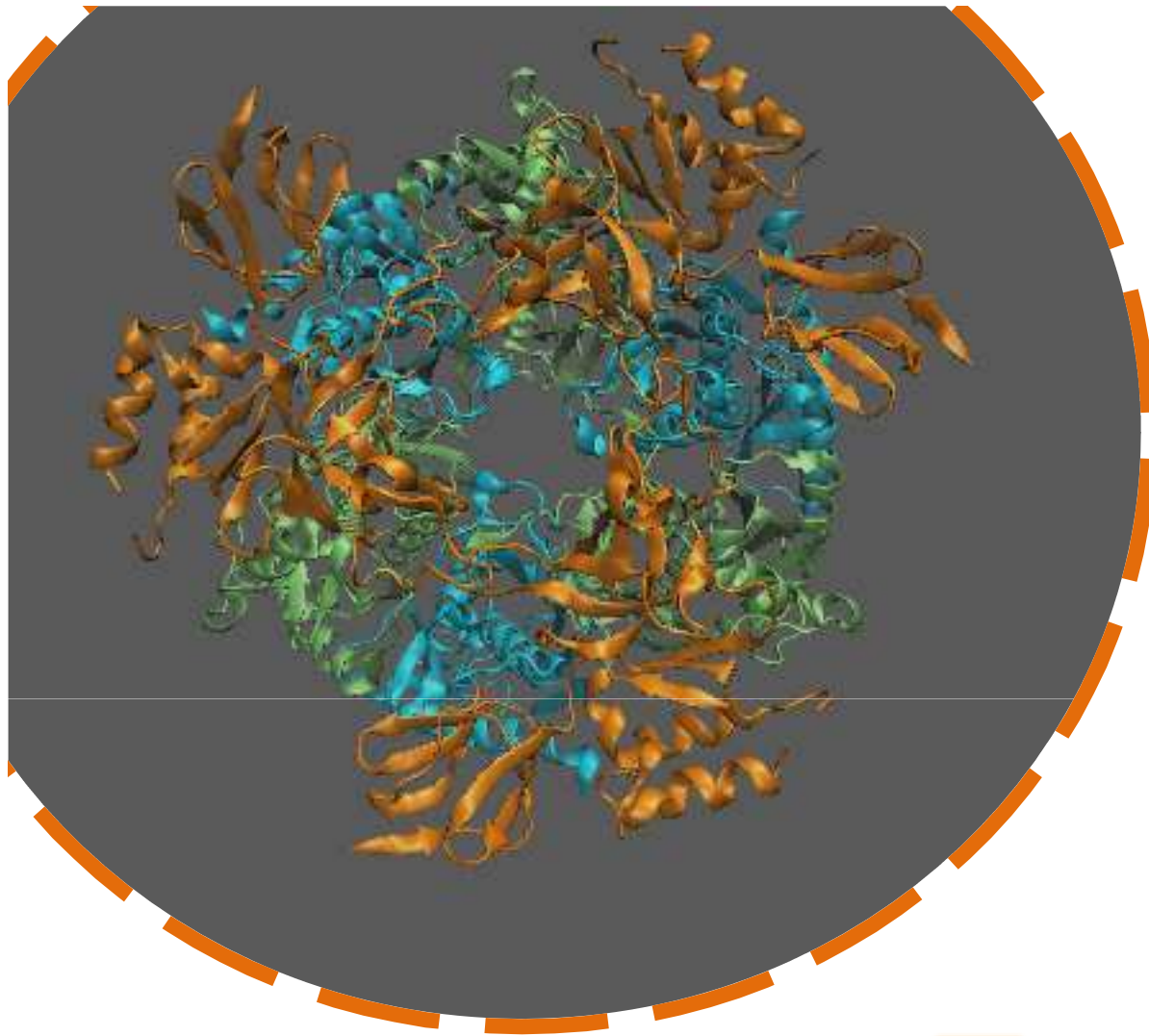


Structural Biology

*Marta Pol, Gerard Prat, Elisa
Ruiz and Raul Sánchez*



The Exosome

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THE ARCHAEL EXOSOME CORE

3.1. Fold

3.2. Interaction between subunits

3.3. Interaction with the RNA

4

EVOLUTION OF THE EXOSOME

4.1. Relationship with the eukaryotic exosome

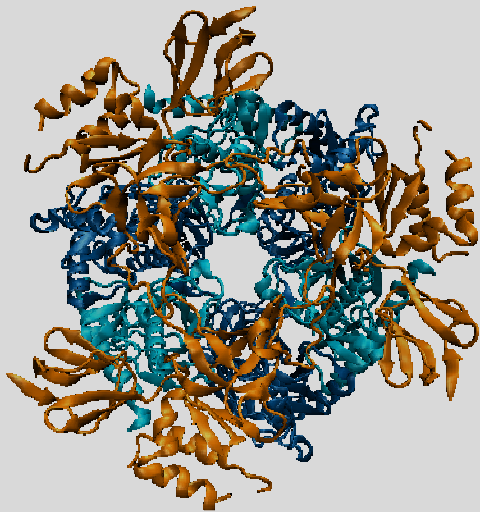
4.2. Evolution of the Cap subunits

4.3. Evolution of the Core subunits

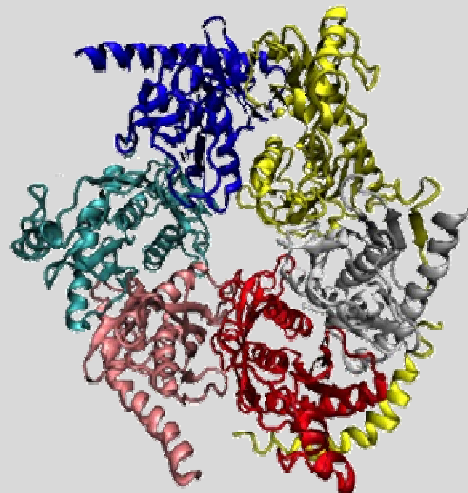
1.1 What's the exosome?

The Exosome is a multiprotein complex with 3'-5' exonuclease activity which can degrade many types of cellular RNAs. It has a critical role in cellular mRNA turnover.

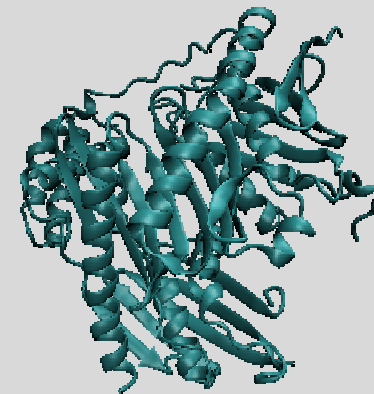
ARCHAEA



EUCARYOTS



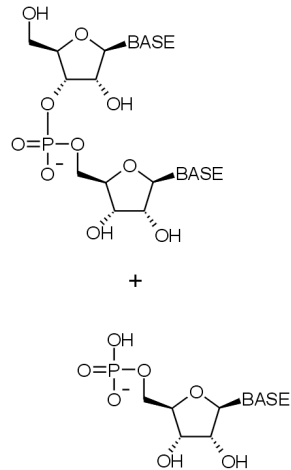
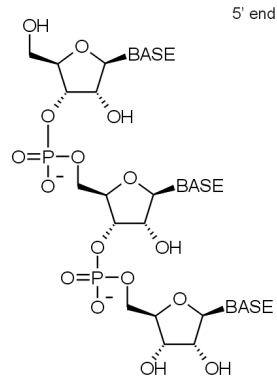
BACTERIA



PNPase & Rnase PH

1.2

The Exosome's Ribonucleolytic activity

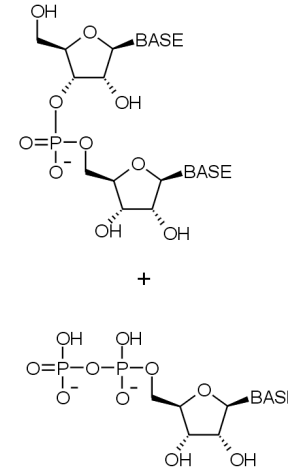
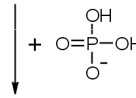
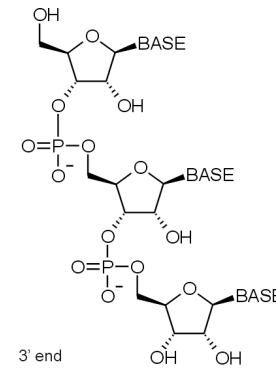


Hydrolytic activity

Uses H₂O molecules to cleave diphosphate bonds.

Nucleotide monophosphates as a product of reaction.

EUKARYOTIC EXOSOME



Phosphorolytic activity

Uses inorganic phosphates to cleave diphosphate bonds.

Nucleotide diphosphates as a product of reaction.

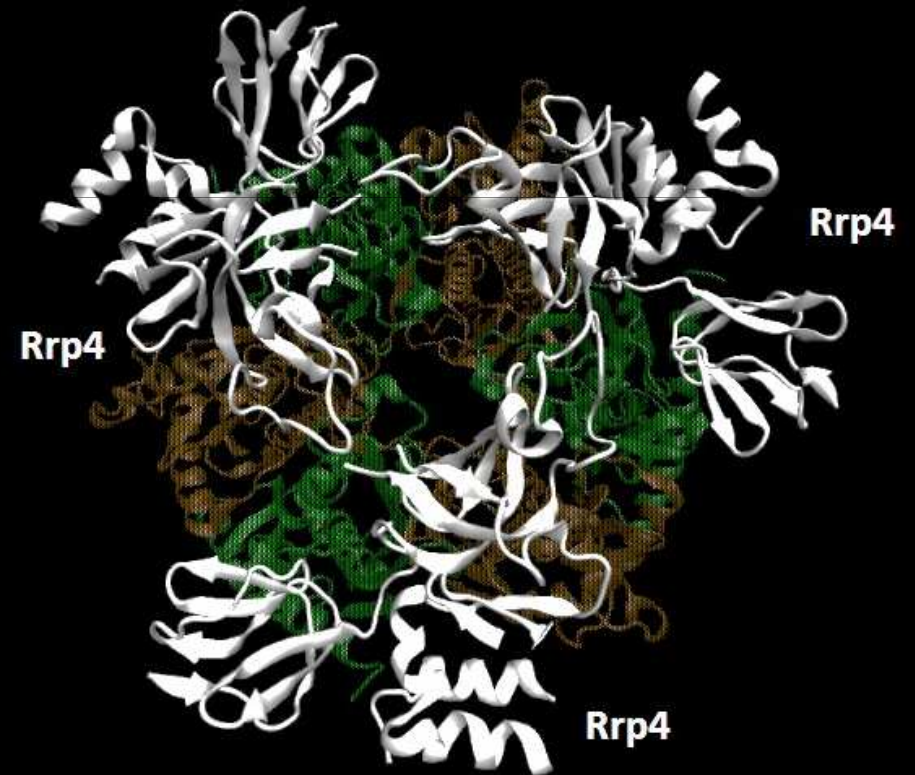
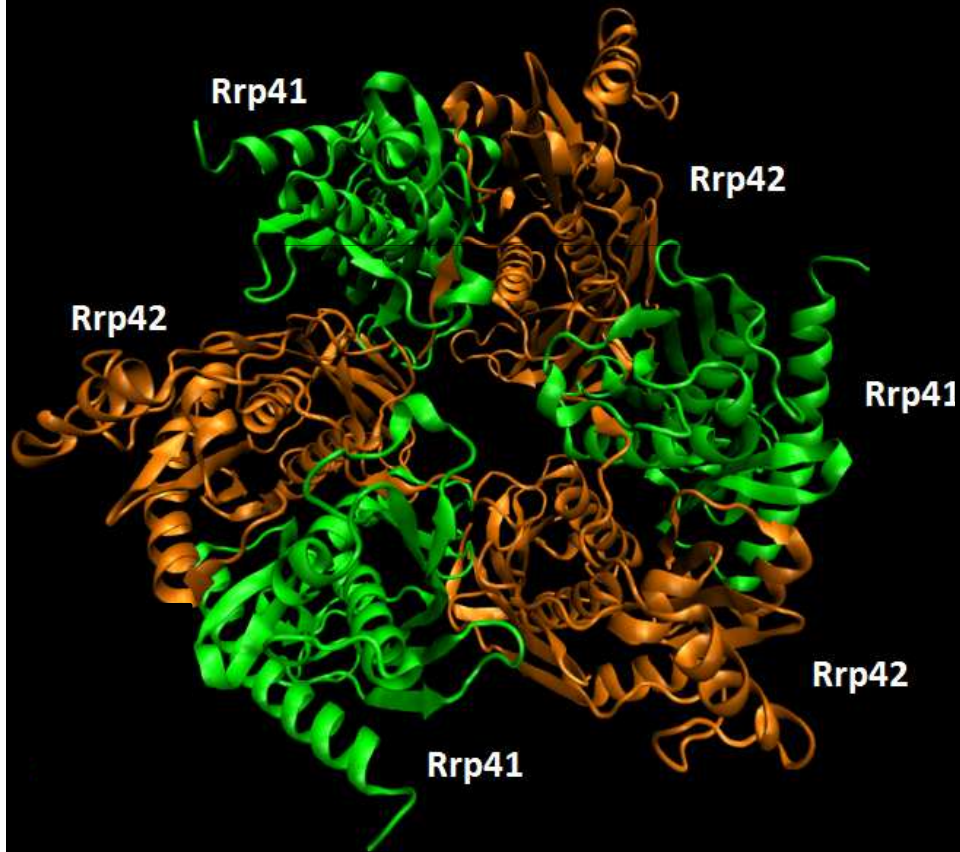
ARCHAEAL EXOSOME

1.1

Exosome structure in archaeae

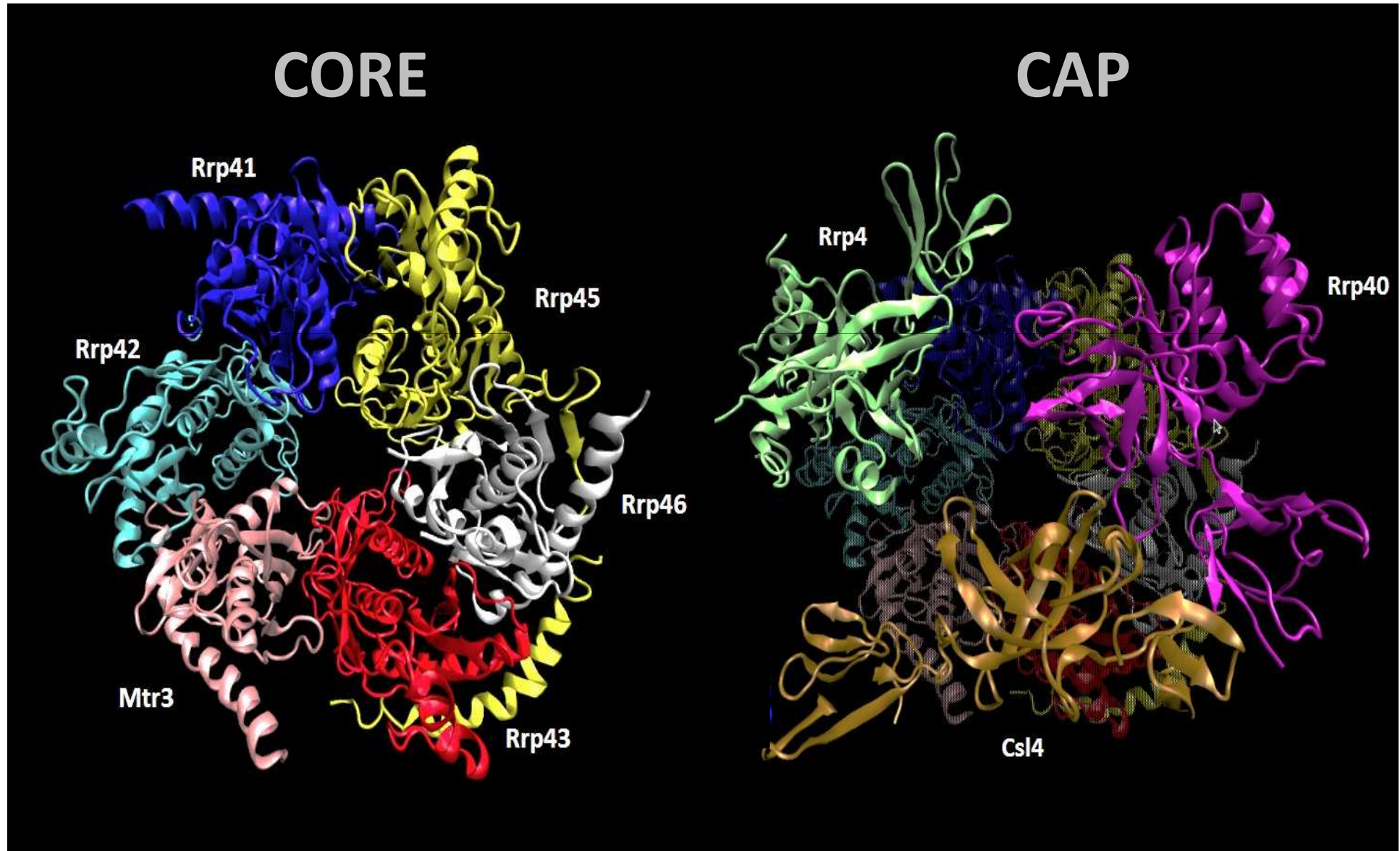
CORE

CAP



1.1

Exosome structure in eukaryots



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- 2.2. Rrp4 Subunit
- 2.3. Core interaction
- 2.4. RNA interaction
- 2.5. Rrp4 vs. Csl4 Subunit

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- 3.1. Fold
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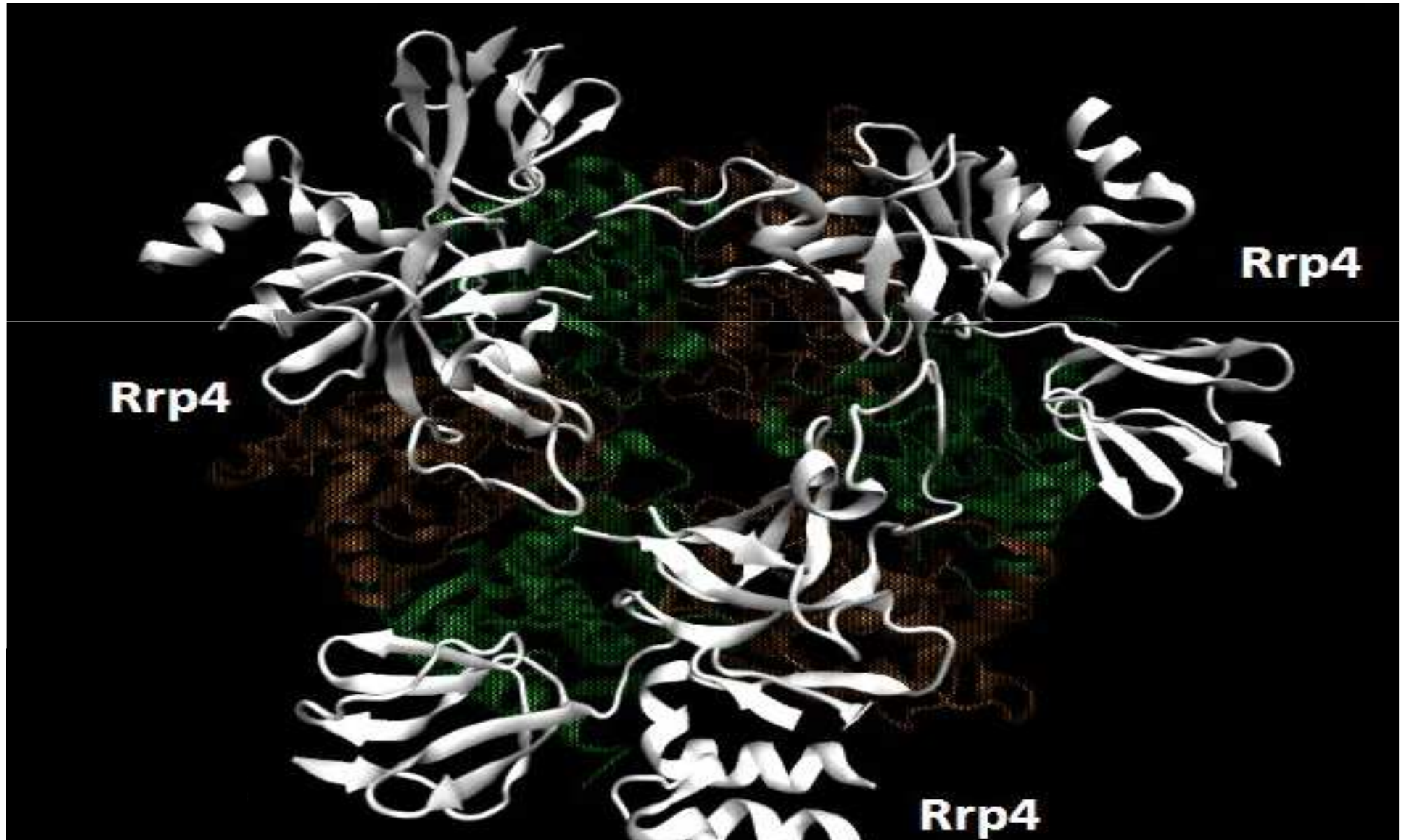
EVOLUTION OF THE EXOSOME

- 4.1. Relationship with the eukaryotic exosome
- 4.2. Evolution of the Cap subunits
- 4.3. Evolution of the Core subunits

2

The archaeal Exosome CAP

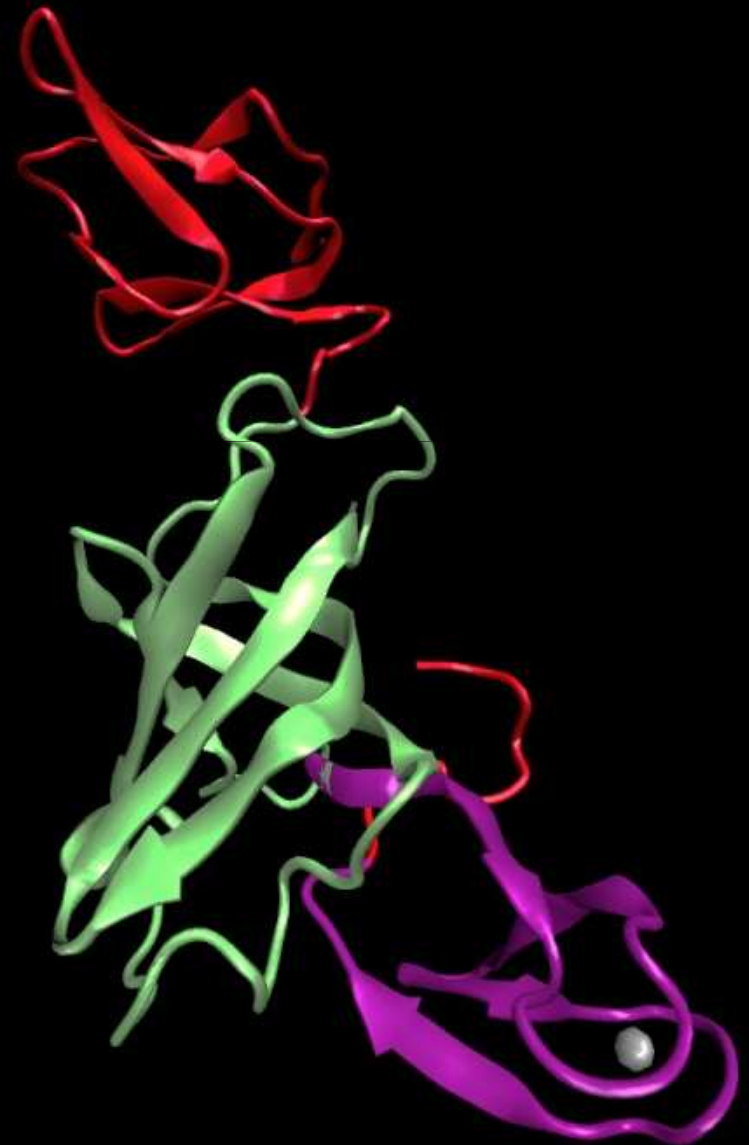
FUNCTION: Select and exclude the RNA substrates.



2.1 Csl4 Subunit

Domains

- N-terminal domain (NTD)
- RNA binding S1
- Zn-ribbons domains

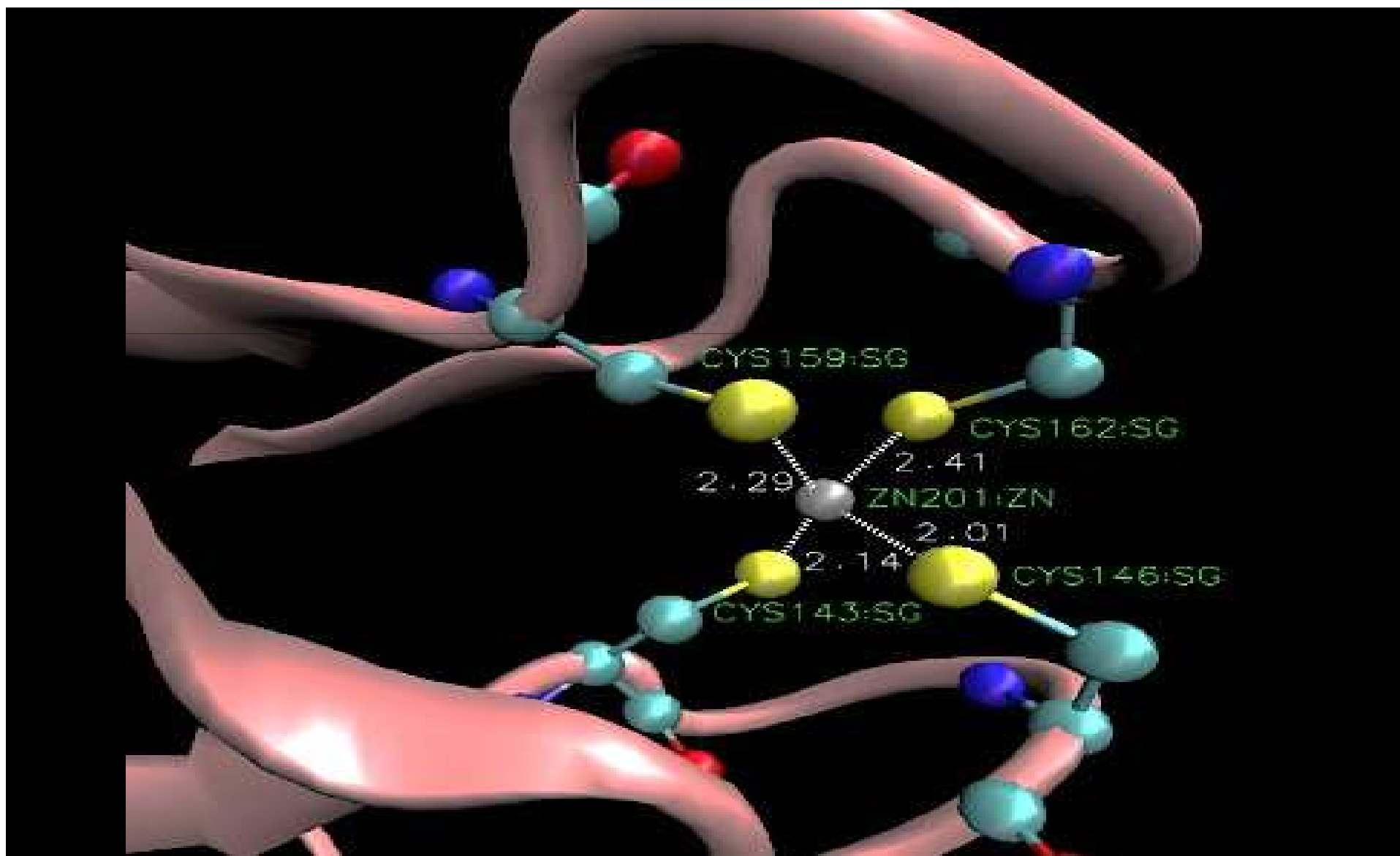


2.1 Csl4 Subunit > Zn-ribbon domain

Lineage:

1. Root: [scop](#)
2. Class: [Small proteins](#) [56992]
Usually dominated by metal ligand, heme, and/or disulfide bridges
3. Fold: [Rubredoxin-like](#) [57769]
metal(zinc or iron)-bound fold; sequence contains two CX(n)C motifs, in most cases $n = 2$
4. Superfamily: [Zinc beta-ribbon](#) [57783]
[Superfamily](#)

2.1 Csl4 Subunit > Zn-ribbon domain

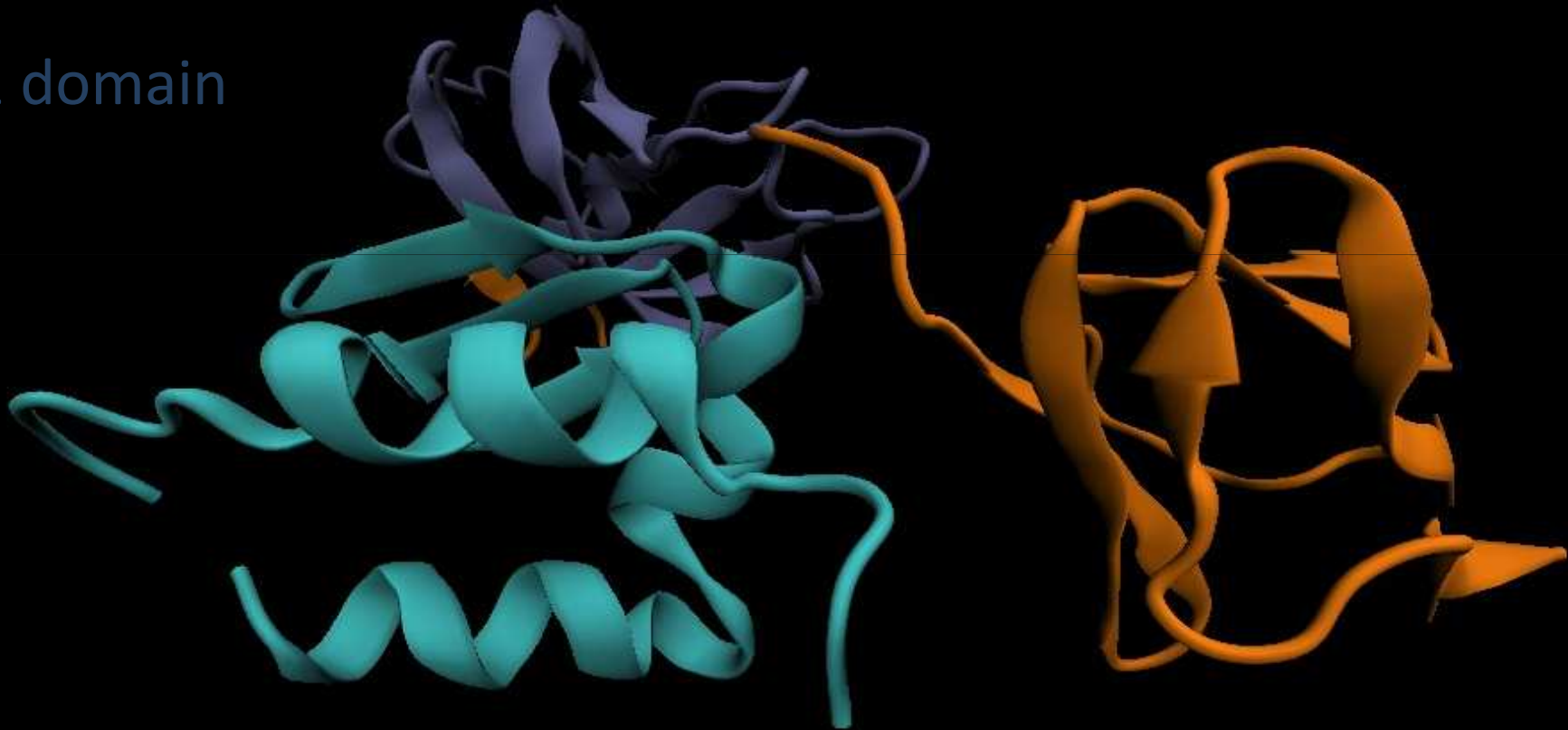


2.2 Rrp4 Subunit

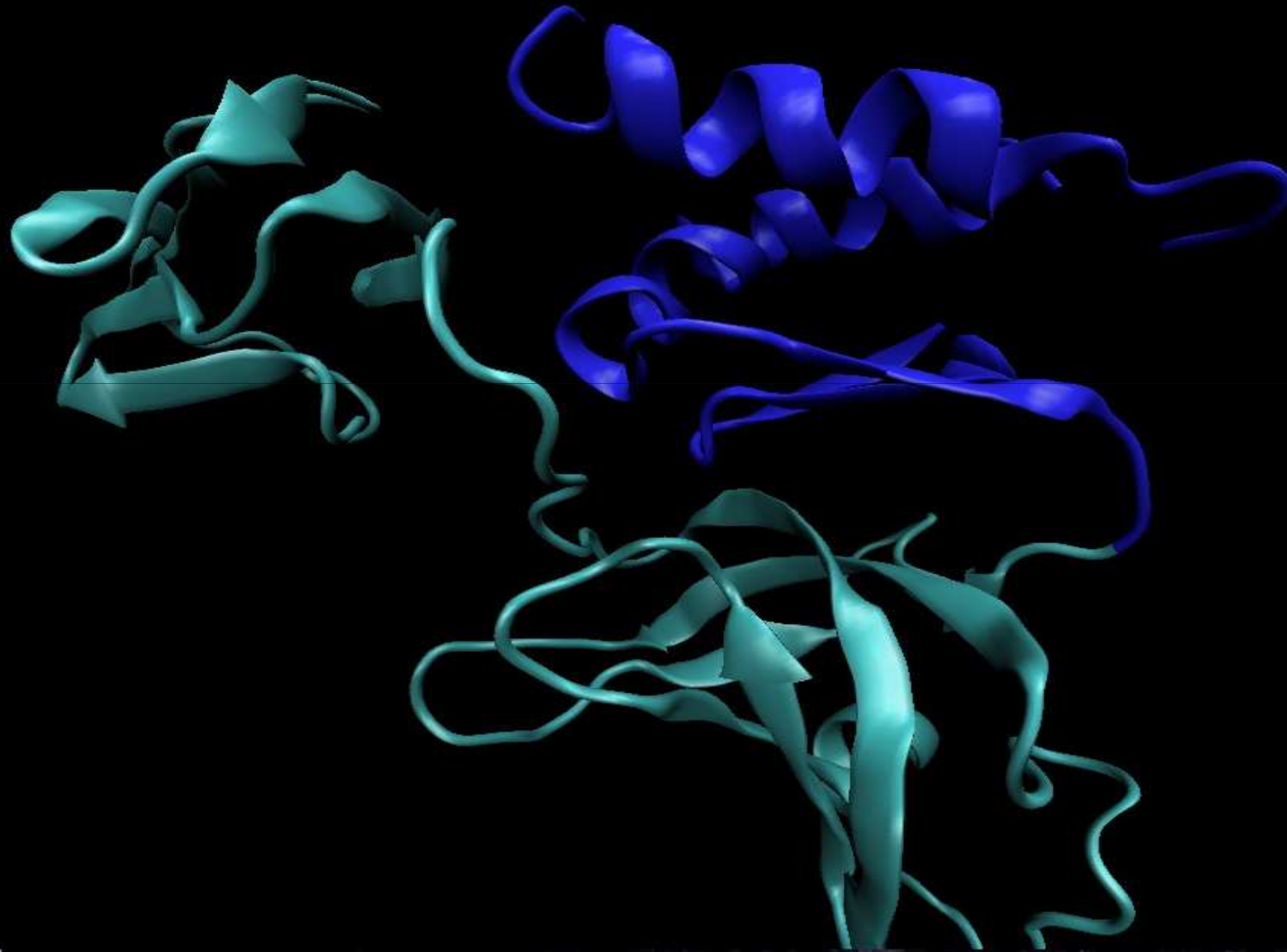
KH domain

NTD

S1 domain



2.2 Rrp4 Subunit > KH domain



2.2 Rrp4 Subunit > KH domain

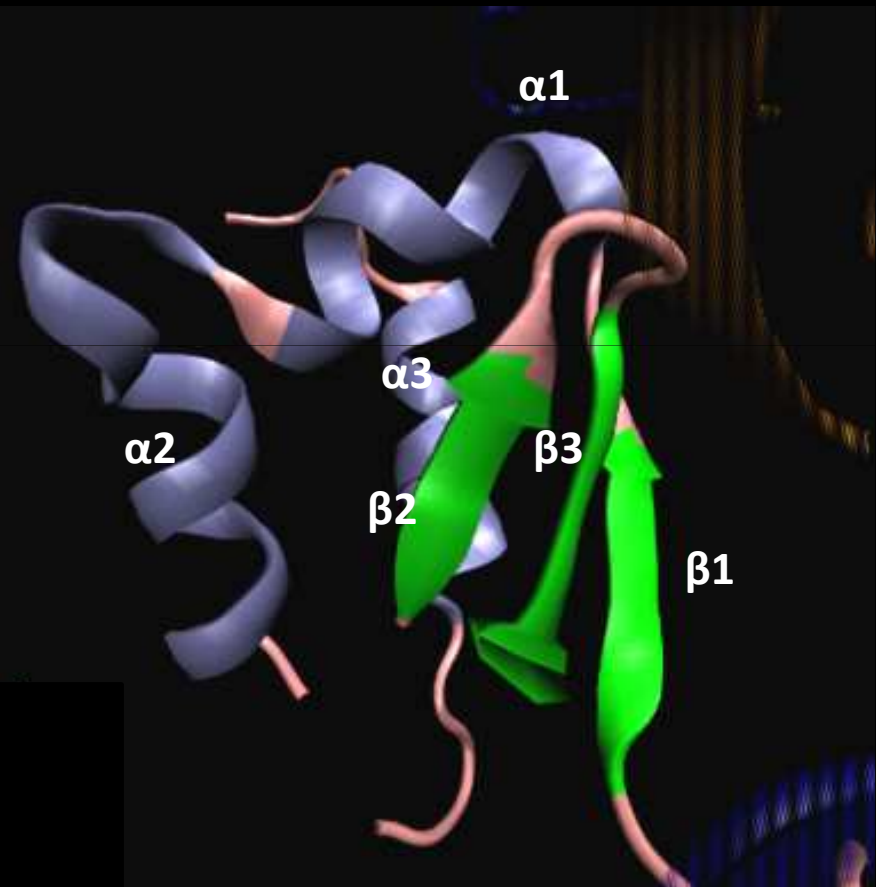
Lineage:

1. Root: [scop](#)
2. Class: [Alpha and beta proteins \(a+b\)](#) [53931]
Mainly antiparallel beta sheets (segregated alpha and beta regions)
3. Fold: [Eukaryotic type KH-domain \(KH-domain type D\)](#) [54790]
beta-alpha(2)-beta(2)-alpha; 2 layers: alpha/beta
4. Superfamily: [Eukaryotic type KH-domain \(KH-domain type D\)](#) [54791]
Prokaryotic and eukaryotic domains share a KH-motif but have different topologies
[Superfamily](#)
5. Family: [Eukaryotic type KH-domain \(KH-domain type D\)](#) [54792]
an RNA-binding domain
6. Protein: Exosome complex RNA-binding protein 1, ECR1 [160229]
7. Species: [Sulfolobus solfataricus \[TaxId: 2287\]](#) [160232]
SQ [Q9UXC4](#) 153-221

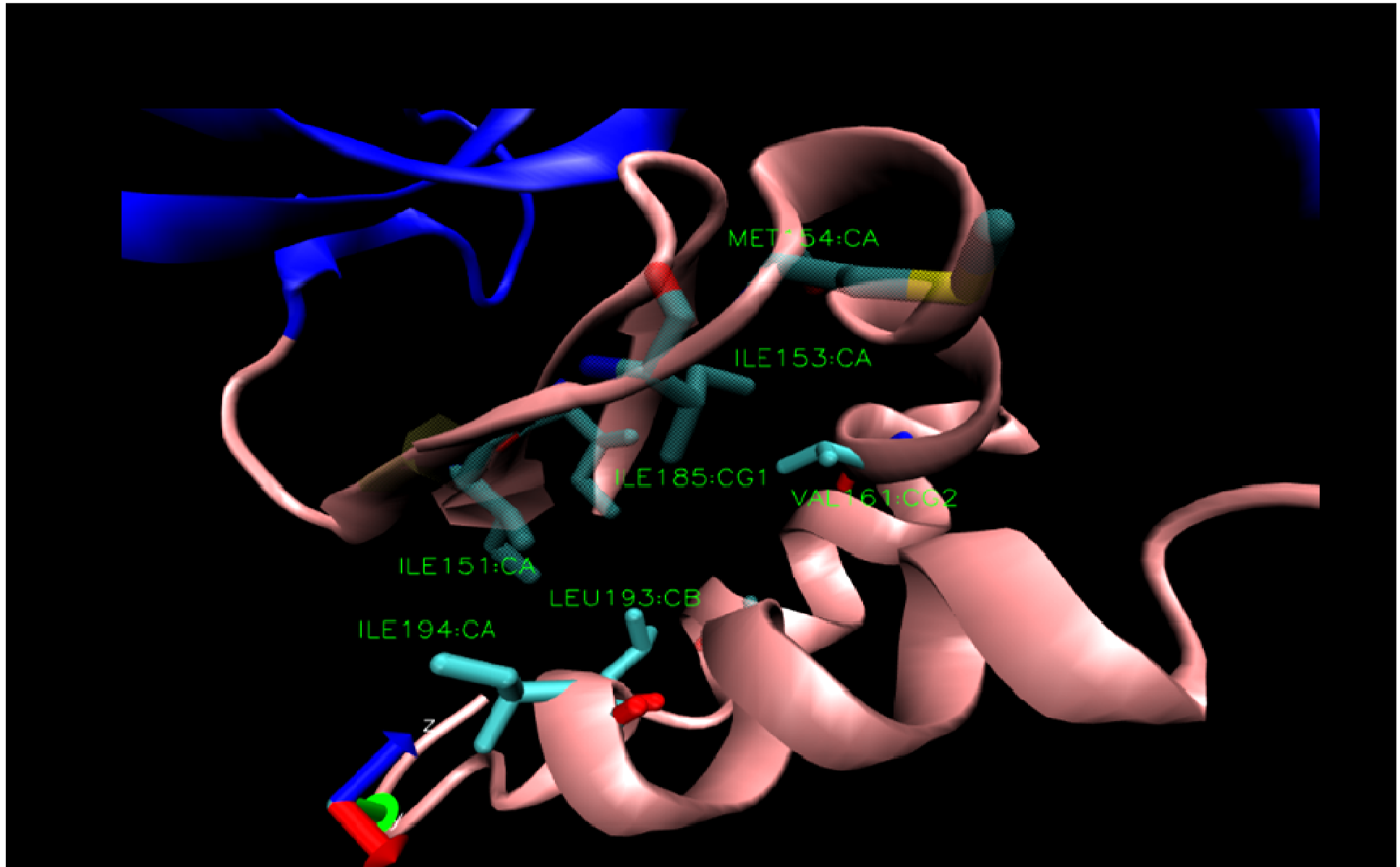
2.2 Rrp4 Subunit > KH domain

Type I KH-domain $\rightarrow \beta\alpha\alpha\beta\beta\alpha$

Characteristic loop (GxNG) but in *S.solfataricus* we find an **AxNG motif**



2.2 Rrp4 Subunit > KH domain



2.2 Rrp4 Subunit > KH domain

Sequence-based alignment: CLUSTALW

```

rrp4_[Sulf/1-197] 1-----KIVLQPR---SIVVPGELLAEGEFQIPWSPYILKINSKYYSTVVG LFDVKDT 49
rrp4_[Aero/1-275] 1MGSSHHHHHSQDPHMAMEMRLPVARKPLSERLGRDTK-KHLVVPGGDTITT-DTGFMRGHGTYMGEELIASVAGSVERVVK 80
rrp4_[Arch/1-179] 1-----MRFVMPGDRIGS-AEEYVKGEVYEEGGELFAAVAGKLIKDR 42
rrp4_[Arab/1-322] 1----MVMRKLQLPLSQTQKVRFERAIERLQSLSSANSASVITDSIPVNHDDAFLKGHGTSEVDGELLATVCG/VERVDK 78
Rrp4_[Caen/1-265] 1-----MSTNAAIDLALDRVDWRDLAAQTEEQPRVYTPGEVLMP-EAGFMRGHGT FVEDENIKSSVAG/IQKVNK 68
rrp4_[Pyro/1-260] 1-----MALEMRLPKARKPLSESLGRDSK-KHLVVPGGDTITT-DTGFMRGHGTYMGEELIASVAGSVERVVK 65
rrp4_[Aede/1-294] 1-----MASNVMIRLASDRANLSLLSGDSN--PRLFTPGEVITS-QQGFMRGHGT YMEGEDIKSSVAG/MVQVVK 66
rrp4_[Meth/1-239] 1-----MPEFELYVEDR---QVVTGELLAR--GQVIASEGTYSGDEVYSKVTG LVDIDGR 51

rrp4_[Sulf/1-197] 50QFEVIPLEGSFYYPKINDIVIGLVEDVEIYGWVVDIKAPYKAYLPAS-----NLLGRSINVGEDLRRYLDVGDYVIAE 124
rrp4_[Aero/1-275] 81LICVKALKTRYI-GEVGDIVVGRITEVQKRWKVETNSRLDSVLLSSMNLPGGELRRRSAEDELAMRGFLQEGDLISAEVQ 161
rrp4_[Arch/1-179] 43VAKVESISPIE-IVKGDVVLGRVVDLRNSIALIEVSSKKGENRGPS--NRGIGLHVSNVDEGYVKEISEAVGYLDILKAR 121
rrp4_[Arab/1-322] 79LVYVRTLRARYK-PEVGDIVVGRVIEVAQKRWRVELNFNQDGV LMLSSMNP DGIQRRRTSVDELNMRNIFVEHVVCAEVR 159
Rrp4_[Caen/1-265] 69LISVRPLKSRYV-GEIGDVVVARVSEVQKRWVVDNLSRLDSILLSSVNLPGGELRRRSAEDELQMMRRYLDQEGDLISAEVQ 149
rrp4_[Pyro/1-260] 66LICVKALKTRYN-GEVGDIVVGRITEVQKRWKVETNSRLDSVLLSSMNLPGGELRRRSAEDELAMRGFLQEGDLISAEVQ 146
rrp4_[Aede/1-294] 67LITVKPLKGRYV-GEIGDVIVARVTDVQKRWKVVDNLSRLDSILLSSVNLPGGELRRRGVEDEQMRKYLQEGDLISAEVQ 147
rrp4_[Meth/1-239] 52RIRVIPLAGPYR-PSPGDFVVGIVEEVKFSSWLDIVRAPLPAI LHV S-----N-AL EEEVDLIETDLSRYRPGDVITAVVR 126

rrp4_[Sulf/1-197] 125NFD-DPVL SVKGKD-----LGRVSN GIVIDIMPVKVPRVIGKN-KSMYETLT----SKFVANNGRIWAIL-----IE 185
rrp4_[Aero/1-275] 162AVFSDGAVSLHTRS----LKYGKLGGQVLVQVSPSLVKR---QK--THFHDLPGASVILGNNGFIWIYP-----TP 224
rrp4_[Arch/1-179] 122VIGDNLRLSTKEEE----MGVLR--ALCSNCKTEMVR---E--GDILKCP-----ECCRVEKRK-----IST 172
rrp4_[Arab/1-322] 160NFQHDGSLQLQARS----QKYGKLEKQQLLKVDPLYVKR---SK--HFFHYVESLGIDLIIIGCNGFIWVGEHVEVRDPMAID 232
Rrp4_[Caen/1-265] 150NIFEEGSLSLYTRS----LKYGKLSQGLLVKVFPA LVKR---RK--MHFHNLP-CGASVILGNNGFIWISP-----TK 212
rrp4_[Pyro/1-260] 147AVFSDGAVSLHTRS----LKYGKLGGQVLVQVSPSLVKR---QK--THFHDLPGASVILGNNGFIWIYP-----TP 209
rrp4_[Aede/1-294] 148NVHSDGVLSLHTRS----LKYGKLGGQILVKVFP SLIKR---RK--THFHNLP-CGASVILGNNGFIWISP-----IV 210
rrp4_[Meth/1-239] 127EVDPVQRVELSLLLEDDAPTRLGRLLQGQVVEIDPVKVP RVIGRKGSMIKMLKRVLGCDIVVGANGRIYVRA-----RE 199

rrp4_[Sulf/1-197] 186AIRKIEN--ESHIK----- 197
rrp4_[Aero/1-275] 225EHKEEEA--GGFIANLEPVSLA-DREVISRLRNCIISLVTQRMMLYDTSILYCY 275
rrp4_[Arch/1-179] 173DYGKGEW----- 179
rrp4_[Arab/1-322] 233DQKDEEMISSSTGKEQSHIPLETQRTICRIGNAIRVLSNLGFTVTLEVIMETVNLSNSKNIDIHMLGSEFHVVAENEAE 314
Rrp4_[Caen/1-265] 213GQEEEGGE--GGFAQNLNEHVPRADREVIARLRNSILALAKCKLMIYDTSIQYAY 265
rrp4_[Pyro/1-260] 210EHKDEDA--GGFIANLEPVSLA-DREVISRLRNCVLLVTQRMMLFDTSILYCY 260
rrp4_[Aede/1-294] 211NTEGEEG--GGFTQNL EESISKQDREVISRLRNCVLLANCKMMLYDTSILYAYEES--LKYEVHELLHQEAMFDIAFLTQH 288
rrp4_[Meth/1-239] 200E-PKKER--ELLAVRAIREIER-----R-SHLRGLTDWLKANLKR LSRW----- 239

```


2.2 Rrp4 Subunit > KH domain

Structure-based alignment: STAMP

```
A.fulgidus_Rrp4/1 1 - - - - - RKIVLP GDLL - STNPRAAGY - GTYVEGGKVYAKII GLFDQ - TETHVRVIP LK 49
S.solfataricus_Rrp 1 QEIVLQPR SIVVPGE LLAEGEFQIPWSPYILKINSKYYSTVV GLFDVKD - TQFEVIP LE 58

A.fulgidus_Rrp4/1 50 C - RYTPSVGDV VIGI IREVAANGWAVDIYSPYQAF LPVSENPEMKPN - - KK - PNEVLDI 104
S.solfataricus_Rrp 59 CSFYYPKINDIVIGLVEDVEIYCWVVDIKAPYKAYLPASN - LLGRSINVGEDLRRLDY 116

A.fulgidus_Rrp4/1 105 CDAI IAKVLNIDPKMKVT LTMKDRICRP IRFGRIVAINPARVPRVIGKKGSMIKLLKSE 163
S.solfataricus_Rrp 117 CDYV IARIENFDRSIDPVL SVK GKDLGRVSN GIVIDIMPVKVPRVIGKNKSMYETLTSK 175

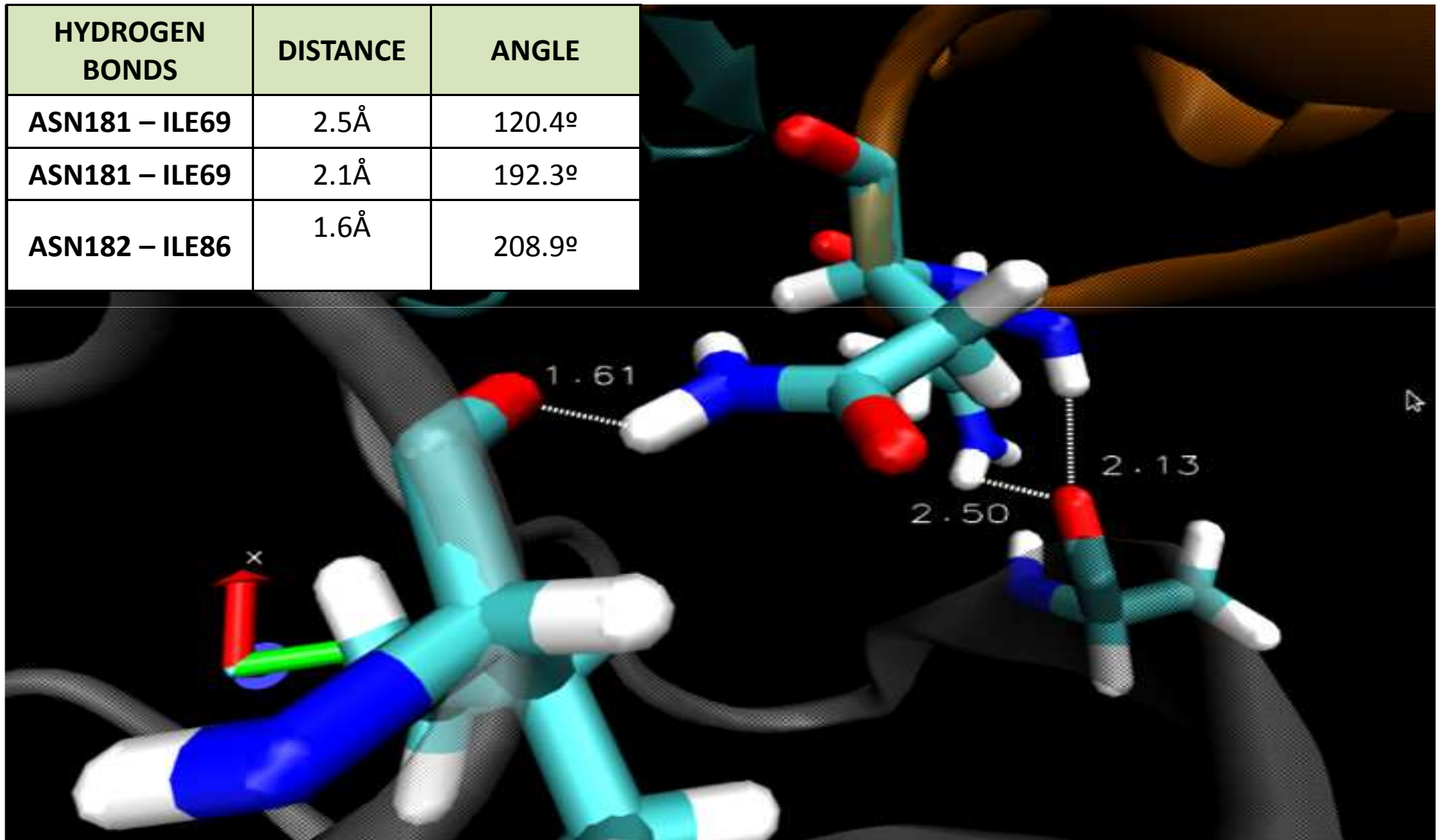
A.fulgidus_Rrp4/1 164 LDVQIVVGQNGLIWVNGDRRKVS - TAE EAIYLT EQEA - - HTEGLTDRVAEFIKRRKAD 218
S.solfataricus_Rrp 176 - - S - IFVANNGRIW - - AF - - - SEEI LIEAIRKI - - ENESH IK - - - - - 207
```

Pair	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs	%I	%S	P(m)
	1	2BA0	2JE6I	5.14	2.49	218	207	212	148	145	0	44.83	100.00	2.98e-27

2.2 Rrp4 Subunit > KH – S1 interaction

Interaction between S1 and KH domain stabilized by hydrogen bonds.

HYDROGEN BONDS	DISTANCE	ANGLE
ASN181 – ILE69	2.5Å	120.4°
ASN181 – ILE69	2.1Å	192.3°
ASN182 – ILE86	1.6Å	208.9°



2.2 Rrp4 Subunit > S1 domain

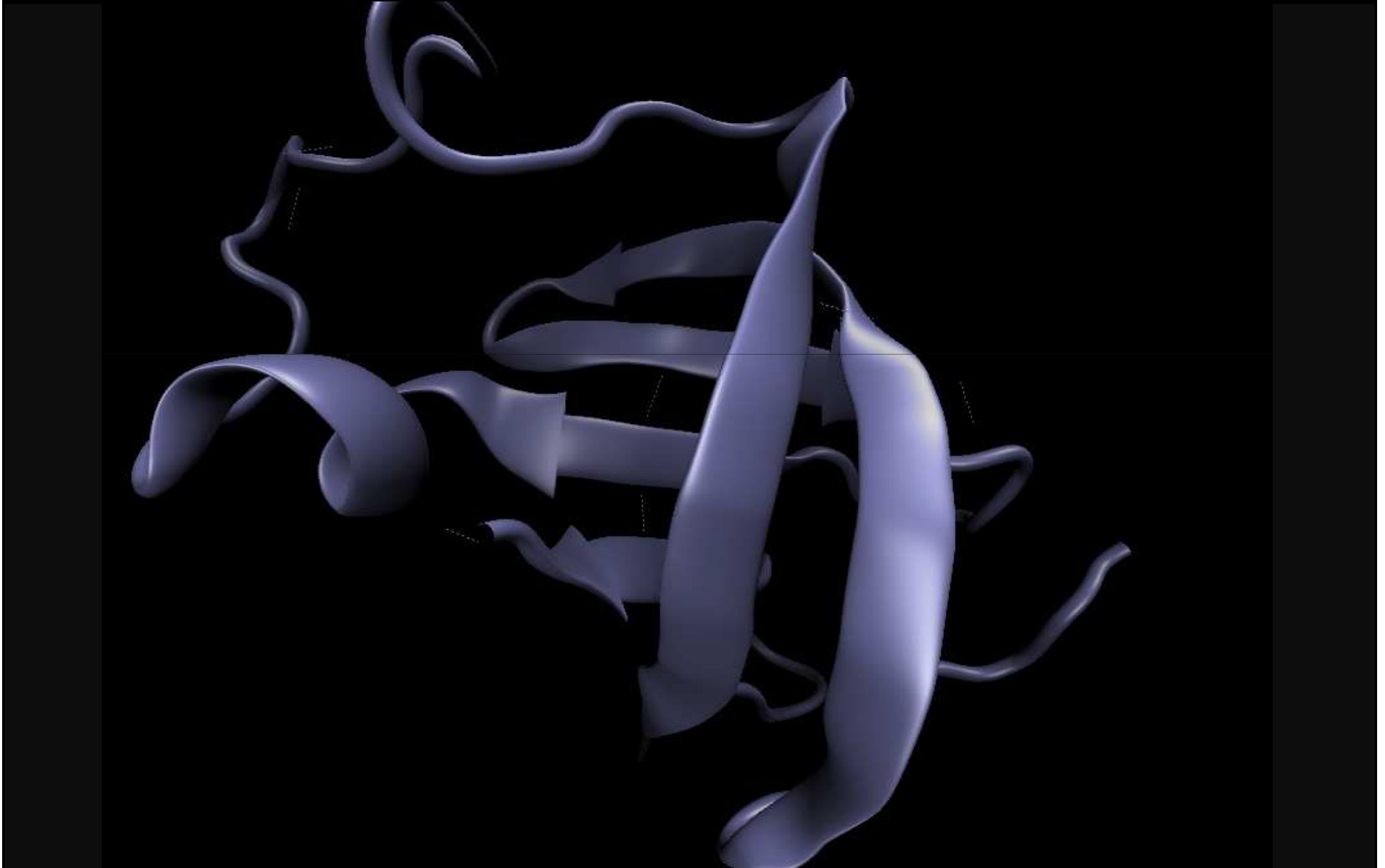


2.2 Rrp4 Subunit > S1 domain

Lineage:

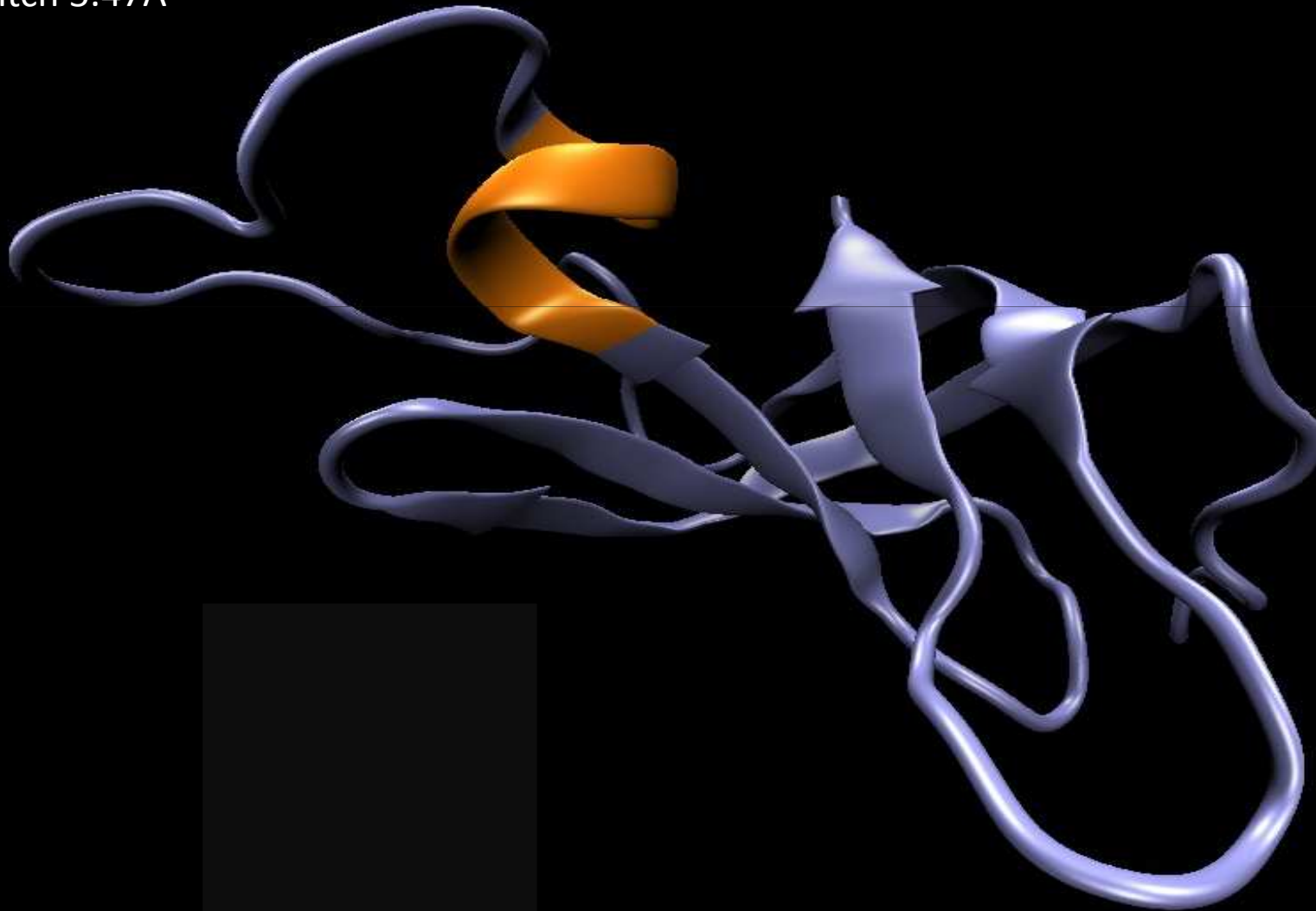
1. Root: [scop](#)
2. Class: [All beta proteins](#) [48724]
3. Fold: [OB-fold](#) [50198]
barrel, closed or partly opened $n=5$, $S=10$ or $S=8$; greek-key
4. Superfamily: [Nucleic acid-binding proteins](#) [50249]
[Superfamily](#)
5. Family: [Cold shock DNA-binding domain-like](#) [50282]
barrel, closed; $n=5$, $S=8$
6. Protein: Eukaryotic initiation factor 2alpha, eIF2alpha, N-terminal domain [74950]
7. Species: [Sulfolobus solfataricus](#) [TaxId: 2287] [141310]
SQ [Q97Z79](#) 1-84

2.2 Rrp4 Subunit > S1 domain

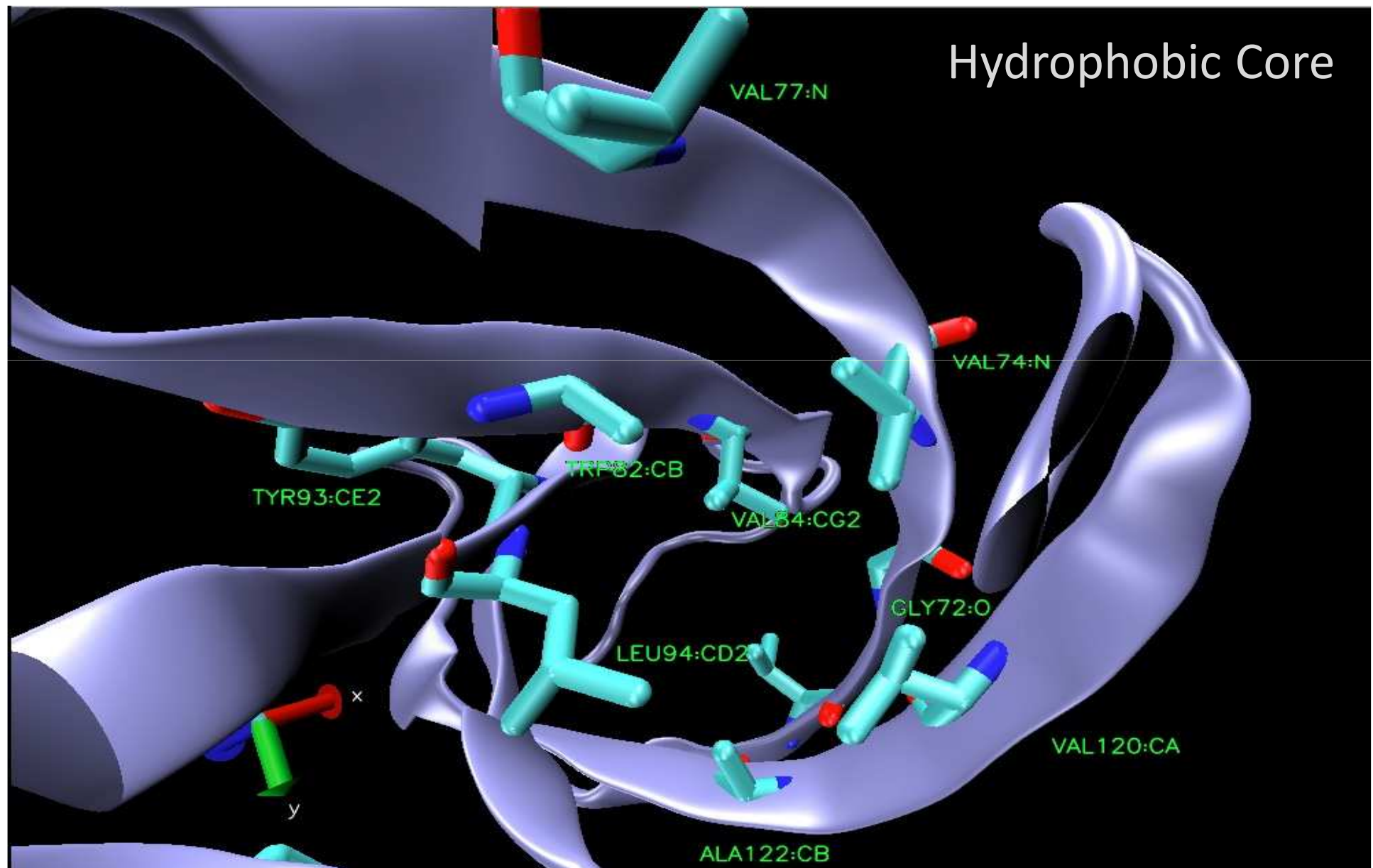


2.2 Rrp4 Subunit > S1 domain

Pitch 5.47Å



2.2 Rrp4 Subunit > S1 domain



2.2

Rrp4 Subunit > S1 domain

Sequence-based alignment: CLUSTALW

```

rrp4_[Sulf/1-197] 1-----KIVLQPR---SIVVPGELLAEGEFQIPWSPYILKINSKYYSTVVG-LFDVKDT 49
rrp4_[Aero/1-275] 1MGSSHHHHHSQDPHMAMEMRLPVARKPLSERLGRDTK-KHLVVPGDTITT-DTGFMRGHGTVMGEEKLIASVAGSVERVNK 80
rrp4_[Arch/1-179] 1-----MRFMVPGDRIGS-AEEYVKGEVYEEGGELFAAVAGKLIKDR 42
rrp4_[Arab/1-322] 1----MVMRKQLPLLSQTQKVRFERAIERLQSLSSANSASVITDSIPVNHDDAFLKGHGTSEVDGELLATVCG/VERVDK 78
Rrp4_[Caen/1-265] 1-----MSTNAAILDLDRVDWRDLAAQTEEQPRVYTPGEVLMPEAGFMRGHGTVEEDENIKSSVAG/IQKVNK 68
rrp4_[Pyro/1-260] 1-----MALEMRLPKARKPLSESLGRDSK-KHLVVPGDTITT-DTGFMRGHGTVMGEEKLIASVAGSVERVNK 65
rrp4_[Aede/1-294] 1-----MASNVMIRLASDRANLSLLSGDSN--PRLFTPGEVITS-QQGFMRGHGTVMGEDIKSSVAG/MVQVNK 66
rrp4_[Meth/1-239] 1-----MPEFELYVEDR---QVVTGELLAR--GQVIASECTYTSGDEVYSKVTGLVDIDGR 51

rrp4_[Sulf/1-197] 50QFEVIPLEGSFYYPKINDIVIGLVEDVEIYGWVVDIKAPYKAYLPAS-----NLLGRSINVGEDLRRYLVDVGYVVARIE 124
rrp4_[Aero/1-275] 81LICVKALKTRYI-GEVGDIVVGRITEVQKRWKVETNSRLDSVLLSSMNLPGGELRRRRAEDELAMRGFLQEGDLISAEVQ 161
rrp4_[Arch/1-179] 43VAKVESISPIE-IVKGDVVLRVVDLRNSIALIEVSSKKGENRGP--NRGIGLHVSNVDEGYVKEISEAVGYLDILKAR 121
rrp4_[Arab/1-322] 79LVYVRTLRARYK-PEVGDIVVGRVIEVAQKRWVVELNFNQDGVMLSSMMPDGIQRRRTSVDLNMNRNIFVEHGVVCAEVR 159
Rrp4_[Caen/1-265] 69LISVRPLKSRYV-GEIGDVVVARVSEVQKRWVVDNLSRLDSILLSSVNLPGGELRRRRAEDELQMMRRYLDEGDLISAEVQ 149
rrp4_[Pyro/1-260] 66LICVKALKTRYN-GEVGDIVVGRITEVQKRWKVETNSRLDSVLLSSMNLPGGELRRRRAEDELAMRGFLQEGDLISAEVQ 146
rrp4_[Aede/1-294] 67LITVKPLKGRYV-GEIGDVIVARVTDVQKRWKVVDNLSRLDSILLSSVNLPGGELRRRGVEDEQQMRKYLQEGDLISAEVQ 147
rrp4_[Meth/1-239] 52RIRVIPLEAGPYR-PSPGDFVVGIVEEVKFSSWLIDVRAPLPAI LHV-----N-ALLEEVDLIETDLSRYRPGDVITAVVR 126

rrp4_[Sulf/1-197] 125NFD-DPVLGVKGD-----LGRVSNIVIDIMPVKVPRVIGKN-KSMYETLT----SKFVANNGRIWAIL-----IE 185
rrp4_[Aero/1-275] 162AVFSDGAVSLHTRS----LKYGKLGQGLVQVSPSLVKR---QK--THFHDLPCGASVILGNNGFIWIYP-----TP 224
rrp4_[Arch/1-179] 122VIGDNLRLSTKEE-----MGVLR--ALCSNCKTEMVR---E--GDILKCP-----ECCRVEKRK-----IST 172
rrp4_[Arab/1-322] 160NFQHDGSLQLQARS---QKYGKLEKQLLKVDPLYVKR---SK--HFFHYVESLGIDLIGCNGFIWVGEHVEVRDPMAD 232
Rrp4_[Caen/1-265] 150NIFEEGSLSLYTRS---LKYGKLSQGLLVKVFPAALVKR---RK--MHFHNLP-CGASVILGNNGFIWISP-----TK 212
rrp4_[Pyro/1-260] 147AVFSDGAVSLHTRS---LKYGKLGQGLVQVSPSLVKR---QK--THFHDLPCGASVILGNNGFIWIYP-----TP 209
rrp4_[Aede/1-294] 148NVHSDGVLSLHTRS---LKYGKLGQGLLVKVFPSLIKR---RK--THFHNLP-CGASVILGNNGFIWISP-----IV 210
rrp4_[Meth/1-239] 127EVDPVQRVELSLLLEDDAPTRLRLQGCQVVEIDPVKVP RVIGRKGSIMKMLKRVLCGDIVVGANGRIYVRA-----RE 199

rrp4_[Sulf/1-197] 186AIRKIEN--ESHIK----- 197
rrp4_[Aero/1-275] 225EHKEEEA--GGFIANLEPVSLA-DREVISRRLRNCIISLVTQRMMLYDTSILYCY 275
rrp4_[Arch/1-179] 173DYGKGW----- 179
rrp4_[Arab/1-322] 233DQKDEEMISSSTGKEQSHIPLETQRTICRIGNAIRVLSNLGFTVTLEVIMETVNLNSKNIDIHDMLGSEFHVVAENAE 314
Rrp4_[Caen/1-265] 213GQEEEGGE--GGFAQNLNEHVPRADREVIARLRNSILALAKCKLMIYDTSIQYAY 265
rrp4_[Pyro/1-260] 210EHKDEDA--GGFIANLEPVSLA-DREVISRRLRNCVLLVTQRMMLYDTSILYCY 260
rrp4_[Aede/1-294] 211NTEGEEG--GGFTQNLSEESISKQDREVISRLRNCVLLANCKMMLYDTSILYAYEES--LKYEVHELLHQEAMFDIAFLTQH 288
rrp4_[Meth/1-239] 200E-PKKER--ELLAVRAIREIER-----R-SHLRGLTDWLKANLKRLSRW----- 239

```

2.2 Rrp4 Subunit > S1 domain

Structure-based alignment: STAMP

```

A.fulgidus_Rrp4/1 1 - - - - - RKIVLP GDLL - STNPRAAGY - GTYVEGGKVYAKII GLFDQ - TETHVRVIP LK 49
S.solfataricus_Rrp 1 QEIVLQPR SIVVPGELLAEGEFQIPWSPYILKINSKYYSTVVGLFDVKD - TQFEVIPLE 58

A.fulgidus_Rrp4/1 50 C - R YTP SVGDV VIGI IREVAANGWAVDIYSPYQAF LPVSENPEMKPN - - KK - PNEVLDI 104
S.solfataricus_Rrp 59 CSFYYPKINDIVIGLVEDVEIYCWVVDIKAPYKAYLPASN - LLGRSINVGEDLRRYLDV 116

A.fulgidus_Rrp4/1 105 CDAI IAKVLNIDPKMKVT LTMKDRICRP IRFGRIVA INPARVPRVIGKKGSMIKLLKSE 163
S.solfataricus_Rrp 117 CDYV IARIENFDRSIDPVL SVK GKDLGRVSN GIVIDIMPVKVPRVIGKNKSMYETLTSK 175

A.fulgidus_Rrp4/1 164 LDVQ I VVGQNGLIWVNGDRRKVS - TAE EAIYLT EQEA - - HTEGLTDRVAEFI KRRKAD 218
S.solfataricus_Rrp 176 - - S - IFVANNGRIW - - AF - - - SEE I L I E A I R K I - - E N E S H I K - - - - - 207

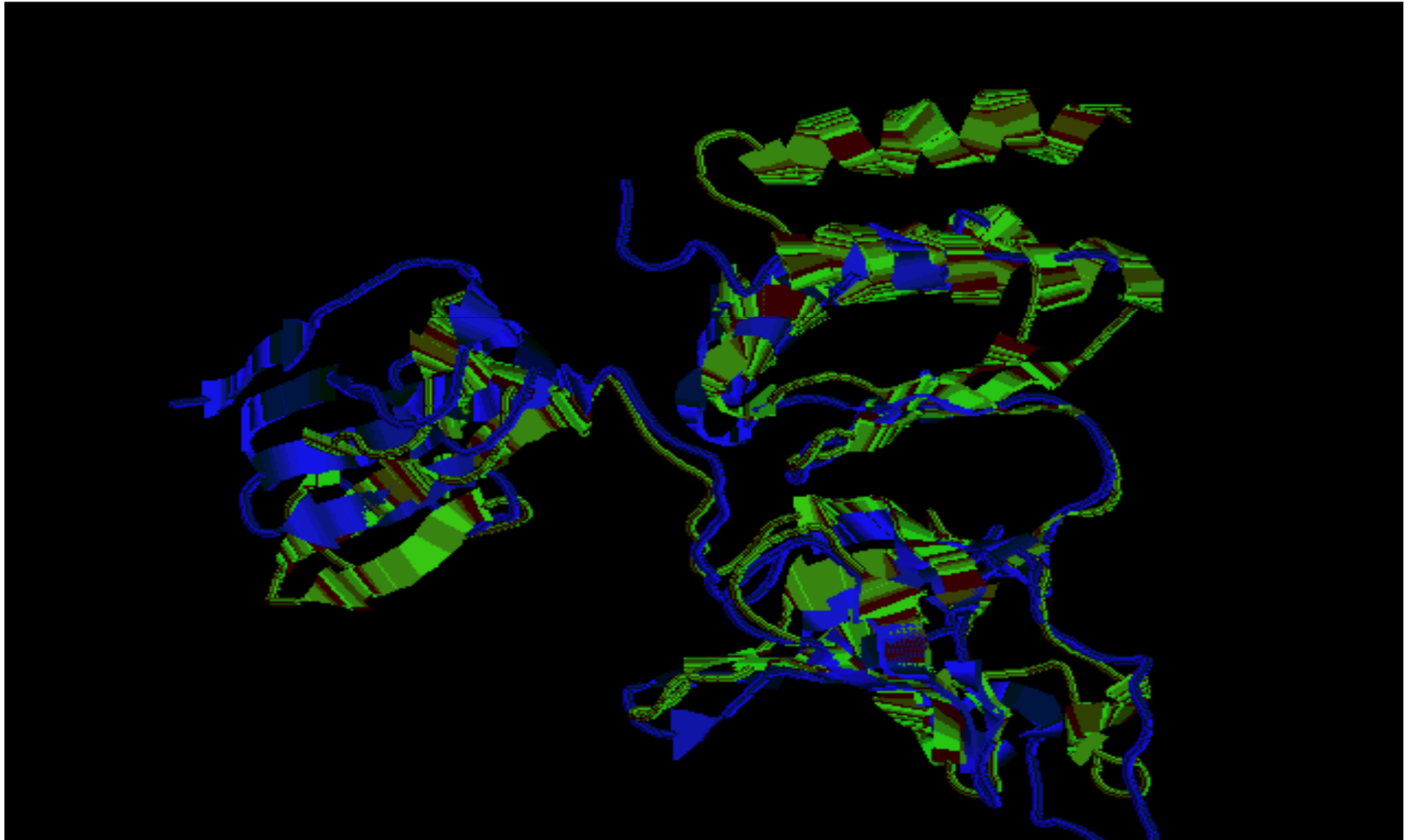
```

Pair	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs	%I	%S	P(m)
1	2BA0	2JE6I	5.14	2.49	218	207	212	148	145	0	44.83	100.00	2.98e-27	

2.2

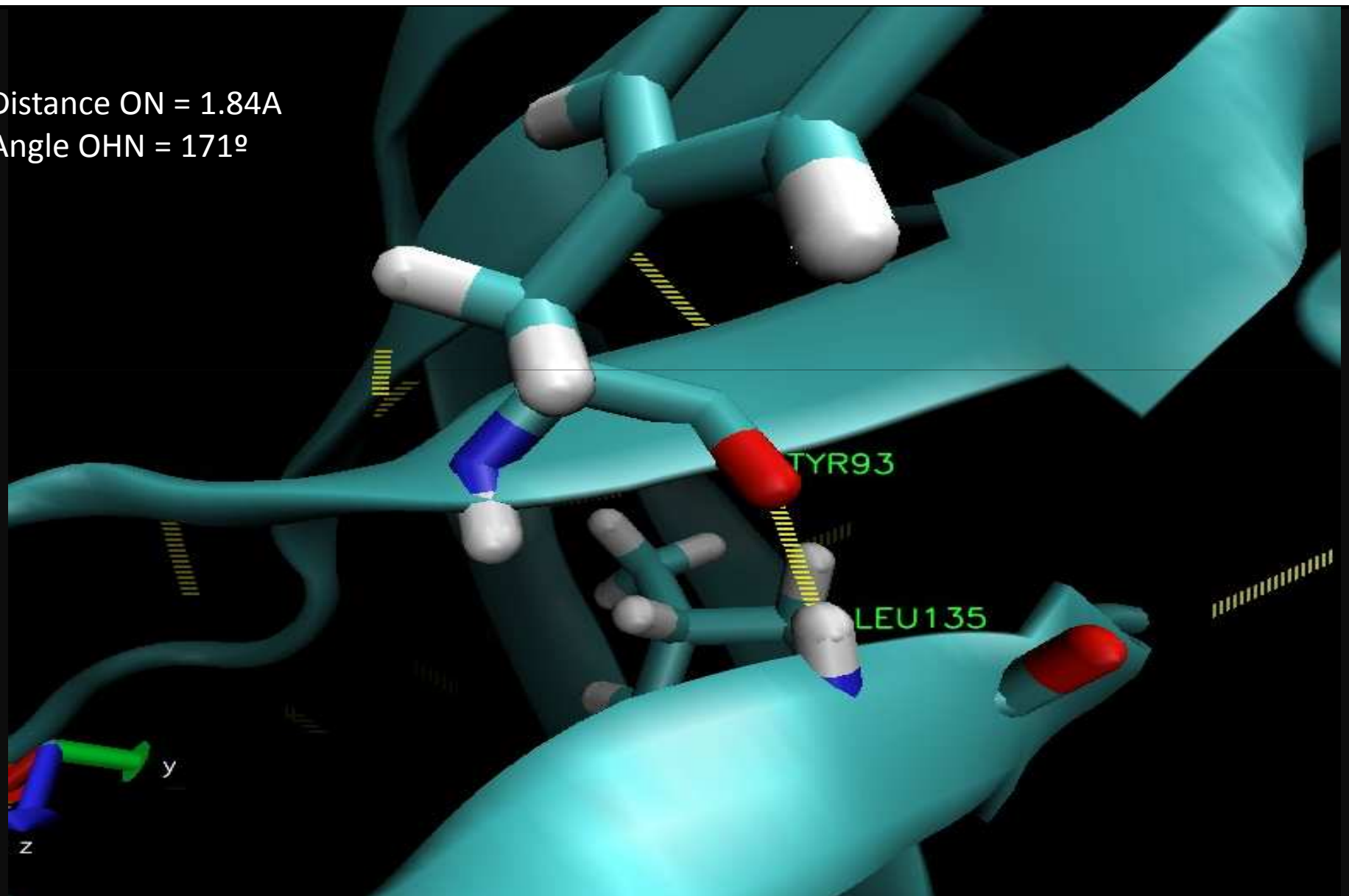
Rrp4 Subunit > S1 domain

Structure-based alignment: STAMP



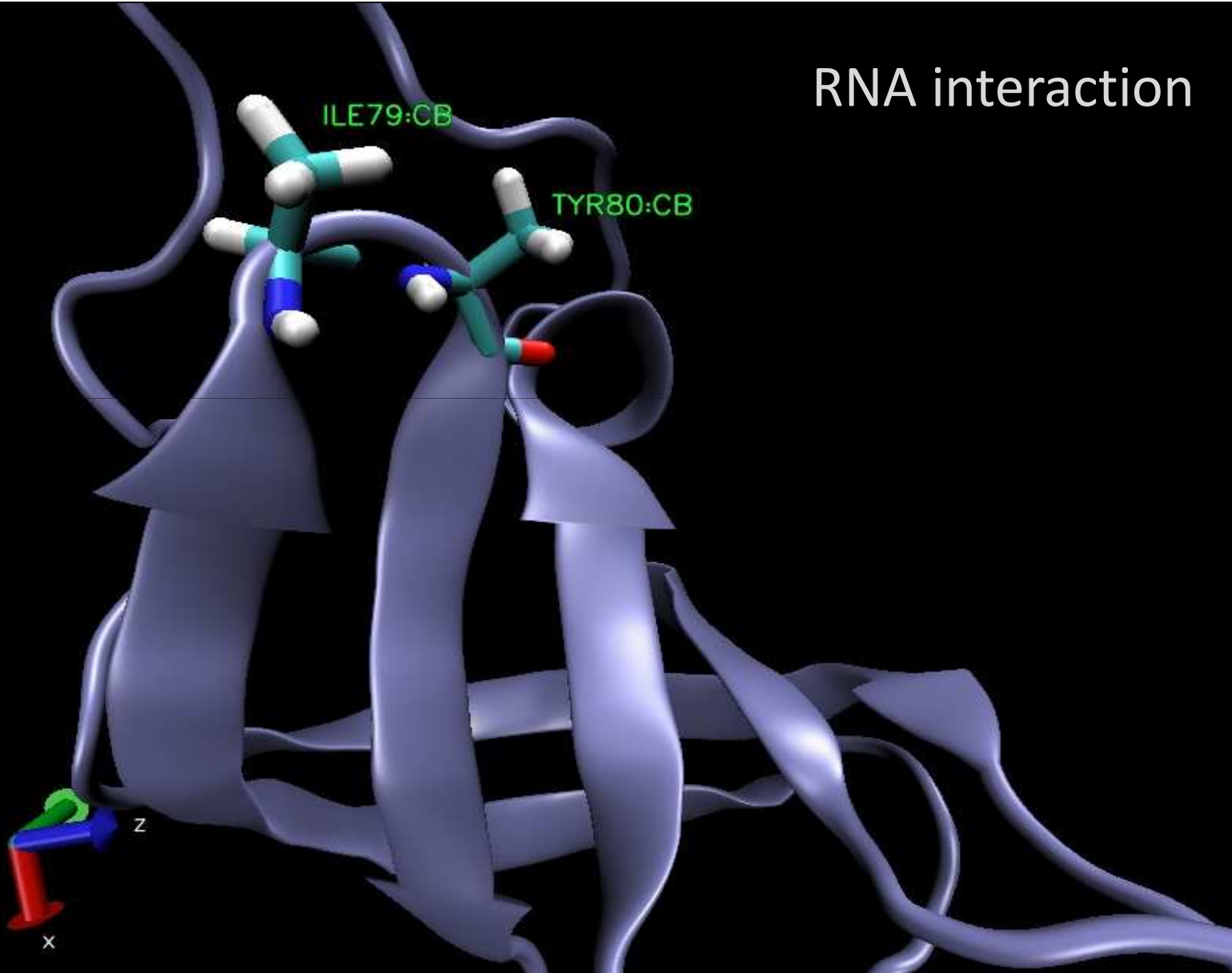
2.2 Rrp4 Subunit > S1 domain

Distance ON = 1.84Å
Angle OHN = 171°



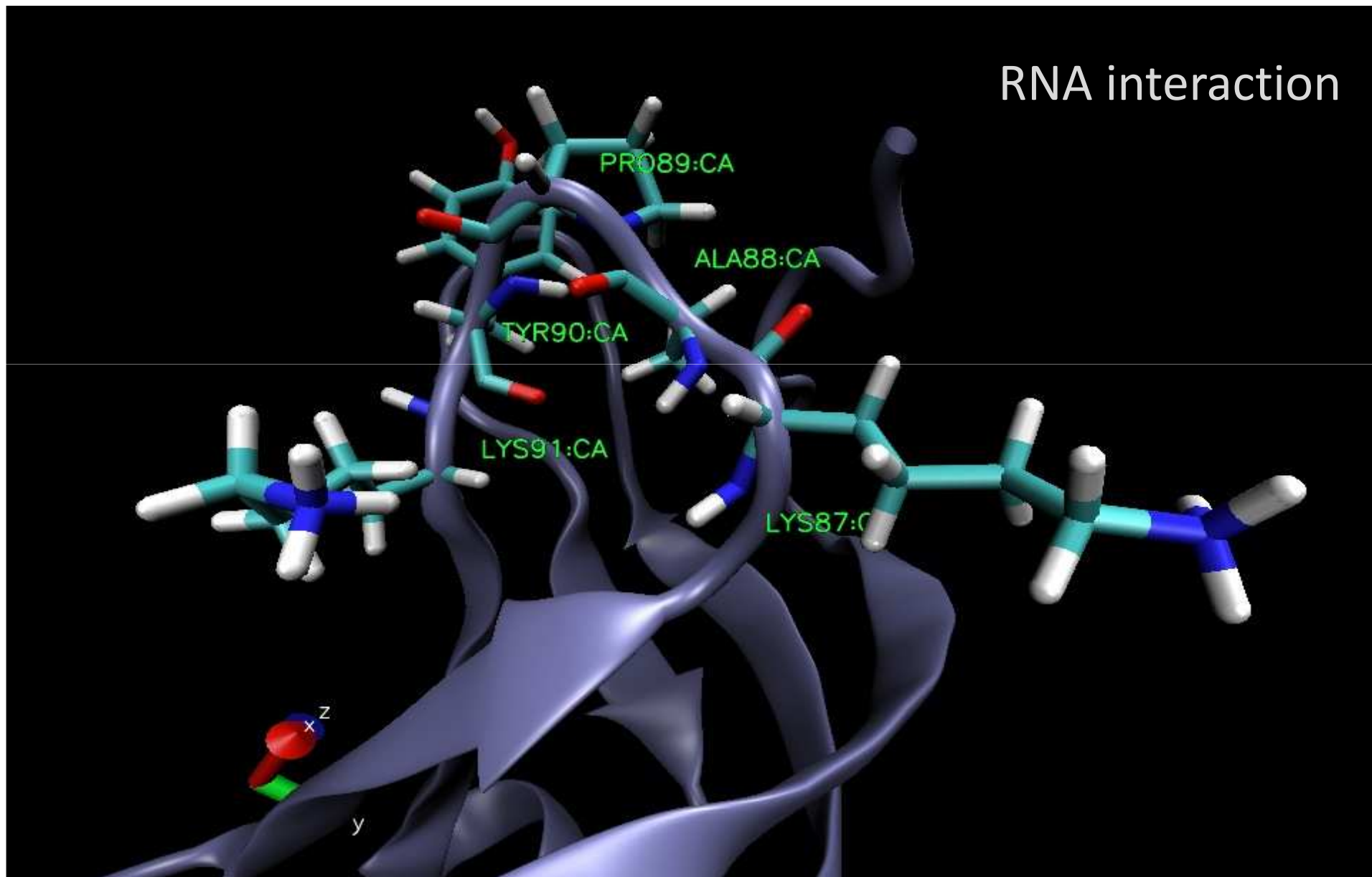
2.2 Rrp4 Subunit > S1 domain

RNA interaction



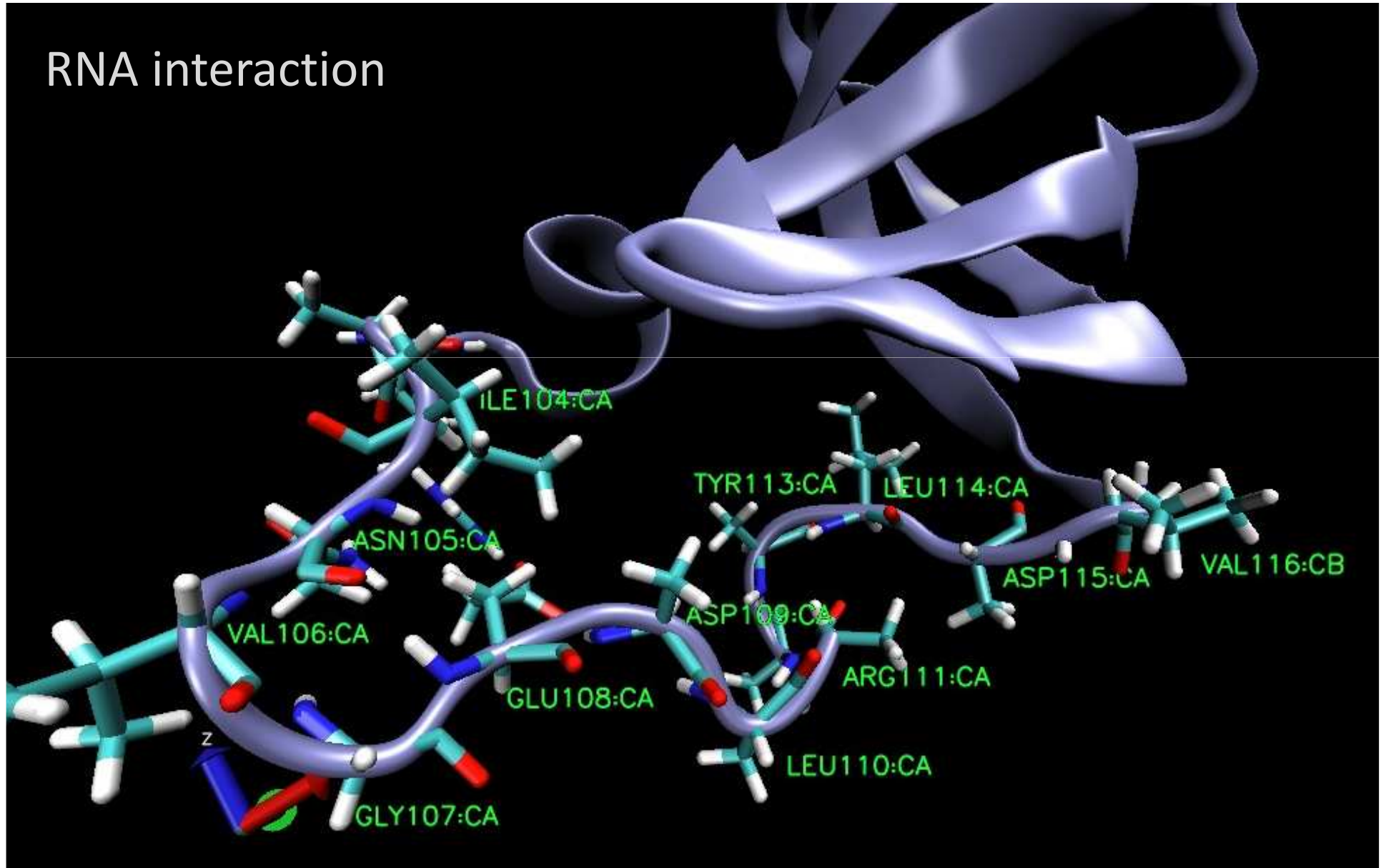
2.2 Rrp4 Subunit > S1 domain

RNA interaction



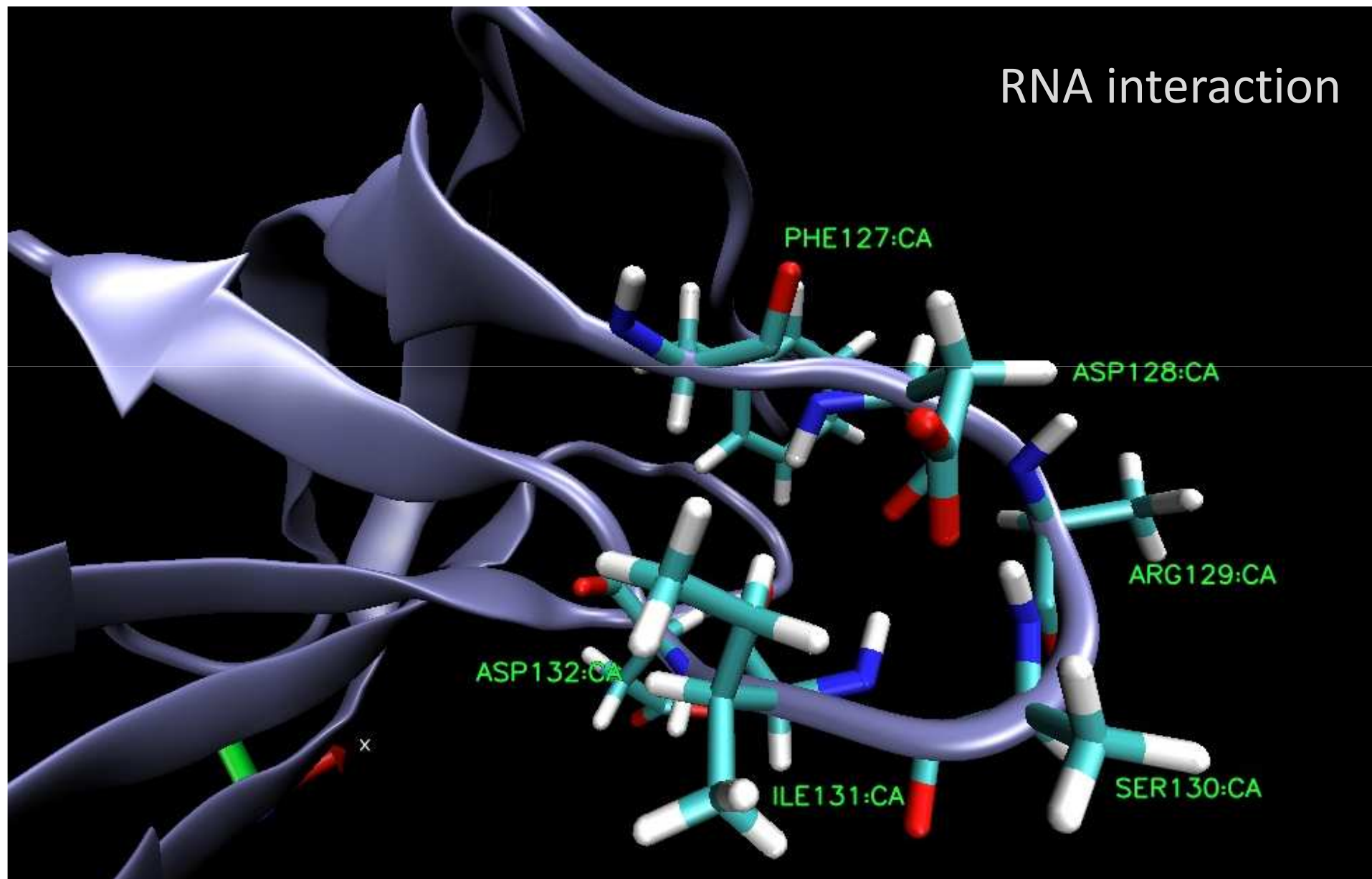
2.2 Rrp4 Subunit > S1 domain

RNA interaction



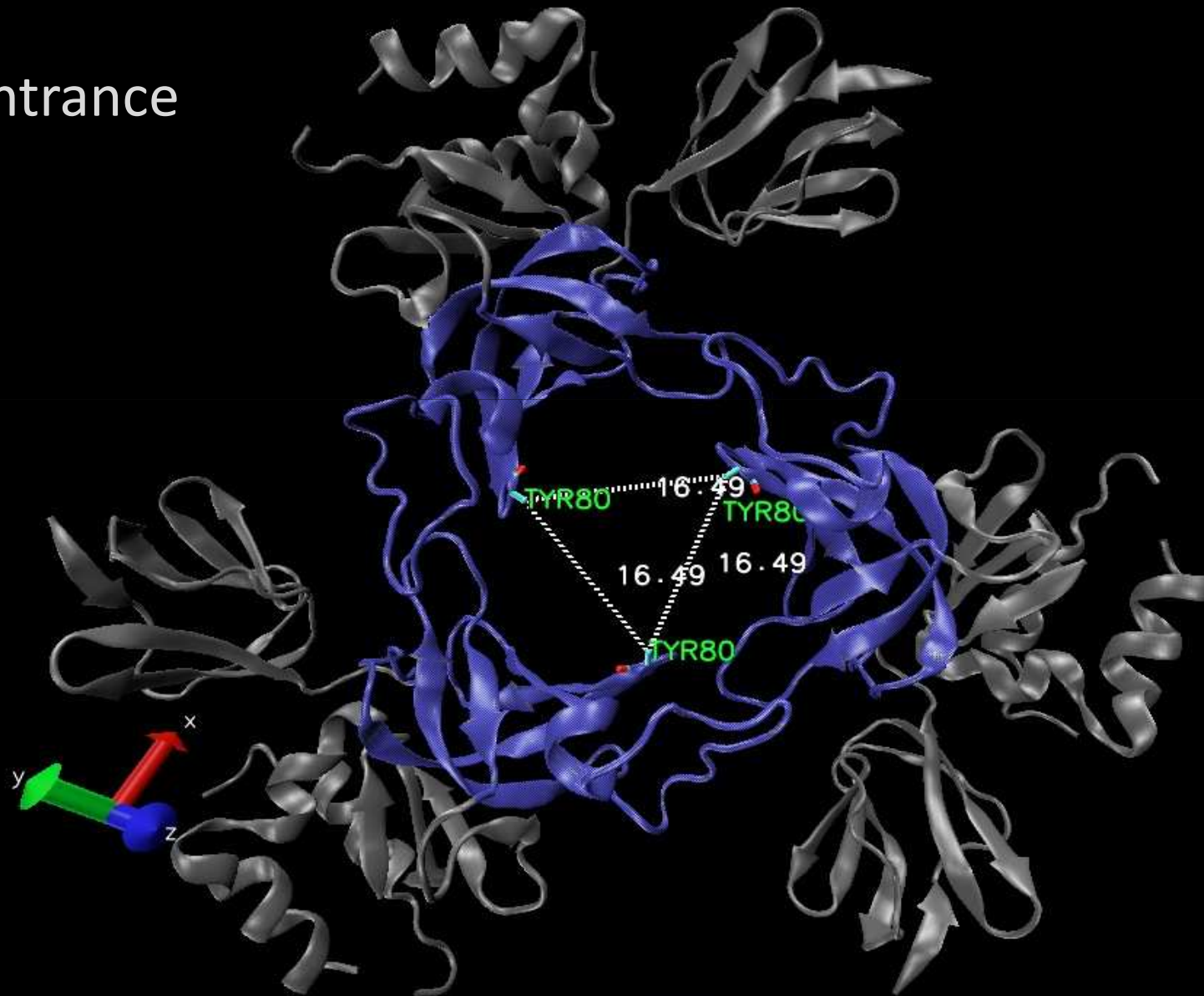
2.2 Rrp4 Subunit > S1 domain

RNA interaction

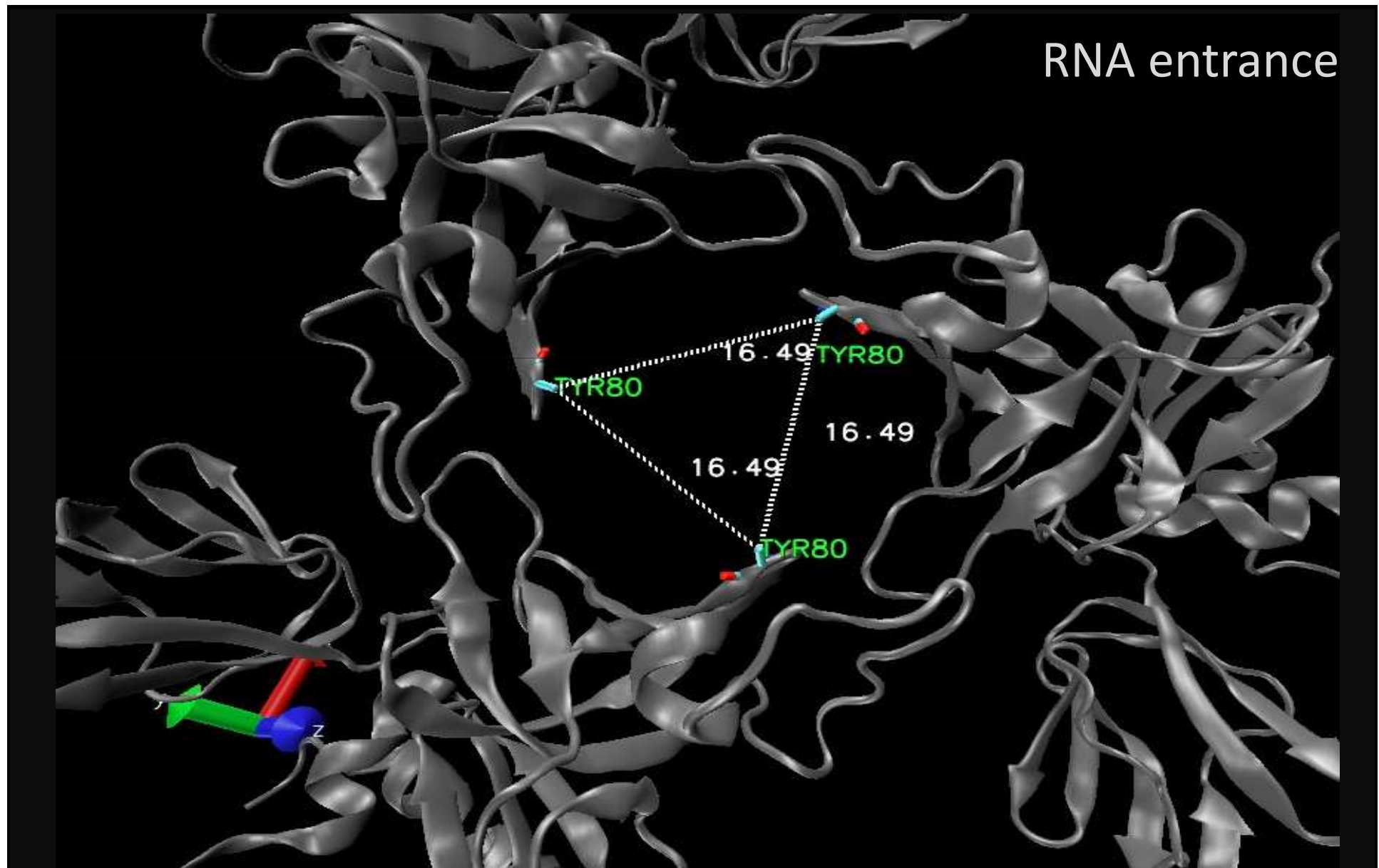


2.2 Rrp4 Subunit > S1 pore

RNA entrance

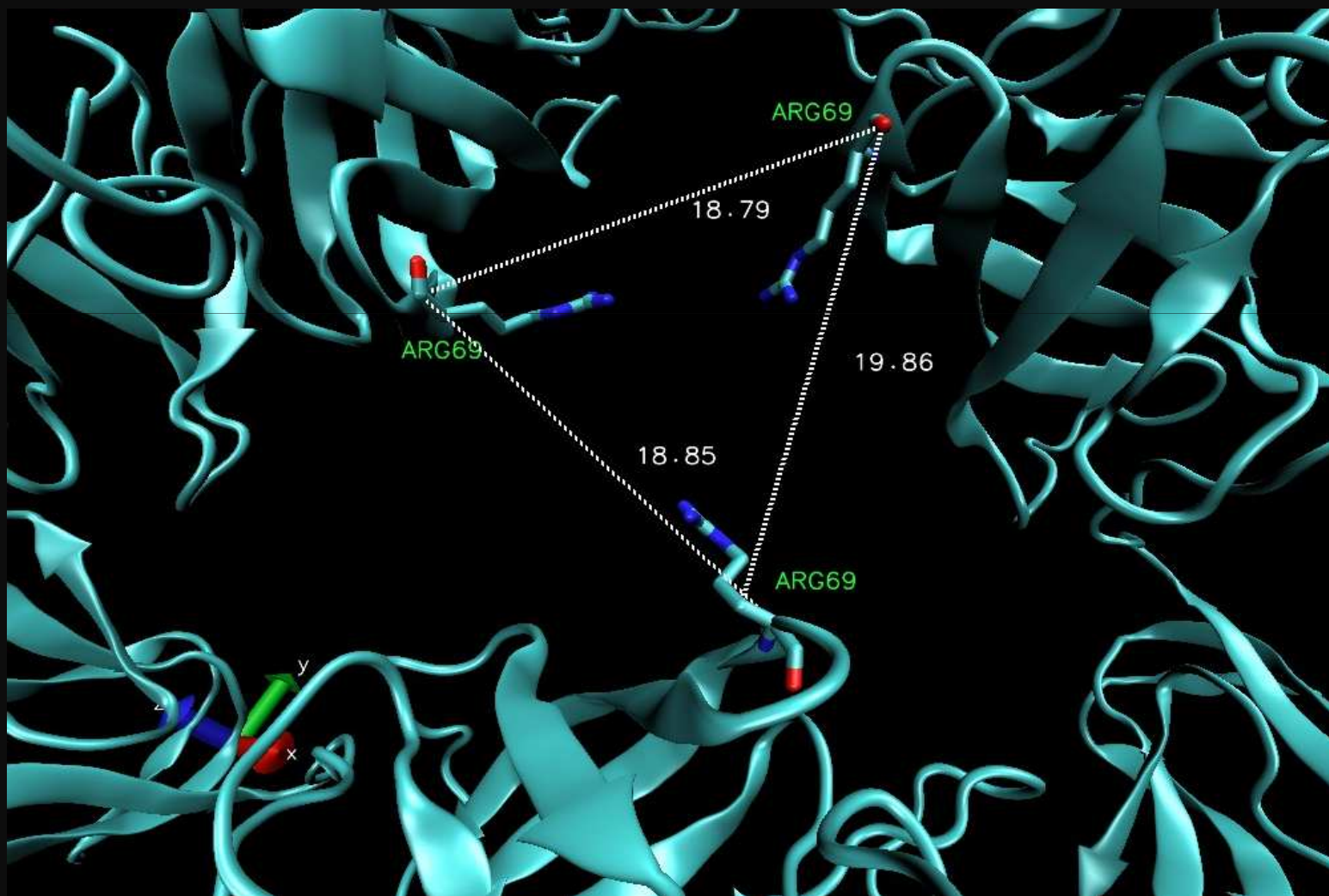


2.2 Rrp4 Subunit > S1 pore

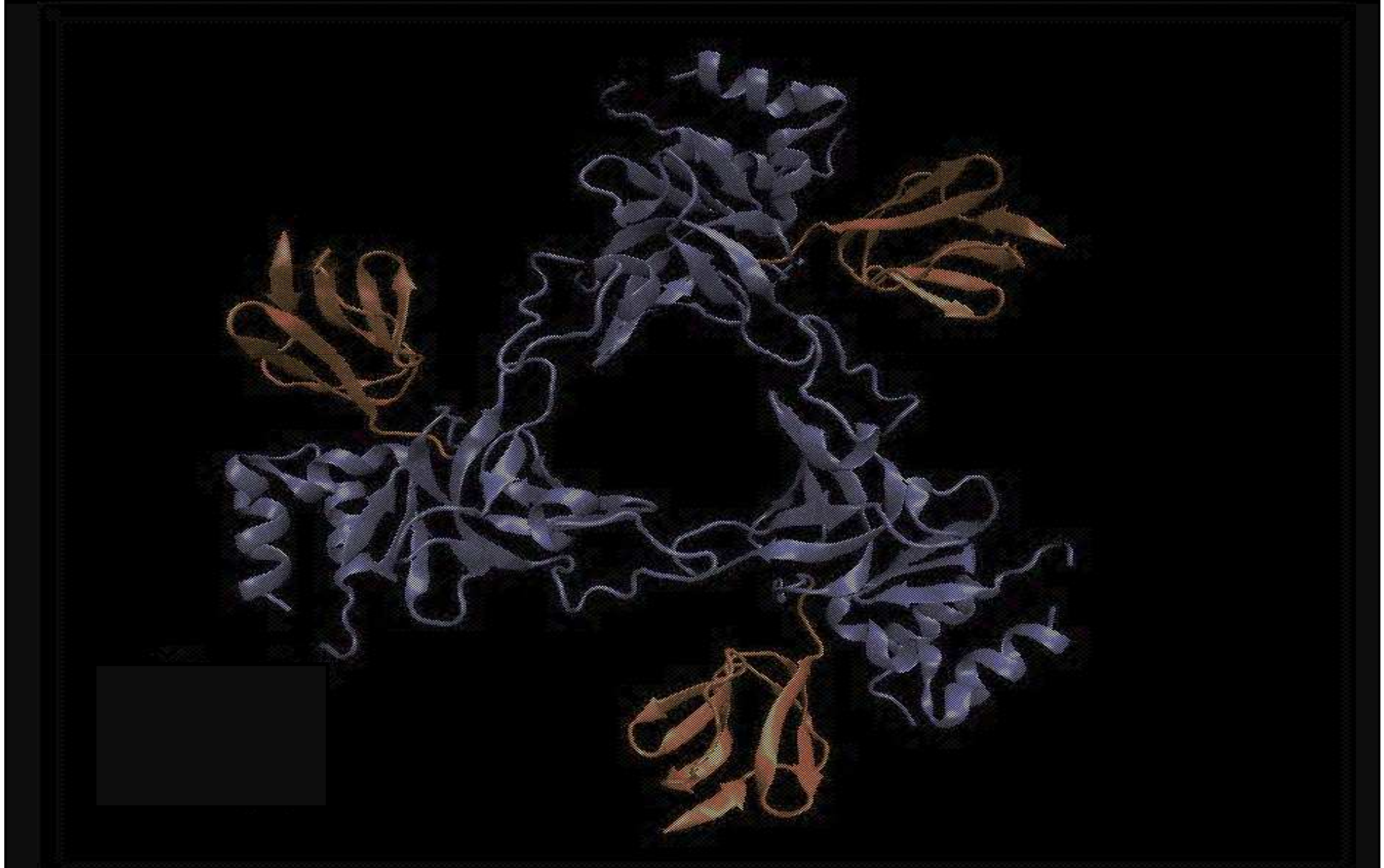


2.2 Rrp4 Subunit > S1 pore

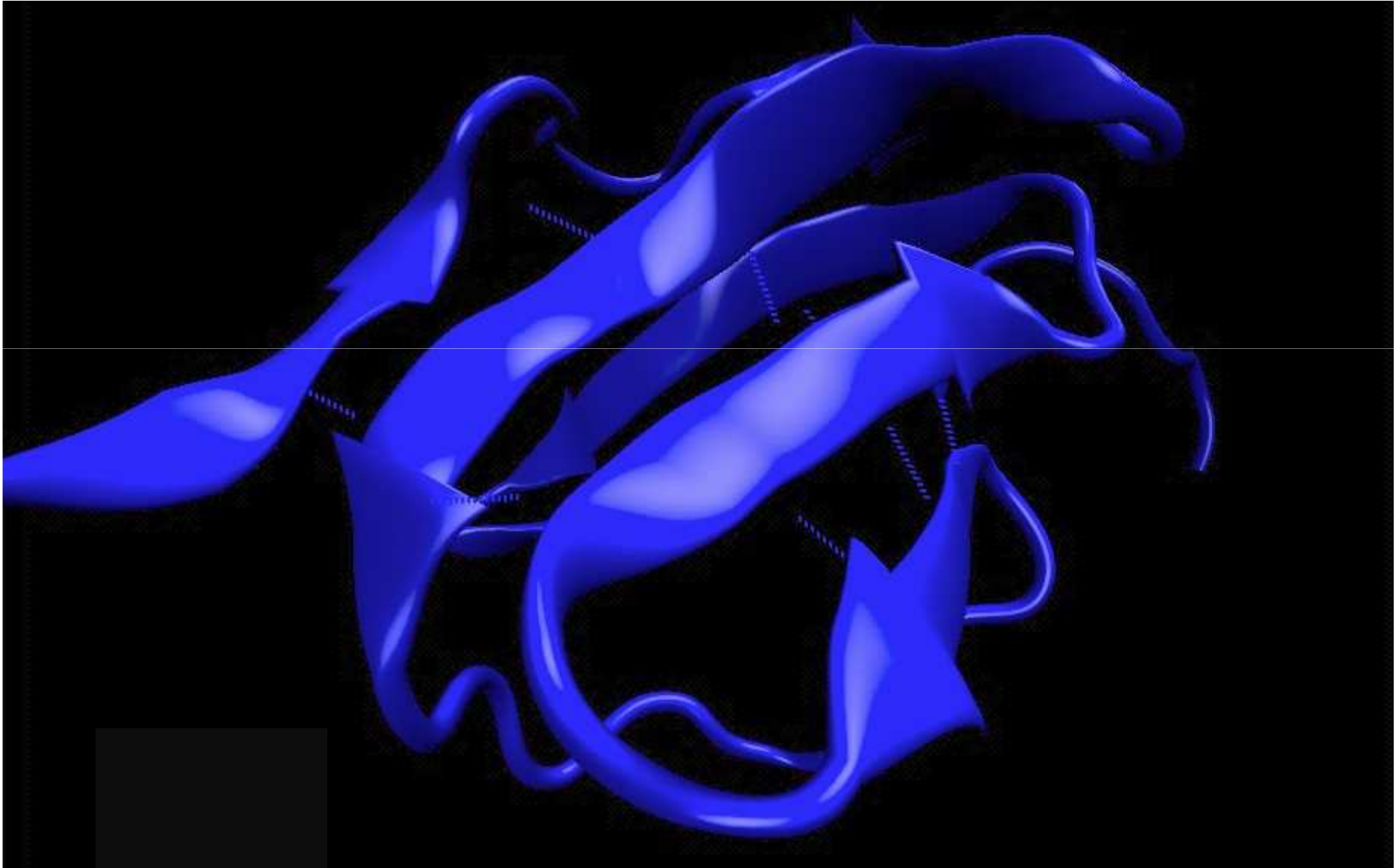
Rrp4 *versus* Csl4



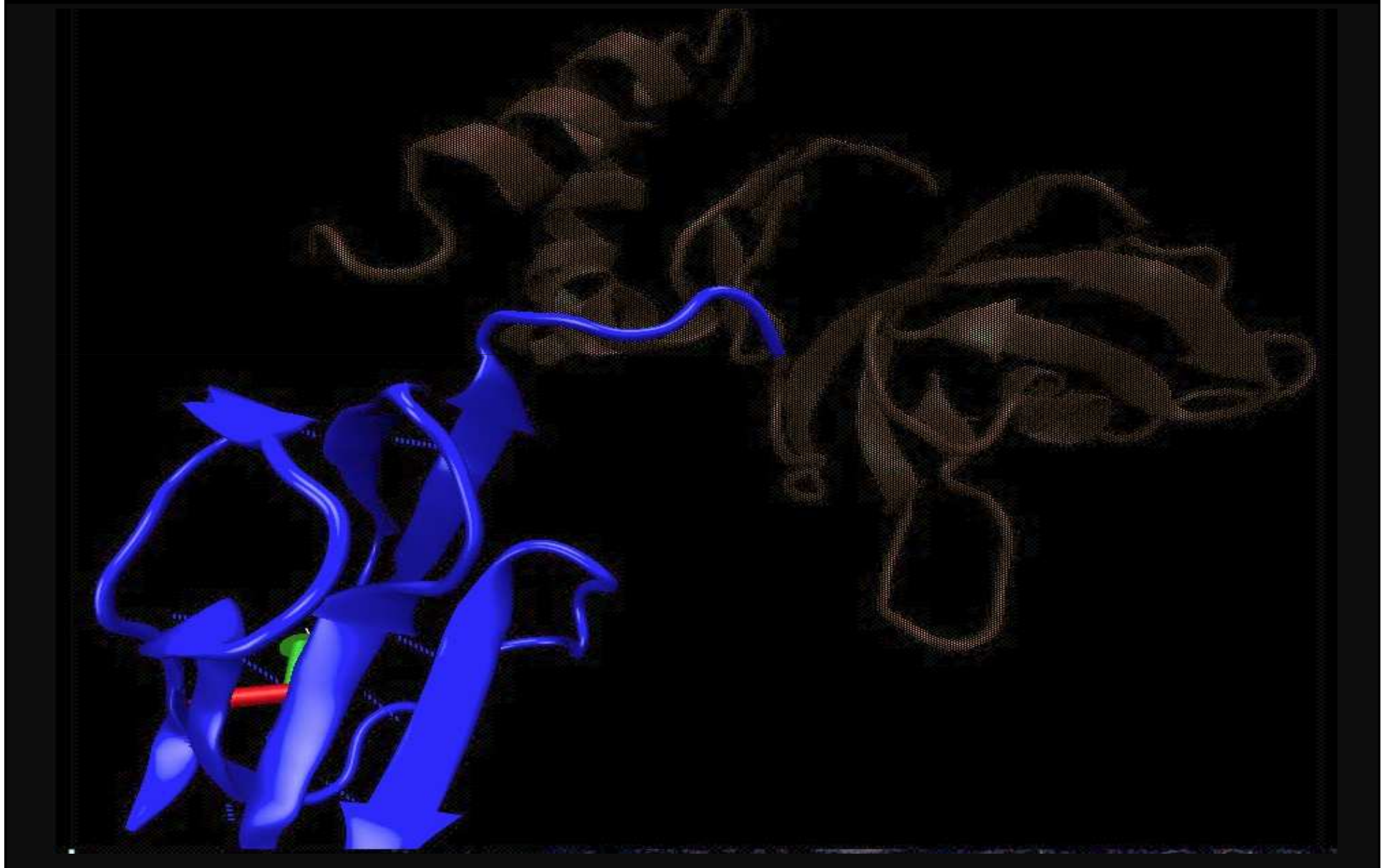
2.2 Rrp4 Subunit > N-terminal domain



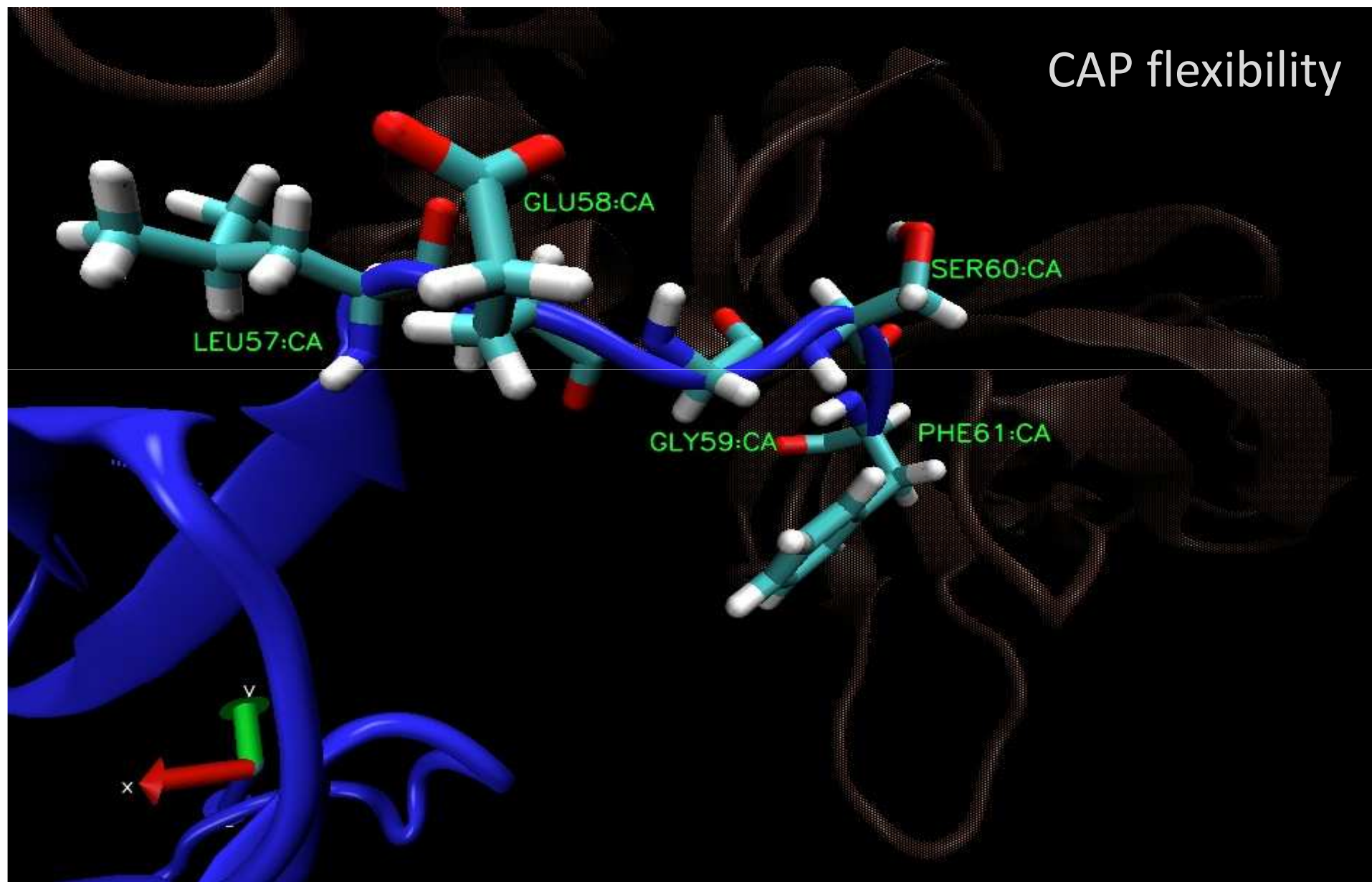
2.2 Rrp4 Subunit > N-terminal domain



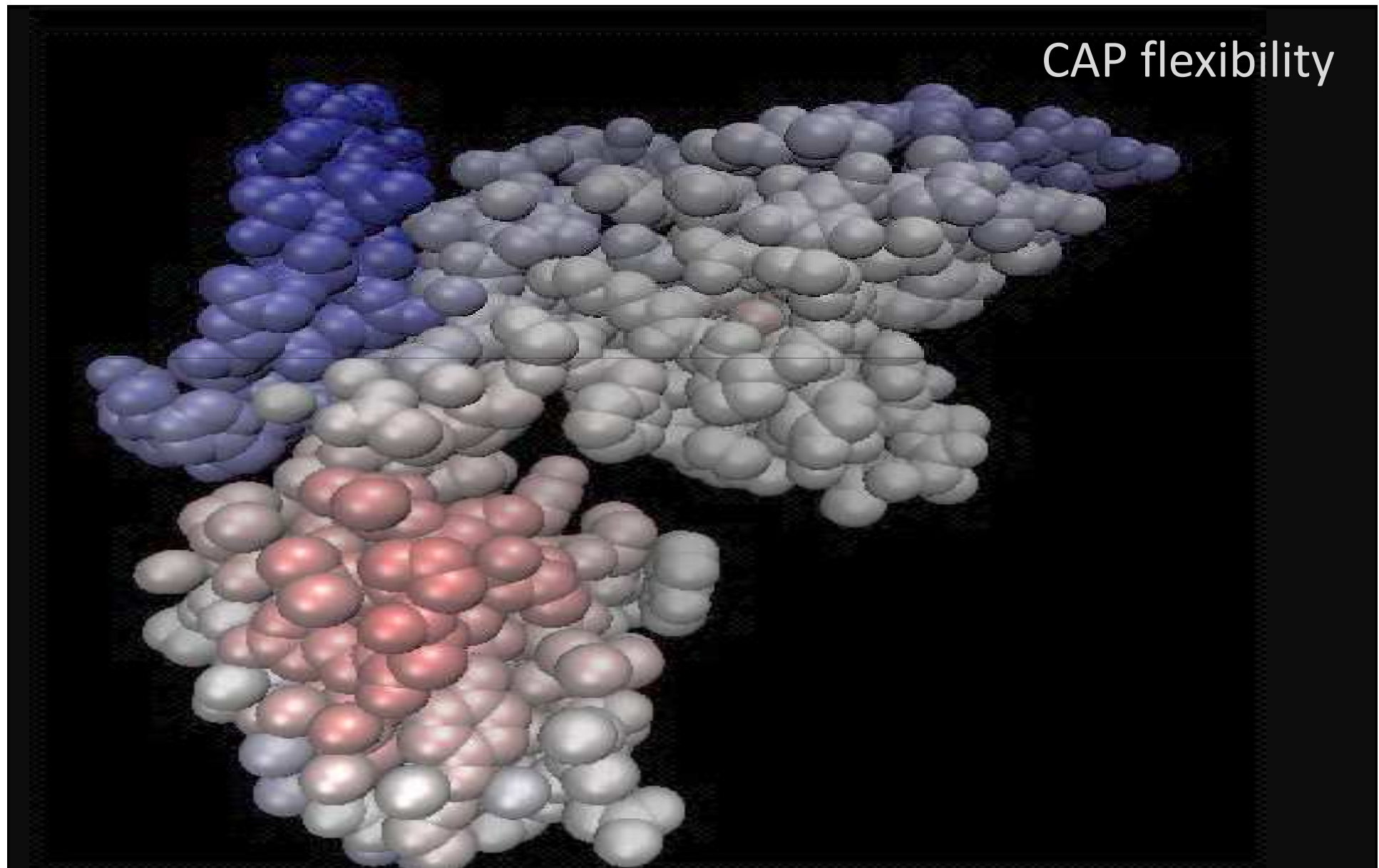
2.2 Rrp4 Subunit > N-terminal domain



2.2 Rrp4 Subunit > N-terminal domain

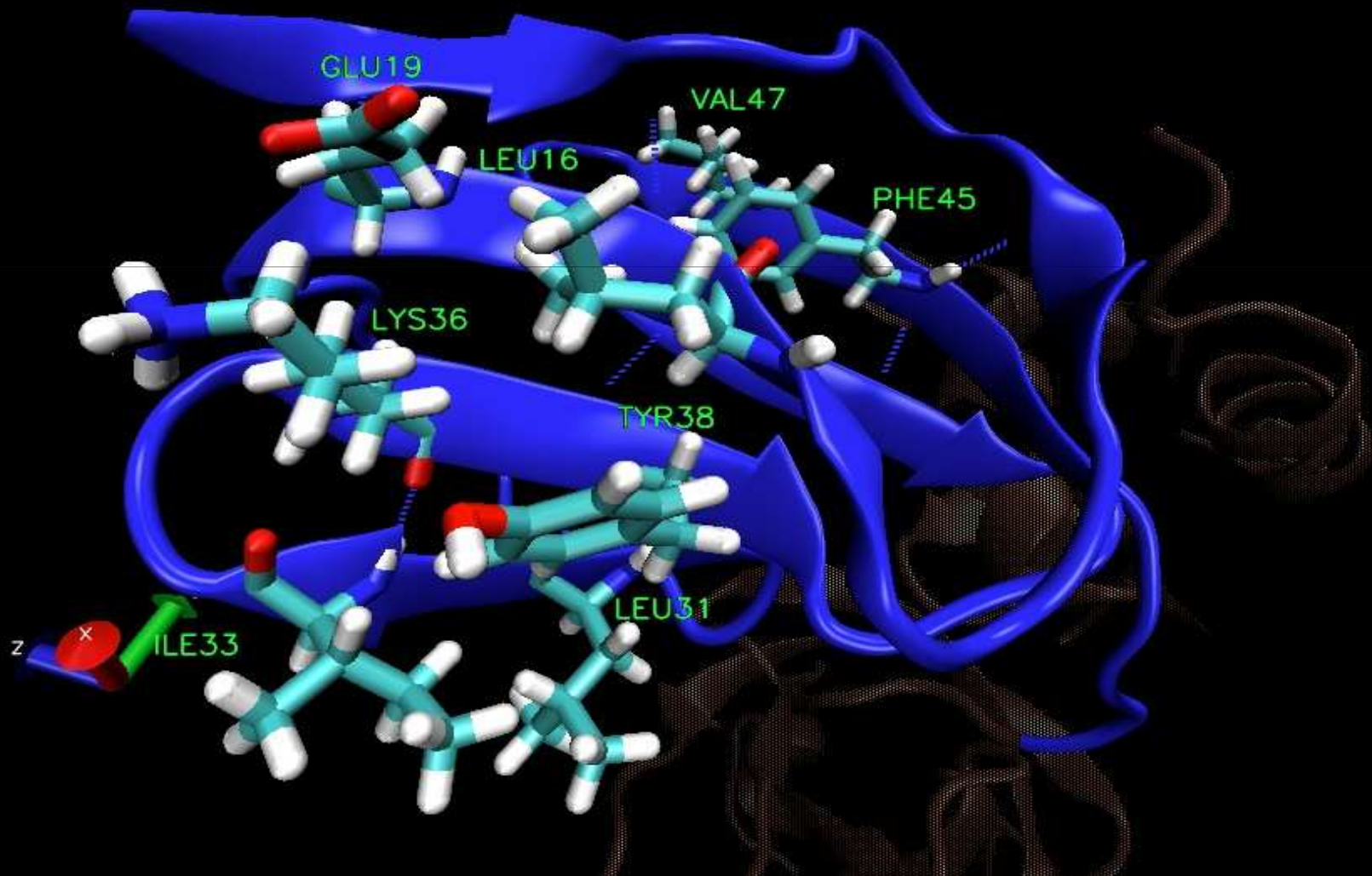


2.2 Rrp4 Subunit > N-terminal domain

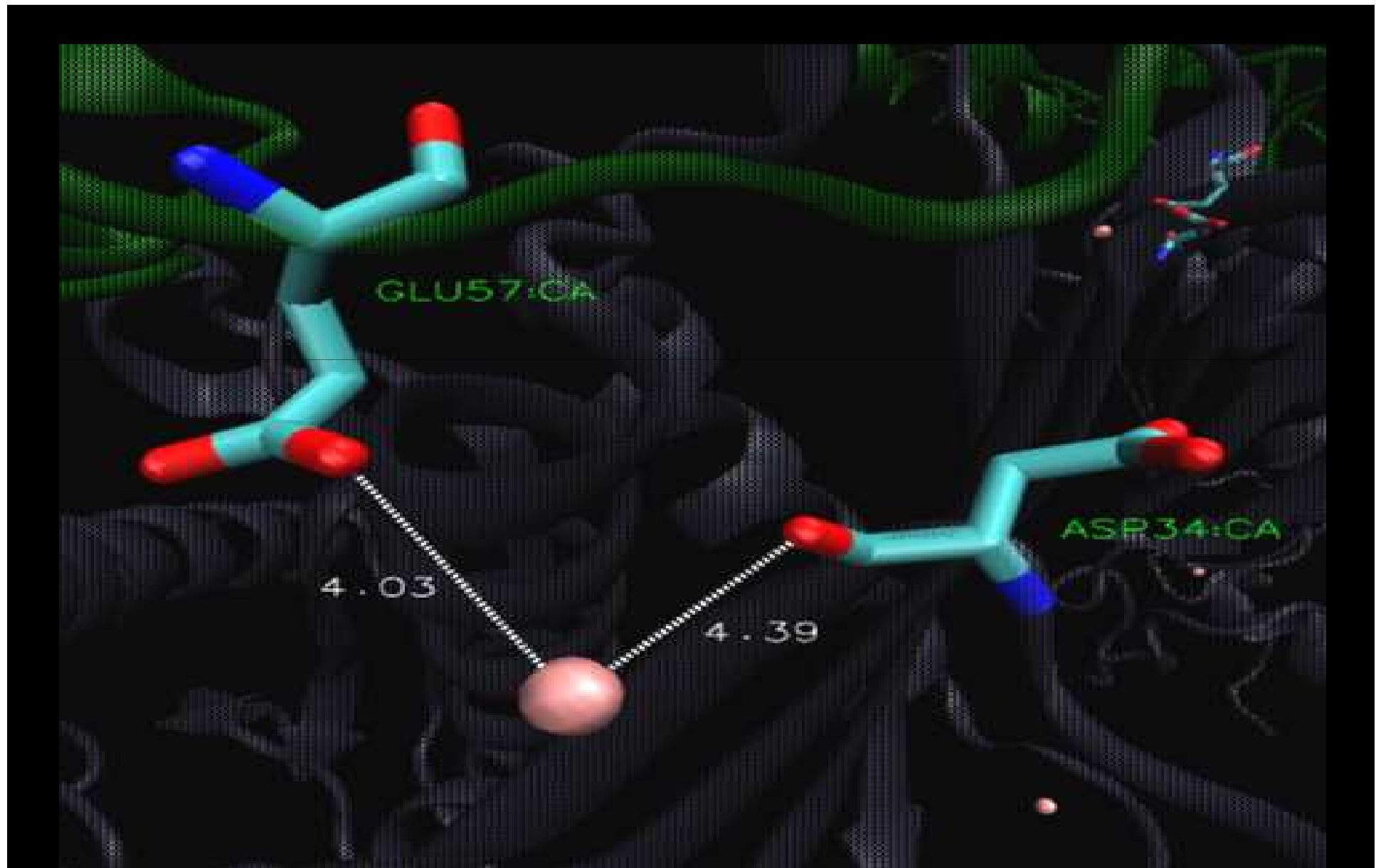


2.2 Rrp4 Subunit > N-terminal domain

RNA interaction

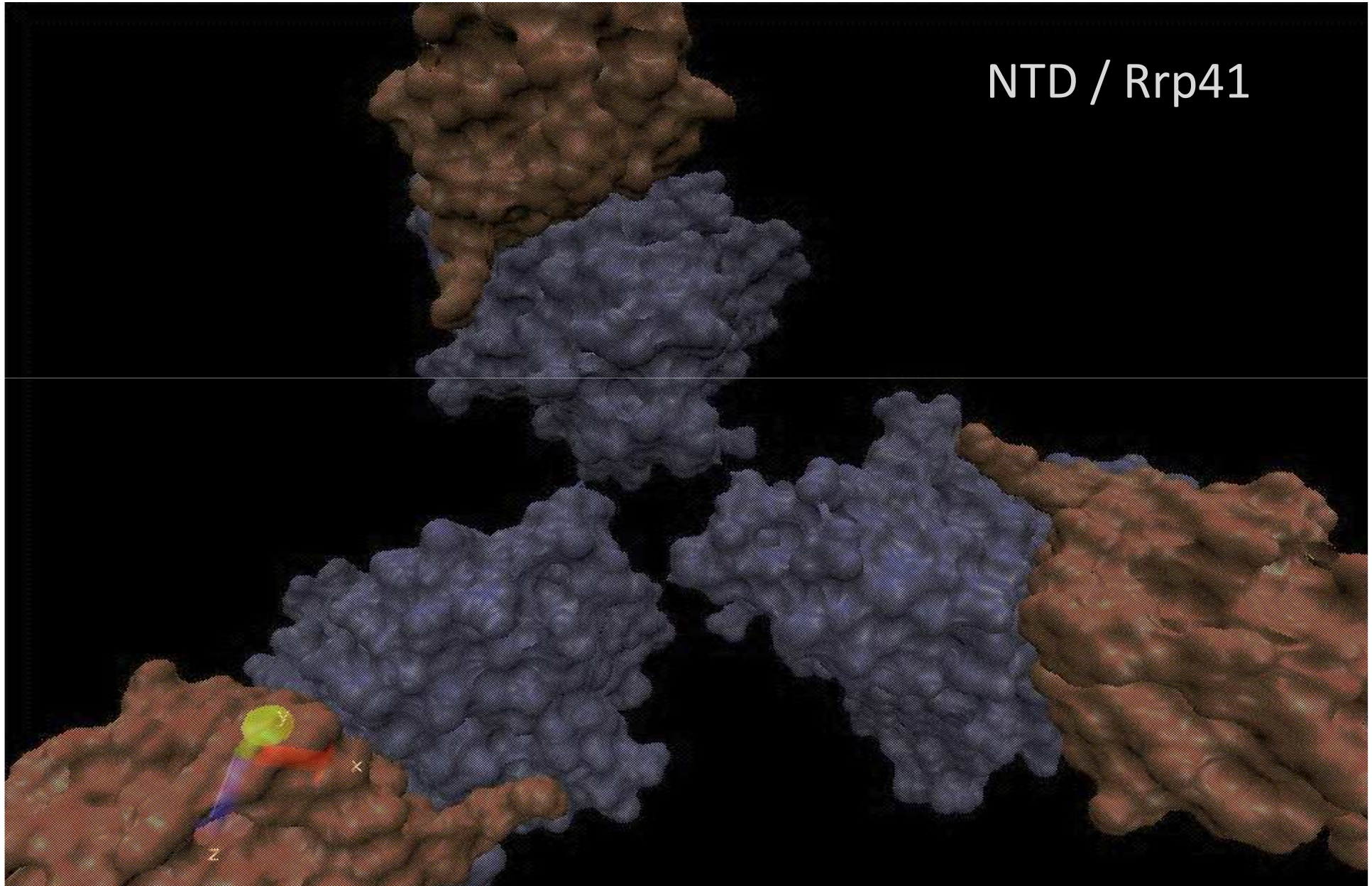


2.2 Rrp4 Subunit > N-terminal domain



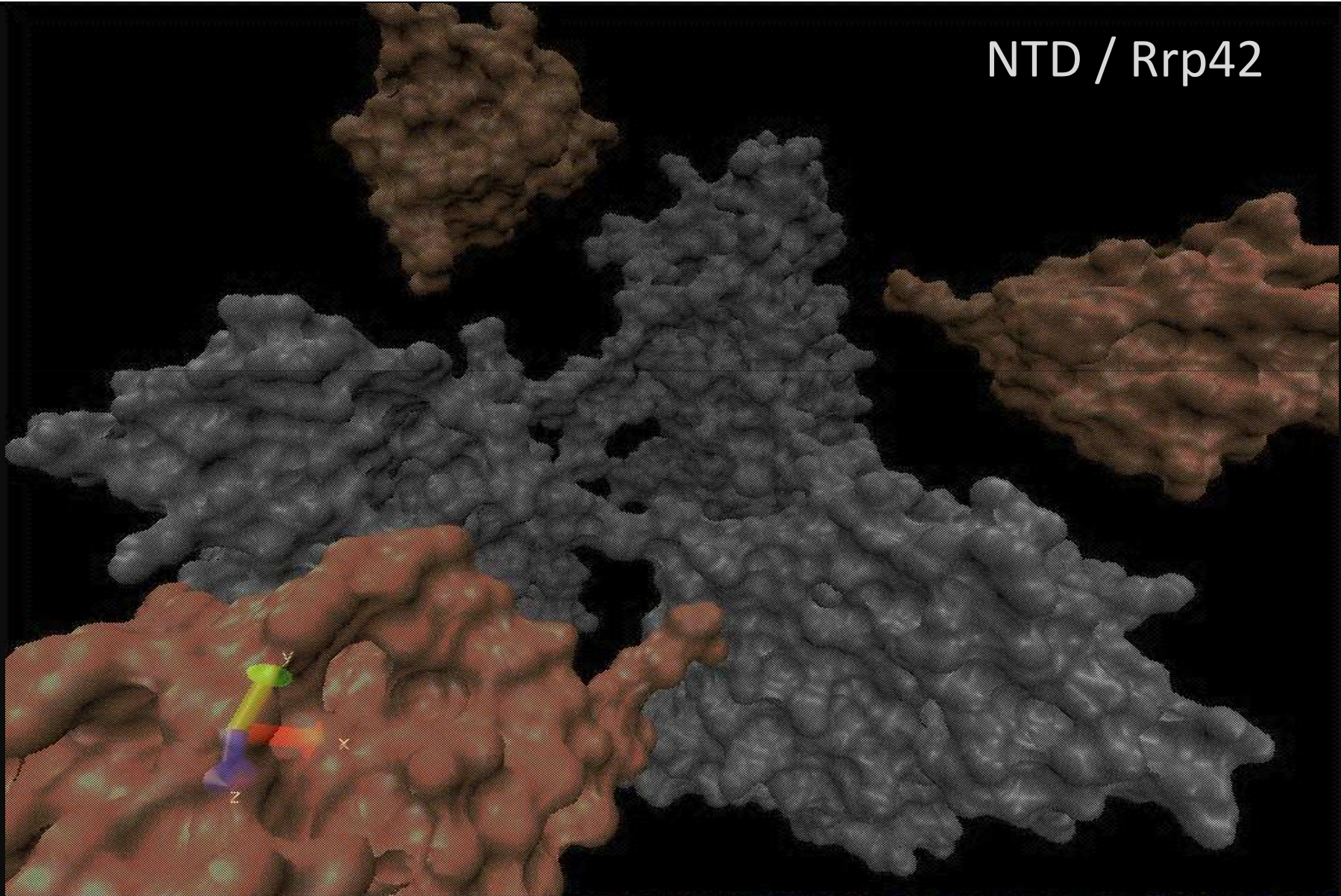
2.2 Rrp4 Subunit > N-terminal domain

NTD / Rrp41



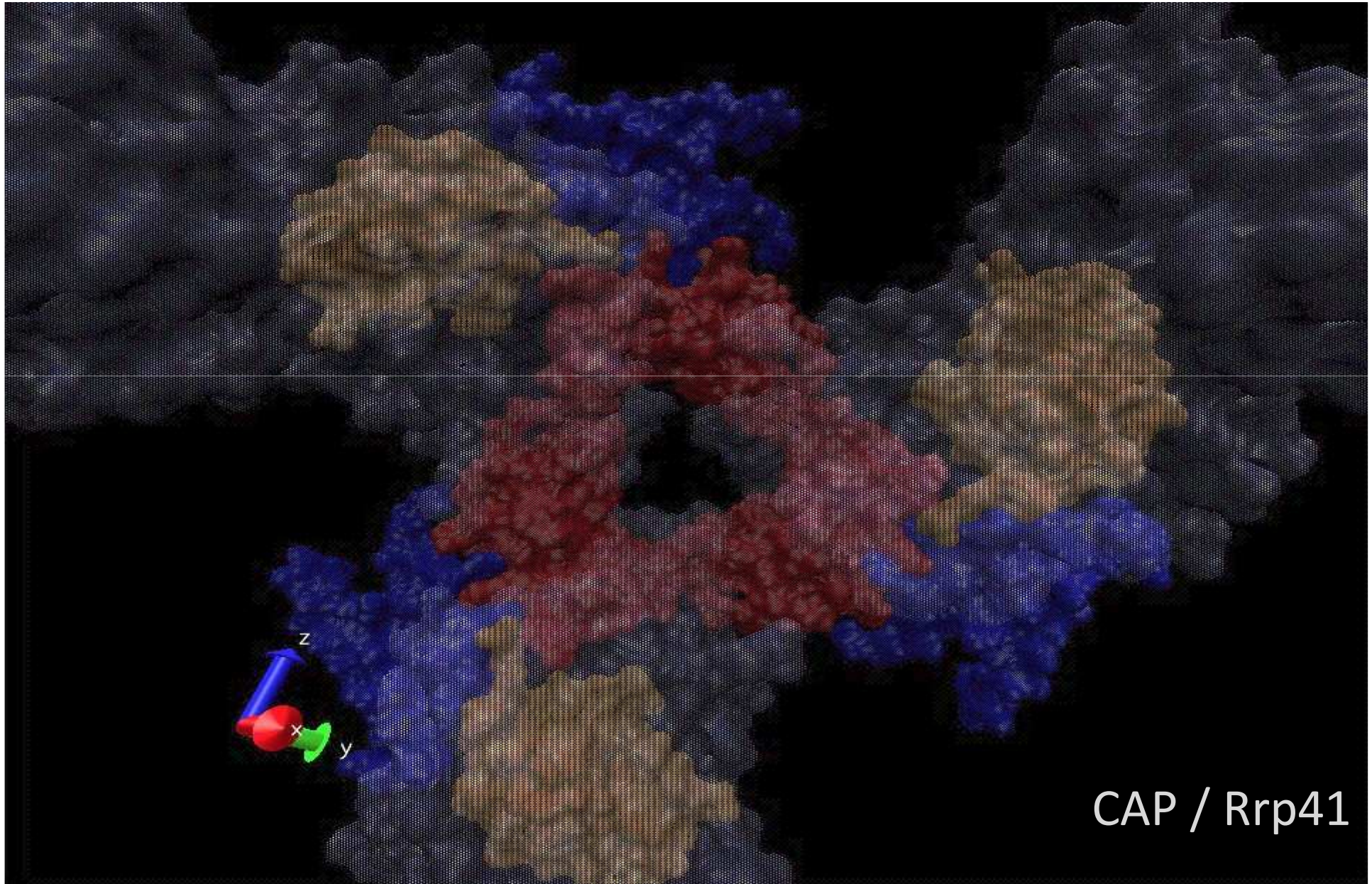
2.2 Rrp4 Subunit > N-terminal domain

NTD / Rrp42



2.3

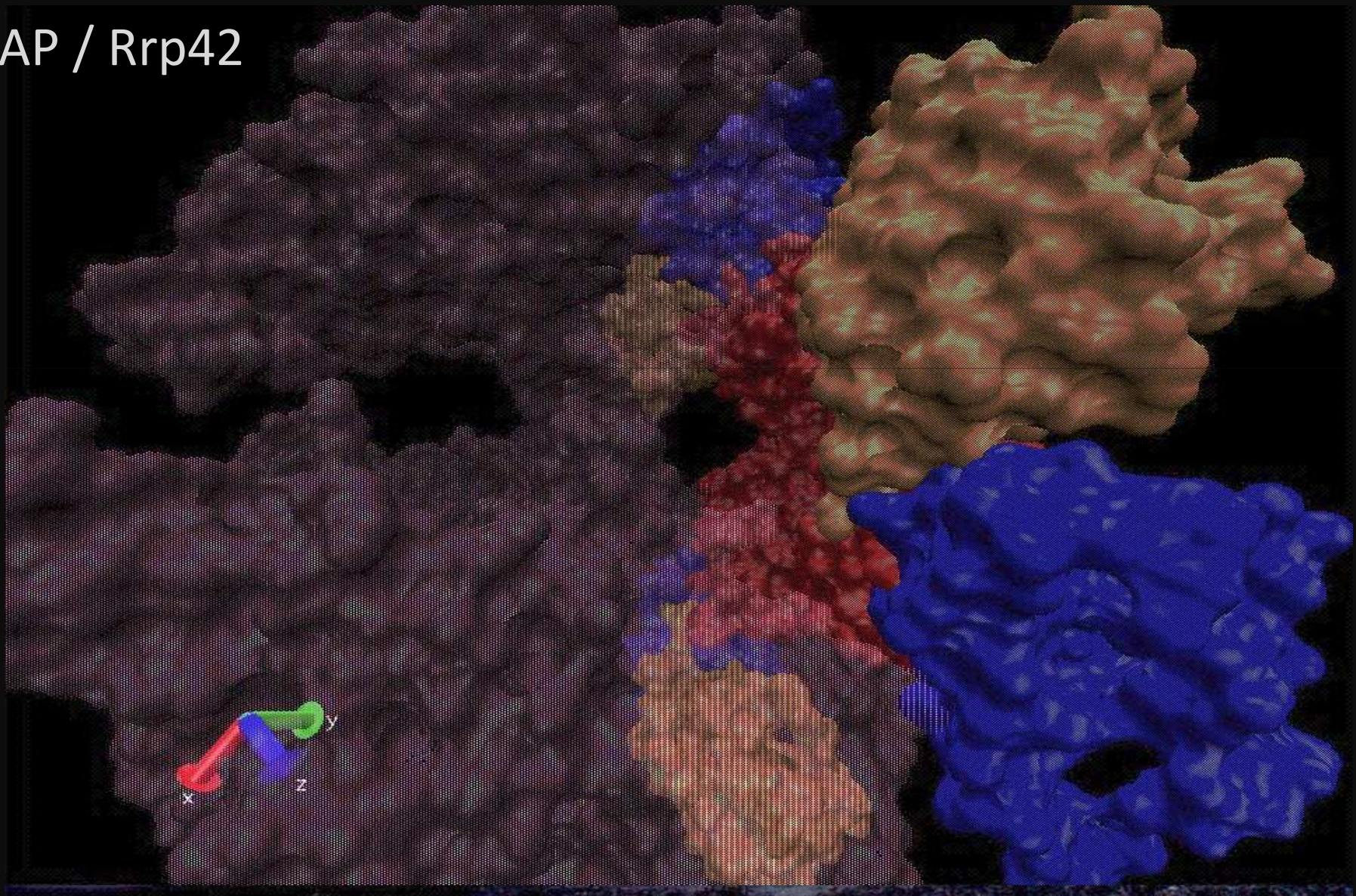
Rrp4/Csl4 CAP - Core interaction



2.3

Rrp4/Csl4 CAP - Core interaction

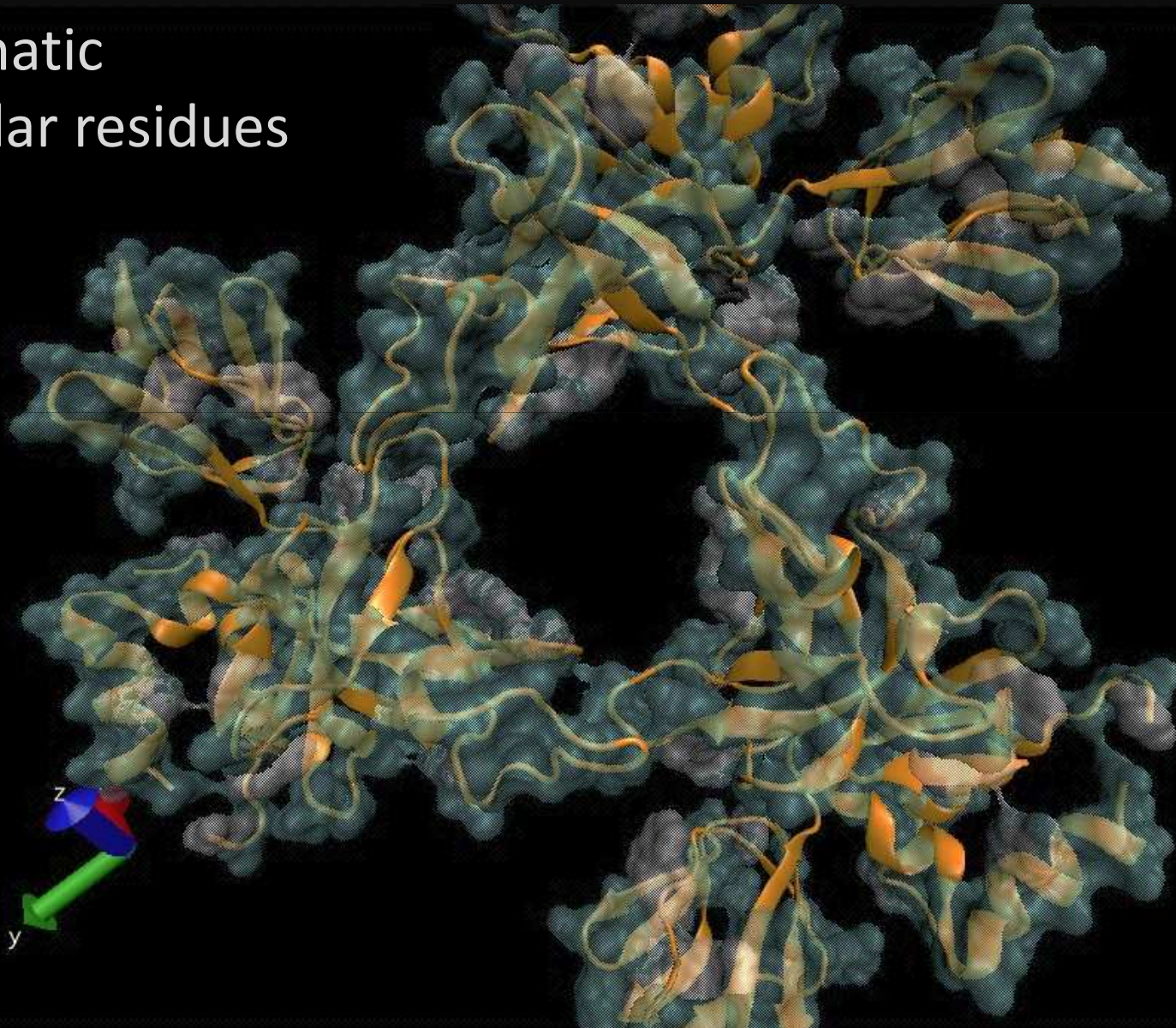
CAP / Rrp42



2.4

Rrp4/Csl4 CAP - RNA interaction

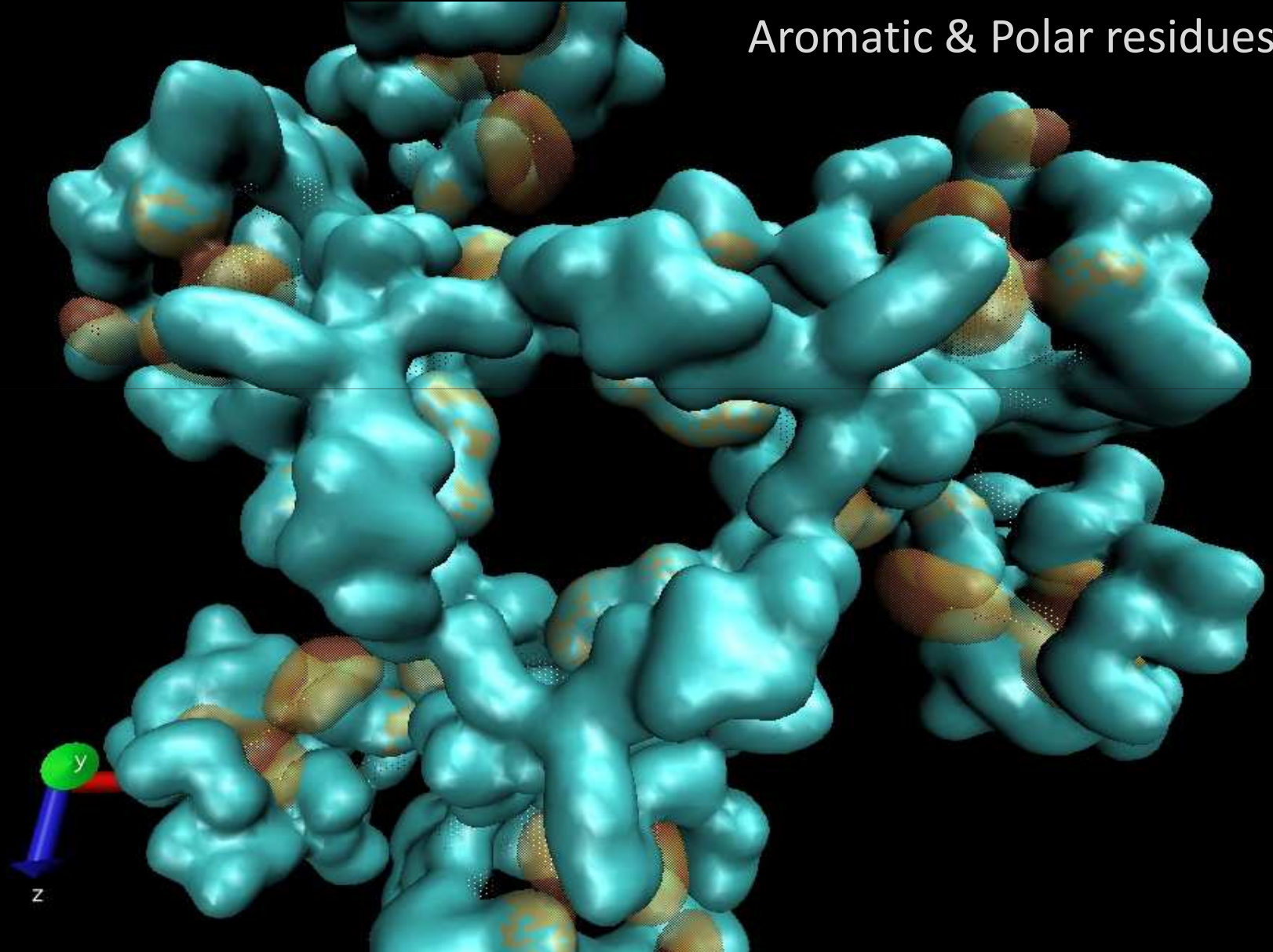
Aromatic
& Polar residues



2.4

Rrp4/Csl4 CAP - RNA interaction

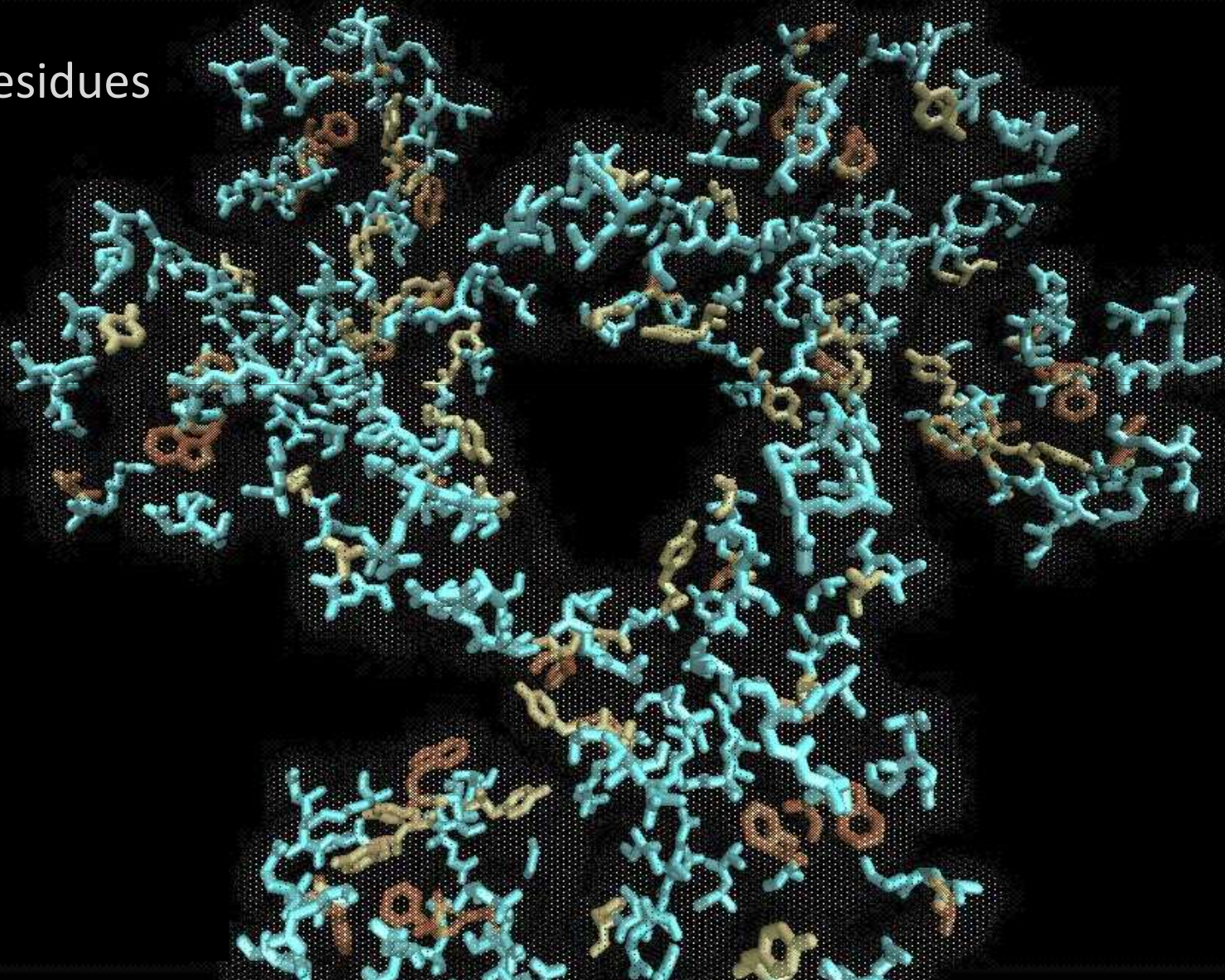
Aromatic & Polar residues



2.4

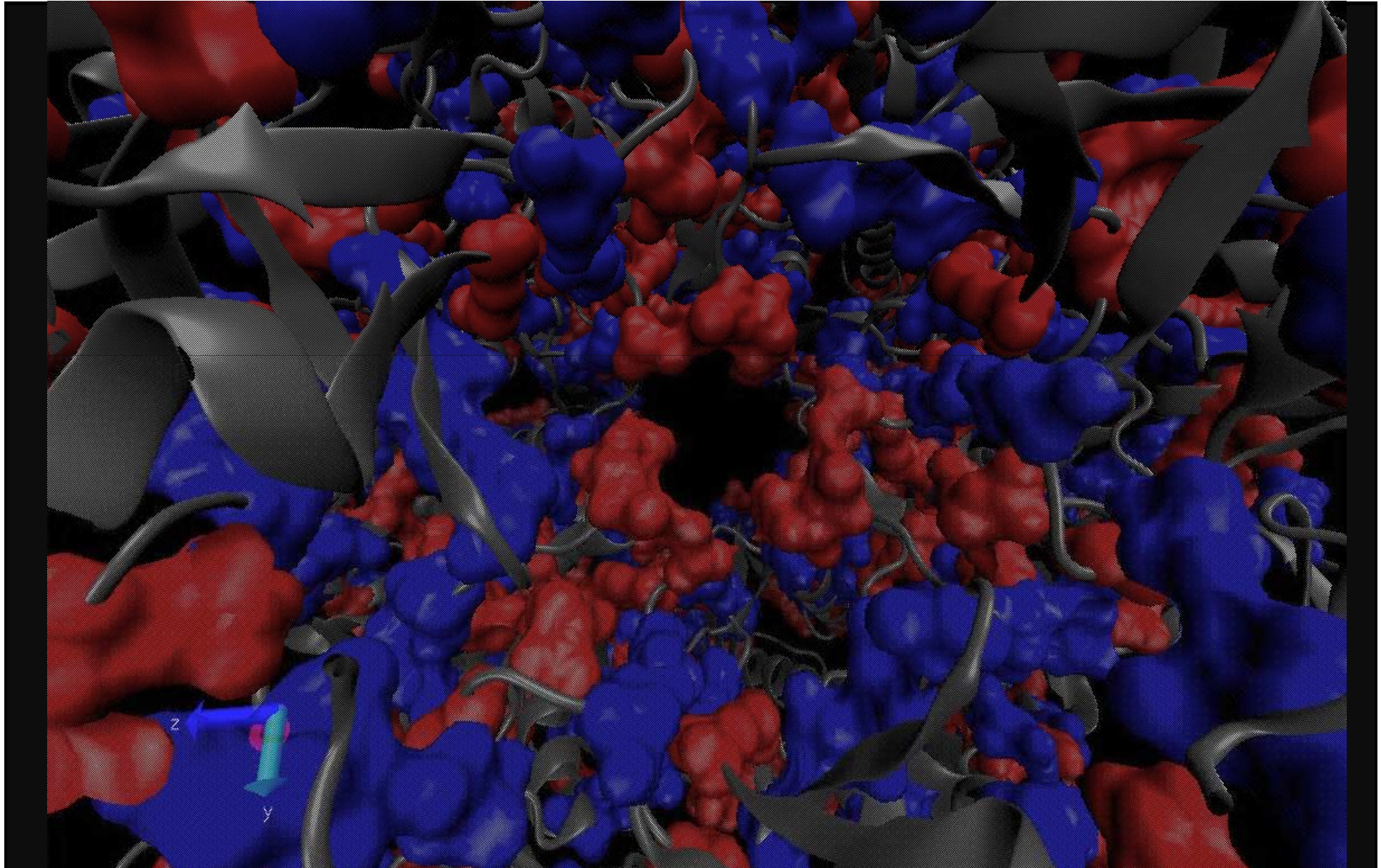
Rrp4/Csl4 CAP - RNA interaction

Aromatic
& Polar residues



2.4

Rrp4/Csl4 CAP - RNA interaction



2.5

Rrp4 vs. Csl4 Subunit

Structure-based alignment: STAMP

```

SsRrp4/1-621 1QEIVLQPRSI VVP GELLAEG--EFQIPWSPYILKINSKYSTVVCLFDV KDTQFEVIPLEGSFYYPKINDIVIGLVEDVEI-----YGWVVD-----IKAPYKAYLPASNLL-- 99
SsCsl4/1-537 1-----MRFMMPGDRIGSAEEYV-KG-EGVYEEGGELFAAAACKLI IKDRVAKVESIS-PIPEI-V-KGDVVLG-RVVDLRNSIALIEVSSKKGENRGPSNRGIGIL--HVS 98

SsRrp4/1-621 100-----LGRSINVGEDLRRY--LDVGDYVI-ARLENFDRSIDPVLSVKGK-DLG-----RV-S-NGIVIDIMPVKVPRVIGKNKSMYE 170
SsCsl4/1-537 99NVDEGYVKE----I--SEAVGYLDI-LKARV-IGD-----NLRLS-TKEEEMGVLRALCSNCKTEMVREGDILKCPECGRVEKRISTDYGKG-----177

SsRrp4/1-621 171TLTSKSI FVANNGRIWAFSEEILIEAIRKIENESHIKQEIVLQ--PRSI VVP GELLAEGEFQIPWSPYILKINSKYSTVVCLFDV KDTQFEVIPLEGSFYYPKINDIVIGLVE 282
SsCsl4/1-537 178-----EWM-RFVMPGDRIGSAEEYVKGEVYEEGGELFAAAACKLI IKDRVAKVESIS-PIPEI--VKGDVVLG-242

SsRrp4/1-621 283DVEI-----YGWVVD-----IKAPYKAYLPASNLL-----GRSINVGEDLRRY--LDVGDYVIARLENFDRSIDPVLSVKGK-DLG-----350
SsCsl4/1-537 243RVVDLRNSIALIEVSSKKGENRGPSNRGIGIL--HVS NVDEGYVKE----EI-SEAVGYLDILKARV-IGD-----NLRLS-TKEEEMGVLRALCSNCKTEMVREGDILKCPEC 341

SsRrp4/1-621 351-----RVS--NGIVIDIMPVKVPRVIGKNKSMYETLTSKSI FVANNGRIWAFSEEILIEAIRKIENESHIKQEIVLQ--RSI VVP GELLAEGEFQIPWSPYILKINSKYYS 453
SsCsl4/1-537 342GRVEKRISTDYGKG-----EWMRFVMPGDRIGSAEEYVKGEVYEEGGELFA 389

SsRrp4/1-621 454TVCLFDV KDTQFEVIPLEGSFYYPKINDIVIGLVEDVEI-----YGWVVD-----IKAPYKAYLPASNLL-----LGRSINVGEDLRRYL-DVGDYVIARI-ENFDRSIDP 547
SsCsl4/1-537 390AAACKLI IKDRVAKVESIS-PIPEI--VKGDVVLG-RVVDLRNSIALIEVSSKKGENRGPSNRGIGIL--HVS NVDEGYVKE----I--SEAVGY-LDILKARVIGD-----NL 485

SsRrp4/1-621 548VLSVKGK-DLG-----RVS--N-GIVIDIMPVKVPRVIGKNKSMYETLTSKSI FVANNGRIWAFSEEILIEAIRKIENESHIK 621
SsCsl4/1-537 486RLS-TKEEEMGVLRALCSNCKTEMVREGDILKCPECGRVEKRISTDYKGGEW-----537

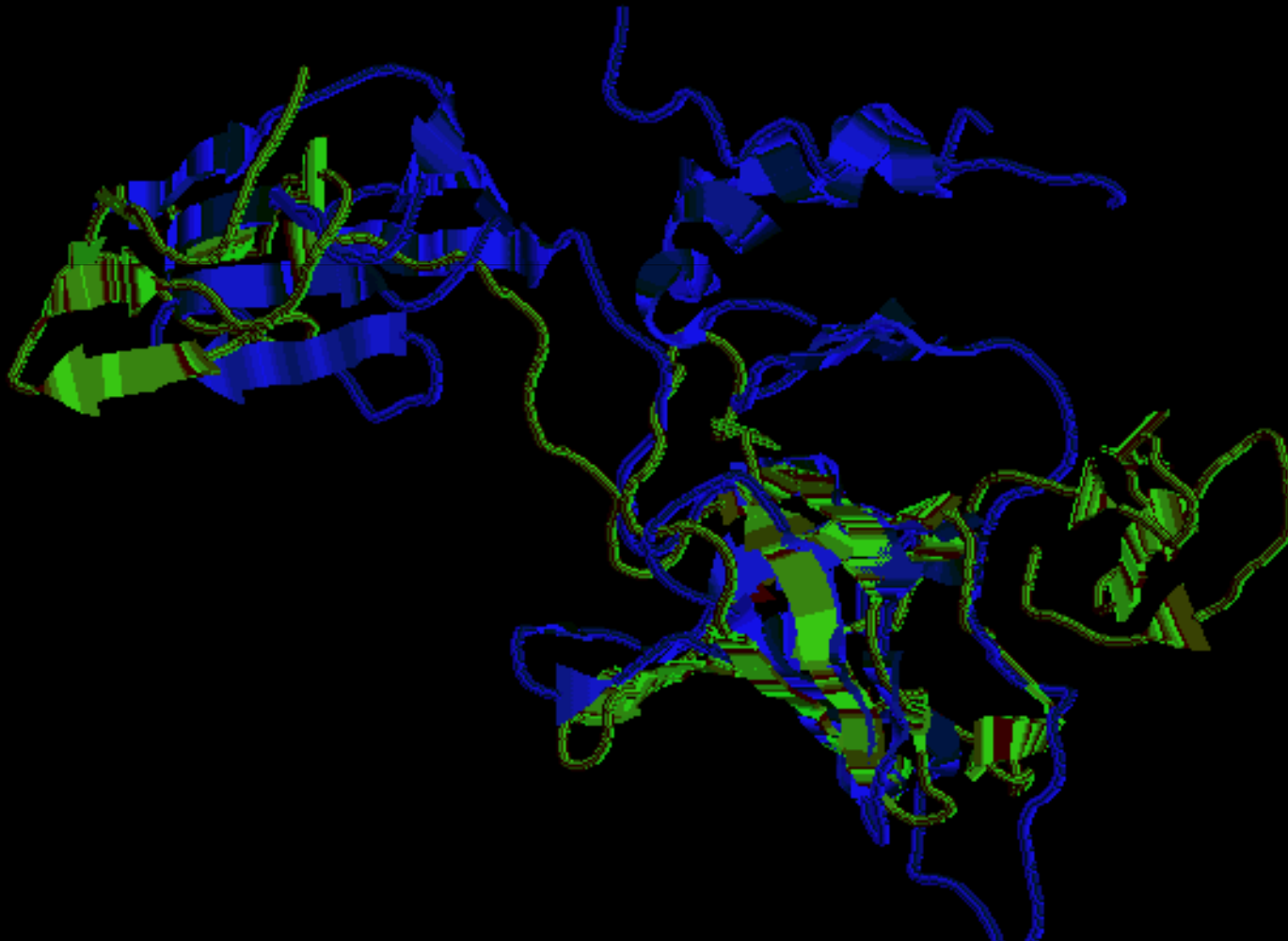
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	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)
Pair	1	2JE6_bioI	2BA1_Csl4	2.41	2.39	621	537	732	203	171	0	18.71	100.00	3.55e-51

2.5

Rrp4 vs. Csl4 Subunit

Structure-based alignment: STAMP



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- 1.2. Exosome fuction
- 1.3. Exosome structure

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- 2.2. Rrp4 subunit

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THE ARCHAEL EXOSOME CORE

- 3.1. Fold
- 3.2. Interaction between subunits
- 3.3. Interaction with the RNA

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EVOLUTION OF THE EXOSOME

- 4.1. Relationship with the eukaryotic exosome
- 4.2. Evolution of the Cap subunits
- 4.3. Evolution of the Core subunits

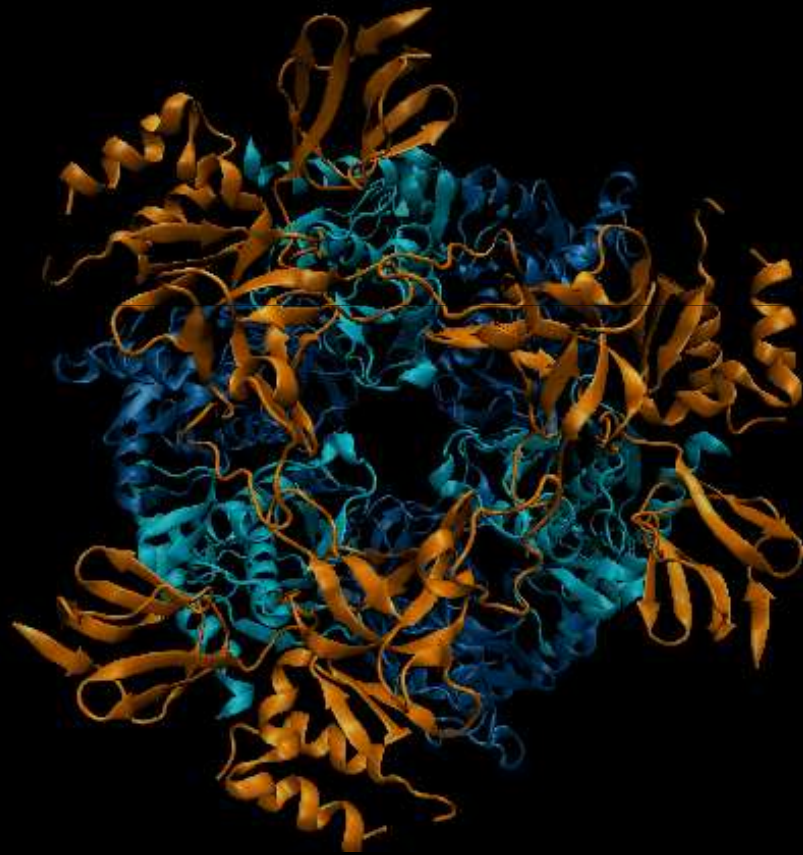
3

The archaeal Exosome CORE

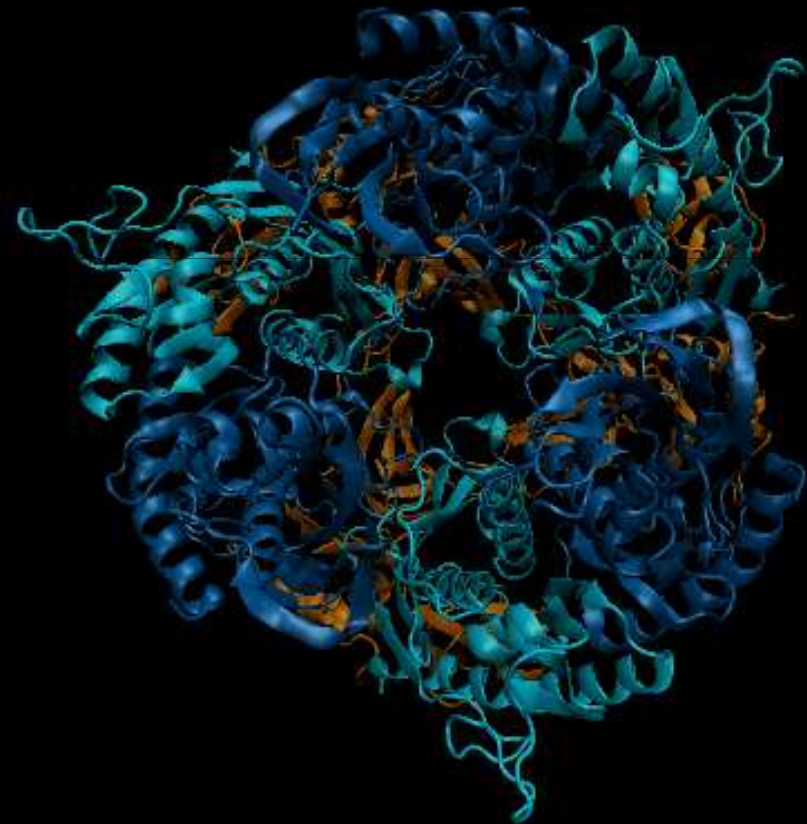
Cap

Rrp42

Rrp41



TOP VIEW



BOTTOM VIEW

Rrp41

Show or hide all alignments.

Rrp42

Show or hide all alignments.

Comments or questions on the site? Send a mail to pfam-help@sanger.ac.uk. Our [cookie policy](#).

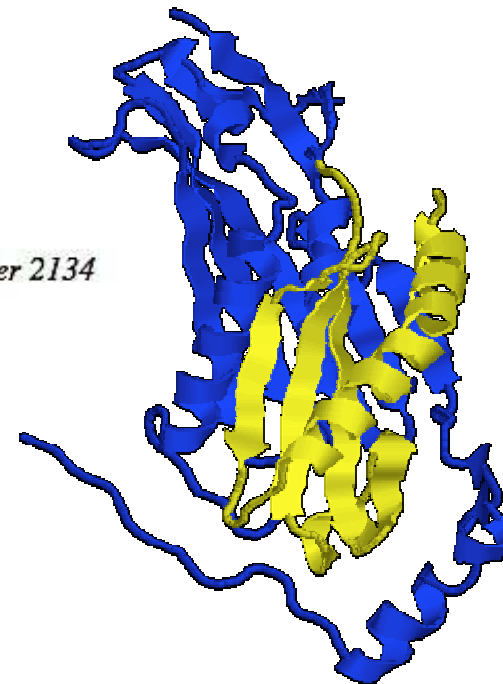
3.1 Exosome Core > Fold

1. Root: [scop](#)
2. Class: [Alpha and beta proteins \(a+b\)](#) [53931]
Mainly antiparallel beta sheets (segregated alpha and beta regions)
3. Fold: [Ribosomal protein S5 domain 2-like](#) [54210]
core: beta(3)-alpha-beta-alpha; 2 layers: alpha/beta; left-handed crossover
4. Superfamily: [Ribosomal protein S5 domain 2-like](#) [54211]
Superfamily
5. Family: [Ribonuclease PH domain 1-like](#) [54229]
6. Protein: Exosome complex exonuclease 1, ECX1 [159923]
7. Species: [Sulfolobus solfataricus](#) [TaxId: 2287] [159924]
SQ Q9UXC2 8-155 Rrp41
SQ Q9UXC0 1-191 Rrp42



Rrp41

1. Root: [scop](#)
2. Class: [Alpha and beta proteins \(a+b\)](#) [53931]
Mainly antiparallel beta sheets (segregated alpha and beta regions)
3. Fold: [Ribonuclease PH domain 2-like](#) [55665]
beta(2)-alpha-beta(2)-alpha; 3 layers: alpha/beta/alpha; antiparallel sheet: order 2134
4. Superfamily: [Ribonuclease PH domain 2-like](#) [55666]
Superfamily
5. Family: [Ribonuclease PH domain 2-like](#) [55667]
6. Protein: Exosome complex exonuclease 1, ECX1 [160590]
7. Species: [Sulfolobus solfataricus](#) [TaxId: 2287] [160591]
SQ Q9UXC2 156-248 Rrp41
SQ Q9UXC0 192-275 Rrp42



Rrp42

3.1 Exosome Core > Fold

First of all, we do a STAMP to study the structural conservation between the two subunits. As you can see at the image and the output, the structure is quite conserved instead the 23% sequence identity



3.1 Exosome Core > Fold

The RNase PH-like domains contain 4 regions implicated in different tasks:

- **Region I**: Residues interacting with region III of the same polypeptide to the maintenance of the fold
- **Region II**: Residues involved in the intermolecular contact to establish the heterodimers between Rrp41-Rrp42
- **Region III**: Residues that form the phosphate binding surface
- **Region IV**: Residues that are forming the catalitical site

Although the 2 subunits have the same RNase PH-like domain, they differ in the capacity of develop the phosphorolytic action, so the difference must be in the RIV

<i>Rrp42_Sso/1-273</i>	1 GHMSSTPSNQNIIP I I K K E S I V - S L F E K G R Q D G R K L T D Y R P L S I T L D Y 48
<i>Rrp41_Sso/1-233</i>	1 - - - - - R - - P K - L I L D D - - G R T D G R K P D E L R S I K I E L G V 29
<i>Rrp42_Sso/1-273</i>	49 A K K A D G S A L V K L G T T M V L A G T K L - E I D - - K - - P Y E D T P N Q G N L I M N V E L 92
<i>Rrp41_Sso/1-233</i>	30 L K N A D G S A I F E M G N T K A I A V Y G P K E M H P R H L S L - - P D R A V L R V R Y H M 75
<i>Rrp42_Sso/1-273</i>	93 L P L A Y E T - F E P G P P D E N A I E L A R V V D R S L R D S K A L D L T K L V I E P G K S V W 140
<i>Rrp41_Sso/1-233</i>	76 T P F S T D E R K N P A - P S R R E I E L S K V I R E A L E S - - A V L V E L F P - - - - R - - T 115
<i>Rrp42_Sso/1-273</i>	141 T V W L D V Y V L D Y G G N V L D A C T L A S V A A L Y N T K V Y K V E Q I S V N K N E V V G K L 189
<i>Rrp41_Sso/1-233</i>	116 A I D V F T E I L C A D A G S R L V S L M A A S L A L A D A - - - - - G I 147
<i>Rrp42_Sso/1-273</i>	190 P L N Y P V V T I S V A K V D K Y L V V D P D L D E E S I M D A K I S F S Y T - P D L K I V G I Q 237
<i>Rrp41_Sso/1-233</i>	148 P M R D L I A G V A V G K A D C V I I L D L N E T E D M W G E A D M P I A M M P S L N Q V T L F Q 196
<i>Rrp42_Sso/1-273</i>	238 K S G K G S M S L Q D I D Q A E N T A R S T A V K L L E E L K K H L G I - - - - 273
<i>Rrp41_Sso/1-233</i>	197 L N - - G S M T P D E F R Q A F D L A V K G I N I I Y N L E R E A L - K S K Y V 233

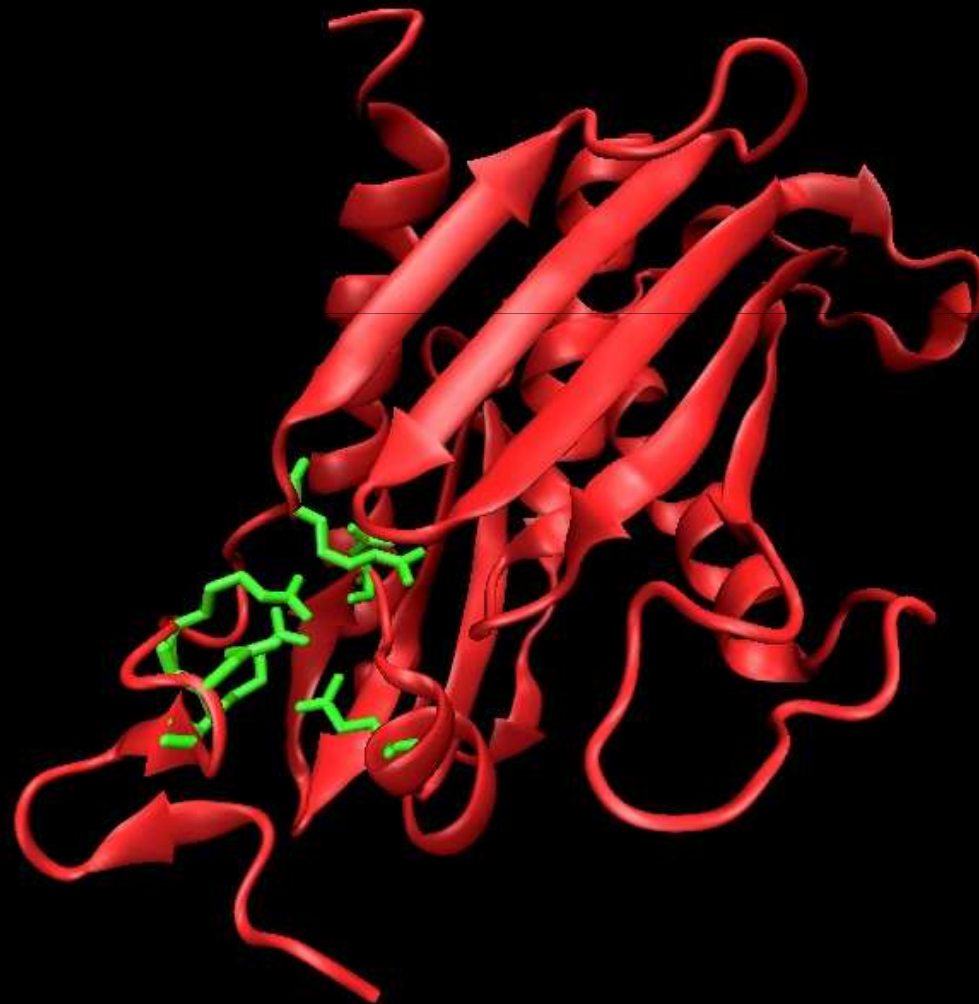
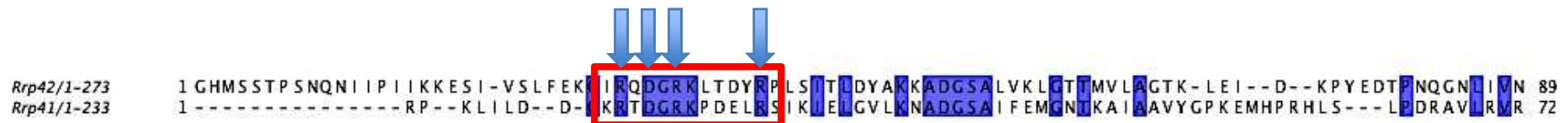
3.1 Exosome Core > Fold

Rrp42/1-273 1 GHMSSTPSNQNIPPIKKESI-VSLFEK **I RQDGRK** LTDYRPLSITLDYAKKADGSA LVKLGTIMVL AGTK-LEI--D--KPYEDT NQGNLIVN 89
Rrp41/1-233 1 -----RP--KLILD--D- **KRTDGRK** PDELSIKIELGVLNADGSA IFEMNTKAI AAVYGPKEMHPRHLS---LPDRAV RVR 72



Rrp42

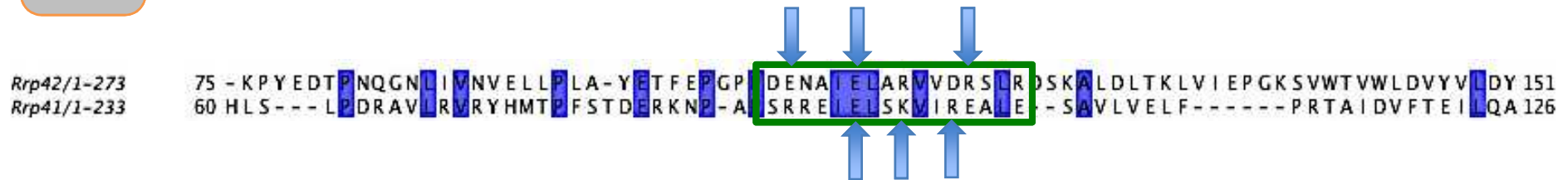
3.1 Exosome Core > Fold



Rrp41

3.2

Exosome Core > Interaction between subunits

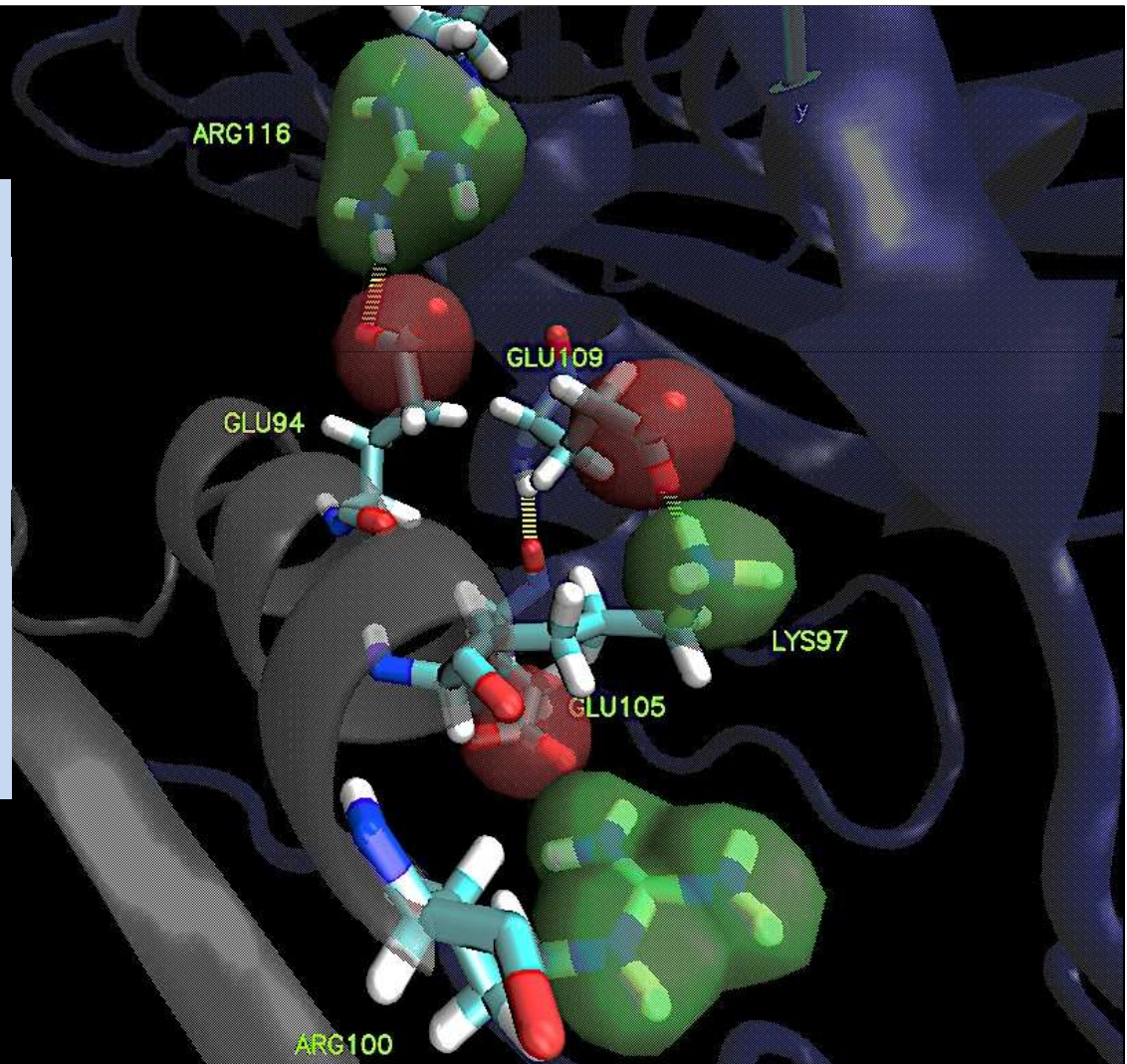


Hydrogen bonds

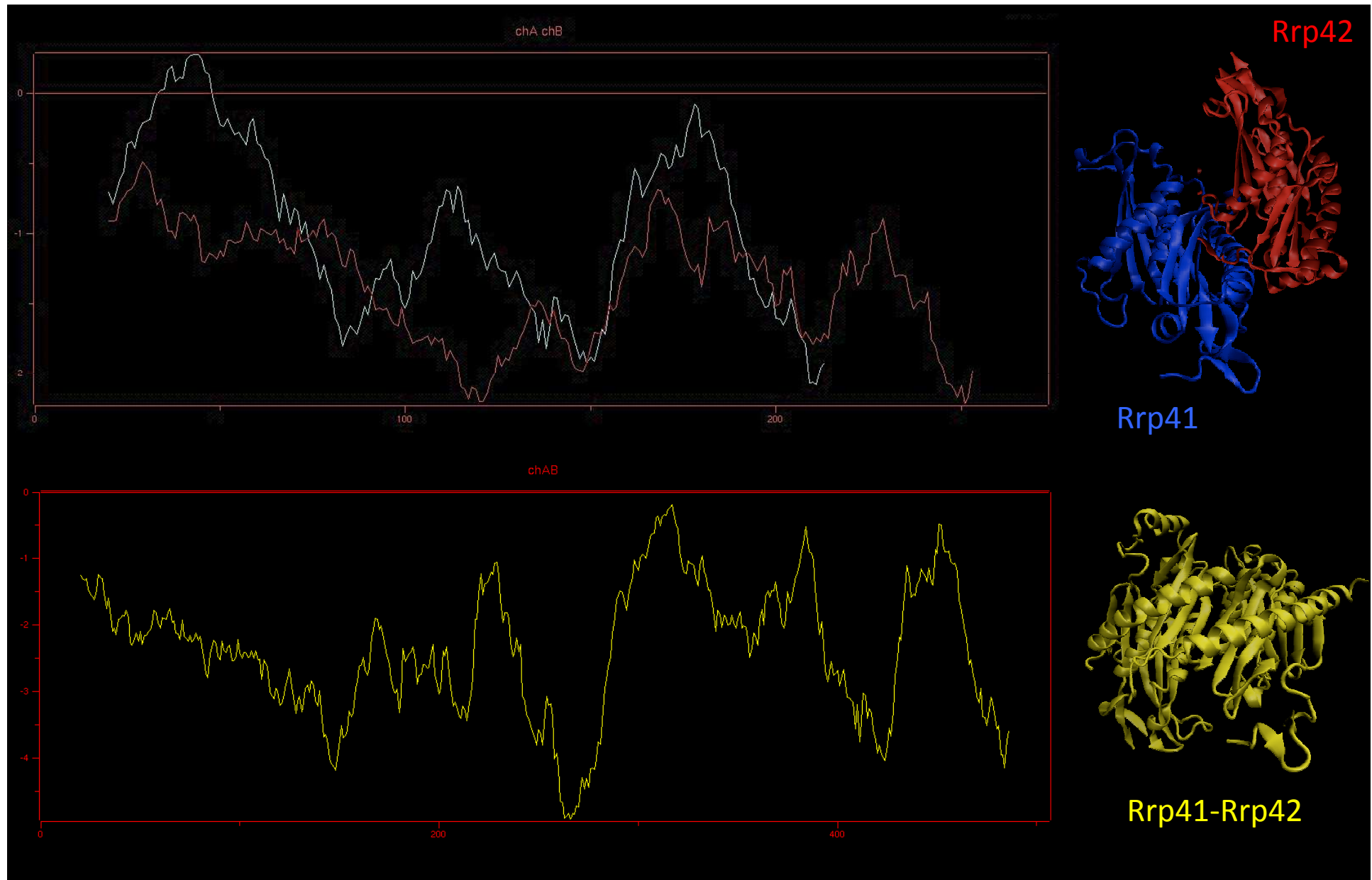
LYS97-GLU109	1'65 A	154'07 °
GLU105-GLU109	1'77 A	163'43 °
ASG116-GLU94	1'98 A	153'19 °

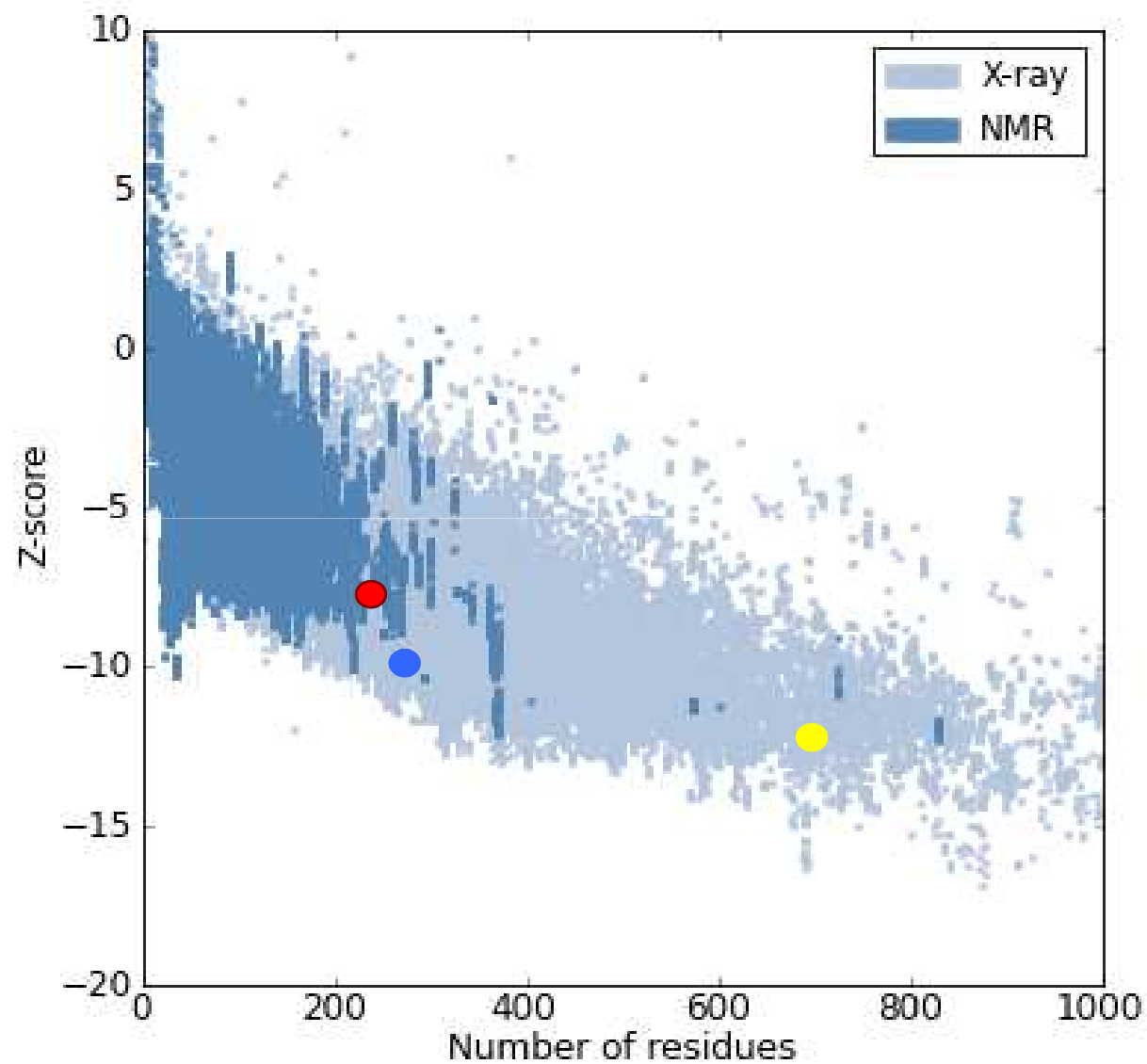
Salt bridges

ARG116-GLU94	2'84 A
GLU109-LYS97	2'63 A
ARG100-GLU105	2'88 A

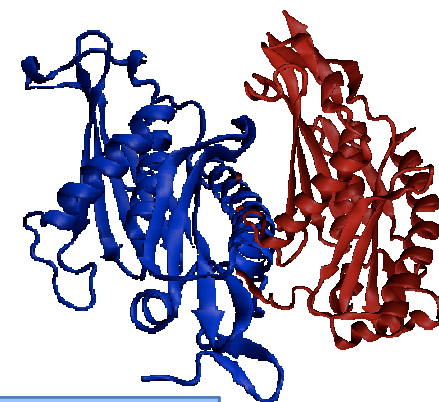


3.2 Exosome Core > Interaction between subunits





Rrp42
Length 273
Zscore -9'38



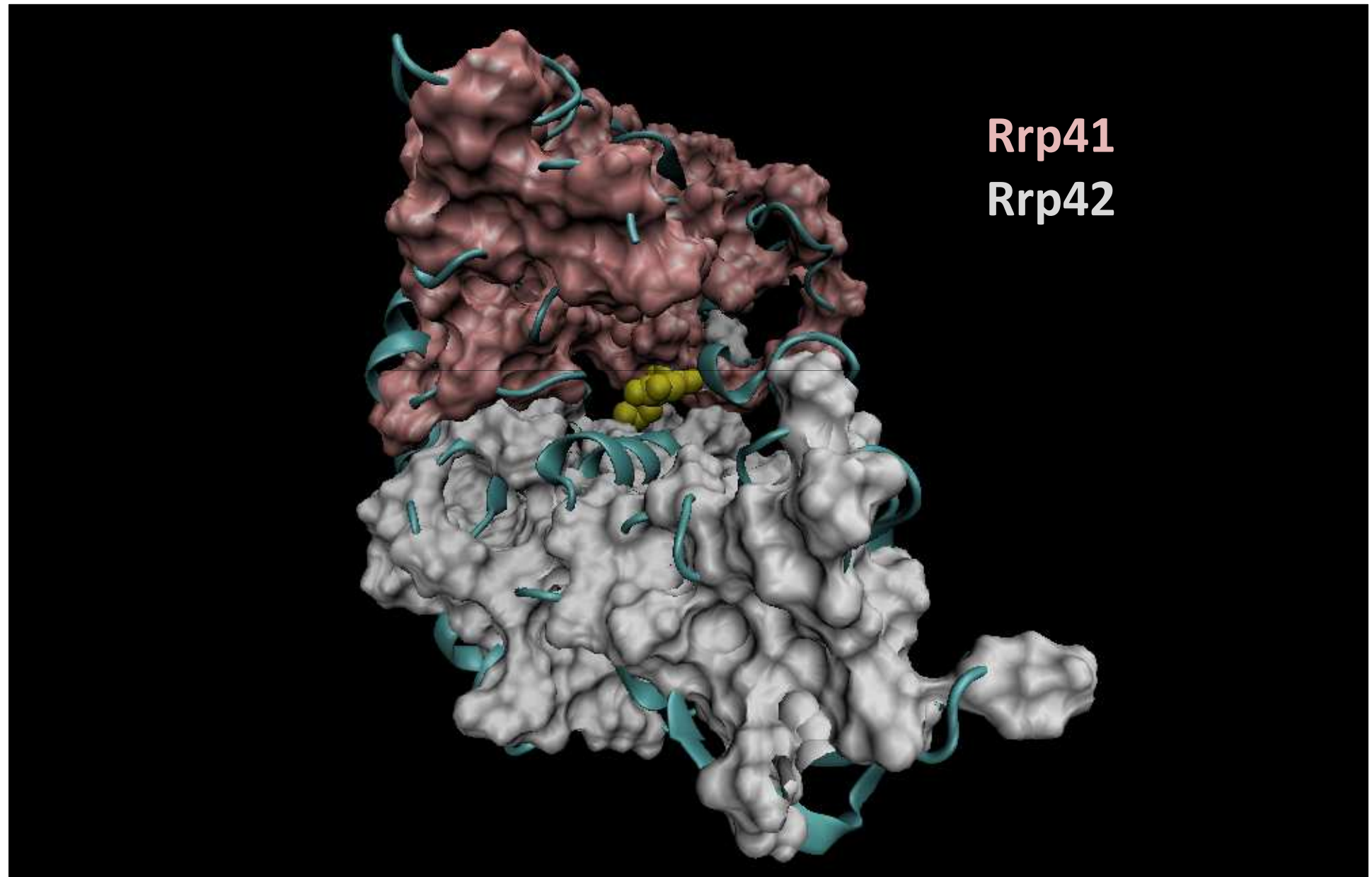
Rrp41
Length 233
Zscore -7'33



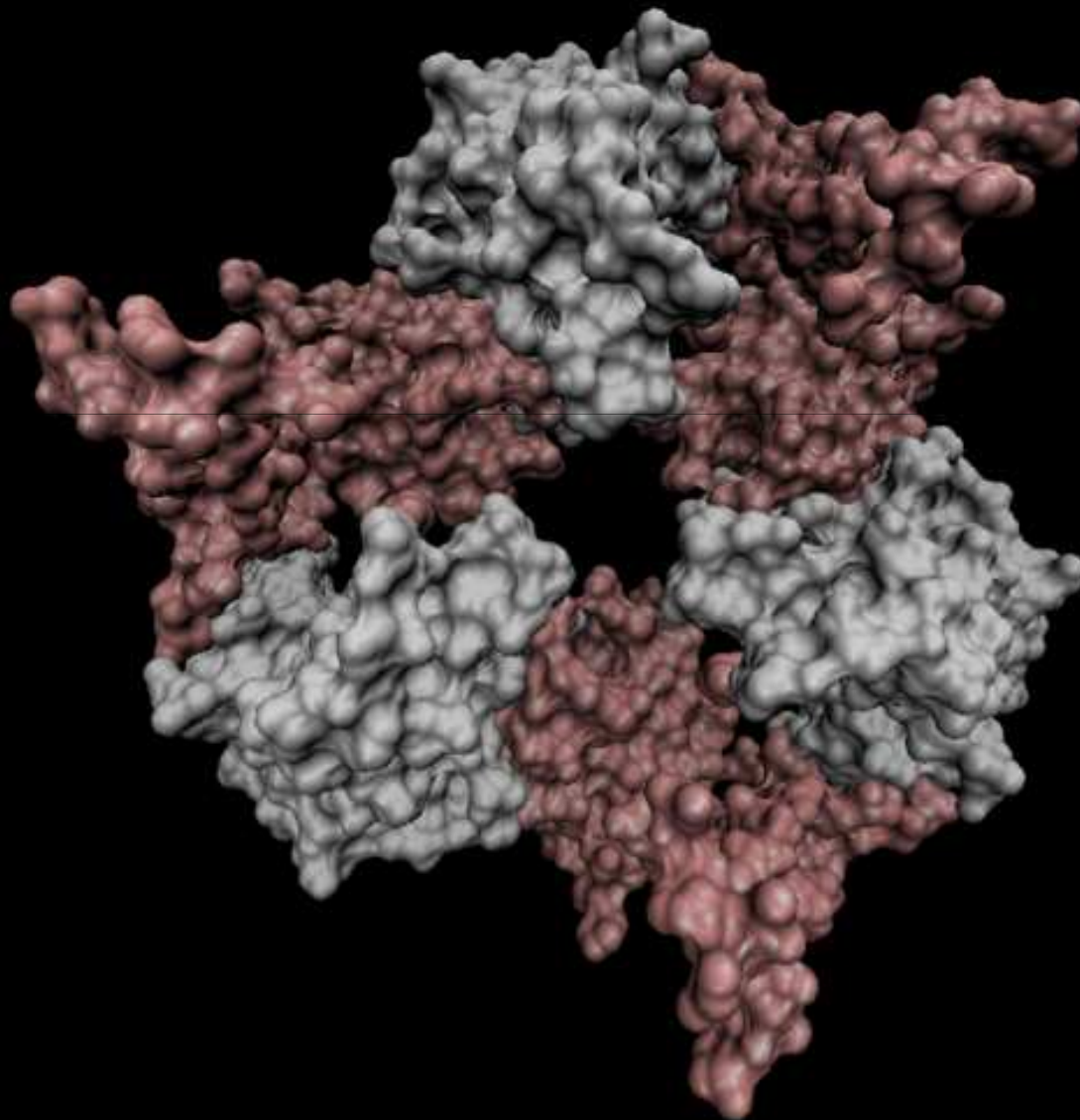
Rrp41-42
Length 739
Zscore -11'74

Rrp41-rrp42

3.2 Exosome Core > Interaction between subunits

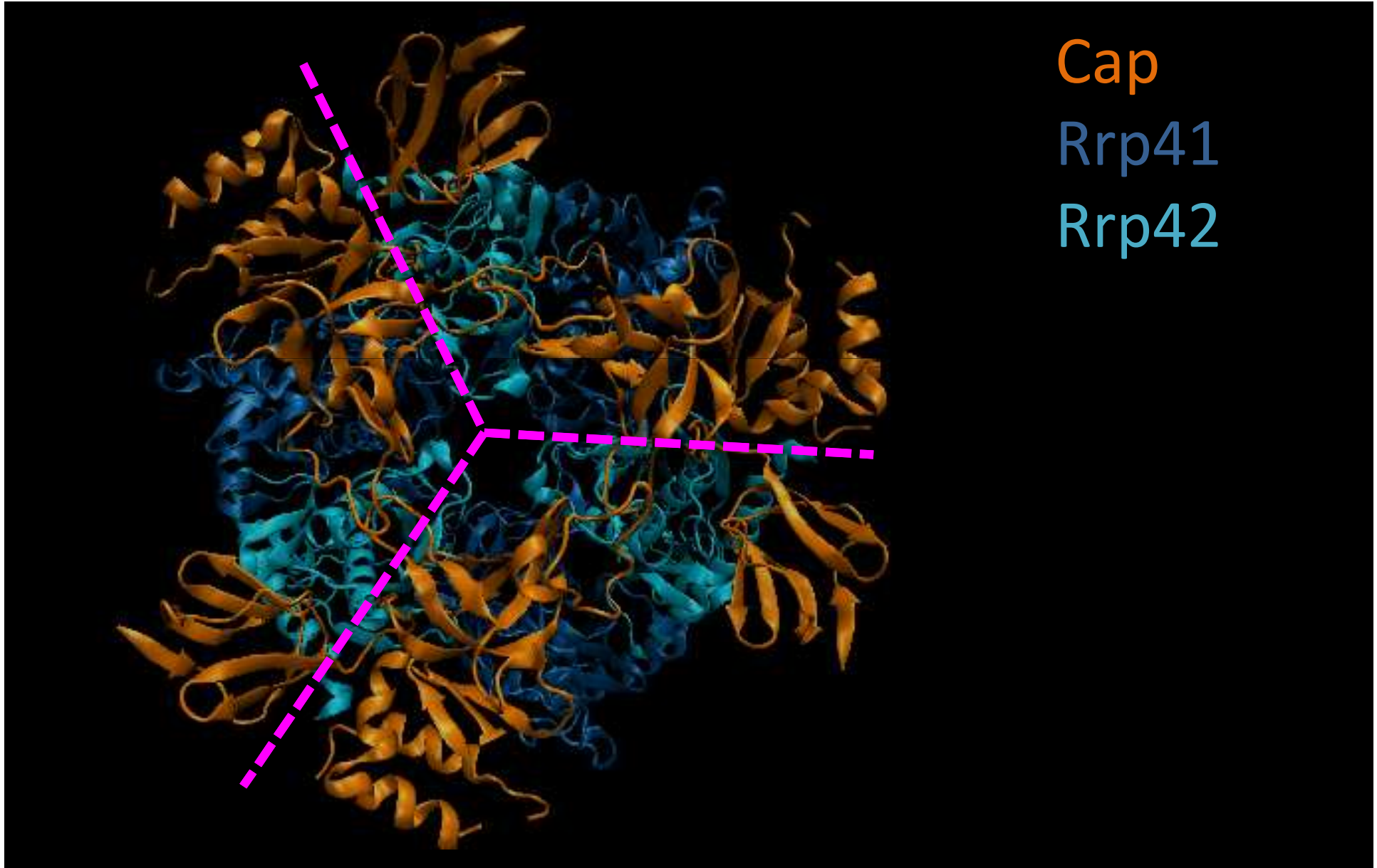


3.2 Exosome Core > Interaction between subunits

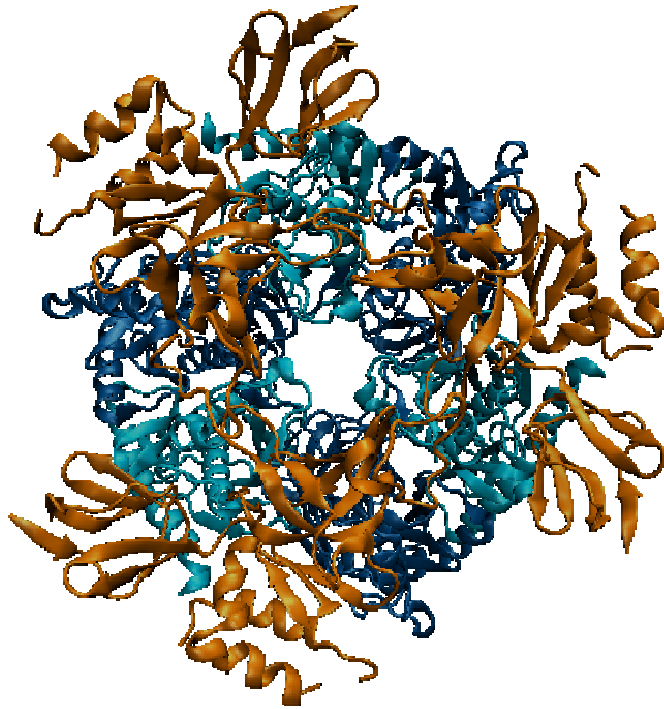


Rrp41
Rrp42

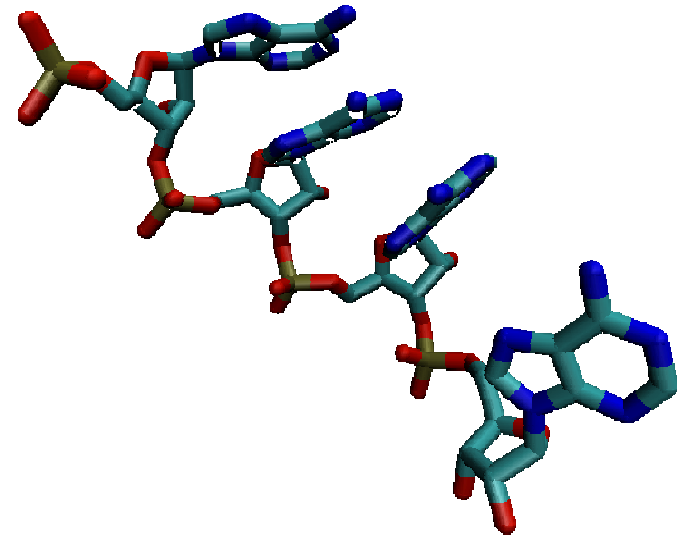
3.2 Exosome Core > Interaction between subunits



3.3 Exosome Core > Interaction with RNA

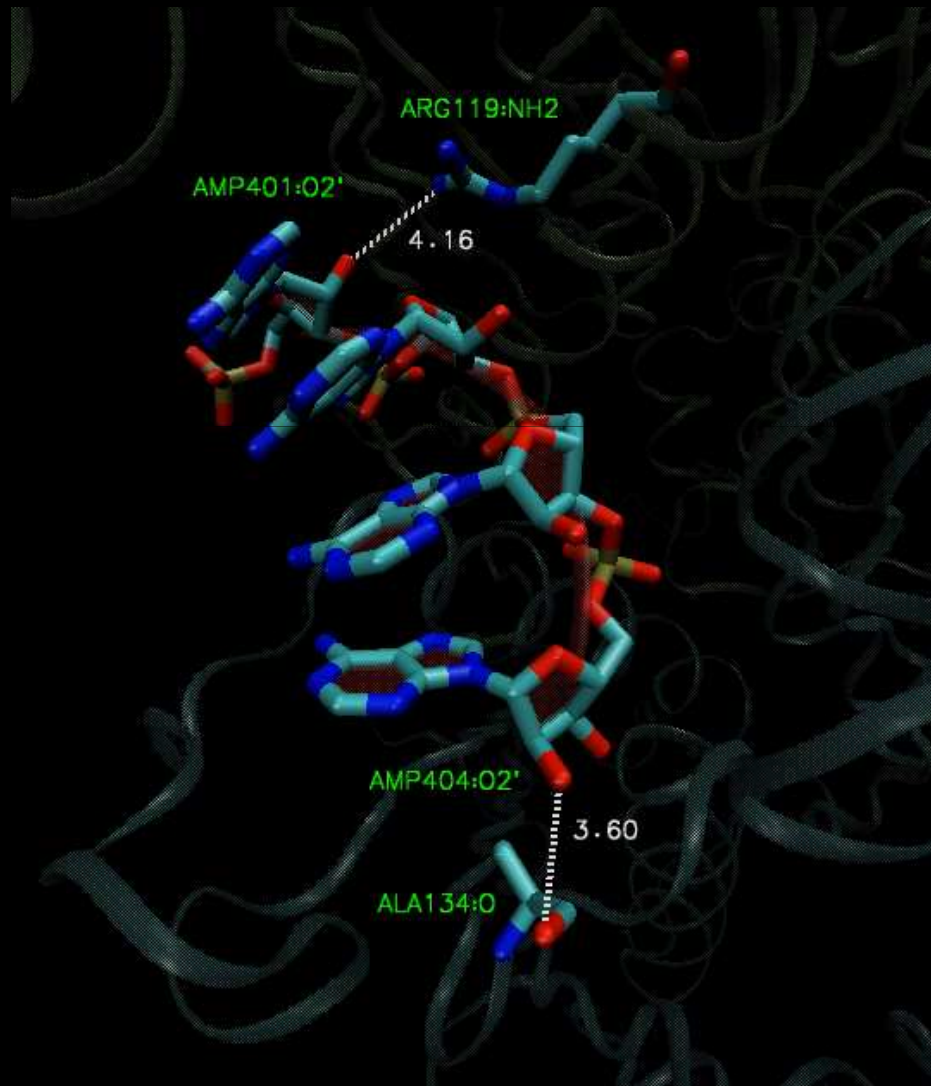


RNA specific

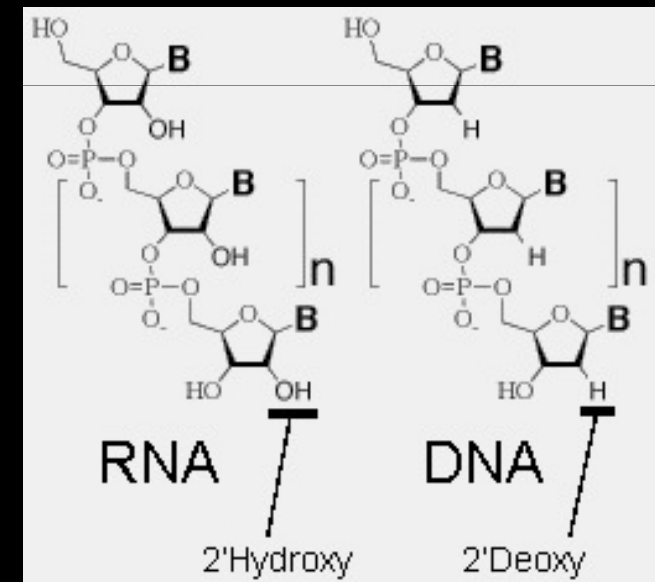


Sequence unspecific

3.3 Exosome Core > Interaction with RNA

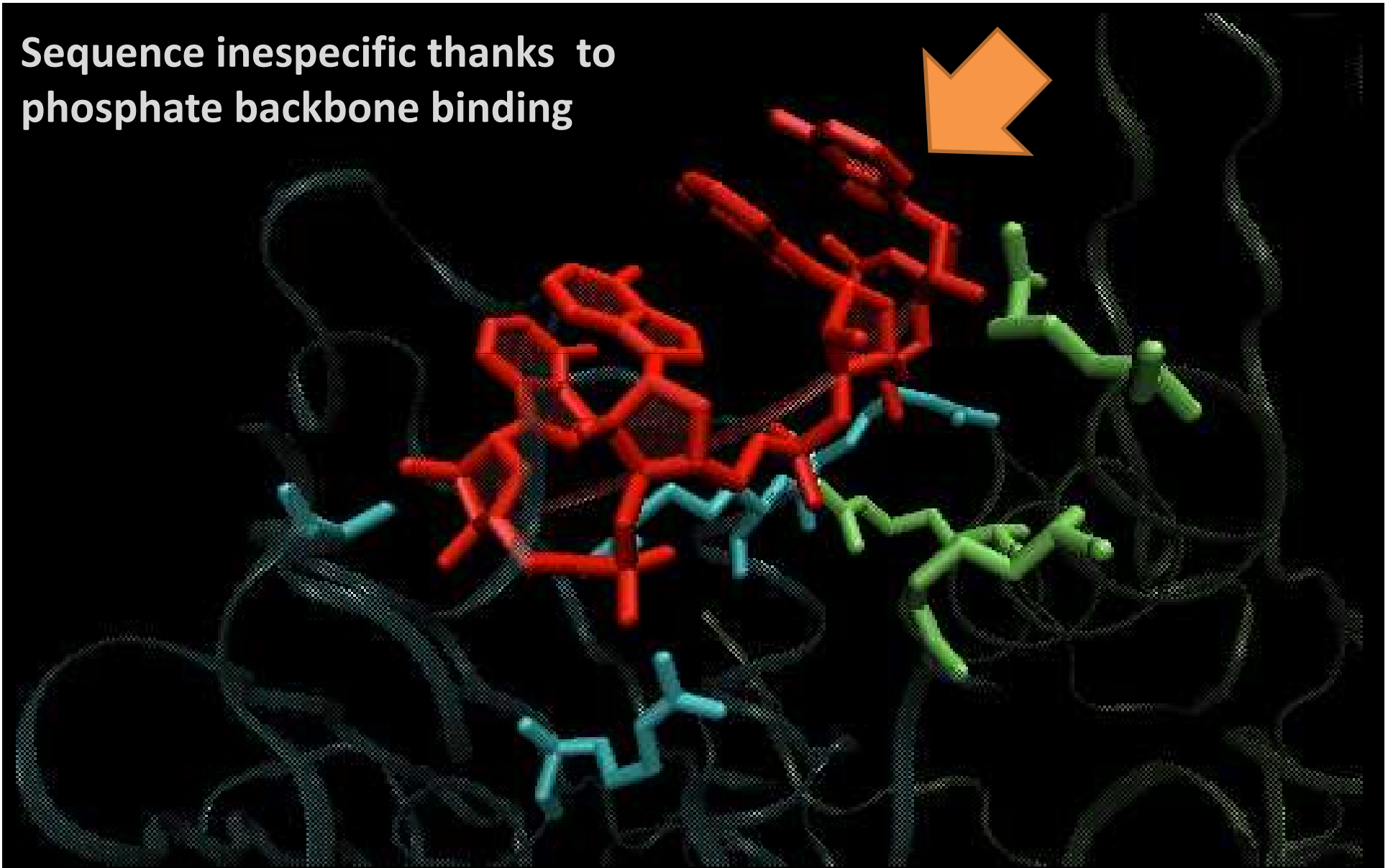


RNA specific thanks
to the 2'OH binding



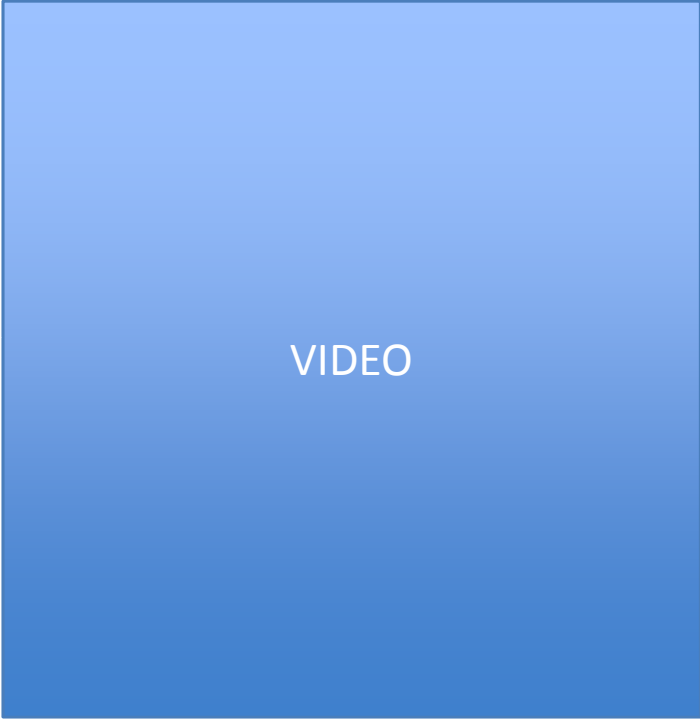
3.3 Exosome Core > Interaction with RNA

Sequence inespecific thanks to
phosphate backbone binding



3.3 Exosome Core > Interaction with RNA

The pathway of RNA within the archaeal Exosome

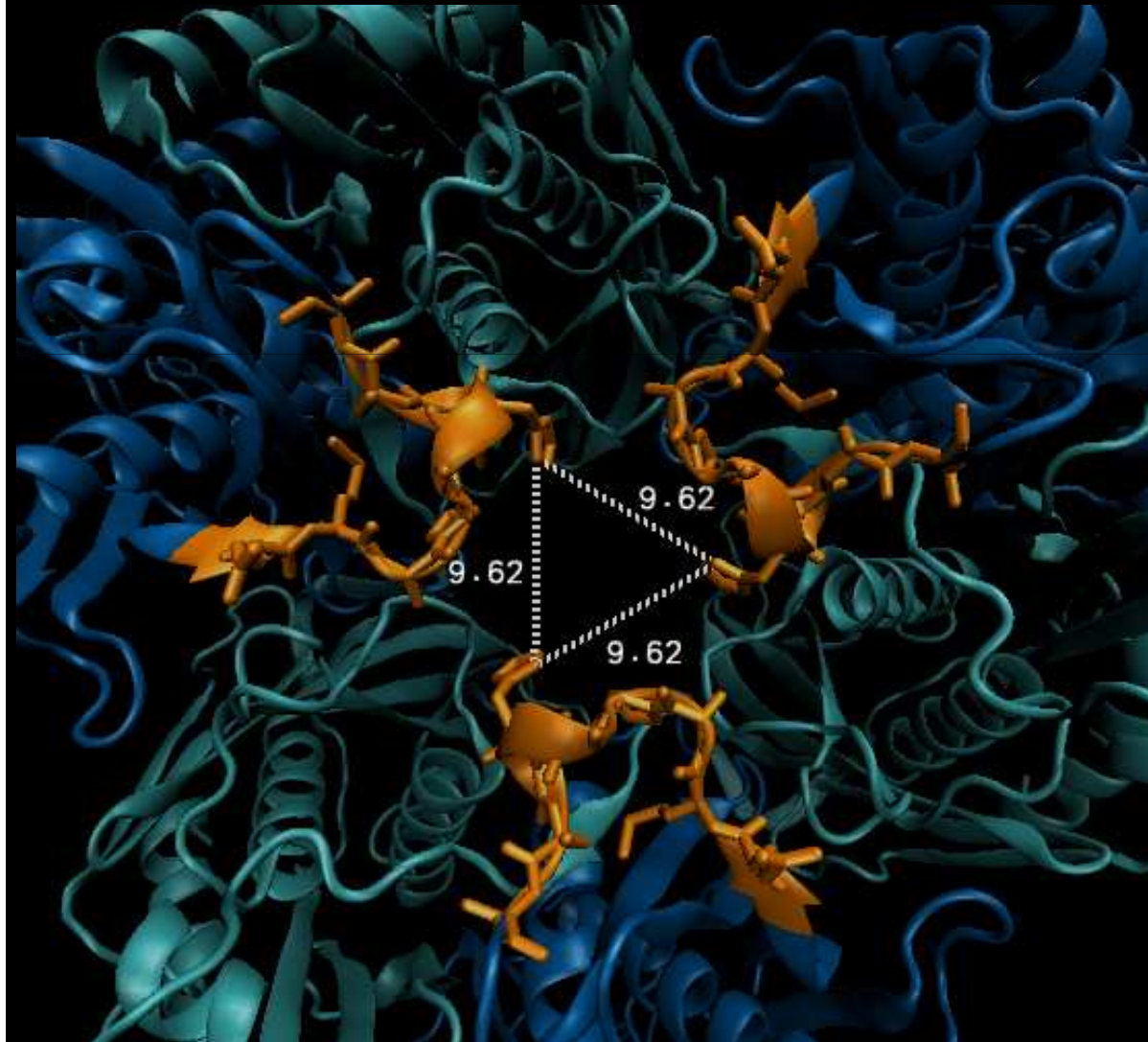


VIDEO

1. Interaction with the CAP
2. 1st interaction surface
3. 2nd interaction surface within the central channel
1. Active site: Degradation
2. Removal of monophosphates

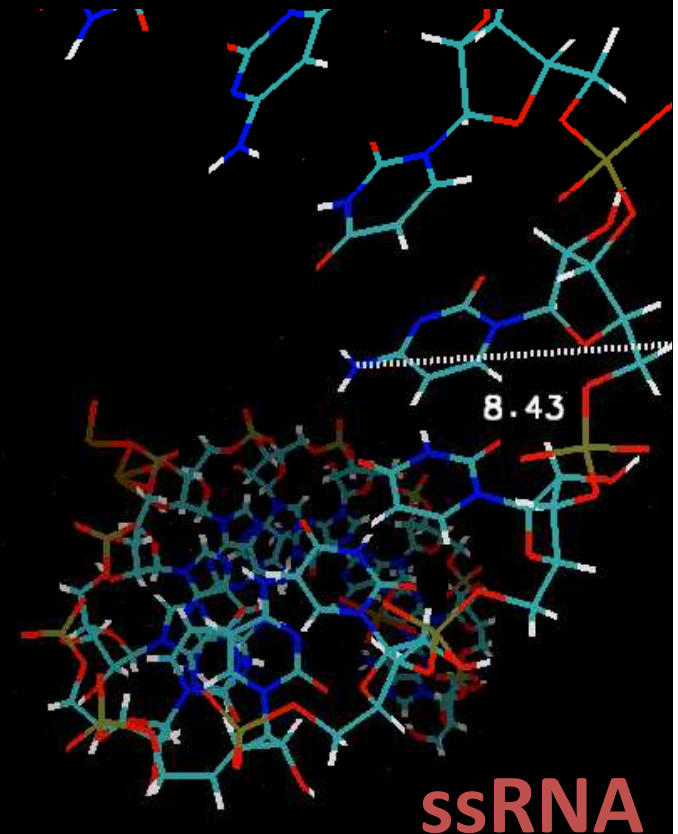
3.3 Exosome Core > Interaction with RNA

1st inteaction surface: The 10A neck of Rrp41



Rrp41

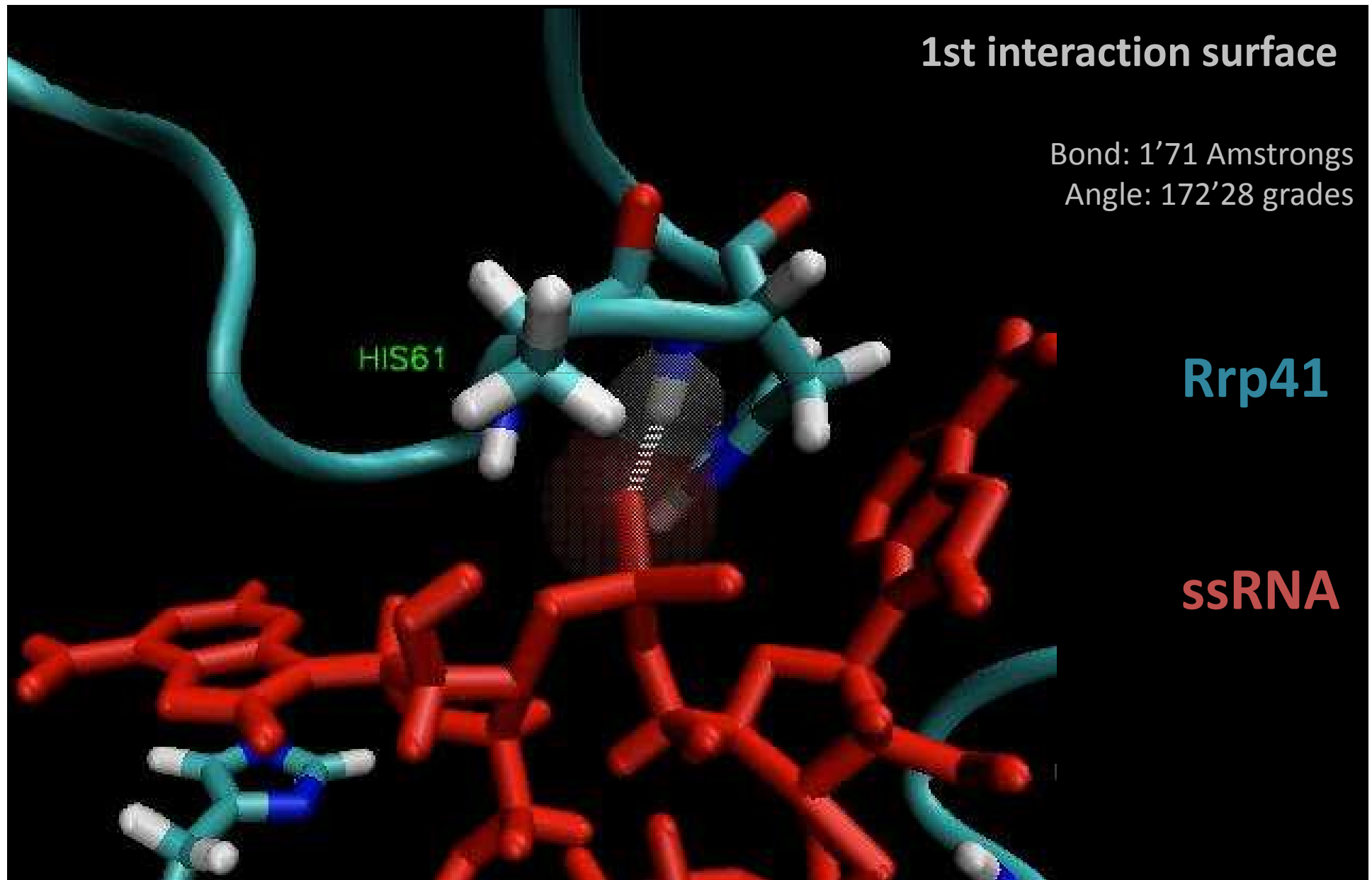
Rrp42



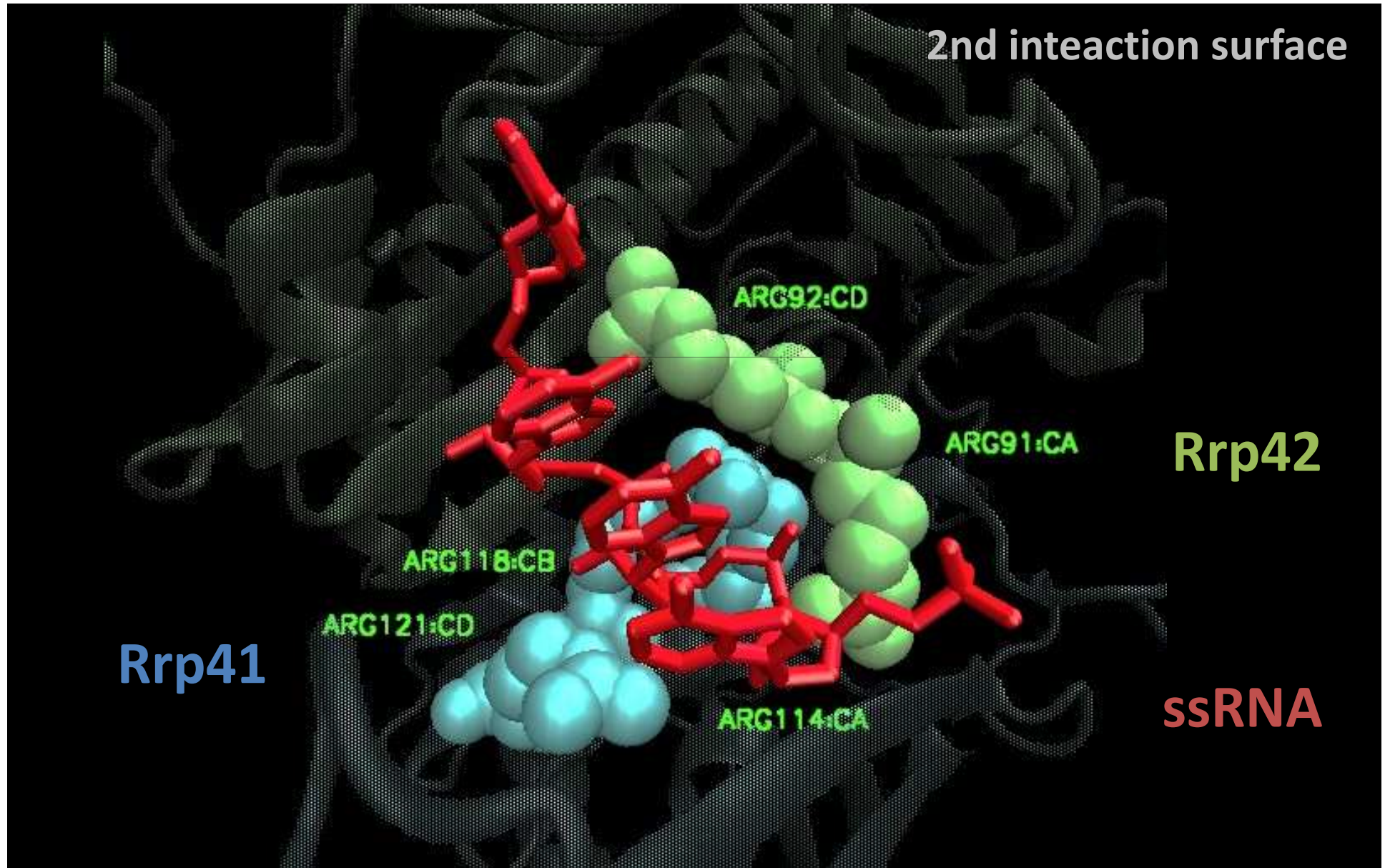
ssRNA

3.3

Exosome Core > Interaction with RNA



3.3 Exosome Core > Interaction with RNA



3.3 Exosome Core > Interaction with RNA

2nd inteaction surface

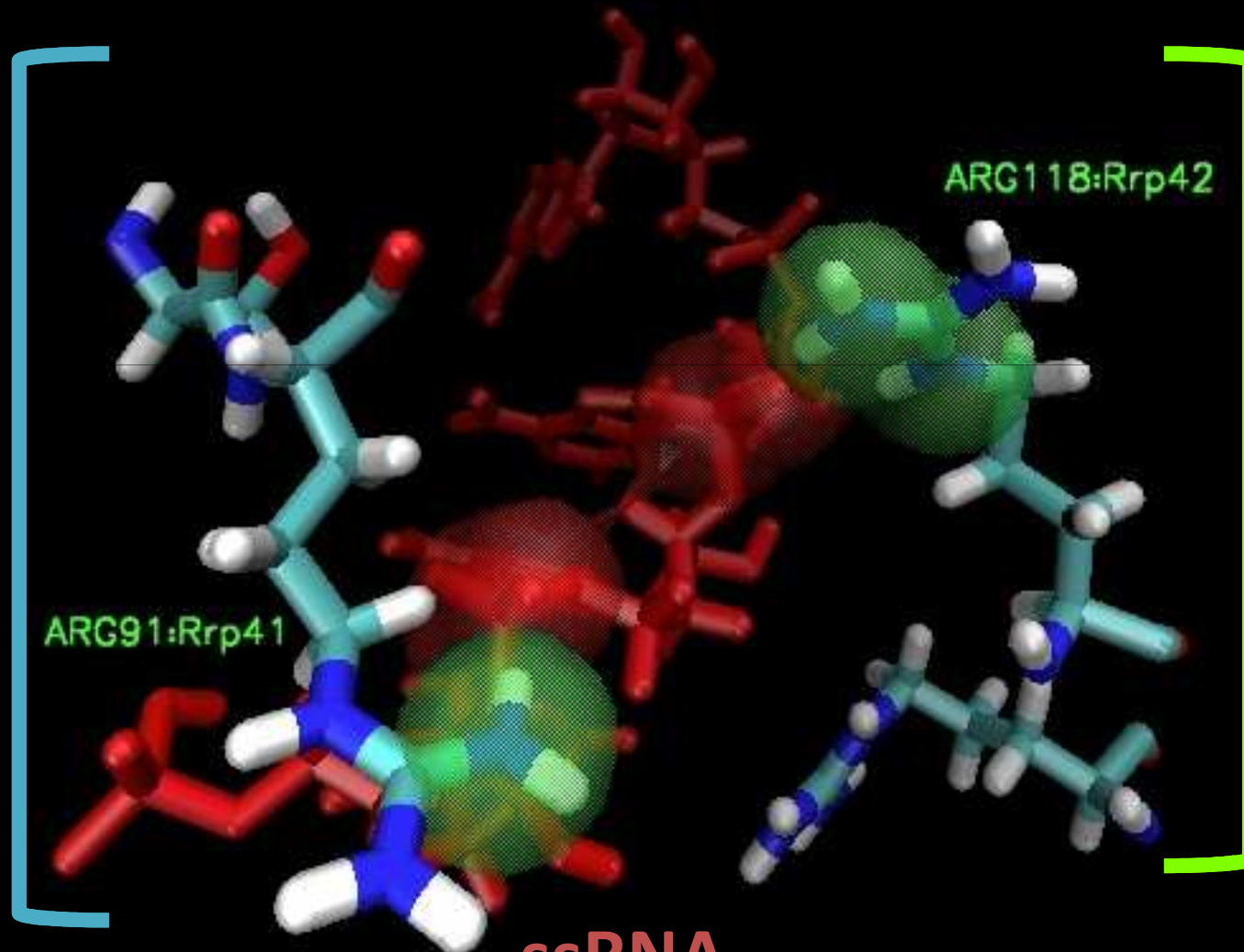
Rrp41

ARG91:Rrp41

ARG118:Rrp42

Rrp42

ssRNA



3.3 Exosome Core > Interaction with RNA

ACTIVE SITE



Rrp42

Rrp41

Active Site

3.3

Exosome Core > Interaction with RNA

Rrp42/1-273 90 VELLPLA-YETFE^{PGPI}DENAE^{ELARVVDRS}LRDSKALDLTKLVI^{EPGKSVWTVWLDVYV}LDYGGNVLD^{ACTLASVAALYN}KY
Rrp41/1-233 73 YHMT^{PFSTD}ERKNP^{ASRREIELSKMIREA}EE--SAVLVELF-----PRTAIDVFTEI^{LCADAGSRLVSLMAASLA}AD--

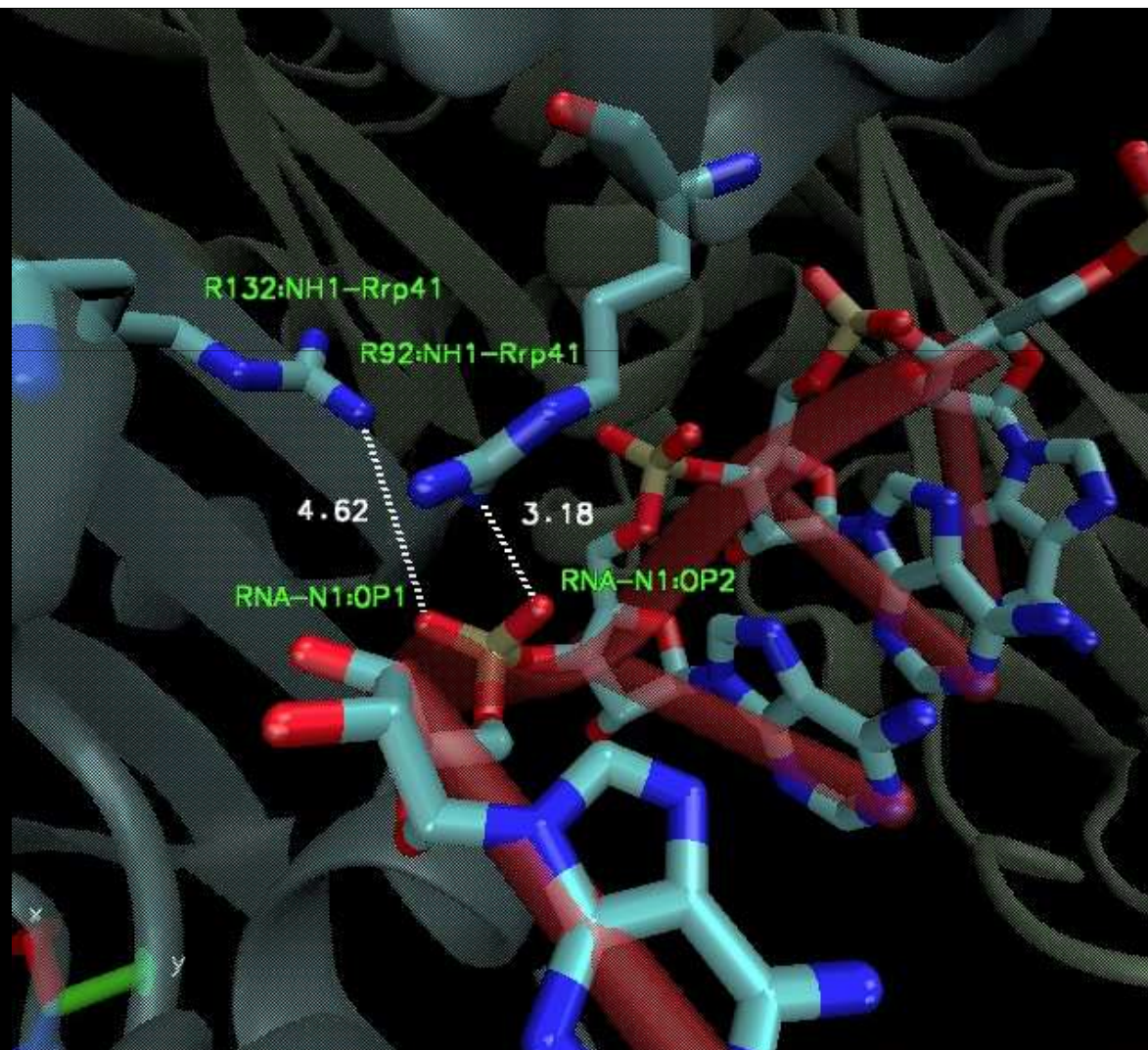


Rrp42

Rrp41

ssRNA

ACTIVE
SITE



3.3

Exosome Core > Interaction with RNA

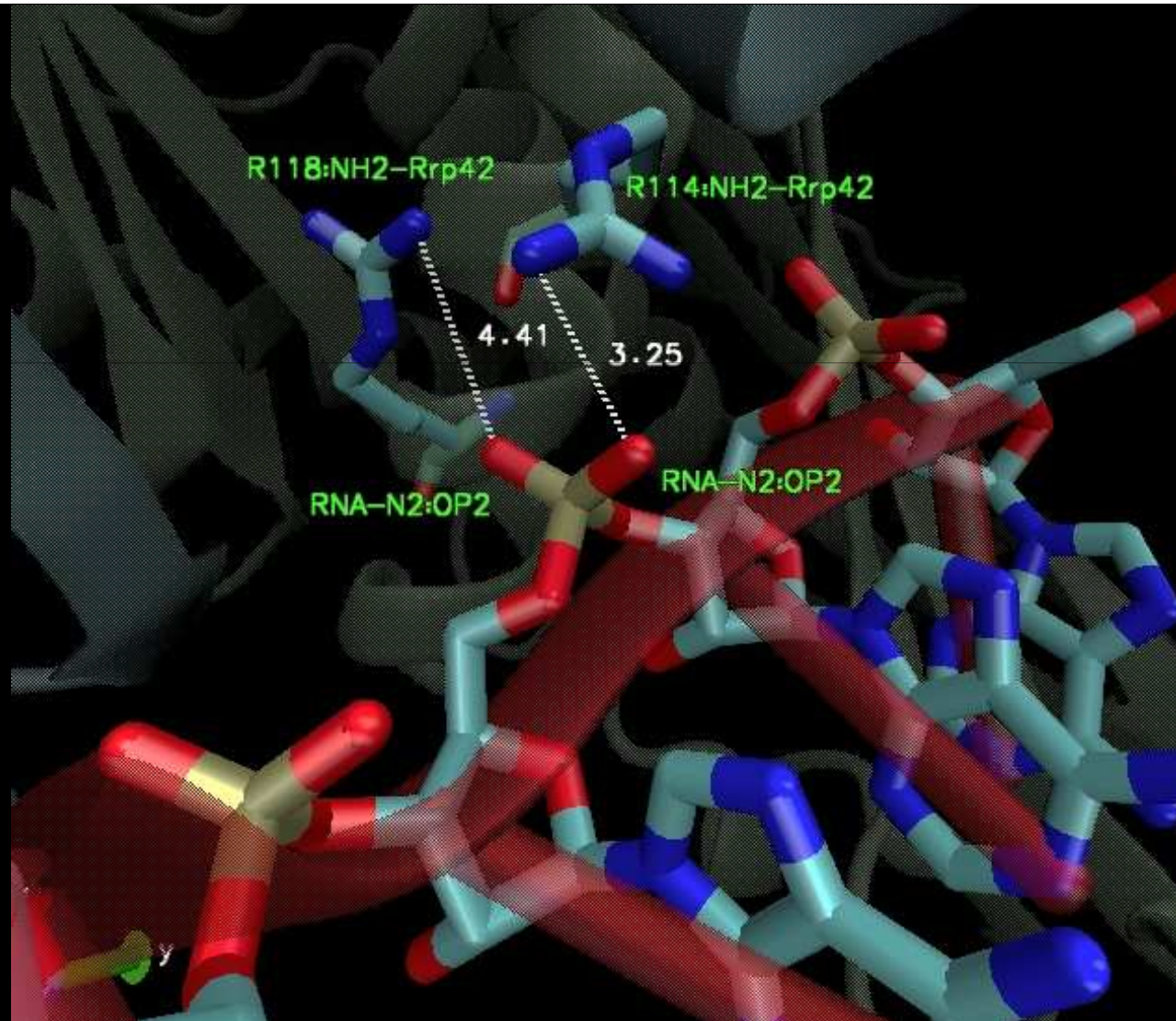


ACTIVE
SITE

Rrp42

Rrp41

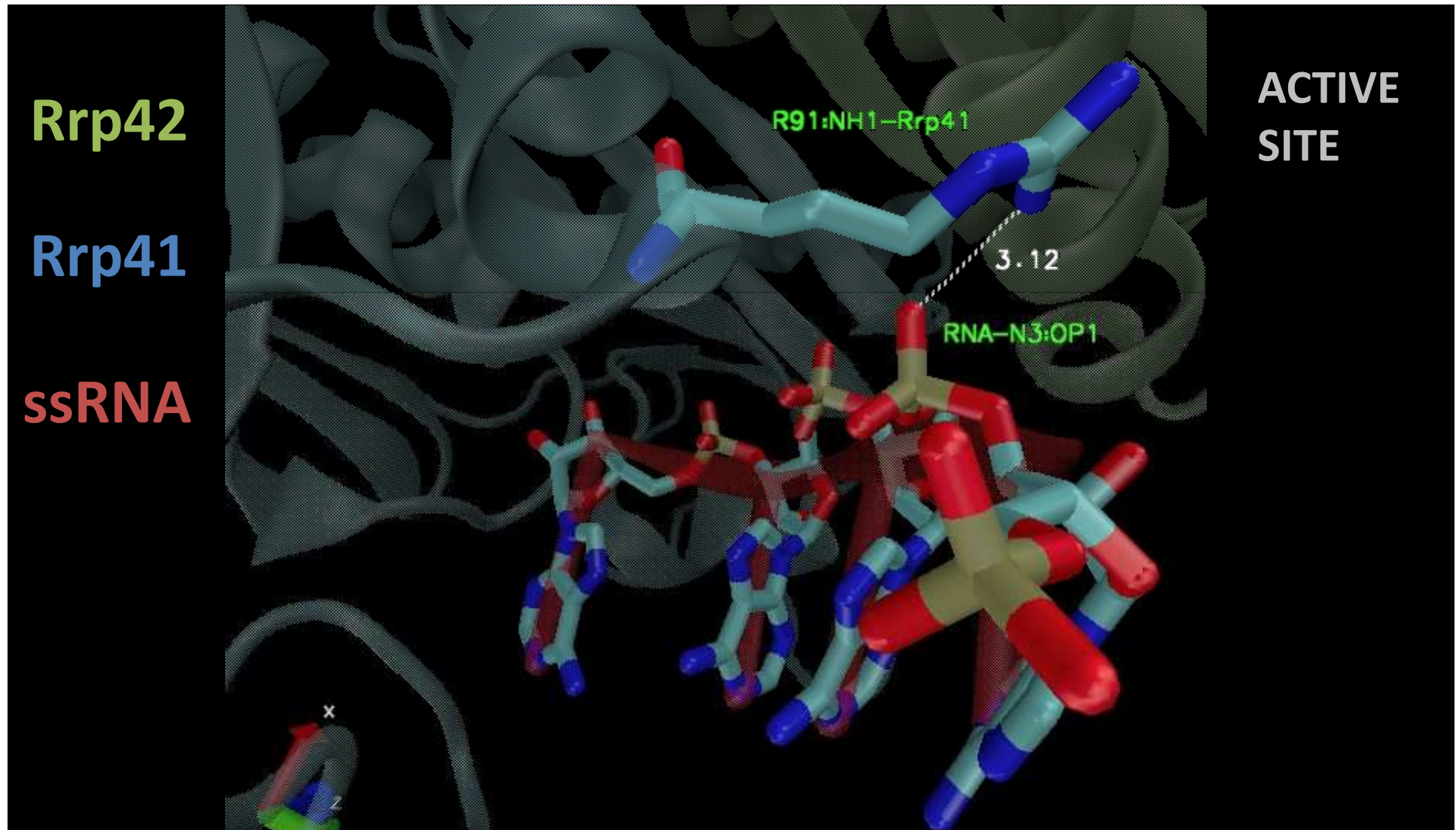
ssRNA



3.3

Exosome Core > Interaction with RNA

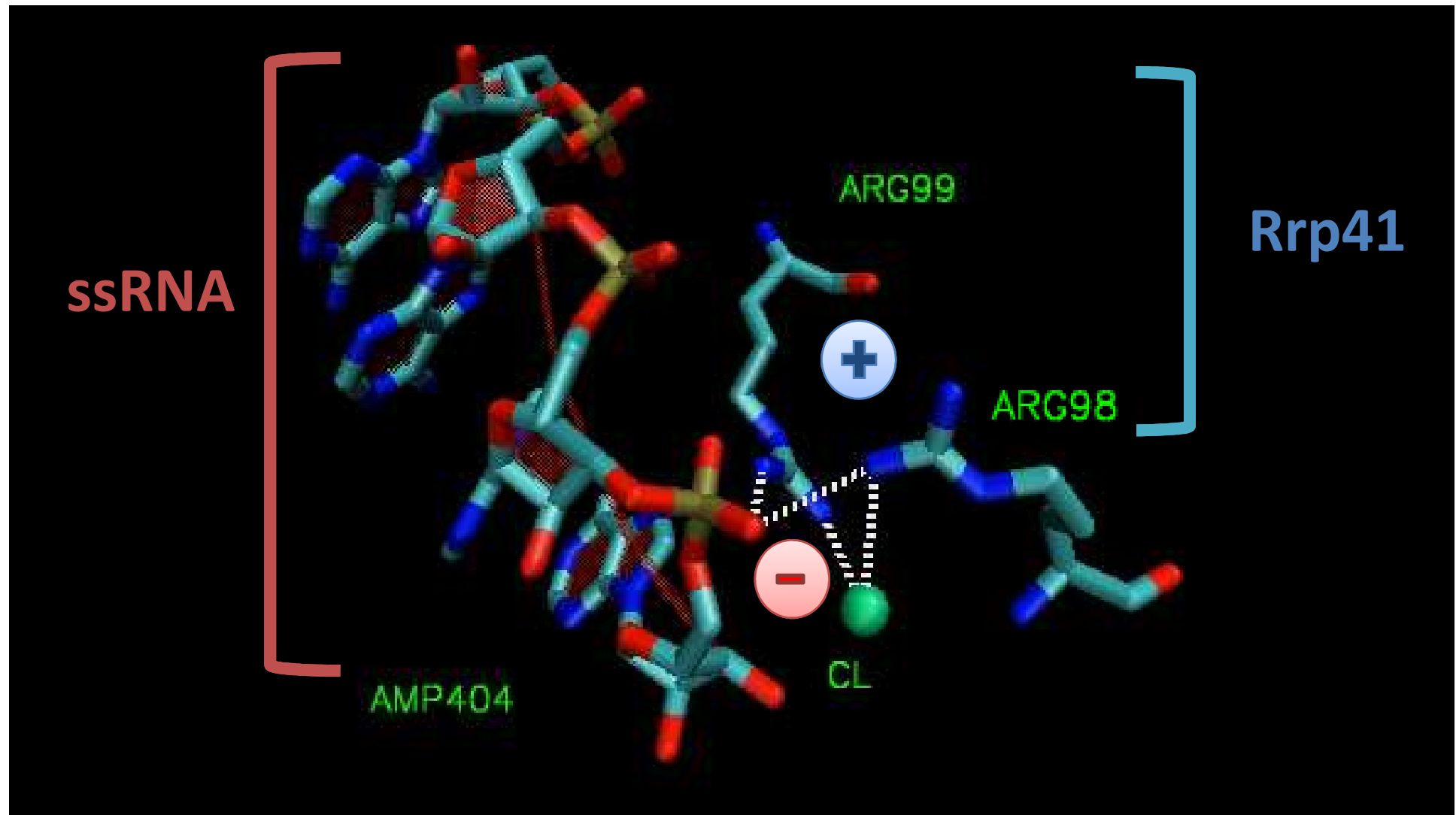
Rrp42/1-273 90 VELLPLA-YETFE^{PGP}DENA^{ELAR}VDRSLRDS
 Rrp41/1-233 73 YHMT^{PF}STD^{ERKNP}-A^{SRRE}ELSKMIREALE--



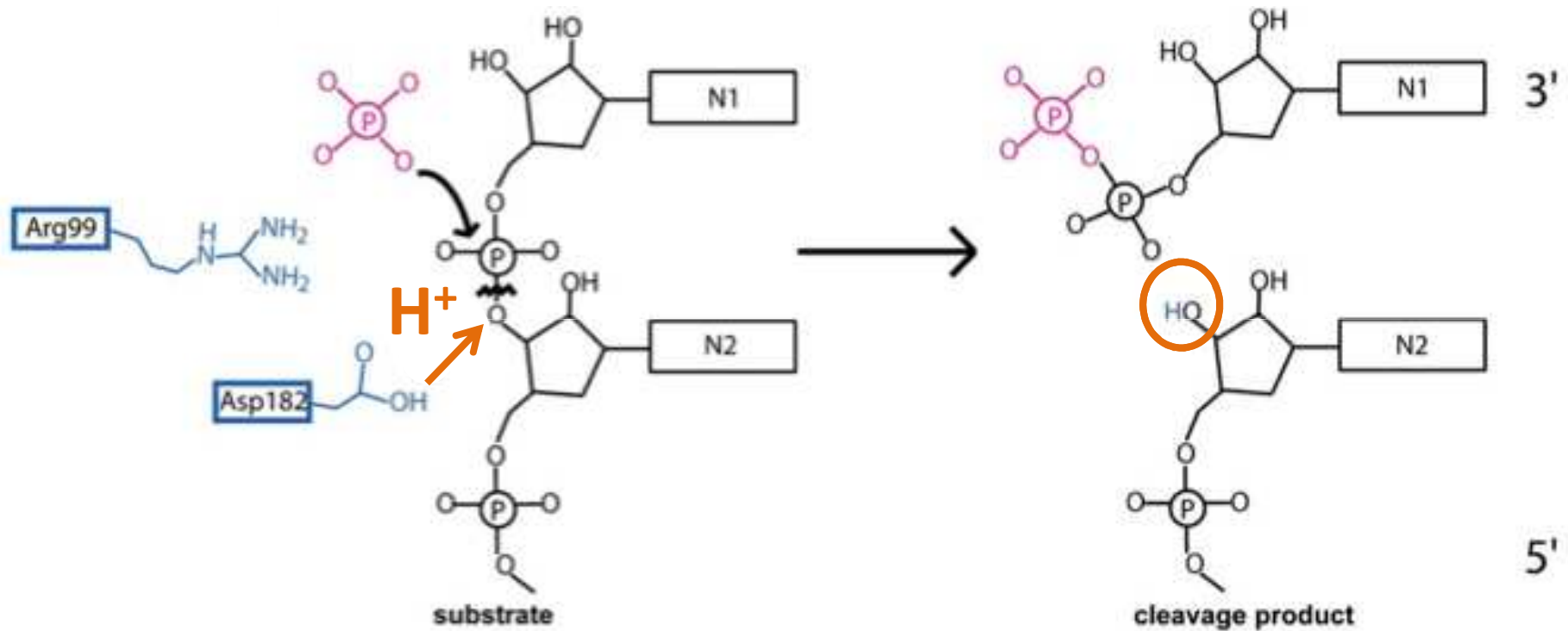
3.3

Exosome Core > Interaction with RNA

Rrp42/1-273 90 VELLPLA-YETFEPPDENAEELARVDRSLRQSKALDLTKLVI EPGKSVWTVWLDVYVLYGGNVLDACTLASVAALYNK
Rrp41/1-233 73 YHMTPFSTDERKNP-ASRRFEISKVIREAF--SAVLVELF-----PRTAIDVFTEICADAGSRLVSLMAASLAAD--

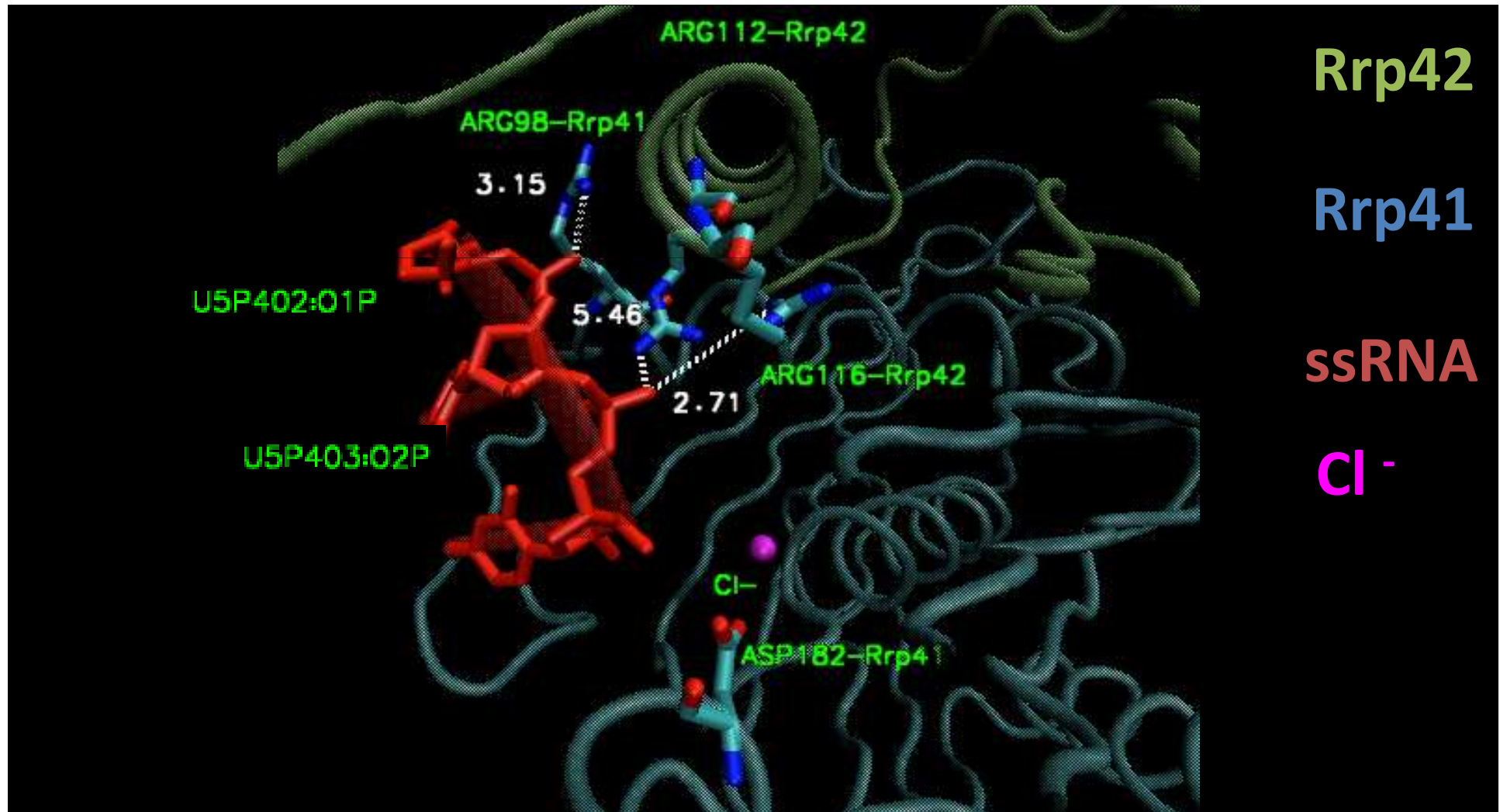


3.3 Exosome Core > Interaction with RNA



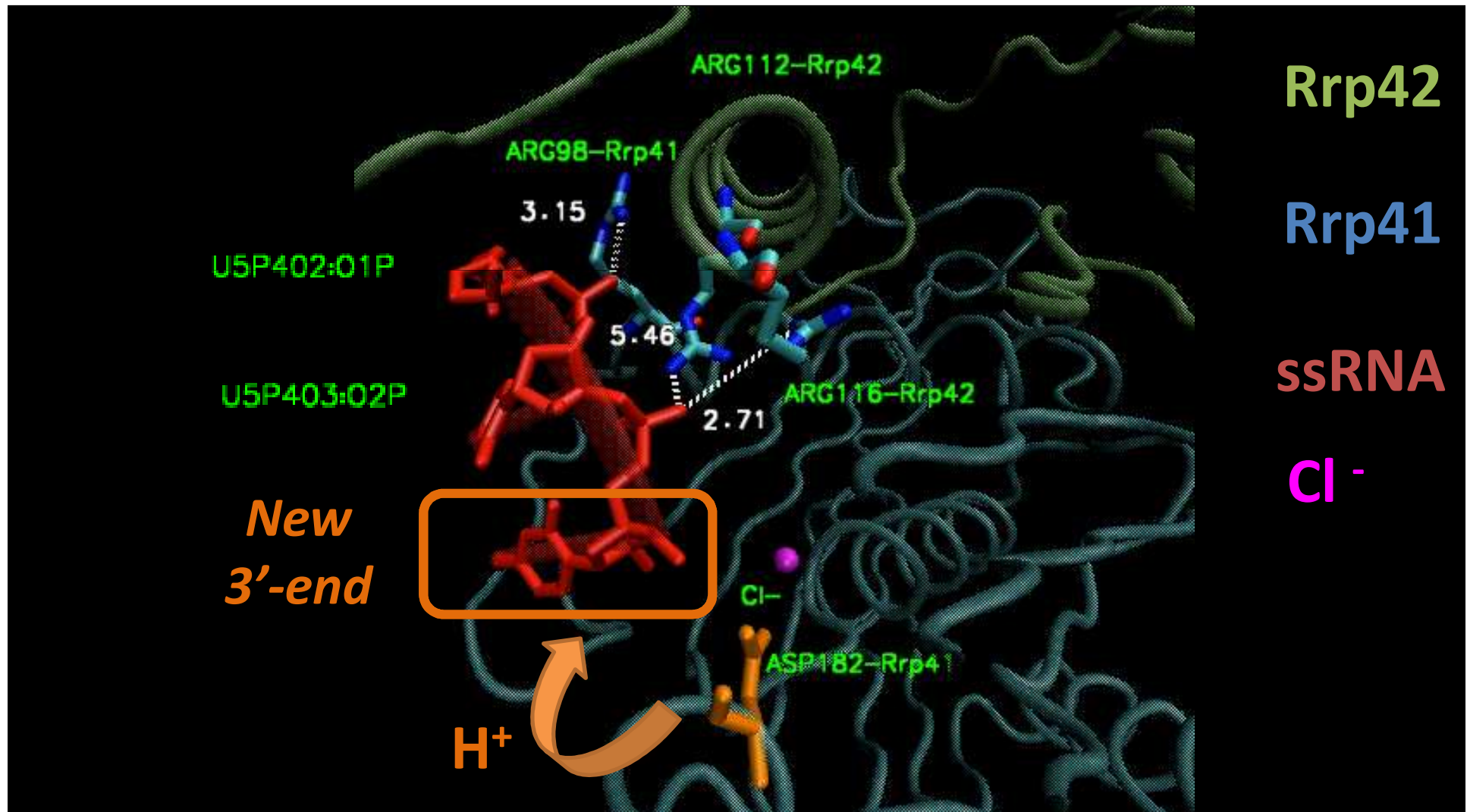
3.3

Exosome Core > Interaction with RNA



3.3

Exosome Core > Interaction with RNA



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- 1.3. Exosome structure

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4

EVOLUTION OF THE EXOSOME

- 4.1. Evolution of the Cap subunits
- 4.2. Evolution of the Core subunits

4.3

Evolution of the CAP subunits > Csl4

Structure-based alignment: STAMP

```

csl4a/1-179  1 MRFVMP . . . . . GD . . . RIGSAEEYVKGEGVYEEGGELFA . . . . . AVAGKLI IKDRVAKV . . 46
csl4eu/1-180 1 . . . . . RYCIPGERLCNLEE . . . . . GSPGSGTYTRHGYIFSSLAGCLMKSSSE . . . . . NG43

csl4a/1-179 47 . . . . . E . . SISPIPEIVKGDVVLGRVVDLRNSIALIEVSSKKGENRG-PSNRGIGILHVSINVDEGYVKEISEAV112
csl4eu/1-180 44 ALPVVSVVRET-ESQLLPDVGAI VTCKVSSINSRFAKVHILYV-GSMPLKNSFRGTIRKEDVRATEKDKVEIYKSF117

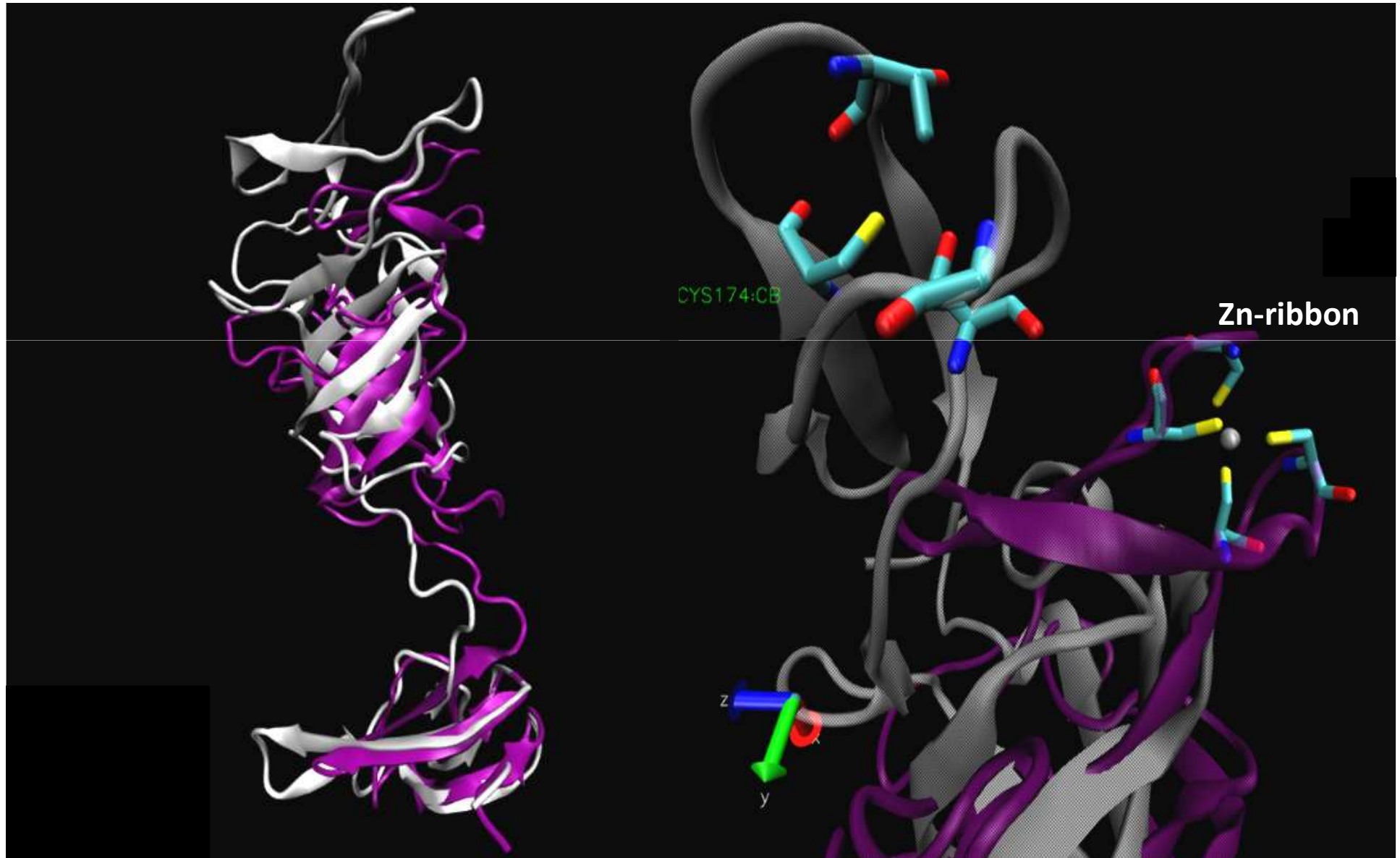
csl4a/1-179 113 GYLDILKARVIG . . . . . DNLRLSTKEEEMQVLRALCSNCKTEMVREG-DILKCPECGRVEKPKISTDYGKGEW 179
csl4eu/1-180 118 RPGDIVLAKVISLGDAQSNYLLTTAENELGVVVAH-SESGIQMVPI SWCEMQCPKTHTKFRKV . . . . . 180

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	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)
Pair	1	csl4ss	csl4eu	4.31	1.44	179	180	212	109	106	0	26.42	100.00	8.95e-07

4.3

Evolution of the CAP subunits > Csl4



4.3

Evolution of the CAP subunits > Rrp4

Structure-based alignment: STAMP

```

Rrp4Euk/1-250  1  - - - - - H L V V P G D T I T T D - T G F M R G H G T Y M G E E K L I A S V A G S V E R V N K L I C V K A L K - T R Y I G E V G D I V 60
Rrp4Ss/1-207  1  Q E I V L Q P R S I V V P G E L L A E G E F Q I P W S P Y I L K I N S K Y Y S T V V G L F D V K D T Q F E V I P L E G S F Y Y P K I N D I V 70

Rrp4Euk/1-250  61  V G R I T E V Q Q K R W K V E T N S R L D S V L L L S S M - - - - N - - E L A - M R G F L Q E G D L I S A E V Q A V F S D G A V S L H T - R 122
Rrp4Ss/1-207  71  I G L V E D V E I Y G W V V D I K A P Y K A Y L P A S N - L L G R S I N V G E D L R R Y L D V G D Y V I A R I E N F D R S I D P V L S V K G 139

Rrp4Euk/1-250  123  S L K Y G K L G Q G V L V Q V S P S L - - - V - - K R Q K - T H F H - - - D L P C G A S V I L G N N G F I W I Y P T P E H G F I A N L E P V 183
Rrp4Ss/1-207  140  K - D L G R V S N G I V I D I M P V K V P R V I G K N - K S M - - - Y E T L T S K - - S I F V A N N G R I W - - - - - - - - - - - - - 186

Rrp4Euk/1-250  184  S L A D R E - V I S R L R N C I I S L V T - - - Q R M M L Y D T S I L Y C Y E A S L P H Q I K D I L K P E I M E E I V M E T R Q R L L E Q E 249
Rrp4Ss/1-207  187  - - - - - A F - S E - E - I L I E A I R K I E N E S H I K - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - 207

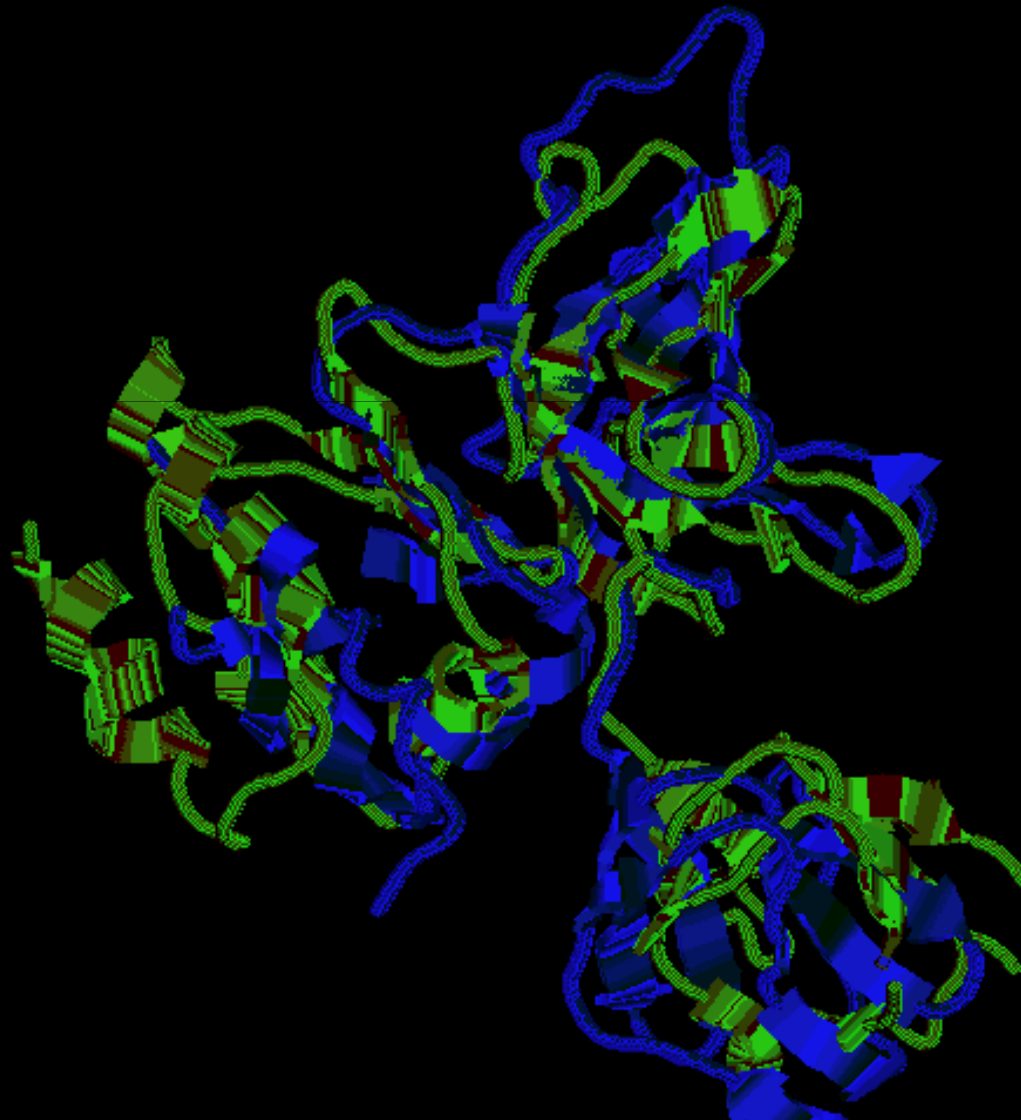
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Pair	1	2nn6H	2JE6I	3.74	2.14	250	207	229	129	123	0	26.83	100.00	2.34e-07

4.3

Evolution of the CAP subunits > Rrp4

Structure-based alignment: STAMP



RMSD: 2'14

Sc: 3'74

4.3

Evolution of the CAP subunits > Rrp4

Structure-based alignment: STAMP

```

Rrp40Euk/1-236  1 ARAA-RTVLG-QV V L P G E E - - L L L P E Q E D A E G P G G A V E R G D R L L V T K C G R L R H K E P G S G S G G - G 59
Rrp45s/1-207   1 - - - Q E I V L Q P R S I V V P G E L L A E G E F - - Q I P W S P Y I L K I - N S K Y Y S T V V G L F D V K - - - - - - - - - - DT 50

Rrp40Euk/1-236  60 V Y W V D S Q - Q K R Y V P V K G D H V I G I V T A K S G D I F K V D V G G S E P A S L S Y L S - F E C A T - - - K R N - R - P 116
Rrp45s/1-207   51 Q F E V I P L E G S F Y Y P K I N D I V I G L V E D V E I Y G W V V D I K A P Y K A Y L P A S N L L - G R S I N V G - E D L R R 112

Rrp40Euk/1-236  117 N V Q V G D L I Y G Q F V V A N K D M E P E M V C I D S C G R A N - G M G V I G Q D G L L F K V T L G L I R K L L - A P D C E I 178
Rrp45s/1-207   113 Y L D V G D Y V I A R I E N F D R S I D P V L S V - - - - - K G K D L G R - V S N G I V I D I M P V K V P R V I G K - N K S M 168

Rrp40Euk/1-236  179 I Q E V G K L Y P L E I V F G M N G R I W V K A K T I Q Q T L I L A N I L E A C - - - - E H M T S D Q R K Q I F S R L A E S 236
Rrp45s/1-207   169 Y E T L T S K - - S - I F V A N N G R I W - - A F - - S - E E I L I E A I R K I E N E S H I K - - - - - - - - - - 207

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	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)
Pair	1	2nn6G	2JE6	4.19	2.33	236	207	238	128	124	0	21.77	100.00	0.00013

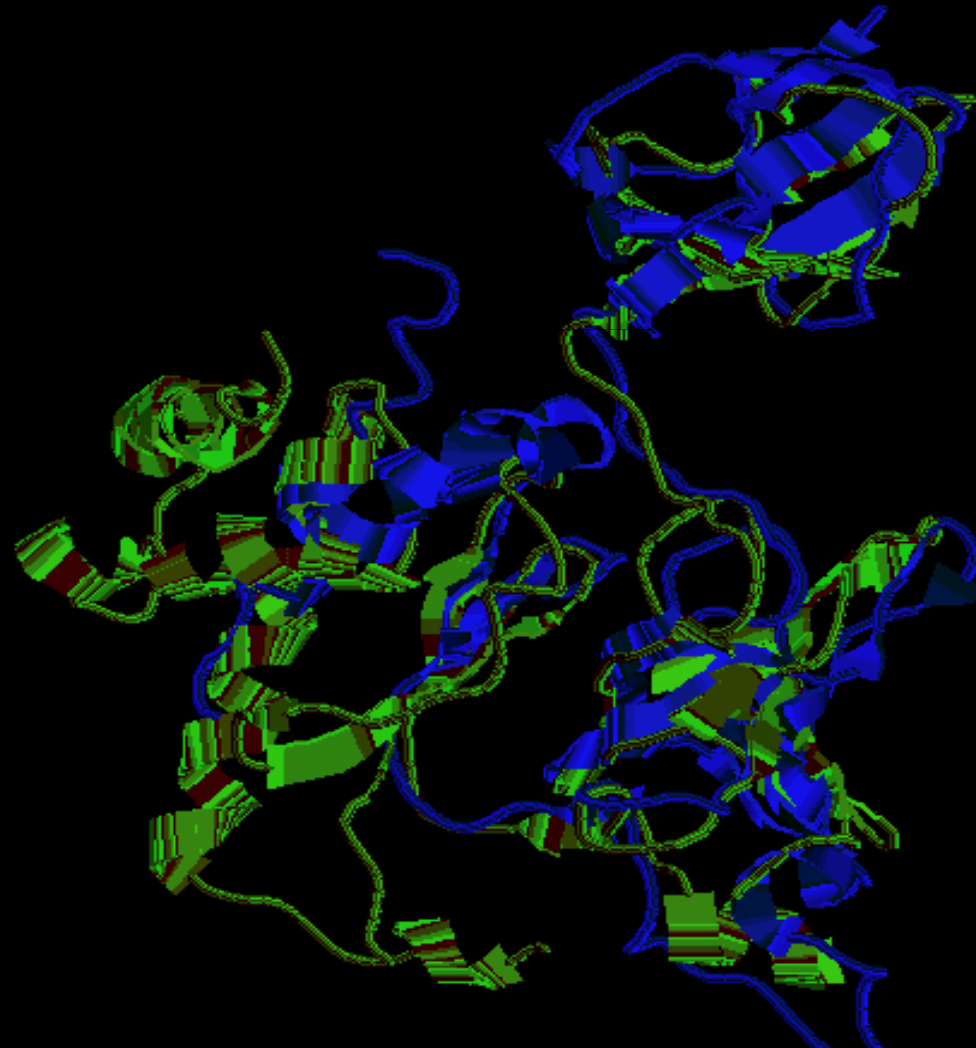
4.3

Evolution of the CAP subunits > Rrp4

Structure-based alignment: STAMP

RMSD: 2'33

Sc: 4'19



4.3

Evolution of the CAP subunits > Rrp4

Structure-based alignment: STAMP

Rrp4eu/Rrp40eu/Rrp4ar

```

rrp4eu/1-250      1 . . . . . H L V V P G D . T I T T D . . T G F M R G H G T Y M G . E . E K L I A S V A G S V E R V . . . . . N K L I C V K A L K . T R Y 52
rrp40/1-236      1 A R A A . R T V L . G Q V V L P G E . . E L L L P E Q E D A E G P G G A V E R G D . R L L V T K C G R L R H K E P G S G S G G . G V Y W V D S Q . Q K R Y 70
rrp4/1-207       1 . . . Q E I V L Q P R S I V V P G E L L A E G E F . . Q I P W S P Y I L K I . . N S K Y Y S T V V G L F D V K . . . . . D T Q F E V I P L E G S F Y 82

rrp4eu/1-250     53 I G E V G D I V V G R I T E V Q Q K R W K V E T N S R L D S V L L L S . S M . . . N . . E . L A . M R G F L Q E G D L I S A E V Q A V F S D G A V S L H 120
rrp40/1-236     71 V P V K G D H V I G I V T A K S G D I F K V D V G G S E P A S L S Y L S F . E . G A T . . . K R N . . R P N V Q V G D L I Y G Q F V V A N K D M E P E M V 140
rrp4/1-207     63 Y P K I N D I V I G L V E D V E I Y G W V V D I K A P Y K A Y L P A S N . . L L G R S I N V G . E D L R R Y L D V G D Y V I A R I E N F D R S I D P V L S 136

rrp4eu/1-250     121 . . . . . T R S L K Y G . K L G Q G V L V Q V S P S L . . V K . R Q . . K . T H F . H D L P C . G A S V I L G N N G F I W I Y P T P E H G F I A N L E 181
rrp40/1-236     141 C I D S C G R A N . . G M G V I G Q D G L L F K V T L G L I R K L L . A P D C E I . I Q E V G K L Y P L E I V F G M N G R I W V K . . . . . 201
rrp4/1-207     137 V . . . . . K G K . D L G R . V S N G I V I D I M P V K V P R V I G K . N K S M . Y E T L T S K . . S . I F V A N N G R I W . . . . . 186

rrp4eu/1-250     182 P V S L A D R E V I S R L R N C I I S L V T . . Q R M M L Y . . D T S I L Y C Y E A . S L P H Q I K D I L K P E I M E E I V M E T R Q R L L E Q E G 250
rrp40/1-236     202 . A . . K T I Q Q T L I L A N I L E A C . . . . E H . . . M T S D Q R K Q I F S R L A E S . . . . . 236
rrp4/1-207     187 . A . . F . . S E . E I L I E A I R K I E N E S H I . . . . K . . . . . 207

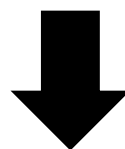
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Pair	2	rrp4eu	rrp4	3.74	2.14	250	207	229	129	123	0	26.83	100.00	2.34e-07
Pair	3	rrp40	rrp4	4.19	2.37	236	207	236	126	122	0	22.95	100.00	3.95e-05

4.3 Evolution of the CAP subunits > S1 domain

Structure-based alignment: STAMP

Pair	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)	
1	1	1SR0	2JE6	0.18	12.72	76	207	199	69	10	0	0.00	100.00	1.00000	LOW SCORE



Pair	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)
1	1	1SR0	2JE6	2.49	1.66	76	207	85	59	58	0	22.41	100.00	0.00275

```

s1_PNPase/1-76      -----
Rrp4Ss/1-207      1 Q E I V L Q P R S I V V P G E L L A E G E F Q I P W S P Y I L K I N S K Y Y S T V V G L F D V K D T Q 51

s1_PNPase/1-76      1 - - - - - A E I E V G R V Y T G K V T R I V D F G A F V A I G G G K E G L V H I S Q I A D K 41
Rrp4Ss/1-207      52 F E V I P L E G S F Y Y P K I N D I V I G L V E D V E I Y G W V V D I K A P Y K A Y L P A S N L L - G 101

s1_PNPase/1-76      42 - R V - - E K - V T D Y L Q M G Q E V P V K V L E V D R Q G R I R L S - I - - - K E A - - - - - 76
Rrp4Ss/1-207      102 R S I N V G E D L R R Y L D V G D Y V I A R I E N F D R S I D P V L S V K G K D L G R V S N G I V I D 152

s1_PNPase/1-76      -----
Rrp4Ss/1-207      153 I M P V K V P R V I G K N K S M Y E T L T S K S I F V A N N G R I W A F S E E I L I E A I R K I E N E 203

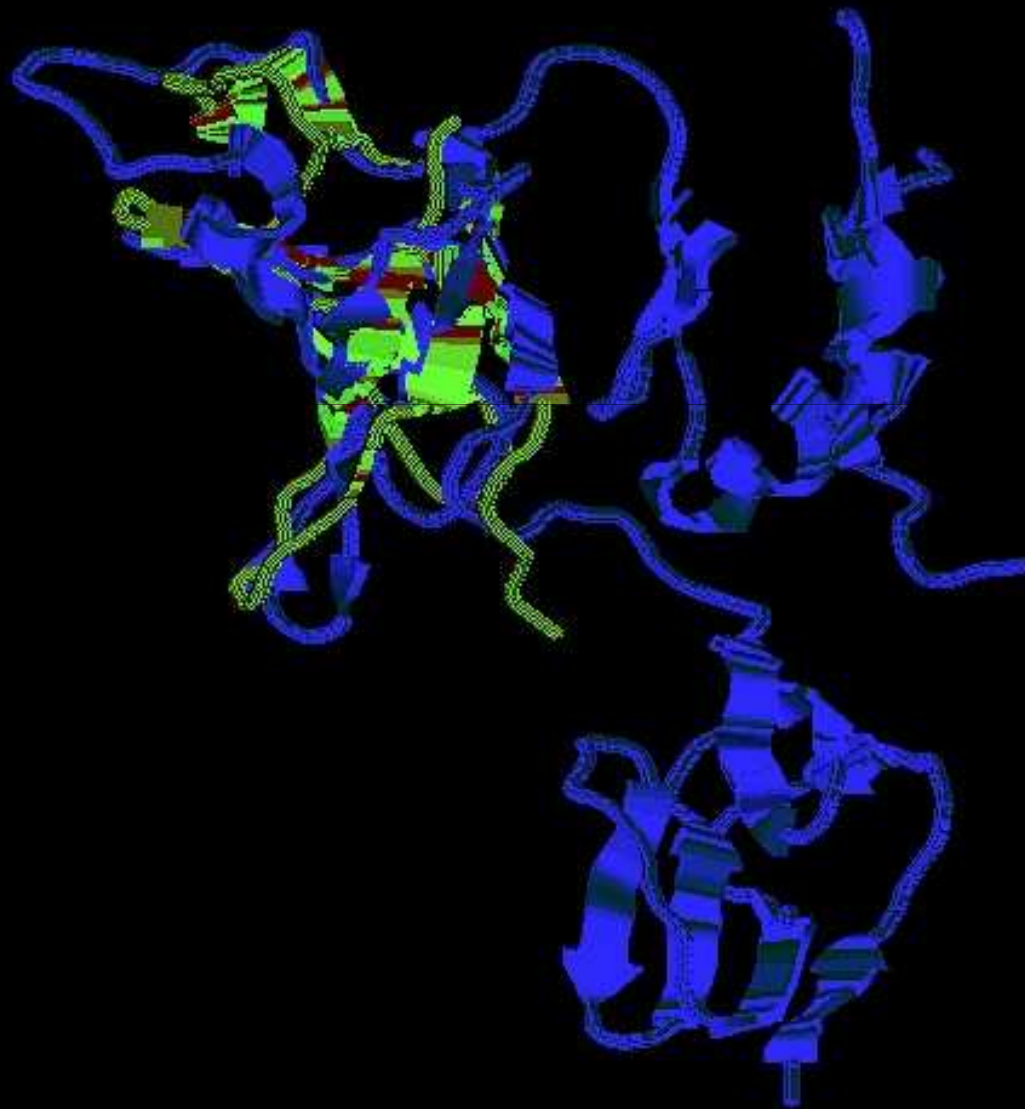
s1_PNPase/1-76      - - - -
Rrp4Ss/1-207      204 S H I K

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207

4.3

Evolution of the CAP subunits > S1 domain



RMSD: 1'66

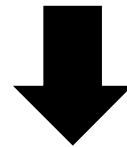
Sc: 2'49

4.3

Evolution of the CAP subunits > S1 domain

Structure-based alignment: STAMP

	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)	
Pair	1	1SR01	2JE6I	0.18	12.72	76	207	199	69	10	0	0.00	100.00	1.00000	LOW SCORE
Pair	2	1SR01	2nn6G	0.10	13.84	76	236	239	51	8	0	25.00	100.00	0.14880	LOW SCORE
Pair	3	1SR01	2nn6H	0.12	14.35	76	250	243	59	3	0	33.33	100.00	1.00000	LOW SCORE
Pair	4	2JE6I	2nn6G	4.23	2.30	207	236	234	123	120	0	23.33	100.00	1.09e-05	
Pair	5	2JE6I	2nn6H	3.76	2.38	207	250	230	132	128	0	25.78	100.00	1.93e-07	
Pair	6	2nn6G	2nn6H	3.81	2.07	236	250	275	135	128	0	24.22	100.00	1.78e-06	



	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)	
Pair	1	1SR01	2JE6I	2.50	1.67	76	207	85	60	59	0	23.73	100.00	0.00318	
Pair	2	1SR01	2nn6G	2.08	1.86	76	236	86	58	56	0	16.07	100.00	0.09038	
Pair	3	1SR01	2nn6H	2.04	1.88	76	250	83	65	59	0	18.64	100.00	0.03598	
Pair	4	2JE6I	2nn6G	3.53	1.83	207	236	243	107	103	0	21.36	100.00	0.00072	
Pair	5	2JE6I	2nn6H	3.49	1.61	207	250	267	108	101	0	26.73	100.00	1.08e-06	
Pair	6	2nn6G	2nn6H	2.84	2.34	236	250	284	97	90	0	17.78	100.00	0.00882	

4.3

Evolution of the CAP subunits > S1 domain

Structure-based alignment: STAMP

```

s1_e.coli/1-76      -----
Rrp4eu/1-250      1 -----HLVPGD-TITTD--T-GF-MRGHGT--YMGE-EKLIASVA-GSV---E 37
Rrp45s/1-207      1 --QEIVLQPRSI VV-PG-ELLAEGEFQ--IP-WSPYIL--K-INSKYYS-TVVGLFDVKD 49
Rrp40eu/1-236      1 ARAARTVL--G-QVVLPGEE--LLLP--EQEDAEGPGGAVERG-D--RLLVTKCG-RLR--- 48

s1_e.coli/1-76      1 -----AEIEVGRVYTCKVTRIVDFGAFVAIGGGKEGLVHISQIAD 40
Rrp4eu/1-250      38 RV-----NKLICVKALK-TRYIGEVGDIVVGRIT EVQQRWVKVETNSRLDSVLLLS-S-M 89
Rrp45s/1-207      50 TQ-----FEVIPLEGSFYYPKINDIVIGLVEDVEIYGWVVDIKAPYKAYLPASNLL- 100
Rrp40eu/1-236      49 HKEPGSGSGGGGVYWDVDS-QQKRYVPVKGDHVIGIVTAKSGDIFKVDVGGSEPA SLSYLS-FE 108

s1_e.coli/1-76      41 KR---V-EK-VTDY LQM CQEVPVKVLEVDROGRIRLS-----I-----KEA----- 76
Rrp4eu/1-250      90 -N---E-LAM-RGFLQECDLISA EVQAVFSDGAVSLH-----TRSLKYG-KLGQGVLVQVS 138
Rrp45s/1-207      101 GRSINVG-EDLRRYLDVGDYVIARIENFDRSIDPVL SV-----KGKDLGR-VSNGIVIDIM 154
Rrp40eu/1-236      109 GAT---KRN--RPNVQVGD LIYQGFVVANKDMEPEMVCIDSCGRAN-GMGVIGQDGLL FKV T 164

s1_e.coli/1-76      -----
Rrp4eu/1-250      139 PSL---VKRQK---THF-HDL-P-CGASVILGNNGFIWIYPTPEHGFIANLEPVSLADREVI 191
Rrp45s/1-207      155 PVKVPRVI-GKNKSM-YETLTSK--S--IFVANNGRI-W-----A--F-S-E- 190
Rrp40eu/1-236      165 LGLIRKLL-APDCEI-IQEVGK-LYPLEIVFGMNGRIWVK-----A--KTIQQT 208

s1_e.coli/1-76      -----
Rrp4eu/1-250      192 SRLRNCIIISLVT-QR--MMLYDTSILYCYEA--SLPHQIKDILKPEIMEEIVMETRQRLLLEQ 248
Rrp45s/1-207      191 EILIEAIRKIENESH- IK----- 207
Rrp40eu/1-236      209 LILANILEAC---EHMT---SDQRKQIFSR LAES----- 236

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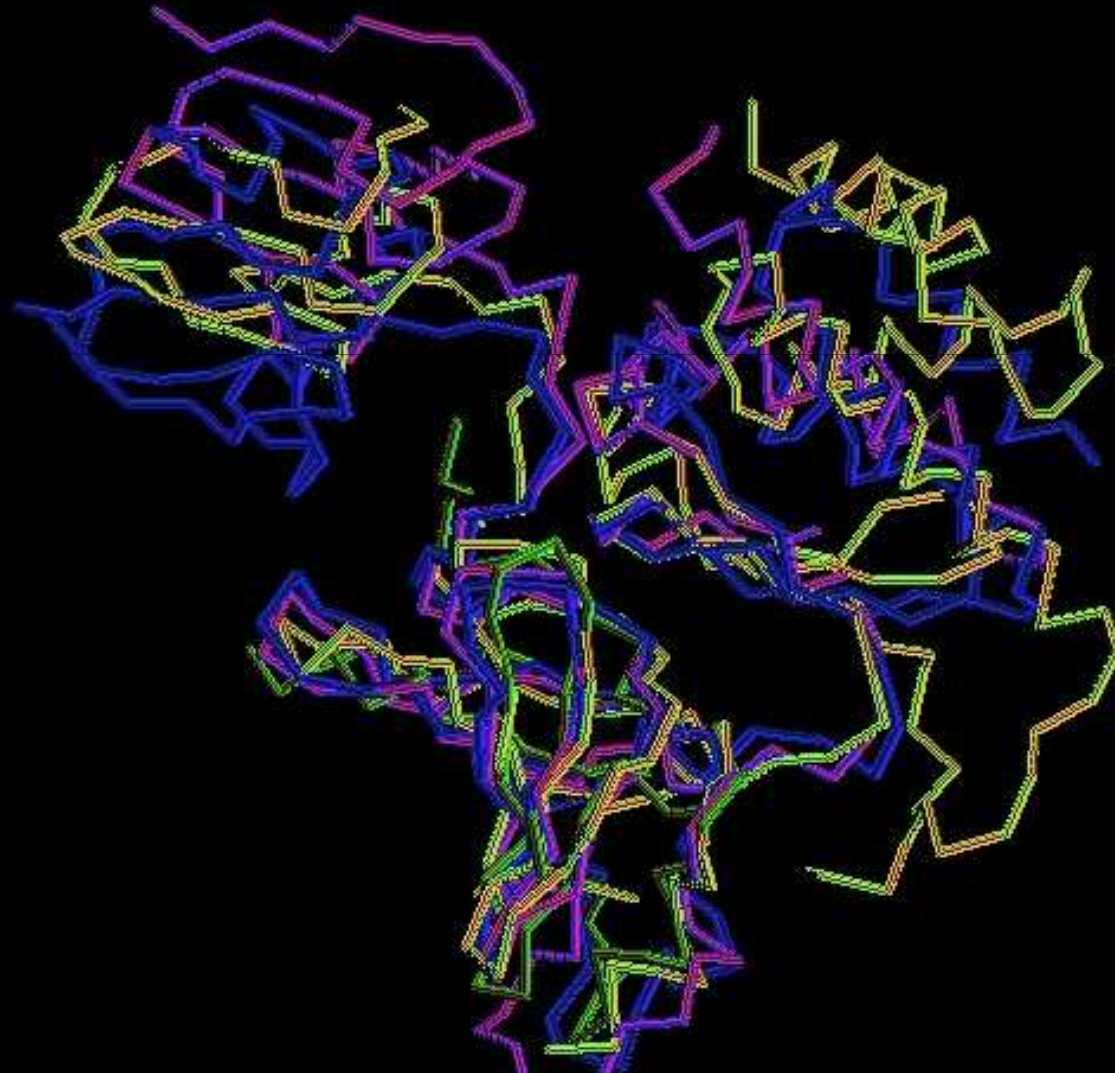
4.3

Evolution of the CAP subunits > S1 domain

Structure-based alignment: STAMP

RMSD: 1'92

Sc: 2'69



4.3

Evolution of the CAP subunits > S1 & KH

Structure-based alignment: STAMP

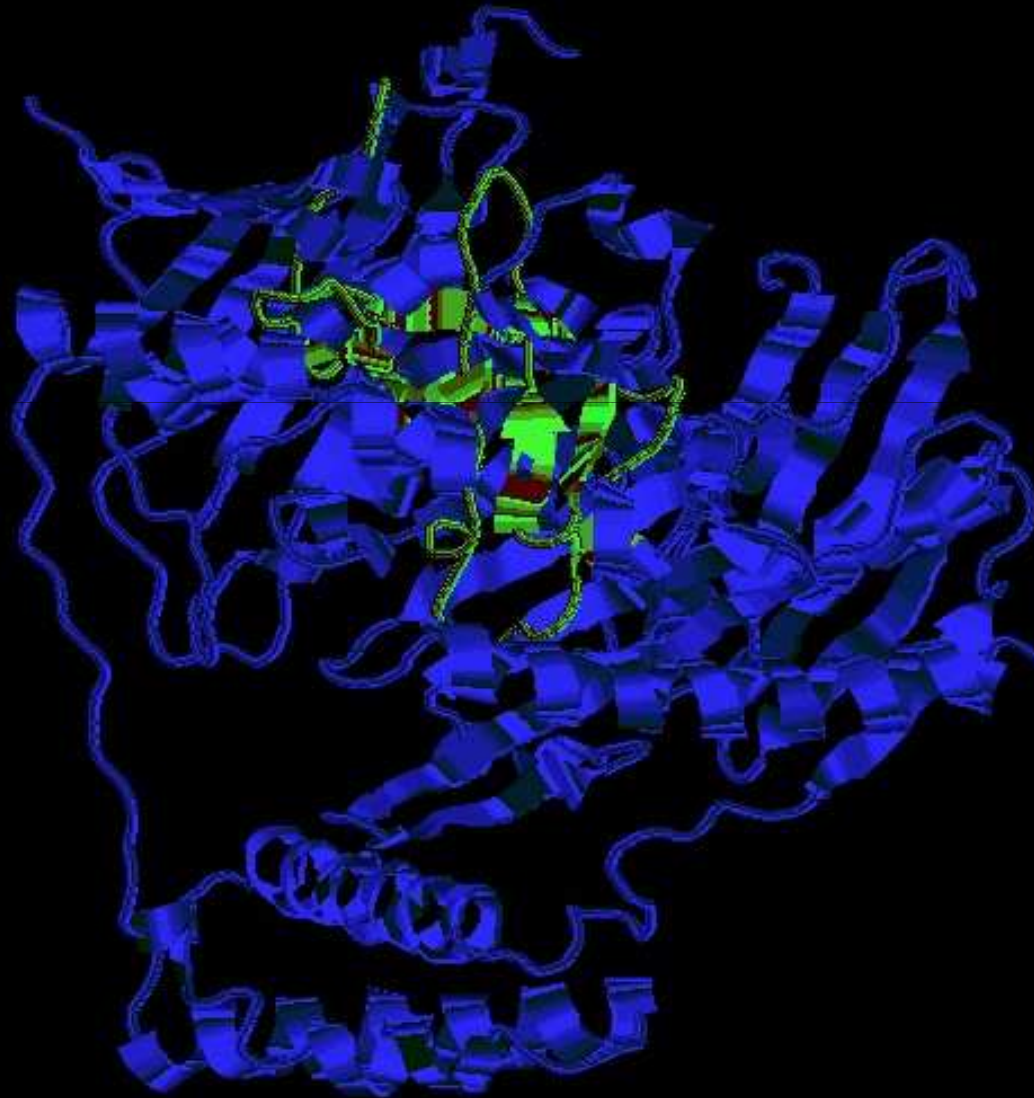
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	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)	
Pair	1	2nn6	3cdi	0.18	1.97	486	516	660	15	4	0	25.00	100.00	1.00000	LOW SCORE
Pair	2	2nn6	2JE6	0.18	2.23	486	621	808	14	12	0	8.33	100.00	1.00000	LOW SCORE
Pair	3	3cdi	2JE6	0.20	2.39	516	621	938	15	8	0	0.00	100.00	1.00000	LOW SCORE
	No.	Domain1	Domain2	Sc	RMS	Len1	Len2	Align	NFit	Eq.	Secs.	%I	%S	P(m)	
Pair	1	3cdiA	1SR0	0.32	1.33	516	76	514	15	12	0	8.33	100.00	1.00000	LOW SCORE

4.3

Evolution of the CAP subunits > S1 & KH

Structural superimposition: XAM

RMSD: >9



4.2

Evolution of the CORE subunits

Conservation among Archaeas

<i>Af_rrp41/1-246</i>	1 K P E K L I V D G R L D G R K F D E L R P K I E A S V L K R A D G S C Y L E M G K N K V I A A V 50
<i>Mth_rrp41/1-222</i>	1 - - - - - S Y R E D G R A F D E L R P K I E A G I L E R A D G S S Y L E F G G N K I L V A V 42
<i>Ss_rrp41/1-234</i>	1 R P K L I L D D G R T D G R K P D E L R S K I E L G V L K N A D G S A I F E M G N T K A I A A V 50
<i>Af_rrp41/1-246</i>	51 F G P R E V H P R H L Q D P S K A I I R Y R Y N M A P F S V E E R K R P G F D R R S I E I S K V S K 100
<i>Mth_rrp41/1-222</i>	43 Y G P R E A Q I R K L Q R P D R A V I R C R Y N M A P F S V E E R K R P G F D R R S V E I S K I T A 92
<i>Ss_rrp41/1-234</i>	51 Y G P K E M H P R H L S L P D R A V L R V R Y H M T P E S T D E R K N P A F S R R E I E L S K V I R 100
<i>Af_rrp41/1-246</i>	101 E A F E A V I M K E L F P R S A I D I F V E V L Q A D A G S R T A C L N A A S V A L V D A G V P M K 150
<i>Mth_rrp41/1-222</i>	93 E A L R P A L I L E K F P R S V I D V F I E V L A E G G T R C A G I T A A S V A L A D A G I P M R 142
<i>Ss_rrp41/1-234</i>	101 E A L E S A V L V E L F P R T A I D V F T E I L Q A D A G S R L V S L M A A S L A L A D A G I P M R 150
<i>Af_rrp41/1-246</i>	151 G M I T S V A V G K A D C Q L V L D P M K E E D N F G E A D M P F A F L I R N G K I E S I A L L Q M 200
<i>Mth_rrp41/1-222</i>	143 D M V V A C A A G K V G D Q V V L D L S E E E D K E G Q A D V P V A I L P R - - - T R E I T L L Q S 189
<i>Ss_rrp41/1-234</i>	151 D L I A G V A V G K A D C V I I L D L N E T E D M W G E A D M P I A M M P S - - - L N Q V T L F D L 197
<i>Af_rrp41/1-246</i>	201 D - G R M T R D E V K Q A I E L A K K G A L Q T Y E M Q R E A I L R R Y I E V G E E M D E I T 246
<i>Mth_rrp41/1-222</i>	190 D - G N L T P E E F E R A L D L A V E G C L R I H E V Q K E A L R K - - - - - 222
<i>Ss_rrp41/1-234</i>	198 N N G S M T P D E F R Q A F D L A V K G I N I I Y N L E R E A L K S K Y V - - - - - 234
<i>Sso_42/1-273</i>	1 G H M S S T P S N Q N - - I P I T K K E S I V S L - F E K G R Q D G R K L T D Y R P L S I T L D Y A K K A D G 54
<i>Af_42/1-253</i>	1 - - - - - E D I L - V D I K R D Y V L S K L R - D N I R I D G R G F D E F R K V E I I P N V I E K A E G 45
<i>Mth_42/1-261</i>	1 - - - - - P E I T R K S I T D L I N - N K I R I D G R S L H E F R D I S I E T G V I S K A E G 41
<i>Sso_42/1-273</i>	55 S A L V K L G T T M V L A G T K L E I D K P Y E D T P N Q G N L I V N V E L L P L A Y E T F E P G P P D E N A I E 111
<i>Af_42/1-253</i>	46 S A L V K L G D T Q V V V G V K M Q P G E P Y P D T P D R G V I I V N A E L V P L A S P T F - E P - P D E N S I E 100
<i>Mth_42/1-261</i>	42 S S R V K L G N T Q I I V G V K P Q I G E P F P D T P E M G V I L T N S E L L P M A S P T F E P G P P D E R S V E 98
<i>Sso_42/1-273</i>	112 L A R V V D R S L R D S K A L D L T K L V I E P G K S V W T V W L D V Y V L D Y G G N V L D A C T L A S V A A L Y 168
<i>Af_42/1-253</i>	101 L A R V V D R G I R E S E A V D L S K L V I E E G E K V W I V F V D I H A L D D G N L L D A S A L A A I A A L M 157
<i>Mth_42/1-261</i>	99 L S R V V D R C I R E S R M I D L E K L C I I E G S K V W M L F L D L H I I E Y D G N L F D A A V L A T V A A L L 155
<i>Sso_42/1-273</i>	169 N T K V - - Y K V E - - - - Q I S V N K N E V V G K L P L N Y P V V T I S V A K V D K Y L V V D P D L D E E S I - 218
<i>Af_42/1-253</i>	158 N T K V P A E R - - - - - F D L - - G - E D Y L L P V R D L P V S V T S L I V G N K Y L V D P S R E E M S - V 203
<i>Mth_42/1-261</i>	156 D T R I P - - A A E V E D G E V V I N - R E K M Q P L P V N R K A L M C T F A K I G N E I V L D P S L E E E D I L 209
<i>Sso_42/1-273</i>	219 M D A K I S F S Y T P D L K I V G I Q K S G K G S M S L Q D I D Q A E N T A R S T A V K L L E E L K K H L G I 273
<i>Af_42/1-253</i>	204 G D T T I T I T T D K D D N V V A M Q K S G G Y L L D E K L F D E L L D V S I N C A R K L R E K F K - - - - 253
<i>Mth_42/1-261</i>	210 - T A R I S I G V T E E G S I C A M Q K G G E G P L T R D D V L K A V S I A V E K V P Q L I E Y L D K S M - - 261

Rrp41

Rrp42

4.2

Evolution of the CORE subunits

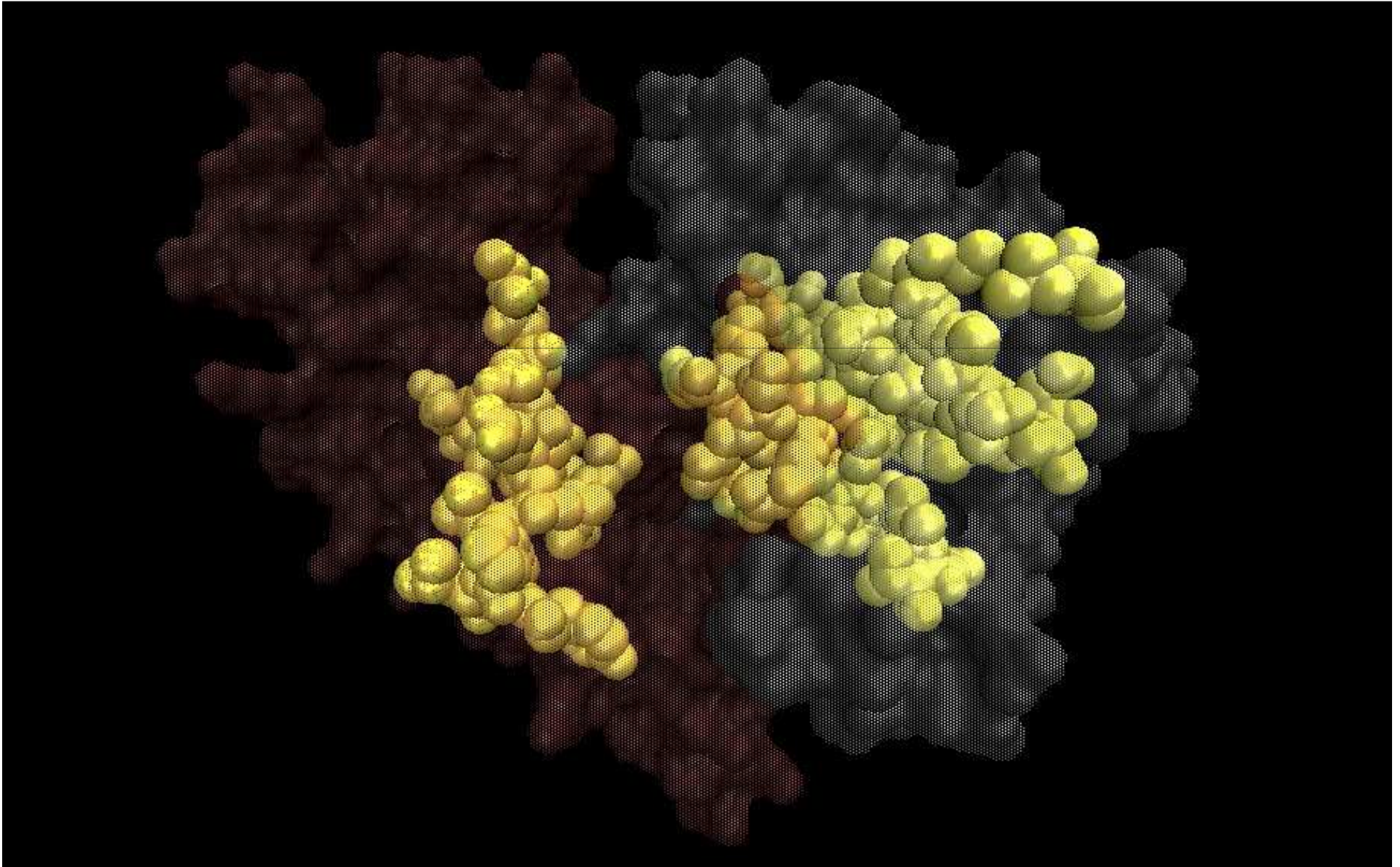
Af_41/1-246	1	PKLI-VGCLLDGKTFDELPPTKLTASVLRADGSCMLMGKNI	50
Sso_41/1-233	1	PKLIDGGRRTDGRAPDEERSKLTLCVLRNADGSAIFLMGNTAIAAV	50
Mth_41/1-222	1	-----SVRFQGRAPDILPPKLTACILTRADGSSYLEFGGNI	42
Af_41/1-246	51	FGPRFVHPRHLDUPSRAITKRYNMAPFSVFERKRPQPRKSTFISNVSR	101
Sso_41/1-233	51	YGPKEMHPRHLSLPDRAVLKVVHYHMTPTSTEDERKNPAPSKKIFLSNVIR	101
Mth_41/1-222	43	YGPKEADIRKLDKPDRAVLKGVNMAPFSVFERKRPQPRKSVLSKITA	93
Af_41/1-246	102	AFLLAVIMKELFPKSAITIFVIVLVAIAGSKTACLNAAASVALVIAQVPMKGM	152
Sso_41/1-233	102	ALGSVVLVLEFPATAIVFTIILDADAGSKLVSEMAASLALADAGIPMRDL	152
Mth_41/1-222	94	ALFPALILEFPASVIVFTIVLLAGGTCAGITAASVALADAGIPMRDM	144
Af_41/1-246	153	ITSVAVCLADGILEVLCRMKEEDNFGCAQMPFAFELINGKLTLSIALLEMDG	202
Sso_41/1-233	153	IAGVAVGKADGVIIILDLNKTEDCMWGEADMPIAMM-----PSLNVTLFQING	199
Mth_41/1-222	145	VVACAAGVYEDVIVLILSEEDKIGDAIVPVAIL-----PSTRITLLSDG	191
Af_41/1-246	203	MTDPEVAGATFLAKGALIVIMIFFATLKYTLVGLMDIT	246
Sso_41/1-233	200	SMTPEFPAQAFILAVKGINIIYNLEKFAKSKVV-----	233
Mth_41/1-222	192	MTPEFPPRALDLAVEGCLTHFVIRKFAK-----	222
Sso_42/1-273	1	GHMSSTPSNQN--IPIIKKESIVSLFEKGIQDGRKLTDRPLSITLDYAKKADG	54
Af_42/1-253	1	-----EDIL-VDIKRDYVLSKLR-DNERIDGRGFDEFKRVIIIPNVIEKAEG	45
Mth_42/1-261	1	-----PEITRKSITDLIN-NKERIDGRSLHEFRDISIETGVISKAEG	41
Sso_42/1-273	55	SALVKLGTTMVLGATKLEIDKPYEDTPNQGNLIVNVELLPLAYETFEPPGPPDENAI	111
Af_42/1-253	46	SALVKLGDTQVVVGVMQPGEPYPTDPDRGVIIVNAELVPLASPTF-EP-PDENSI	100
Mth_42/1-261	42	SSRVKLGNTQIIIVGVKPOIGEPFPDTPEMGVILTNSSELLPMASPTFEPPGPPDERSVE	98
Sso_42/1-273	112	LARVVDRSLRDSKALDLTKLVI EPGKSVWTVWLDVYVLDYGGNVLDACTLASVAALY	168
Af_42/1-253	101	LARVVDRGIRESEAVDLSKLVIEEGEKVWIVFVDIHALDDDGNNLLDASALAAIAALM	157
Mth_42/1-261	99	LSRVVDRCIRESRMIDLEKLCITEGSKVWMLFLDLHIIDYDGNLFDAAVLATVAALL	155
Sso_42/1-273	169	NTKV--YKVE---QISVNKNEVVGKLPINYPVVTISVAKVDKYLVVDPDLDEES	218
Af_42/1-253	158	NTKVPAER-----FDL--G-EDYLLPVRDLPSVSTSLIVGNKYLVDP SREEMS-V	203
Mth_42/1-261	156	DTRIP--AAEVEDGEVVIN-REKMQPLPVNRKALMCTFAKIGNEIVLDP SLEEDIL	209
Sso_42/1-273	219	MDAKISFSYTPDLKIVGIIQSGKGSMSLQDI DQAENTARSTAVKLLLEELKKHLGI	273
Af_42/1-253	204	GDTTLTITTDKDDNVVAMQSGGYLLDEKLFDELIDVSI NCARKLREKFK-----	253
Mth_42/1-261	210	TARISIGVTEEGSICAMQKGGEGPLTRDDVLKAVSIAVEKVPQLIEYLDKSM--	261

Rrp41

Rrp41

4.2

Evolution of the CORE subunits



4.2

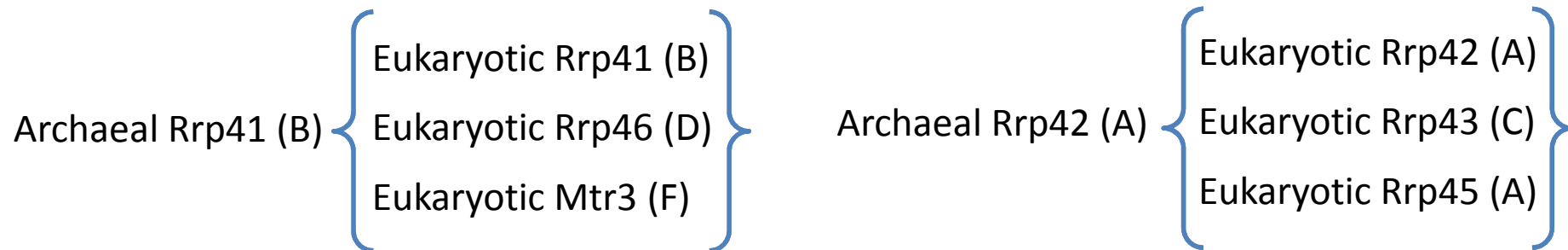
Evolution of the CORE subunits

What bibliography says...

- Core eukaryotic subunits derivate from the achaeal subunits
- Human exosome doesn't have phosphorolytic activity
- They conserve the same fold

4.2

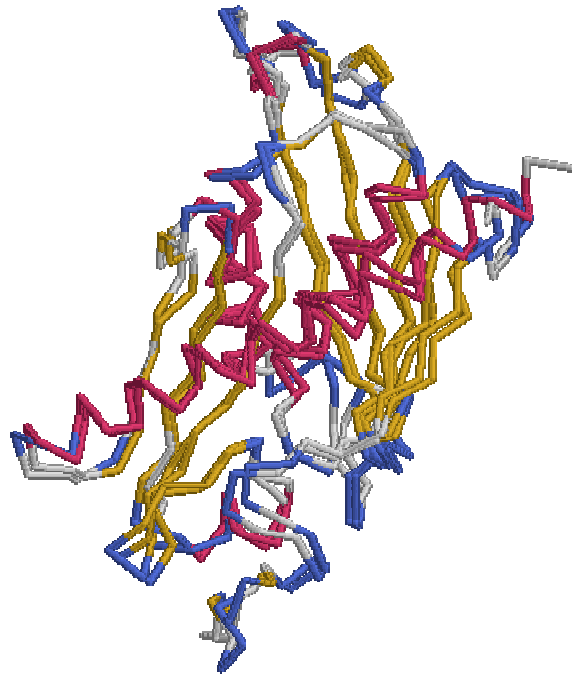
Evolution of the CORE subunits



2NN6A/1-340	1	-----MK-----ETPLSNCERRFLLRATIEKKRLDGRQTYD-----YRNIRIS-----	38
2NN6D/1-205	1	-----GCSLRHFACEQNL-LSRPDGSASFLOGDTSVLGVY-----GPA-E---V---KNKATLE-VILRPK-	53
2NN6F/1-223	1	-----G---TRDPTRLRPYYARAGL-LSQAKGSAYLEAGGTKVLCVVS-----GPR-----QA---LRGRLL-CDRRAP	57
2JEBB/1-233	1	RPKLILDDGKRITDGRKPDRLRSIKIELGV-LKNADGSAIFEMGNTKATAAVY-----GPKE-MHPRHLSLPDRAVLR-VRYHMT	77
2NN6B/1-235	1	-----LS-DGGYRVDGRRAGELRKIQARMGV-FAQADGSAYIEGNTKALAVVY-----GPHEIRGSRARALPDRAVLR-CQYSAT	74
2NN6E/1-275	1	-----GHSSTPSN-----TLSEAEKVYIVHGVQEDLRVDGRGCEDY-----RCVEVETDV-----	37
2JEBB/1-273	1	-----GHMSSTPSN-----QNIIPYIKKESIVSLFEKGIQDGRKLTQY-----RPLSITLDY-----	48
2NN6C/1-270	1	-----TV-EPLEYRRFLKENCPRDGRRELGEF-----RTTTVNIIGS-----	35
2NN6A/1-340	39	-----FGT--DY--GC--C--I--V--ELGKTRVLG--QVSCELVSPKLNREGI-LFF-NLELSQMAAPAFEPGRQSDLLVKL-NR-----	104
2NN6D/1-205	54	-----I--GLPGVAEKSRLIRNTCEAVVLGT-LHPRTSITVVLQVVS-D-----AGSLLACC-----LNAACMALVDAGVPM	118
2NN6F/1-223	58	FAGRKRRA-PPGGCEERELALALQEALEPAV-RLGRYPRAQLEVSALLLE-D-----GGSALAAA-----LTAALALADAGVEM	129
2JEBB/1-233	78	FSTDERKNP-APSRREIELSKVIREALESAY-LVELFPRTAIDVFTEILQ-A-----DAGSLVVS-----LMAASLALADAGIPM	149
2NN6B/1-235	75	FSTGERKRRPHGDRKSCMGLOLRQTFAAI-LTQLHPRSQIDYVQVQLQ-A-----DGGTYAAC-----VNAATLAVLDAGIPM	147
2NN6E/1-275	38	-----VSN-TSG--SA--R--V--K--LGHTDILVG--VKAEMGTPKLEKPNEGYL-EFF-VDCSASATPEFEGRGDDDLGTEIA-NT-----	104
2JEBB/1-273	49	-----AKK-ADG--SA--L--V--K--LGTTMVLG--TKLEIDKPYEDTPNQGNL-IVN-VELLPPLAYETFEPPDENAIELA-RV-----	115
2NN6C/1-270	36	-----IST-ADG--SA--L--V--K--LGNTTVICG--VKAFAAPSTDAPDKGYV-VPN-VDLPLLCSSRFSGPPGEEAQVAS-QF-----	102
2NN6A/1-340	105	LMERCLRNKSCIDTESLC-----VV-----AG-----EKVWQIRVDLHLLNHGNIIDAASIA-----AIVALCHFRRPDVSQGDDEVTLTYTEERD--P--VP--	184
2NN6D/1-205	119	R--AL--FCG-V--ACALD-S-DGTLVLDPTSKQKE-ARAVLT-----FALDSVERKL-LM--SSTKGL-----YSDTELQOCL	180
2NN6F/1-223	130	Y--DL--VVG-C--GLSLAPGPAPTWLLDPTREEER-AAAGLT-----VALMPVLNQV-AG--LLGSGE-----GGLTESWAEAV	194
2JEBB/1-233	150	R--DL--IAG-V--AVGKA--D-GVILDLNETEDMWG-EADMP-----IAMPPLNQV-TL--FQLNGS-----M-TPDEFROAF	210
2NN6B/1-235	148	R--DF--VCA-C--SAGFV--D-GTALADLSHVEEA-AGGPOLA-----LALLPASGOI-AL--LEMDAR-----L-HEDHLERVL	208
2NN6E/1-275	105	LYRIFNNKSSVDLKTLCI-----SP-----RE-----HCWVLYVDVLLLECGGNLFDASIAV-----KAALFNTRIIPRVVLEDIELSDDP-Y-D--CI--RL--	182
2JEBB/1-273	116	VDRSLRDSKALDLTKLVI-----EP-----GK-----SVWTWLDVYVLDYGGNVLDACLTAS-----VAALYNTKVKYKVE---QISVNKN-EV-V--G--KL--	189
2NN6C/1-270	103	ADVIENTSQIQKEDLCI-----SP-----GK-----LVWVLYCDLICLDYDGNILDACTFAL-----LAALKNVQLPEVTINEETALAEVN--LKK-KS--YL--	181
2NN6A/1-340	185	LSI-HH-MPICVSFAFFQOQTYLLVDPNEREERVMDGLVLIAMNKHRE-IC-TIQ--S--SGGIMLLKBDQVLRCSKIAGVKVAEITELIKALENDQKVRKEGGKFGF	284
2NN6D/1-205	181	AAAAAASQ-----HV-----FRFYRESLQRRYS--KS-----	205
2NN6F/1-223	195	RLGLECCQ-----RL-----YPVLQQLVRAAR-RRGAAA-----	223
2JEBB/1-233	211	DLAVKGIN-----II-----YNLEREALKSKYV-----	233
2NN6B/1-235	209	EAAAQAAR-----DV-----HTLLDRVVRQHVR-EASI-----	235
2NN6E/1-275	183	SVE-NV-PCIVTLCKI-G-YRHVVDATLQEEACSLASLLVSVTSKGVV-TC-MRK--VGKGS-L-DPESIFEMMETGKRVGKVLHASLQSVVHKEESLG-PKRQ--	275
2JEBB/1-273	190	PLN-YP-VVTISVAKVD-KYLVVDPDLDEESIMDAKISFSYTPDLKI-VG--IQK--SGKGSMS--LQDIDQAENTARSTAVKILLELKKHL--GI--	273
2NN6C/1-270	182	NIR-TH-PVATSAFVFD-TLLIYDPTGEEHULATGLTIYMDDEEGKL-CC--LHK--P-GGSGLTGAKLQDCMSRAVTRHKEVKKLMDEVIKSMKPK-----	270

4.2

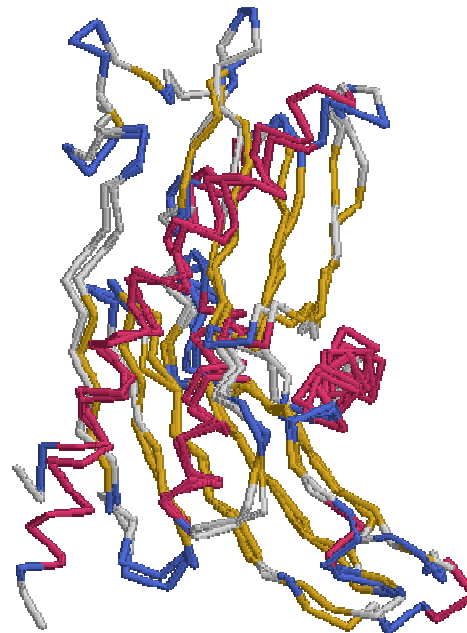
Evolution of the CORE subunits



Rrp41 Sso vs Rrp41 Hs

Sc: 8'18

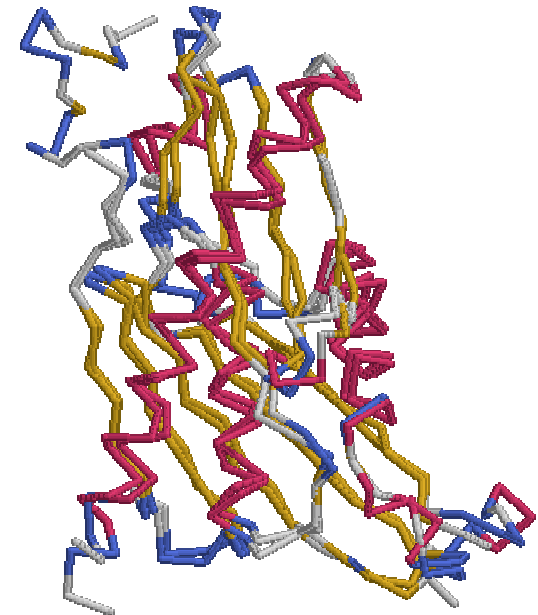
RMSD: 1'32



Rrp41 Sso vs Mtr3 Hs

Sc: 7'33

RMSD: 1'38



Rrp41 Sso vs Rrp46 Hs

Sc: 7'27

RMSD: 1'26

4.2

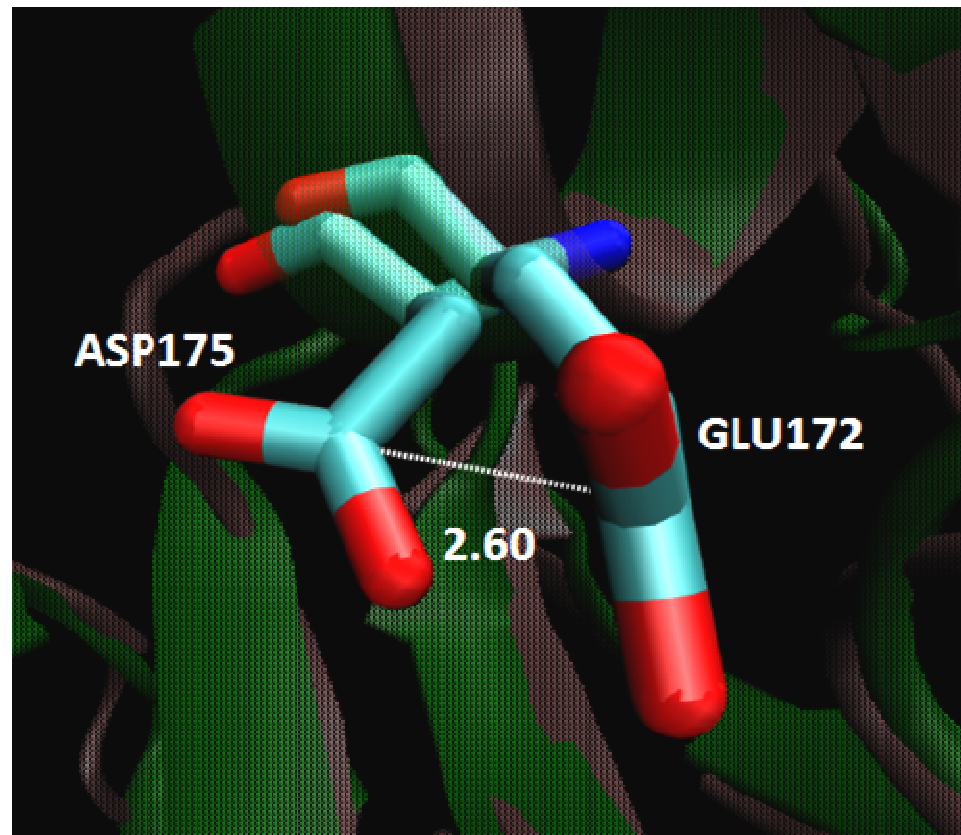
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Structural alignment with alignfit between archaeal rrp41 and its derivated subunits in eukaryotic

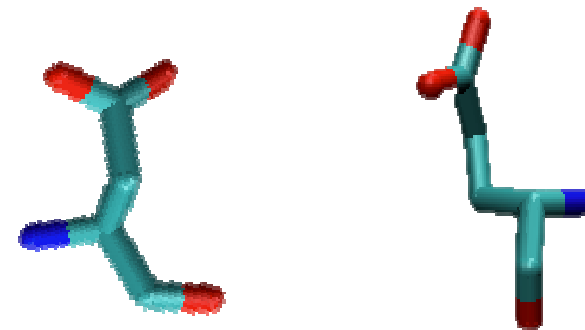
4.2

Evolution of the CORE subunits

<i>rrp46_Hs/1-205</i>	117	PMRALFCGVACA-LDS-DGTLVLDP	TSKQEE	KE-ARAVLTFALDSVERKLL	163
<i>Mtr3_Hs/1-223</i>	128	EMYDLVVGCGLSLAPGPAPT	TWLLDP	TRLEER-AAAGLTVALMPVLNQVA	176
<i>rrp41_Sso/1-233</i>	148	PMRDLIAGVAVGK-A-D-GV	IILD	LNEDMWG-EADMP	IAMMP
<i>2NN6B/1-235</i>	146	PMRDFVCACSAGF-V-D-GT	ALAD	LSHV	EE-AAGGPQLALALLPASGQIA
					191

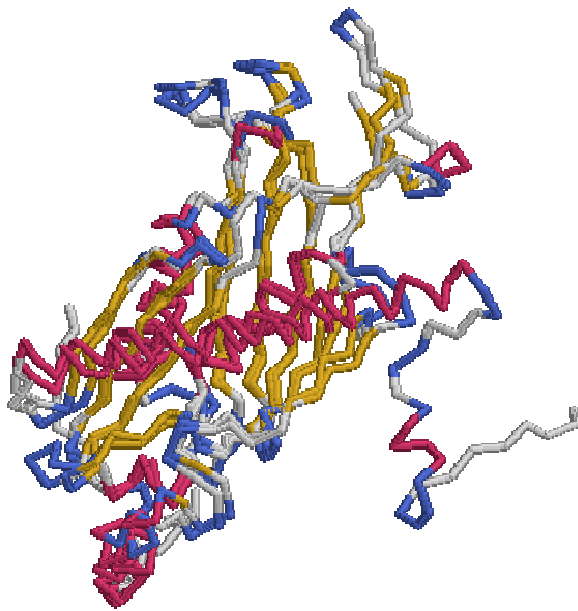


Asp → Glu
(Archaea) *(Eucaryot)*



4.2

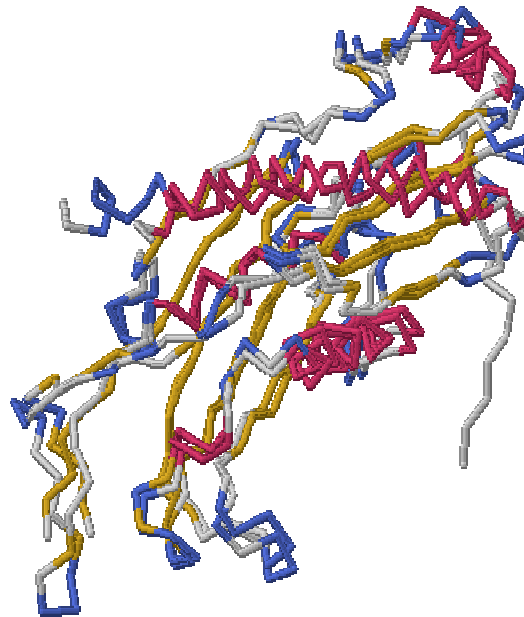
Evolution of the CORE subunits



Rrp42 Sso vs Rrp42 Hs

Sc: 5'67

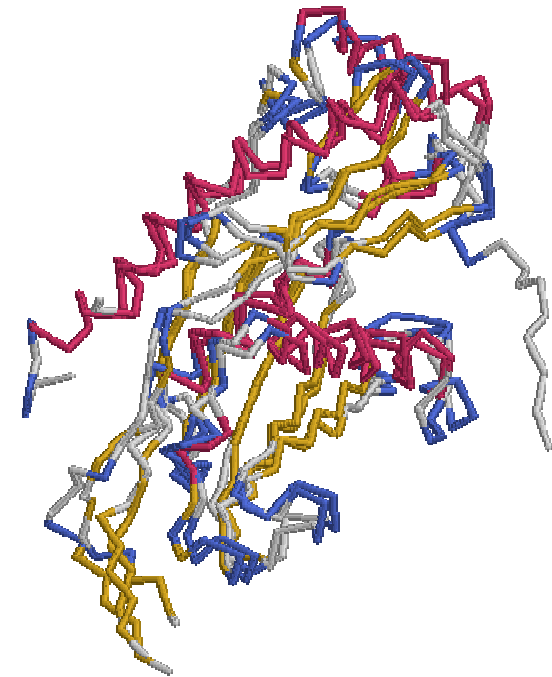
RMSD: 1'58



Rrp42 Sso vs Rrp43 Hs

Sc: 7'13

RMSD: 1'68



Rrp42 Sso vs Rrp45 Hs

Sc: 7'11

RMSD: 1'73

But some questions remain to be investigated...

- Why the evolution has allow the lack of function in the eukaryotic exosome?
- How interact the eukaryotic exosome with the subunits that bring the hydrolitic function?
- Which is the relationship between Rrp41-42 and the bacterial analog PNPase PH?
- Is there any relationship between the bacterial KH domain and archaeal KH domain?
- Coevolution of Rrp41 and Rrp42



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