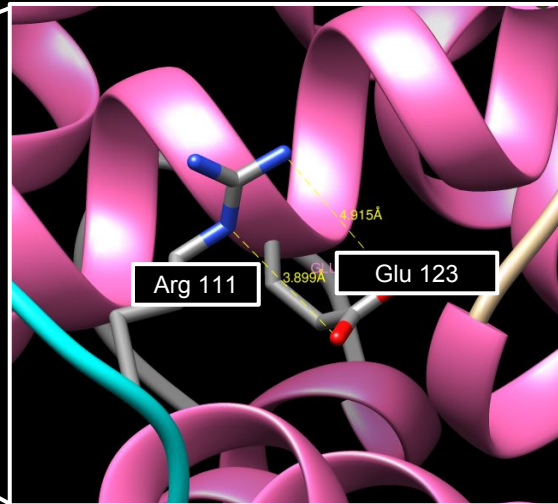
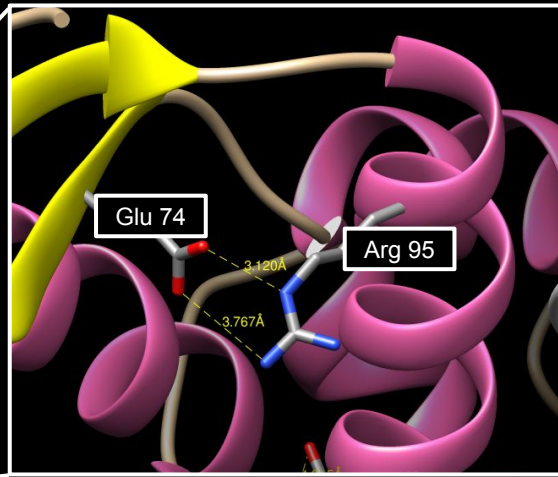
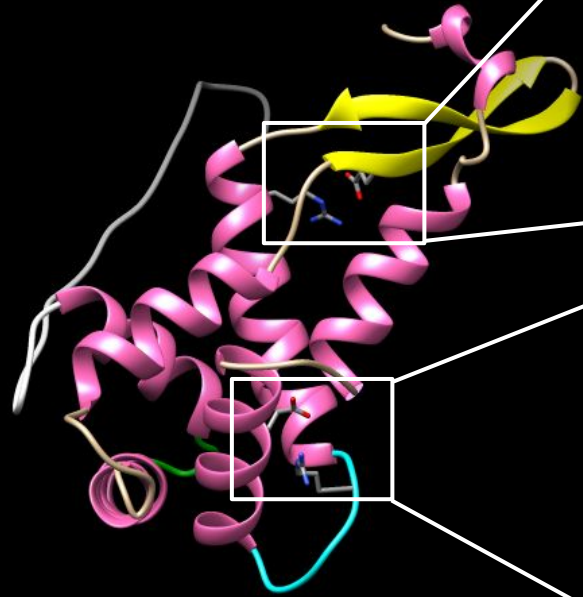
Class	All alpha protein
Fold	Ribosomal protein S7
Superfamily	Ribosomal protein S7
Family	Ribosomal protein S7
Protein	Ribosomal protein S7

Biological importance

- Initiation of ribosomal folding
- Inhibits bacterial growth (overexpression)



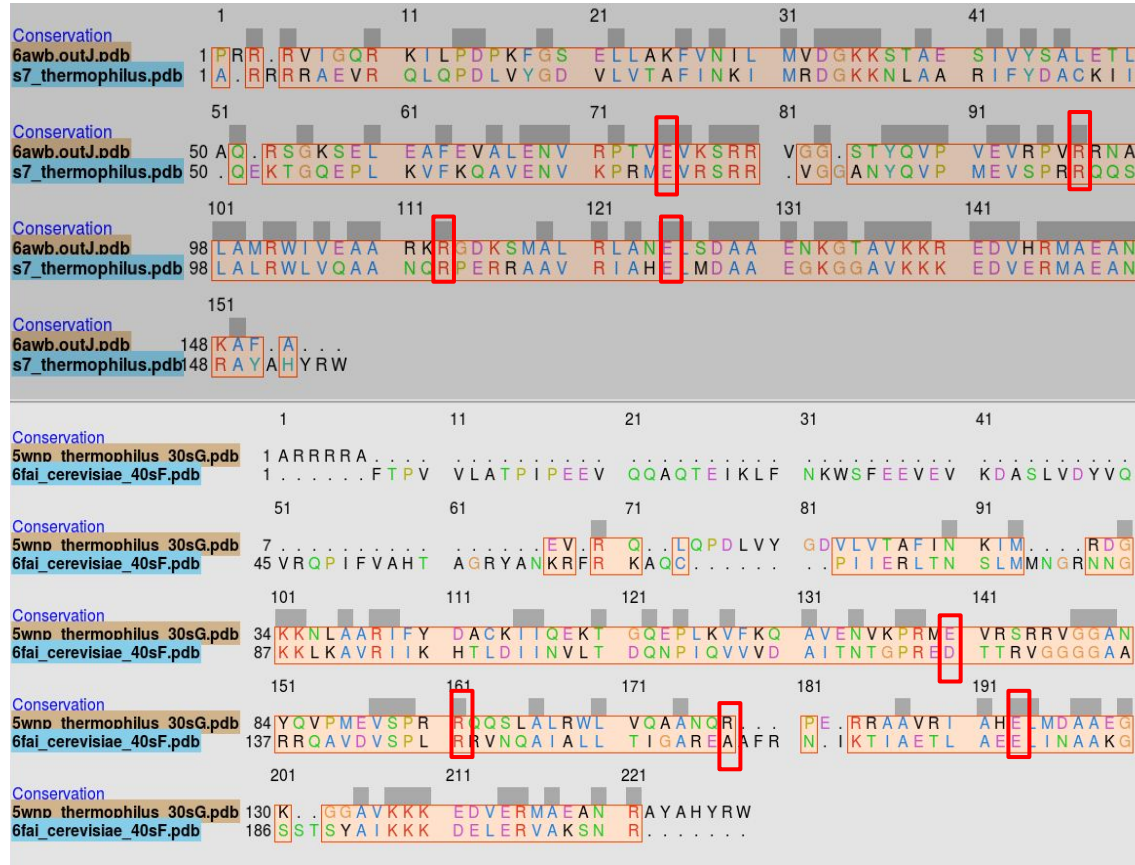
Salt bridges in helices



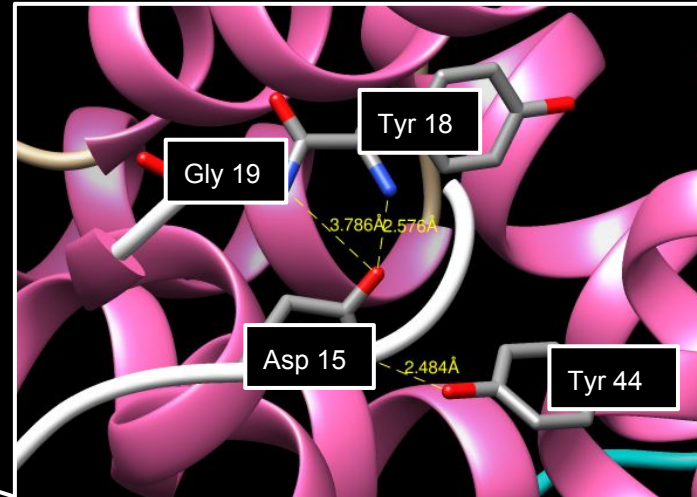
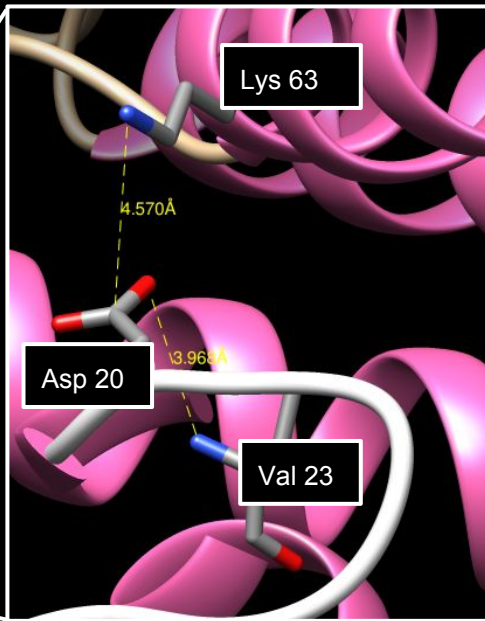
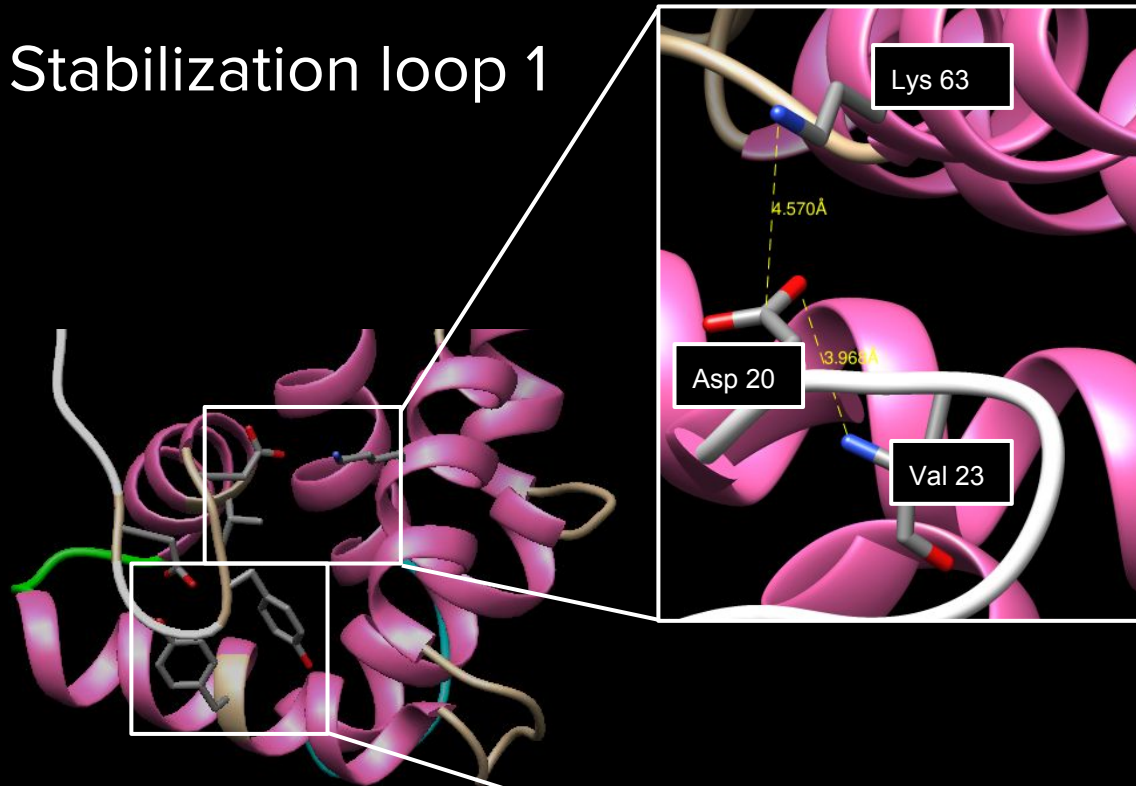
Sequence conservation

Homo	DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Mus	DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio	DYIAVKEKYAKYLPHSSGRYAAKFRKAQCPIVERVTNSMMMHGRNNGKKLLTVRIVKHA
Xenopus	DYIAVKEKYAKFLPHSGGRYAAKFRKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila	DYISVKEKFARYLPHSAGRYAAKFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces	DYVQVRQP--IFVAHTAGRYANKRFRKAQCPIIERLTNSLMMNGRNNNGKKLKAVRIIKHT
spDeinococcus	-----MARRRRAEVRPVQPDVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus	-----MARRRRAEVRQLQPDVYGDVLVTAFINKIMRDGKKNLAAIRIFYDA
Escherichia	-----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVVSA
	. * * .: . . :: :*** : *. :
Homo	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNVQAIWLLCT
Mus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNVQAIWLLCT
Danio	FEIIHLLTGENPLQILVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNVQAIWLLCT
Xenopus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNVQAIWLLCT
Drosophila	FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNVQAIWLLCT
Saccharomyces	LDIINVLTQNPQIVVVDAITNTGPREDTTRVGGGGAARRQAVDVSPLRVNVQAIALLTI
spDeinococcus	CRLVQERTGQEPLKVFKQAYDNVVKPRVVRSSRVGGSTYQVPVEVGPRRQSLTLRWMS
Thermus	CKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQSLALRWLVQ
Escherichia	LETLAQRSGKSELEAFEVALENVRPTVEVKSRRVGGSTYQVPVEVRPVRNALAMRWIVE
	: :.: :. * * * : .*: : .: * * *: : :
Homo	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Mus	GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Danio	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Xenopus	GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Drosophila	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces	GAREAAFRNIKTIAETLAEELINAAGSSSTSYAIAKKKDELERVAKSNR-----
spDeinococcus	AVDG--RPERTAIERLACEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus	AANQ--RPERRAAVRIAEIMDAAEGKGG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia	AARK--RGDKSMALRLANESDAANKGT--AVKKREDVHRMAEANKAFAHYRWLSLRS
	.. * : : * : : * : : * : : * : : * : : *

Structural conservation



Stabilization loop 1



Sequence conservation

Homo	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Mus	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Xenopus	DYIAVKEKYAKFLPHSGGRYAAKRFRKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila	DYISVKEKFARYLPHSAGRYAAKRFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces	DYVQVRQP--IFVAHTAGRYANKRFRKAQCPITIERLTNSLMMNGRNNGKKLKAVRIKHT
spDeinococcus	-----MARRRRAEVRVPQPDLVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus	-----MARRRRAEVRQLQPDLVYGDVLVTAFINKIMRDGKKNLAAIRIFYDA
Escherichia	-----MPRRRVIGQRKILPDPKFGESELLAKFVNILMVDGKKSTAESIVYSA
	. * * .: . . :: :*** : *. :
Homo	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNQAIWLLCT
Mus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNQAIWLLCT
Danio	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNQAIWLLCT
Xenopus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNQAIWLLCT
Drosophila	FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRVNQAIWLLCT
Saccharomyces	LDIINVLTQNPVIQVVDAITNTGPREDTTRVGGGGAARRQAVDVSPLRVNQAIALLTI
spDeinococcus	CRLVQERTGQEPLKVFKQDAYDNVKPRVEVRSRRVGGSTYQVPVEVGPRRQSSLTLRWMIS
Thermus	CKIIQEKTGQEPLKVFKQDAENVKPRMEVRSRRVGGANYQVPMEVSPRRQSSLALRWLVQ
Escherichia	LETLAQRSKGKSELEAFQVALENVRPTEVKSRRVGGSTYQVPVEVRPVRNALAMRWIVE
	: :.: .: . * * * : .*: : .:* * *: : :
Homo	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Mus	GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Danio	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Xenopus	GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Drosophila	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces	GAREAAFRNIKTIAETLAEELINAAGSSSTSYAIAKKKDELERVAKSNR-----
spDeinococcus	AVDG---RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus	AANQ---RPERRAAVRIAHELMDAAEGKGG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia	AARK---RGDKSMALRLANELSDAAENKGT--AVKKREDVHRMAEANKAFAYRWLSLRS
	.. * : : * * : * * . * : * : * : * : * :

Structural conservation



Beta hairpin



```

Homo      -----MTEWETAAPAVAETPDIKLFGKWSTDDVQINDISLQ
Mus       -----MTEWEAATPAVAETPDIKLFGKWSTDDVQINDISLQ
Danio     -----MAEDWEAAPAVAETPEIKLFGKWSTDDVQINDISLQ
Xenopus   -----MSDWET-VPVGAETPEIKLFGKWSTDDVQINDISLQ
Drosophila MAEVAENVVETFEPPAAPMEA EVAETILETNVVSTTELPEIKLFGRWSCDDVTVNDISLQ
Saccharomyces -MSDTEAPVEVQEDFEVVVEEFTPVVLATPIPEEVQQAQTEIKLFNKWSFEEVEVKDASLV
spDeinococcus -----
Thermus   -----
Escherichia -----
    
```

```

Homo      DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Mus       DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio     DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Xenopus   DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Drosophila DYISVKEKFARYLPHSAGRYAAKFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces DYVQVRQP--IFVAHTAGRYANKRFRKAQCPITERLTNSLMMNGRNNGKKLKAVRIIKHT
spDeinococcus -----MARRRRRAEVRPVQPDLVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus     -----MARRRRRAEVRQLQPDLVYGDVLVTAFINIKIMRDGKKNLAA RIFYDA
Escherichia -----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVYSA
    
```

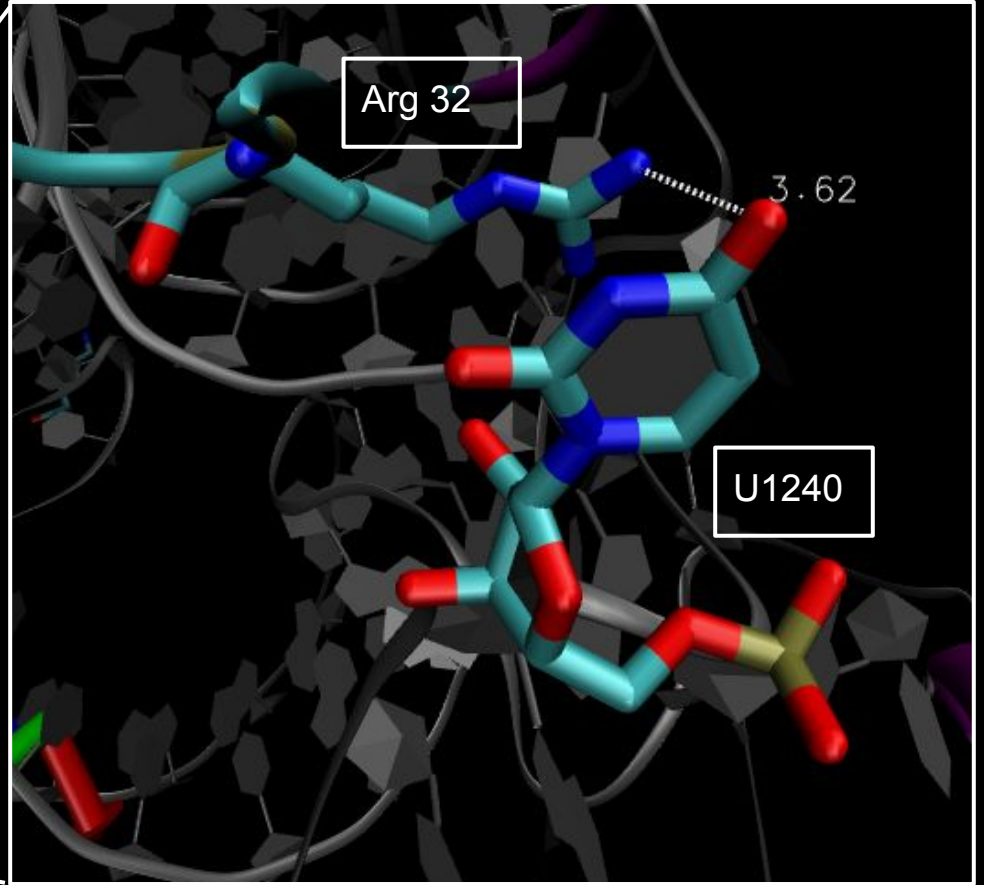
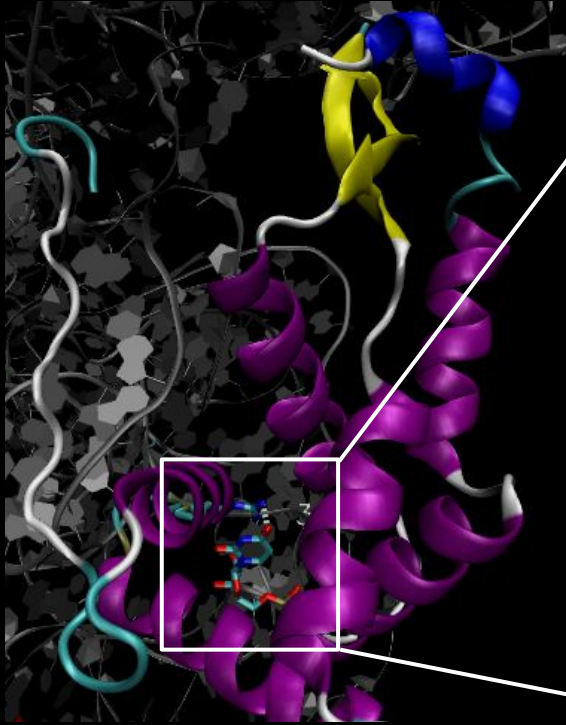
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Homo      FEIIHLLTGENPLQVLVNAIINSCP EDSTRIGRAGTVRRCAVDVSP.LRRVNQAIWLLCT
Mus       FEIIHLLTGENPLQVLVNAIINSCP EDSTRIGRAGTVRRCAVDVSP.LRRVNQAIWLLCT
Danio     FEIIHLLTGENPLQVLVNAIINSCP EDSTRIGRAGTVRRCAVDVSP.LRRVNQAIWLLCT
Xenopus   FEIIHLLTGENPLQVLVNAIINSCP EDSTRIGRAGTVRRCAVDVSP.LRRVNQAIWLLCT
Drosophila FEIIHLLTGENPLQILVSAIINSCP EDSTRIGRAGTVRRCAVDVSP.LRRVNQAIWLLCT
Saccharomyces LDIINVLTDQNP IQVVDAITNTCP EDTRVRGGGGAARRCAVDVSP.LRRVNQAIALLTI
spDeinococcus CRLVQERTGQEPLKVFKQAYDNVKKP MEVRSRRVGGSTYQVPVEVCPRRQQSLTLRWKIS
Thermus     CKIIQEKTGQEPLKVFKQAVENVKPP MEVRSRRVGGGANYQVPMEVSPRRQQSLALRWLVQ
Escherichia LETLAQRSKGKSELEAFEVALENVRP MEVKSRRVGGSTYQVPVEVSP.VRRNALAMRWIVE
    
```

```

Homo      GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Mus       GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Danio     GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Xenopus   GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Drosophila GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces GAREAAFRNIKTIAETLAEELINAAGSSNSTSYAIAKKKDELERVAKSNR-----
spDeinococcus AVDG--RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus     AANQ--RPERRAAVRIAHELMDAEKGKG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia AARK--RGDKSMALRLANELSDAAENKGT--AVKKKREDVHRMAEANKAFAHYRWLSLRS
    
```

S7-16S rRNA (loop2)



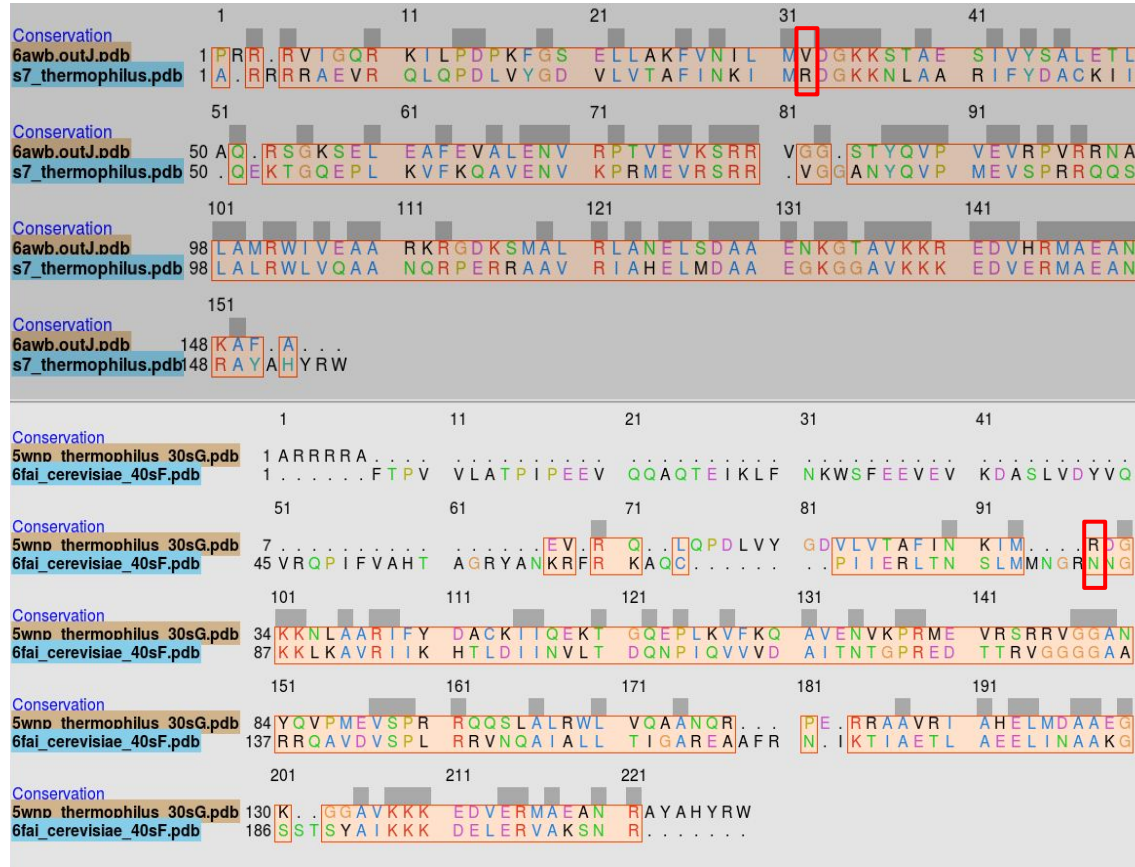
Sequence conservation

Homo	DYIAVKEKYAKYLPHSAGRYAAKRFKAQCPIVERLTNSMMMHGRN	NGKKLMTVRIVKHA
Mus	DYIAVKEKYAKYLPHSAGRYAAKRFKAQCPIVERLTNSMMMHGRN	NGKKLMTVRIVKHA
Danio	DYIAVKEKYAKYLPHSSGRYAAKRFKAQCPIVERVTNSMMMHGRN	NGKKLLTVRIVKHA
Xenopus	DYIAVKEKYAKFLPHSGGRYAAKRFKAQCPIVERFTNSLMMHGRN	NGKKLMTVRIVKHA
Drosophila	DYISVKEKFARYLPHSAGRYAAKRFKAQCPIVERLTCSLMMKGRN	NGKKLMACRIVKHS
Saccharomyces	DYVQVRQP--IFVAHTAGRYANKRFRKAQCPIIERLTNSLMMNGRN	NGKKLKAVRIKHT
spDeinococcus	-----MARRRRAEVRPVQPDLVYQDVLVSAMINRIMR	DGKKNLASRIFYGA
Thermus	-----MARRRRAEVRQLQPDLVYGDVLVTAFAINKIMR	DGKKNLAAIRIFYDA
Escherichia	-----MPRRRVIGQRKILPDPKFGSELLAKFVNILMV	DGKKSTAESIVYSA
	. * * .: . . :: :*** : *. :	

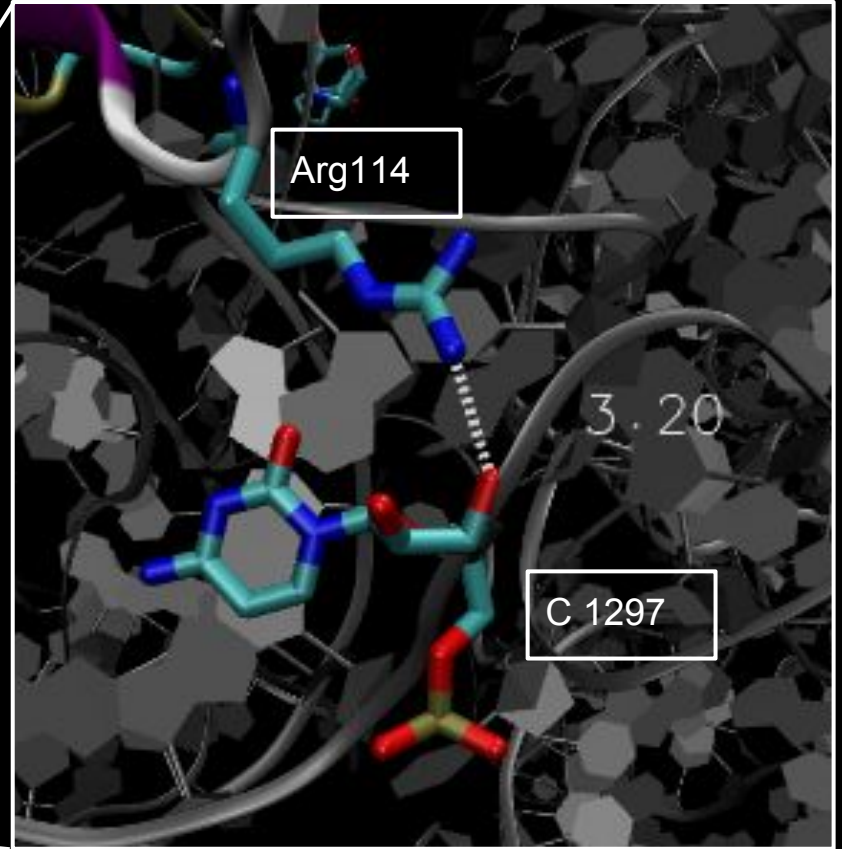
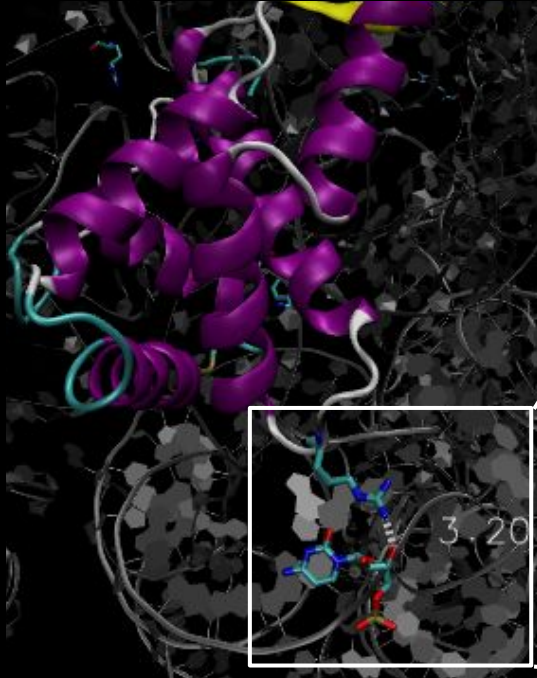
Homo	FEIIHLLTGENPLQVLVNAINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Mus	FEIIHLLTGENPLQVLVNAINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Danio	FEIIHLLTGENPLQILVNAINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Xenopus	FEIIHLLTGENPLQVLVNAINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Drosophila	FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Saccharomyces	LDIINVLTQNPQIVVVDAITNTGPREDTTRVGGGGAARRQAVDVSPLRRVNQAIALTI
spDeinococcus	CRLVQERTGQEPLKVFKQAYDNVVKPRVEVRSRRVGGSTYQVPVEVGPRRQQLTLRWMS
Thermus	CKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQQLSLRLWLQ
Escherichia	LETLAQRSGKSELEAFEVALENVRTVEVKSRRVGGSTYQVPVEVPRVRNALAMRWIVE
	: :.. :: . * * * : .*: : .:* * *: :: :

Homo	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Mus	GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Danio	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Xenopus	GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Drosophila	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces	GAREAAFRNIKTIAETLAELINAAGSSSTSYAIAKKKDELERVAKSNR-----
spDeinococcus	AVDG---RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus	AANQ---RPERRAAVRIAHELMDAAEGKGG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia	AARK---RGDKSMALRLANELSDAAENKGT--AVKKREDVHRMAEANKAFAYHRLSLRS
	.. * : :* *: **: . . *::: :.::*: :

Structural conservation



S7-16S rRNA (loop5)



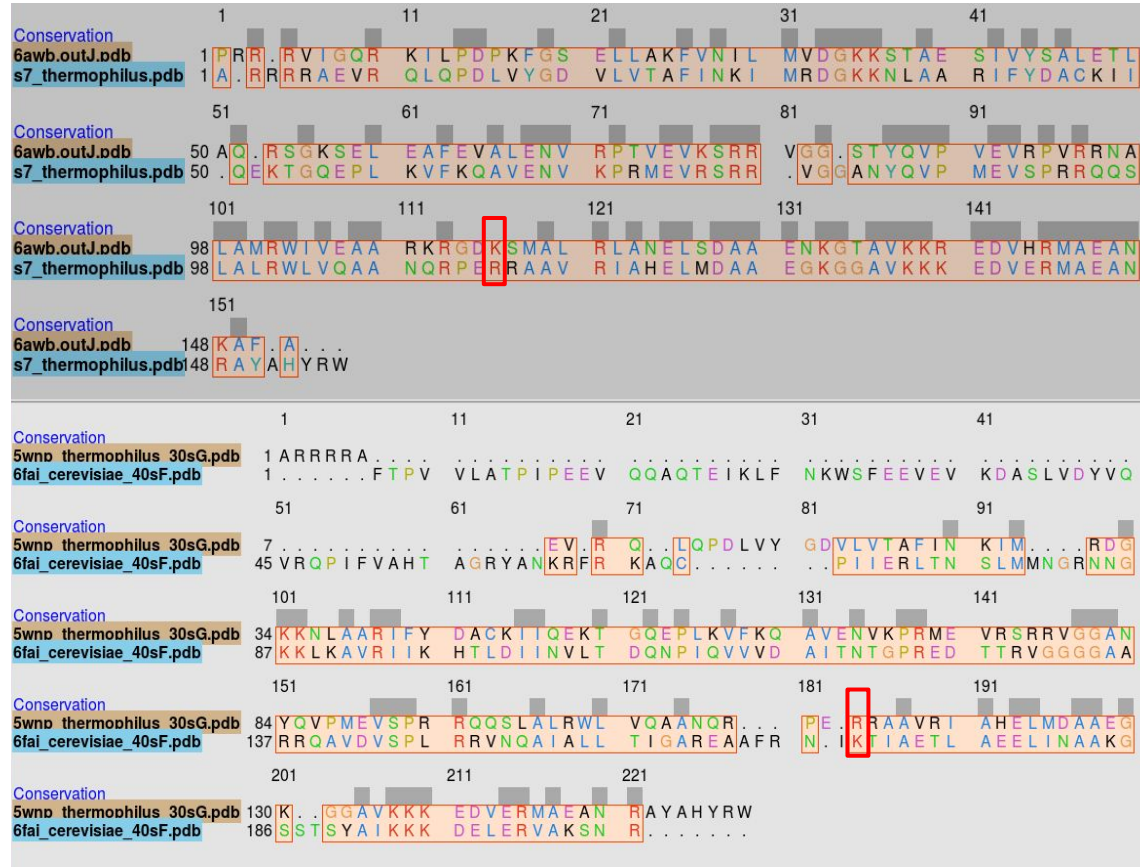
Sequence conservation

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Mus       DYIAVKEKYAKYLPHSAGRYAAKRFKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio     DYIAVKEKYAKYLPHSAGRYAAKRFKAQCPIVERLTNSMMMHGRNNGKKLLTVRIVKHA
Xenopus   DYIAVKEKYAKFLPHSGGRYAAKRFKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila DYISVKEKFARYLPHSAGRYAAKRFKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces DYVQVRQP - - IFVAHTAGRYANKRFRKAQCP I IERLTNSLMMNGRNNGKKLKAVRIIKHT
spDeinococcus -----MARRRRAEVRPVQPD LVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus     -----MARRRRAEVRQLQPD LVYGDVLVTAFINKIMRDGKKNLAA RIFYDA
Escherichia -----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVYSA
          . *      *      .:      . .      ::      :*** : * . :

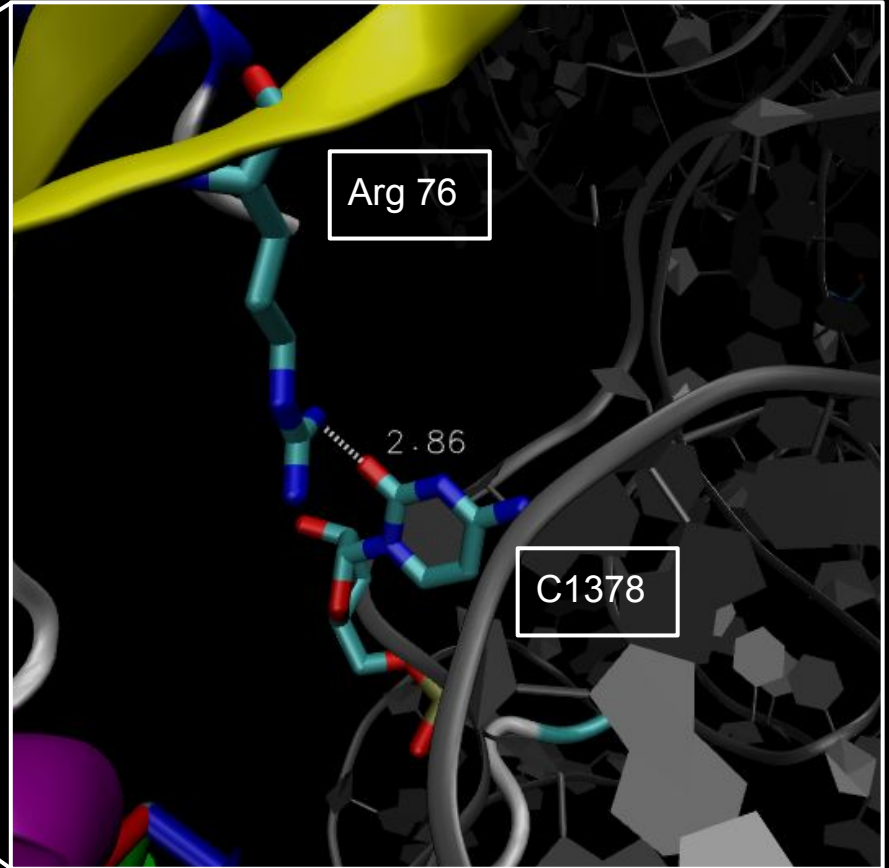
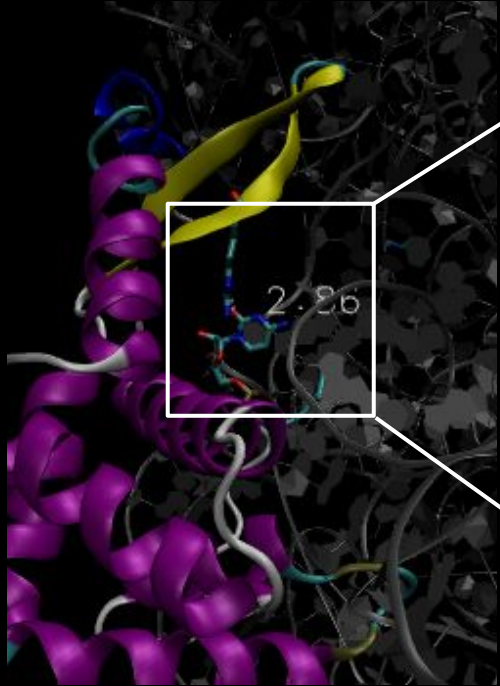
Homo      FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Mus       FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Danio     FEIIHLLTGENPLQILVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Xenopus   FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Drosophila FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Saccharomyces LDII NVLTQDNPIQVVVDAITNTGPREDTTRVG GGAARRQAVDVSPLRRVNQAIALLTI
spDeinococcus CRLVQERTGQEPLKVFKQAYDNVKPRVEVRSRRVGGSTYQVPVEVGPRRQQSLTLRWIS
Thermus     CKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQQSLALRWLVQ
Escherichia LETLAQRSGKSELEAFEVALENVRPTVEVKSRRVGGSTYQVPVEVRPVRRNALAMRWIVE
          :      :.: .: . * * * :      .*: : .:* * *:      :: :

Homo      GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR -----
Mus       GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR -----
Danio     GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR -----
Xenopus   GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR -----
Drosophila GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR -----
Saccharomyces GAREAAFRNIKTIAETLAEELINAAGSSSTSYAIAKKKDELERVAKSNR -----
spDeinococcus AVDG - - - RPERTAIERLAGEIMDAAQGRGG - - AIKKKDDVERMAEANRAYAHYRW - - -
Thermus     AANQ - - - RPERRAAVRIAHELMDAAEGKGG - - AVKKKEDVERMAEANRAYAHYRW - - -
Escherichia AARK - - - RGD KSMALRLANELSDAAENKGT - - AVKKREDVHRMAEANKAFAHYRWLSLRS
          ..      *      :      : * *: :*: . .      *:*:*:*:*:*:*:*:
```

Structural conservation



S7-16S rRNA (beta-hairpin)



Sequence conservation

```
Homo      DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHHGRNNGKKLMTVRIVKHA
Mus       DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHHGRNNGKKLMTVRIVKHA
Danio     DYIAVKEKYAKYLPHSSGRYAAKRFRKAQCPIVERVTNSMMMHHGRNNGKKLLTVRIVKHA
Xenopus   DYIAVKEKYAKFLPHSGGRYAAKRFRKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila DYISVKEKFARYLPHSAGRYAAKRFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces DYVQVRQP--IFVAHTAGRYANKRFRKAQCPIERLTNSLMMNGRNNGKKLKAVRIIKHT
spDeinococcus -----MARRRRAEVRPVQPDLVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus     -----MARRRRAEVRQLQPDLVYGDVLVTAFAINKIMRDGKKNLAAIRIFYDA
Escherichia -----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVYSA
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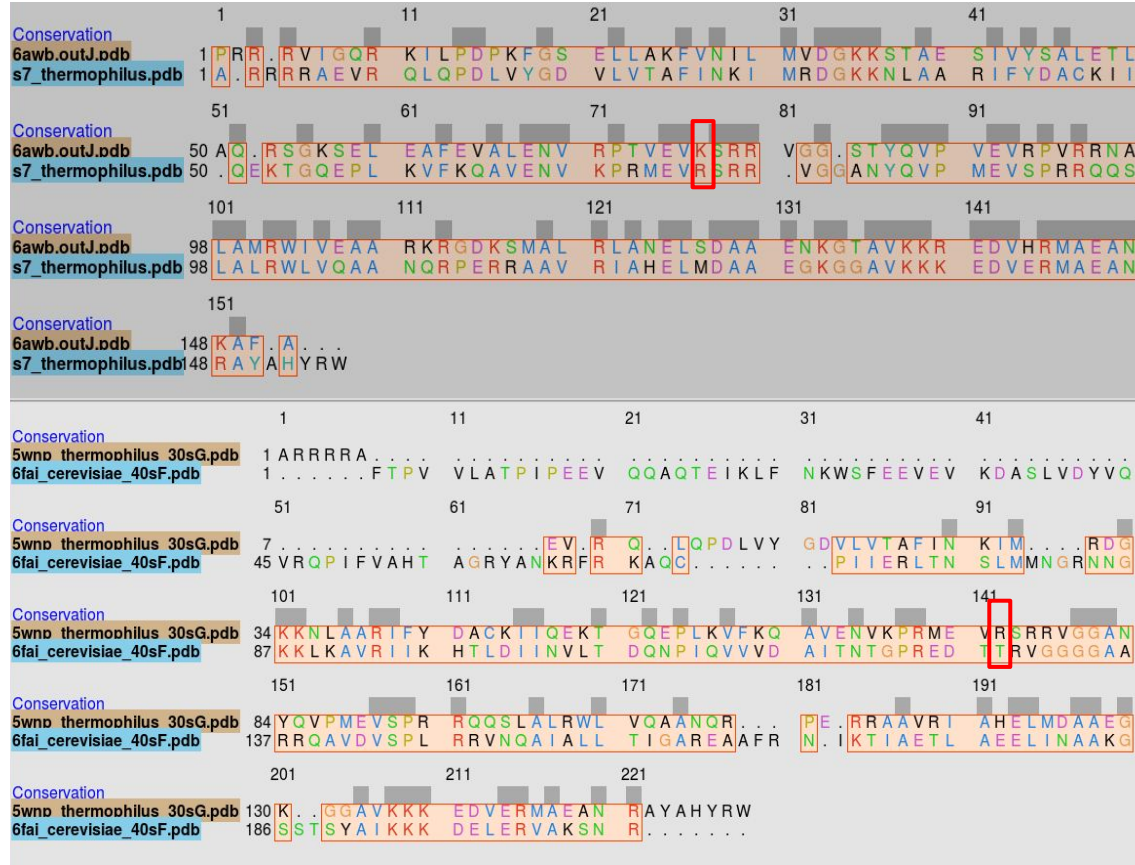


```
Homo      FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Mus       FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Danio     FEIIHLLTGENPLQILVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Xenopus   FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Drosophila FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Saccharomyces LDIIINVLTQNP IQVVDAITNTGPREDTTRVGGGGAARRQAVDVSPLRRVNQAIALLTI
spDeinococcus CRLVQERTGQEPLKVFKQAYDNVKPRVEVRSRRVGGSTYQVPVEVGPRRQQLTRWMIS
Thermus     CKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQQSLALRWLVQ
Escherichia LETLAQRSGKSELEAFEVALENVRPTVEVRSRRVGGSTYQVPVEVRPVRNALAMRWIVE
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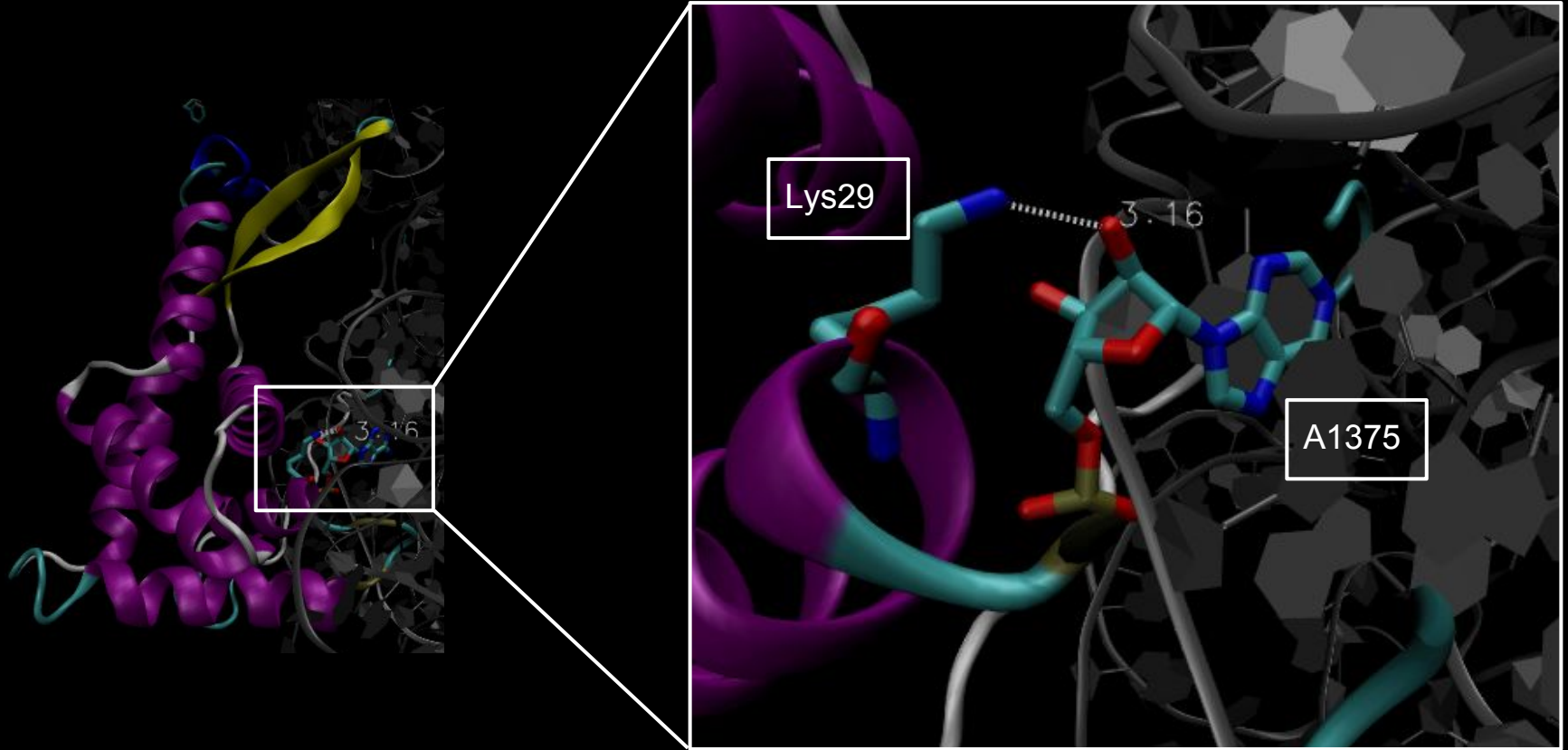


```
Homo      GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Mus       GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Danio     GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Xenopus   GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Drosophila GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces GAREAAFRNIKTIAETLAEELINAAGSSSTYAIAKKKDELERVAKSNR-----
spDeinococcus AVDG--RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus     AANQ--RPERRAAVRIAHELMDAAEKGKG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia AARK--RGDKSMALRLANELSDAAENKGT--AVKKREDVHRMAEANKAFAHYRWLSLRS
          ..      *  :      :*  *:  :*:  .  .      *::*:*:*:*:*::
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Structural conservation



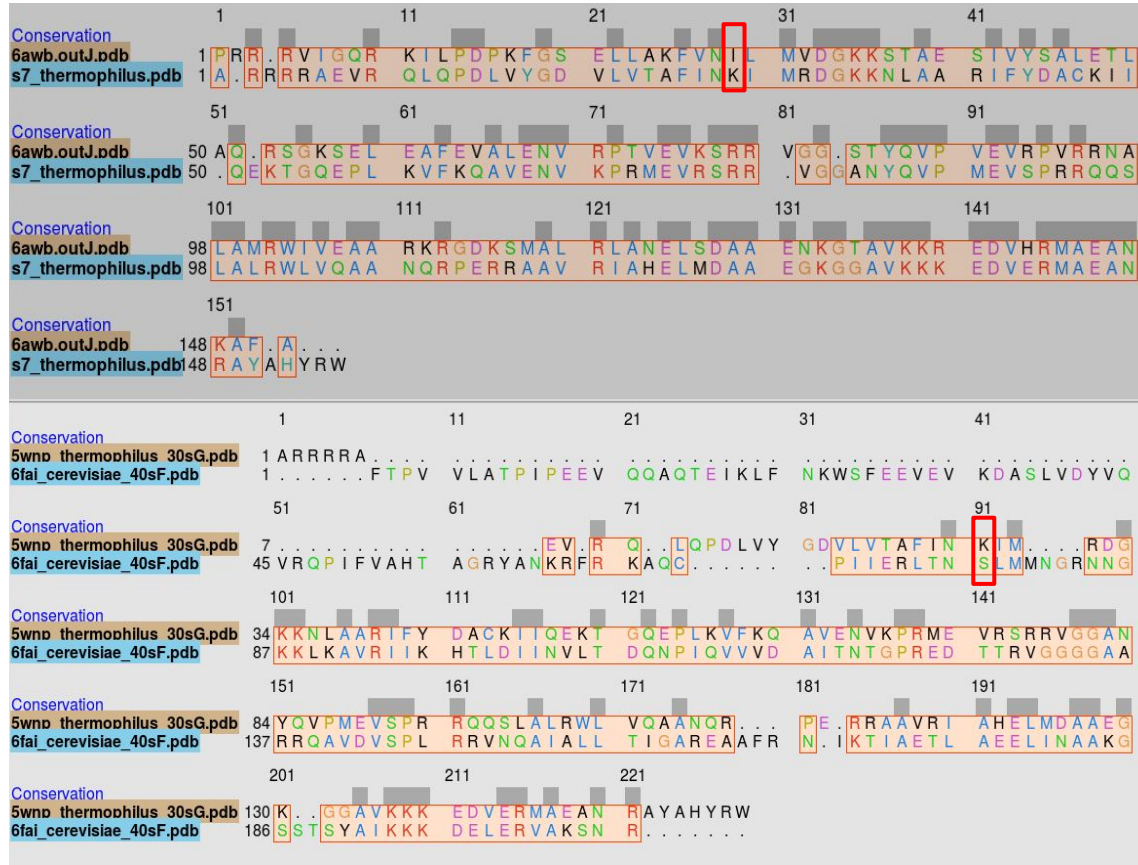
S7-16S rRNA (alfa-1)



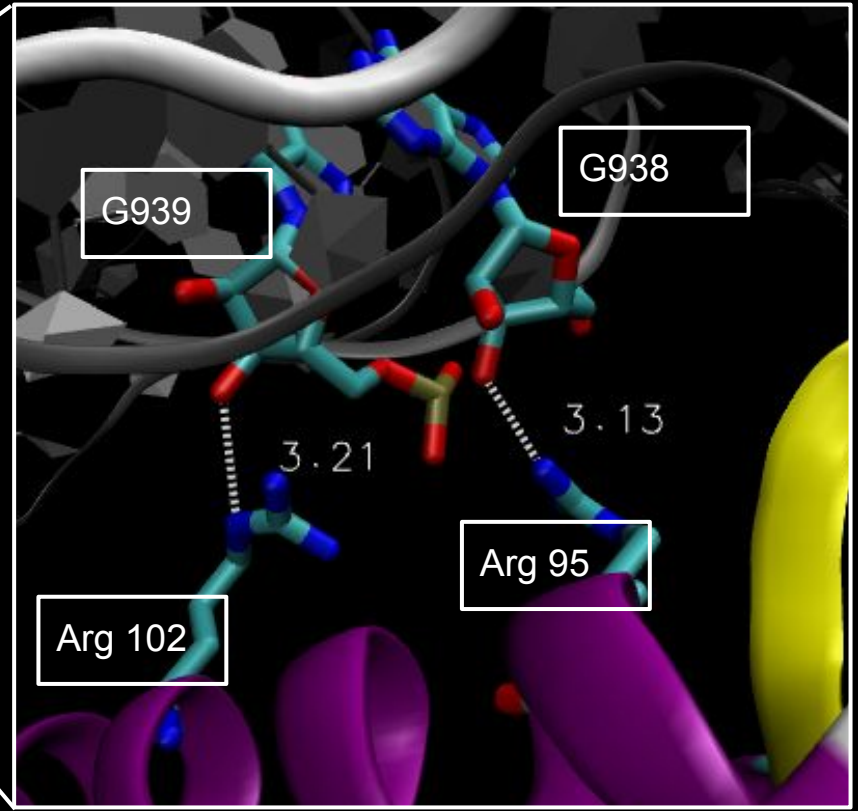
Sequence conservation

Homo	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Mus	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Xenopus	DYIAVKEKYAKFLPHSGGRYAAKRFRKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila	DYISVKEKFARYLPHSAGRYAAKRFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces	DYVQVRQP--IFVAHTAGRYANKRFRKAQCPIIERLTNSLMMNGRNNGKKLKAVRIIKHT
spDeinococcus	-----MARRRRAEVRPVPQDLVYQDVLVSAMINIMRDGKKNLASRIFYGA
Thermus	-----MARRRRAEVRQLQPDLVYGDVLVTAFINIMRDGKKNLAAIRIFYDA
Escherichia	-----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVYSA
	. * * .: . . :: :*** : *. :
Homo	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Mus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Danio	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Xenopus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Drosophila	FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Saccharomyces	LDIINVLTQNPQVVDVAITNTGPREDTTRVGGGGAARRQAVDVSPLRRVNQAIALLTI
spDeinococcus	CRLVQERTGQEPLKVFKQAYDNVVKPRVEVRSRRVGGSTYQVPVEVGPRRQSLTLRWMS
Thermus	CKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQSLALRWLVQ
Escherichia	LETLAQRSGKSELEAFEVALENVRPTVEVKSRRVGGSTYQVPVEVRPVRNALAMRWIVE
	: :.: :. * * * : .*: : .:*** *: : :
Homo	GAREAAFRNIKTIAECLADELINAAKGSSNSYAIAKKKDELERVAKSNR-----
Mus	GAREAAFRNIKNIAECLADELINAAKGSSNSYAIAKKKDELERVAKSNR-----
Danio	GAREAAFRNIKTIAECLADELINAAKGSSNSYAIAKKKDELERVAKSNR-----
Xenopus	GAREAAFRNIKTIAECVADELINAAKGSSNSYAIAKKKDELERVAKSNR-----
Drosophila	GAREAAFRNIKTIAECLADELINAAKGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces	GAREAAFRNIKTIAETLAEELINAAKGSSSTSYAIAKKKDELERVAKSNR-----
spDeinococcus	AVDG--RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus	AANQ--RPERRAAVRIAHELMDAAEKGKG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia	AARK--RGDKSMALRLANELSDAAENKGT--AVKKREDVHRMAEANKAFAHYRWLSLRS
	.. * : :* *: :*: . . *:***:.*:***:

Structural conservation



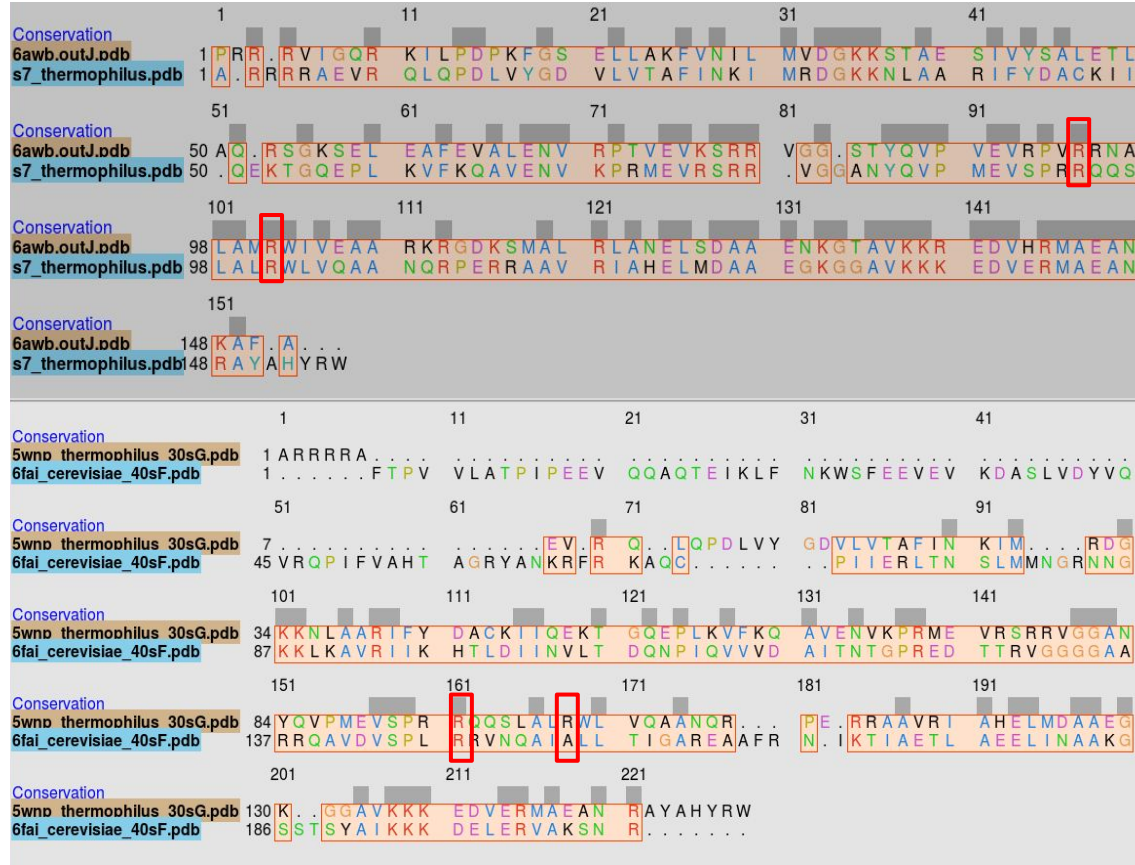
S7-16S rRNA (alfa-4)



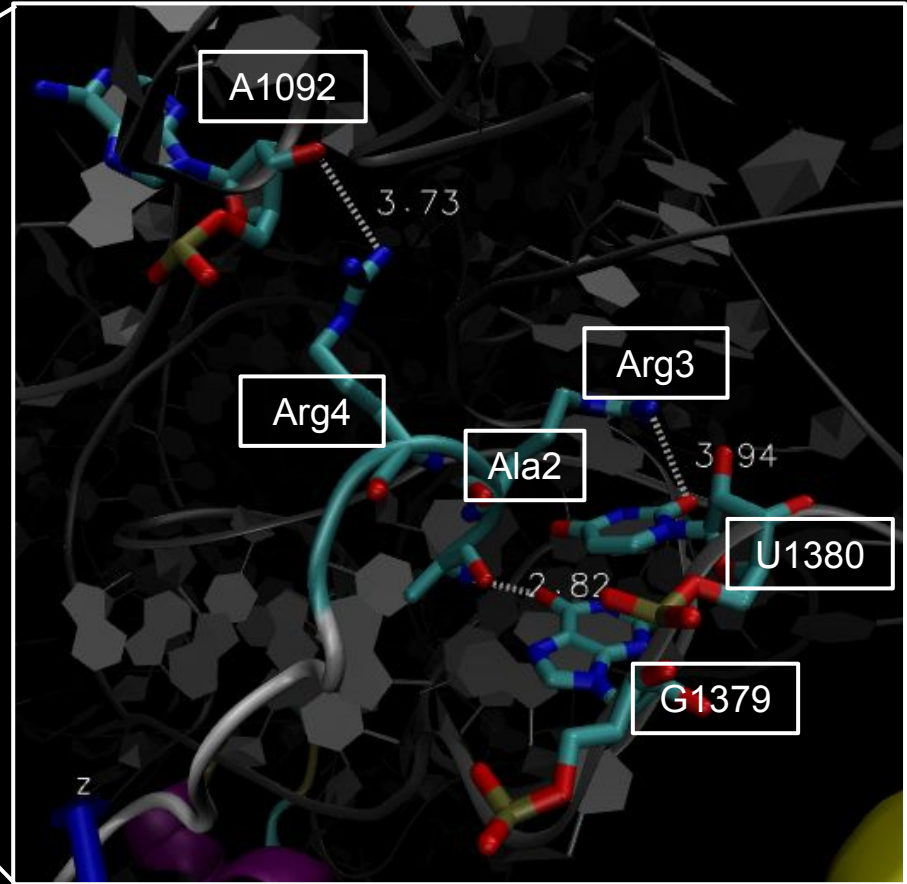
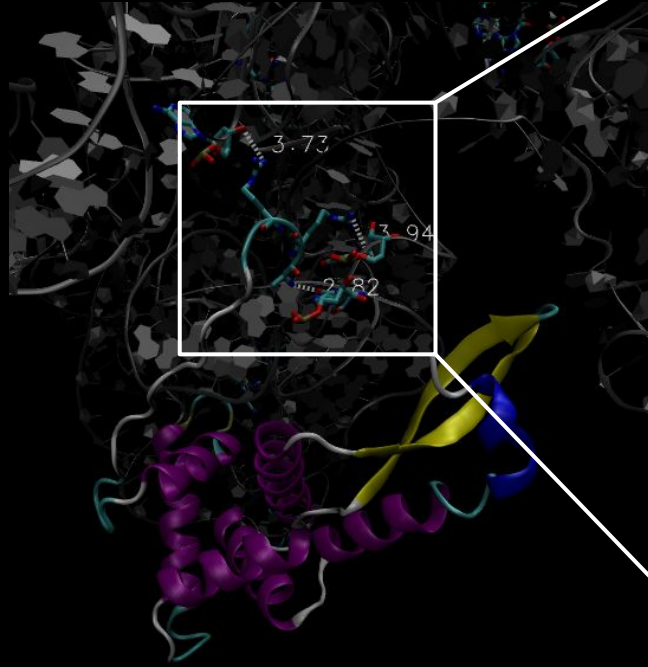
Sequence conservation

Homo	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Mus	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio	DYIAVKEKYAKYLPHSAGRYAAKRFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Xenopus	DYIAVKEKYAKFLPHSSGRYAAKRFRKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila	DYISVKEKFARYLPHSAGRYAAKRFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces	DYVQVRQP--IFVAHTAGRYANKRFRKAQCPIIERLTNSLMMNGRNNGKKLKAVRIIKHT
spDeinococcus	-----MARRRRAEVRPVPQDLVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus	-----MARRRRAEVRQLQPDLVYGDVLVTAFINRIMRDGKKNLAAIRIFYDA
Escherichia	-----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVYSA
	. * * .: . . :: :*** : * . :
Homo	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSP [→] LRVNQAIWLLCT
Mus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSP [→] LRVNQAIWLLCT
Danio	FEIIHLLTGENPLQILVNAIINSGPREDSTRIGRAGTVRRQAVDVSP [→] LRVNQAIWLLCT
Xenopus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSP [→] LRVNQAIWLLCT
Drosophila	FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSP [→] LRVNQAIWLLCT
Saccharomyces	LDIINVLTQDNPIQVVDAITNTGPREDTTRVG [→] GGAARRQAVDVSP [→] LRVNQAIWLLTI
spDeinococcus	CRLVQERTGQEPLKVFKQAYDNV [→] KPRVEVRSRRVGGSTYQVPVEVGPRRQ [→] QSLT [→] LRWMIS
Thermus	CKIIQEK [→] TGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSP [→] RRQ [→] QSLA [→] LRWL [→] VQ
Escherichia	LETLAQRS [→] GKSELEAFEVALENV [→] RPTVEVKSRRVGGSTYQVPVEV [→] RPVRNALAN [→] RWIVE
	: :.: .: . * * * : .*: : .: * * *: : :
Homo	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVA [→] SNR-----
Mus	GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVA [→] SNR-----
Danio	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVA [→] SNR-----
Xenopus	GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVA [→] SNR-----
Drosophila	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVA [→] SNR-----
Saccharomyces	GAREAAFRNIKTIAETLAEELINAAGSSSTSYAIAKKKDELERVA [→] SNR-----
spDeinococcus	AVDG--RPERTA [→] IERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus	AANQ--RPERRAAVRIAHELM [→] DAEGKGG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia	AARK--RGDKSMALRLANELSDAAENKGT--AVKKREDVHRMAEANKAFAHYRWLSLRS
	.. * : : * *: :*: . . * :*: :*: :*: :*: :

Structural conservation



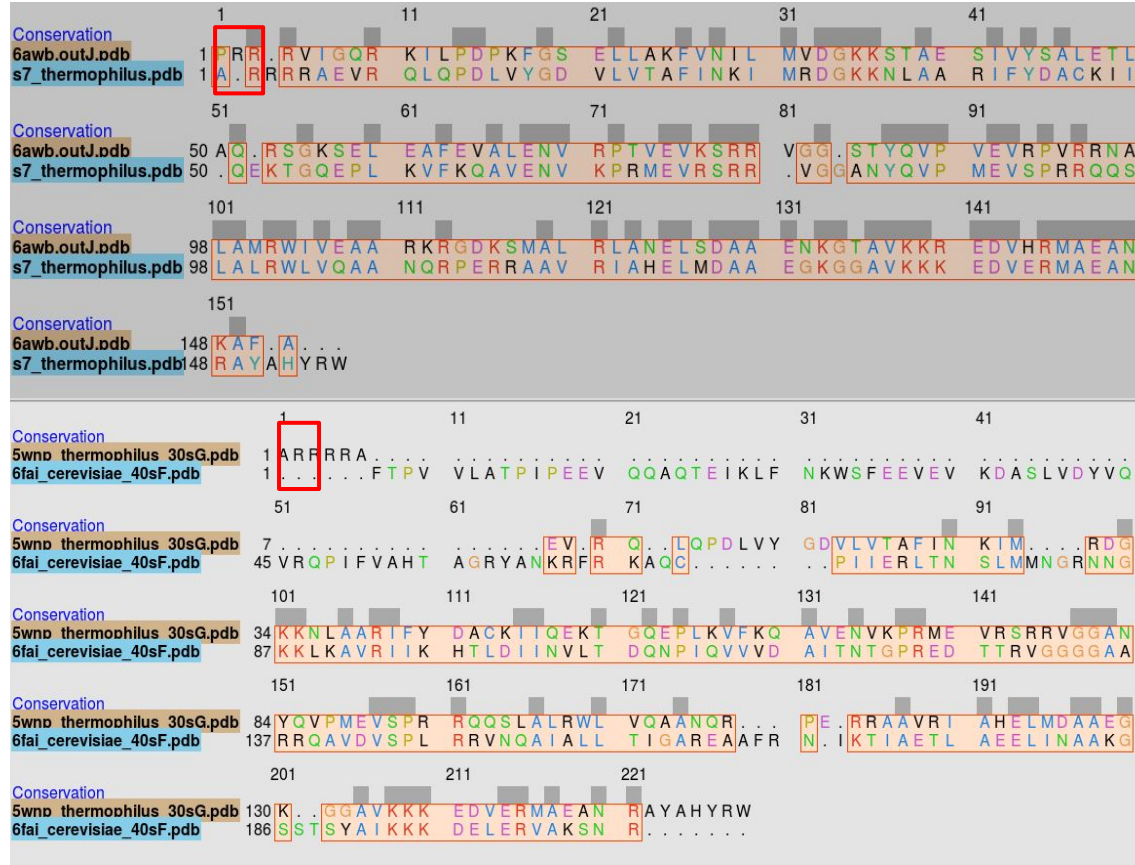
S7-16S rRNA N-terminal



Sequence conservation

Homo	DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Mus	DYIAVKEKYAKYLPHSAGRYAAKFRKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
Danio	DYIAVKEKYAKYLPHSSGRYAAKFRKAQCPIVERVTNSMMMHGRNNGKKLLTVRIVKHA
Xenopus	DYIAVKEKYAKFLPHSGGRYAAKFRKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
Drosophila	DYISVKEKFARYLPHSAGRYAAKFRKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
Saccharomyces	DYVQVRQP--IFVAHTAGRYANKRFRKAQCPIIERLTNSLMMNGRNNGKKLKAVRIKHT
spDeinococcus	-----MARRRAEVRPVQPDLVYQDVLVSAMINRIMRDGKKNLASRIFYGA
Thermus	-----MARRRAEVRQLQPDLVYGDVLVTAFINKIMRDGKKNLAAARIFYDA
Escherichia	-----MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAESIVYSA
	. * * .: . . :: :*** : * . :
Homo	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Mus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Danio	FEIIHLLTGENPLQILVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Xenopus	FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Drosophila	FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSPLRRVNQAIWLLCT
Saccharomyces	LDIINVLTQNPQIQQVVDAITNTGPREDTTRVGGGGGAARRQAVDVSPLRRVNQAIALLTI
spDeinococcus	CRLVQERTGQEPLKVFKQAYDNVVKPRVEVRSRRVGGSTYQVPVEVGPRRQQLTLRWMS
Thermus	CKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQQLALRWLVQ
Escherichia	LETLAQRSGKSELEAFEVALENVRPTVEVKSRRVGGSTYQVPVEVRPVRNALAMRWIVE
	: :... :: . * * * : .*: : .:* * *: :: :
Homo	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Mus	GAREAAFRNIKNIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Danio	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Xenopus	GAREAAFRNIKTIAECVADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Drosophila	GAREAAFRNIKTIAECLADELINAAGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces	GAREAAFRNIKTIAETLADELINAAGSSNSTSYAIAKKKDELERVAKSNR-----
spDeinococcus	AVDG---RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus	AANQ---RPERRAAVRIAHELMDAAEGKGG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia	AARK---RGDKSMALRLANELSDAAENKGT--AVKKKREDVHRMAEANKAFAHYRWLSLRS
	.. * : : * *: :*: . * :*:*:*:*:*:*:*:*

Structural conservation



Sequence conservation in bacteria

CLUSTAL 2.1 multiple sequence alignment



Helices
stabilization

Conserved in eukaryotes
and prokaryotes except
Glu 74.

Loops
stabilization

D-15 and Y-44 are highly
conserved in bacteria

Y-18 Q-19, D-20, V-22 →
two groups in bacteria

K-63 → 3 different
groups in bacteria

RNA-binding

N-terminal and R102 in
alpha4 highly conserved
in bacteria and R95
conserved in evolution

Lys 29 alpha 1 depends
on the specie

R32, R76, R114 → 2
groups in bacteria

Sequence conservation

Homo DYIAVKEKYAKYLPHSAGRYAAKRFKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
 Mus DYIAVKEKYAKYLPHSAGRYAAKRFKAQCPIVERLTNSMMMHGRNNGKKLMTVRIVKHA
 Danio DYIAVKEKYAKYLPHSSGRYAAKRFKAQCPIVERVTNSMMMHGRNNGKKLMTVRIVKHA
 Xenopus DYIAVKEKYAKFLPHSGGRYAAKRFKAQCPIVERFTNSLMMHGRNNGKKLMTVRIVKHA
 Drosophila DYISVKEKFARYLPHSAGRYAAKRFKAQCPIVERLTCSLMMKGRNNGKKLMACRIVKHS
 Saccharomyces DYYVQRQP--IFVAHTAGRYANKRFKAQCPIERLTNSLMMGRNNGKKLKAVRIKHT
 spDeinococcus -----MARRRAEVRVPQPDLYYQDYLVSAMINIMRGKKNLASRIFYGA
 Thermus -----MARRRAEVRQLQPDLYYGDYLVAFINKIMRGKKNLAAIRIFYDA
 Escherichia -----MRRRVIGORKILDPKFGSELLAKFVNIMVGKKSTAESIVSA

Conserved residues

RNA-binding residues

Structure stabilization

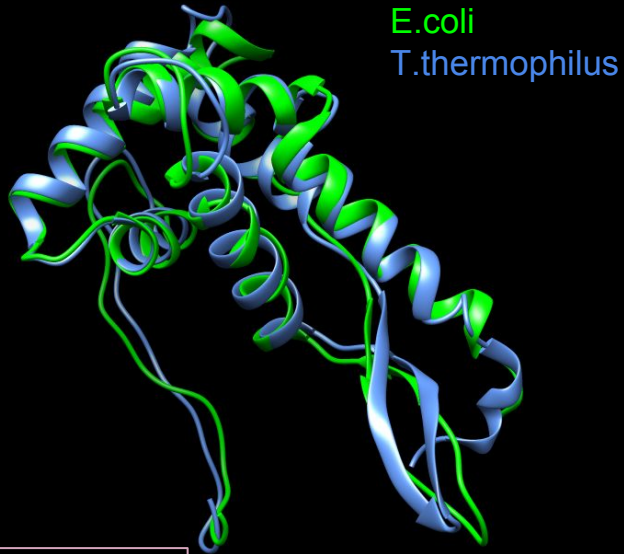
Homo FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSP^LLRVNQAIIWLLCT
Mus FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSP^LLRVNQAIIWLLCT
Danio FEIIHLLTGENPLQILVNAIINSGPREDSTRIGRAGTVRRQAVDVSP^LLRVNQAIIWLLCT
Xenopus FEIIHLLTGENPLQVLVNAIINSGPREDSTRIGRAGTVRRQAVDVSP^LLRVNQAIIWLLCT
Drosophila FEIIHLLTGENPLQILVSAIINSGPREDSTRIGRAGTVRRQAVDVSP^LLRVNQAIIWLLCT
Saccharomyces LDIIINVLTQDNPTQVVVDAITNTGPREDSTRVGGGGAARRQAVDVSP^LLRVNQAIALITI
spDeinococcus CRLVQERTGQEPLKVFKAAYDNVKPRVEVSRRRVGGSTYQVPVEVGPRRQSLSLIRWMIS
Thermus CKIIQEKTGQEPLKVFKAAYENVKPRVEVSRRRVGGANYQVPMEVSPRRQSLSLRWLVS
Escherichia LETLAQRSGSELEAFEALNVRTPEVKSRRRVGGSTYQVPVEVRPNRNALANRWIVE

: : : : * * : : : : * : : : : *

Homo GAREAAFRNIKTTIAECLADEFLINAAKGSSNSYAIAKKKDELERVAKSNR-----
Mus GAREAAFRNIKNTIAECLADEFLINAAKGSSNSYAIAKKKDELERVAKSNR-----
Danio GAREAAFRNIKTTIAECLADEFLINAAKGSSNSYAIAKKKDELERVAKSNR-----
Xenopus GAREAAFRNIKTTIAECVADEFLINAAKGSSNSYAIAKKKDELERVAKSNR-----
Drosophila GAREAAFRNIKTTIAECLADEFLINAAKGSSNSYAIAKKKDELERVAKSNR-----
Saccharomyces GAREAAFRNIKTTIAETLAEFLINAAKGSSTSYAIAKKKDELERVAKSNR-----
spDeinococcus AVDG---RPERTAIERLAGEIMDAAQGRGG--AIKKKDDVERMAEANRAYAHYRW----
Thermus AANQ---RPERRAAVRIAHEIMDAAEGKGG--AVKKKEDVERMAEANRAYAHYRW----
Escherichia AARK---RGDKSMALRLANELSDAAENKGT--AVKKKREDVHRMAEANKAFAHYRWLSLRS

Structural conservation

Bacteria/Bacteria



RMSD = 1,659
Q-score = 0,717
% id. = 49,01%

Bacteria/Eukaryote

T. thermophilus
S. cerevisiae



RMSD = 1,284
Q-score = 0,468
% id. = 29,03%

GTPase ERA



ERA classification

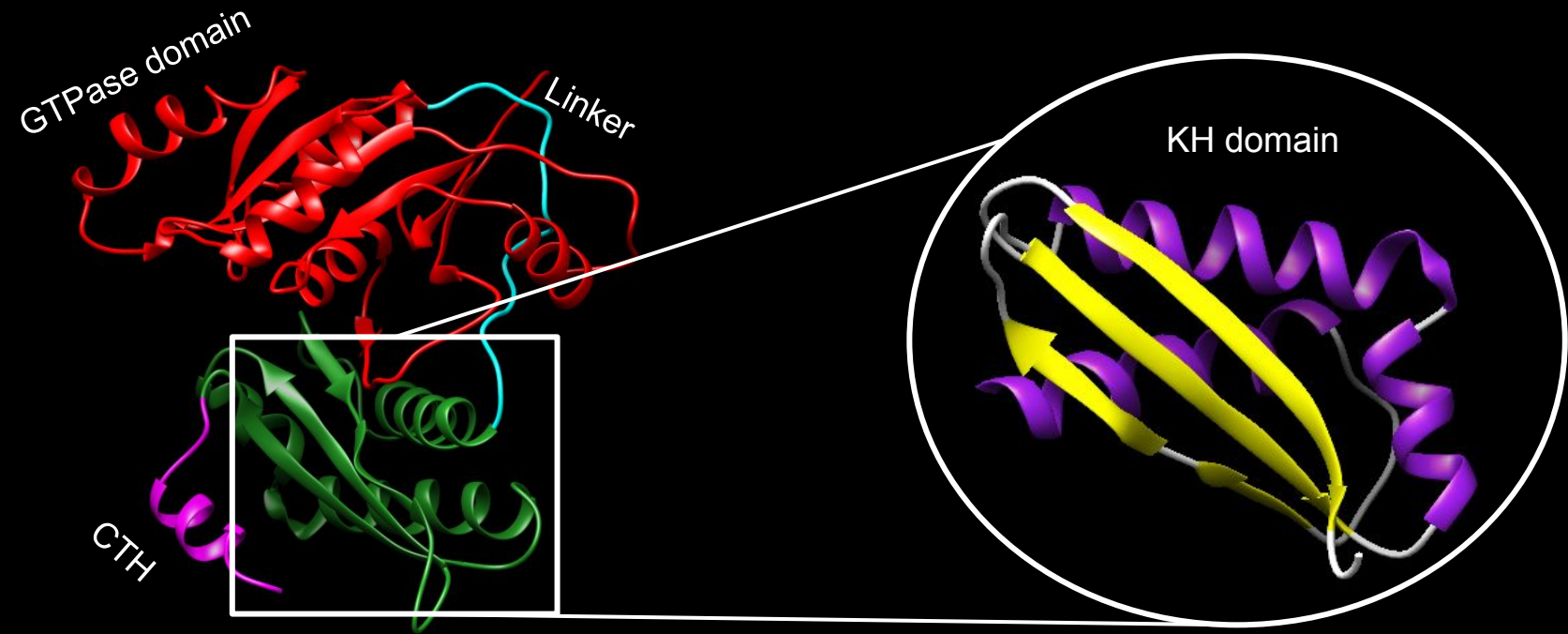
CATH

Class	Alpha Beta
Architecture	3-Layer Sandwich
Topology	Rossmann fold
Homologous Superfamily	P-loop containing nucleotide triphosphate hydrolases

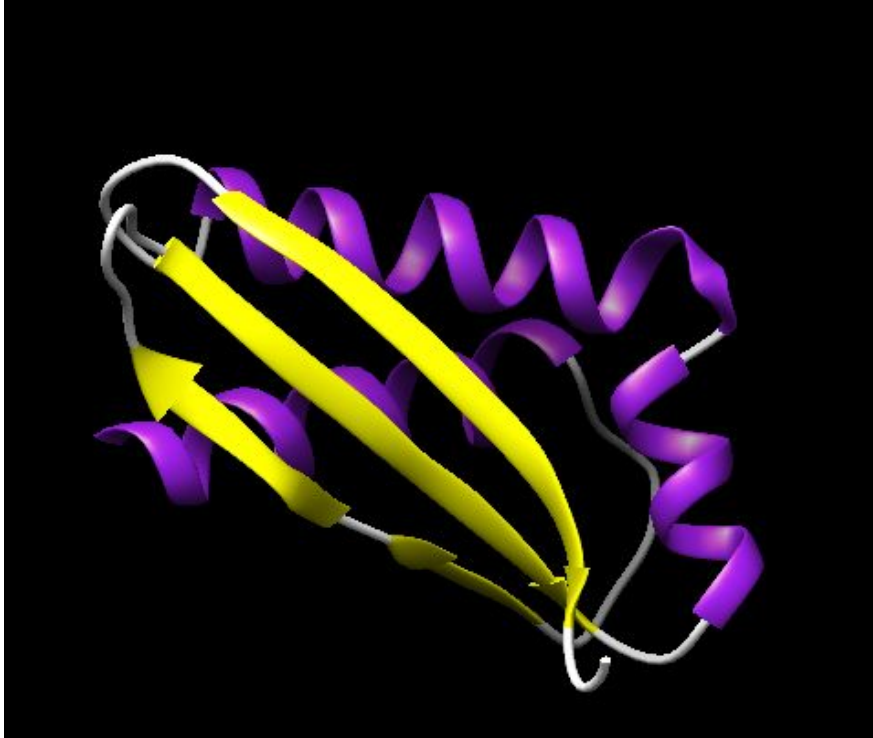
SCOP

Class	Alpha and beta proteins
Fold	P-loop containing nucleotide triphosphate hydrolases
Superfamily	P-loop containing nucleotide triphosphate hydrolases
Family	G proteins
Protein	GTPase ERA

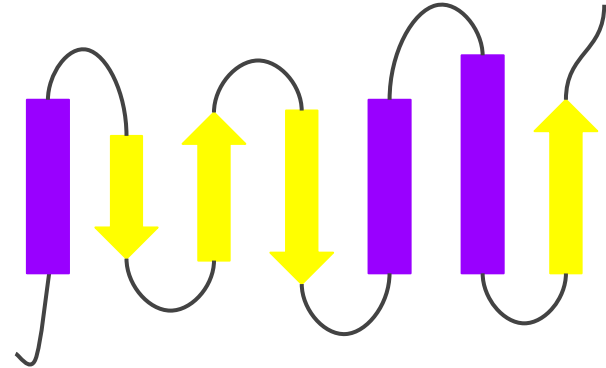
GTPase ERA



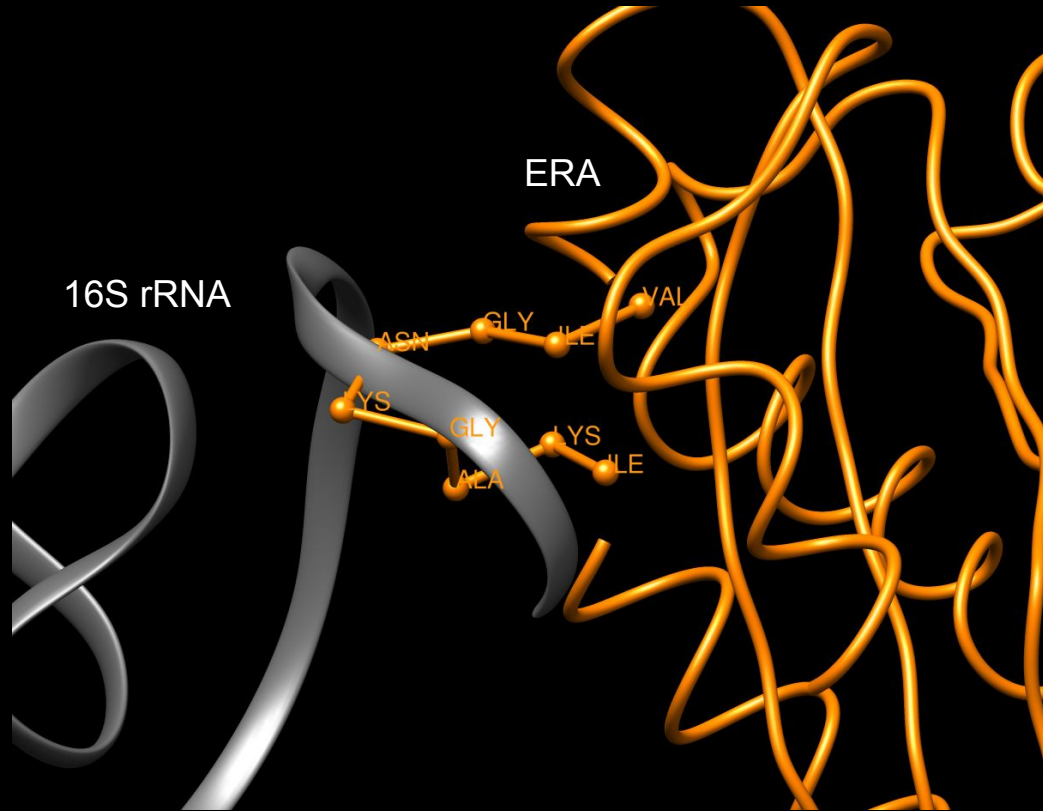
KH domain



- RNA-binding motif
- Interaction 16S rRNA

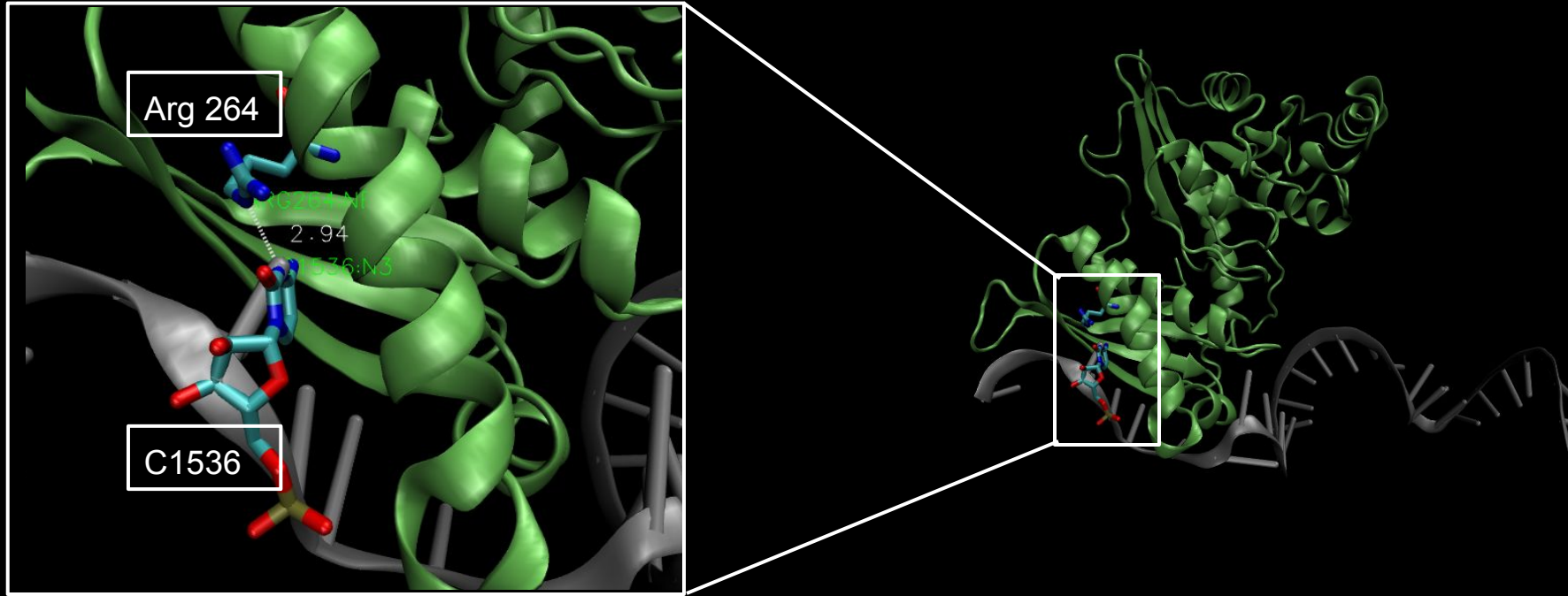


KH domain sequence

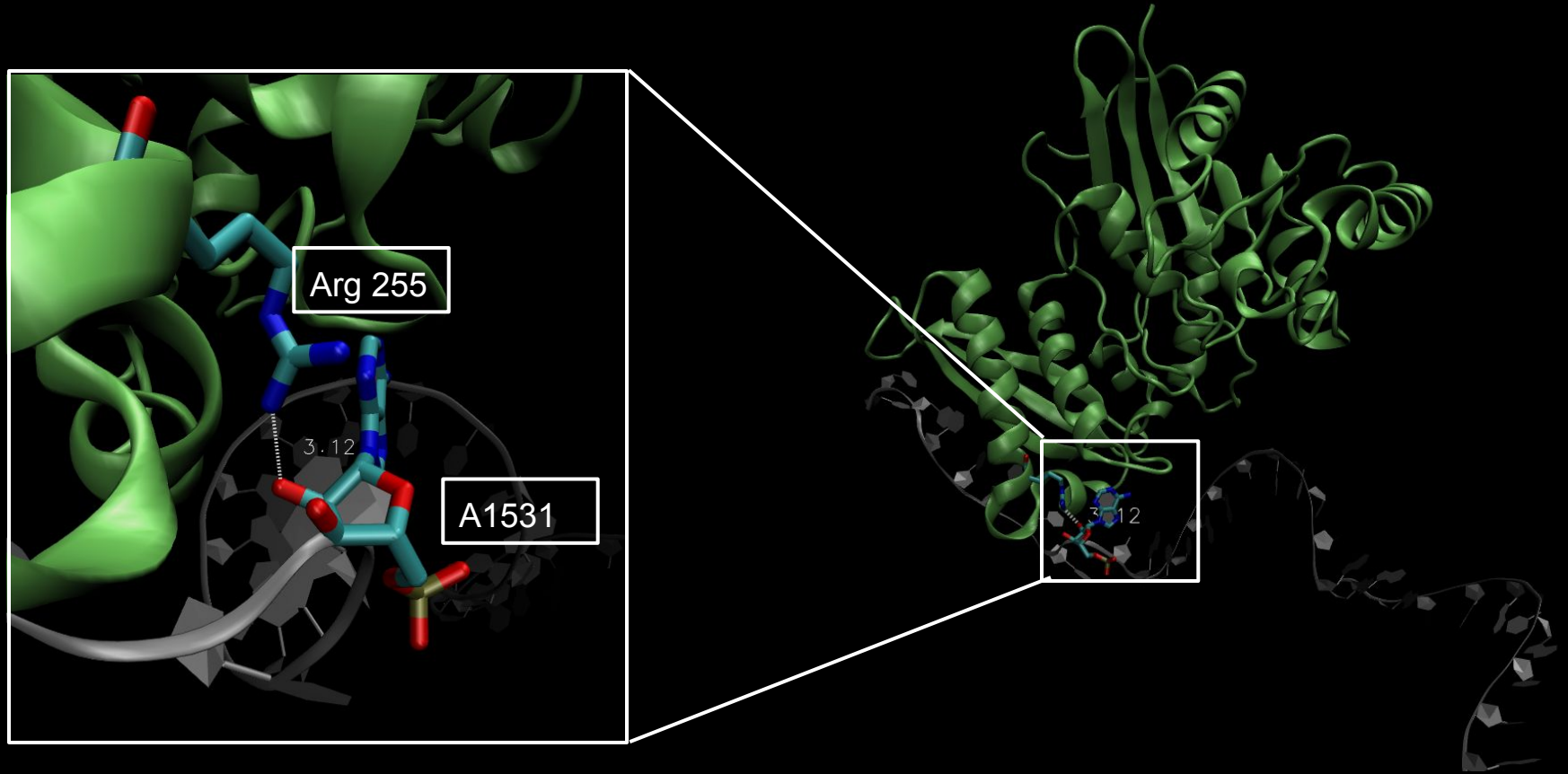


Conserved sequence
246 VIGxxGxxI 254

Interactions with 16S rRNA



Interactions with 16S rRNA



Sequence conservation

CLUSTAL 2.1 multiple sequence alignment

```

sp|P06616|ERA_ECOLI      -----MSIDKSYCGFIAIVGRPNVGKSTLLNKLGLGQKISITSRKAQTTTHRIVGIH
sp|Q56057|ERA_SALTY      -----MSTDKTYCGFIAIVGRPNVGKSTLLNKLGLGQKISITSRKAQTTTHRIVGIH
sp|A5UF17|ERA_HAEIG      -----MTEQFDKTYCGFIAIVGRPNVGKSTLLNKLGLGQKISITSRKAQTTTHRIVGIH
sp|Q67800|ERA_AQUAE      -----MKVGYVAIVGKPNVGKSTLLNNLLGTKVSIISPAGKTTMRVLGVK
sp|Q9RWM0|ERA_DEIRA      MTDFSASPDLQDPTTHAGFVAIVGKPNVGKSTLLNAFLGTKVAPTSPRPQTTRRGVRGIY
sp|Q5SM23|ERA_THET8      -----MAEKTSYGFVAIVGKPNVGKSTLLNNLLGVKVPAPISRPQTTTRKRLRGIL
                               *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

```

```

sp|P06616|ERA_ECOLI      TEG-AYQAIYVDTPGLHMEEK-AINRLMNKAASSSIGDVELVIFVVEGTR-WTP-DDEM
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sp|A5UF17|ERA_HAEIG      TEG-AYQEIYVDTPGLHIEEK-AINRLMNRAASSAIGDVLIFVVGTH-WNA-DDEM
sp|Q67800|ERA_AQUAE      NIPNEAQIIFLDTPGIYEPKSDVLGHSVVEIAKQSLLEADVLI FMDIATEGWRPRDEEI
sp|Q9RWM0|ERA_DEIRA      TLD-NRQLIFVDTPGLHKPKDA--LGKYMNSEVHSALSDVDVAVVWVVDLRHPPTD-EDRL
sp|Q5SM23|ERA_THET8      TEG-RRQIVFVDTPGLHKPMDA--LGEFMDQEVYEALADVNAVWVWVVDLRHPPTP-EDEL
                        *      *      *      *      *

```

```

sp|P06616|ERA_ECOLI      VLNKLREGK--APVILAVNKVDNVQEKADLLPHLQFLASQM-NFLDIVP--ISAETGL-N
sp|Q56057|ERA_SALTY      VLNKLRLDGK--APVTLAVNKVDNVQEKVDLLPHLQFLASQM-NFLDIVP--ISAETGM-N
sp|A5UF17|ERA_HAEIG      VLNKLRNAK--APVVLAVNKVDNIKNKDDLLPFITDLSKSF-NFAHIVP--ISAQRGN-N
sp|Q67800|ERA_AQUAE      YQNF1KPLN--KPVIVVINKIDK7GPAKNVPLIDEIHKKHPELTIVP--ISALKGA-N
sp|Q9RWM0|ERA_DEIRA      VANSVRDLP--KPLFLVGNTDAAKYPEEAMKLYGALLEGRGSDLPVSETMLSAQNSVNA
sp|Q5SM23|ERA_THET8      VARALKPLVGKPVILLVGNKDAAKYPEEAMKAYHELLP-----EAEPRMLSALDER-Q

```

GTPase domain (NTD)

Linker

KH-domain

HTH of CTD

CTH (C-terminal helix)

Sequence conservation

sp|P06616|ERA_ECOLI
sp|Q56057|ERA_SALTY
sp|A5UFI7|ERA_HAEIG
sp|O67800|ERA_AQUAE
sp|Q9RWM0|ERA_DEIRA
sp|Q5SM23|ERA_THET8

VDTIAAIVRKHLPEATHHFPED-YITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIER
VDTIAGIVRKHLPEATHHFPED-YITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIER
VHELEKIVRQSLREGVHHFPED-YVTDERSQRFMASEIIREKLMRFTGEELPYSVTVEIEQ
LDELVKITLKYLPEGEPLFPED-MITDLPRLLLAAEIVREKAMMLTREEVPTSIAVKINE
VATLREQLLLEVLNPFPPFPQG-AASDQSREMWAEEIREEAMKKLRDELPAVATRVNR
VAELKADLLALMPEGPPFFYPEDYAKSDQTFGEWVAEILREEAMKRLWHEVPYAVATKVEE
: : : : * :*: :* . :*:*: * *: * :*:*:~

sp|P06616|ERA_ECOLI
sp|Q56057|ERA_SALTY
sp|A5UFI7|ERA_HAEIG
sp|O67800|ERA_AQUAE
sp|Q9RWM0|ERA_DEIRA
sp|Q5SM23|ERA_THET8

FVSNERGG--YDINGLILVEREGQKKNVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELW
FVTNERGG--YDINGLILVEREGQKKNVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELW
FKVNERTG--YEINGLILVEREGQKKNVIGAGGQKIKTIGMEARADMERLFDNKVHLELW
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VAERENGV--LYIKAILYVERPSQKAVIGEGGRKIKTIGQATRKQLEALLGKKVYLDLE
: . *: :*: * :*: * :*: * :*: * :*: *

sp|P06616|ERA_ECOLI
sp|Q56057|ERA_SALTY
sp|A5UFI7|ERA_HAEIG
sp|O67800|ERA_AQUAE
sp|Q9RWM0|ERA_DEIRA
sp|Q5SM23|ERA_THET8

VKVKSGWADDERALRSLGYVDDL-
VKVKSGWADDERALRSLGYVDDL-
VKVKSGWADDERALRSLGYMDE--
VKVVPDWRRRPEYVRLFGYAL---
VIVIPGWREDEEALRELGYE---
VKVYPDWRKDPEALRELGYRSSVG
* * ..* . :* :*

GTPase domain (NTD)

Linker

KH-domain

HTH of CTD

CTH (C-terminal helix)

Conserved sequence
VIGxxGxxI

Conclusions

- Ribosome sequence is highly conserved in bacteria and in eukaryotes but not between these groups.
- The conservation of the sequence correlates with the protein function.
- Although some residues are not conserved, they don't affect the conservation of the protein structure.
- The alignments and superimpositions can help us to corroborate the protein homology.
- The structure of the proteins are similar with their eukaryotic homologues.

Tools used

- PDB
- UniProt
- PDBePISA
- EMBL-EBI
- CATH
- SCOP
- STAMP
- CLUSTALW
- CHIMERA
- VMD

Bibliography

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PEM questions

1. Which of the following sentences is not true about the ribosome:
 - a. It's involved in protein biosynthesis
 - b. It's universally conserved
 - c. It's composed of RNA and proteins
 - d. It's located in the nucleus
 - e. It's bound to mRNA and tRNA
2. In relation with the S7 ribosomal protein:
 - a. It's involved in the initiation of ribosomal folding
 - b. Allows the union of other proteins in 16S rRNA
 - c. The two previous ones are correct
 - d. It binds to S11 ribosomal protein
 - e. All of them are correct
3. S11 binds principally with the 16s rRNA through:
 - a. VDW
 - b. Hidrogen bonds
 - c. Hydrophobic interactions
 - d. Ionic bonds
 - e. It does not interact with 16S rRNA
4. Which is the homologous of the ribosomal protein L2?
 - a. L8
 - b. S16
 - c. L13
 - d. L4
 - e. S8

5. Which of the following structure corresponds to S7?

- a. Five-stranded beta-sheet and two alpha-helices
- b. Six alpha-helices and one beta-hairpin
- c. Two beta-barrels and three alpha-helices
- d. All alpha
- e. Ten antiparallel beta-sheet and one alpha-helix

6. Choose the correct answers in relation with ERA GTPase

- 1. It's composed by two domains and one linker
- 2. It's a specific GTPase of *E.coli*
- 3. The KH domain is the one that binds to the rRNA
- 4. It binds to 23S rRNA
 - a. 1, 2, 3
 - b. 1, 3
 - c. 2, 4
 - d. 4
 - e. 1, 2, 3, 4

7. In relation with the ribosomal conservation:

- a. All the bacterial ribosomal proteins have homologous in eukaryotes
- b. Eukaryotes and prokaryotes have the same number of ribosomal proteins
- c. The two previous are correct
- d. L2, S7 and S11 are conserved between bacteria
- e. All of them are correct

8. In relation with the structural conservation of the ribosome, choose the correct answer:

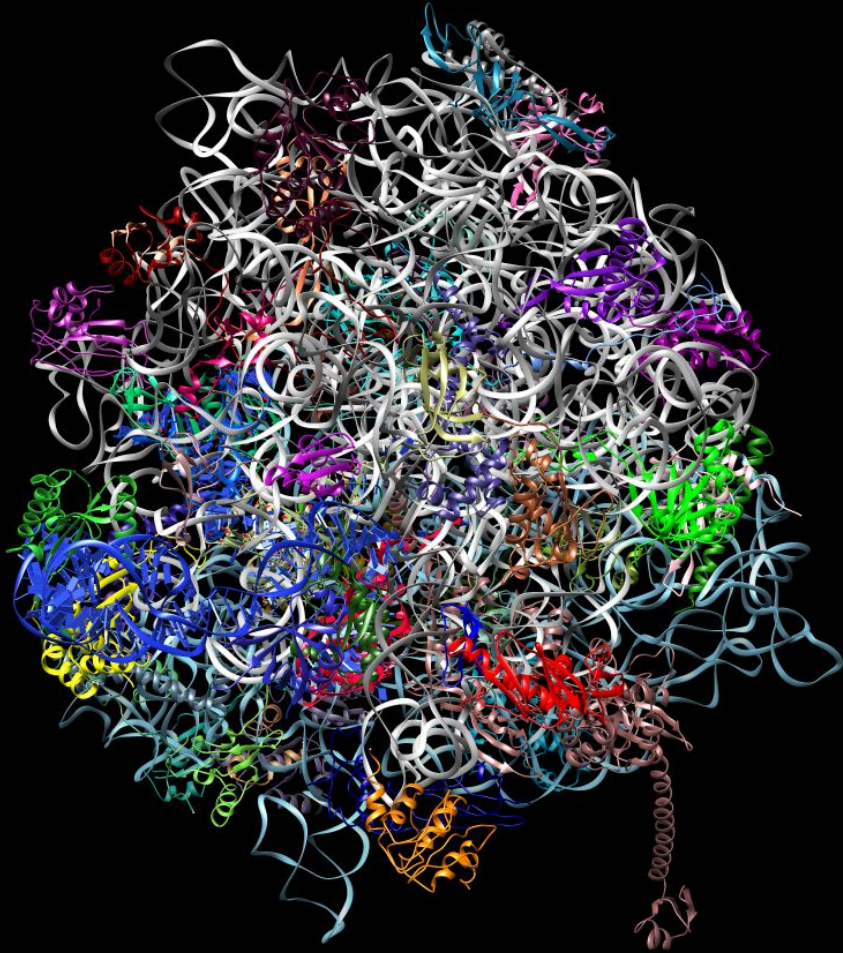
- a. The structure is more conserved between bacteria and eukaryote rather than between bacteria
- b. The principal characteristic of eukaryotes is that they have incorporated beta-hairpins on their structure
- c. The global structure of the ribosomal proteins has not changed much between bacteria and eukaryotes
- d. A change in an aminoacid always alters the structure
- e. The RMSD always correlates with the % ID

9. Choose the correct answer about ribosomal proteins:

- a. All residues implicated in the interactions are conserved
- b. There is no interactions that allow the stabilization of the S7 protein
- c. Ribosomal proteins interact with rRNA
- d. There is no interaction between ribosomal proteins
- e. No external protein to the ribosome participate in translation process

10. Choose the correct answer about ribosomal proteins:

- a. Amino acids are usually changed for ones with similar properties
- b. Q-score is lower in bacteria/bacteria superimpositions
- c. The two previous are correct
- d. Structural information do not help much to determine homology between proteins
- e. All of them are correct



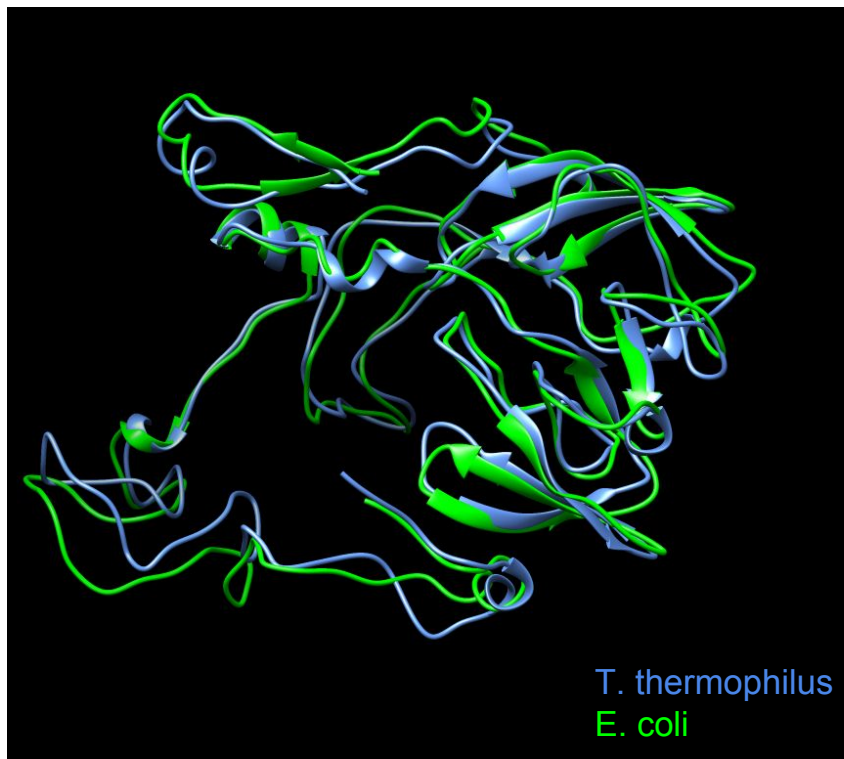
The Ribosome

Structural biology

Arola Altimir
Emma Bigas
Irene Calderón
Joana Oliver

ANNEX

Superimposition Bacteria L2



Conservation	1	11	21	31	41	
3i8a_ecoli_50sC.pdb	1	AVVKCKPTSP	GRRHVVKVVN	PEL.HKK.KPF	APLLEKNSKS	GGRNNNGRIT
5j8b_thermophilus_50SD.pdb	1	AVKKFKPYTP	SRRFMTVADF	SEITKT.EPE	KSLVKPLKKT	GGRNNQGRIT
Conservation	51	61	71	81	91	
3i8a_ecoli_50sC.pdb	50	TRHTGGGHKQ	AYRIVDFKH.	NKDGIPAVVE	RLEYDPNRSA	NIALVLYKDG
5j8b_thermophilus_50SD.pdb	50	VRFRGGGHKR	LYRIIDFKRW	DKVGIPAKVA	AIEYDPNRSA	RIALLHYVDG
Conservation	101	111	121	131	141	
3i8a_ecoli_50sC.pdb	99	ERRYTLAPKG	LKAGDQIQSG	VDAATKPGNT	LPMRNIPVGS	TVHNVEMKPG
5j8b_thermophilus_50SD.pdb	100	EKRYIIAPDG	LQVGGQVVAG	PDAPIQVQNA	LPLRFIPVGT	VVHAVELEPK
Conservation	151	161	171	181	191	
3i8a_ecoli_50sC.pdb	149	KGGQLARSAG	TYVQIVARDG	AYVTLRLRSG	EMRKVEADCR	ATLGEVGNAE
5j8b_thermophilus_50SD.pdb	150	KGAKLARAAG	TSAQIQGREG	DYVILRLPSG	ELRKVHGE CY	ATVGAVGNAD
Conservation	201	211	221	231	241	
3i8a_ecoli_50sC.pdb	199	HMLRVLGKAG	AARWRGV RPT	VRGTAMNP.VD	HPHGG.GEGR	NFG.KHPV.T
5j8b_thermophilus_50SD.pdb	200	HKNIVLGKAG	RSRWLGRRPH	VRGAAMNP.V	DHPHGGGEGR	AP.RGRP.PA
Conservation	251	261	271	281		
3i8a_ecoli_50sC.pdb	246	..PWGVQTK	GKKTRSN..K	RTDKFIVRRR	S.	
5j8b_thermophilus_50SD.pdb	247	SPWGW..QTK	GLKTRK..RR	K PSSRFIIARR	KK	

Evaluating superpositions across all 264 fully populated columns in the final alignment:

RMSD of 3j8g_ecoli_50sC.pdb with 5j8b_thermophilus_50SD.pdb: 1.553

Overall RMSD: 1.553

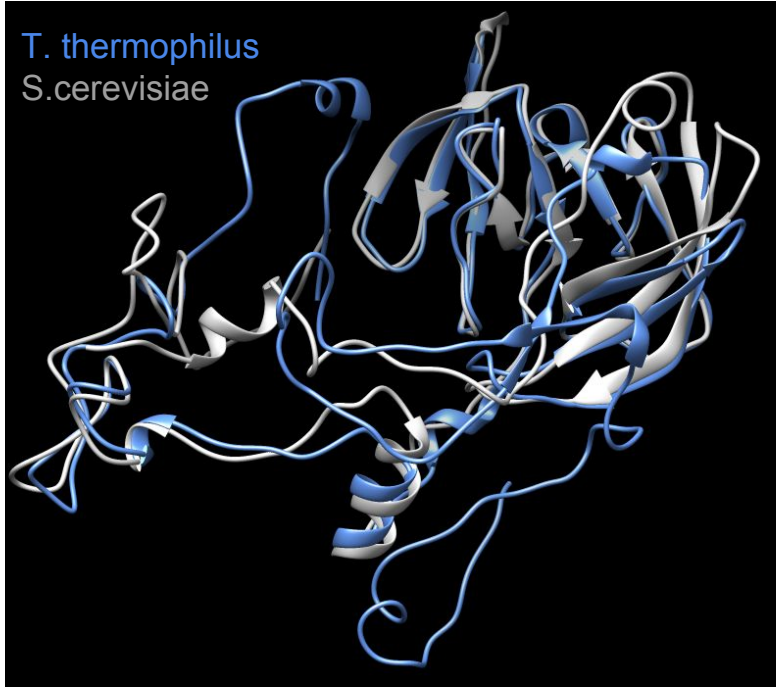
Sequence lengths: 271 275

SDM (cutoff 5.0): 30.484

Q-score: 0.737

5j8b_thermophilus_50SD.pdb vs. 3j8g_ecoli_50sC.pdb: 55.72% identity

Superimposition Bacteria/Eukaryote L2/L8



Conservation	1	11	21	31	41
5i8b_thermophilus_50SD.pdb	1 AVKKFKPYTP	SRRFMTVADF	SEITKTEPEK	SLVKPLKKT.	RVIRNQKGA
cerevisiae60s.D.pdb	1	...	...	...	...
Conservation	51	61	71	81	91
5i8b_thermophilus_50SD.pdb	40 ..GGRNNQGR	ITVRFRRGGH	K...RLYRI	..DFKRWDK.	..V...GIP
cerevisiae60s.D.pdb	12 GSIF.....	...	..TSHTRLRQG	AA..KLR..T.L	..YAE..RHGYIR
Conservation	101	111	121	131	141
5i8b_thermophilus_50SD.pdb	76 AKVAAI...EYDP	NRSARIALLLH	YV...D...	G EKRYI...IAPDG	LQVGGQVVVAG
cerevisiae60s.D.pdb	42 GIVKQIVHDS	GRGAPLAKVV	F..RD...PYKYRL	REEIFIANEG	VHTGQFIYAG
Conservation	151	161	171	181	191
5i8b_thermophilus_50SD.pdb	120 PDAPITQVNGA	LPLRFIPVGT	VVHAVELEPK	KGAKLAHAAG	TSAQIQGRE.
cerevisiae60s.D.pdb	91 KKASLNVGNV	LPLGSPVEGT	IVSNVEEKPG	DRGALARASG	NYVIIIGHNP
Conservation	201	211	221	231	241
5i8b_thermophilus_50SD.pdb	169 G...DYVILRLP	SGELRKVHGE	CYATVGA VGN	ADHKNTI..VLG	KAGRSRW..LG
cerevisiae60s.D.pdb	141 D...ENKTRVRLP	SGAKKVISSD	ARGVIGVIAG	GGRVDKPL..L	KAGRAFH..KYR
Conservation	251	261	271	281	291
5i8b_thermophilus_50SD.pdb	216 ...RRPHVR	GAAMNPVDHP	HGGGEGRAPR	GRPPASP...	WGW..Q
cerevisiae60s.D.pdb	190 LKRNSWPKTR	GVAMNPVDHP	HGGGNH..QHI	GKAS...TIS	RGAVSGQKAG
Conservation	301	311	321	331	
5i8b_thermophilus_50SD.pdb	253 TKG...LKTRKR	RKPSSRFIIA	RRK...TGLL	R...K...TQ	
cerevisiae60s.D.pdb	236 L...IA.....	...	...ARRTGLL	RGSQK...TQ	

Evaluating superpositions across all 190 fully populated columns in the final alignment:

RMSD of 5i8b_thermophilus_50SD.pdb with cerevisiae60s.D.pdb: 1.722

Overall RMSD: 1.722

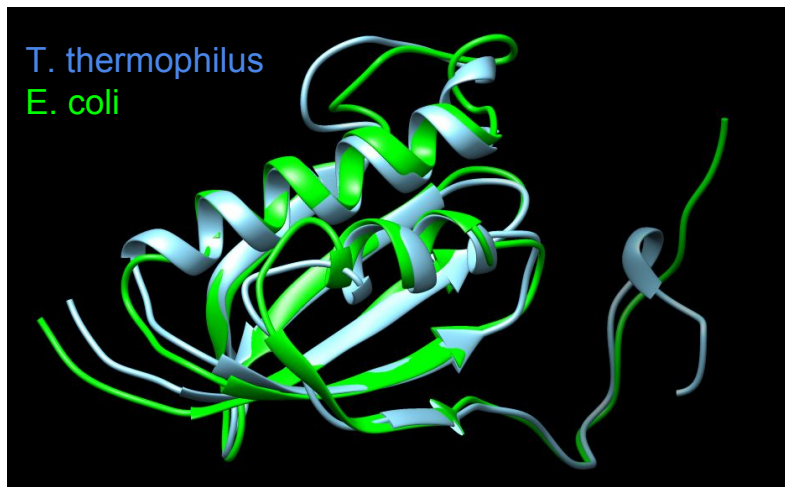
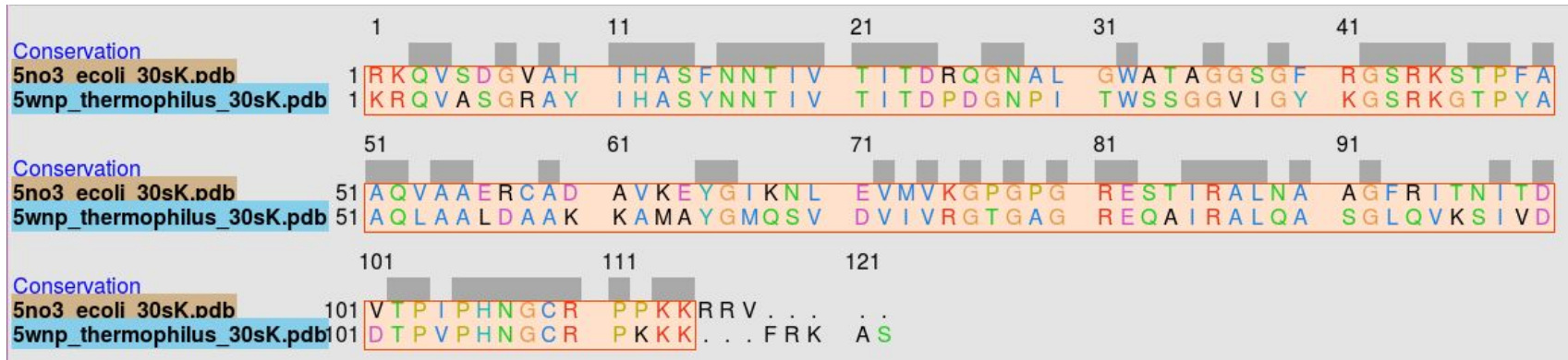
Sequence lengths: 275 252

SDM (cutoff 5.0): 37.893

Q-score: 0.392

5i8b_thermophilus_50SD.pdb vs. cerevisiae60s.D.pdb: 25.79% identity

Superimposition Bacteria S11



Evaluating superpositions across all 114 fully populated columns in the final alignment:

RMSD of 5wnp_thermophilus_30sK.pdb with 5no3_ecoli_30sK.pdb: 1.316

Overall RMSD: 1.316

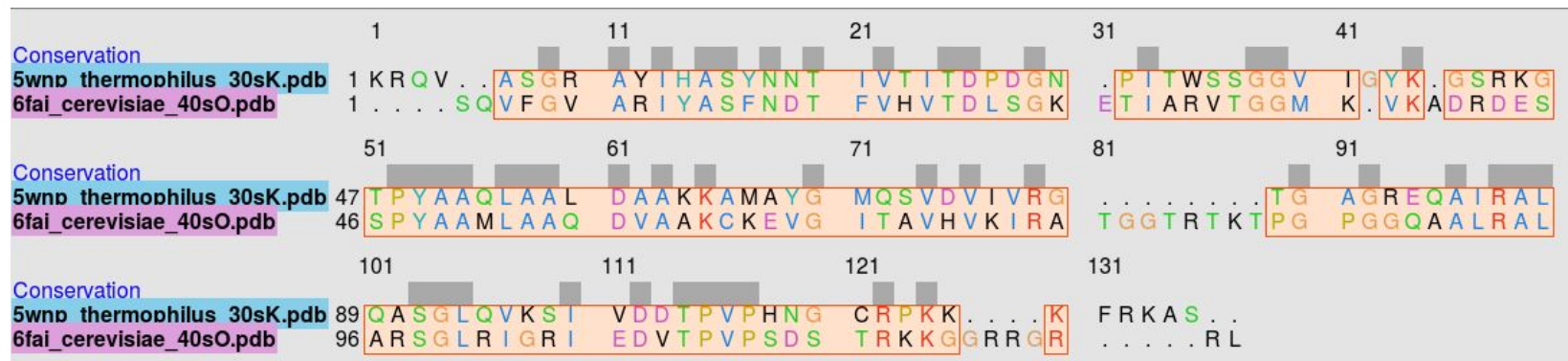
Sequence lengths: 119 117

SDM (cutoff 5.0): 26.000

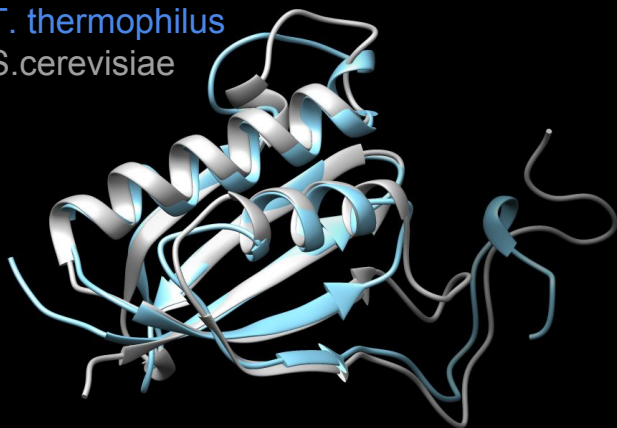
Q-score: 0.783

5wnp_thermophilus_30sK.pdb vs. 5no3_ecoli_30sK.pdb: 52.99% identity

Superimposition Bacteria/Eukaryote S11/S14



T. thermophilus
S.cerevisiae



Evaluating superpositions across all 109 fully populated columns in the final alignment:

RMSD of 5wnp_thermophilus_30sK.pdb with 6fai_cerevisiae_40sO.pdb: 1.327

Overall RMSD: 1.327

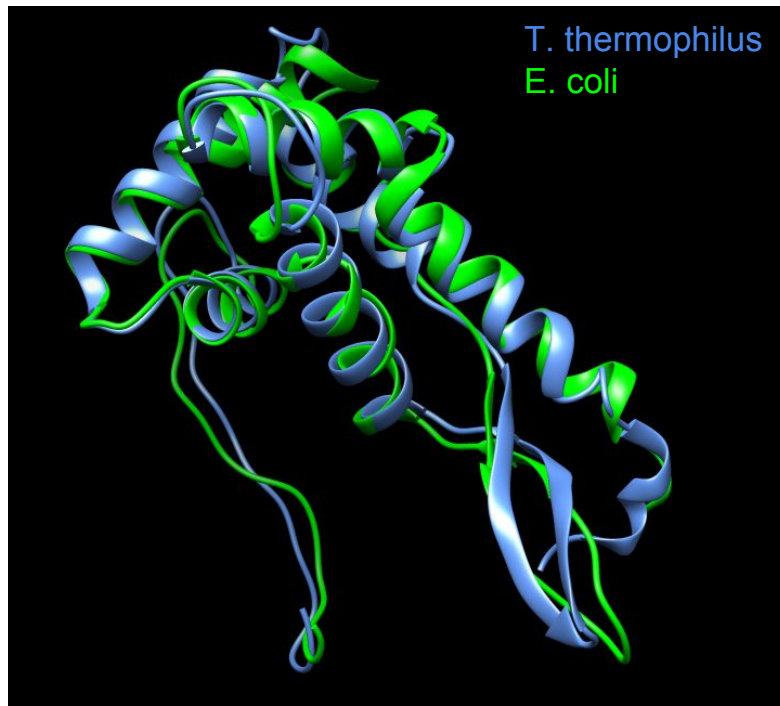
Sequence lengths: 119 127

SDM (cutoff 5.0): 26.624

Q-score: 0.657

5wnp_thermophilus_30sK.pdb vs. 6fai_cerevisiae_40sO.pdb: 38.66% identity

Superimposition Bacteria S7



Conservation

6awb.outJ.pdb

s7_thermophilus.pdb

1

11

21

31

41

1

P

R

R

R

V

T

G

O

R

K

I

L

P

D

F

K

F

G

S

E

L

L

A

K

F

V

N

I

L

M

V

D

G

K

K

S

T

A

E

S

T

I

V

Y

S

A

E

T

L

1

A

R

R

R

R

A

E

V

R

Q

L

Q

P

D

L

V

Y

G

D

V

L

V

T

A

F

I

N

K

I

M

R

D

G

K

K

N

L

A

A

R

I

F

Y

D

A

C

K

I

I

Conservation

6awb.outJ.pdb

s7_thermophilus.pdb

51

61

71

81

91

50

A

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S

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S

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V

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M

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Q

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Conservation

6awb.outJ.pdb

s7_thermophilus.pdb

101

111

121

131

141

98

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A

E

G

K

G

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A

V

K

K

K

E

D

V

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R

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A

E

A

N

Conservation

6awb.outJ.pdb

s7_thermophilus.pdb

151

148

K

A

F

A

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148

R

A

Y

A

H

Y

R

W

Evaluating superpositions across all 148 fully populated columns in the final alignment:

RMDS of 6awb.outJ.pdb with s7_thermophilus.pdb: 1.659

Overall RMSD: 1.659

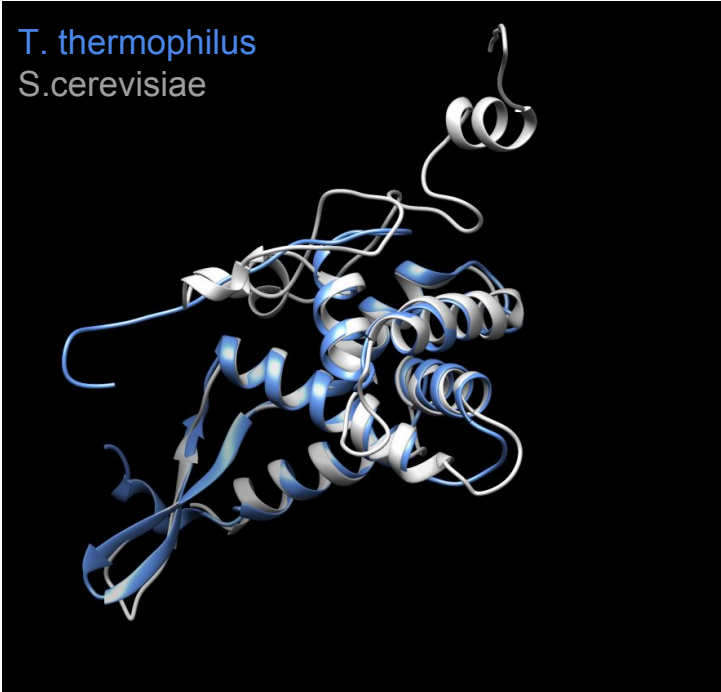
Sequence lengths: 151 155

SDM (cutoff 5.0): 32.422

Q-score: 0.717

s7_thermophilus.pdb vs. 6awb.outJ.pdb: 49.01% identity

Superimposition Bacteria/Eukaryote S7/S5



Conservation	1	11	21	31	41
5wnp_thermophilus_30sG.pdb	1	A R R R R A			
6fai_cerevisiae_40sF.pdb	1	 F T P V	V L A T P I P E E V	Q Q A Q T E I K L F	N K W S F E E V E V
Conservation	51	61	71	81	91
5wnp_thermophilus_30sG.pdb	7				
6fai_cerevisiae_40sF.pdb	45	V R Q P I F V A H T	A G R Y A N K R F R	K A Q C	G D V L V T A F I N
Conservation	101	111	121	131	141
5wnp_thermophilus_30sG.pdb	34	K K N L A A R I F Y	D A C K I I O E K T	G O E P L K V F K Q	A V E N V K P H M E
6fai_cerevisiae_40sF.pdb	87	K K L K A V R I I K	H T L D I I N V L T	D Q N P I Q V V V D	A I T N T G P R E D
Conservation	151	161	171	181	191
5wnp_thermophilus_30sG.pdb	84	Y Q V P M E V S P R	R Q O S L A L R W L	V Q A A N Q R I . . .	P I E . R R A A V R I
6fai_cerevisiae_40sF.pdb	137	R R Q A V D V S P L	R R V N Q A I A L L	T I G A R E A A F R	N . I K T I A E T L
Conservation	201	211	221		
5wnp_thermophilus_30sG.pdb	130	K . . G G A V K K K	E D V E R M A E A N	R A Y A H Y R W	
6fai_cerevisiae_40sF.pdb	186	S T S Y A I K K K	D E L E R V A K S N	R	

Evaluating superpositions across all 133 fully populated columns in the final alignment:

RMSD of 5wnp_thermophilus_30sG.pdb with 6fai_cerevisiae_40sF.pdb: 1.284

Overall RMSD: 1.284

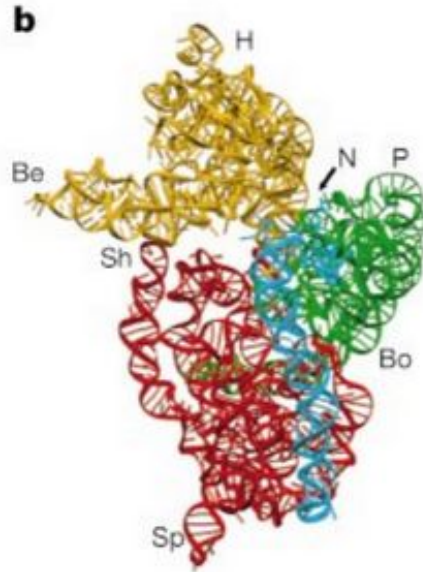
Sequence lengths: 155 206

SDM (cutoff 5.0): 26.645

Q-score: 0.468

5wnp_thermophilus_30sG.pdb vs. 6fai_cerevisiae_40sF.pdb: 29.03% identity

Structure of 70S ribosome



Head
Beck
Neck
Platform
Shoulder
Spur
Body

