

RNA polymerase in Prokaryotes

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RNA polymerase

SUBUNITS

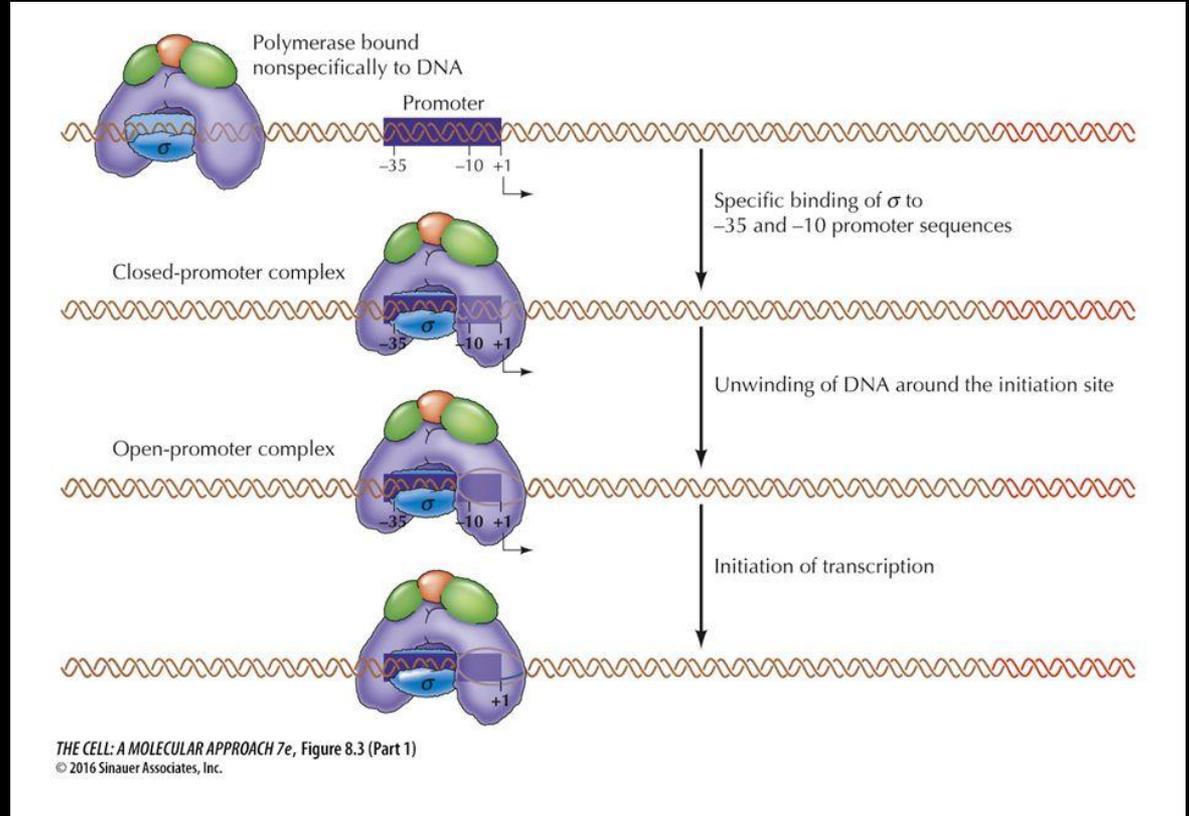
Core

| | |
|---|----------------------|
| - | β' |
| - | β |
| - | $\alpha 1, \alpha 2$ |
| - | ω |
| - | σ |



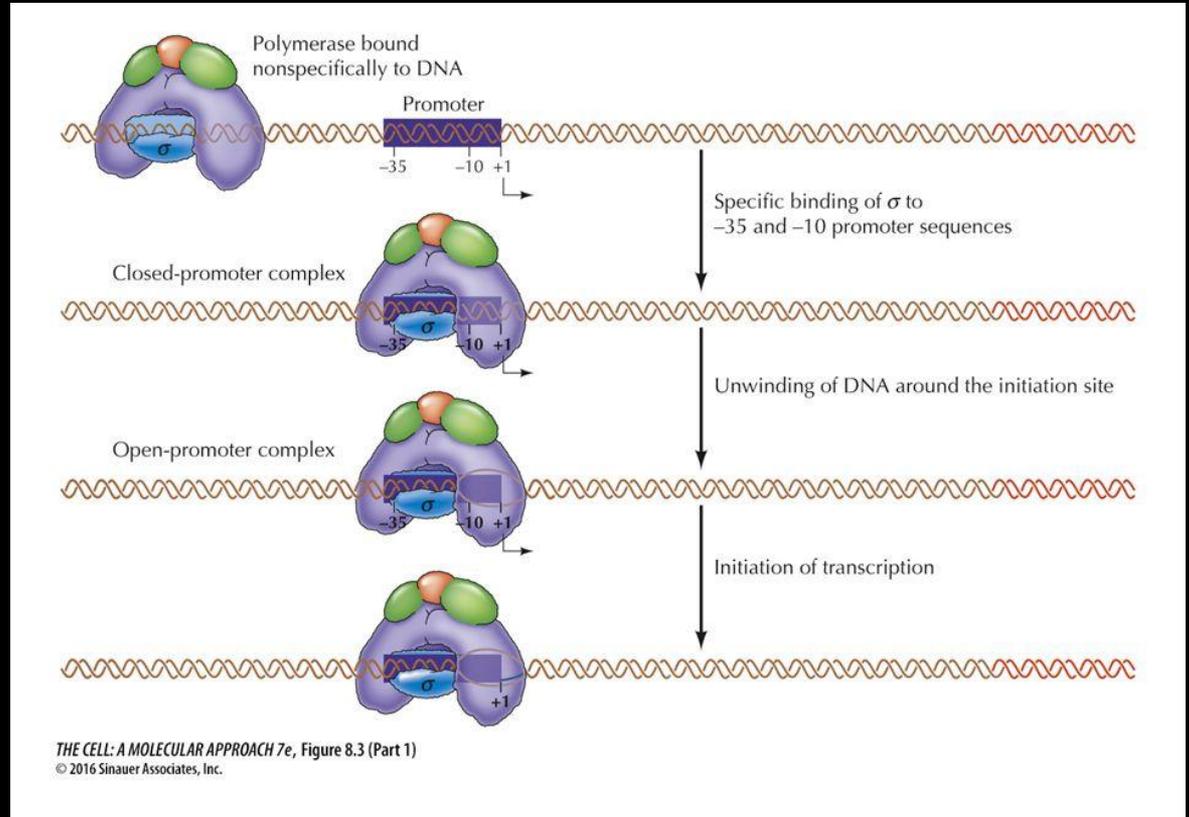
Transcription

- Initiation
- Elongation
- Termination

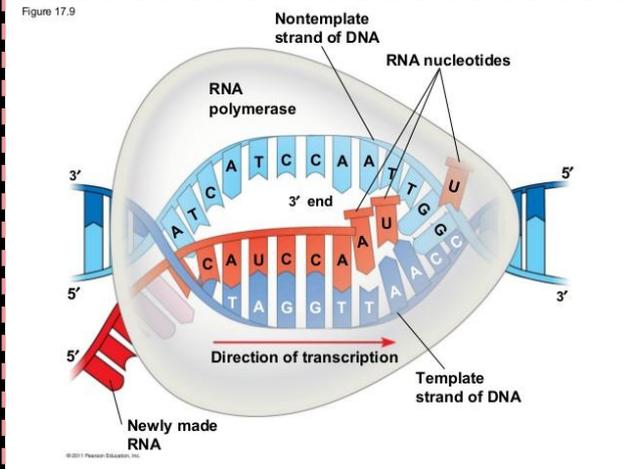


Transcription

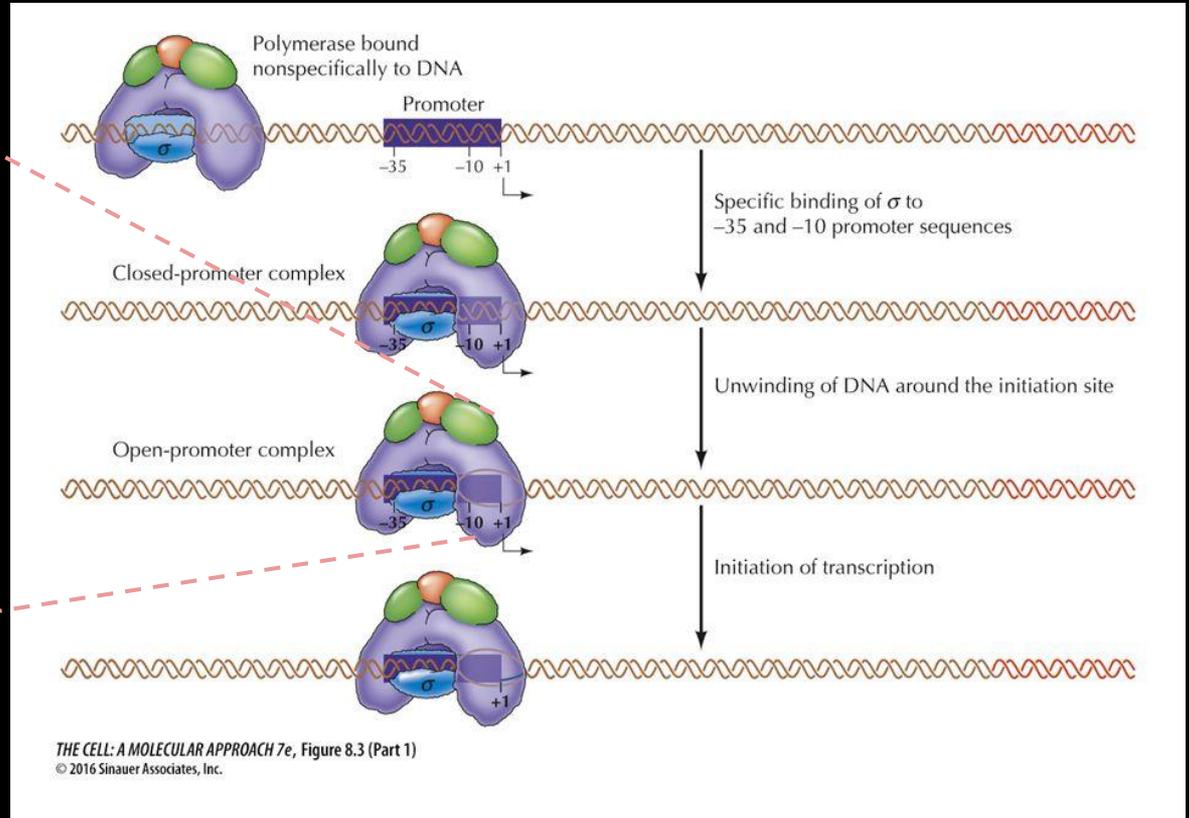
- Initiation
- Elongation
- Termination



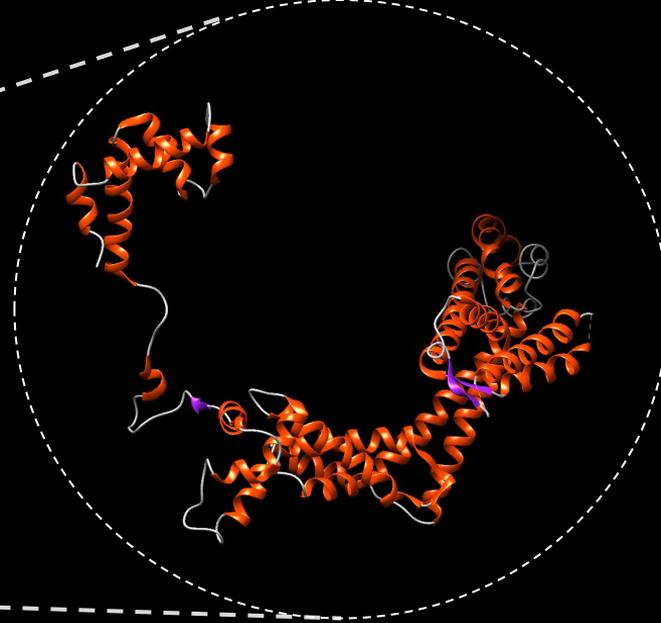
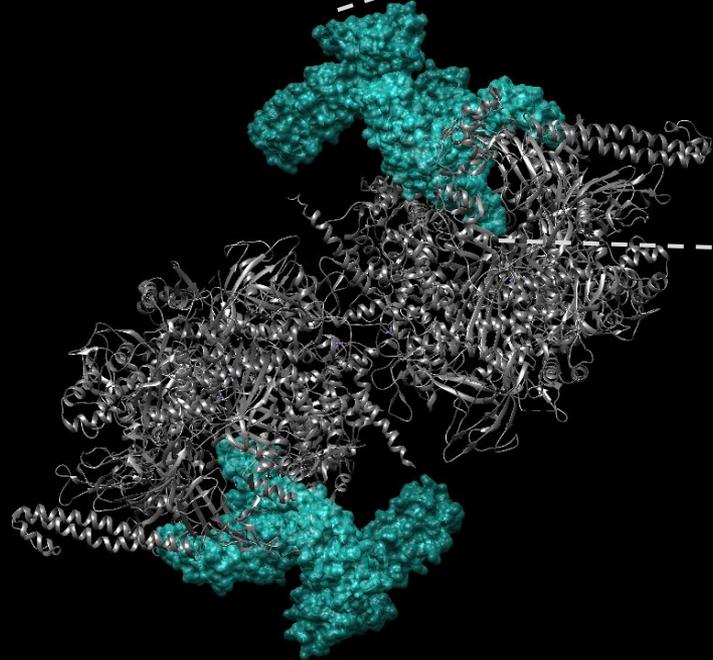
Transcription



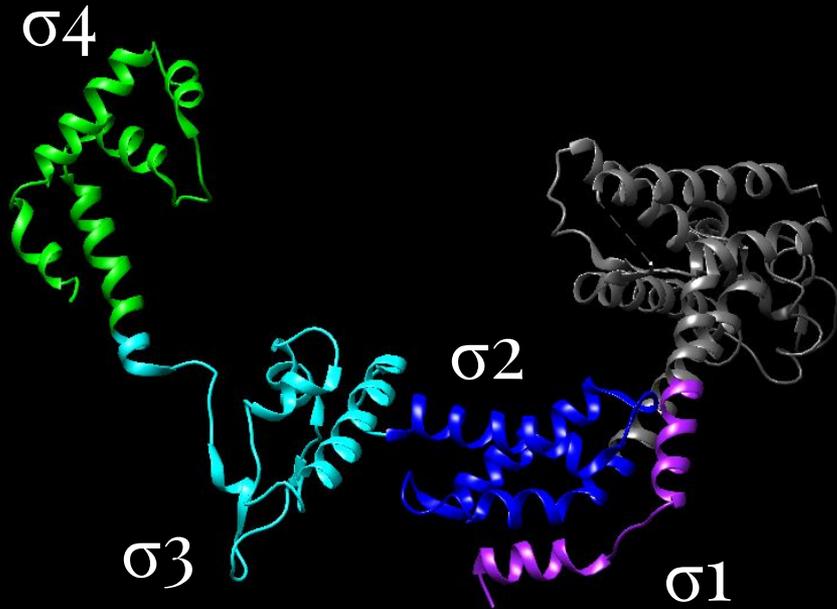
<https://www.slideshare.net/kindarspirit/17-from-gene-to-protein-22899119>



Sigma 70 (σ 70) subunit

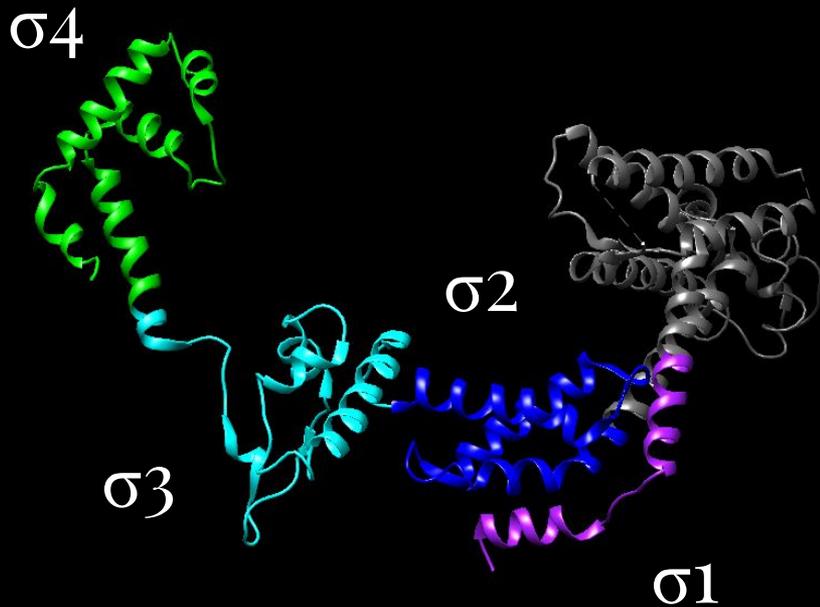


Sigma70: Regions



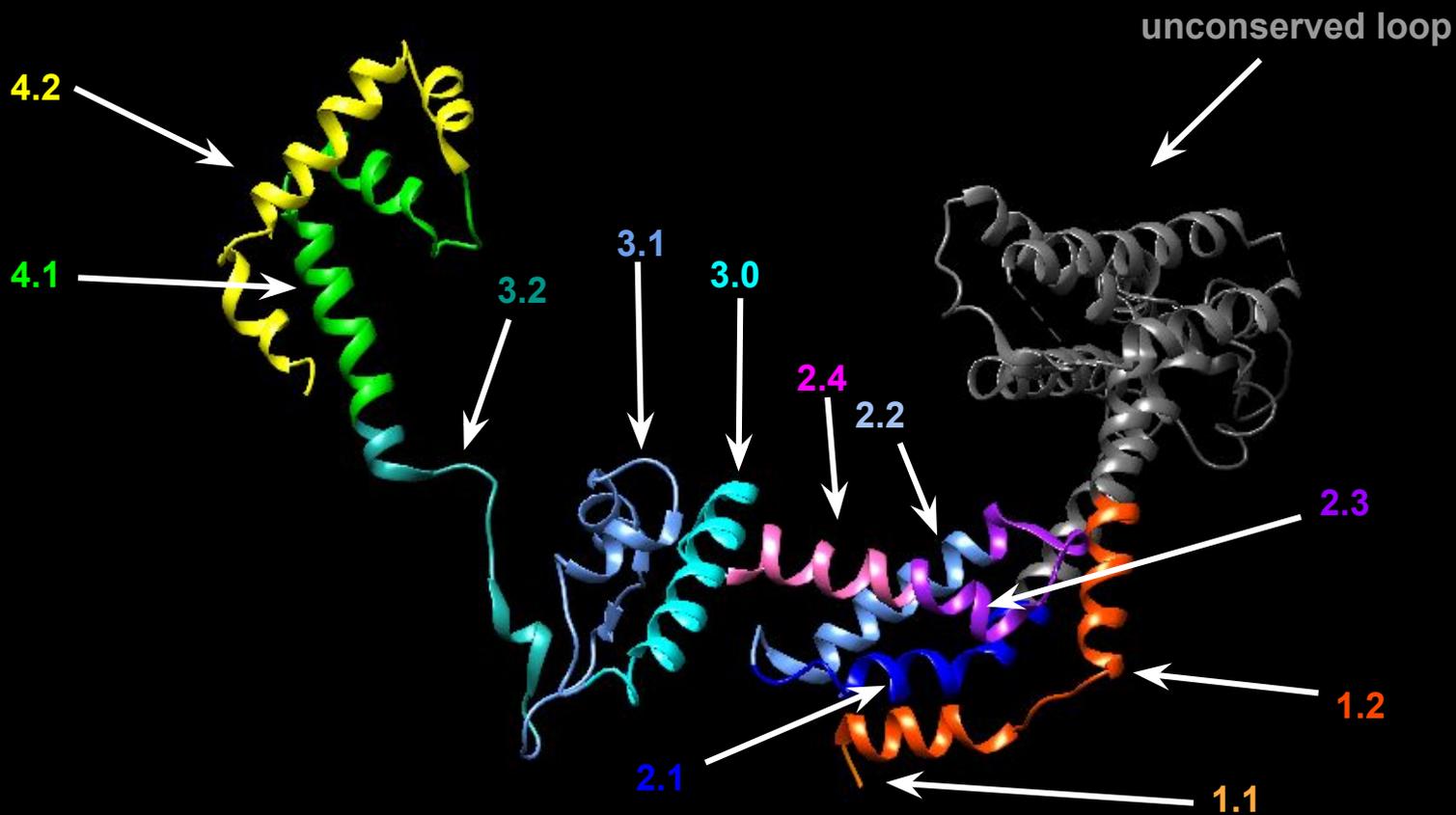
| | | |
|----------------------|--|-----|
| sp P00579 RP0D_ECOLI | MEQN PQS Q L K L L V T R G K E Q G Y L T Y A E V N D H L P E D I V D S D L E D I I Q M I N D Y G I Q V W E E A P D A D L L M A E N T -- A D E A A E | 78 |
| sp P0A2E4 RP0D_SALTI | MEQN PQS Q L K L L V T R G K E Q G Y L T Y A E V N D H L P E D I V D S D L E D I I Q M I N D Y G I Q V W E E A P D A D L L M A E N T T S T D E D A E E | 80 |
| tr Q0WJ27 Q0WJ27_YER | MEQN PQS Q L K L L V T R G K E Q G Y L T Y A E V N D H L P E D I V D S D L E D I I Q M I N D Y G I Q V W E E A P D A D L L M A E N T T D T D D A A E | 80 |
| tr A0A085Q539 A0A085 | MDN PQS Q L K L V L R G K E Q G Y L T Y A E V N D H L P A E I V D S E Q E D I I Q M I N D Y G K V V E T A P D A D L L A L S D D T T I T D E A A E | 80 |
| sp Q7ZL95 SIGA_THET2 | KKSKRKKVA0AEFA0ETEMVDFEAEELPEEPEGEEDPDLFDPPDLAFDDLDLDFEEGGLD-----LFFFEED | 69 |
| sp P00579 RP0D_ECOLI | AAAVQLSSVESEIGRTTDPVRYVMREYGVIVELLTRGEEDIKAKRIEDSINVOQCSVAEYPEAITYLLEQYDRVEAEEARL | 158 |
| sp P0A2E4 RP0D_SALTI | AAAVQLSSVESEIGRTTDPVRYVMREYGVIVELLTRGEEDIKAKRIEDSINVOQCSVAEYPEAITYLLEQYDRVEAEEARL | 160 |
| tr Q0WJ27 Q0WJ27_YER | AAAVQLSSVESEIGRTTDPVRYVMREYGVIVELLTRGEEDIKAKRIEDSINVOQCSVAEYPEAITYLLEQYDRVEAGESRL | 160 |
| tr A0A085Q539 A0A085 | AAAAALSSVESEIGRTTDPVRYVMREYGVIVELLTRGEEDIKAKRIEDSINVOQSAEAYPTIPYILLEQFDRVQAEELRL | 160 |
| sp Q7ZL95 SIGA_THET2 | LPDKTS-----TSDPVRYVMREYGVIVELLTRGEEDVFAKVFVFAFAK-----K | 116 |
| sp P00579 RP0D_ECOLI | SDLITGFVDPNAEEDLAPTATHVGSSELSQEDLDD-----EDEDGDDGDDSDADDNS-----IDPELAREKFAELRAQY | 228 |
| sp P0A2E4 RP0D_SALTI | SDLITGFVDPNAEEEMAPTATHVGSSELSQEDLDD-----EDEDGDDGDDAADDNS-----IDPELAREKFAELRAQY | 230 |
| tr Q0WJ27 Q0WJ27_YER | SDLITGFVDPNAEEDLAPTATHVGSSELSSTEEMD-----EDEDEE-----DDAEEDNS-----IDPELAREKFSDLREQY | 227 |
| tr A0A085Q539 A0A085 | TDLISGFVDPNDEMTEAPTATHVGSSELSEADLADDEDADVVEDEDEDGDDGESSDSEEVGIDPELAREKFNELRGKFL | 240 |
| sp Q7ZL95 SIGA_THET2 | SEITG-----TSDPVRYVMREYGVIVELLTRGEEDVFAKVFVFAFAK-----LDPDLIRE----- | 129 |
| sp P00579 RP0D_ECOLI | VVTRDTIKAKGRSHATAQEEILKSEVFKQFRLVPKQFDYLVNSMRYMMDRVRTQERLIMKLCEVQCKPKKKNFITLFTG | 308 |
| sp P0A2E4 RP0D_SALTI | VVTRDTIKAKGRSHAAAQEEILKSEVFKQFRLVPKQFDYLVNSMRYMMDRVRTQERLIMKLCEVQCKPKKKNFITLFTG | 310 |
| tr Q0WJ27 Q0WJ27_YER | ENARMEIKKGRNHNAAAEEILKSEVFKQFRLVPKQFDYLVNSMRYMMDRVRTQERLIMKLCEVQCKPKKKNFITLFTSS | 307 |
| tr A0A085Q539 A0A085 | QNLQLANEFGRSDHQASEASDLVDLDFREFRLTPKQFDHLVETLTSMDRVRTQERLVMAKVEVAVKPKKSFIALFTG | 320 |
| sp Q7ZL95 SIGA_THET2 | --VRAKILGSGAR-----VRIHP-----GLKLETD-----PKT----- | 155 |
| sp P00579 RP0D_ECOLI | NETSDTWFNAAIAMNKPWSEKLDHVS EYHRALQKIQEETGLTIEQVKDINRRMSIGEAKARAKKEMEANLRLVI | 388 |
| sp P0A2E4 RP0D_SALTI | NETSETWFNAAIAMNKPWSEKLDHVAEEYQRCLQKIQEETGLTIEQVKDINRRMSIGEAKARAKKEMEANLRLVI | 390 |
| tr Q0WJ27 Q0WJ27_YER | NETSDTWFNAAVAMGKPVSEKLDKDVSEYQKSLQKIQEETGLTIEQVKDINRRMSIGEAKARAKKEMEANLRLVI | 387 |
| tr A0A085Q539 A0A085 | NESNEEMLDKVLASDKPYVAKVREQEETIRRSIQKIQEETGLTIEQVKDINRRMSIGEAKARAKKEMEANLRLVI | 400 |
| sp Q7ZL95 SIGA_THET2 | ---VEED---QKLLKPKHEH---KRYLHIAI-----EGSAARQHLTEANLRLVI | 196 |
| sp P00579 RP0D_ECOLI | SIAKKYYTRGLQFLDLIQEIGNGLKAVDKFEYRRGKFKSTYATWWRQAITRSIADQRTIRIRPVHMJETINKLNRISR | 468 |
| sp P0A2E4 RP0D_SALTI | SIAKKYYTRGLQFLDLIQEIGNGLKAVDKFEYRRGKFKSTYATWWRQAITRSIADQRTIRIRPVHMJETINKLNRISR | 470 |
| tr Q0WJ27 Q0WJ27_YER | SIAKKYYTRGLQFLDLIQEIGNGLKAVDKFEYRRGKFKSTYATWWRQAITRSIADQRTIRIRPVHMJETINKLNRISR | 467 |
| tr A0A085Q539 A0A085 | SIAKKYYTRGLQFLDLIQEIGNGLKAVDKFEYRRGKFKSTYATWWRQAITRSIADQRTIRIRPVHMJETINKLNRISR | 480 |
| sp Q7ZL95 SIGA_THET2 | SIAKKYYTRGLSFLDLIQEIGNGLKAVDKFEYRRGKFKSTYATWWRQAITRSIADQRTIRIRPVHMJETINKLNRISR | 276 |
| sp P00579 RP0D_ECOLI | QMLQEMGREPTPEELAERM--LMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLLEPLDATTESLRATH | 546 |
| sp P0A2E4 RP0D_SALTI | QMLQEMGREPTPEELAERM--LMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLLEPLDATTESLRATH | 548 |
| tr Q0WJ27 Q0WJ27_YER | QMLQEMGREPTPEELAERM--LMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLLEPLDATTESLRATH | 545 |
| tr A0A085Q539 A0A085 | QMLQEMGREPLPEELAERM--QMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLLEPLDATTESLKAATR | 558 |
| sp Q7ZL95 SIGA_THET2 | QLQDELGREPTYEEIAEAMGPWDAAKRVETLKIAPQVPSLVEPIGDEKDSYFGDFIDPEHLPSPVDATQSLGSEEL | 356 |
| sp P00579 RP0D_ECOLI | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRRHPSRSEVLRSLFDL | 613 |
| sp P0A2E4 RP0D_SALTI | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRRHPSRSEVLRSLFDL | 615 |
| tr Q0WJ27 Q0WJ27_YER | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRRHPSRSEVLRSLFDL | 612 |
| tr A0A085Q539 A0A085 | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRRHPSRSEVLRSLFDE | 625 |
| sp Q7ZL95 SIGA_THET2 | LSKLSERAEVLRMRFGIDMNTDHTLLEEVGAEQFDVTRERIRQIEAKALRKLRRHPSRIRKLRFELD | 423 |

σ 70 Subunit: 1.2 - 2.1 nonconserved Loop



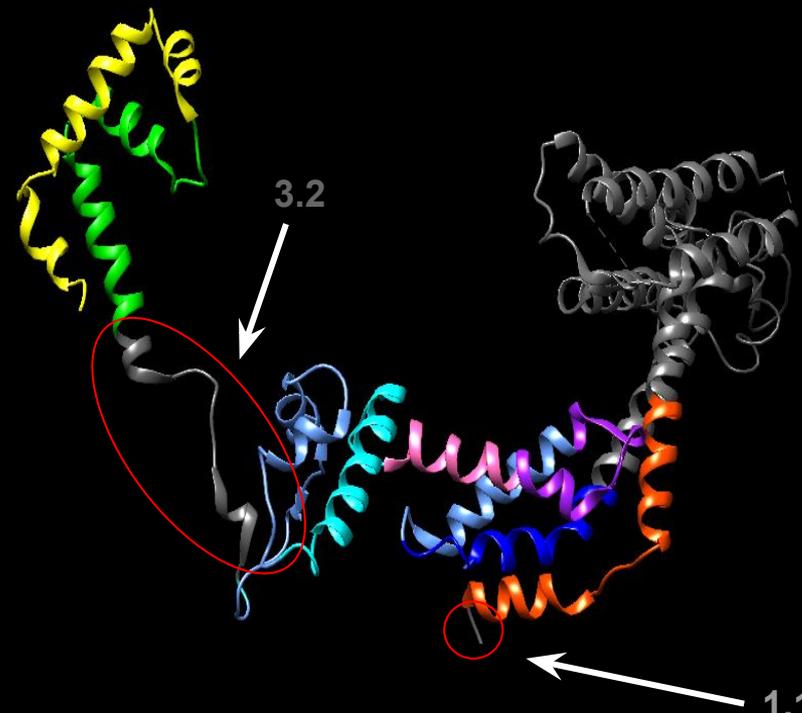
| | | |
|----------------------|--|-----|
| sp P0A2E4 RP0D_SALT1 | MEQNPOSQIKLLVTRGKEGYLYTVAEYNDHLFEDIVSQQEEDIIQMINDKGIQVVEEPPADDLLLAENTTSTDDEAAEAARQVLSVSESEIGRTIDPV | 100 |
| tr Q0WJ27 Q0WJ27_YER | MEQNPOSQIKLLVTRGKEGYLYTVAEYNDHLFEDIVSQQEEDIIQMINDKGIQVVEEPPADDLLLAENTTSTDDEAAEAARQVLSVSESEIGRTIDPV | 100 |
| tr A0A0850539 A0A085 | MDQNPOSQIKQLVLRGKEGYLYTVAEYNDHLFAEIVSQQEEDIIQMINDKGIQVVEEPPADDLLSDOTTIDDEAAEAARQVLSVSESEIGRTIDPV | 100 |
| sp Q72L95 SIGA_THET2 | WKKSKRKLQAQEAQETVIVQEAELPEFTEGEPDPILEDPLALEDDLIDPEEGLD-----LSEEEEDLIPPKTS-----TSDPV | 81 |
| sp P0A2E4 RP0D_SALT1 | RVMMEKGVVELLREGEIDIAKRIEDGIVQCSVAEYPEATITLLEQYDRVVEAEARLSDLIITGFVDPNAEEEMAPTATHVGSSELQEDLDD----- | 195 |
| tr Q0WJ27 Q0WJ27_YER | RVMMEKGVVELLREGEIDIAKRIEDGIVQCSVAEYPEATITLLEQYDRVVEAEARLSDLIITGFVDPNAEEDIAPTATHVGSSELTEEMD----- | 194 |
| tr A0A0850539 A0A085 | RVMMEKGVVELLREGEIDIAKRIEDGIVQSAIAEYPTIPYILLEQYDRVQAEELRLDLSITGFVDPNDEETAPTATHVGSSELSEADLEDDAVV | 200 |
| sp Q72L95 SIGA_THET2 | ROYLIEGVVPLTTEVELLARKVEEGEATK-----KLSSETG----- | 121 |
| sp P0A2E4 RP0D_SALT1 | DEDEDEDGDDAADDNS-----DPELAREKFAELRAQYVYTRDTIKAKRSHHAAAGEELIKLSEVFKQFLVQKQFDYLVNMSVNMHGVVTRQERLIM | 280 |
| tr Q0WJ27 Q0WJ27_YER | EPEDEE-----DDAEDDNS-----DPELARKKFSDLREQYENARMEKKRGRSHANAAAEELKLSVFKQFLVQKQFDYLVNMSVNMHGVVTRQERIM | 287 |
| tr A0A0850539 A0A085 | EDEDEDDEDGDESSDEEEVGTPELAREKFNELRKGQNLQLANEFRRSHQASEASDLVLDIFREFLTKQFDHVELTILSMGVVTRQERLYM | 300 |
| sp Q72L95 SIGA_THET2 | DEDEDEDGDESSDEEEVGTPELAREKFNELRKGQNLQLANEFRRSHQASEASDLVLDIFREFLTKQFDHVELTILSMGVVTRQERLYM | 152 |
| sp P0A2E4 RP0D_SALT1 | KLCVEQCKPKKNFVITLFTGNETSETWFNAATAMNKPWSEKLDHVAEYVQRCLQKLRHEEYGLTIEQVDTINRMSIGEAARRKIKEMVEANLRLV | 390 |
| tr Q0WJ27 Q0WJ27_YER | KLCVEQCKPKKNFVITLFTGNETSETWFNAAVAMGKPVSEKLDVSEVQRSLKRLQHEEYGLTIEQVDTINRMSIGEAARRKIKEMVEANLRLV | 387 |
| tr A0A0850539 A0A085 | KAVVEVAKPKKSFIALFTGNESEEWLDKVLASDKPYAVKREQEELRSTOKLMEIEETLSLSVERKDISRMSIGEAARRKIKEMVEANLRLV | 400 |
| sp Q72L95 SIGA_THET2 | PKT-----VEFD-----KRLSKPKHE-----KRYLHAR-----EEEAHQHLEANRLVY | 196 |
| sp P0A2E4 RP0D_SALT1 | SIAKKYYTRGLDFLDLQEGNIGLWAVDKFEYRRGVKFSYATWIRQATIFSIADQARTIRIPVHMIEITINKLRISRMQLENGREPTPEELAEVY | 489 |
| tr Q0WJ27 Q0WJ27_YER | SIAKKYYTRGLDFLDLQEGNIGLWAVDKFEYRRGVKFSYATWIRQATIFSIADQARTIRIPVHMIEITINKLRISRMQLENGREPTPEELAEVY | 486 |
| tr A0A0850539 A0A085 | SIAKKYYTRGLDFLDLQEGNIGLWAVDKFEYRRGVKFSYATWIRQATIFSIADQARTIRIPVHMIEITINKLRISRMQLENGREPTPEELAEVY | 499 |
| sp Q72L95 SIGA_THET2 | SIAKKYYTRGLDFLDLQEGNIGLWAVDKFEYRRGVKFSYATWIRQATIFSIADQARTIRIPVHMIEITINKLRISRMQLENGREPTPEELAEVY | 296 |
| sp P0A2E4 RP0D_SALT1 | -LMPEDKTRKVLKIAEPISEETPIGDDSDSLGDFIEDITLLEPLDSATSESRATHDLAGLIPAREAVLWRGGDMNTHDITLLEVGKQVTRER | 588 |
| tr Q0WJ27 Q0WJ27_YER | -LMPEDKTRKVLKIAEPISEETPIGDDSDSLGDFIEDITLLEPLDSATSESRATHDLAGLIPAREAVLWRGGDMNTHDITLLEVGKQVTRER | 585 |
| tr A0A0850539 A0A085 | -QMPEDKTRKVLKIAEPISEETPIGDDSDSLGDFIEDITLLEPLDSATSESRATHDLAGLIPAREAVLWRGGDMNTHDITLLEVGKQVTRER | 598 |
| sp Q72L95 SIGA_THET2 | PGWDKRVVEETLKIAEPISEETPIGDDSDSLGDFIEDITLLEPLDSATSESRATHDLAGLIPAREAVLWRGGDMNTHDITLLEVGKQVTRER | 396 |
| sp P0A2E4 RP0D_SALT1 | IRTEAKALRKLRFPSRSEVLRSLDD | 615 |
| tr Q0WJ27 Q0WJ27_YER | IRTEAKALRKLRFPSRSEVLRSLDD | 612 |
| tr A0A0850539 A0A085 | IRTEAKALRKLRFPSRSEVLRSLDE | 625 |
| sp Q72L95 SIGA_THET2 | IRTEAKALRKLRFPSRTRKRLDFLD | 423 |

σ 70 Subunit: Subregions



σ 70 Subunit: Flexible Linkers

| | | |
|--------------------------|--|-----|
| sp P00579 RP0D_ECOLI | MEQNQPSQKLLVTRGKEQGYLYTAAEVNDHLPEDIVSDQVIEDIIQMINDMGTQVLEEAPDADLLMLAENT--ADEDAAE | 78 |
| sp P0A2E4 RP0D_SALTI | MEQNQPSQKLLVTRGKEQGYLYTAAEVNDHLPEDIVSDQVIEDIIQMINDMGTQVLEEAPDADLLMLAENTTSDDEAAE | 80 |
| tr Q0WJ27 Q0WJ27_YER | MEQNQPSQKLLVTRGKEQGYLYTAAEVNDHLPEDIVSDQVIEDIIQMINDMGTQVLEEAPDADLLMLAENTTDDDDAAE | 80 |
| tr A0A085Q539 A0A085 | MEQNQPSQKLLVTRGKEQGYLYTAAEVNDHLPAAEIVSEQVEDIIQMINDMGTQVLEEAPDADLLSDDTTITDEDAE | 80 |
| sp Q72L95 SIGA_THET2 | MKSKRKNAAQQAQFAQETVAVLQFAELPPEEPEGEPPDQVLEDDPDLALEDLIDLPPEEREGID-----LLEEEFF | 69 |
| sp P00579 RP0D_ECOLI | AAQVMSVSEVEIGRTTQVRYMVRREYGVVLELITREGEIDIAKRIEDCINQVCSVAEYPEAITYLLEQYDRVEAEEARL | 158 |
| sp P0A2E4 RP0D_SALTI | AAQVMSVSEVEIGRTTQVRYMVRREYGVVLELITREGEIDIAKRIEDCINQVCSVAEYPEAITYLLEQYDRVEAEEARL | 160 |
| tr Q0WJ27 Q0WJ27_YER | AAQVMSVSEVEIGRTTQVRYMVRREYGVVLELITREGEIDIAKRIEDCINQVCSVAEYPEAITYLLEQYDRVEAGESRL | 160 |
| tr A0A085Q539 A0A085 | AAQAAASVSEVEIGRTTQVRYMVRREYGVVLELITREGEIDIAKRIEDCINQVSAIAEYPGTIPYILEQFDRVQAEELRL | 160 |
| sp Q72L95 SIGA_THET2 | LPPIKIS-----TSDVRYVQLHEHGQVPLLTLEEVELARKVVEEYFAIK-----KLI | 116 |
| sp P00579 RP0D_ECOLI | SDLITGFVDPNAEEDLAPTATHVGSSELSEQEDLDDDD----EDEDDEEDGDDSDADDNNS----IDPELAREKFAELRAQY | 228 |
| sp P0A2E4 RP0D_SALTI | SDLITGFVDPNAEEMAPTATHVGSSELSEQEDLDDDD----EDEDDEEDGDDSDADDNNS----IDPELAREKFAELRAQY | 239 |
| tr Q0WJ27 Q0WJ27_YER | SDLITGFVDPNAEEDLAPTATHVGSSELSTEEMDD----EDEDDEE--DDBAEDNNS----IDPELAREKFSDLRQY | 227 |
| tr A0A085Q539 A0A085 | TDLISGFVDPNDETEAPTATHVGSSELSEADLADEDAVVEDEDEDGDEGDESSDSEEEVGLIDPELAREKFNELRGKFL | 240 |
| sp Q72L95 SIGA_THET2 | SEITG-----LDPDLIRE | 129 |
| sp P00579 RP0D_ECOLI | VVTRDTIKKAGGRSHATAQEEIILKSEVFKQFRLVPKQFDYLVNSMVMMDRVRTQERLIMKLCVEQCKMPPKKNFITLFTG | 308 |
| sp P0A2E4 RP0D_SALTI | VVTRDTIKKAGGRSHAAQEEIILKSEVFKQFRLVPKQFDYLVNSMVMMDRVRTQERLIMKLCVEQCKMPPKKNFITLFTG | 310 |
| tr Q0WJ27 Q0WJ27_YER | ENARMETIKMGRNHANAQEEIILKSEVFKQFRLVPKQFDYLVNSMVMMDRVRTQERLIMKLCVEQCKMPPKKNFVTLFSS | 307 |
| tr A0A085Q539 A0A085 | QNLQLAVNEFGRSDHQSEASDLVLDIFREFLTPKQFDHLVETLITSMDRVRTQERLYMKAVVEVAKMPPKKSFIALFTG | 320 |
| sp Q72L95 SIGA_THET2 | VVRAKILGSRAR-----VRHIP-----GLMETLD-----PKT----- | 155 |
| sp P00579 RP0D_ECOLI | NETSDTWFNAATAMNKPWSEKLDHVSVEVHRAQLKQVEETGLTIEQVKDINRMSIGEAKARAKKEMVEANLRVLI | 388 |
| sp P0A2E4 RP0D_SALTI | NETSETWFNAATAMNKPWSEKLDHVAEYQRCLQKLRQVEETGLTIEQVKDINRMSIGEAKARAKKEMVEANLRVLI | 390 |
| tr Q0WJ27 Q0WJ27_YER | NETSDTWFNAAVMGPWSEKLDKDSVEDYQRSQKLRQVEETGLTIEQVKDINRMSIGEAKARAKKEMVEANLRVLI | 387 |
| tr A0A085Q539 A0A085 | NESNEEWLDKVLASDKPYVAKVREQEETRRISQKLMTEQTSLSVERIKDTSRMSIGEAKARAKKEMVEANLRVLI | 400 |
| sp Q72L95 SIGA_THET2 | VEETD--QKLSLQKHEH---KRYLHAR-----EGFAAQHLEANLRVLI | 196 |
| sp P00579 RP0D_ECOLI | SIAKKYYTRGLQFLDLIQEENIGLMAVDKFEYRRQYKFSYATWVIROAITRSTADQARTIRIPVHMVETINKLNRISR | 468 |
| sp P0A2E4 RP0D_SALTI | SIAKKYYTRGLQFLDLIQEENIGLMAVDKFEYRRQYKFSYATWVIROAITRSTADQARTIRIPVHMVETINKLNRISR | 470 |
| tr Q0WJ27 Q0WJ27_YER | SIAKKYYTRGLQFLDLIQEENIGLMAVDKFEYRRQYKFSYATWVIROAITRSTADQARTIRIPVHMVETINKLNRISR | 467 |
| tr A0A085Q539 A0A085 | SIAKKYYTRGLQFLDLIQEENIGLMAVDKFEYRRQYKFSYATWVIROAITRSTADQARTIRIPVHMVETINKLNRISR | 489 |
| sp Q72L95 SIGA_THET2 | SIAKKYYTRGLQFLDLIQEENIGLMAVDKFEYRRQYKFSYATWVIROAITRSTADQARTIRIPVHMVETINKLNRISR | 276 |
| sp P00579 RP0D_ECOLI | QLQLEGREPTPEELAEARM--LMPEDKTRKVLKIAKEPISMETPIGDDESHLGDFTIEDTILELPIDSAITESLRATHD | 546 |
| sp P0A2E4 RP0D_SALTI | QLQLEGREPTPEELAEARM--LMPEDKTRKVLKIAKEPISMETPIGDDESHLGDFTIEDTILELPIDSAITESLRATHD | 548 |
| tr Q0WJ27 Q0WJ27_YER | QLQLEGREPTPEELAEARM--LMPEDKTRKVLKIAKEPISMETPIGDDESHLGDFTIEDTILELPIDSAITESLRATHD | 545 |
| tr A0A085Q539 A0A085 | QLQLEGREPTPEELAEARM--QMPEDKTRKVLKIAKEPISMETPIGDDESHLGDFTIEDTILELPIDSAITATSLKATRD | 558 |
| sp Q72L95 SIGA_THET2 | QLQLEGREPTYEELAEARMGPGWDAKVEETLKIAQEPVSLTETPIGDEKDSFYGDFIDPEELPSPVDAATSLSEELEK | 356 |
| sp P00579 RP0D_ECOLI | VLAGLITAREAVLNRFRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFD | 613 |
| sp P0A2E4 RP0D_SALTI | VLAGLITAREAVLNRFRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFD | 615 |
| tr Q0WJ27 Q0WJ27_YER | VLAGLITAREAVLNRFRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFD | 612 |
| tr A0A085Q539 A0A085 | VLAGLITAREAVLNRFRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFD | 625 |
| sp Q72L95 SIGA_THET2 | ALSKLSREAVLNRKGLIDGRHTLLEEVGAFVTRERIRQIEAKALRKLHPSRIRKLRDFLD | 423 |



1.1

sp|P00579|RP0D_EC0LI MEQNPQSOLKLLVTRGKEQGYLTYAEVNDHLPEDIVSDQIEDIIQMINDMGIQVMEAPDADDLMLAENT--ADEDAAE 78
sp|P0A2E4|RP0D_SALTI MEQNPQSOLKLLVTRGKEQGYLTYAEVNDHLPEDIVSDQIEDIIQMINDMGIQVMEAPDADDLMLAENTTSDDEDAAE 80
tr|Q0WJ27|Q0WJ27_YER MEQNPQSOLKLLVTRGKEQGYLTYAEVNDHLPEDIVSDQIEDIIQMINDMGIQVLEAPDADDLMLAENTTDDDDAAE 80
tr|A0A085Q539|A0A085 MDQNPQSOLKQLVLRGKEQGYLTYAEVNDHLPEDIVSDQIEDIIQMINDMGIKVVEAPDADDLALSDDTTITDDDDAAE 80
sp|Q72L95|SIGA_THET2 MKKSKRKNAAQAEQAEETVLVQEEAEELPEFPEGEPPD-LEDPDLALEDDLPLPEEGGLD-----LEEEED 69

sp|P00579|RP0D_EC0LI AAAQVLSVSEIEGRITDPVRYMYRREMGTVLELLTREGIEDIAKRIEDSINOVQCSVAEYPEAITYLLEQYDRVEAEEARL 158
sp|P0A2E4|RP0D_SALTI AAAQVLSVSEIEGRITDPVRYMYRREMGTVLELLTREGIEDIAKRIEDSINOVQCSVAEYPEAITYLLEQYDRVEAEEARL 160
tr|Q0WJ27|Q0WJ27_YER AAAQVLSVSEIEGRITDPVRYMYRREMGTVLELLTREGIEDIAKRIEDSINOVQCSVAEYPEAITYLLEQYDRVEAEESRL 160
tr|A0A085Q539|A0A085 AAAAALSSVSEIEGRITDPVRYMYRREMGTVLELLTREGIEDIAKRIEDSINOVQSAIAEYPGTIPYILEQFDRVQAEELR 160
sp|Q72L95|SIGA_THET2 LPTPKIS-----TSDPVRYQLHEIQVPLLLTLEEVEVLARKVVEEEMAIK-----KL 116

sp|P00579|RP0D_EC0LI SDLITGFVDPNAEEDLAPTATHVGSSELSQEDLDD-----EDEDEEDGDDSDADDNS-----IDPELAREKFAELRAQY 228
sp|P0A2E4|RP0D_SALTI SDLITGFVDPNAEEMAPTATHVGSSELSQEDLDD-----EDEDEEDGDDAADDNS-----IDPELAREKFAELRAQY 230
tr|Q0WJ27|Q0WJ27_YER SDLITGFVDPNAEEDIAPTATHVGSSELSSTEMDD-----EDEDEE--DDAEDDNS-----IDPELAREKFSDLREQY 227
tr|A0A085Q539|A0A085 TDLISGFVDPNDMETEAPTATHVGSSELSEADLADEDDAVVEDEDEDEDEGDGESSDSEEEVGIIDPELAREKFNLRGKF 240
sp|Q72L95|SIGA_THET2 SEITG-----LDPDLIRE----- 129

sp|P00579|RP0D_EC0LI VVTRDTIKAKGRSHATAQEEIILKLVSEVFKQFRLVLPKQFDYLVNSMFRVMMDRVRTQERLIMKLCVEQCKMPKKNFITLFTG 308
sp|P0A2E4|RP0D_SALTI VVTRDTIKAKGRSHAAAQEEIILKLVSEVFKQFRLVLPKQFDYLVNSMFRVMMDRVRTQERLIMKLCVEQCKMPKKNFITLFTG 310
tr|Q0WJ27|Q0WJ27_YER ENARMEIKKNGRNHANAAAEEIILKLVSEVFKQFRLVLPKQFDYLVNMMRAMMDRVRTQERLIIMKLCVEQCKMPKKNFITLFSG 307
tr|A0A085Q539|A0A085 QNLQLAVNEFGRDSSHQASEADLVLDIFREFRLTPKQFDHLVETLRITSMDRVRTQERLVMKAVVEVAKMPKKSFIALFTG 320
sp|Q72L95|SIGA_THET2 -VVRAKILGSAR-----VRHIP-----GLKETLD-----PKT----- 155

sp|P00579|RP0D_EC0LI NETSDTFWNAAIAMNKPWSEKLDHVSSEVHRALQKLQRIEEETGLTIEQVKDINRRMSIGEAKVRAAKKEMVEANLRLVI 388
sp|P0A2E4|RP0D_SALTI NETSETWFAAIAMNKPWSEKLDHVAEEVQRCLQKLQRIEEETGLTIEQVKDINRRMSIGEAKVRAAKKEMVEANLRLVI 390
tr|Q0WJ27|Q0WJ27_YER NETSDTFWNAAVAMGKPWSEKLDKVSDEDRSLQKLQRIEEETGLTIEQVKDINRRMSIGEAKVRAAKKEMVEANLRLVI 387
tr|A0A085Q539|A0A085 NESNEEWLDKVLASDKPYVAKVREQEETRRSIQKLQRIEEETGLTIEQVKDINRRMSIGEAKVRAAKKEMVEANLRLVI 400
sp|Q72L95|SIGA_THET2 -----VEEID---QKLKSLPKHE---KRYLHIAE-----EAEARQHLLEANLRLVI 196

sp|P00579|RP0D_EC0LI SIAKKYTVRGLQFLDLIQEGNIGLMAKAVDKFEYRRGYKFSTYATWVIRQAITRSIADQARTIRIPVHMETINKLNRISR 468
sp|P0A2E4|RP0D_SALTI SIAKKYTVRGLQFLDLIQEGNIGLMAKAVDKFEYRRGYKFSTYATWVIRQAITRSIADQARTIRIPVHMETINKLNRISR 470
tr|Q0WJ27|Q0WJ27_YER SIAKKYTVRGLQFLDLIQEGNIGLMAKAVDKFEYRRGYKFSTYATWVIRQAITRSIADQARTIRIPVHMETINKLNRISR 467
tr|A0A085Q539|A0A085 SIAKKYTVRGLQFLDLIQEGNIGLMAKAVDKFEYRRGYKFSTYATWVIRQAITRSIADQARTIRIPVHMETINKLNRISR 480
sp|Q72L95|SIGA_THET2 SIAKKYTVRGLSFLDLIQEGNIGLIRAVEKFEYKRRFKFSTYATWVIRQAINRAIADQARTIRIPVHMETINKLNRISR 276

sp|P00579|RP0D_EC0LI QMLQEMGREPTPEELAERM--LMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLELPLDSATTESLRAATHD 546
sp|P0A2E4|RP0D_SALTI QMLQEMGREPTPEELAERM--LMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLELPLDSATTESLRAATHD 548
tr|Q0WJ27|Q0WJ27_YER QMLQEMGREPTPEELAERM--LMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLELPLDSATSESLSRATHD 545
tr|A0A085Q539|A0A085 QMLQEMGREPLPEELAERM--QMPEDKIRKVLKIAKEPISMETPIGDDSDSHLGDFTEDTTLELPLDSATATSLKAATRD 558
sp|Q72L95|SIGA_THET2 QLQQLGREPTYEEIAEAMGPGWDAKRVEETLKIAQEPVSLLETPIGDEKDSFYGDFIPDEHLPSVDAATQSLSEELEK 556

sp|P00579|RP0D_EC0LI VLAGLTAREAKVLRMRFGIDMNTDHTLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFDD 613
sp|P0A2E4|RP0D_SALTI VLAGLTAREAKVLRMRFGIDMNTDHTLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFDD 615
tr|Q0WJ27|Q0WJ27_YER VLAGLTAREAKVLRMRFGIDMNTDHTLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFDD 612
tr|A0A085Q539|A0A085 VLAGLTPREAKVLRMRFGIDMNTDHTLEEVGKQFDVTRERIRQIEAKALRKLHPSRSEVLRSLFDE 625
sp|Q72L95|SIGA_THET2 ALSKLSEREAVLKLKRGIDTGREHTLEEVGAFQVTRERIRQIENKALRKLKHSRTRKLRDFLD- 423

σ70 Subunit: Conserved regions

| | | |
|----------------------|--|-----|
| sp P00579 RP0D_ECOLI | MEQNPQSLKLLVTRGKQGYLTYAEVNDHLPEDIVDSIQIEDIQIQMINMGIQVMEAPDAADLLAENT--ADEDAALAAAQVLSVSESEIGRTITPV | 98 |
| sp P0A2E4 RP0D_SALTI | MEQNPQSLKLLVTRGKQGYLTYAEVNDHLPEDIVDSIQIEDIQIQMINMGIQVMEAPDAADLLAENTTSTDEDAEAAAQVLSVSESEIGRTITPV | 100 |
| tr Q0WJ27 Q0WJ27_YER | MEQNPQSLKLLVTRGKQGYLTYAEVNDHLPEDIVDSIQIEDIQIQMINMGIQVLEAPDAADLLAENTTDDDAEAAAQVLSVSESEIGRTITPV | 100 |
| tr A0A085Q539 A0A085 | MDQNPQSLKLLVTRGKQGYLTYAEVNDHLP AEIVDSIQVEDIQIQMINMGIKVVEAPDAADLLASDDTTITDEDAEAAAALSVSESEIGRTITPV | 100 |
| sp Q72L95 SIGA_THET2 | MKKSRRKNAQAQEAQETVFLVQEEALPELPEPEGEPPI--LEPDLALEDLLDLPEEGELD-----LEEEEDLPIPKIS-----TSLPV | 81 |
| sp P00579 RP0D_ECOLI | RYMYMRMGTVELLTRGEGIDIAKRIEDSINQVQCSVAEYPEAITYLLEQYDRVEAEEAALSDLITGFVDPNAEEDLAPTATHVGSELSQEDLDDD----- | 193 |
| sp P0A2E4 RP0D_SALTI | RYMYMRMGTVELLTRGEGIDIAKRIEDSINQVQCSVAEYPEAITYLLEQYDRVEAEEAALSDLITGFVDPNAEEEMAPTATHVGSELSQEDLDDD----- | 195 |
| tr Q0WJ27 Q0WJ27_YER | RYMYMRMGTVELLTRGEGIDIAKRIEDSINQVQCSVAEYPEAITYLLEQYDRVEAGESALSDLITGFVDPNAEEDIAPTATHVGSELSTEEMDD----- | 194 |
| tr A0A085Q539 A0A085 | RYMYMRMGTVELLTRGEGIDIAKRIEDSINQVQSAIAEYPTGPIYILEQFDRVQAEELRLDLSLITGFVDPNDMEAPTATHVGSSELSEADLADEDDAVV | 200 |
| sp Q72L95 SIGA_THET2 | RYMYMRMGTVELLTRGEGIDIAKRIEDSINQVQSAIAEYPTGPIYILEQFDRVQAEELRLDLSLITGFVDPNDMEAPTATHVGSSELSEADLADEDDAVV | 221 |
| sp P00579 RP0D_ECOLI | EDEDEEDGDDSDADDNS-----IDPELAHEKFAELRAQYVVRTDITKAKGSHATAQEEILKLVSEVFKQFLVLPKQFDYLVNSMVMRRVVRTQERLIM | 288 |
| sp P0A2E4 RP0D_SALTI | EDEDEEDGDDDAADDNS-----IDPELAHEKFAELRAQYVVRTDITKAKGSHAAAQEEILKLVSEVFKQFLVLPKQFDYLVNSMVMRRVVRTQERLIM | 290 |
| tr Q0WJ27 Q0WJ27_YER | EDEDEE-----DDDAEDNS-----IDPELAHQKFDLREQYENARMEIKKNGNHANAAAEILKLVSEVFKQFLVLPKQFDYLVNSMVMRRVVRTQERLIM | 287 |
| tr A0A085Q539 A0A085 | EDEDEDEDEDGDESSDSEEVGIDPELAHEKFNELRGKFNQLQAVNEFGDSHQASEASDLVDLDFREFLTPKQFDHVELTSMRRVVRTQERLVM | 300 |
| sp Q72L95 SIGA_THET2 | -----LDPDLIE-----VVRAKILGSAI-----V--HIP-----GL--ETLI----- | 152 |
| sp P00579 RP0D_ECOLI | KLCVEQCKMPKKNFITLFTGNSETDWFNAAIAMNKPWSEKLDHVSVEVHRALQKLRQIIEETGLTIEQVKDINRMSIGEAAARRAKEMVFNANLRLVI | 388 |
| sp P0A2E4 RP0D_SALTI | KLCVEQCKMPKKNFITLFTGNSETDWFNAAIAMNKPWSEKLDHVAEVQRCLQLRQIEEETGLTIEQVKDINRMSIGEAAARRAKEMVFNANLRLVI | 390 |
| tr Q0WJ27 Q0WJ27_YER | KLCVEQCKMPKKNFVTLFSSNETDWFNAAVAMGPKWSEKLDVSDVQRCLQLRQIEEETGLTIEQVKDINRMSIGEAAARRAKEMVFNANLRLVI | 387 |
| tr A0A085Q539 A0A085 | KAVVEVAKMPKSFIALFTGNSENEWLDKVLASDPYVAKVRELEIRRSIQKLMIEQETLSLVERIKDISRMSIGEAAARRAKEMVFNANLRLVI | 400 |
| sp Q72L95 SIGA_THET2 | -----P--T-----LDPDLIE-----VVRAKILGSAI-----V--HIP-----GL--ETLI----- | 196 |
| sp P00579 RP0D_ECOLI | SIAKKYTNRGLQFDLDTIQEGNIGLMAVDKFEYRAGKFFSYATWIRQAITSIAADQATIRIPVMVETINKLNISRQMLQEMGREPTPEELAEARM- | 487 |
| sp P0A2E4 RP0D_SALTI | SIAKKYTNRGLQFDLDTIQEGNIGLMAVDKFEYRAGKFFSYATWIRQAITSIAADQATIRIPVMVETINKLNISRQMLQEMGREPTPEELAEARM- | 489 |
| tr Q0WJ27 Q0WJ27_YER | SIAKKYTNRGLQFDLDTIQEGNIGLMAVDKFEYRAGKFFSYATWIRQAITSIAADQATIRIPVMVETINKLNISRQMLQEMGREPTPEELAEARM- | 486 |
| tr A0A085Q539 A0A085 | SIAKKYTNRGLQFDLDTIQEGNIGLMAVDKFEYRAGKFFSYATWIRQAITSIAADQATIRIPVMVETINKLNISRQMLQEMGREPTPEELAEARM- | 499 |
| sp Q72L95 SIGA_THET2 | SIAKKYTGGLSELDLDTIQEGNIGLMAVDKFEYRAGKFFSYATWIRQAITSIAADQATIRIPVMVETINKLSTARQLQDLGREGPTPEELAEARMG | 296 |
| sp P00579 RP0D_ECOLI | -LMPEDIRKVLKIAKEPISMTPIGDDKESHLGDIETLLELPDLSA--TESLRAATHDVLAGLTAREAKVLRMFGIDMNTDHTLEEYVKGQFDVTRER | 586 |
| sp P0A2E4 RP0D_SALTI | -LMPEDIRKVLKIAKEPISMTPIGDDKESHLGDIETLLELPDLSA--TESLRAATHDVLAGLTAREAKVLRMFGIDMNTDHTLEEYVKGQFDVTRER | 588 |
| tr Q0WJ27 Q0WJ27_YER | -LMPEDIRKVLKIAKEPISMTPIGDDKESHLGDIETLLELPDLSA--SESLRSATHDVLAGLTAREAKVLRMFGIDMNTDHTLEEYVKGQFDVTRER | 585 |
| tr A0A085Q539 A0A085 | -QMPEDIRKVLKIAKEPISMTPIGDDKESHLGDIETLLELPDLSA--ATSLKAAATRDVLAGLTAREAKVLRMFGIDMNTDHTLEEYVKGQFDVTRER | 598 |
| sp Q72L95 SIGA_THET2 | PGWDAKIVETLQIAQPVSLTPIGDEKDSFYGDIPVHEHLPSPVDA--QSLLSEELKALSKLSEKAMVLRKGLIDGREGHTLEEYVGAFFGVTRER | 396 |
| sp P00579 RP0D_ECOLI | IRQIEANALRKLK--HPSRSEVLRSFLDD | 613 |
| sp P0A2E4 RP0D_SALTI | IRQIEANALRKLK--HPSRSEVLRSFLDD | 615 |
| tr Q0WJ27 Q0WJ27_YER | IRQIEANALRKLK--HPSRSEVLRSFLDD | 612 |
| tr A0A085Q539 A0A085 | IRQIEANALRKLK--HPSRSEVLRSFLDE | 625 |
| sp Q72L95 SIGA_THET2 | IRQIEANALRKLK--HPSRSEVLRSFLDD | 423 |

σ1

12 acidic residues
0 basic residues

σ2

12 acidic residues
15 basic residues

σ3

14 acidic residues
8 basic residues

σ4

7 acidic residues
13 basic residues

σ 70 Subunit: region 1 and 2

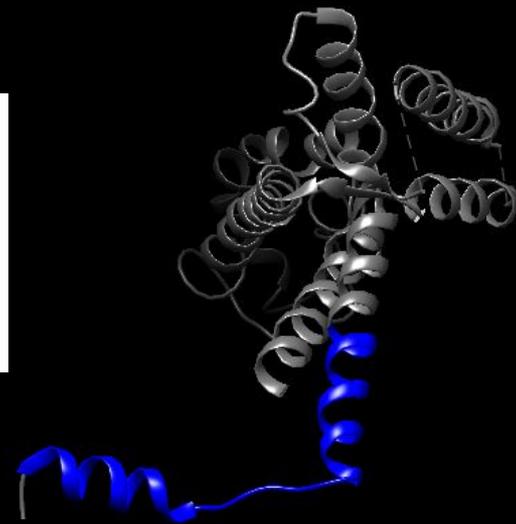
non-conserved loop

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sp|P00579|RP0D_ECOLI MEQNPQSLLKLVTRGKEGGYLYAEVNDHLPEDIVDSQIEDIIQMINDYGIQVMEAPDADDLMLAENT--AEDAAE*78
sp|P0A2E4|RP0D_SALTI MEQNPQSLLKLVTRGKEGGYLYAEVNDHLPEDIVDSQIEDIIQMINDYGIQVMEAPDADDLMLAENTTSTDEDAAE*80
tr|Q0WJ27|Q0WJ27_YER MEQNPQSLLKLVTRGKEGGYLYAEVNDHLPEDIVDSQIEDIIQMINDYGIQVMEAPDADDLMLAENTTDTDDDAE*80
tr|A0A085Q539|A0A085 MDQNPQSLLKLVLRGKEGGYLYAEVNDHLP AEIVDSQVEDIIQMINDYGIQVMEAPDADDLALSDTTITDEDAAE*80
sp|Q72L95|SIGA_THET2 MKKSKRKNAAQAEAEQETEMLVQEFEEELPEFPEGEPPDPLEDPDLALEDLIDLPEEGGLD-----LEEEED*69

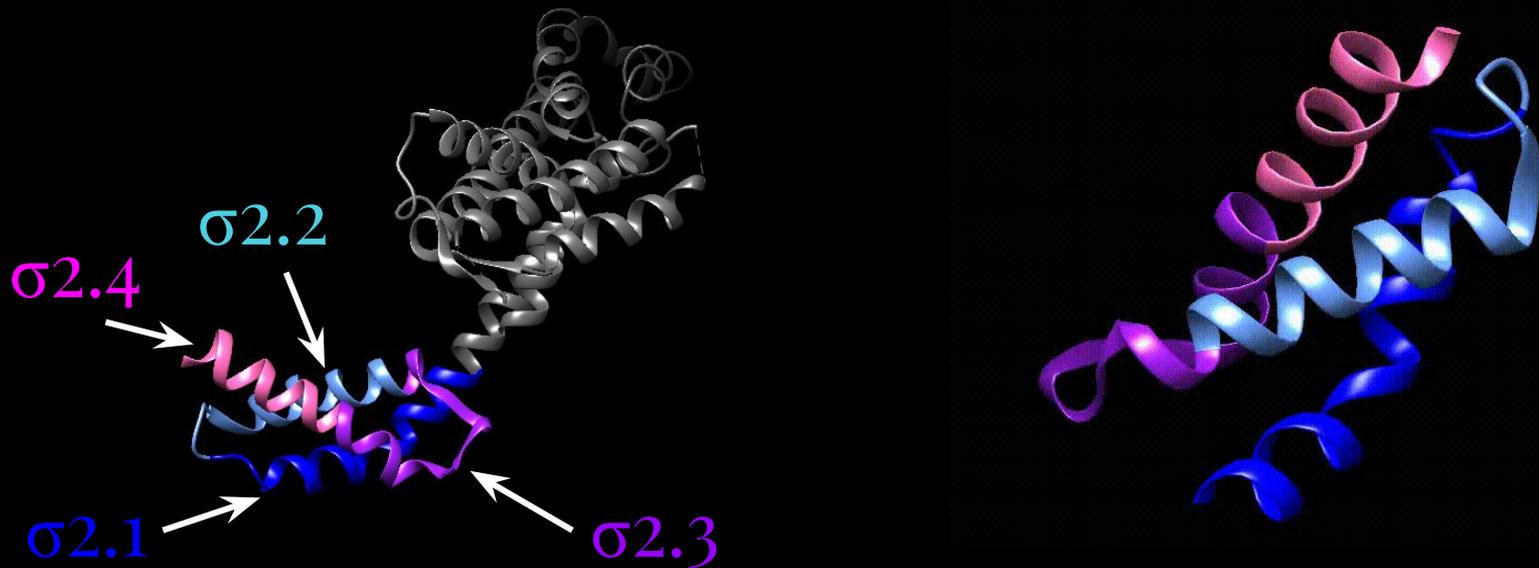
sp|P00579|RP0D_ECOLI AAQVLSVSESEIGRTTD*VRMYMREMGTVELLTREGIEDIAKRIEDGIIQVQCSVAEYPEAITYLLEQYDRVEAEEARL 158
sp|P0A2E4|RP0D_SALTI AAQVLSVSESEIGRTTD*VRMYMREMGTVELLTREGIEDIAKRIEDGIIQVQCSVAEYPEAITYLLEQYDRVEAEEARL 160
tr|Q0WJ27|Q0WJ27_YER AAQVLSVSESEIGRTTD*VRMYMREMGTVELLTREGIEDIAKRIEDGIIQVQCSVAEYPEAITYLLEQYDRVEAGESRL 160
tr|A0A085Q539|A0A085 AAQVLSVSESEIGRTTD*VRMYMREMGTVELLTREGIEDIAKRIEDGIIQVQSAIAEYPGTIPYILEQFDRVQAEELRL 160
sp|Q72L95|SIGA_THET2 LPIPKTS-----TSD*VRQYLHEIGQVPLLTLEEEVELARKVEEEMKATK-----KL 116
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σ 1.1

σ 1.2



σ 70 Subunit: region 2

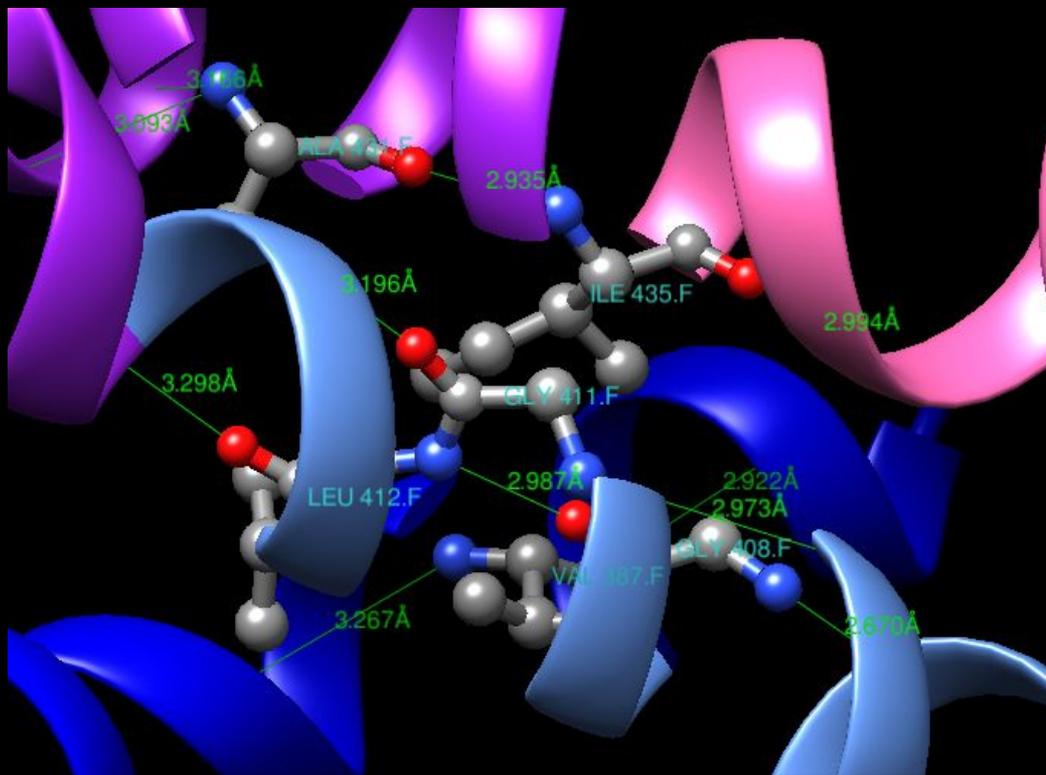


| | | | | | | | | | |
|-------|------------|------------|-----------------------------|------------------------|--------------------------|----------------------|-----------------------|-------|-----|
| sp | P00579 | RPOD_ECOLI | =NETSDTWFNAAIAMNKPWSEKLDHVS | EEVHRALQKLRQ | EEETGLTIEQVKDINRRMSIGEAK | RRRAKEMVEANRLVI | 388 | | |
| sp | P0A2E4 | RPOD_SALTI | =NETSETWFNAAIAMNKPWSEKLDHVA | EEVQRCLQKLRQ | EEETGLTIEQVKDINRRMSIGEAK | RRRAKEMVEANRLVI | 399 | | |
| tr | Q0WJ27 | Q0WJ27_YER | =NETSDTWFNAAVAMGKPWSEKLDKDV | SEDPVQRSLQKLRQ | EEETGLTIEQVKDINRRMSIGEAK | RRRAKEMVEANRLVI | 387 | | |
| tr | A0A085Q539 | A0A085 | =NESNEEWLDKVLASDKPYVAKVREQ | EEIIRRSIQKLRQ | EEETLSLVERIKDISRRMSIGEAK | RRRAKEMVEANRLVI | 400 | | |
| sp | Q72L95 | SIGA_THET2 | -----VEEID--QKLSLPKEH--- | KRYLHTAR----- | EEEAAROHLTEANRLVI | | 196 | | |
| | | | | | | | | | |
| sp | P00579 | RPOD_ECOLI | SI | AKKYTNRGLQFLDLIQEGNIGL | MKAVDKFEYRRG | YKFSTYATWWIRQAITRSI | ADQARTIRIPVHMIETINKLN | RISK | 468 |
| sp | P0A2E4 | RPOD_SALTI | SI | AKKYTNRGLQFLDLIQEGNIGL | MKAVDKFEYRRG | YKFSTYATWWIRQAITRSI | ADQARTIRIPVHMIETINKLN | RISK | 470 |
| tr | Q0WJ27 | Q0WJ27_YER | SI | AKKYTNRGLQFLDLIQEGNIGL | MKAVDKFEYRRG | YKFSTYATWWIRQAITRSI | ADQARTIRIPVHMIETINKLN | RISK | 467 |
| tr | A0A085Q539 | A0A085 | SI | AKKYTNRGLQFLDLIQEGNIGL | MKAVDKFEYRRG | YKFSTYATWWIRQAITRSI | ADQARTIRIPVHMIETINKLN | RISK | 480 |
| sp | Q72L95 | SIGA_THET2 | SI | AKKYTERGLSFLDLIQEGNIGL | TRAVEKFEYRRR | YKFSTYATWWIROATINRAI | ADQARTIRIPVHMIETINKLN | SRISK | 276 |

σ 70 Subunit: region 2 - folding residues

σ 2.3

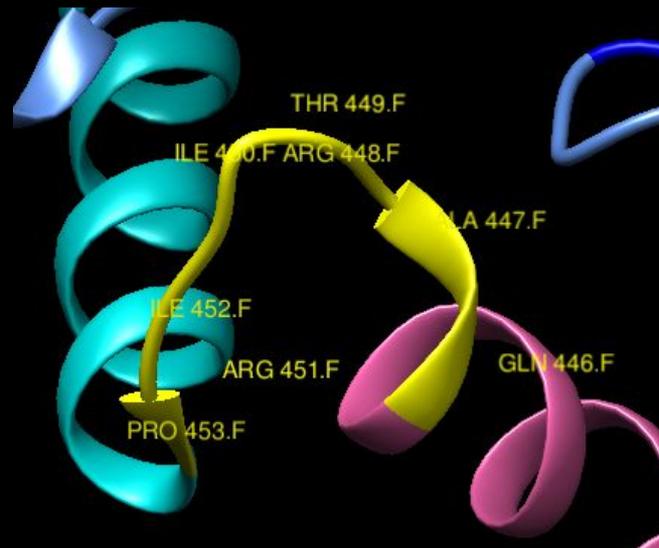
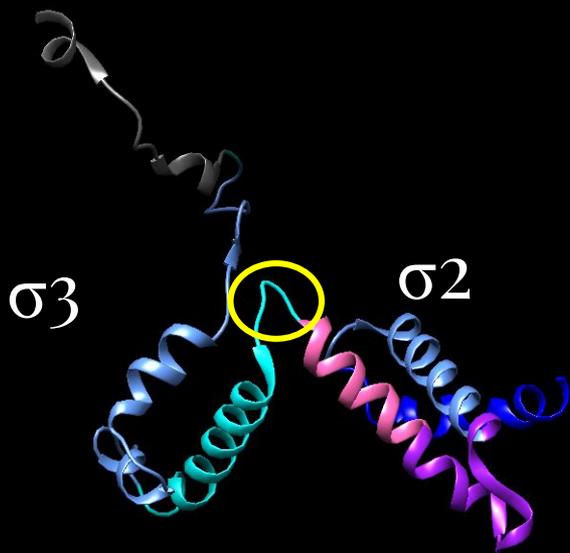
σ 2.4



σ 2.1

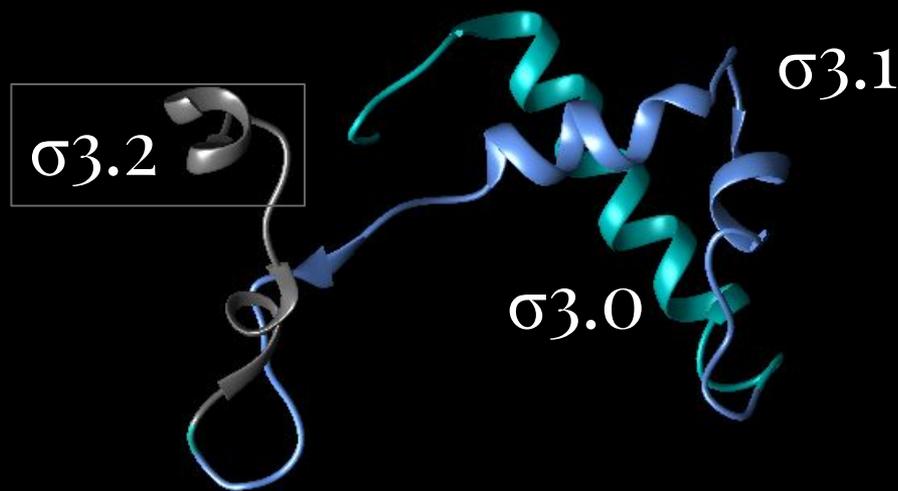
σ 2.2

σ 70 Subunit: 2.4-3.0 linker



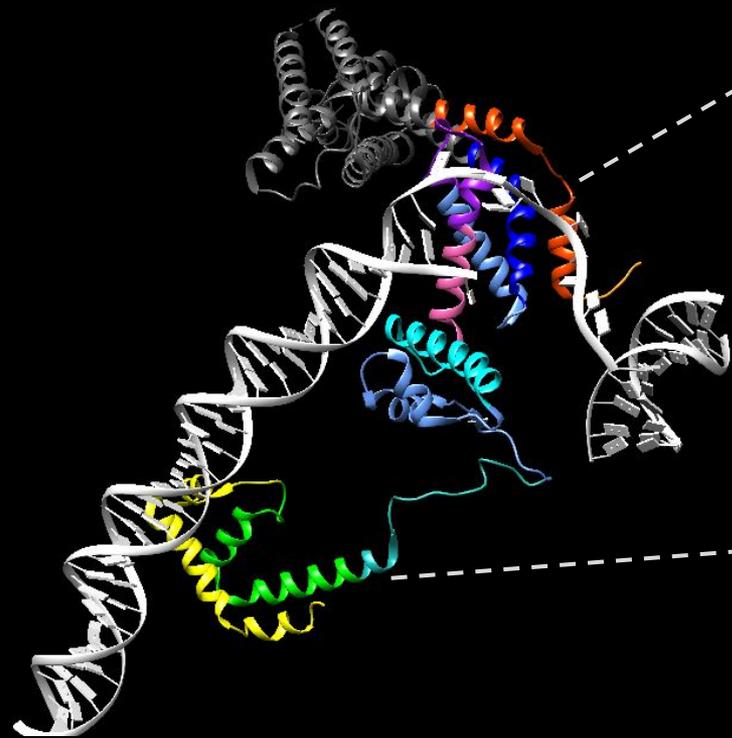
| | | | | | | | | | | | | | | | | |
|----------------------|----|------|--------|-----------|---|-----|------|---------|-----------------------|----------|----------|-----------|---------------------------|--------------------------|-----|-----|
| sp P0A2E4 RP0D_SALT1 | SI | AKKY | TNRGLQ | FLDLIQEGN | I | GLM | KAVD | KFEYRRG | YKFSTYATWWIRQAIT | RSIAD | QARTIRIP | / | HMIETINKL | NRISRQMLQEMGREPTPEELAERY | - | 489 |
| tr Q0WJ27 Q0WJ27_YER | SI | AKKY | TNRGLQ | FLDLIQEGN | I | GLM | KAVD | KFEYRRG | YKFSTYATWWIRQAIT | RSIAD | QARTIRIP | / | HMIETINKL | NRISRQMLQEMGREPTPEELAERY | - | 486 |
| tr A0A085Q539 A0A085 | SI | AKKY | TNRGLQ | FLDLIQEGN | I | GLM | KAVD | KFEYRRG | YKFSTYATWWIRQAIT | RSIAD | QARTIRIP | / | HMIETINKL | NRISRQMLQEMGREPLPEELAERY | - | 499 |
| sp Q72L95 SIGA_THET2 | SI | AKKY | TNRGLS | FLDLIQEGN | Q | GLI | RAVE | KFEYKRR | YKFSTYATWWIRQAINRAIAD | QARTIRIP | / | HMVETINKL | SRTARQLQDELGREPTYEEIAEAVG | - | 296 | |

σ 70 Subunit: region 3



| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|------------|------------|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-----|---|-----|-----|
| sp | P00579 | RP0D_ECOLI | SI | AK | Y | T | N | R | G | L | Q | F | L | D | L | I | Q | E | G | N | I | G | L | M | K | A | V | D | K | F | E | Y | R | R | G | Y | K | F | S | T | Y | A | T | W | W | I | R | Q | A | I | T | R | S | I | A | D | Q | A | R | T | I | R | I | P | V | H | M | I | E | T | I | N | K | L | N | R | I | S | R | 468 | |
| sp | P0A2E4 | RP0D_SALTI | SI | AK | Y | T | N | R | G | L | Q | F | L | D | L | I | Q | E | G | N | I | G | L | M | K | A | V | D | K | F | E | Y | R | R | G | Y | K | F | S | T | Y | A | T | W | W | I | R | Q | A | I | T | R | S | I | A | D | Q | A | R | T | I | R | I | P | V | H | M | I | E | T | I | N | K | L | N | R | I | S | R | 470 | |
| tr | Q0WJ27 | Q0WJ27_YER | SI | AK | Y | T | N | R | G | L | Q | F | L | D | L | I | Q | E | G | N | I | G | L | M | K | A | V | D | K | F | E | Y | R | R | G | Y | K | F | S | T | Y | A | T | W | W | I | R | Q | A | I | T | R | S | I | A | D | Q | A | R | T | I | R | I | P | V | H | M | I | E | T | I | N | K | L | N | R | I | S | R | 467 | |
| tr | A0A085Q539 | A0A085 | SI | AK | Y | T | N | R | G | L | Q | F | L | D | L | I | Q | E | G | N | I | G | L | M | K | A | V | D | K | F | E | Y | R | R | G | Y | K | F | S | T | Y | A | T | W | W | I | R | Q | A | I | T | R | S | I | A | D | Q | A | R | T | I | R | I | P | V | H | M | I | E | T | I | N | K | L | N | R | I | S | R | 480 | |
| sp | Q72L95 | SIGA_THET2 | SI | AK | Y | T | N | R | G | L | S | F | L | D | L | I | Q | E | G | N | Q | G | L | I | R | A | V | E | K | F | E | Y | K | R | R | F | K | F | S | T | Y | A | T | W | W | I | R | Q | A | I | N | R | A | I | A | D | Q | A | R | T | I | R | I | P | V | H | M | V | E | T | I | N | K | L | S | R | T | A | R | 276 | |
| sp | P00579 | RP0D_ECOLI | Q | M | L | Q | E | M | G | R | E | P | T | P | E | E | L | A | E | R | M | -- | L | M | P | E | D | K | I | R | K | V | L | K | I | A | K | E | P | T | S | M | E | T | P | I | G | D | D | E | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | S | A | T | T | E | S | L | R | A | A | T | H | D | 546 | |
| sp | P0A2E4 | RP0D_SALTI | Q | M | L | Q | E | M | G | R | E | P | T | P | E | E | L | A | E | R | M | -- | L | M | P | E | D | K | I | R | K | V | L | K | I | A | K | E | P | T | S | M | E | T | P | I | G | D | D | E | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | S | A | T | T | E | S | L | R | A | A | T | H | D | 548 | |
| tr | Q0WJ27 | Q0WJ27_YER | Q | M | L | Q | E | M | G | R | E | P | T | P | E | E | L | A | E | R | M | -- | L | M | P | E | D | K | I | R | K | V | L | K | I | A | K | E | P | T | S | M | E | T | P | I | G | D | D | E | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | S | A | T | S | E | S | L | R | S | A | T | H | D | 545 | |
| tr | A0A085Q539 | A0A085 | Q | M | L | Q | E | M | G | R | E | P | L | P | E | E | L | A | E | R | M | -- | Q | M | P | E | D | K | I | R | K | V | L | K | I | A | K | E | P | T | S | M | E | T | P | I | G | D | D | E | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | S | A | T | S | L | K | A | A | T | R | D | 558 | | | |
| sp | Q72L95 | SIGA_THET2 | Q | L | Q | E | L | G | R | E | P | T | Y | E | E | I | A | E | A | M | G | P | G | W | D | A | K | R | V | E | E | T | L | K | I | A | Q | E | P | V | S | L | E | T | P | I | G | D | E | K | D | S | F | Y | G | D | F | I | P | D | E | H | L | P | S | P | V | D | A | A | T | Q | S | L | S | E | E | L | E | K | 356 |

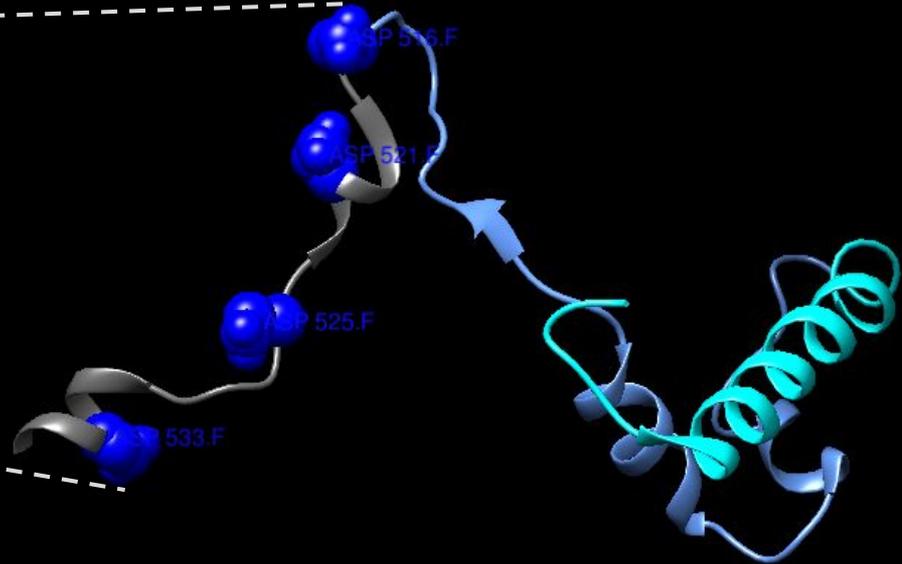
σ_{70} Subunit: region 3



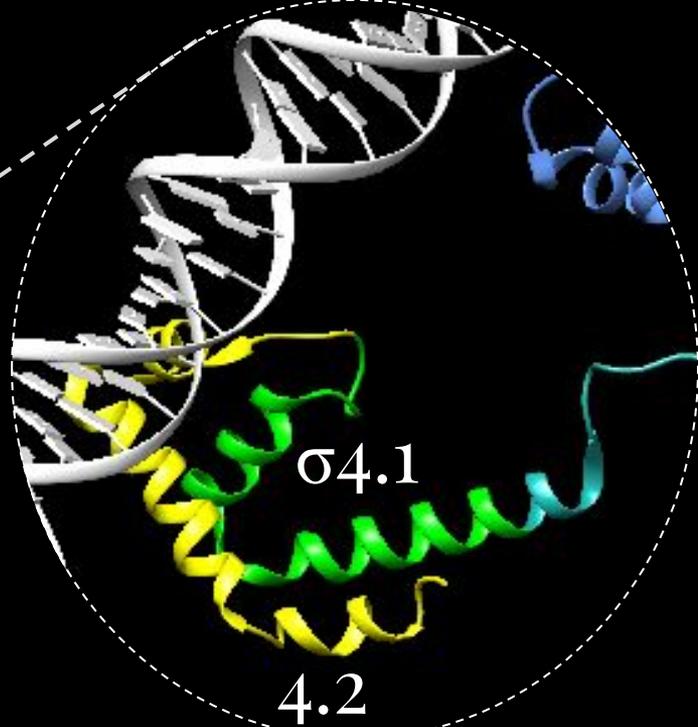
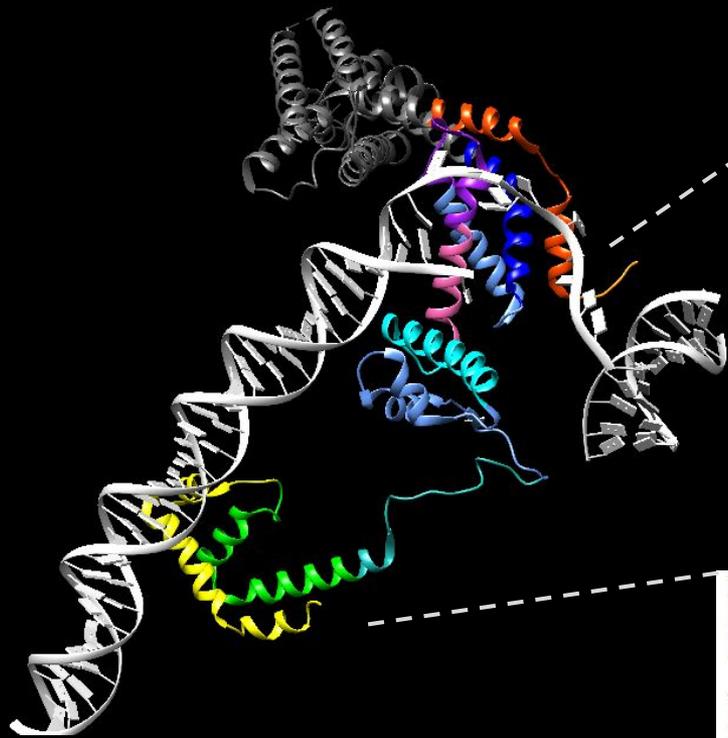
Hydrophobic
face

σ 70 Subunit: region 3.2 - flexible linker

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| D | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | D |
| D | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | D |
| D | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | D |
| D | S | H | L | G | D | F | I | E | D | T | T | L | E | L | P | L | D |
| D | S | F | Y | G | D | F | I | P | D | E | H | L | P | S | P | V | D |



σ 70 Subunit: region 4

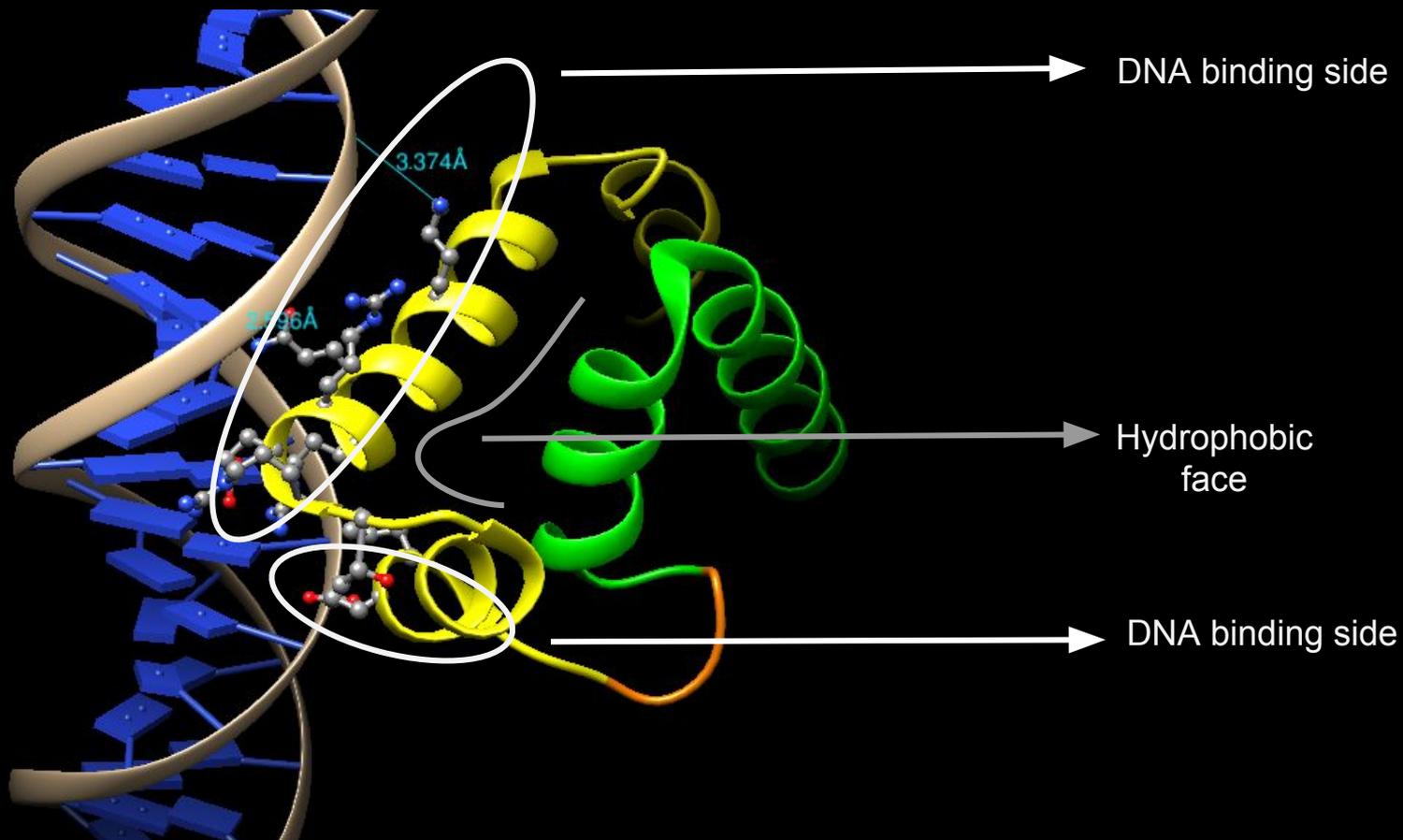


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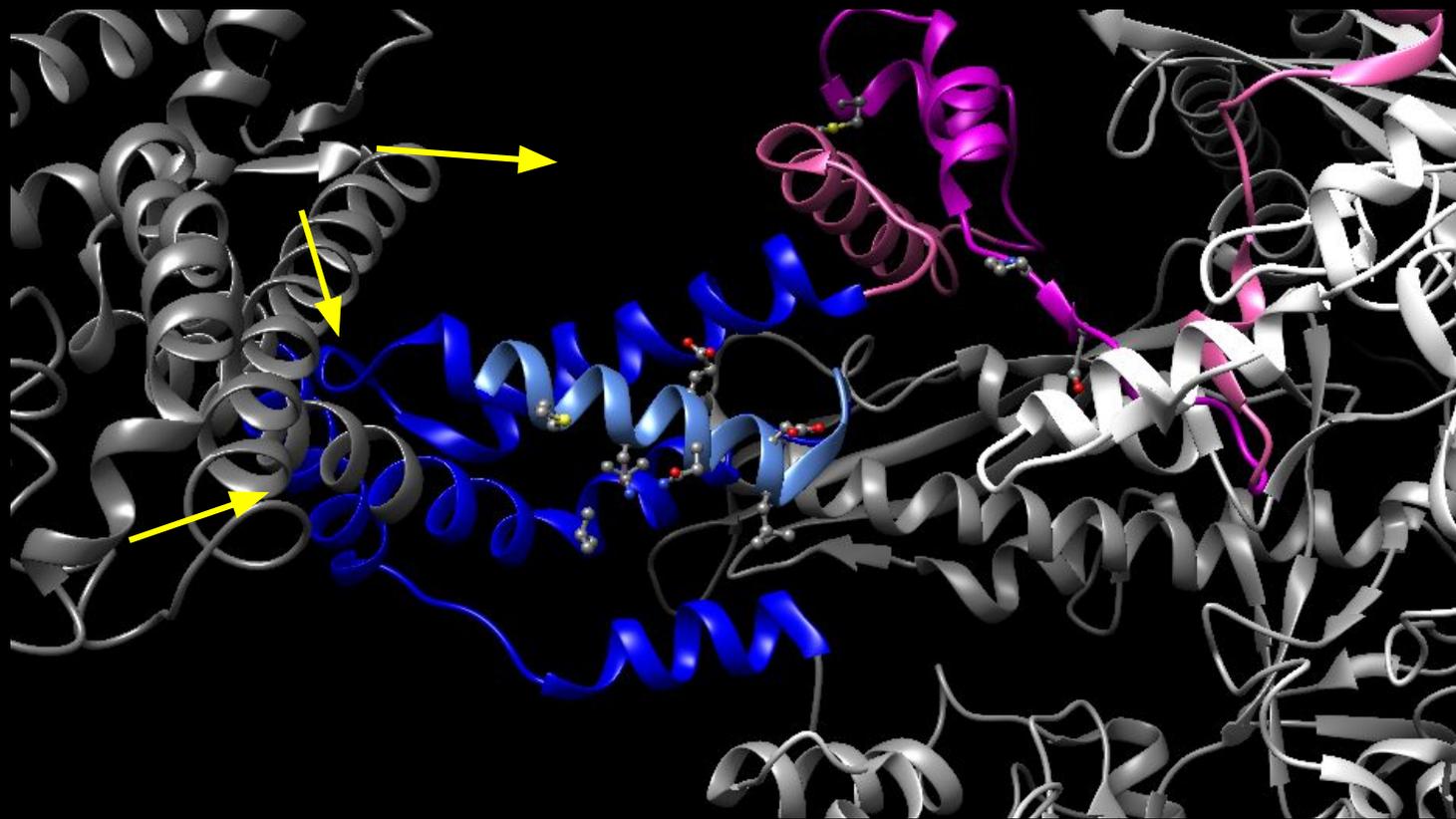
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sp | P0A2E4 | RPOD_SALTI | QNLQEMGREPTPEELAEKRV--LMPEDKTRKVLKIAKEPISMETPIGDDEDSHLGDFIEDITILELPDLSATTESLRAATHD 548
tr | Q0WJ27 | Q0WJ27_YER | QNLQEMGREPTPEELAEKRV--LMPEDKTRKVLKIAKEPISMETPIGDDEDSHLGDFIEDITILELPDLSATTESLRSATHD 545
tr | A0A085Q539 | A0A085 | QNLQEMGREPLPEELAEKRV--QMPEDKTRKVLKIAKEPISMETPIGDDEDSHLGDFIEDITILELPDLSATATSLKAAATRD 558
sp | Q72L95 | SIGA_THET2 | QLQQLGREPTYEETIABAVGPGWDAKRVETLKIAGEPVSLMETPIGDDEKDSFYGDFIPDEKLPSPVDAATQSLISEELEK 356

sp | P00579 | RPOD_ECOLI | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRFHFSRSSEVLRSLFDD 613
sp | P0A2E4 | RPOD_SALTI | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRFHFSRSSEVLRSLFDD 615
tr | Q0WJ27 | Q0WJ27_YER | VLAGLTAREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRFHFSRSSEVLRSLFDD 612
tr | A0A085Q539 | A0A085 | VLAGLTPREAKVLRMRFGIDMNTDHTLLEEVGKQFDVTRERIRQIEAKALRKLRFHFSRSSEVLRSLFDE 625
sp | Q72L95 | SIGA_THET2 | ALSKLSREAVVLRKRGKLDGREDHTLLEEVGAFEFVTRERIRQIENKALRKLRFHFSRTIRKLRFLLD- 423
    
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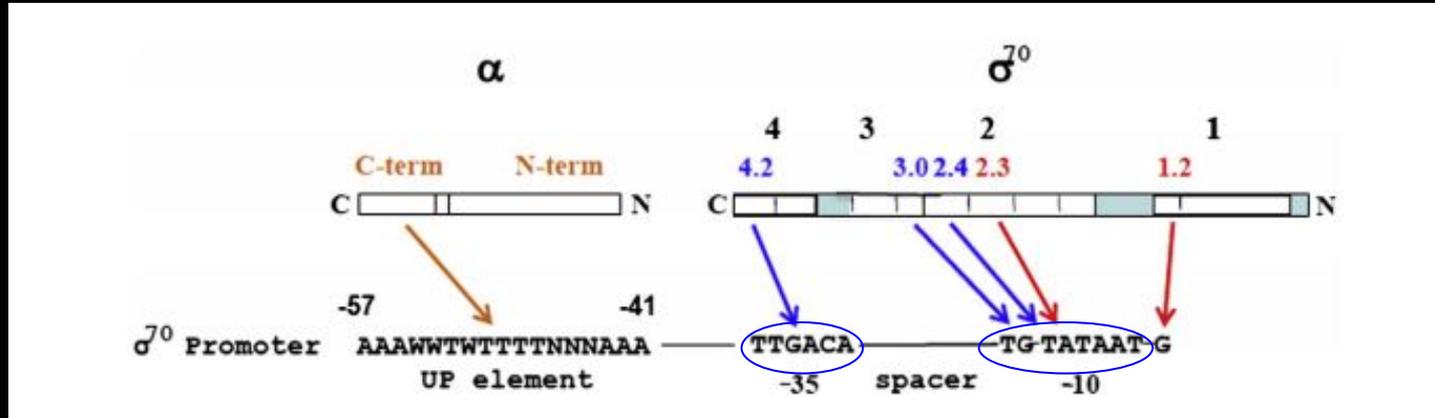
σ 70 Subunit: region 4.2



σ 70 Subunit: core RNP binding



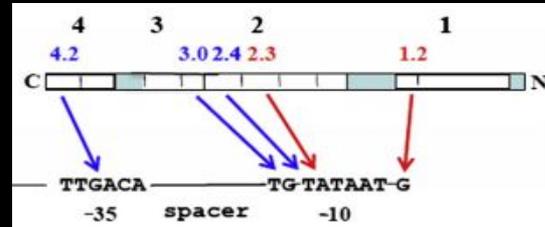
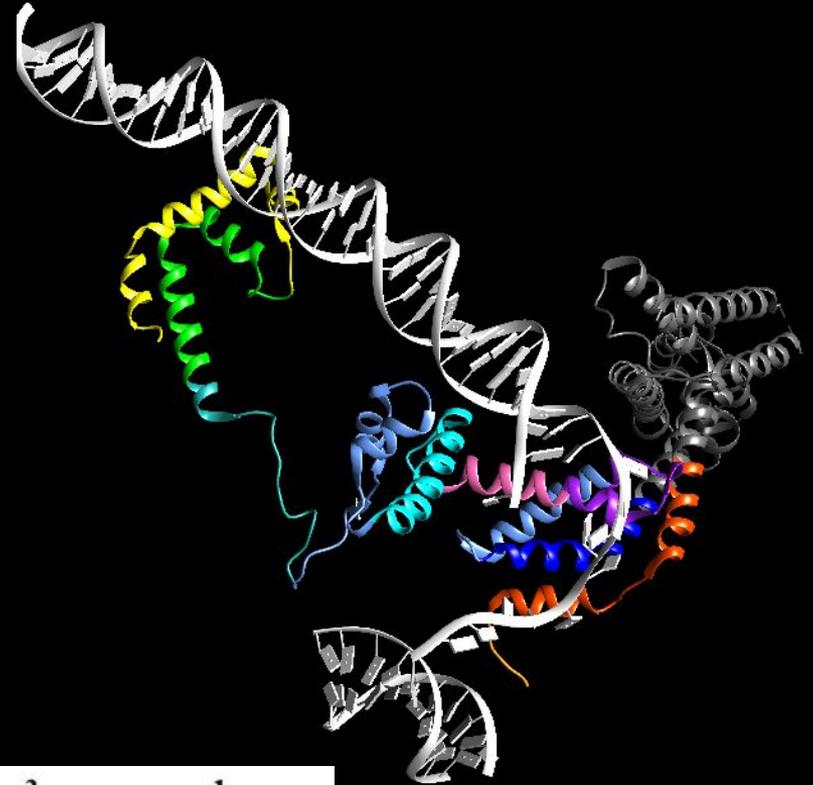
Transcription: Promoters recognition



Saecker, R. and Record, M. (2011). *Journal of Molecular Biology*. pp.754-771.

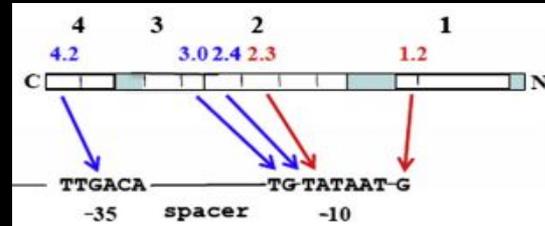
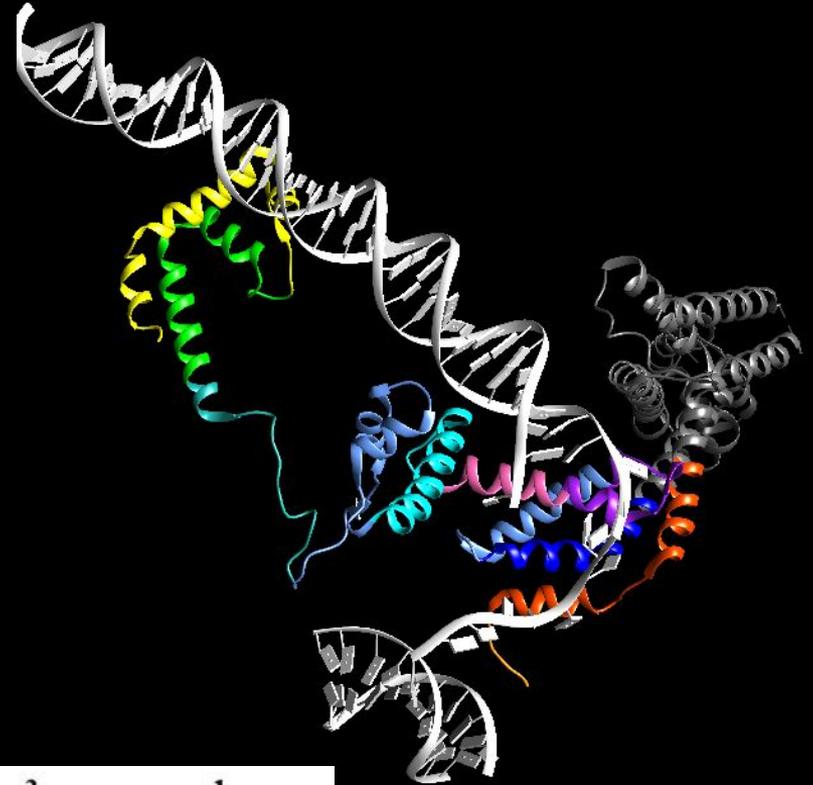
σ_{70} Subunit: DNA BINDING

- Sigma binds DNA by to specific domains: σ_2 and σ_4
 - - 10 element $\Rightarrow \sigma_2$
 - -35 element $\Rightarrow \sigma_4$

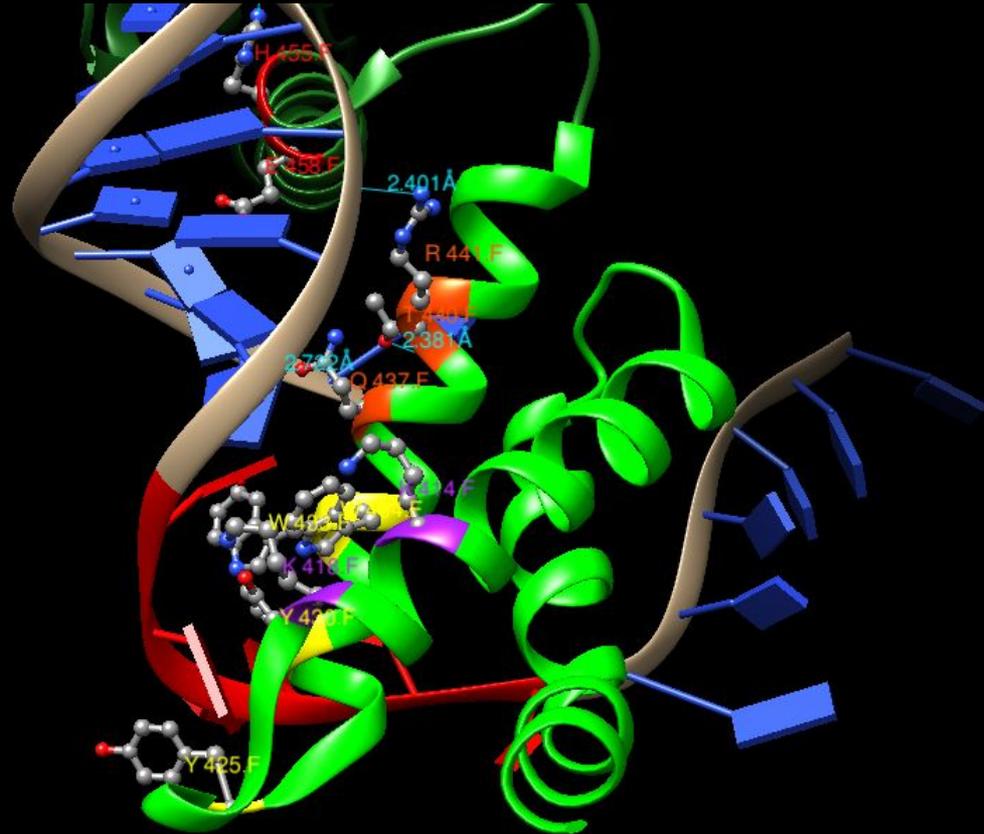


σ_{70} Subunit: DNA BINDING

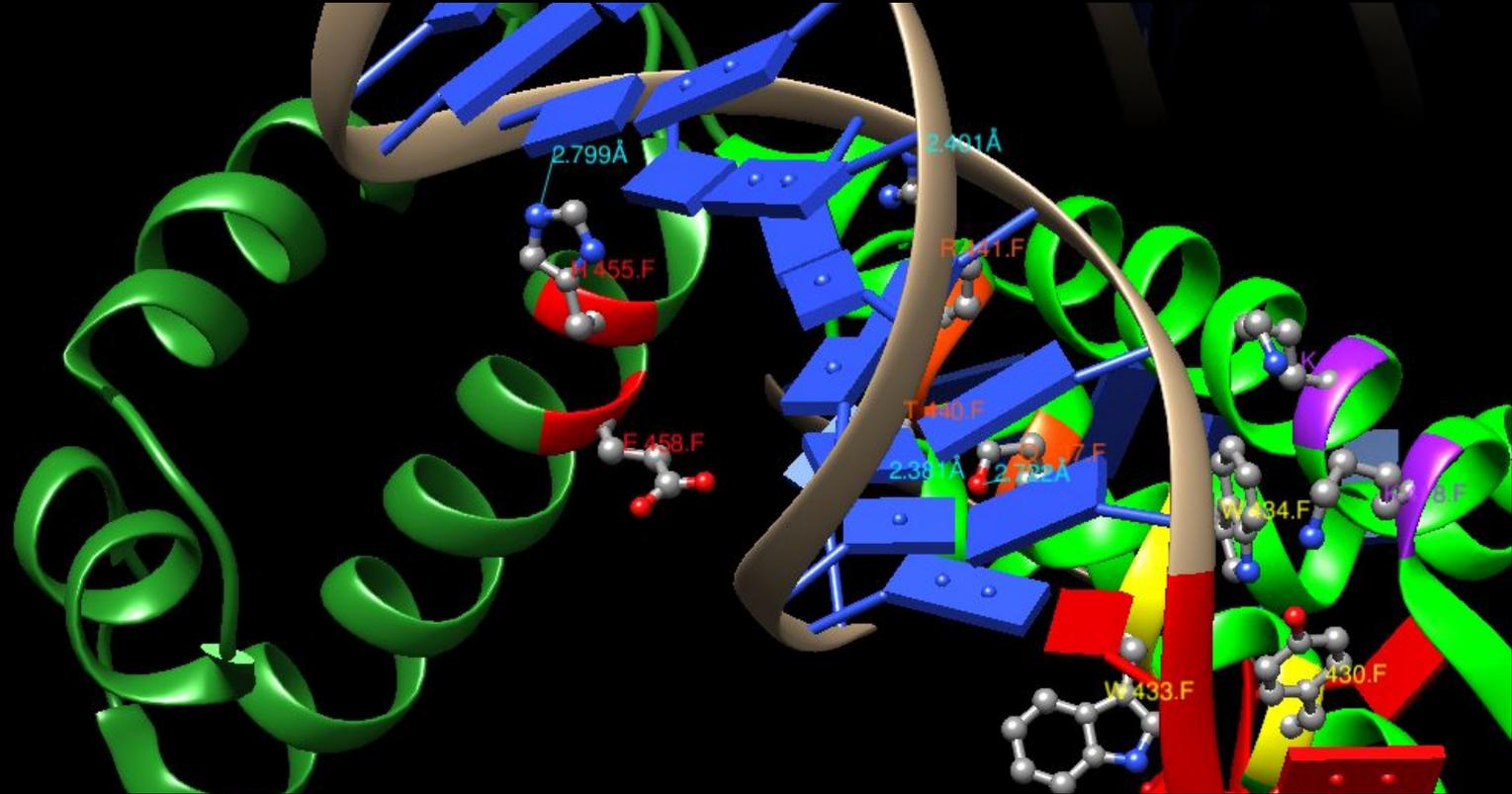
- Sigma binds DNA by to specific domains: σ_2 , σ_4 and σ_3
 - - 10 element $\Rightarrow \sigma_2$
 - -35 element $\Rightarrow \sigma_4$
 - -10 extended $\Rightarrow \sigma_3$



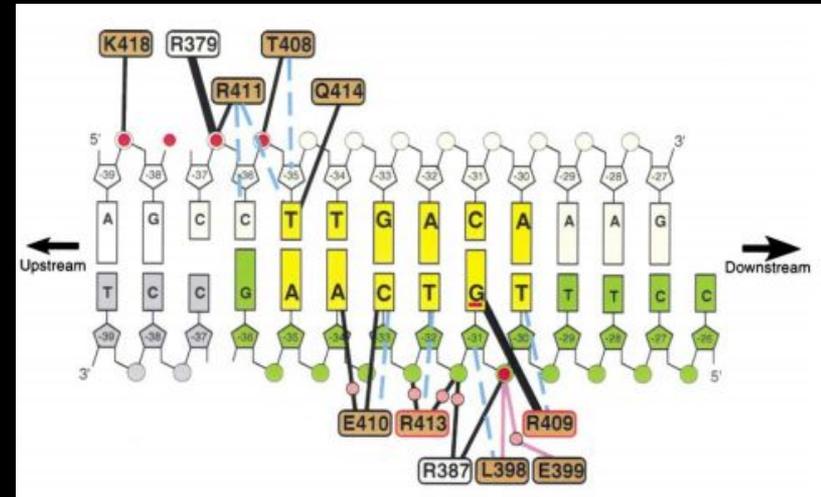
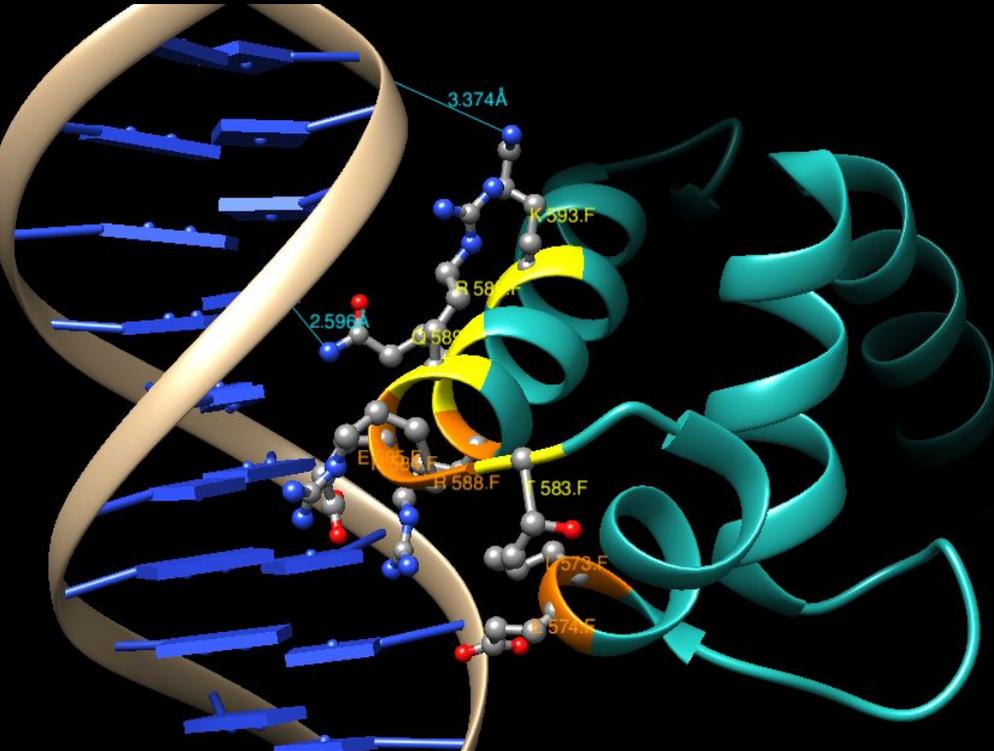
σ 70 Subunit: -10 element recognition



σ 70 Subunit: -10 extended recognition



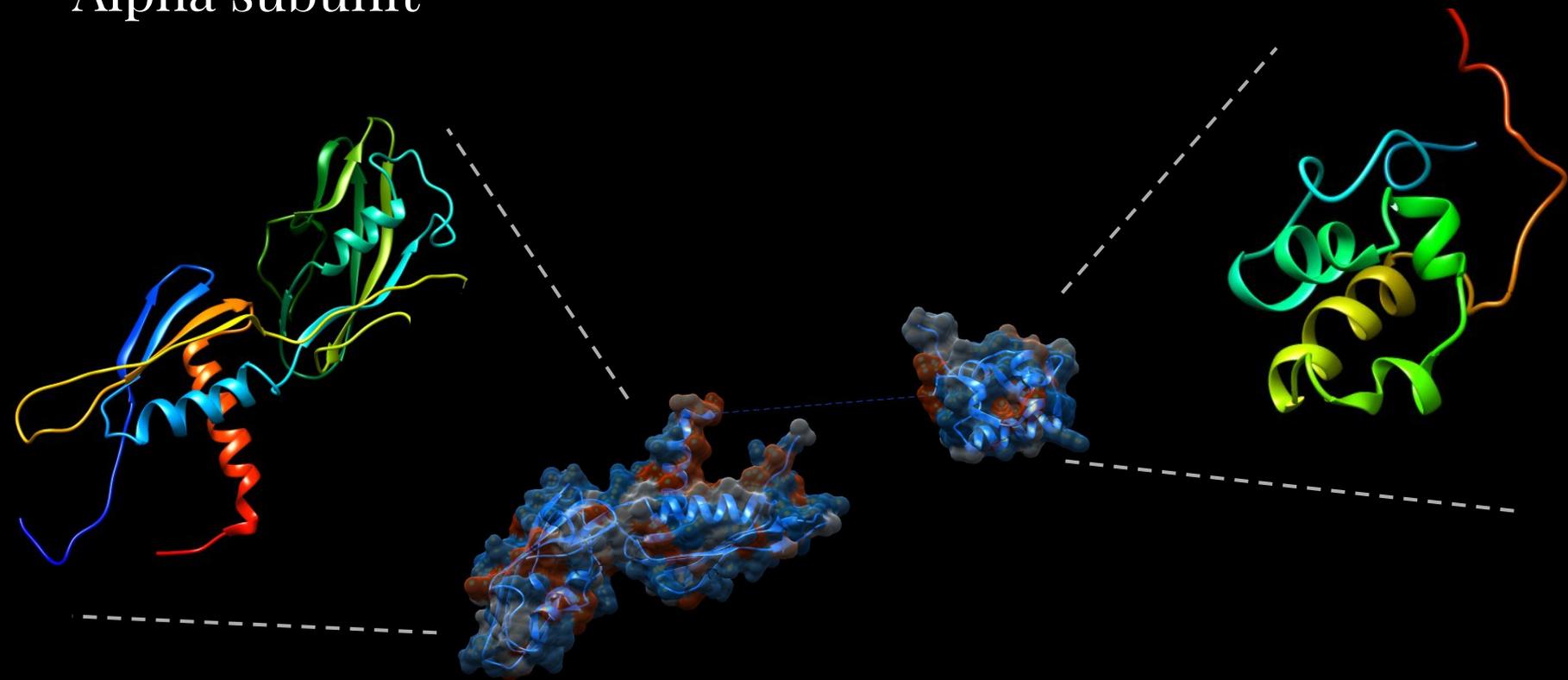
σ 70 Subunit: -35 recognition



Campbell, E., Muzzin, O., Chlenov, M., Sun, J., Olson, C., Weinman, O., Trester-Zedlitz, M. and Darst, S. (2002). Structure of the Bacterial RNA Polymerase Promoter Specificity σ Subunit. *Molecular Cell*, 9(3), pp.527-539.

Alpha subunit

C-terminal domain (CTD)



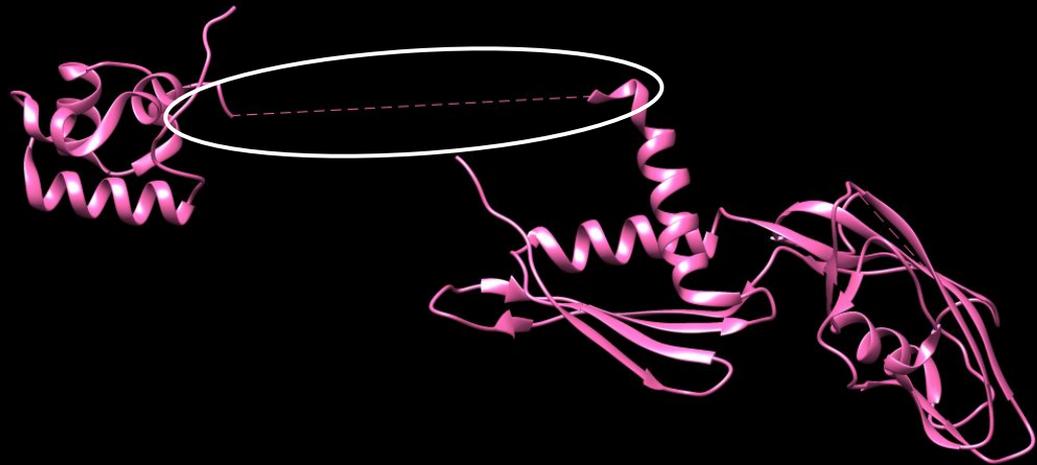
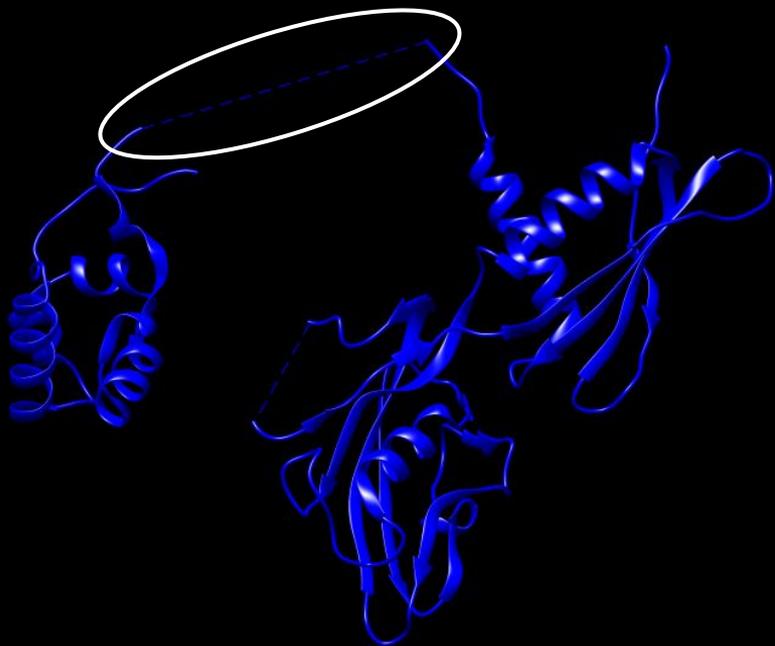
N-terminal domain (NTD)

Alpha subunit

Functions

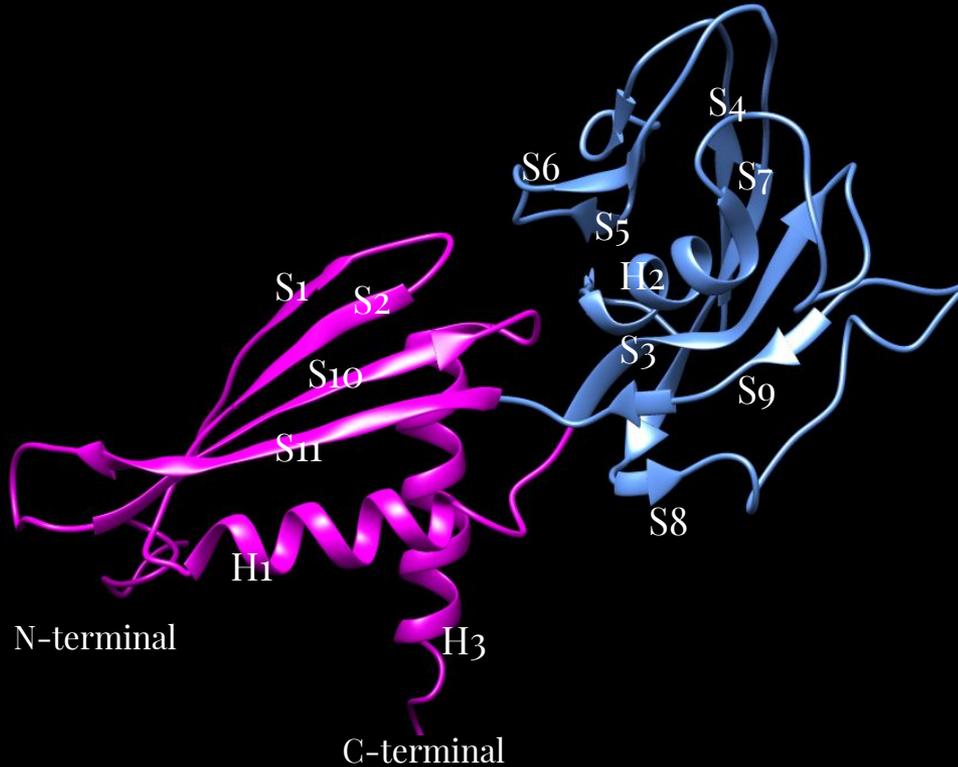
1. Initiates RNAP assembly
2. Participates in promoter recognition
 - Non-sequence-non-specific interactions with most promoters
 - Sequence-specific interactions with UP element containing promoters
3. Target of a set of transcription regulator proteins

Alpha subunit: linker



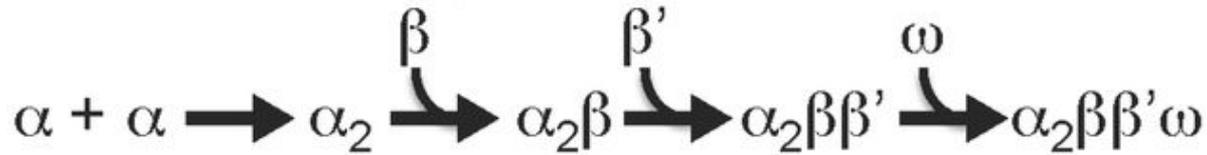
Alpha subunit: N-terminal domain

Domain 1



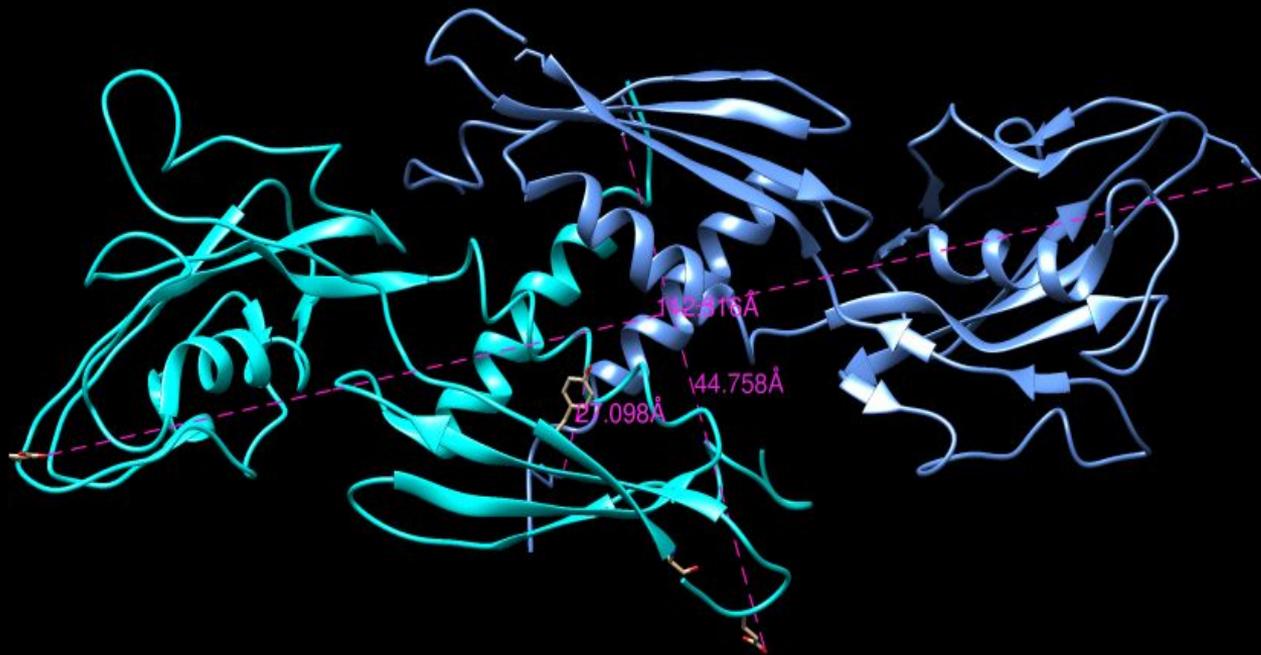
Domain 2

Alpha subunit: N-terminal domain

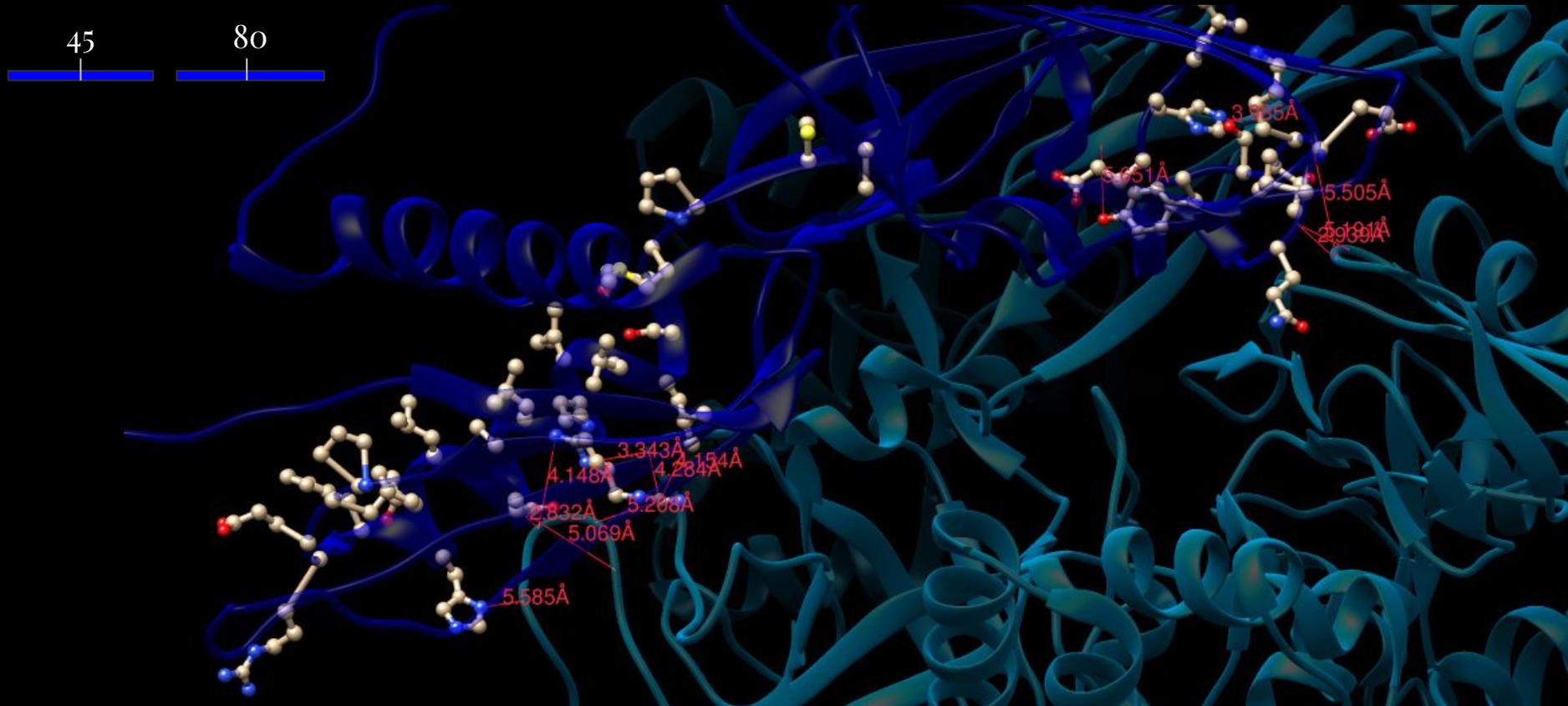


Alpha subunit: N-terminal domain

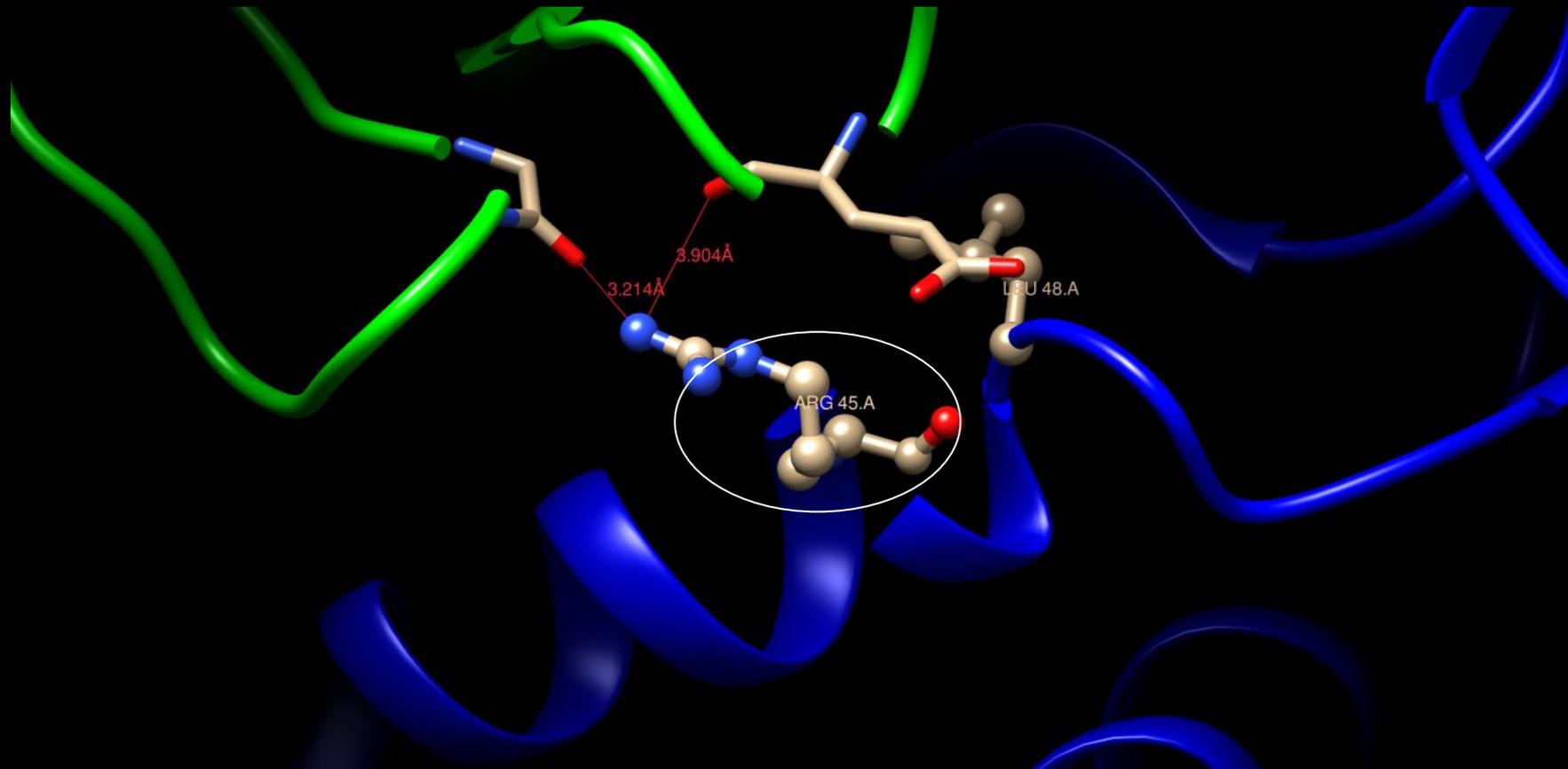
120Å
60Å
25Å



Alpha-beta interaction

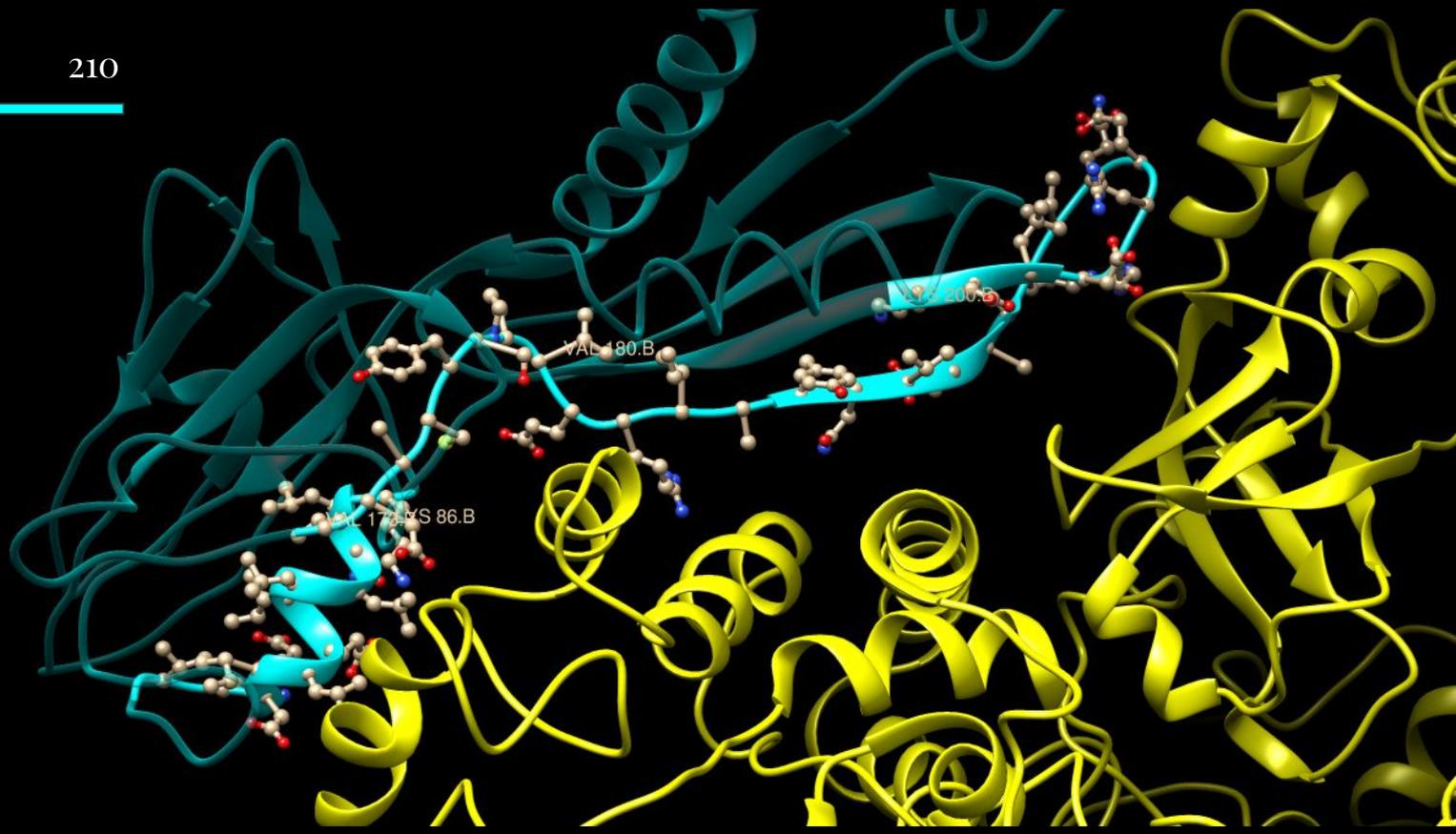


Alpha-beta interaction

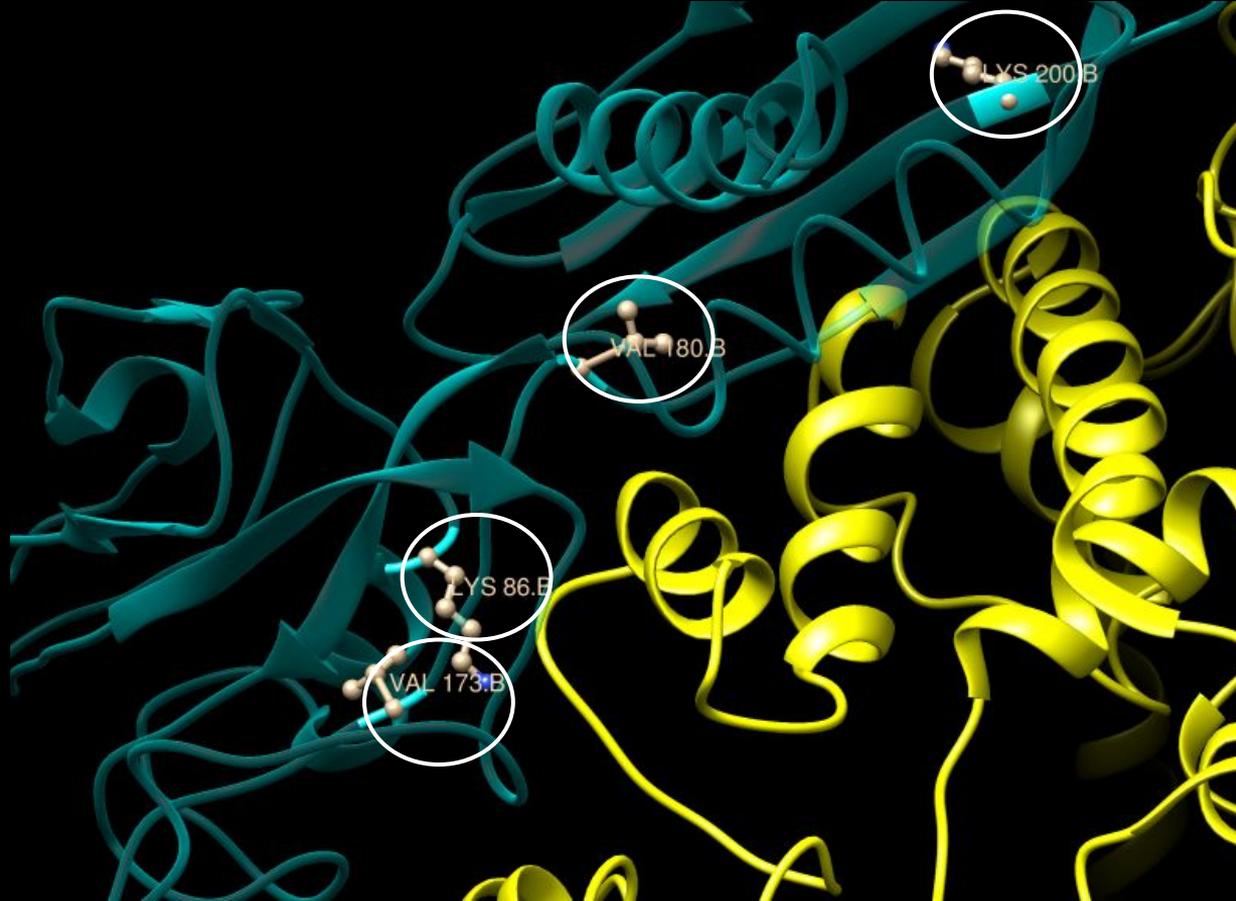


Alpha-beta' interaction

80 175 210

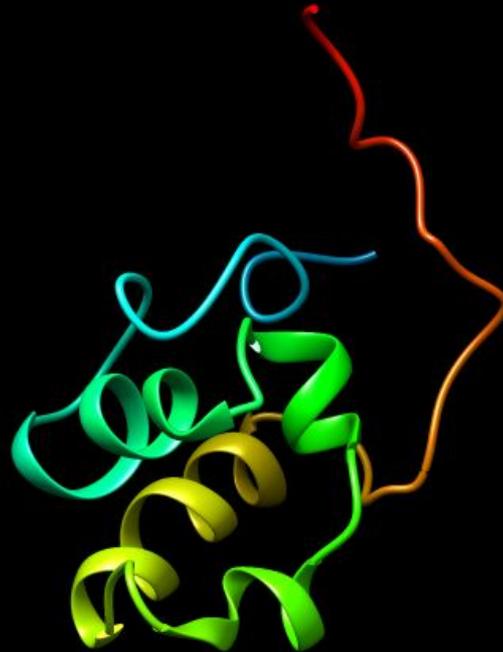


Alpha-beta' interaction

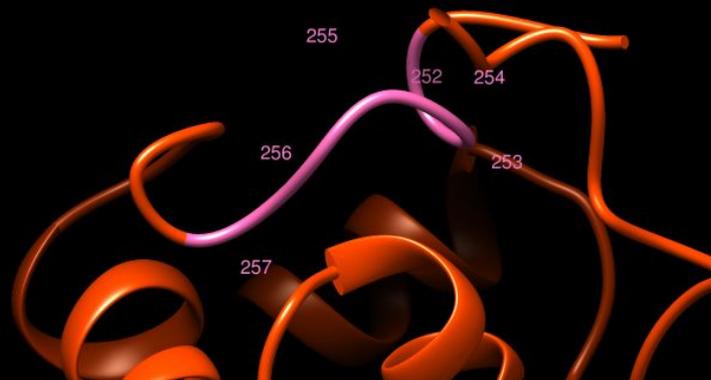


Alpha subunit: C-terminal domain

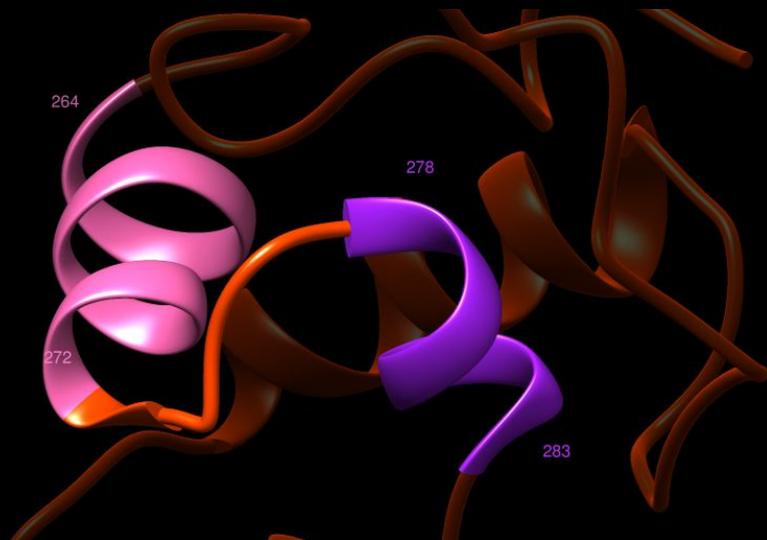
C-terminal domain (CTD)



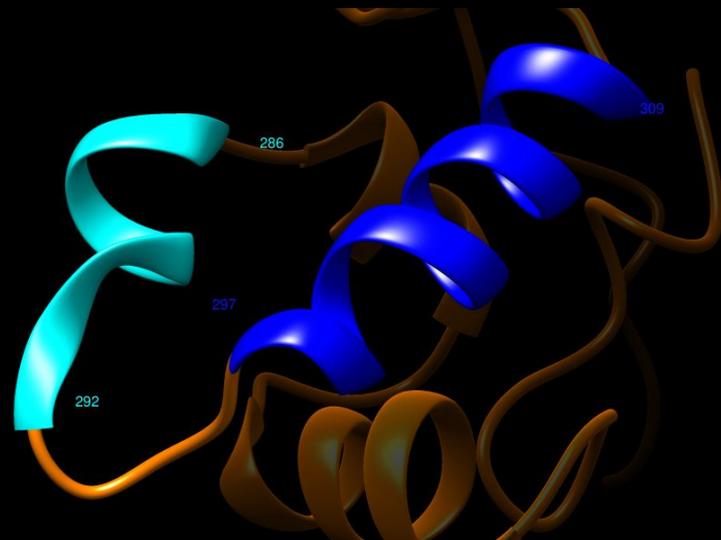
Nonstandar helix



Helix 1 and 2

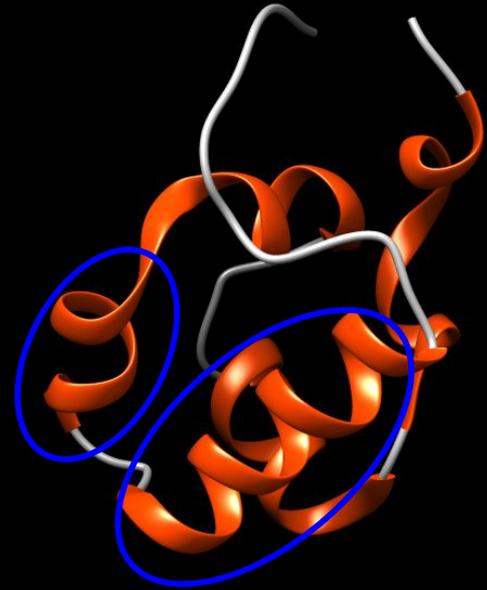
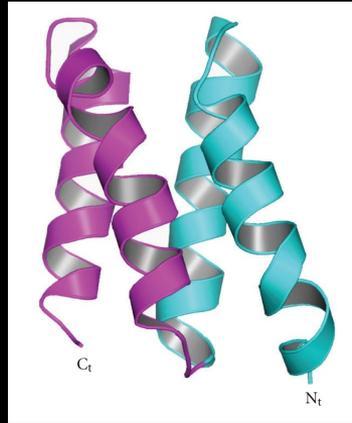
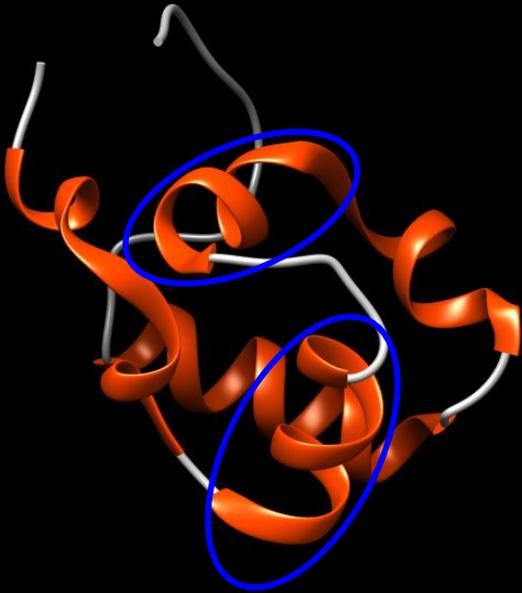


Helix 3 and 4

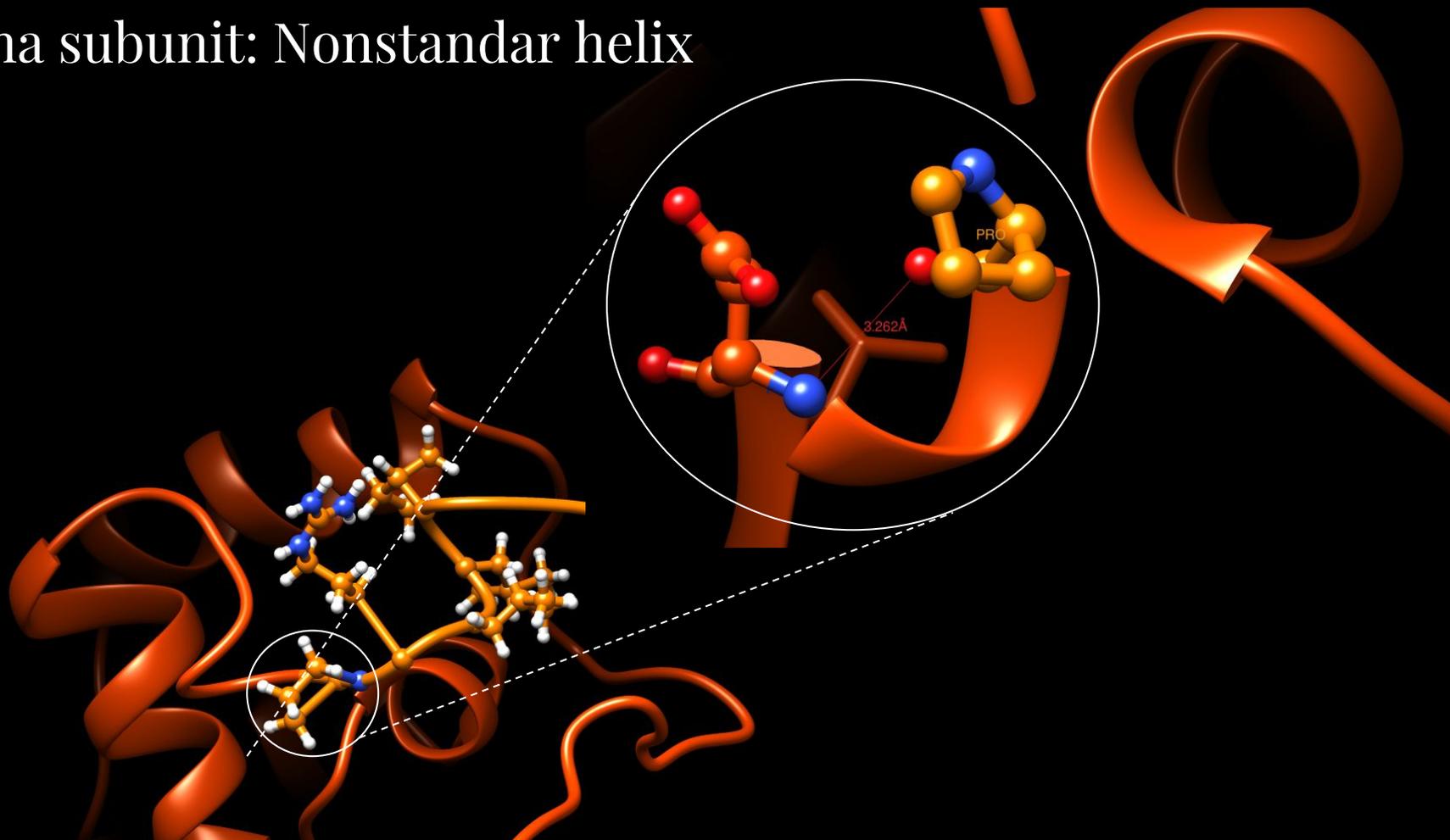


Alpha subunit: C-terminal domain

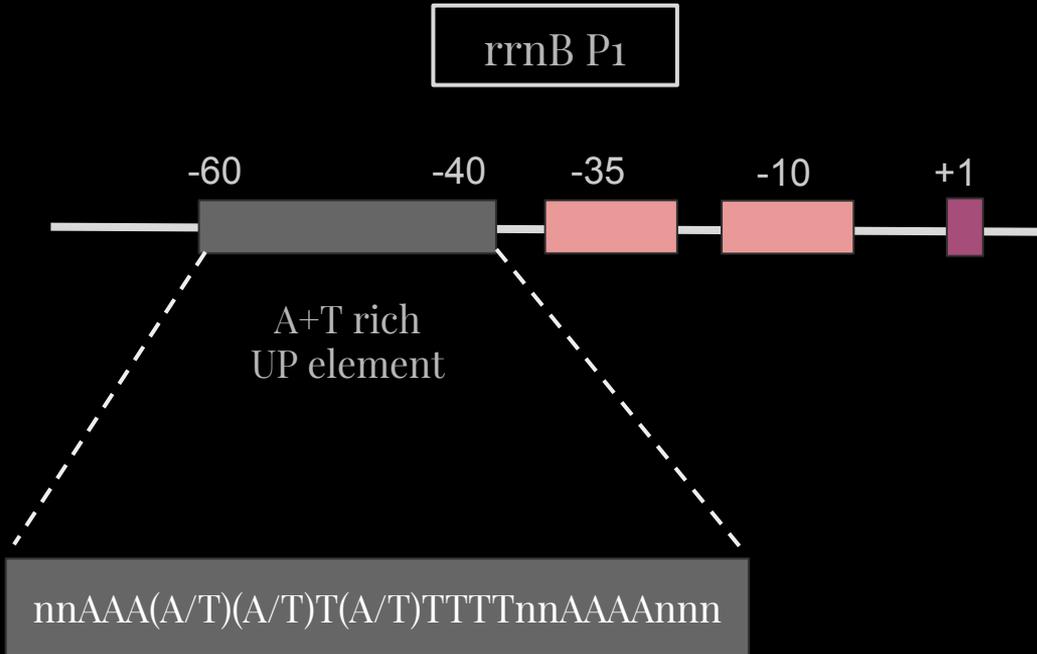
(Helix-hairpin-Helix)₂ domain



Alpha subunit: Nonstandard helix

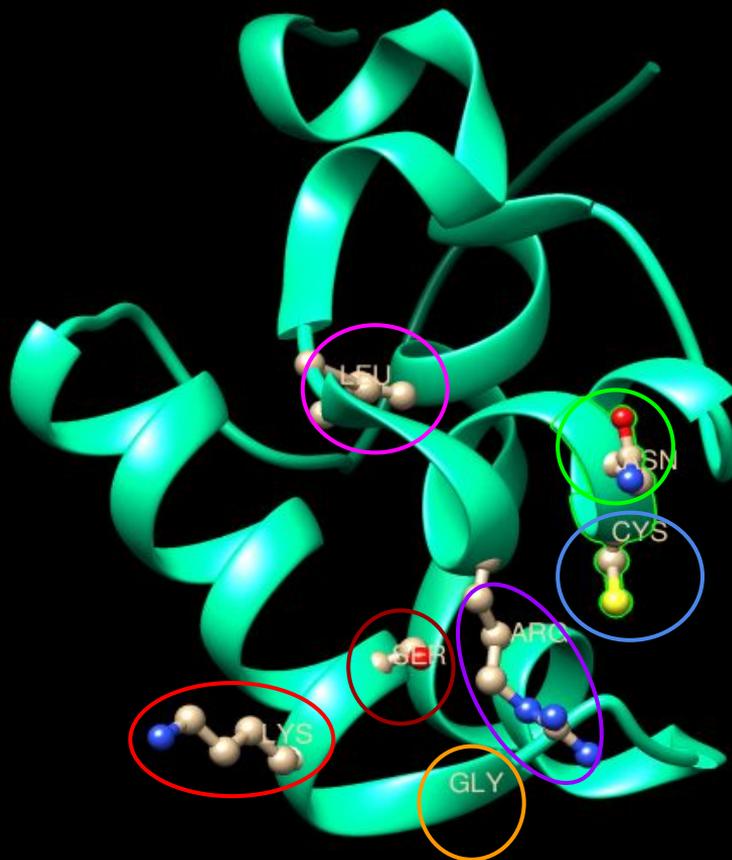


Alpha subunit: Promoter recognition



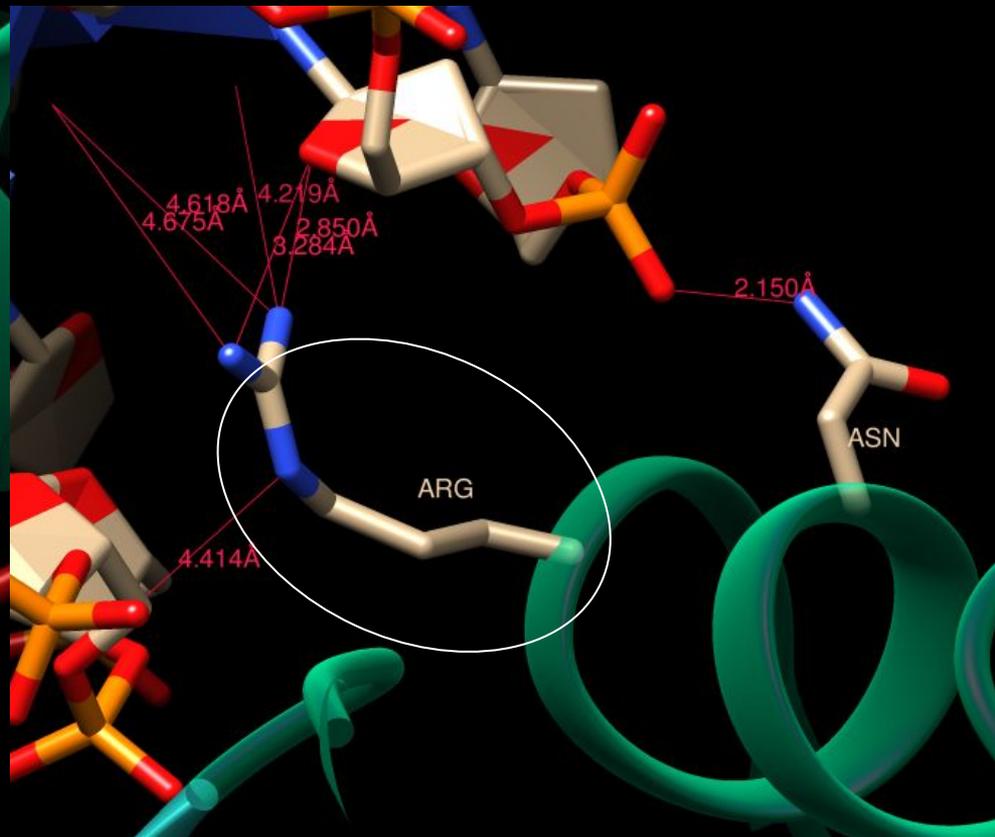
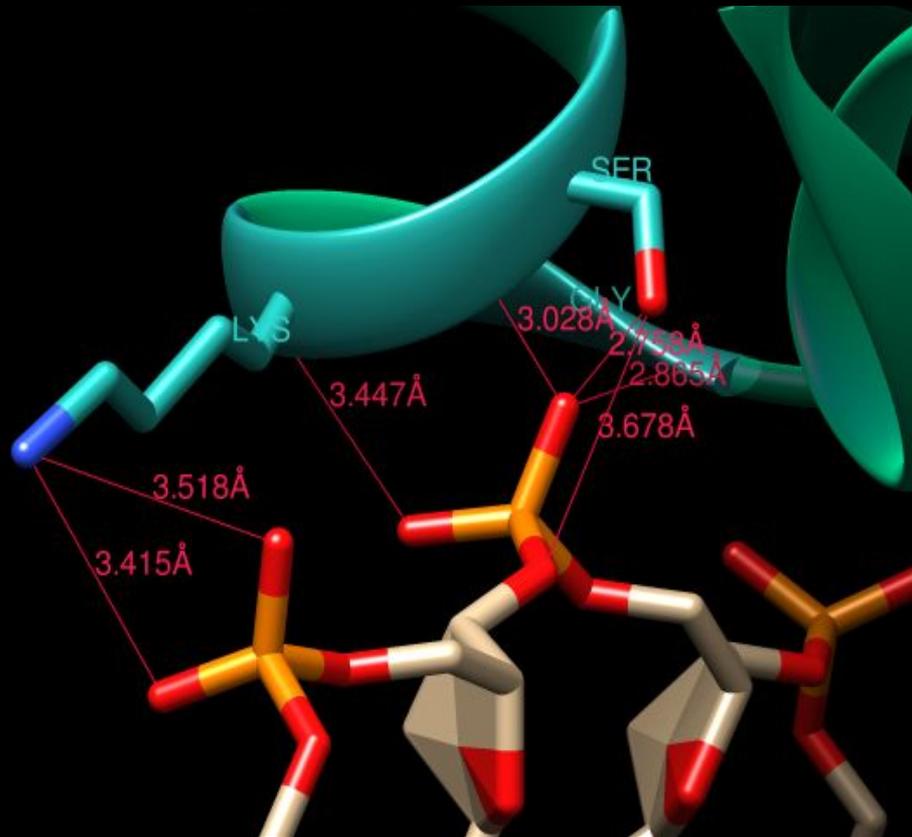
Alpha subunit: Promoter recognition

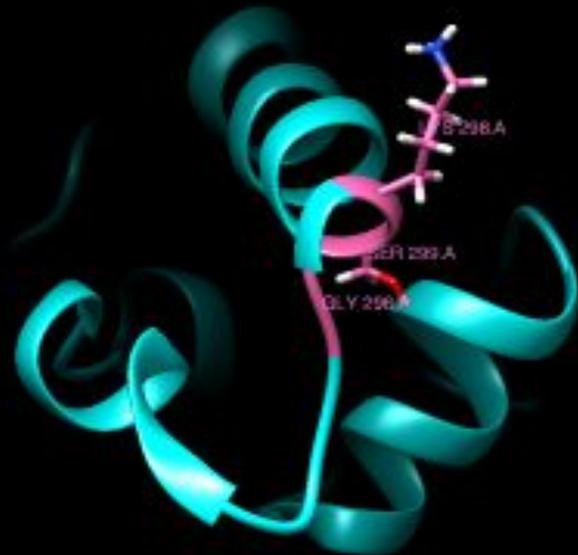
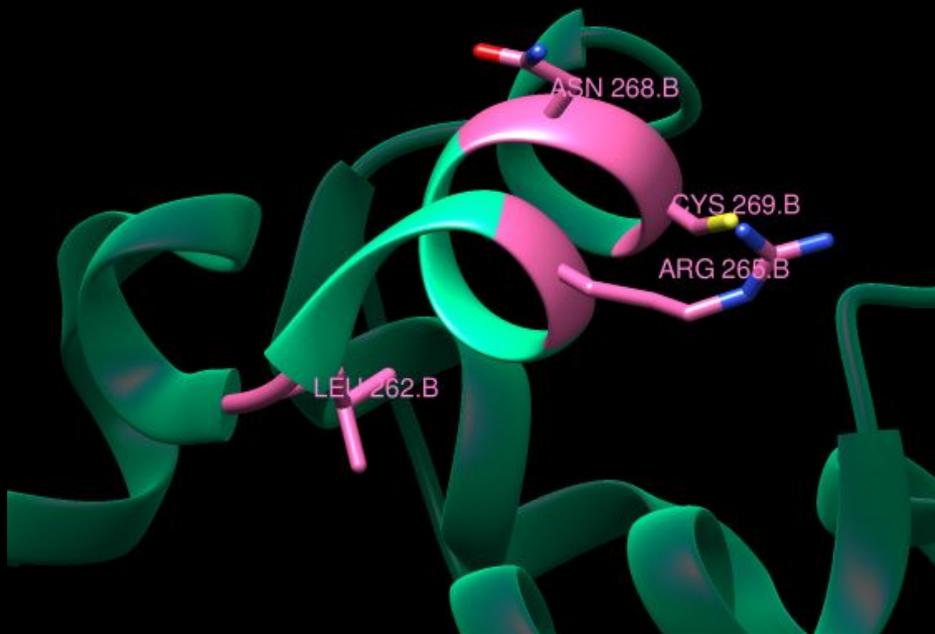
Consensus
 Conservation
 E coli
 Salmonella tiphy
 Yersinia pestis
 Vibrio Cholerae
 Therus aquaticus

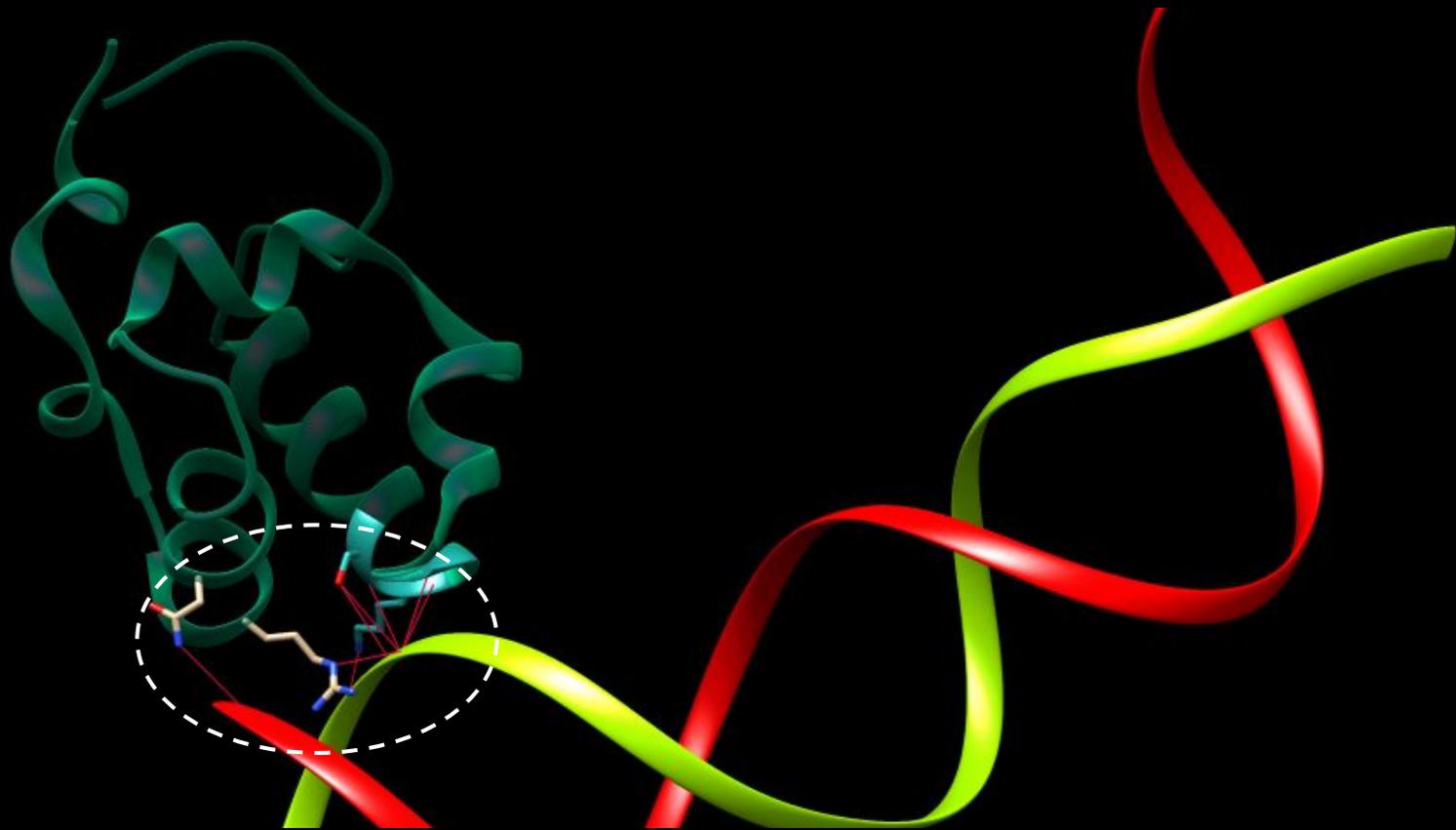


| | |
|------------|------------|
| RPVDDLELTV | RSANCLKAEA |
| LPLEELGLST | RVLHSLKEEG |

| |
|-----------|
| LGKKSLEIK |
| IGERSLEIR |
| LGKKSLEIK |
| LGKKSLEIK |
| LGKKSLEIK |
| IGERSLEIR |

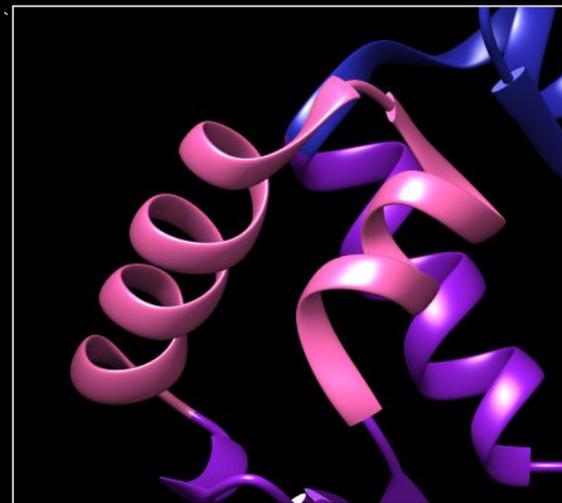
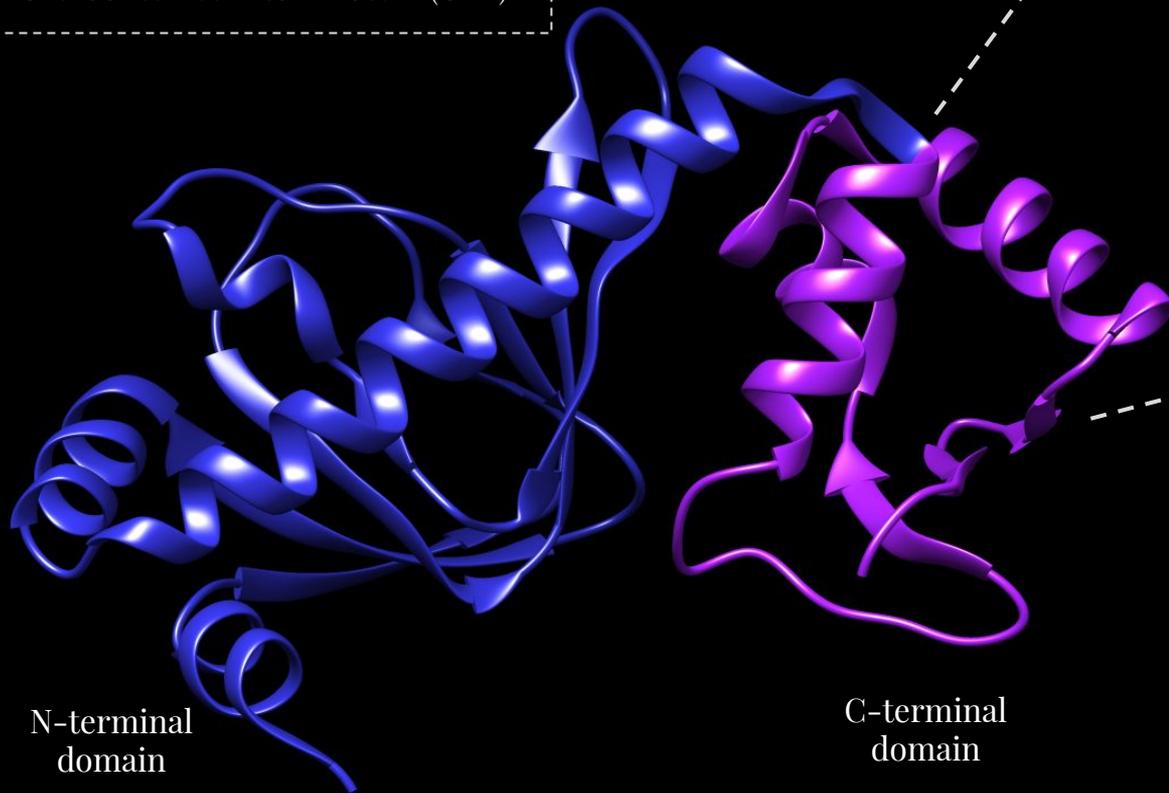




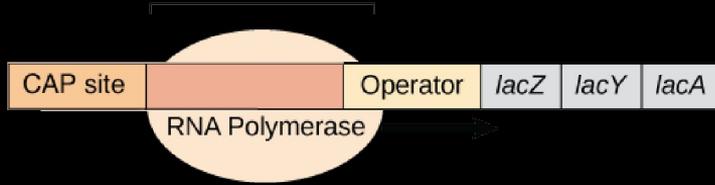


Alpha subunit: interaction with CAP

Catabolite Activator Protein (CAP)

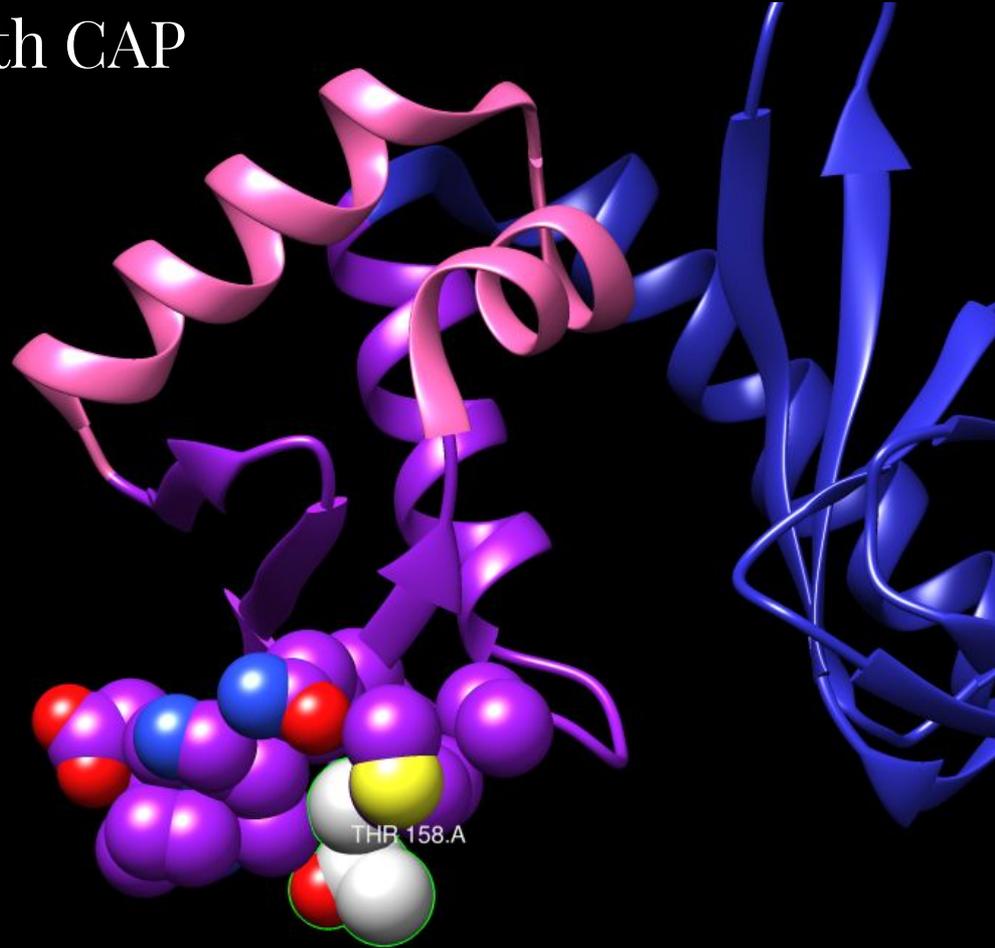


Alpha subunit: interaction with CAP

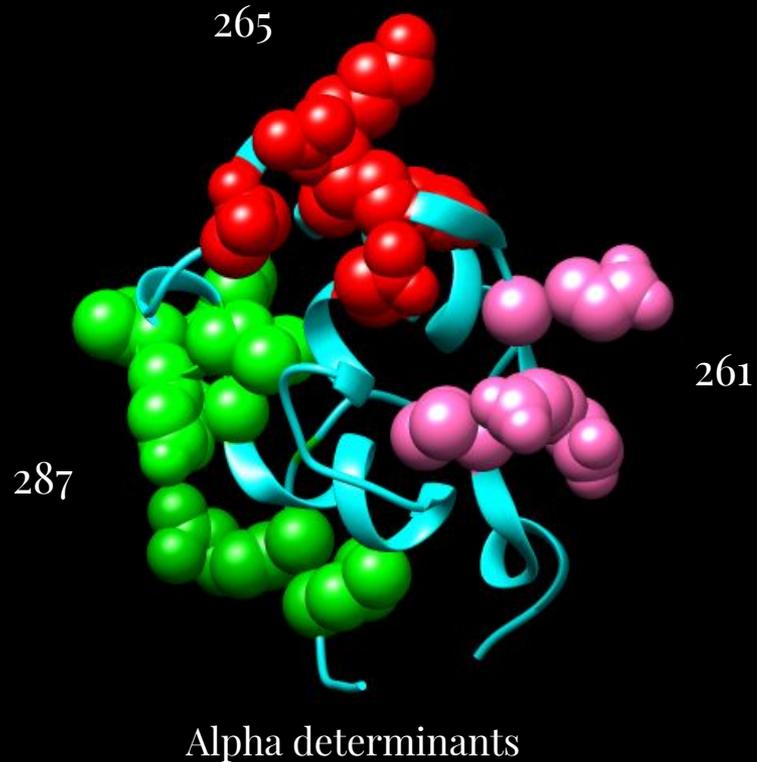


CAP determinants

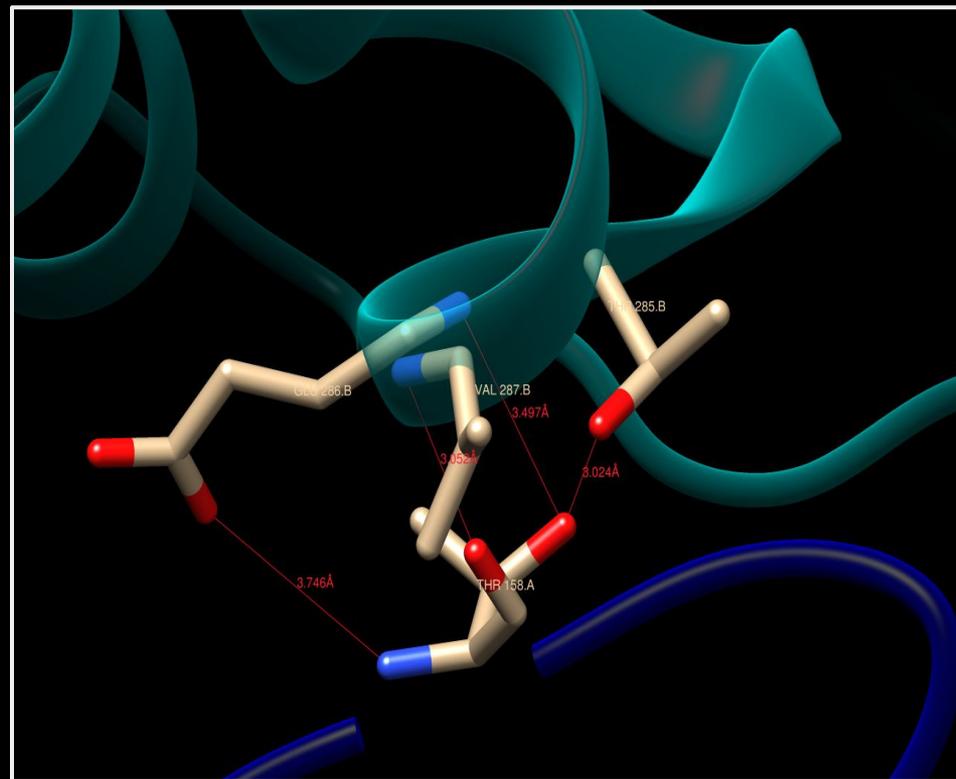
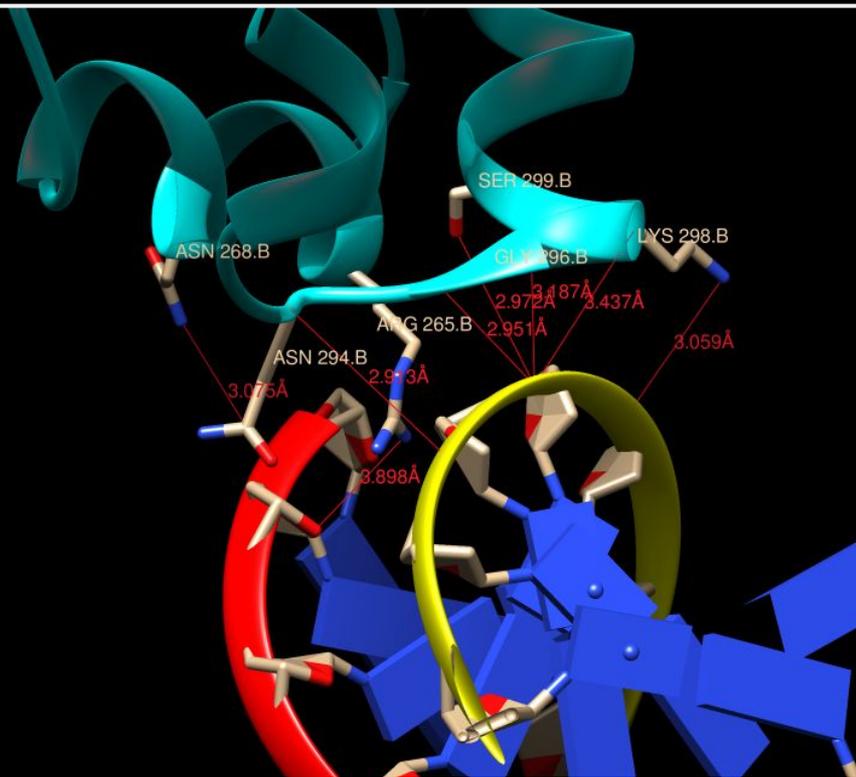
Activation Region 1 (AR1)
Residues 156-164



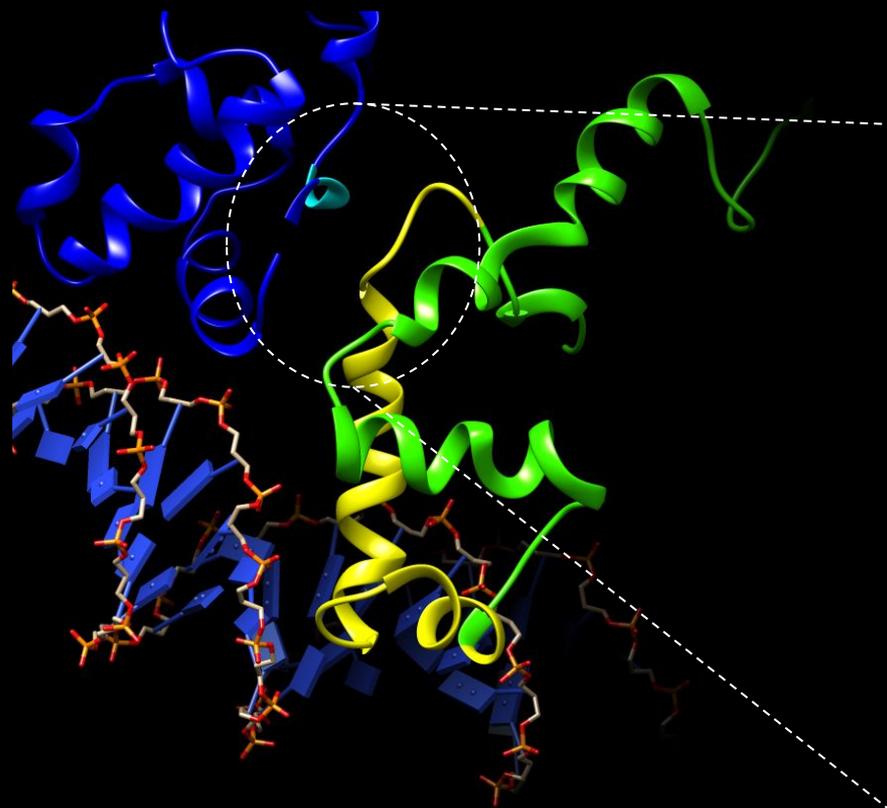
Alpha subunit: interaction with CAP



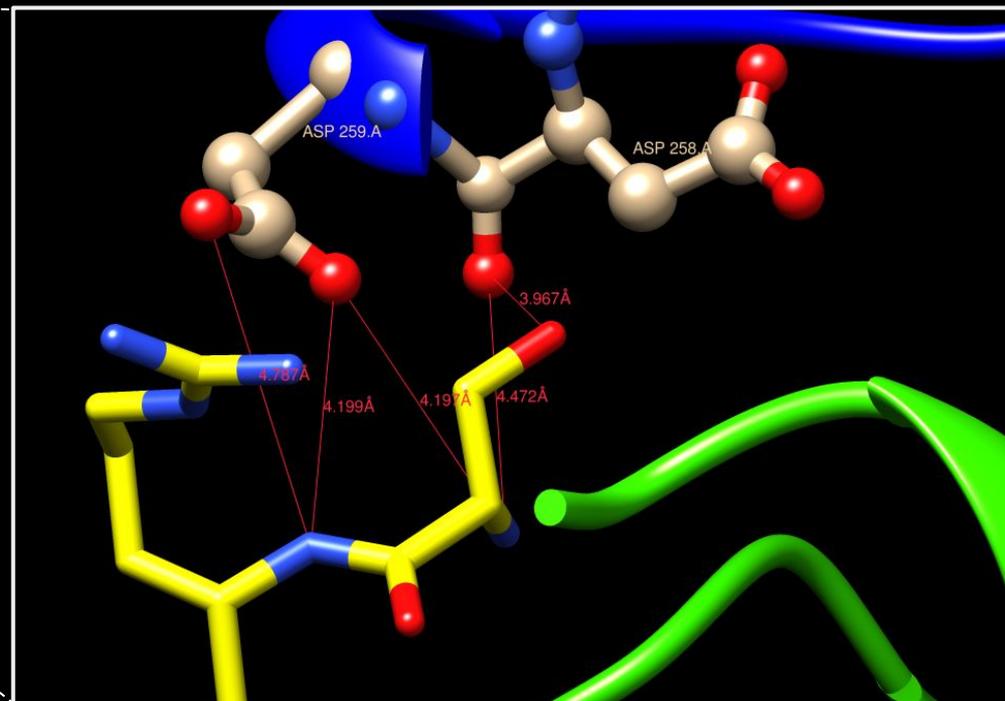
265 determinant



287 determinant

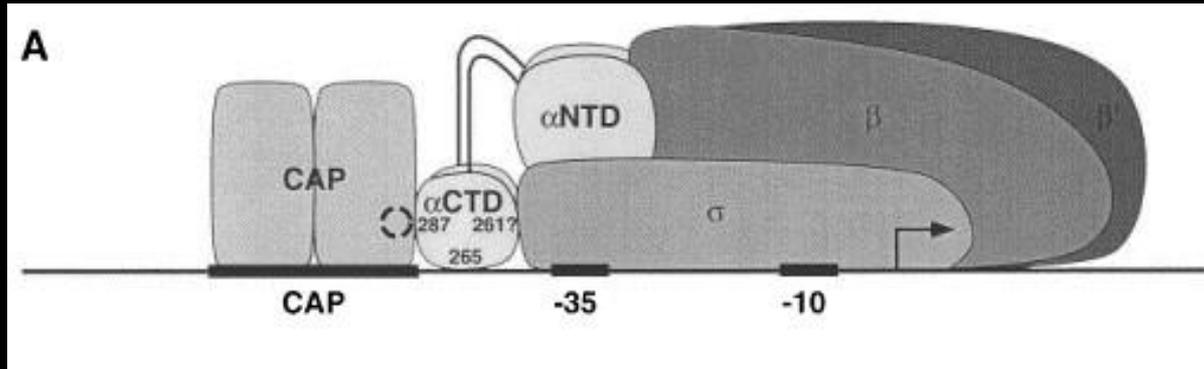


261 determinant

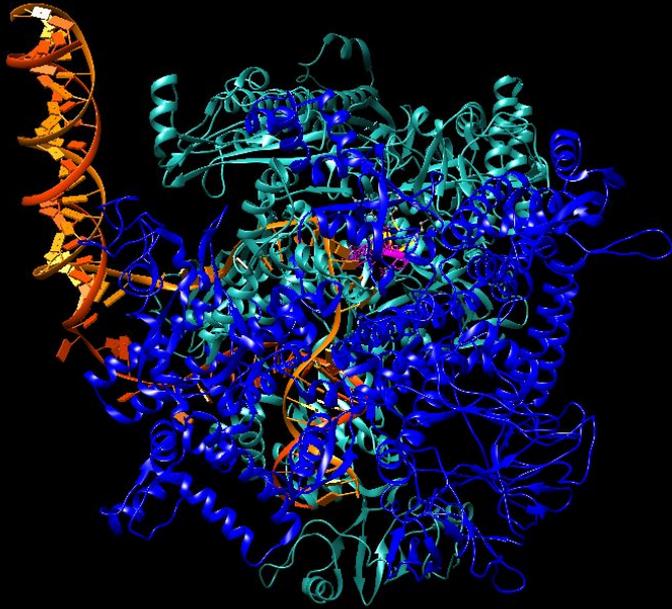


Alpha subunit: interaction with CAP

Class I CAP-dependent promoter



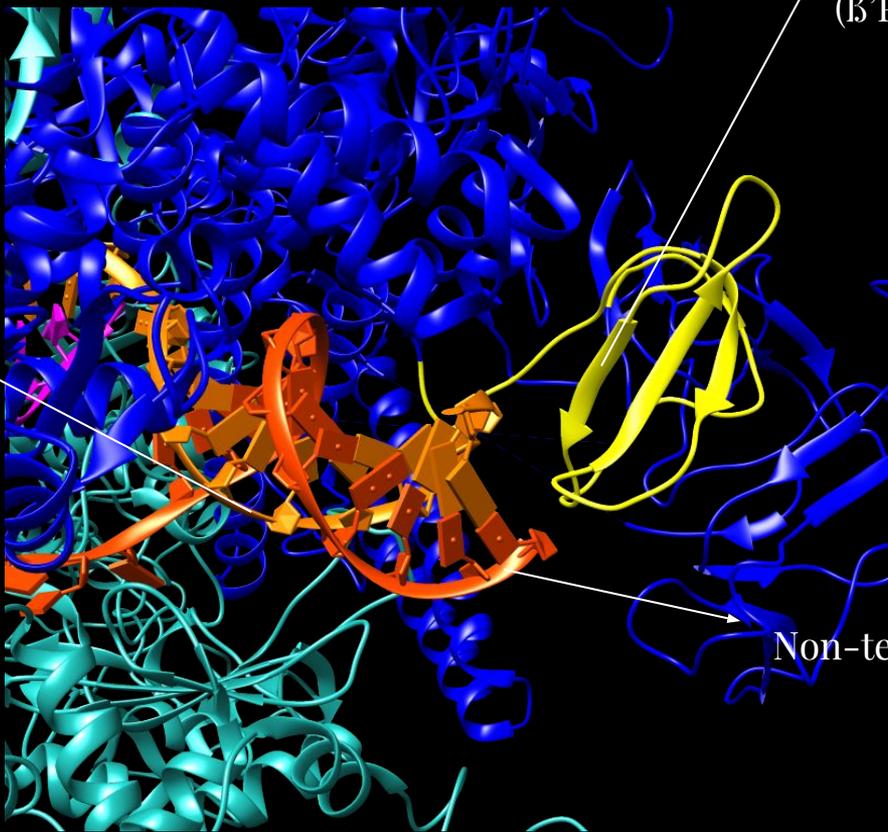
β and β' subunits: structures and functionality



- Jaw
- Clamp
- The Fork-loop 2 (FL2)
- The catalytic center
- Access to the catalytic center: RNA polymerase channels and regions
- The lid and the rudder

The Jaw

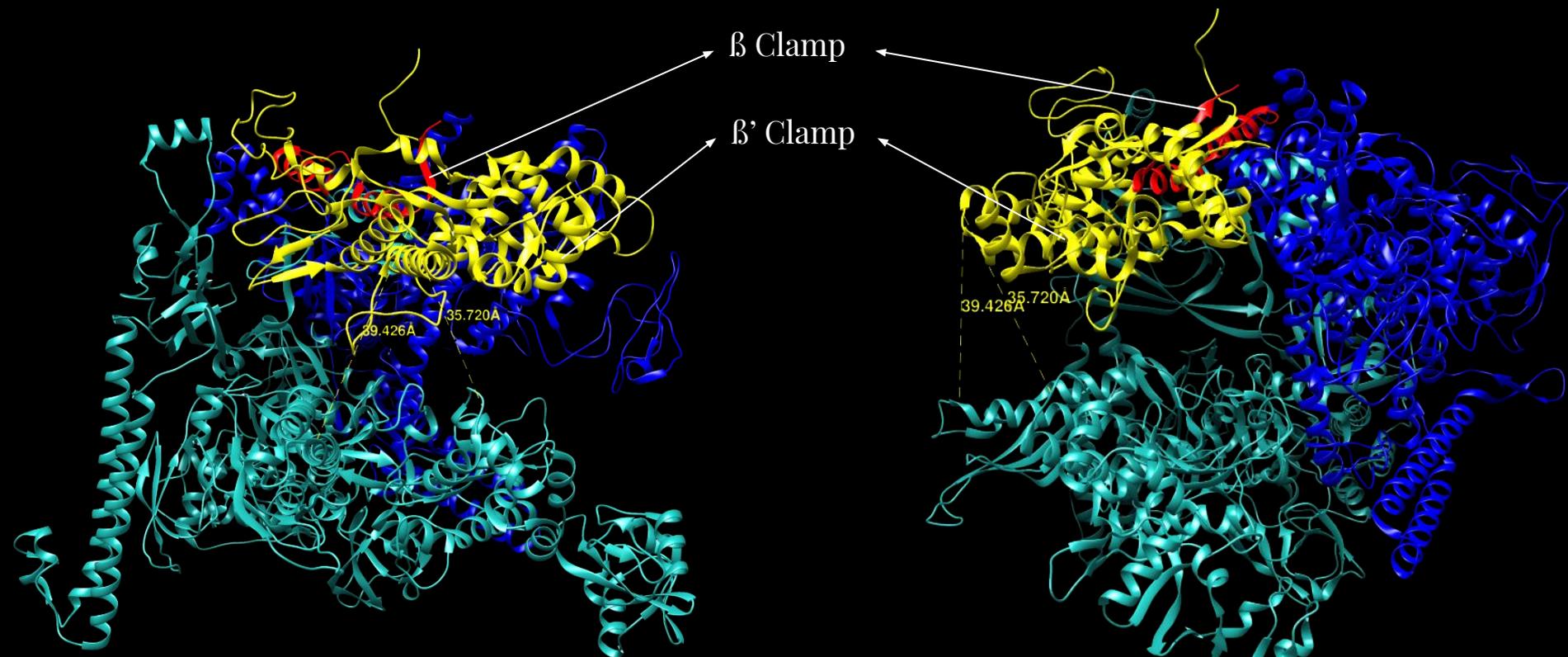
Template DNA



Jaw
(β'Pro1150-β'Asp1208)

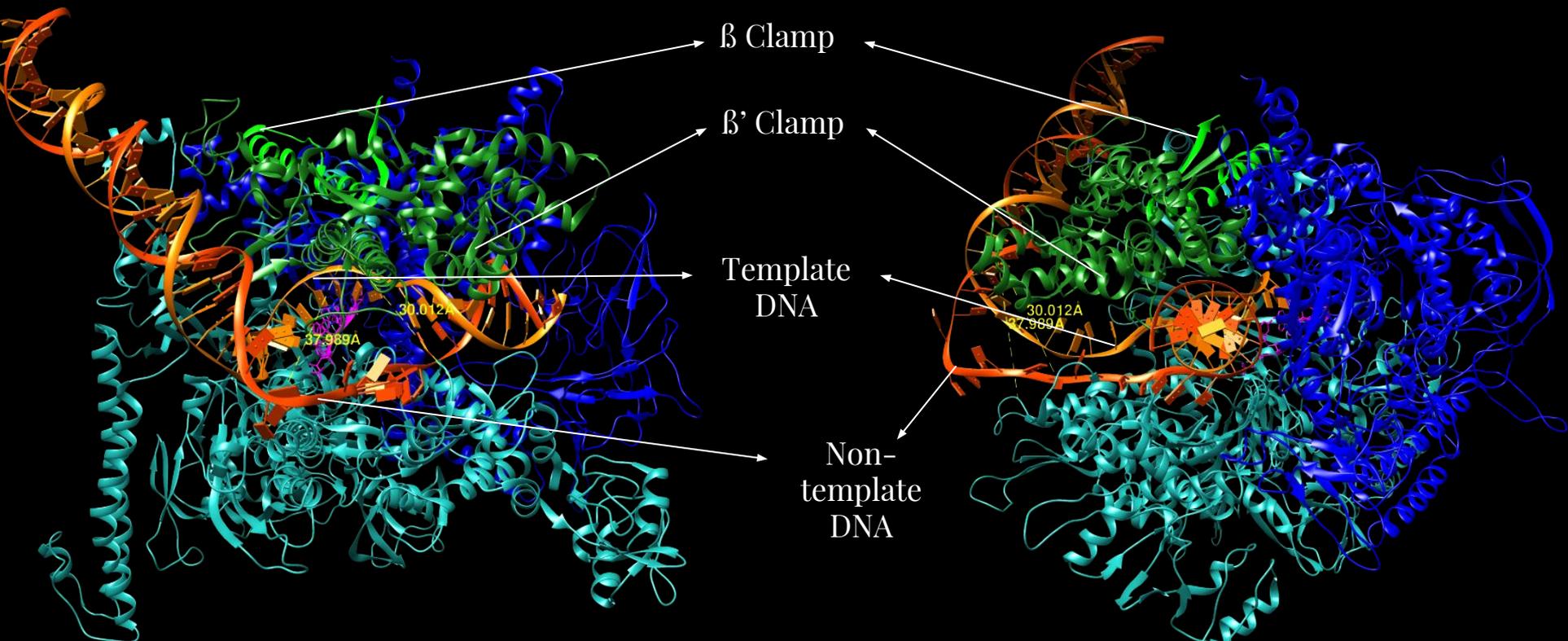
Non-template DNA

The Clamp



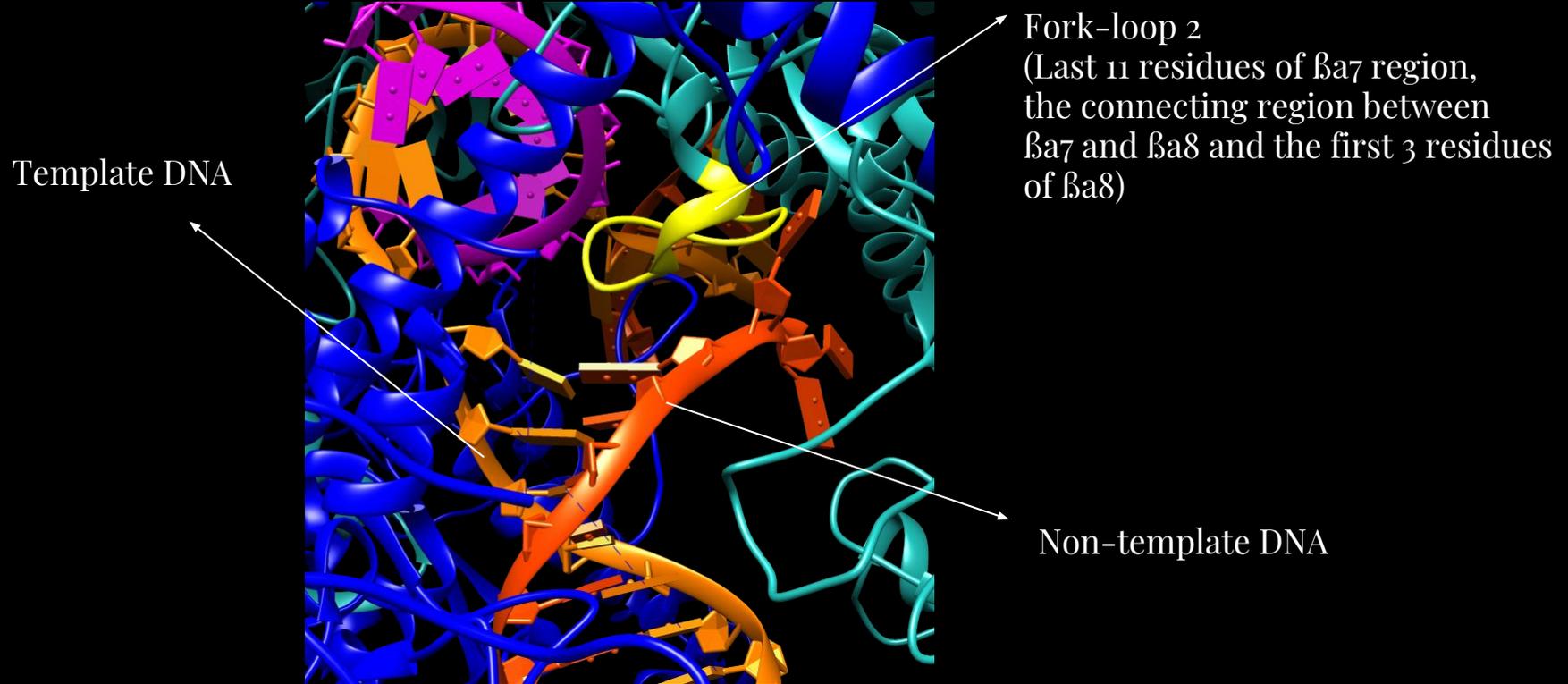
DISTANCES: β Leu481---(39.427Å)--- β' Ala286---(35.720Å)--- β Pro375

The Clamp

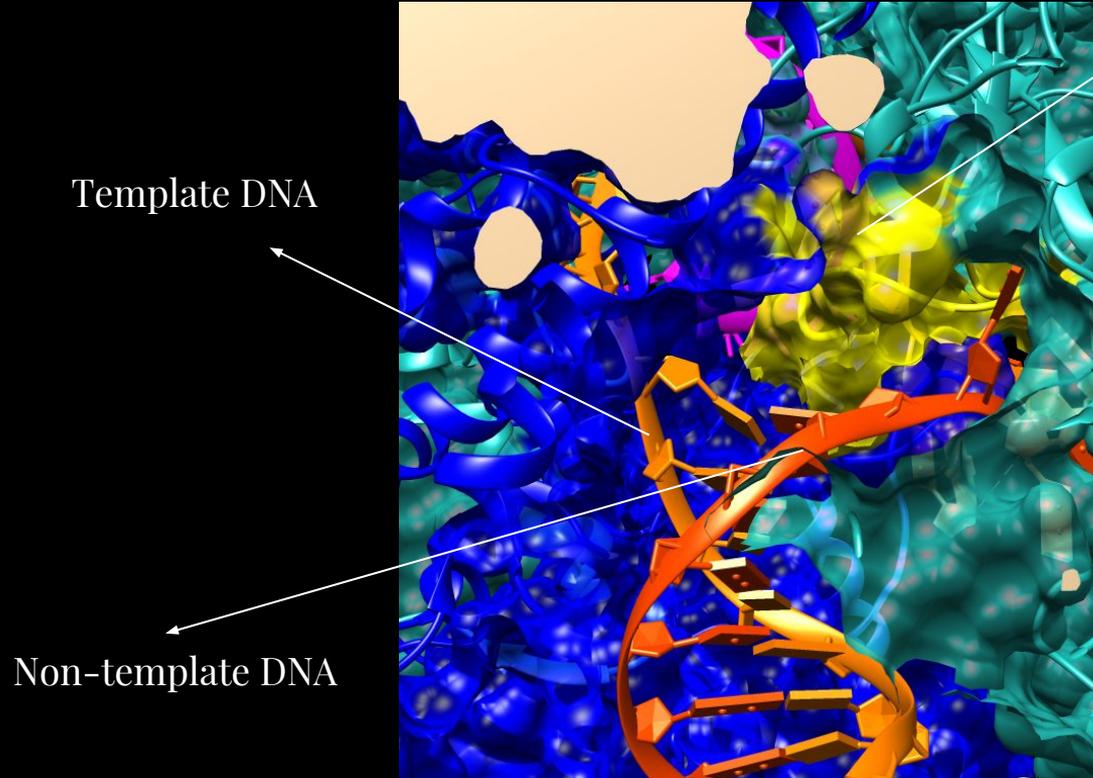


DISTANCES: β Leu481---(37.989A)--- β' Ala286---(30.012A)--- β Pro375

The Fork-loop 2 (FL2)



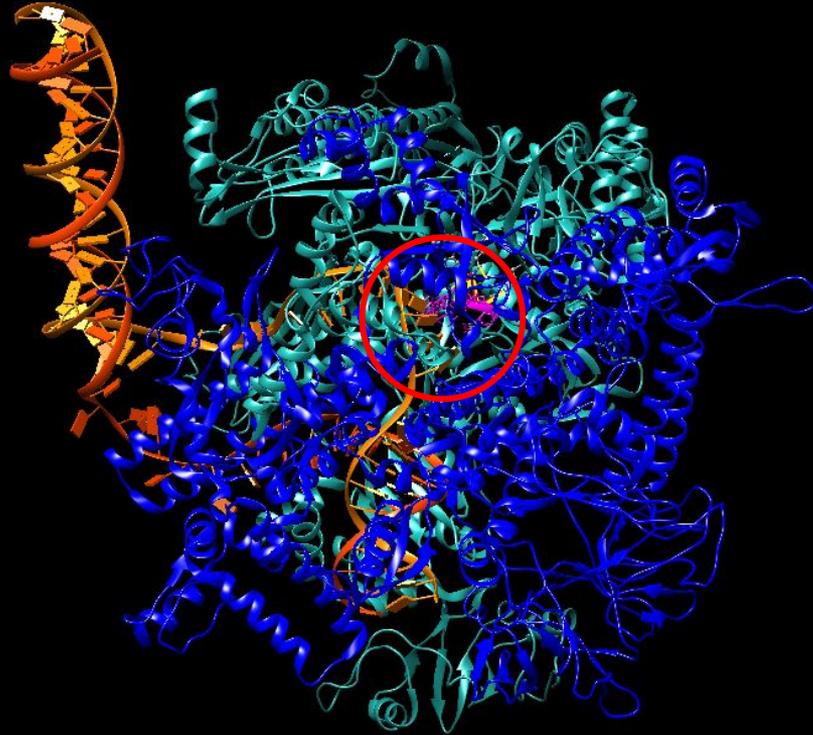
The Fork-loop 2 (FL2)



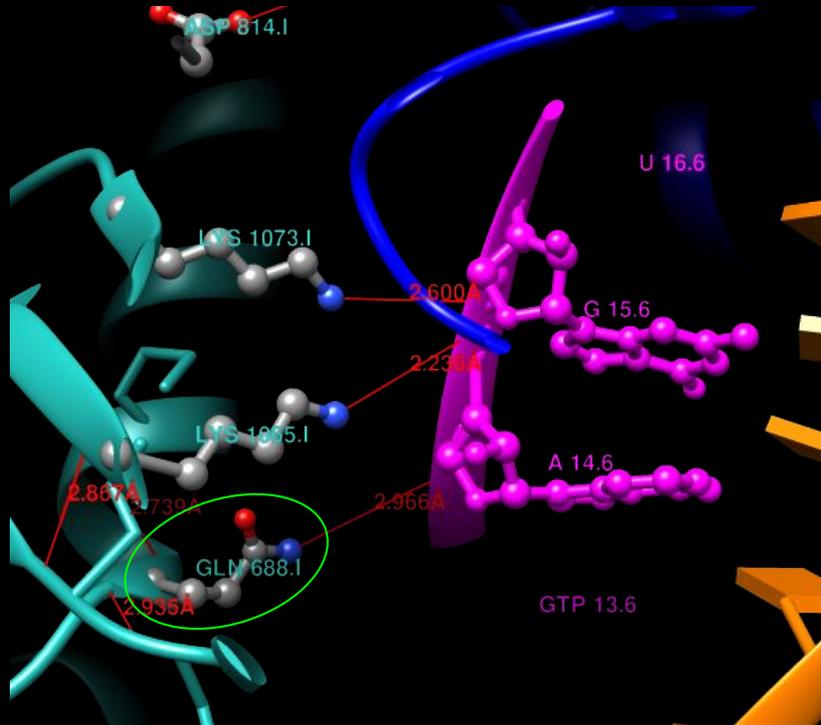
Fork-loop 2
(Last 11 residues of β a7 region,
the connecting region between
 β a7 and β a8 and the first 3 residues
of β a8)

Naji, Souad, et al. "Structure–function analysis of the RNA polymerase cleft loops elucidates initial transcription, DNA unwinding and RNA displacement." *Nucleic acids research* 36.2 (2007): 676–687.

The catalytic center



The catalytic center: β a10 region

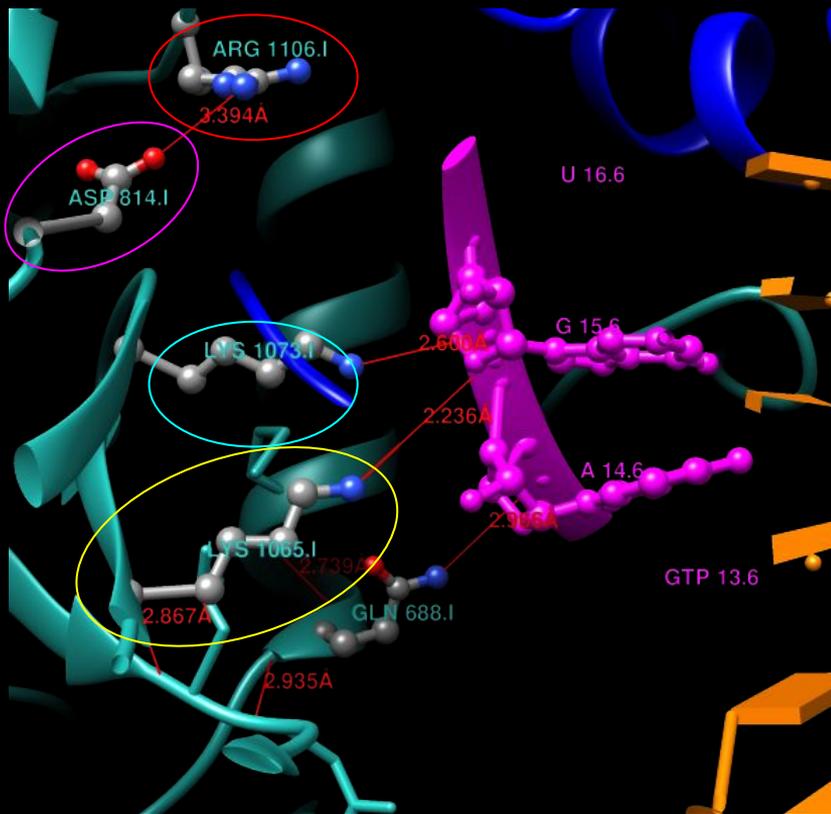


Bln688

| | 701 |
|----------------------|--|
| Consensus | QRQAVPTLRA |
| Conservation | QRQAVPTLRA |
| spIP0A8V2IRPOB_ECOLI | QRQAVPTLRA |
| spIQ8Z320IRPOB_SALTI | QRQAVPTLRA |
| spIQ8ZAP5IRPOB_YERPE | QRQAVPTLRA |
| spIQ9KV30IRPOB_VIBCH | QRQAVPTLRS |
| spIQ8RQE9IRPOB_THET8 | QTQAVPLIRA |

Bln688 N.....OP RNA (-3) - 2,966A

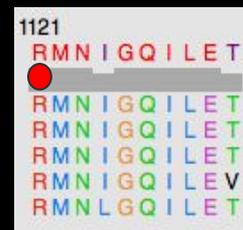
The catalytic center: β a11 and β a14 regions



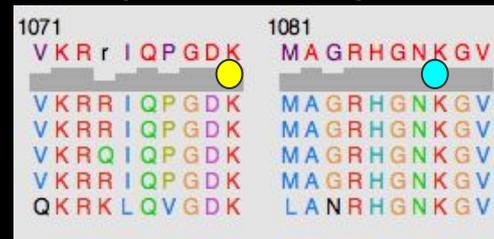
β Asp814



β Arg1106

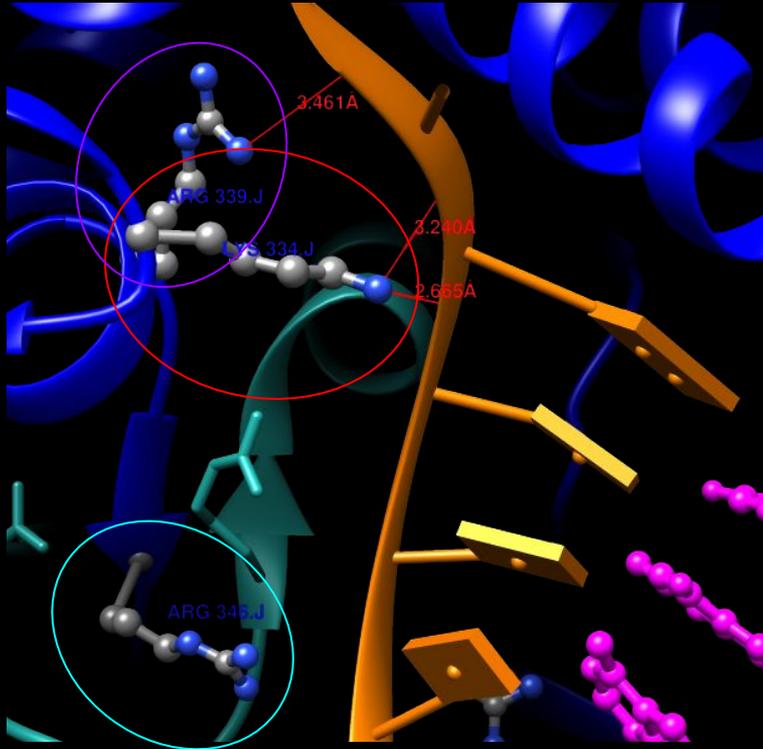


β Lys1065 and β Lys1073

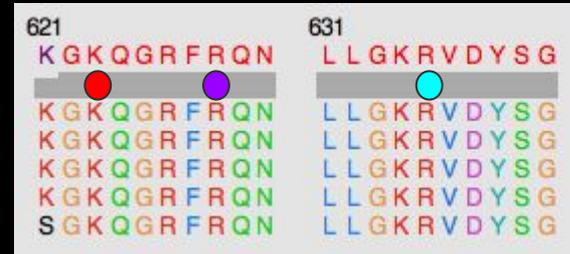


β Asp814 O.....NH2 β 1106 - 3,394Å
 β Lys1065 N.....OP RNA (-1) - 2,236Å
 β Lys1073 N.....O1' RNA (-2) - 2,600Å

The catalytic center: β' a11 region (Sw2)

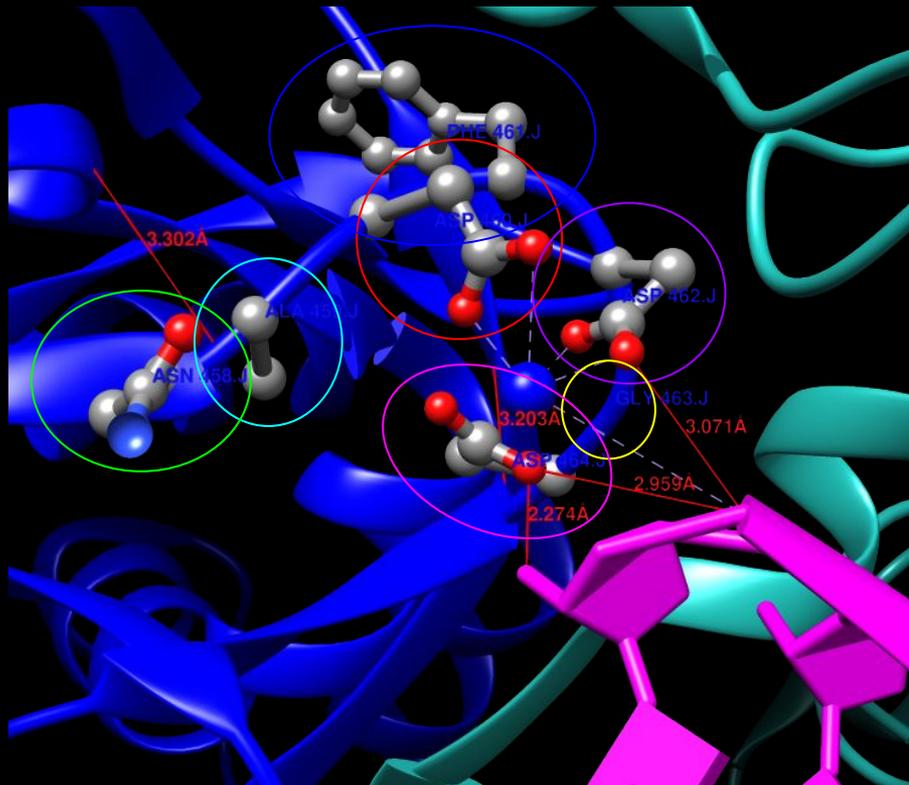


β' Lys334, β' Arg339 and β' Arg346



β' Lys334 N.....OP2' tDNA (+1) - 2,665A
 β' Lys334 N.....OP1' tDNA (-1) - 3,240A
 β' Arg339 N.....OP1' tDNA (+2) - 3,461A

The catalytic center: β' a12 region (β' -NADFDGD motif)



| Consensus | 781 |
|----------------------|---------------------|
| Conservation | N A D F D G D q M a |
| spiP0A8T7IRPOC_ECOLI | N A D F D G D Q M A |
| spiP0A2R5IRPOC_SALTI | N A D F D G D Q M A |
| spiQ8D1H3IRPOC_YERPE | N A D F D G D Q M A |
| spiQ8KV29IRPOC_VIBCH | N A D F D G D Q M A |
| spiQ8RQE8IRPOC_THET8 | N A D F D G D Q M A |
| spiP04050IRPB1_YEAST | N A D F D G D E M N |
| spiP24928IRPB1_HUMAN | N A D F D G D E M N |

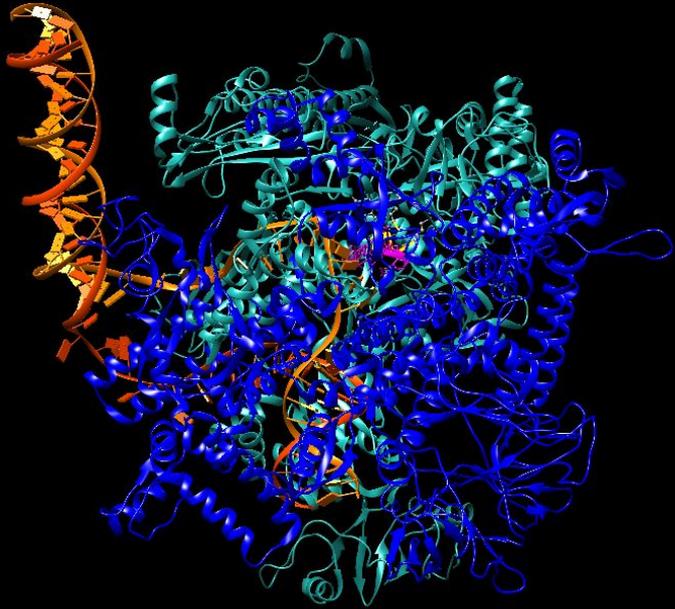
HYDROGEN BONDS:

| | | |
|--------------------------------------|---|--------|
| β' Asp462 O2'.....O3' RNA (-1) | - | 3,071A |
| β' Asp464 O1'.....O3' RNA (-1) | - | 2,959A |
| β' Asp464 O1'.....O2' RNA (-1) | - | 2,274A |

ELECTROSTATIC INTERACTIONS:

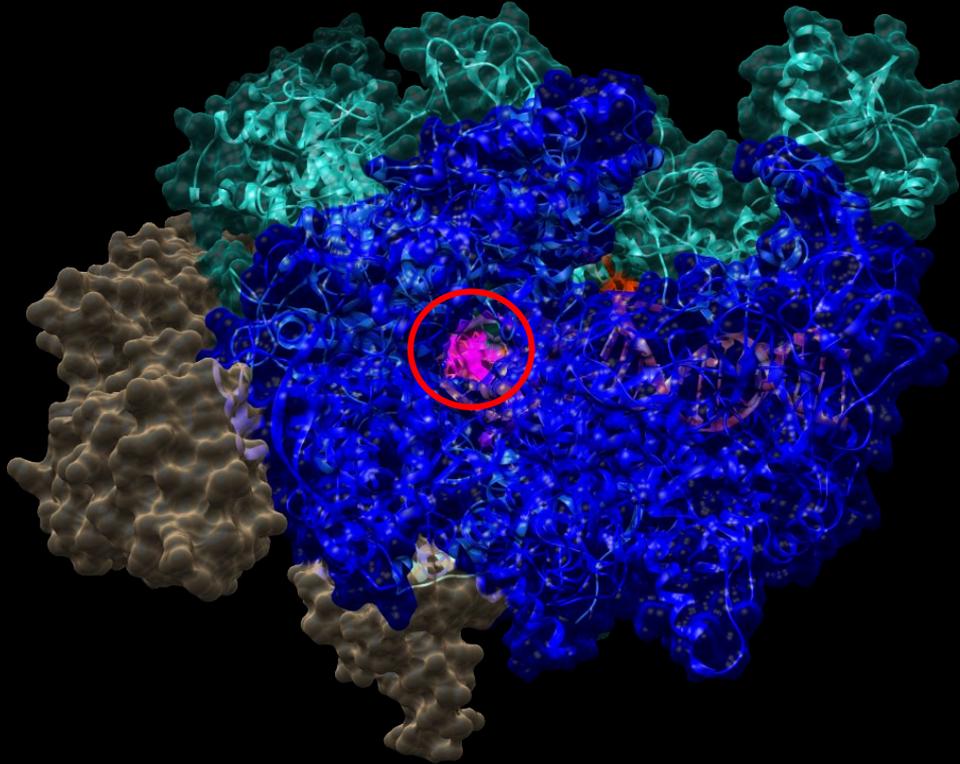
| | | |
|------------------------------|---|--------|
| [Mg].....O3' RNA (-1) | - | 2,088A |
| β' Asp460 O1'.....[Mg] | - | 2,158A |
| β' Asp460 O2'.....[Mg] | - | 2,772A |
| β' Asp462 O1'.....[Mg] | - | 2,961A |
| β' Asp462 O2'.....[Mg] | - | 2,159A |

Access to the catalytic center: RNA polymerase structural channels and regions



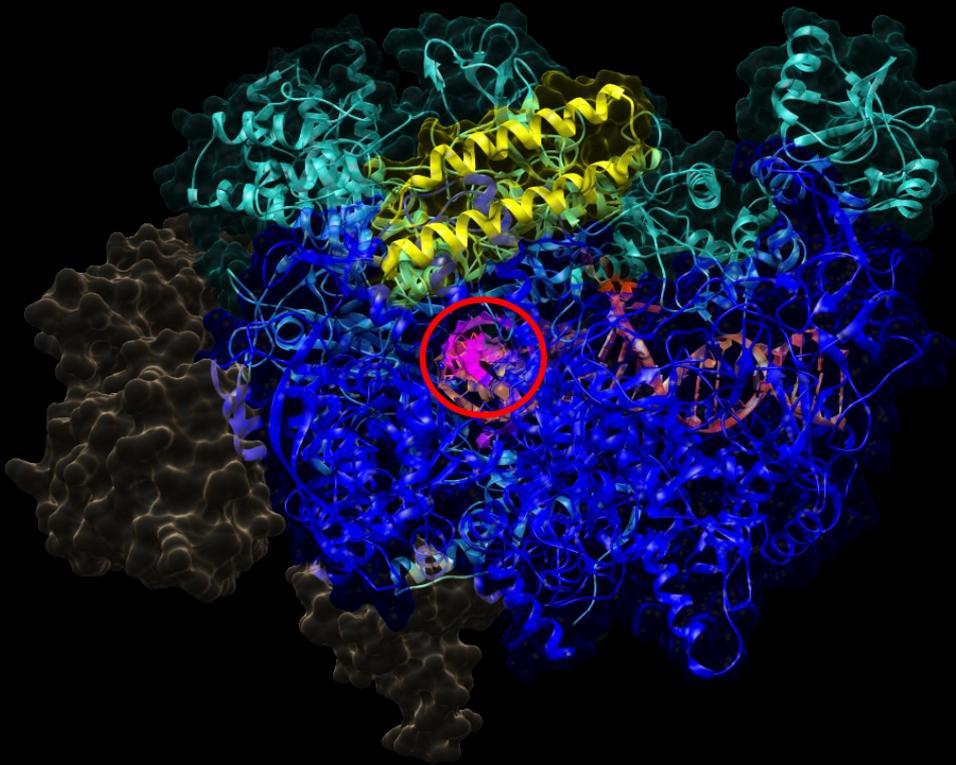
- Secondary channel
- RNA exit channel
- Switch 3

RNAP structural channels: Secondary channel



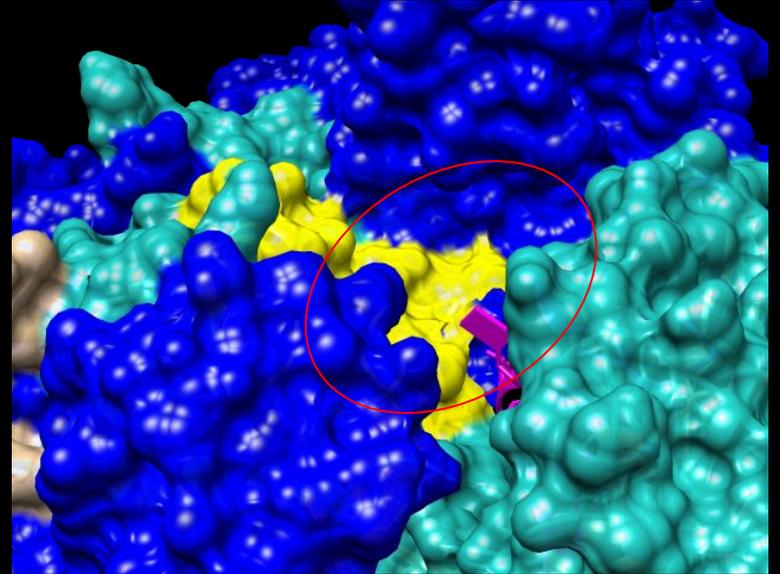
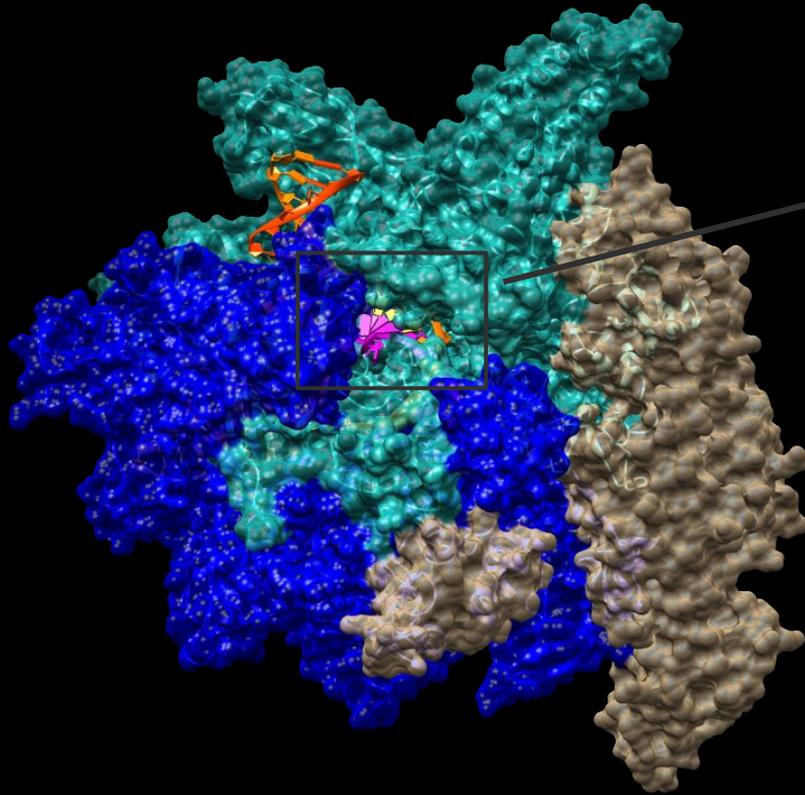
- Direct path for the nucleotide substrate
- Exit for the RNA transcript during backtracking
- Direct access to the RNAP active center for extrinsic factors

RNAP structural channels: Secondary-channel rim helices



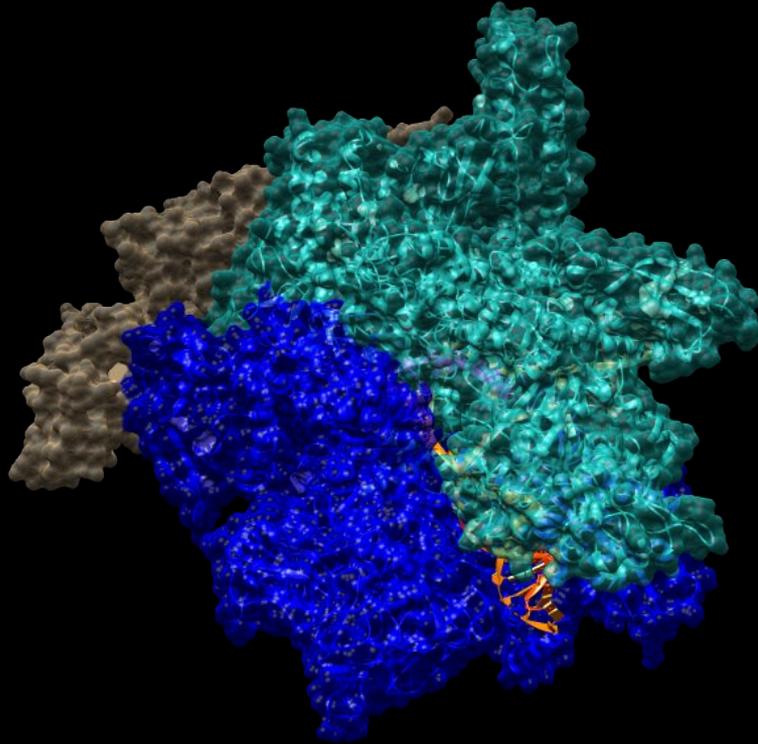
- $\beta'a_{13}$ region (C-terminal helix) and $\beta'a_{14}$ (N-terminal helix)
- $\beta'Ile646$ - $\beta'aThr703$
- Binding of Gre-factors which may regulate the transcription

RNAP structural channels: RNA exit channel



β_{a15} region: β Gly1249- β Leu1259

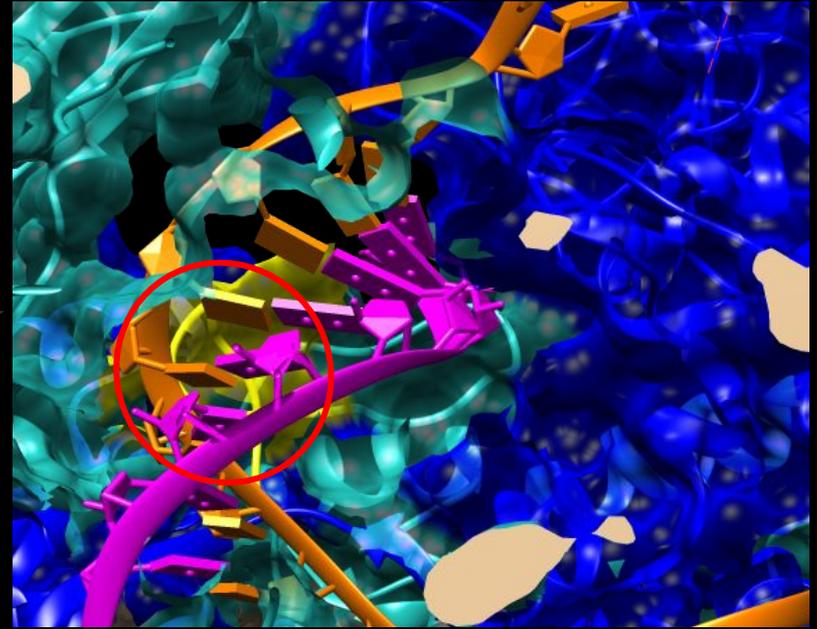
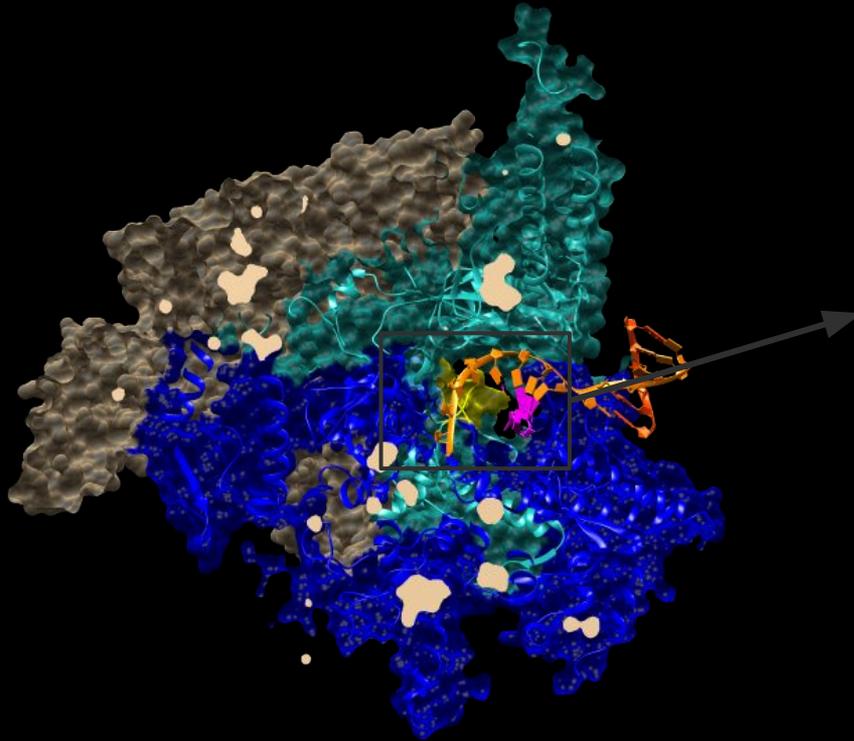
RNAP structural channels: Switch 3



| | 1271 | | 1281 | |
|----------------------|------|--------|------|-------|
| Consensus | TQQP | LGGKAQ | FGG | QRFGE |
| Conservation | | | | |
| spIP0A8T7IRPOC_ECOLI | TQQP | LGGKAQ | FGG | QRFGE |
| spIP0A2R5IRPOC_SALTI | TQQP | LGGKAQ | FGG | QRFGE |
| spIQ8D1H3IRPOC_YERPE | TQQP | LGGKAQ | FGG | QRFGE |
| spIQ9KV29IRPOC_VIBCH | TQQP | LGGKAQ | FGG | QRFGE |
| spIQ8RQE8IRPOC_THET8 | TQQP | LGGKAQ | FGG | QRFGE |
| spIP04050IRPB1_YEAST | TQQP | LGGKAQ | FGG | QRFGE |
| spIP24928IRPB1_HUMAN | TQQP | LGGKAQ | FGG | QRFGE |

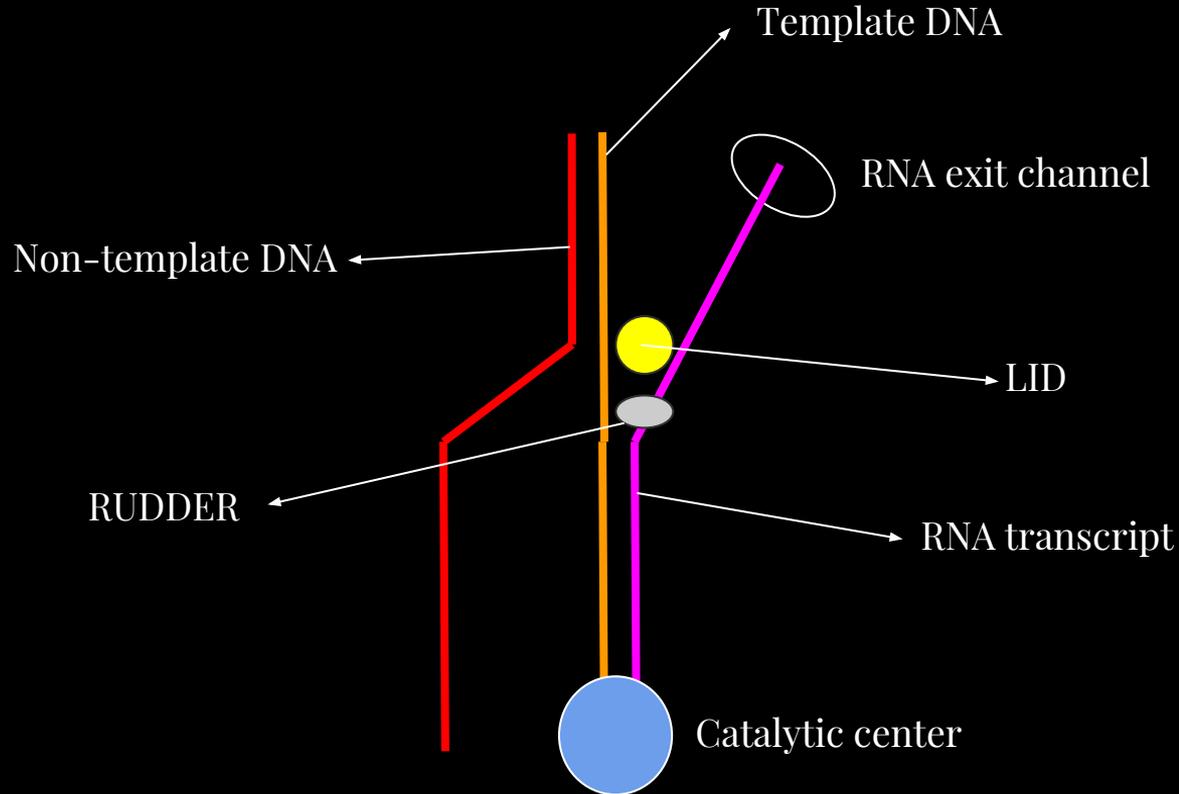
β_{a15} region: β Gly1260- β Gly1267

RNAP structural channels: Switch 3

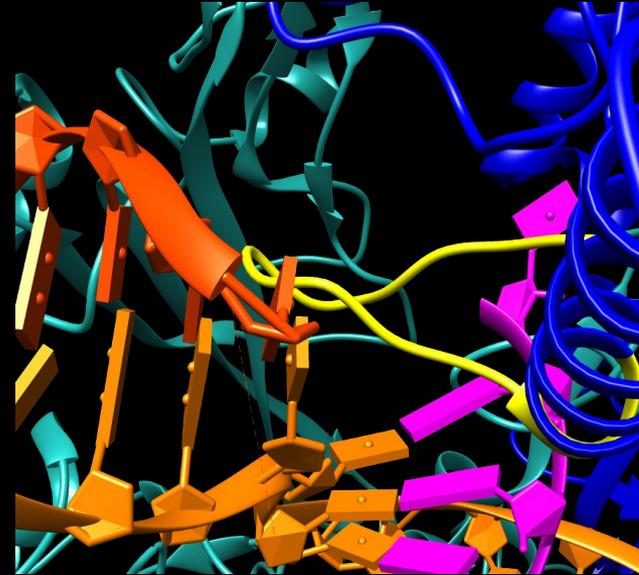
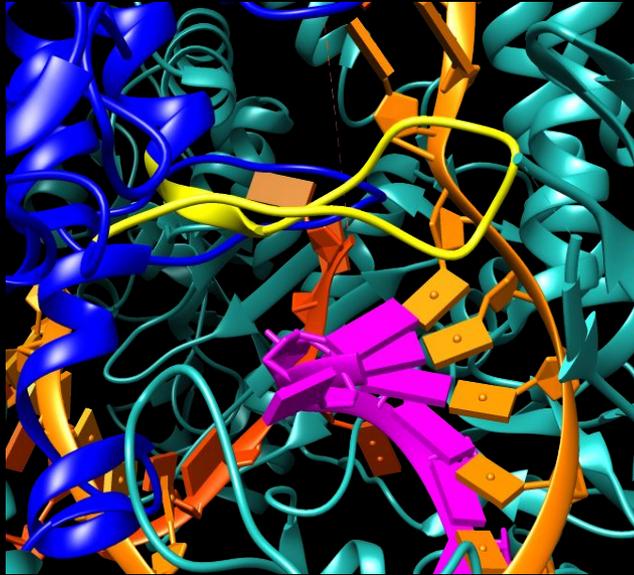


β a15 region: β Gly1260- β Gly1267

The lid and the rudder



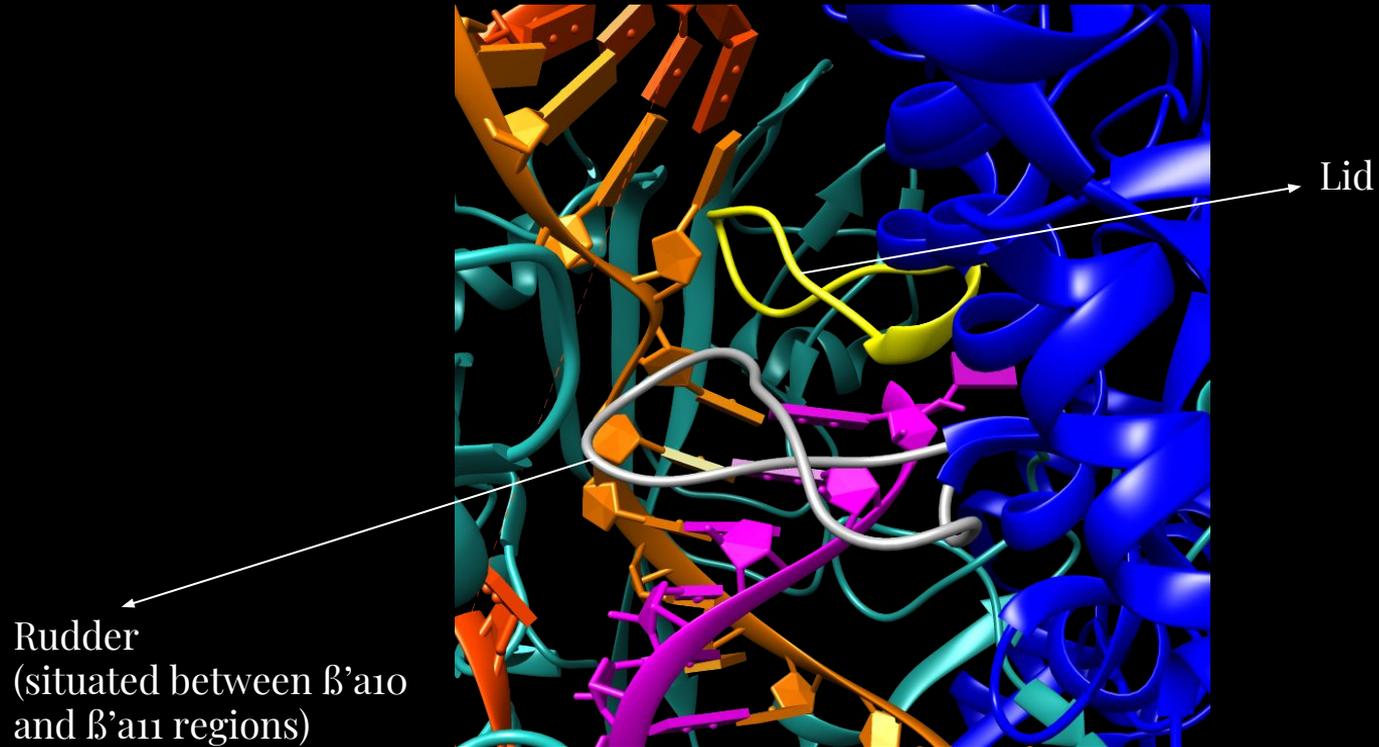
The lid



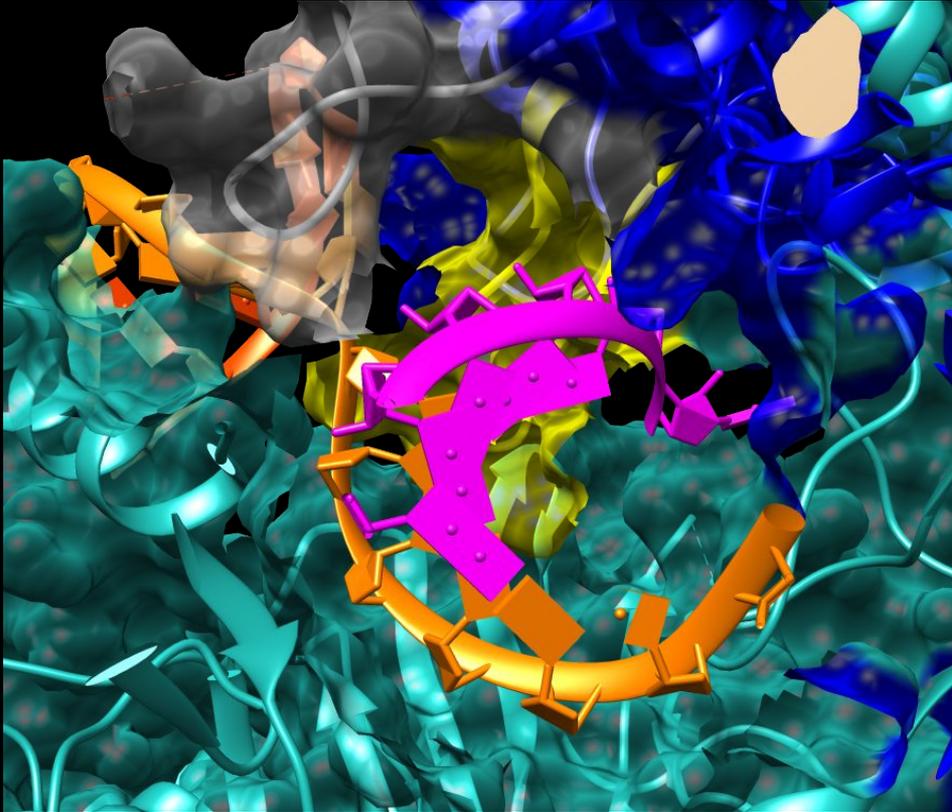
β' a8 (C-terminal) and β' a9 (N-terminal)
regions: β' Arg250- β' Lys265

| | 531 | | 541 | | 551 |
|----------------------|---------|-----|------------|--|------------|
| Consensus | PVLPPDL | RPL | VPLDGGRFAT | | SDLNDLYRRV |
| Conservation | | | | | |
| spIP0A8T7IRPOC_ECOLI | PVLPPDL | RPL | VPLDGGRFAT | | SDLNDLYRRV |
| spIP0A2R5IRPOC_SALTI | PVLPPDL | RPL | VPLDGGRFAT | | SDLNDLYRRV |
| spIQ8D1H3IRPOC_YERPE | PVLPPDL | RPL | VPLDGGRFAT | | SDLNDLYRRV |
| spIQ8KV29IRPOC_VIBCH | PVLPPDL | RPL | VPLDGGRFAT | | SDLNDLYRRV |
| spIQ8RQE8IRPOC_THET8 | PVLPPDL | RPL | VPLDGGRFAT | | SDLNDLYRRV |
| spIP04050IRPB1_YEAST | PVLPPDL | RPL | VQVDGGRFAT | | SDLNDLYRRV |
| spIP24928IRPB1_HUMAN | PVLPPDL | RPM | VQVDGGRFAT | | SDLNDLYRRV |

The rudder



The lid and the rudder



Toulokhonov, Innokenti, and Robert Landick. "The role of the lid element in transcription by *E. coli* RNA polymerase." *Journal of molecular biology* 361.4 (2006): 644-658.



Non-essential role of the lid
in elongation

Conclusions

- Regions and residues responsible for the specific binding of RNA polymerase to DNA have been proven to be highly conserved among prokaryotic and non prokaryotic species.
- It has been proven that both Sigma and Alpha subunits are responsible for the binding of RNAP to promoter regions of the DNA. Therefore, allowing promoter dependent transcription.
- β and β' subunits play the most important role in the catalytic activity of RNA polymerase.
- Both Mg^{+} element and its interactions with β' -NADFDGD motif are responsible for the assembly of RNA transcript to the polymerase.

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Questions

- ❖ Which is the largest subunit of RNAP?
 - a. Alpha
 - b. Beta
 - c. Beta'
 - d. Sigma
 - e. b and c
- ❖ Which subunits comprises the catalytic core of RNAP?
 - a. Alpha(2), Beta, Beta', Omega
 - b. Alpha(2), Beta, Beta, Sigma
 - c. Beta, Beta', Sigma, Omega
 - d. Alpha(2), Beta, Beta'
 - e. Alpha(2), Beta, Sigma
- ❖ Which type of interaction does alpha subunit with DNA?
 - a. Non-specific interactions with UP-element DNA
 - b. Non-specific interactions with non-UP-element DNA
 - c. Sequence-specific interactions with UP-element DNA
 - d. Sequence-specific interactions with non-UP-element DNA
 - e. b and c

Questions

- ❖ Which structure separates the template DNA and the non-template DNA?
 - a. The lid
 - b. The rudder
 - c. The RNA exit channel
 - d. The fork-loop 2 (FL2)
 - e. The clamp
- ❖ Which structure “pinches” the DNA strand ?
 - a. The rudder
 - b. The RNA exit channel
 - c. The clamp
 - d. The lid
 - e. Any subunit does it, the DNA is free in the RNA polymerase
- ❖ Through which structure does usually the RNA transcript leave the RNA polymerase?
 - a. The secondary channel
 - b. The RNA exit channel
 - c. The main channel
 - d. The jaw
 - e. The clamp

Questions

- ❖ Which are the DNA-binding functions related to Sigma?
 - a. -10 element recognition
 - b. -10 element melting
 - c. -35 element recognition
 - d. -10 element recognition and melting
 - e. All options are correct
- ❖ Which is the most conserved region of Sigma subunit ?
 - a. 1
 - b. 2
 - c. 3
 - d. 4
 - e. 2 and 4 are equally conserved
- ❖ Select the wrong affirmation about Sigma2:
 - a. It is highly conserved
 - b. It is responsible for -35 element recognition
 - c. It is responsible for the -10 element recognition
 - d. It includes subregion 1.2
 - e. It takes part in the core binding

Questions

- ❖ Which of these is not a main characteristic of Sigma70?
 - a. It is a primary factor of sigma family
 - b. All of its regions are conserved
 - c. It recognizes DNA binding promoters
 - d. It is not the only protein of sigma family
 - e. It's secondary structure is almost entirely helical

RNA polymerase in Prokaryotes

Sofía Ardiles, Lorea Jordana, Aina Nicolás & Lluís Zacarías