

Supplementary Material

Article title: Structural complexity and functional diversity of plant NADPH Oxidases

Journal: Amino Acids

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S1 File

>AtRbohA_O81209

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

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S1 File

>OsRbohB_Q5ZAJ0

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S1 File

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ATPMVSILREICSA RAPAKLAGIADASDDDIRGIRAGTQHGTLDL SKQETSAQ LLD RIRKSG ILSMYM KERV G IFQ TETR IDRLRAFV LSS LWLFS
LLWMLYISLTIYVIANAF DANVALVADFTSSA VLLFLFSFTIASDMLV TLDPPRWRVYGT PRGFV SLSVC LLVADL VVGATLFGIEQHSSHYMDGA
GNAMRII ALVLF CIKSIM FALTRI FYL PRPW RIQLR VRH LGRK AS ALLS RRG NGL TAVA Q QRCV QSD DKV SHV EQQEQQEQQEQQEQQ
EQ QEQ
QGRPRFETFIEDL LDLRDPYEFERLFGNI IQVKQFN RVSGFSNDVQRG IFFCGNPALGASVRRAMHKVQRQPERL GTKPKILFIQERF

>CmRboh2_M1UWF8

S1 File

MQRRAAVDAQECHEDTRFSPNSGGAFGRAPNLAAAAAIQSTPRHRRLSHVRIALVPRSFCFLDEVWMKPSLPPVPLGACAITTMRPRNRIRAQLDLWN
ERVGESGLFFSLLVAYWCSQAWFFVYGVKYALSIALFSWDSRYMLIFGRGFGYVATFNALLPITVNRTLTNILYRLPLYDIFSVARWLPLDHAIIA
RWFTIAGWIHGILLSVAYGVGTLFPLFSNTIPTTMVFVTGCALMAFLLAIVLLSLGSVRRRVYRWFASHVPLAILTyaALVFHGLRGGRILW
SVYFFGLPVVLYILDRLYHSFAAAFTPFRVLSVELSHKNSNVVRLVIERGRKFVAGQYFKLAWKFHVCSHLAVAGEWHFPTVASSPLLDKDRIIFF
IAATGKWTNALRALALQQHQHDENLEHASSTSPTPKSLATEAMPHAVDKSSITCLPINRRWILLSGPYGAPAQSHPQNFAHQLLIGTVGASPMF
SIVQELCGRATPCDNNNNKDASLECSDVSTGGDLENCLASVSDTSPRESTDLPNFEKLKASTTANDSSEVVPSVQALPPVLAARLGTLRGDTF
LDRFSAAVLNSNLWLFSLWICLADLTVSICASAFSHIVAFIGSLALFVVIITMICLTVIADMRLSVNPPRWHYVLLRGILLLWFAVALTNAVLCS
LLIVEYFLASNDRMASISKSEWLFWMVVTVPVHITIFVLLFFFFLPRSWTWRRTVTAKFRRCLQGSWDHQQRSNKVVSARNAEWNASHIRTWT
FVWVVRVYVEDLWFLEKLYELASQQDASDPCCRPLRIHVITRLGHDDADPVSSLPANCGEILQFHCGPDFGEYVAELVNEDHTTPLAGRKPG
APASIRRFQRTAFSNKVHHGIFCGGRSVRSVHQSIARAAAARGLPQRNVFFMKENF

>PyRboh_Q2F9N3

MGDDKPPPKSRVSRVESYLSTNGFVLTFGLYILANVILFFFATPERRLWPVGHYRRNLTPVARGAGNLINFNSAVILLVSARKFMSWLRNTPLN
MVVPFDKAMPAPHMLVGRVFLAASVSVHVGFLPVYVVSCKPWGPYNGFTQLFITGSMIVALFAILFTSVRVNRSKRYELFWYSHAICASLGFVLLM
IHGLHYGVWTYRWAAGPMAYIIDRLMRVEQKEVRMEVSRDVGAIKGNMLCLRLPRSFTYPEPGQYAEVKVPASISSLVQWHPFTIASAPEPELVF
YIKKSGDWTTNLHAMFASTDPTQVEIKVRGPYGSPAQHVGQFENVVLIAGGVGSTPFASVVKSAHNWMAASSTRGPEMSPSSFNAAAGQVSVPAAT
ARDATTVPASASLSARLTMQHSTSAATVTAQARMPTVDLADMDEDLSSNGSRIPAARLSDDAALRPPQAPSSFTSDVLERVAELDRLYSIADKED
NDRVFPPPSSVQSVVEQDMTGHAVIDMDGEDGALSDDDSRLDEEEEDQLQSQQSIGRVLRHSAFINSTAGQQLIGLALDADAVVKQRAAAKEGAN
RRTSVLGAFFGGLKGDDRRGTLPESEVVRARTKRAVILQILHSVSVSALLWAMVARFAIVALASIMRGFSPSTAGLAMFNTTRGLVVADLVLASACA
VPLAVSLGCEASILGVSVYFRQRGSLVDTLFLLPLLLAGVITDALALAGHGRSAAWFASVNLLVLPLLLFAFLFRRLTRVGSRLVLAQNLQSSHSL
RSLDFVWTSPSPEHDawlveellpisrsgtvrlhrhitrsaaevepwmldydevplktykrpdwaaifagitersrgsvvvgvffcgphpmksiq
DGIARATALSLARGYRRGAIGLDGSREMRT

EF-hand-like I

OsRbohB_Q5ZAJ0
 AtRbohB_Q9SBI0
 OsRbohH_Q2QP56
 ANC-C6AB_AtB-OsBH_N3
 OsRbohF_Q0J595
 OsRbohG_Q69LJ7
 AtRbohE_O81211
 ANC-C3AB_AtE_OsFG_N3
 OsRbohA_Q0JJJ9
 OsRbohc_Q65XC8
 AtRbohF_O48538
 ANC-4AB_AtF-OsAC_N4
 OsRbohE_Q8S1T0
 OsRbohd_Q0DHH6
 AtRbohH_Q9FJD6
 AtRbohJ_Q9LZU9
 ANC-C2AB_AtHJ-OsDE_N3
 ANC-C6AB_INV_N3
 ANC-C3AB_INV_N3
 ANC-4AB_INV_N4
 ANC-C2AB_INV_N3
 DISCRIM_2-3-4-6AB

----KRLDRTKSSAAVALKGLQFVTAKVGDWAAVEKRFNQI-----Q--VGVLL
 ----RRLDRSKFGAMFALRGLRFIAKNDRGWDEVAMRFDEKIA--VEGKLP
 ----PRLDRSMTGAARALRGLQFLNNSANGWPEVEKRFERIA--VDGFLL
 ----PRLDRSKTGAARALRGLQFLNQSVEGWPVEKRFDRIA--VDGFLL
 ----ARLNRSRSRGARRALKGLRFISRTTELWTRVEHRFNAIS--RDGLLS
 ----ARLNRSSTGAKRALKGLRFISRTTELWRRVEDRFNAIA--RDGLLS
 ----AKLQRSTSQAQRALKGLQFINKTTQWKKVEKRFESIIS--KNGLLA
 ----AKLQRSSRAQRALKGLQFINKTTQLWKKVEKRFESIIS--KNGLLA
 -----A--RDGYLS
 ----AQLDRTKSGAQRRAIRGLRFISPKNKAWIEVQANFDERIA--RDGYLS
 ----AQLDRTSSAQRALRGLRFISPKNQDGWNDVQSNFEKE--KNGYIY
 ----AQLDRTSGAHKALRGLKFISNRSDADEVQSNFDKIA--TDGFLK
 ----GRMTRMQSSAQVGLRLRFLDKTS--GWKSVERRFDEMNR--NGRLP
 ----KLKRTHSSAQPALRGLRFLDKTS--GWNVEKRFDEMSEA--DGRLP
 ----QRVERTTSSAARGLQSLRFLRTVDWRSIENRFNQPSV--DGKLP
 ----QRVERTTSSAARGLQSLRFLRTVDWRSIENRFNQPAV--DGRLP
 ----QRVERTTSSAARGLKSRLFLRTVDWRSIEKRFNQPAV--DGKLP
 -----GW-----R-----L-
 -----R---A---LKGL-FI-----V---F---I-----GLL-
 -----AQL-R-----A---L-F-S-----W-V---F-----G-
 -----R-S-A-----LRFLD-T---W---RF-----L-
 -----X-X-X-X-----X-X-X-X-----X-X-X-X-----X-X-X-X

EF-hand-like II

OsRbohB_Q5ZAJ0
 AtRbohB_Q9SBI0
 OsRbohH_Q2QP56
 ANC-C6AB_AtB-OsBH_N3
 OsRbohF_Q0J595
 OsRbohG_Q69LJ7
 AtRbohE_O81211
 ANC-C3AB_AtE_OsFG_N3
 OsRbohA_Q0JJJ9
 OsRbohc_Q65XC8
 AtRbohF_O48538
 ANC-4AB_AtF-OsAC_N4
 OsRbohE_Q8S1T0
 OsRbohd_Q0DHH6
 AtRbohH_Q9FJD6
 AtRbohJ_Q9LZU9
 ANC-C2AB_AtHJ-OsDE_N3
 ANC-C6AB_INV_N3
 ANC-C3AB_INV_N3
 ANC-4AB_INV_N4
 ANC-C2AB_INV_N3
 DISCRIM_2-3-4-6AB

RSRGKICIGMD-GSDEFAVQMFDSDLARKRGIVKQVLTKDELKDFYEQLTD
 KSKFGHCIGMV-ESSEFVNELFEALVRRGTTSSSITKTLEFEFWEQITG
 RSRFGQCIGMV-GSEEFAVQIFDSLARPGITAQLLTKDQREFWEQLSD
 RSRFGQCIGMV-GSEEFAVOLFDSLARPGITAQVLTKDELREFWEQLSD
 RDNFGDCIGME-DSKEFAVGIFDALARPRRQELEIRISKEELEYDFWL---
 RDDFGEIGMV-DSKEFAVGIFDALARPRRNLERITREELYDFWLQISD
 RDDFGEVGVMV-DSKDFAVSVFDSLARPRRQKLEKITKDELHDFWLQISD
 RDDFGEVGVMV-DSKDFAVGVFDALARPRRQKLEKITKDELHDFWLQISD
 RSDFAECIGMT-ESKEFALELFDTLSRPRQMKVDTINKDELREIWQOITD
 RDDFPQCIGMT-ESKEFAMELFDTLSRPRQMQVDKINKEELREIWQOITD
 RSDFAQCIGMK-DSKEFALELFDALSRPRRLKVEKINHDELYEYWSQIND
 RTDFAQCIGMK-DSKEFALELFDALSRKRRRLRAEKISREELFEFWSQITD
 KESFGKCIGMG-DSKEFAGELVALARPRLNLEPDGITKEQLEFWEEEMTD
 QESFAKICIGMA-DSKEFASEVFVALARPRSIKPDGITKEQLEFWEEELTD
 KEKFGVCIGMG-DTMFEEAAYEALGRPRQIETNGIDKEQLEKFWEDMIK
 KDKFGVCIGMG-DTLEFAAKVYEALGRPRQIKTNGIDKEQLEKFWEDMIK
 KDKFGVCIGMG-DTKEFAGELYEALGRPRQIKTNGIDKEQLEKFWEDMIK
 --F---C---G-----F-----L-R-R-----Q---
 R-FG-C-GM---SK-FA---DAL-RP-----I---E-L---FW-QISD
 R-F---I---S-E-A-ELFD-L-R-----I---L---QI---
 --F---C-G-----FA-----RP-----G-----FW-----
 -----X---X-X-----X---X-X-----X---X-----XXXX

EF-hand I**EF-hand II**

OsRbohB_Q5ZAJ0
 AtRbohB_Q9SBI0
 OsRbohH_Q2QP56
 ANC-C6AB_AtB-OsBH_N3
 OsRbohF_Q0J595
 OsRbohG_Q69LJ7
 AtRbohE_O81211
 ANC-C3AB_AtE_OsFG_N3
 OsRbohA_Q0JJJ9
 OsRbohc_Q65XC8
 AtRbohF_O48538
 ANC-4AB_AtF-OsAC_N4
 OsRbohE_Q8S1T0
 OsRbohd_Q0DHH6
 AtRbohH_Q9FJD6
 AtRbohJ_Q9LZU9
 ANC-C2AB_AtHJ-OsDE_N3
 ANC-C6AB_INV_N3
 ANC-C3AB_INV_N3
 ANC-4AB_INV_N4
 ANC-C2AB_INV_N3
 DISCRIM_2-3-4-6AB

QGFDNRLRTFFDMVDKNADGRITAEEVKIIALSASANKLSKIKERADEY
 NSFDDRLQIFFDMVDKNLDGRITGDEVKEIIALSASANKLSKIKENVDEY
 PGFDAKLQIFFDMVDKNADGQITEEELKEVLTLTASANKLSKILERVDEY
 -----IVLSASANKLSKIKEQAEYY
 QSF达尔QIFFDMVDKNADGRITEEVKEIIMLSASANKLSRKEQAEYY
 QSF达尔QIFFDMADSNEDGKITREEIKELLMLSASANKLAKIKEQAEYY
 QSF达尔QIFFDMADSNEDGKITREEIKELLMLSASANKLAKIKEQAEYY
 NSFDSRLQIFFFMVDKNADGRITEEVKEIIMLSASANKLSRKEQAEYY
 NSFDSRLQIFFDMVDKNADGHITEAEVKIIIMLSASANKLSRKEQAEYY
 ESFDSRLQIFFDIVDKNEDGRITEEVKEIIMLSASANKLSRKEQAEYY
 QSFDSRLQIFFDMVDKNEDGRITEEVKEIIMLSASANRLSRKEQAEYY
 QNFDSRLRIFFDMCDKNGDGMLTEDEVKEVIVLVAANKLAKIKSHAATY
 KDLDCRLQIFFDMCDKNGDGMLTEEVKEVIVLVSASANRGNIKKNAAY
 KDLDCRLQIFFDMCDKNGDGMLTEEVKEVIVLVSASANRLVNIKKNAASY
 KDLDCRLQIFFDMCDKNGDGMLTEEVKEVIVLVSASANRGNIKKNAAY
 --FD-----VDK---DG-----E---L-AS-NKLSK-----EY
 QSF达尔QIFFD---N-DG-I-R-E---EL--LSASANKL-KIKEQA--Y
 -SFDSRLQI-FD-VDK---DG-I-E-EV-E-I-LSASAN-L-R---QAEED-
 -----RL---FFDMCDK-GDG-L-E-EV-E-I-LSA---N-L---IK---A-Y
 XX---XX---X-X-X-----X-----X-----X-X-X-X-----X-X-X-X

EF-hand II

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohc_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohd_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

TALIMEELDPNTNLGYIEMEDLEALLLQSPSEAAATTHSSKLSKALSMKLA
AALIMEELDRDNLGYIELHNLETLLLQVPSGSN-SANKRALNKMLISQKLI
TALIMEELDPDQLGYIDISNLESLLLPPSQAPSVTTHSSNISQLISQKLV
TALIMEELDPDNLGVIELSNLESLLLQPPSQAPSVTTHSSNLSQLLSQKLV
ASLIMEELDPEDLGVIELWQLEALLLQRDAYMNYSGSTAQWSQNLLGGGN
ASLIMEELDPENLGVIELWQLEALLLQRDSYMNYTASGAQWSQNLLGGGAAG
ASLIMEELDPENFGYIELWQLETLLLQRDAYMNYYTSGGVSTPRRNLLIR-
ASLIMEELDPENFGYIELWQLETLLLQRDAYMNYYTSGGVWTPRMNLLIR-
AALIMEELDPEGLGYIELWQLETLLLQKDTYMN-----YTSQALSQNL
AALIMEELDPEQLGYIELWQLETLLLQKDTYVN-----YTSQALSQNL
AALIMEELDPERLGVIELWQLETLLLQKDTYLN-----YTSQALSQNL
AALIMEELDPLGLGYIELWQLETLLLQKDTYLN-----YTSQALSQNL
ASLIMEELDPDPRGYIEIWQLETLLRGMVSAQAA-EKMKTTSLLARTMI
ASLIMEELDPDHGRGYIEIWQLETLLRGMVTAQGP-EKVKLASASLARTMV
ASLIMEELDPDHKGYIEMWQLEIILTGMVTNADTK---MKKSQTLTRAMI
ASLIMEELDPNEQGYIEMWQLEVLLTGVISNADSK---VVRKSQQLTRAMI
ASLIMEELDPDHQGYIEMWQLEIILRGMVSNETKKLLMMKSQTLTRAMI
--LI-EELDD---G-I----L---LLL-----S---
A-LIMEELDPE-GYIELWQLE-LLL-D-YM-Y-----
AALIMEELDPE-GYIE-WQLETLLLQKDTY-N-----TSQALSQNL-
--LIMEELDPE-G-I-----LL-----L---M---
-----X-----XXXXXX-----XXXX-XXXX-----

TMD - I

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohc_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohd_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

SNKEMSPVRYHQWQQFMYFLEENWKRSWVMTLWISICIALFIWKFIQYRNR
PTKDRNPVKRFAMNISYFFLENWKRIWVLTLWISICITLFTWKFIQYKRK
PTKDRNPRLRGLRRLSYFMEDNWKRVWVMALWAINAGLFTWKFMAYKRH
PTKDRNPRLRGLRRLSYFMEDNWKRVWVMALWAINAGLFTWKFMAYKRH
DWRRRWSPRRAARAQVAEEENVRRAWVLALWFAAMAGLFIAWKFVQYRRT
GW---G---VRKAARVRVAEEENVRRAWVALWFAAMASLFWVKFVQYRRT
---RHVVQCRKKLQCLILDNVQRSWVLLVVVMLMAILFWVKFLEYREK
---RHVVQCRCSKKLQCLILDNVQRAWVLLVVWMAMAILFWVKFLEYREK
GLRKKSIRKISTSLSYYFEDNWKRWLVLALWIGIMAGLFTWKFMQYRNR
GLRKRSPIRKISTKLSSYLEDNWKRWLVLALWIGIMAGLFIWKFIQYRHR
GLRGKSRIHRMSSDFVYIMQENWKRIWVLSLWIMIMIGLFLWKFFQYKQK
GLRKSPPIRMSRRLVYYLQENWRRLWVLTWVCIMIGLFTWKFIQYKRK
PSRYSRPLKRHVSRTVDVFHENWKRIWLVALWLVNVGLFAYKEFYERR
PSSHRPMQRRENKTVDFIHENWKRIWVLSSLWAINLIALFMYKVFQYSSR
PERYRTPMSKVSVTAELMHENWKKLWLVLALWAIINVYLFMWKYEEFMRN
PKRYRTPTSKVYVVTAEMLYEHWWKKIWIWVTLWLAVNVVLFMWKYEEFTTS
PKRYRTPMSKVSVTAEFMHENWKKIWIWVTLWLAINVVLFMWKFEEFMRS
----P-----F---NW-R-W---LW-----LF-WKF---Y---
-----W-R-W---W-----WF-W---Y---
--R---I-----Y---NW-R-W---W---M-GLF-WKF---Y---
P---R-P-----W-W---LW---N-L---K---
X-X-X-X-----X-----X-X-X-X-X-----

A-loop**TMD - II****B-loop**

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohc_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohd_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

AVFGIMGYCVTTAKGAAETLKFNMALVLPLVCRNTITWLRSTQVGAVVP
TVFEVGMGYCVTVAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
PTFDVGMGYCVCVAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
PVFDVGMGYCVCVAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
PAFRVMGYCILPTAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
PAFRVMGYCILPTAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
AAFKVMGYCILPTAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
AAFKVMGYCILPTAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
YVFDVGMGYCVTTAKGAAETLKLNMAIILLPVCNRNTITWLRSTSCKGSVP
YVFNVMGYCVTTAKGAAETLKLNMAIILLPVCNRNTITWLRSTSCKGSVP
DAFHVMGYCILPTAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
DAFQIMGYCILLAAGKAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
AAFQVMGHCVCVAKGAAEVILKLNMALILLPVCNRNTITWLRSTSCKGSVP
DAFQVMGHCVCVAKGAAEVILKLNMALILLPVCNRNTITWLRSTSCKGSVP
PLYNITGRCVCAAKGAAETLKLNMALILVPVCRKTLTILRSTF-LNRVVP
PLYNITGRCLCAAKGAAETLKLNMALILVPVCRKTLTILRSTF-LNRVVP
PLFNITGYCVCVAKGAAETLKFNMALILLPVCNRNTITWLRSTSCKGSVP
--F---GYCV--AKG-AET-KFNMAL-L-P-CRNTITW-R----G---P
--F-VM-YC---AKGAAETLK-NMAL-LLPVCNRNTITWLRSTSCKGSVP
----MG-C---AK---A-TL---MA-I---P-CRNTIT-LR-T----P
----C-C-AK---AE-LK-NMA-I---R-TLT---R---L---P
-----X-----X-----X-----X-----X-----X-----X-----

TMD - III

C-loop

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohc_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

FNDNINFHKVIAAGVAVGVALHAGAHLTCDFPRLHASDAQYELM-KPFF
FDDNINFHKVVAFGIAGVIGILHAISHLACDFPRLHAKNVEFEPM-KKFF
FNDNINFHKVVAGGVVVGVALHGVTHTCDFPRLHASDAAYEPM-KKYF
FNDNINFHKVVAGGVAVGVALHVATHTCDFPRLHASDAAYEPM-KAYF
FDDSTIFHKVEATAIALGICHTAGTHLACDFPRLGSSREYEYLL-SGFF
FDDNITFHMKIATAIVVGITLHAGNHLCDFPRLIASGPEEYRLV-ADAF
FDDNINFHKIIACACAIAIGILVHAGTHLACDFPRIINSSPEQFVL-ASAF
FDDNINFHKIIACACAIAIGILVHAGTHLACDFPRLINSSPEQFVL-ASAF
FDDNINFHKTIAAAIVVGIIHLHAGHNHLVCDFPRLIKSSDEKYAPL-GQYF
FDDNINFHKTIAAAIVVGIVLHGGHLHVCDFPRLIGSSEEKYAPL-GKYF
FDDNINFHKTIAGAIVAVVAVLHAGDHLCDFPRIVRATEVDYNRYLFHYF
FDDNINFHKTIAGAIVIGILHAGDHLCDFPRLVSTSESYEKYLKGVF
FDDNINFHKVIAATIAATAVHTLAHVTCDFPRLINCPSDKFMATLGPNF
FDDNINFHKVIALTIAIGAATHTLAHVTCDFPRLVSCPRDKFEATLGPYF
FDDNINFHKVIAVMIAFQALLHTALHIFCNYPRLSSCSYDVFLTYAGAAL
FDDNINFHKLIAVIAVISLHTALHMLCNYPRLSSCPNFYSDYAGNLL
FDDNINFHKVIAVAYIAAFQALIHTALHILCNYPRLSSCPYDVFLTYAGALL
F-DN-NFHKV-A-G---H---HL-CDFP-LLH-----F
FD-I-FHK---A-AI----HAG-HL-CDFP---S-E-L---F
-D-NINFHKT-A-A----LH-G-H-CDFP---Y-----F
FDDNI-FHK-A----H-H-C-P-L-C----G---
-----X-----XX-----XX-----X-X-X-X--X-X

TMD-IV

D-loop

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohc_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

GEKRPPNYWWFVKGTBGTWTGVVMVLMAIATLTLAQWPWFRRNKLDSNPLK
GDERPENYGWFMKGTBGTWTGVTMVVLMLVAVYVLAQSFRNRRANLPKSLK
GQTRIPDYWWFVRGVEGITGVIMVVLMAIATLAHPWFRRSKLDSDNPLK
GQKRPPNYWWFVRGVEGITGVIMVVLMAIATLAHPWFRRNKLDSNPLK
GASRP-TYRGLLLAGVEGTGIVMVVLMSFTLATRPLRKREAPLPFPLG
GPEKP-TYVGLLSGVEGTGIVMVVLMTSFTLATHPFRKGEKGGGSPFN
NGTKP-TFKDLMTGARGITGISMVILTTIAFTLASTHFRRNRRVRLPAPLD
NGTKP-TFKDLMTGVEGTGISMVILMTIAFTLATLATHFRRNRRVRLPAPLD
GEIKP-TYFTLVKGVEGTGIVMVVCMIIAFTLATRWFRRSLVKLPKPF
GETKP-TYTLTVKGVEGTGIVMLVCMIIAFTLATRWFRRSLVKLPKPF
QTKQP-TYFDLVKGPEGITGILMVIILMIIISFTLATRWFRRNLVKLPKPF
GDRKP-SYVLDLVKGVEGTGVLMVVLMIIAFTLATKWFRRNLIKLPKPF
GYRQP-TYADLLESAPGTGILMIIIMSFTLATHSFRRSVVKLPSPHL
NYVQP-TYSSLVASTBGTWTGILMIIIMSFTLATHSFRRSVVKLPSPHL
GNTQP-SYLGMLMTSVITGVLMIFFMGFSFTLAMHYFRRNIVVKLPKPF
GAKQP-TYLGMLMLTPSVTGVLMIIFMGISFTLAMHYFRRNIVVKLPKPF
GYKQP-TYLGMLMLTSVITGVLMIFFMGFSFTLAMHYFRRNIVVKLPKPF
G-----Y-WF---G-TG---VLM---LA---W---R-----
----P---L---G-BG-TG---MV-L---FTLA---R-----
----P---Y---L---G-G-TG---M-----F-LAT-WFRR-L-K---PF-
---QP-----G-----M---F-LA-H-FR---LP---
X-----X-X-X-X-----XX-----XX-----XXX-----X-X-X-X

TMD-V

E-loop

TMD-VI

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohc_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

KMTGFNAFWFTHHLFIVYVTLFVHGTCLYLSRKWYKTTTWMYLAVPVVL
RLTGFNAFWYSSHLLFIVYVLLIVHGFYVYLSKEWYHKTWTWMLAVPVLL
RLSGFNMFWYSSHLLFIVYIAYVVFVHCVCLYINRTWKQTTTWMLAIPILL
KLSGFNMFWYSSHLLFIVYVLLFIVHGCVCLYISRKWYKTTTWMLAIPILL
HLAGFNAFWYSSHLLFIVYVLLIVHGFWMFVLTWKWHQRTTWMYIAVPLML
RLAGFNAFWYSSHLLGIVYLLIAHGYFLFLVRRWLKTTTWMYISVPLML
RLTGFNAFWYTHHLLVVVYIMLIVHGTLFLFADWKWYQTTTWMLAISVPLVL
RLTGFNAFWYTHHLLVVVYILLIVHGTLFLADWKWYQTTTWMLAISVPLVL
KLTGFNAFWYSSHLLFIVYVLLIVHGCVCLYIHGVYRRTTWMLAISVPLVL
KLTGFNAFWYSSHLLFIVYVLLIVHGCVCLYIHGVYRRTTWMLAISVPLVL
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HLAGFNAFWYAHLLVLAYVLLVHSYFIFLTREWYKTTTWMLAISVPLVL
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VLAGFNAFWYAHLLVLAYVLLVHSYFIFLTREWYKTTTWMLAISVPLVL
VLAGFNAFWYAHLLVLAYVLLVHSYFIFLTREWYKTTTWMLAISVPLVL
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RLAGFNAFWYAHLLVLAYVLLVHSYFIFLTREWYKTTTWMLAISVPLVL
---GFN-FW---HHL---IVY---HG---Y---W---TWMY-A-P---
-L-GFN-AFWY-HHL---VY---L---HG-F---W---TWY-YI---P---L
--TG-NAFWYSSHLL---Y---L---HG---W---TWMY---VP---
-LAGFN-FWYAH-LL---Y---L---H-Y---W---TWM-----P---
---X-----X-X-X

TMD-VI

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohC_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

YVSERILRLFRSH-DAVGIQKVAVYPGNVLALYMSKPPGFRYRSGQYIFI
YAFERLIRAFPGAKAVKVAVYPGNVLISLYMSKPKGFKYTSQYIYI
YAGERIFRALPSGFTTVRIEKVAVYPGNVIAIHMTKPHGFKYKSGQYIYV
YAGERLLRALPSGFTTVRIEKVAVYPGNVLALHMSKPHGFKYKSGQYIYV
YVGERTLRAFFSKAYAVKILKVCILPGLNVITITMSKPYGFYRSGQYIFL
YVGEMRLRALPSNAYAVKILKVCILPGLNVITITMSKPYGFYRSGQYIFL
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VVAERSLRACSKHYSVKILKVSMLPGEVLSLIMSCKPPGFKYKSGQYIFL
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YGGERTLRYFRSGSYSSVRLLKVAIYPGNVITLQMSKPPTFRYKSGQYMFV
YASERILRFLSGLYTVRLGKVAIYPGNVITLQMSKPPTFRYKSGQYMFV
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YSCERTIRRVRESSYGVTVIAAIYPGNVLSIHMNKPFSSFKYKSGMYMFV
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YASERLFSRLOEHNNHRVNIIKAIVYSGNVNLALYMTKPPGFKYKSGMYMFV
Y---ER---R-----V---V---Y-G-----KP-GF-Y-SQY---
Y---ER---R---RS---V---V---KV---LPG-V---SKP-GF-Y-SQYIFL
---ER---R-FRSG---VR---KVAIY-GNVITLQ---KP---FRYKSGQYMFV
Y---ER-----A---Y-G-VL-----P---FKY-SGMY-F---
-----X-XXXX---X-XXXXX---X---X-----X-----X---

FAD-I

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AtRbohB_Q9SBI0
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJJ9
OsRbohC_Q65XC8
AtRbohF_O48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DHH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

KCTAVSPYEWHPFSITSAPGDDYLSVHIRTGIDWTSRLRTVFSEACRPPT
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NCGEVSPFHWHPFTITSAPDDSYLSMHIRCRGIDWTSFFRAIFSQCICRPPM
NCSEVSPFHWHPFTITSAPGDDYLSMHIRCRGIDWTSRLRALFSQVCRPPT
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QCPTISPFWHPFSITSAPGDDYLSVHIRTNGIDWTRQELKRIFVENY-FSP
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QCPAVSPFWHPFSITSAPGDDYLSVH1VRLQGIDWTRELKRVFAACEPPA
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KCPDISKFHWHPFSITSAPGDDYLSVH1RALGIDWTTELRNLFAKTCCEPHQ
-C---S---WHPF---SA---D---Y-S---IR---GIWT-----C---
QCP---S---FWHPF---ITSAPGD---VH---GIWT---EL-----
QC-AVS-FWHPFSITSA---D---S-H-R-LGIWT---EL---F---C---P---
K-P---S-FWHPFSITSAP---LSVH-R---GIWT---E---F-----
X-XX---X---X-X---X-X---X-X-----X-X-----X-X-

FAD-II

EGESGLLRADLSDEKARFPKLVDGPGYGAPAQDYREYDVILLIGLGIGAT
TSQSGLLFIADIG-NITRFPPLLIDGPGYGAPAQDYRNYDVILLVGLGIGAT
NGQSGLLRADCM-HHSRFPKLIDGPGYGAPAQDYWKYDVILLIGLGIGAT
NGQSGLLRADFA-NNSRFPKLIDGPGYGAPAQDYRKYDVILLIGLGIGAT
SAFGALGMAEQK-----PPRLLVDGPGYGAPAQDFRNYDVILLVGLGIGAT
HAFSELGATEPR----PRLLVDGPGYGAPAQDFRNYDVILLVGLGIGAT
CSFSAYCNIDMI----RPKLLVDGPGYGAPAQDYRSYDVILLIGLGIGAT
CSFGAYCNIDMI----RPKLLVDGPGYGAPAQDYRSYDVILLIGLGIGAT
GGKSGLLRADE--TKKILPKLIDGPGYGSPAQDYSKYDVILLVGLGIGAT
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GGKSGLLRADE--TJKSLPKLIDGPGYGAPAQDYRKYDVILLVGLGIGAT
SGKSGLLRADE--TJKSLPKLKIDGPGYGAPAQDYKKYDVILLVGLGIGAT
TSKATLRSLETTDA---FPKVLIDGPGYGAPAQNYKKYDVILLIGLGIGAT
SSKATLARLETTDG---FPKVFIDGPGYGAPAQNYKKYDVILLIGLGIGAT
APPNSLMRMETRVN-P-FPKIFIKGPYGAPAQNYQKFDILLLVGLGIGAT
KPPNDLIRMETRAN-P-FPRIFIKGPYGAPAQSYYQKFDILLIGLGIGAT
APPNSLMRMETRANYP-FPKIFIKGPYGAPAQNYQKFDILLIGLGIGAT
-----A-----P---DPYG-PQDY---Y-V---LL-GLGIGAT
---F-----P-L-VDGPYGAPAQD---DVILL-GLGIGAT
-G-SGLLR-E---K---P-L-ID-PYG-P---D---YDVILLVGLGIGAT
---L-R-ET-----P---I-GP-GAPAQ-Y---D-L-L-GLGIGAT
-XXXXXXXXX---X-----X-----X-----X-----X-----X-----

NADPH-I

NADPH-I

```

OsRboH_B_Q5ZAJ0
AtRboH_B_Q9SB10
OsRboH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRboH_F_Q0J595
OsRboH_G_Q69LJ7
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ANC-C3AB_AtE_OsFG_N3
OsRboh_A_Q0JJ9
OsRboh_C_Q65XC8
AtRboh_F_Q48538
ANC-4AB_AtF-OsAC_N4
OsRboh_E_Q8S1T0
OsRboh_D_Q0DH6
AtRboh_H_Q9FJD6
AtRboh_J_Q9LZU9
ANC-C2AB_AthJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2B_INV_N3
DISCRIM 2-3-4-6AB

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P1ISILRDLNNNIKLADLMDL--T---ASAYRTSRAFYWVTREPGS
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P1ISILKDLNNSRDEQ-----YTTATPTKKAVKAFYWVTREPGS
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P1ISILKDMNLHLKPGIPKSGQ----KKFPORAYFYWVTREQAS
P1ISI-----LN-----T---Y-YW-TRE-GS
P1ISI-DLNN-----A-FYWVTREE-S
P1ISILKDL--I-MEE-----TTN-FYWVTREQ-S
P1-ISI-KD-LN-K-----R-F-WVTREQ-S
-----X-XXX-----XXXXXX-----XX

```

OsRbohB_Q5ZAJ0
AtRbohB_Q9SBIO
OsRbohH_Q2QP56
ANC-C6AB_AtB-OsBH_N3
OsRbohF_Q0J595
OsRbohG_Q69LJ7
AtRbohE_O81211
ANC-C3AB_AtE_OsFG_N3
OsRbohA_Q0JJ9
OsRbohC_Q65XC8
AtRbohF_Q48538
ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LZU9
ANC-C2AB_AtHJ-OsDE_N3
ANC-C6AB_INV_N3
ANC-C3AB_INV_N3
ANC-4AB_INV_N4
ANC-C2AB_INV_N3
DISCRIM_2-3-4-6AB

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FEWFRGVMNEVADRDAGIELHNHNTSVEEGDARSALVTMLQALHHAF
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FEWKFGVMNEVAEMDKKGVLIELHNLYLTSVYEEARDARSTLLSMVQALNHA
FEWFKGVMNEVAEMDKKGVLIELHNLYLTSVYEEARDARTTLMSVQALNHA
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FDWFKGVMNEIAELDQRNIEIEMHNLYLTSVYEEGDARSALITMLQALNHA
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FDWFKGVMDDIAEYDTHVIEMHNLTSMYEAGDARSALIAMVQLQHAF
FEWKFGVMDIAVYDTNVIEMHNLTSMYEAGDARSALIAMVQLQHAF
FEWFKGVMDIAEYDNHVIEMHNLTSMYEEGDARSALIAMVQLQHAF
-EWF---M-----D----ELHN-C--V--EGD--SAL--MLQ-----F
--WF-GVM-E---MD-G-IE-HNLYLTSVY-E-DAR-TL--M-QA--HAF
FDWFKG-MNE-AE-DQ---IEMHNLTSVYEEGDARS-L-TM-QAL-HAF
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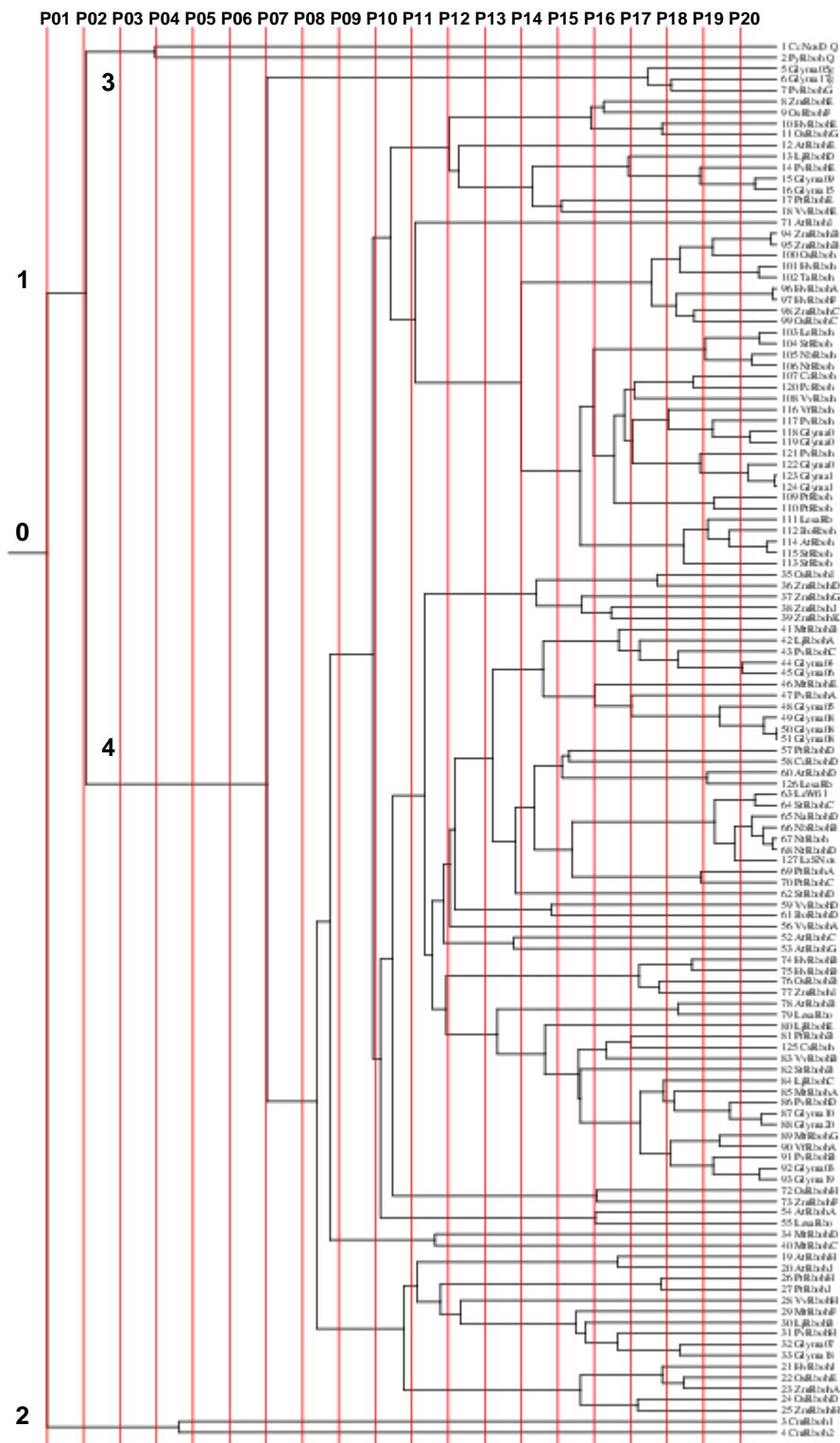
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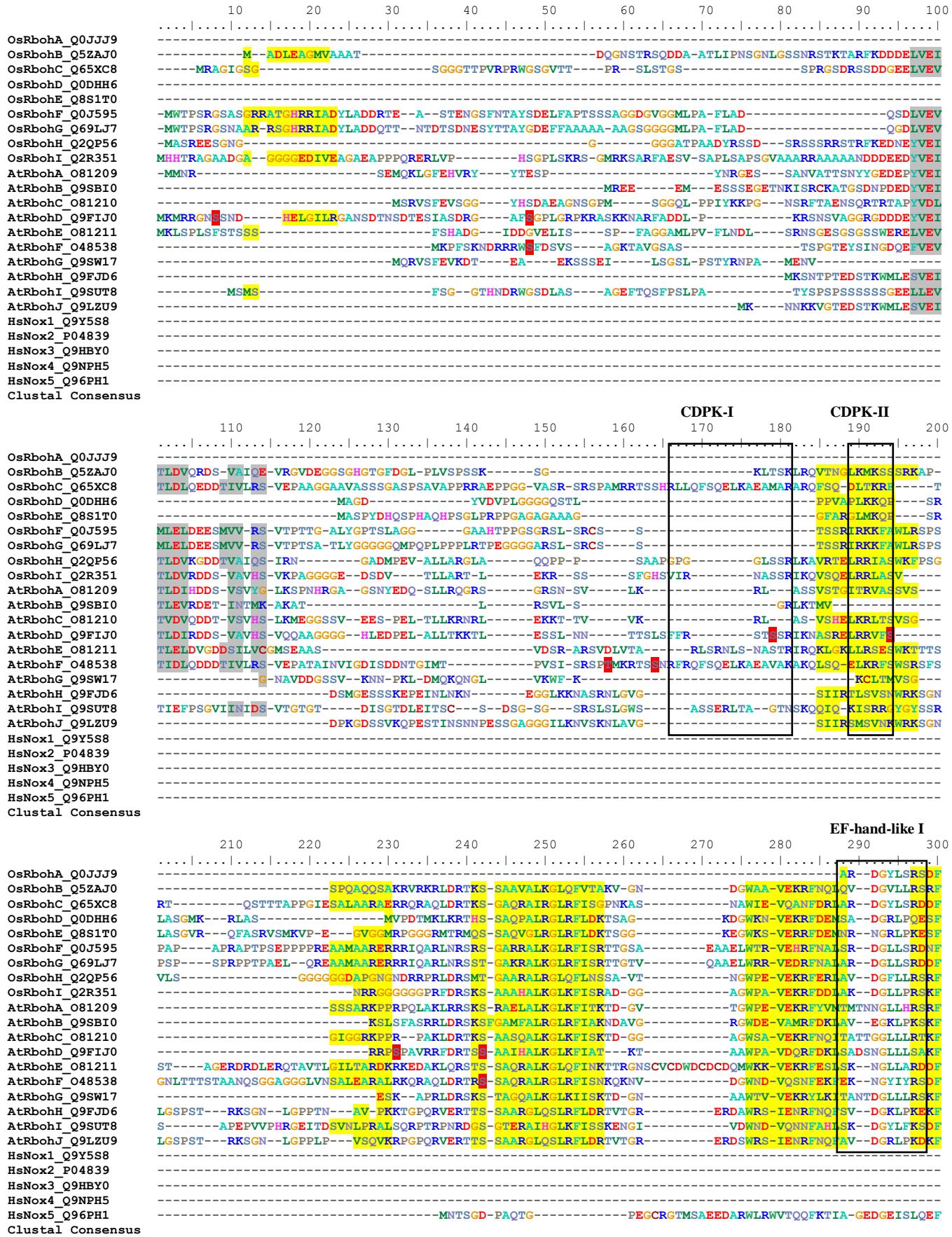
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OsRbohC_Q65XC8
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ANC-4AB_AtF-OsAC_N4
OsRbohE_Q8S1T0
OsRbohD_Q0DH6
AtRbohH_Q9FJD6
AtRbohJ_Q9LUZ9
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ANC-C6AB_INV_N3
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DISCRIM_2-3-4-6AB

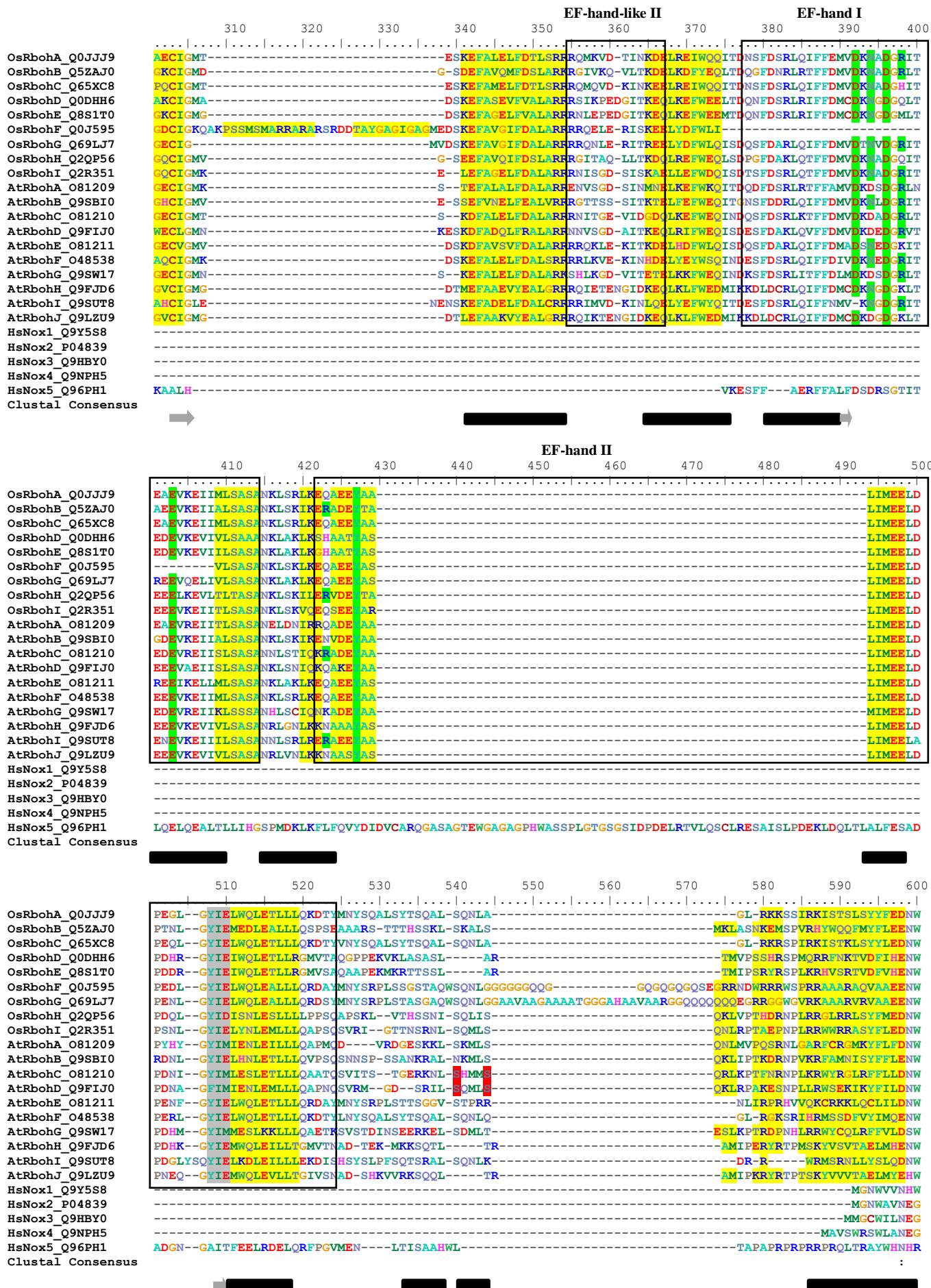
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SG IDIV SGTR VR TH FARP NWRS VF KHV AV NHN QR VG V F Y C G NT I I GEI
NGV DVS SGTR VR TH FARP SWRD VF KRV A VH NQG QR VG V F F C G D Q AL TPEI
SGDV VS SGTR VR TH FARP NW RDVF KRV A VH NQG QR VG V F Y C G D Q AL TPEI
HGVD I SGTR VR TH FARP NW KE VF TRIA SKH PNST VG V F Y CG K P LAKEI
HGVD I SGTR VR TH FARP NW KE VF TRIA SKH PNST VG V F Y CG AP LAKEI
HGVD I SGTR VR TH FARP NW KE VF SSI ARK H PN ST VG V F Y CG I Q TVAKEI
HGVD I SGTR VR TH FARP NW KE VF SKI AS KH PNST VG V F Y CG I Q TVAKEI
NGVD I SGTK VR TH FARP NW RK VL SKISS KH P YA KIG V F Y CG AP LAQEI
NGVD I SGTK VR TH FARP NW FK VL SKI AS KH P YA KIG V F Y CG AP LAQEI
NGVD I SGTR VR TH FARP NW KK VL LT KSS KH CNAR I G V F Y CG VP LV GK EI
NGVD I SGTR VR TH FARP NW KK VF SKM CS KH CNR G I G V F Y CG AP LAKERI
NGVD I SGSR IR TH FARP NW RK VF SD LANAH KNS RIG V F Y CG SP LT KQI
NGVD I SGSK IR TH FARP NW RK VF SD LANAH QNS RIG V F Y CG SP LT KMI
NGVD I SESR IR TH FARP NW RK VF SEL SS KH EAC RIG V F Y CG SP LV RP I
NGVD I SESR IR TH FARP NW RK VF SEL SNK HETS RIG V F Y CG SP LV RP I
NGVD I SESR IR TH FARP NW RK VF SEL ANTHEAS RIG V F Y CG SP LV KP I
-G-D-S-T-V-THF-RP-WR-V-----GVF-CG-----I
HGVD I SGTR VR TH FARP NW-EVF--IA-K-P--TVG V F Y CG --A-I
NGVD I VSG--RTHFA-PN-----KH-----GVF-C--P-L--EI
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X-----X-X-----X-X-X-X-----XX-----X-X

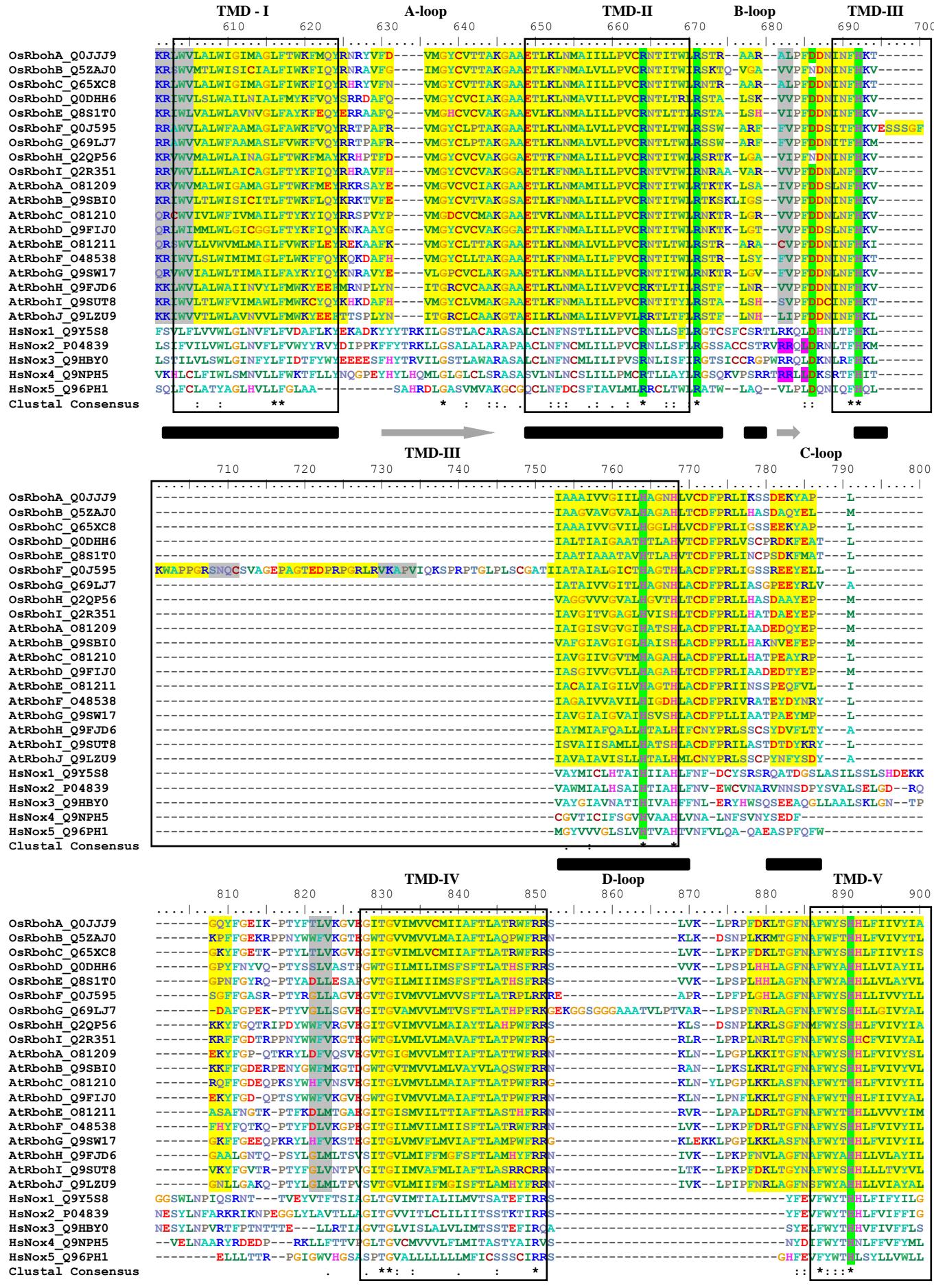
S2 File

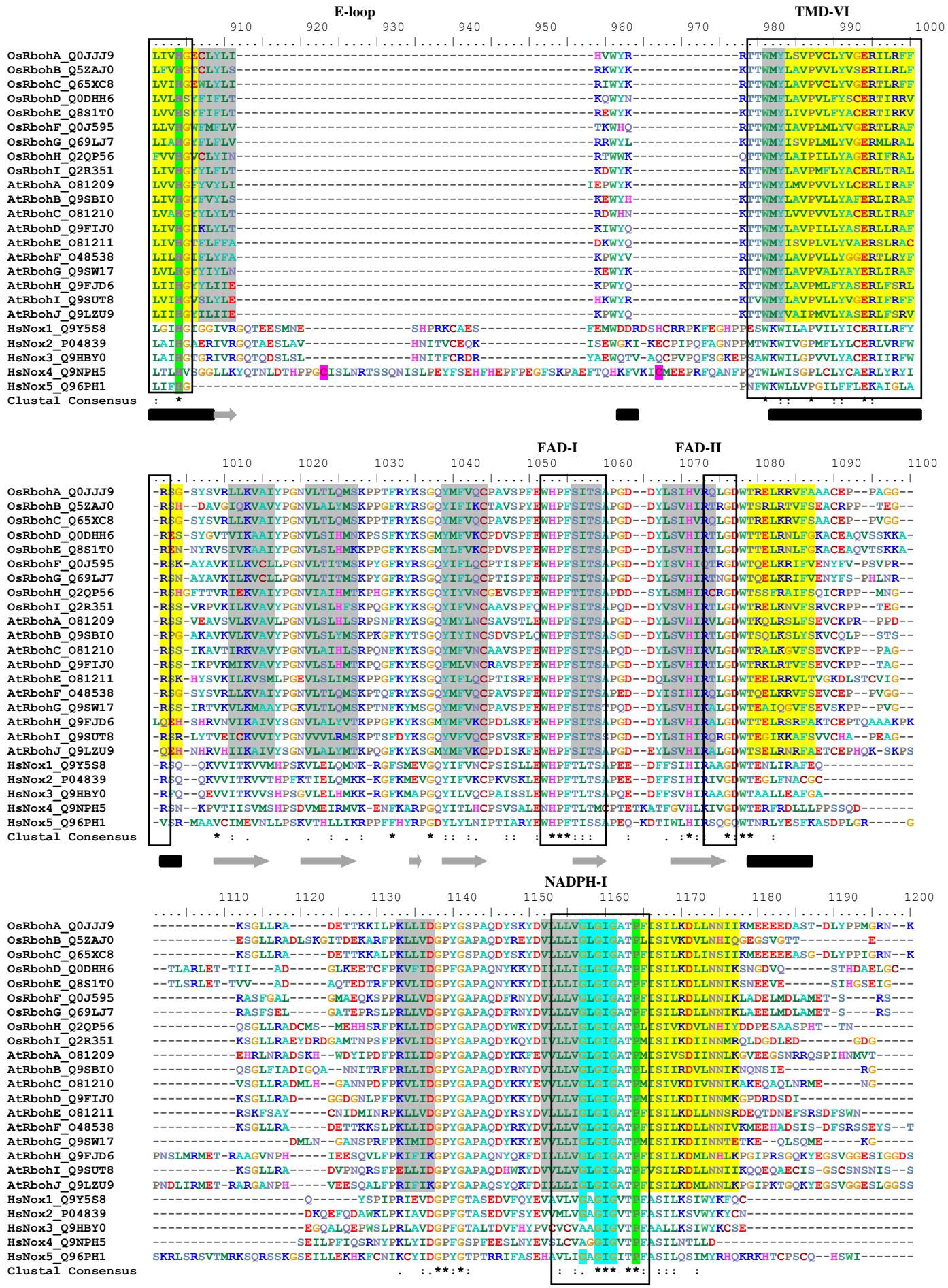
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ANC-C6AB_AtB-OsBH_N3	RRLSQDFSHKTTFKFVFKENF
OsRbohF_Q0J595	KKLSLDMSHKTTTRFHFKKEYF
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AtRbohE_081211	KKQAQDMSQKTTTRFEFHKEHF
ANC-C3AB_AtE_OsFG_N3	KKQAQDMSQKTTTRFEFHKEHF
OsRbohA_Q0JJ9	SKLCHEFNGKCTTKFEFHKEHF
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AtRbohJ_Q9LZU9	KSLCQEFSLESSTRFTFHKENF
ANC-C2AB_AtHJ-OsDE_N3	KELCQEFSLNSSTRFTFHKENF
ANC-C6AB_INV_N3	-----DF----T-T-F-FHKEN-
ANC-C3AB_INV_N3	K-----T-TRF-FHKE-F
ANC-4AB_INV_N4	--LC---N----KFEFHKE-F
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DISCRIM_2-3-4-6AB	X-XX-XXX--X---X---X-

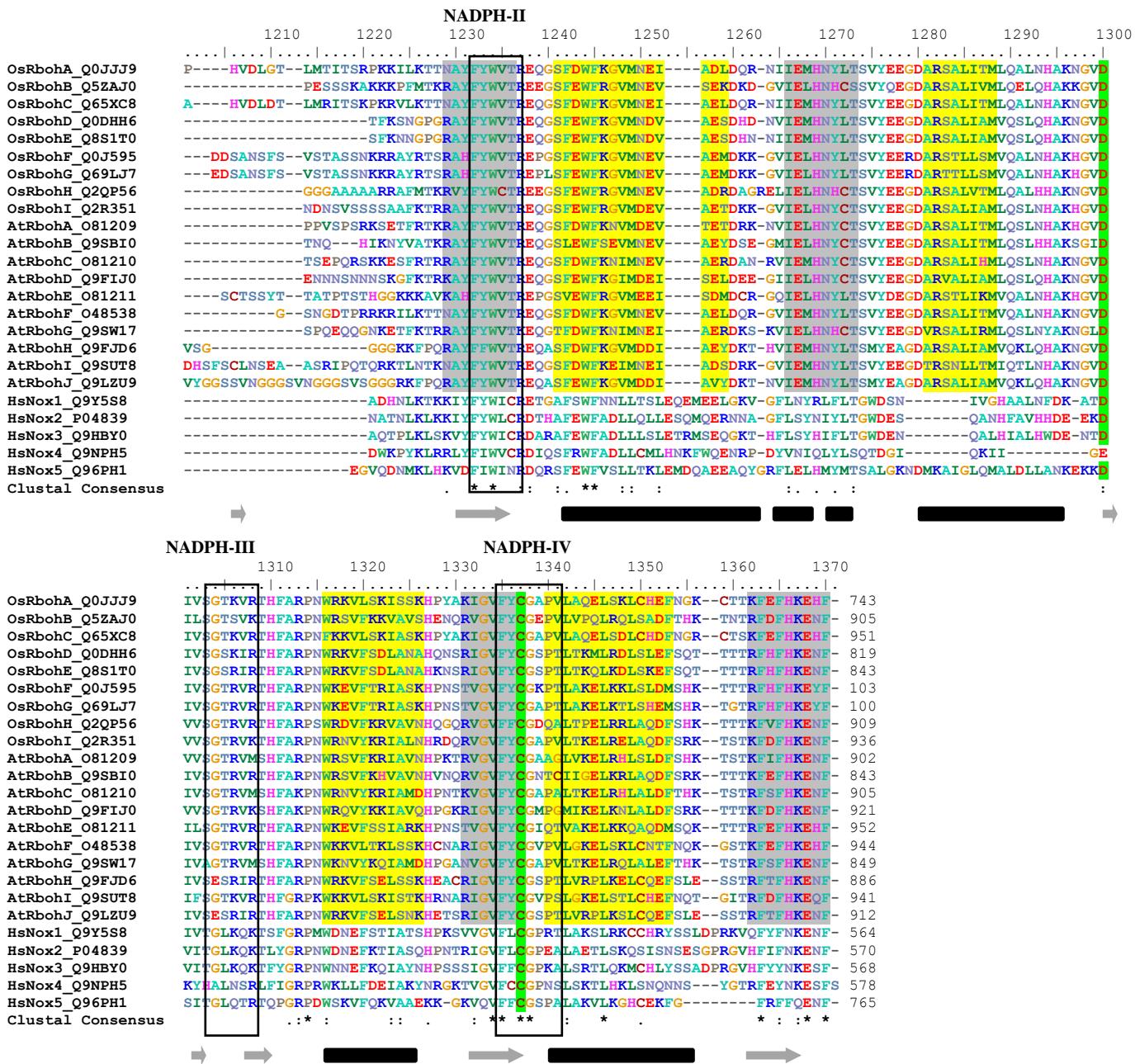




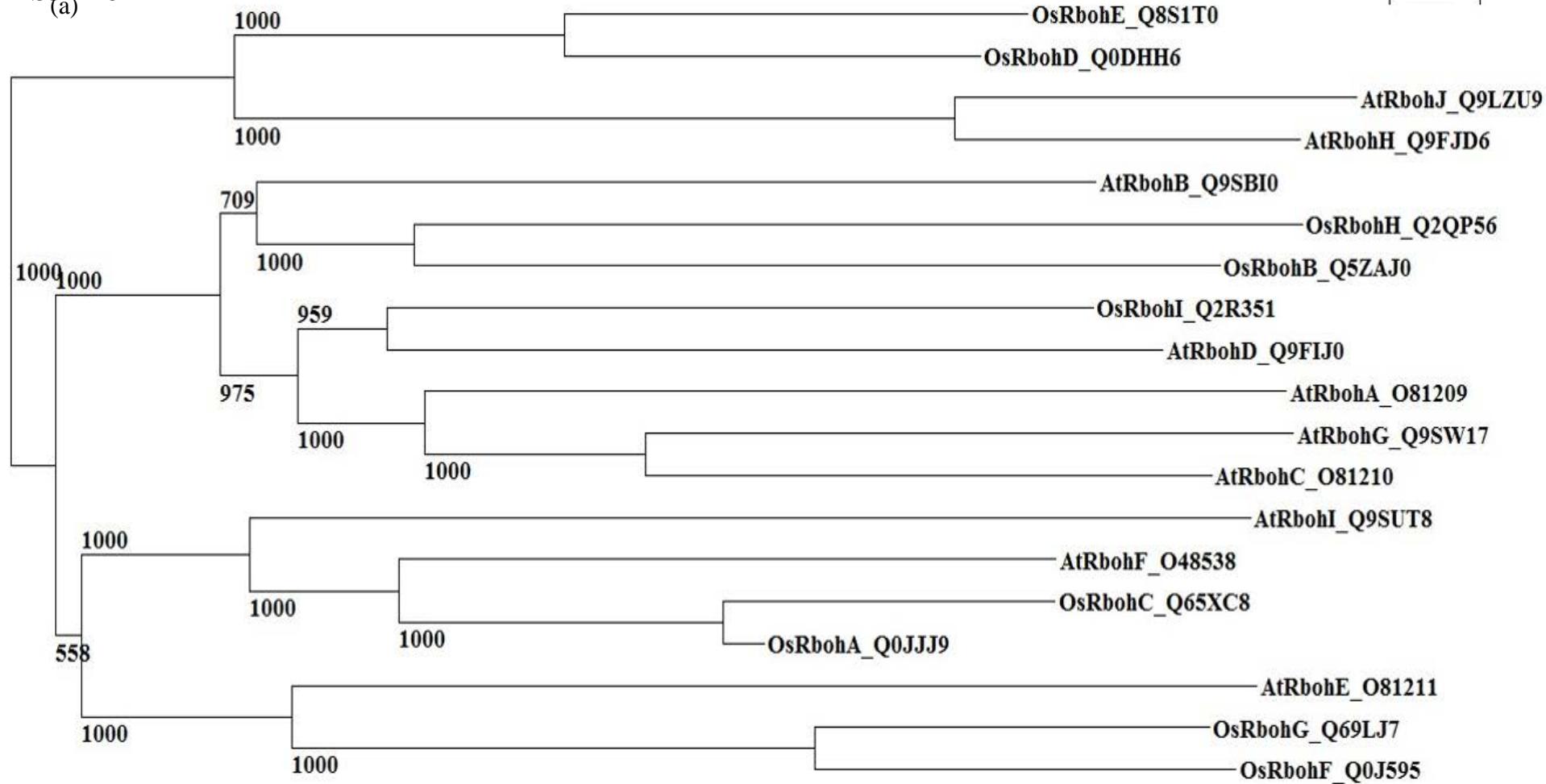








(a)



Rbohs	Putative Orthogous		
	InParanoid 8	OMA Browser	Ortholog ID
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AtRbohB	-	OsRbohB	OsRbohI
AtRbohC	OsRbohB	-	OsRbohI
AtRbohD	OsRbohB	OsRbohI	OsRbohI
AtRbohE	OsRbohG, OsRbohF	-	OsRbohG, OsRbohF
AtRbohF	OsRbohC, OsRbohA	OsRbohA	OsRbohC
AtRbohG	-	-	OsRbohI
AtRbohH	OsRbohE, OsRbohD	OsRbohE, OsRbohD	OsRbohE
AtRbohI	-	-	OsRbohC
AtRbohJ	OsRbohE, OsRbohD	OsRbohE, OsRbohD	OsRbohE
OsRbohA	AtRbohF	-	-
OsRbohB	AtRbohD, AtRbohC	AtRbohB	AtRbohB
OsRbohC	AtRbohF	-	AtRbohI, AtRbohF
OsRbohD	AtRbohH, AtRbohJ	AtRbohH, AtRbohJ	AtRbohJ, AtRbohH
OsRbohE	AtRbohH, AtRbohJ	AtRbohH, AtRbohJ	AtRbohJ, AtRbohH
OsRbohF	AtRbohE	AtRbohE	AtRbohE
OsRbohG	AtRbohE	AtRbohE	AtRbohE
OsRbohH	-	-	AtRbohB
OsRbohI	-	AtRbohD	AtRbohD

Ca-interacting residues in template 3A8R (D-242, N-244, D-246, R-248, E-253)

RMSD_Monomer (C-alpha atoms)

Deletion associated with Ca-binding site on EF-I in 2 Rbohs : OsRbohF (Major deletion), AtRbohI (Minor deletion)

Mutations suggested for Ca-binding site on EF-I in 5 Rbohs : AtRbohA,C, D, G, J

Insertions associated with N-ter

Deletions associated with N-ter

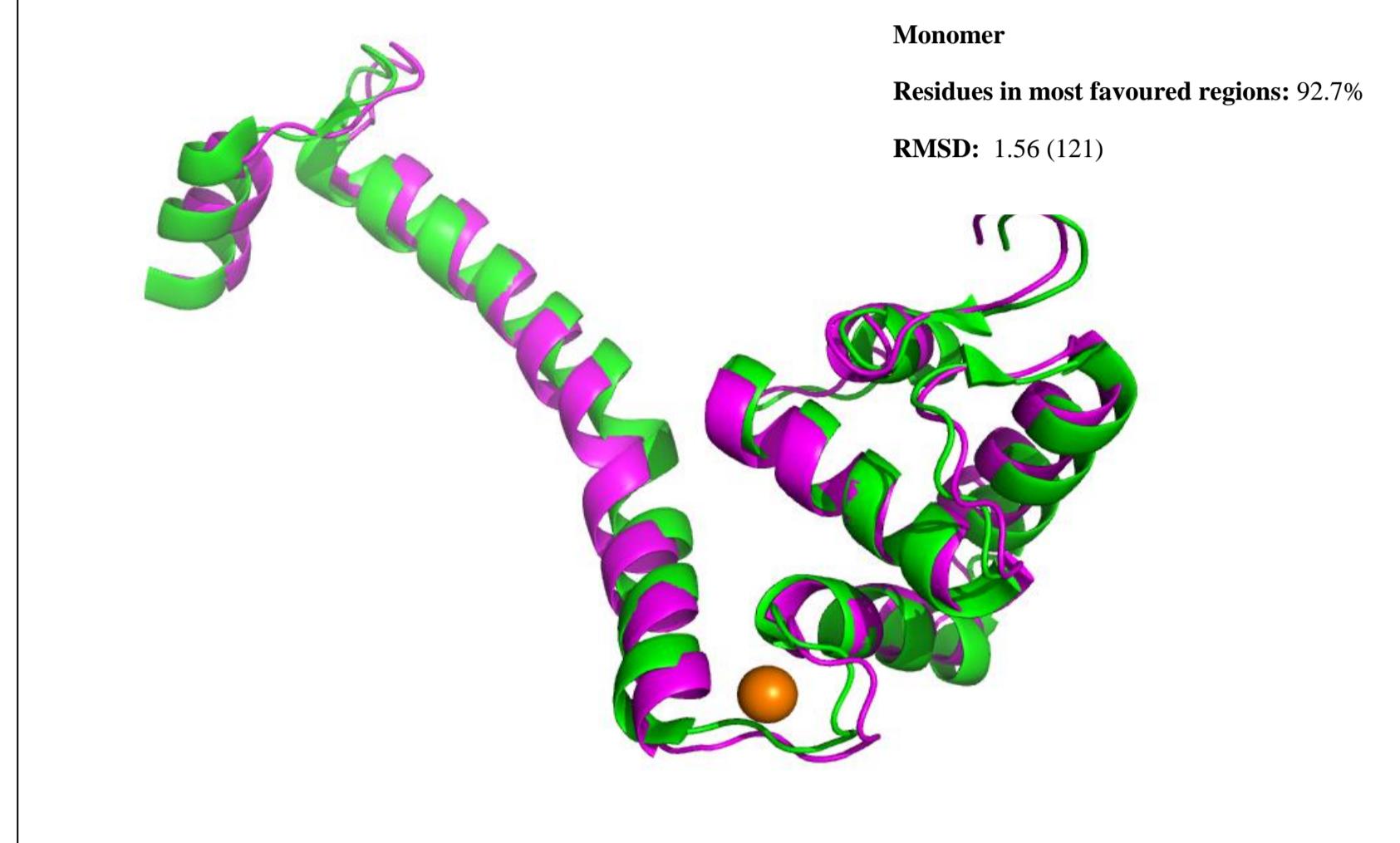
1. OsRbohA (NP_001044165 – 143 aa)

- Sequence alignment of OsRbohA with template using **Modeller9v8** is given as follow

Model: OsRbohA.B99990001.pdb

- Edited alignment

3A8RA QVDGVLLRSRGKCIQMDGSDEFAVQMFDSLARKRGIVKQVLTDELKDFYEQLTDQGFDNRLRTFFDMVDKNADGRILTAEEVKEIIALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDLEAL
OsRbohA ARDGYLSRSDFAECIGMTESKFALELFDTLSRRQMKVDTINKDELREIWQQITDNSFDSRLQIFFEMVDKNADGRITEAEVKEIIMLSASANKLSRLKEQAEYYAALIMEELDPEGLGYIELWQLET



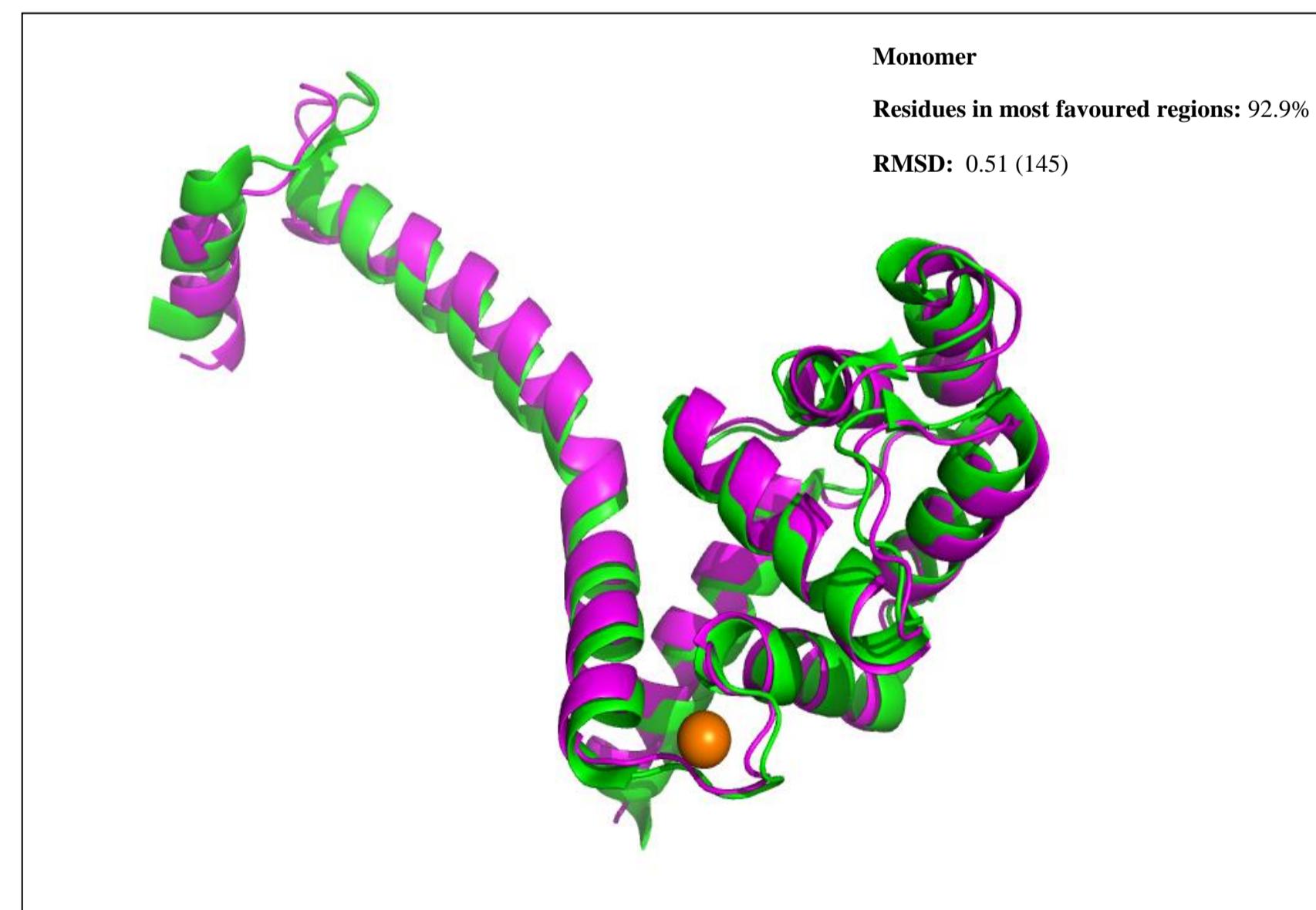
2. OsRbohC (NP_001056115 – 178 aa)

- Sequence alignment of OsRbohC with template using **Modeller9v8** is given as follow

Model: OsRbohC.B99990001.pdb

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVG-NDGWAABEKRNFNLQVDGVLLRSRGKCIAMDGSDEFAVQMFDLARKRGIVKQVLTKDELKDFYEQLTDQGFDNRLRTFFDMVDKNAIGRLTAEEVKEIIALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDLEALL
OsRbohC 174 TKSGAQRAIRGLRFISGPNKASNAWIEVQANFDRLARDGYLSRDDFPQCIGMTESKEFAMELFTLSRRRQMVDKINKEELREIWQQITDNSFDSRLQIFFDMVDKNAIGHTEAVKEIIMLSASANKLSRLKEQAEEYAAALIMEELDPEQLGYIELWQLETLL

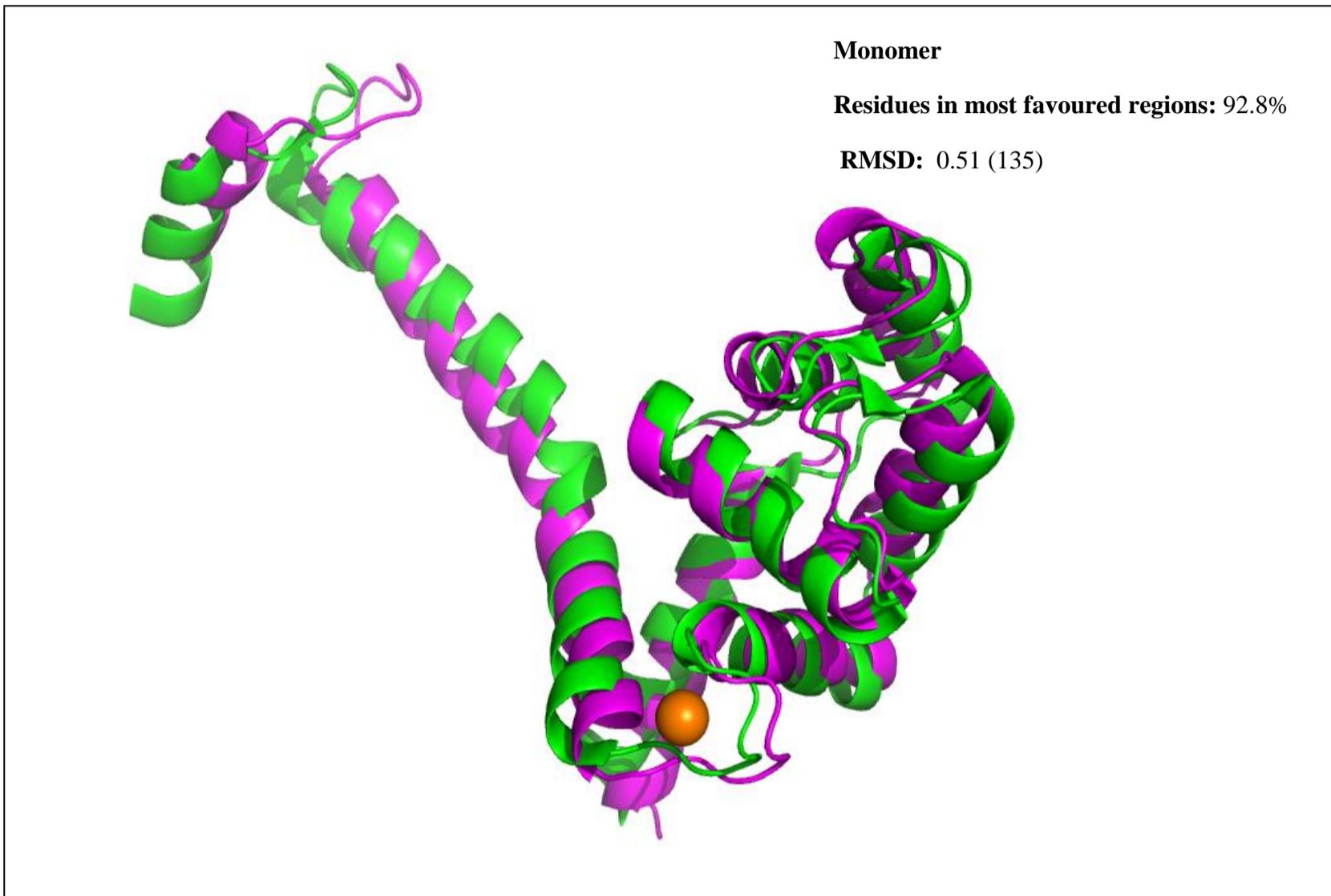


3. OsRbohD (NP_001055783 – 179 aa)

- Sequence alignment of OsRbohD with template using **Modeller9v8** is given as follow

Model: OsRbohD.B99990001.pdb

- Edited alignment



4. OsRbohE (NP_001044725 - 179 aa)

- Sequence alignment of OsRbohE with template using **Modeller9v8** is given as follows

Sequence alignment showing conservation across three proteins: 3A8RA, OsRbohE, and Consrvd. The alignment highlights conserved amino acids with purple and green boxes. Amino acid positions are indicated above the sequence.

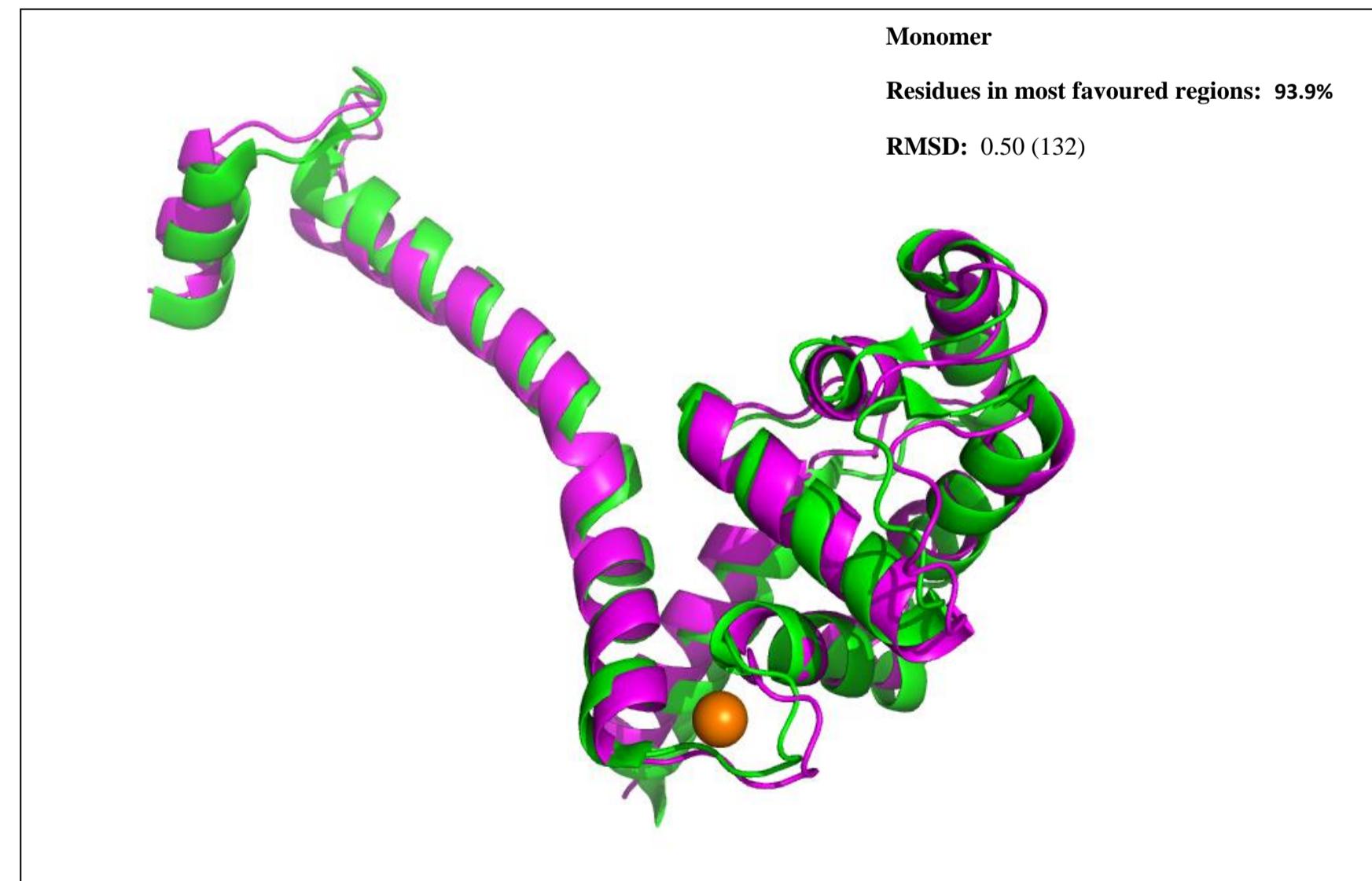
	146	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	303		
3A8RA	138	TKSSAAVALKGLQFVTAKVG-NDGWAAYEKRNFNQLQVDGVLLRSRGKCIGMDGSDEFQVQMFDSLARKRGIV-KQVLTKDELKDFYEQLTDQGFDRNRLLRTFFDMV	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	303	
OsRbohE	76	MQSSAQVGLRGLRFILDKTSGGKEGWKSVERRFDEMNRNRGLPKESFGKICMGDSKEFAGELFVALARRNIEPEDGITKEQLKEFWEEMTDQNFDSSLRRIFFDMC	138	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	303
Consrvd	***	*	*	***	*	***	*	**	***	***	***	***	***	***	***	***	***		

Regions highlighted: G-96 (purple box), P-149 (green box), and D-182 (blue box).

Model: OsRbohE.B99990001.pdb

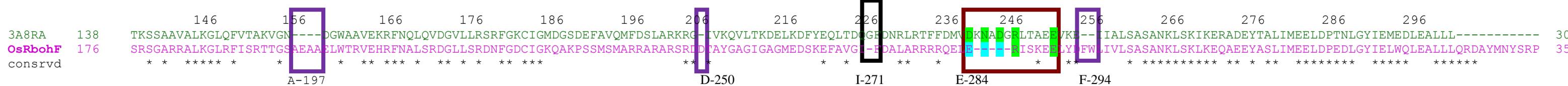
- **Edited alignment**

3A8RA 138 TKSSAAVALKGLQFVTAKVG-NDGWAABEKRFRNQLQVDGVLLRSRFGKCIGMDGSDEFAVQMFDLARKRGIV-KQVLTKEDELKFYEQLTDQGFDNRRLRTFFDMVILKNAADGRLTAEEVKEIIALSASANKLSIKERADEYTALIMEELDPTNLGYIEMEDLEALL
OsRbohE 76 MQSSAQVGLGLRFLDKTSGGKEGWKSVERRFDEMNRNGRLPKESFGKCIGMGSKEFAGELFVALARRNLEPEDGITKEQLKEFWEEMTDQNFDSSLRIFFDMCIIKGQGMLTEDEVKEVIIILSASANKLAKLGHAATYASLIMEELDPDDRGYIEIWQLETLL



5. OsRbohF (NP_001061956 – 178 aa)

- Sequence alignment of OsRbohF with template using **Modeller9v8** is given as follows:

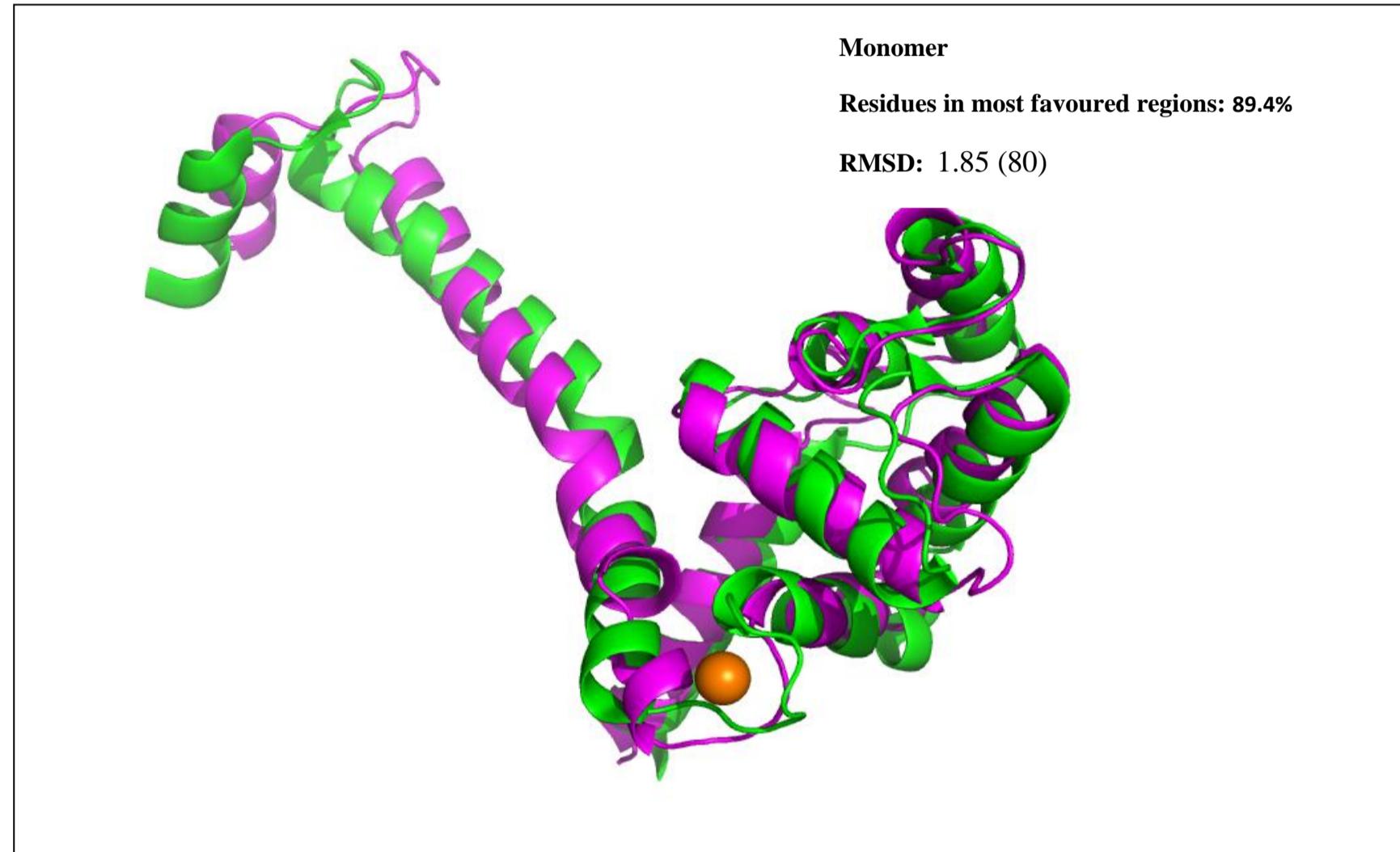


Deletion associated with Ca-binding site : D-242, N-244, D-246, R-248, E-253 are absent in OsRbohF (Major deletion)

Edited alignment

Sequence alignment of OsRbohF with template using **Modeller9v8** is given as follows:

3A8RA	138	TKSSAAVALKGLQFVTAKGVN	146	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	
OsRbohF	176	SRSGARRALKGLRFISRTTGSAEAEELWTRVEHRFNALS RDGLLSRDNGCIGKQAKPSSMSMARRARARSRRDTAYGAGIGAGMEDSKFAVGI	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	303
consrvd			*	*	*****	*	*	*	*	*	*	*	*	*	*	*	*	353	



6. OsRbohG (NP_001063267 – 181 aa)

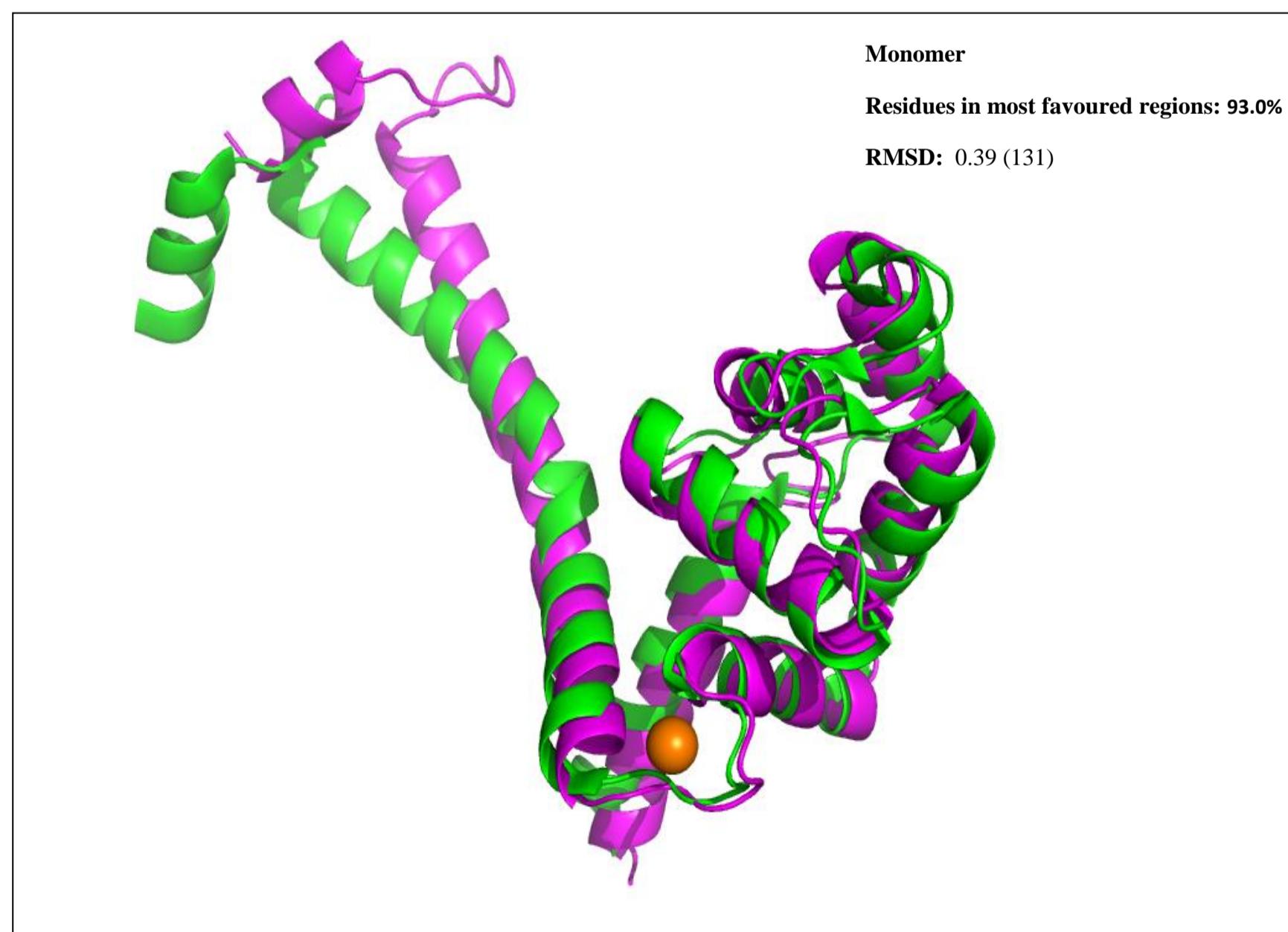
- Sequence alignment of OsRbohG with template using **Modeller9v8** is given as follows:



Edited alignment

Sequence alignment of OsRbohG with template using **Modeller9v8** is given as follows:

3A8RA	138	TKSSAAVALKGLQFVTAKGVN	146	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	
OsRbohG	180	SSTGAKRALKGLRFISRTTGTVQAELWRRVEDRFN ALARDGLLSRDDFGECIGMVDSKEFAVGIFDALARRRNLERITREELYDFWLQISDQSFDARLQIFFDMV	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	303
consrvd			*	*	*****	*	*	*	*	*	*	*	*	*	*	*	*	360	



7. OsRboH (NP_001066954 – 198 aa)

- Sequence alignment of OsRboH with template using **Modeller9v8** is given as follows

The figure shows a sequence alignment between 3A8RA (residues 138-303) and OsRbohH (residues 138-335). The alignment highlights conserved regions with green bars and P-loop motifs with purple boxes. The conserved regions are labeled with their respective residue numbers above the sequence. The P-loop motifs are labeled D-242, D-293, and P-316 below the sequence.

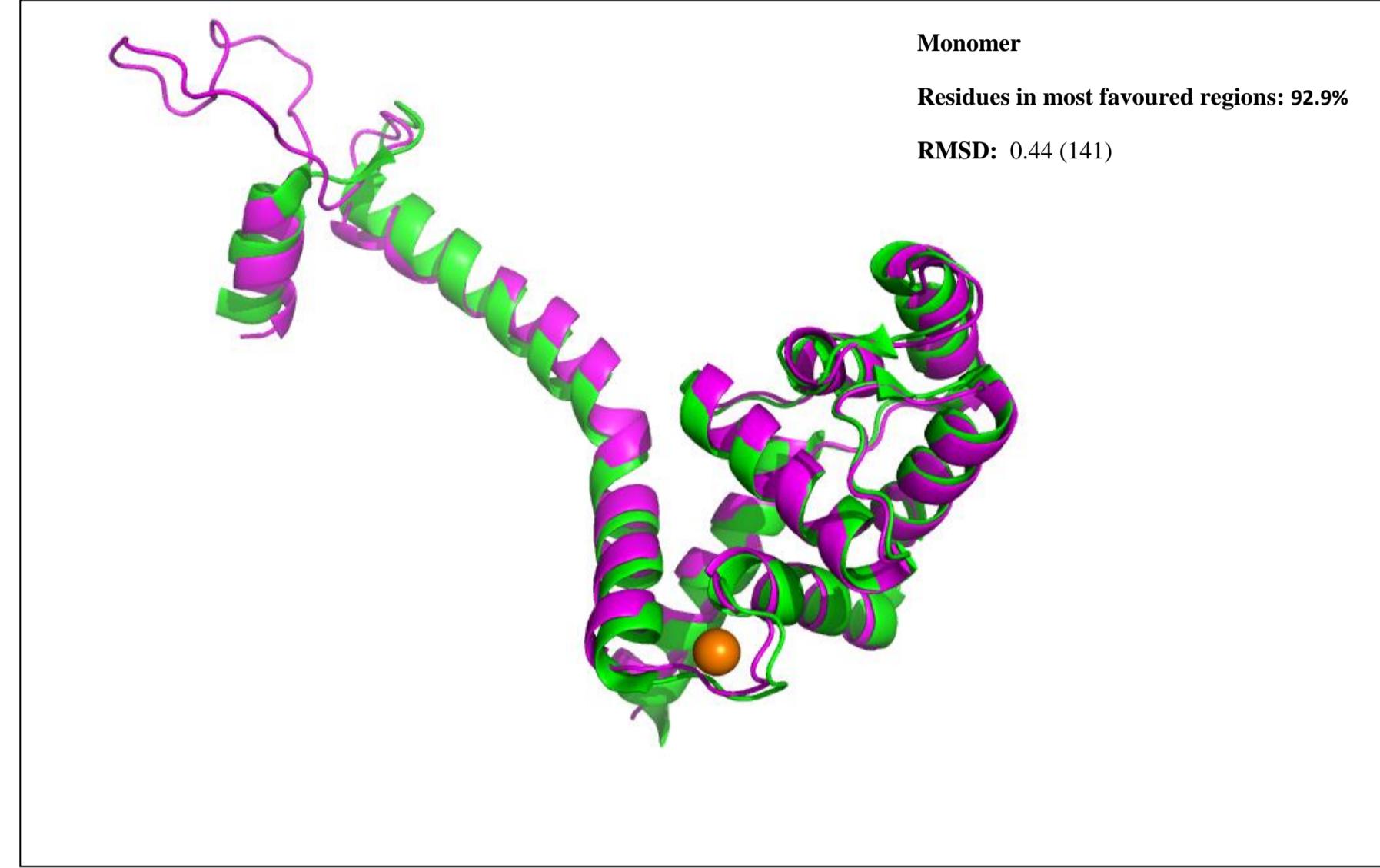
	146	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	303
3A8RA	TKSSAAVALKGLQFVTAKVGNDGWA 138	NQLQVDGVLLRSRGKCI	GMDSDEFAVQMFDLARKRGIV 138	KQVLTKDELKDFYEQLTDQGF DNLRLTFFDMV	DNLRLTFFDMV	IKNA	DGR	TAE	VKEII	IALSASANKLSK	IERADEYTA LIMEELDP	PTNLGYI	-	-	-	MEDLEALLL	303
OsRbohH	SMTGAARALRGIQFLN 138	SAVTNGWPEVEKRFERIA VQIFDSLARRGITAQLLT KDQLREFWEQLSDPGFDA KLQTFDMV	LGFLRSRGQCIGMVSEEF AVQIFDSLARRGITAQLLT KDQLREFWEQLSDPGFDA KLQTFDMV	IKNA	DGR	QITEE	LKEVLT	LTASANKLSK	ILERVDEYTA LIMEELDP	DQLGYIDSTRVA SAILNSDTVHGHPF	HISNLESLLLPPSQAPSK	335					
consrvd	***	***	*****	**	*****	*	*****	*****	*****	*	**	*	*****	*****	*****	*****	***
	***	***	*****	**	*****	*	*****	*****	*****	*	**	*	*****	*****	*****	*****	***

P-242 D-293 P-316

Model: OsRbohH.B99990001.pdb

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGNDGWAABEKRNFNQLQVDGVLLRSRGKCIAMDGSDEFAVQMFDSLARKRGIVKQVLTKDELKDFYEQLTDQGFDNRLRTFFDMVUKIADGRLTAEVKKEIIALSASANKLSKIERADEYTA
OsRbohH 138 SMTGAARALRGLQFLNSSAVTNGWPEVEKRFERLAVDGFLRSRGQCIGMVGSEEFAVQIFDSLARRGITAQLLTDQREFWEQLSDPGFDAKLQTFDMVUKIAGQITEELKEVLTASANKLSKILERVDEYTA
-----MEDLEALLL-----



OsRbohH_909 (166 aa)

ClustalW alignment

OsRboH_892	KFPGVLSGGGGGDAPNGNDRRPLDRS	SMTGAARALRGLQFLNSAVTNGWPEVEKRF	168
OsRboH_909	KFPGVLSGGGGGDAPNGNDRRPLDRS	SMTGAARALRGLQFLNSAVTNGWPEVEKRF	168
3A8R	KAPS-----PQAQQSAKVRVKRLDR	TKSSAAVALKGLQFVTAKVGNDGWAACEKRF	168
	* ***	:* . .: * *****: : . ** * :*****: :**. *****	
OsRboH_892	ERLAVDGFLRSRFGQCIGMVGSEEF	AVQIFDSLARRGITAQLLTDQLREFWEQLSDP	228
OsRboH_909	ERLAVDGFLRSRFGQCIGMVGSEEF	AVQIFDSLARRGITAQLLTDQLREFWEQLSDP	228
3A8R	NQLQVDGVLLRSRFGKCIGMDGSDEF	AVQMFDSSLARKRGIVKQVLTKDELKDFYEQLTDQ	228
	: :* ***.*****:***** * :*****:*****:*****:***. * :*****:*: :*:****:*		
OsRboH_892	GFDALKQTFFDMVDKNADGQITEEE	LKEVLTLTASANKLSKILERVDEYTALIMEELDPD	288
OsRboH_909	GFDALKQTFFDMVDKNADGQITEEE	LKEVLTLTASANKLSKILERVDEYTALIMEELDPD	288
3A8R	GFDNRLRTFFDMVDKNADGRITAEEVKEI	IIALSASANKLSKIKERADEYTALIMEELDPT	288
	*** :*:*****:*****: :* * * :*: :*:*****:***** * *.*****:*****		
OsRboH_892	QLGYIDSTRVAVSAILNSDTVHGHL	LPFPKISNLESLLLPPSQAPSK-LVTHSSNISQLI	347
OsRboH_909	QLGYID-----	ISNLESLLLPPSQAPSK-LVTHSSNISQLI	324
3A8R	NLGYIE-----	MEDLEALLLQSPSEAARSTTHSSKLSKAL	

Modeller alignment (used for model)

8. OsRbohI (ABA94089 – 176 aa)

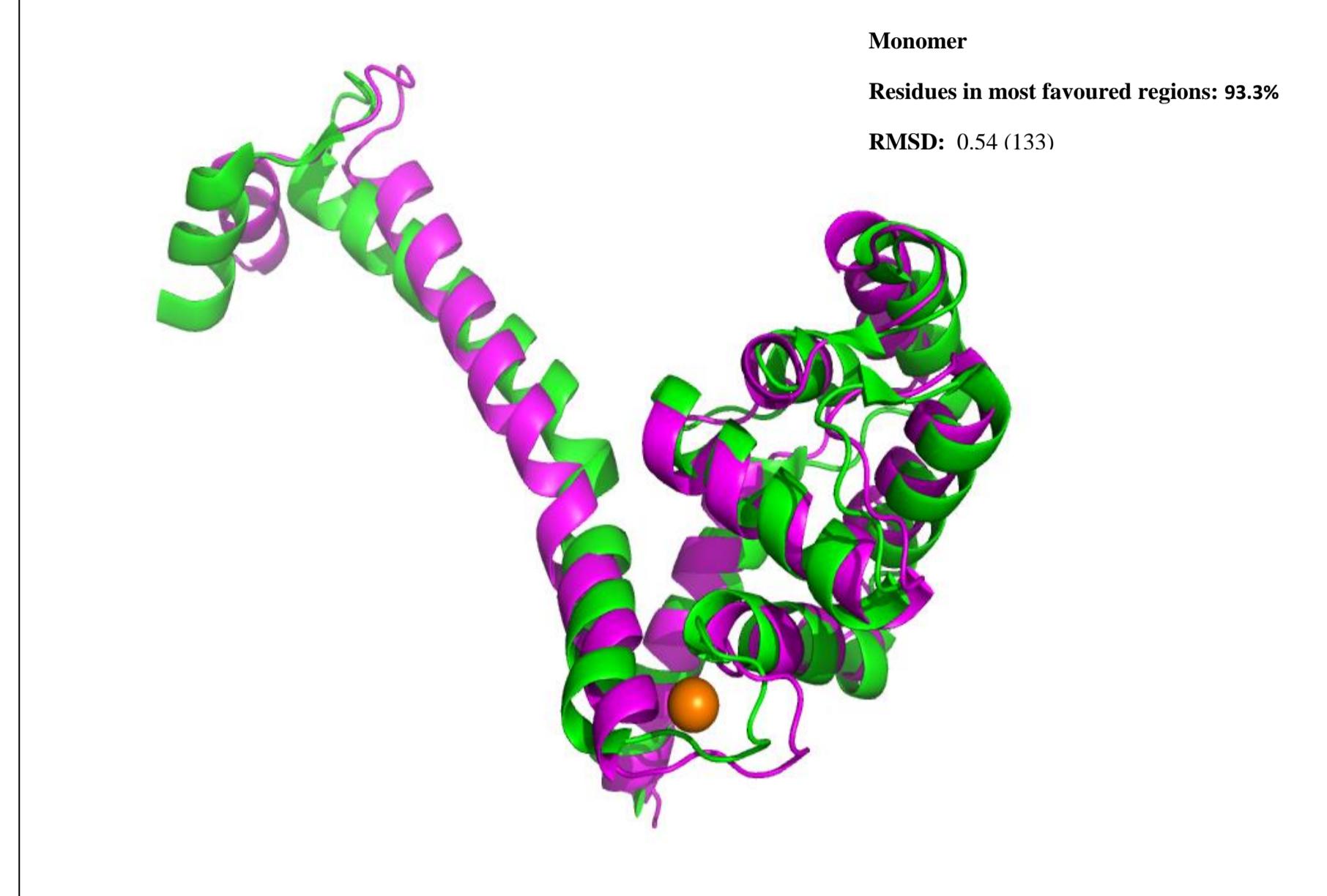
- Sequence alignment of OsRboH1 with template using **Modeller9v8** is given as follow:

Sequence alignment of 3A8RA (138) and OsRbohI (168) showing conserved regions (black bars) and mutations (green bars). The alignment highlights conserved regions (black bars) and mutations (green bars) across the sequence. The conserved regions are located at positions 146-156, 166-176, 186-196, 206-216, 226-236, 246-256, and 266-276. Mutations are indicated by green bars above the sequence, with specific labels K-219 and D-271 pointing to the sequence.

Model: OsRbohI.B99990001.pdb

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGNQWAAVEKRFNQLQVDGVLLRSRGKCIGMDGSDFAVQMFDSLARKRKGIVKQVLTKDELKDFYEQLTDQGFDNRLRTFFDMVKNA
OsRbohI 168 SKSAAAHALKGLKFISRADGGAGWPAVEKRFDDLAKGGLLPRSKFGQCIGMK-ELEFAGELFDALARRNISGDSISKAELLEFWDQISDTSFDSRLQTFFDMVKNA
GRITEEVKEIITLSASANKLSKVQEQQSEYYARLIMEELDPSNLGYIELYNLEMILLIS



9. AtRbohA (AAC39475 – 178 aa)

- Sequence alignment of AtRbohA with template using **Modeller9v8** is given as follow

TKSSAAVALKGLQFVTAKVGNNDGWAABEVKRFNQLOV--DGVLRLRSRGKCIQMDGSDEFAVQMFDSLARKRGIVKQVLTKDELKDFYEQLTDQGFNRRLRTFFDMVLUKADGRLTAEVKIIALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDLEALLL----- 303
SKSRAELALKGLKFITKTDGVTGWPEVEKRFYVMTMTNIGLLHRSRGECIGMK-STEFLALALFDALARRENVSGDSINMNELKEFWKQITDQDFDSRLRTFFAMVUKDSDGHLNEA2VREIITLSASANELDNIRQADEYAALIMEELDPYHYGYIMIENLEILLQAPMQDVRDGE 306

3A8RA 138
AtRbohA 129
Consrvd

146 156 166 176 186 196 206 216 226 236 246 256 266 276 286

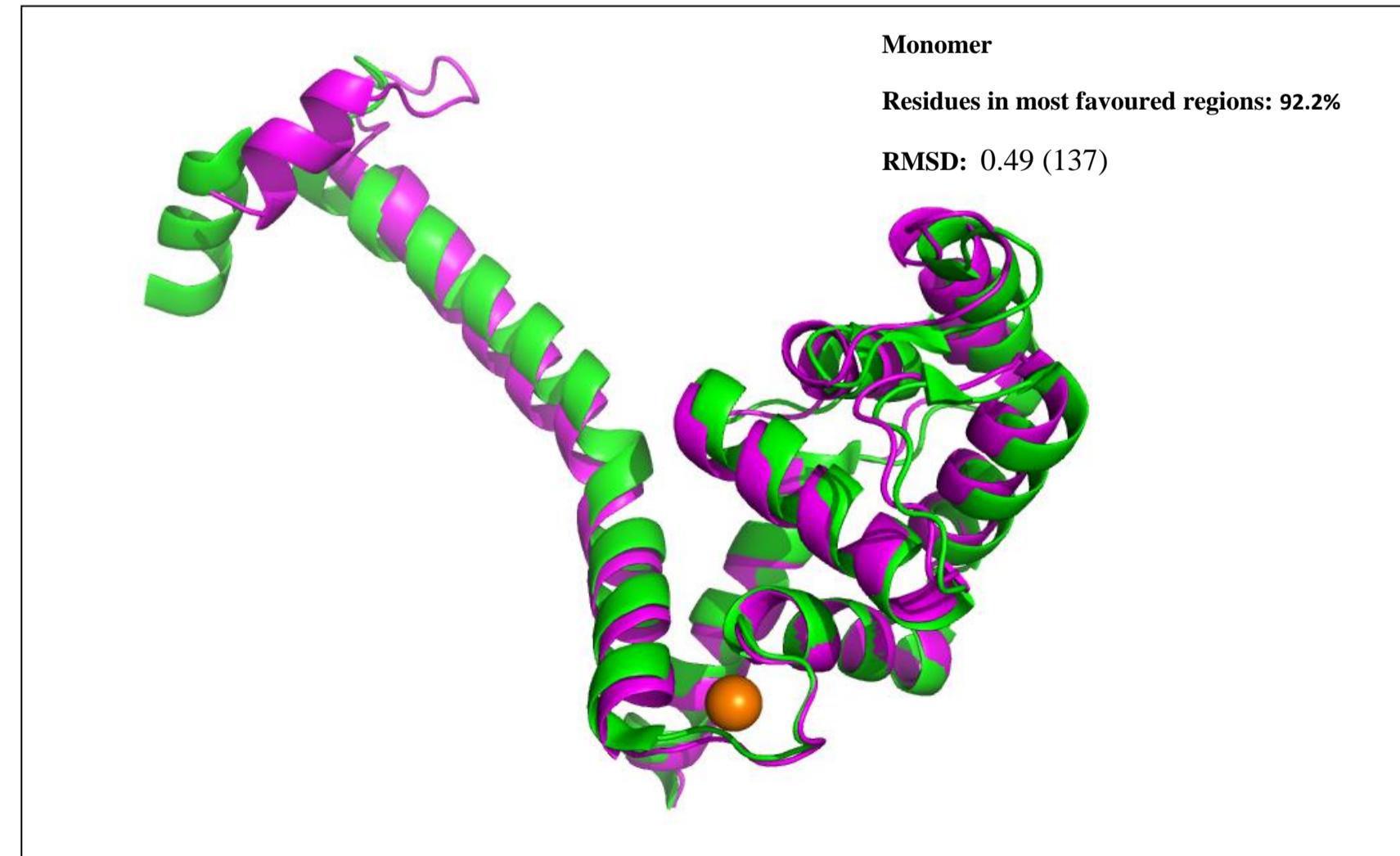
T-165 D-234

Model: AtRbohA.B99990001.pdb

Mutations suggested for Ca-binding site in following Rbohs : Mutate D to N in AtRbohA (because N is replaced by D)

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGNQWAEEKRFNQLQV--DGVLLRSRGKCIGMDGSDEFQMFDSLARKRGIVKQVLTKDELKDFYEQLTDQGFDNRLRTFFDMV**DKNAGRLTAEEVKEII**ALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDEALLIS
AtRbohA 129 SKSRAELALKGLKFITKTDGVTGWPEVEKRFYVMTMTNNGLLHRSRGECIGMK-**STEFALALFDALARRENVSGDSINMNELEFWKQITDQDFDSRLRTFFAMV**DKDSEGR**LNEAEVREIITLSASANE**LDNIRRQADEYAALIMEELDPYHYGYIMIENLEILLIS****



10. AtRbohB (AAC39476 -178 aa)

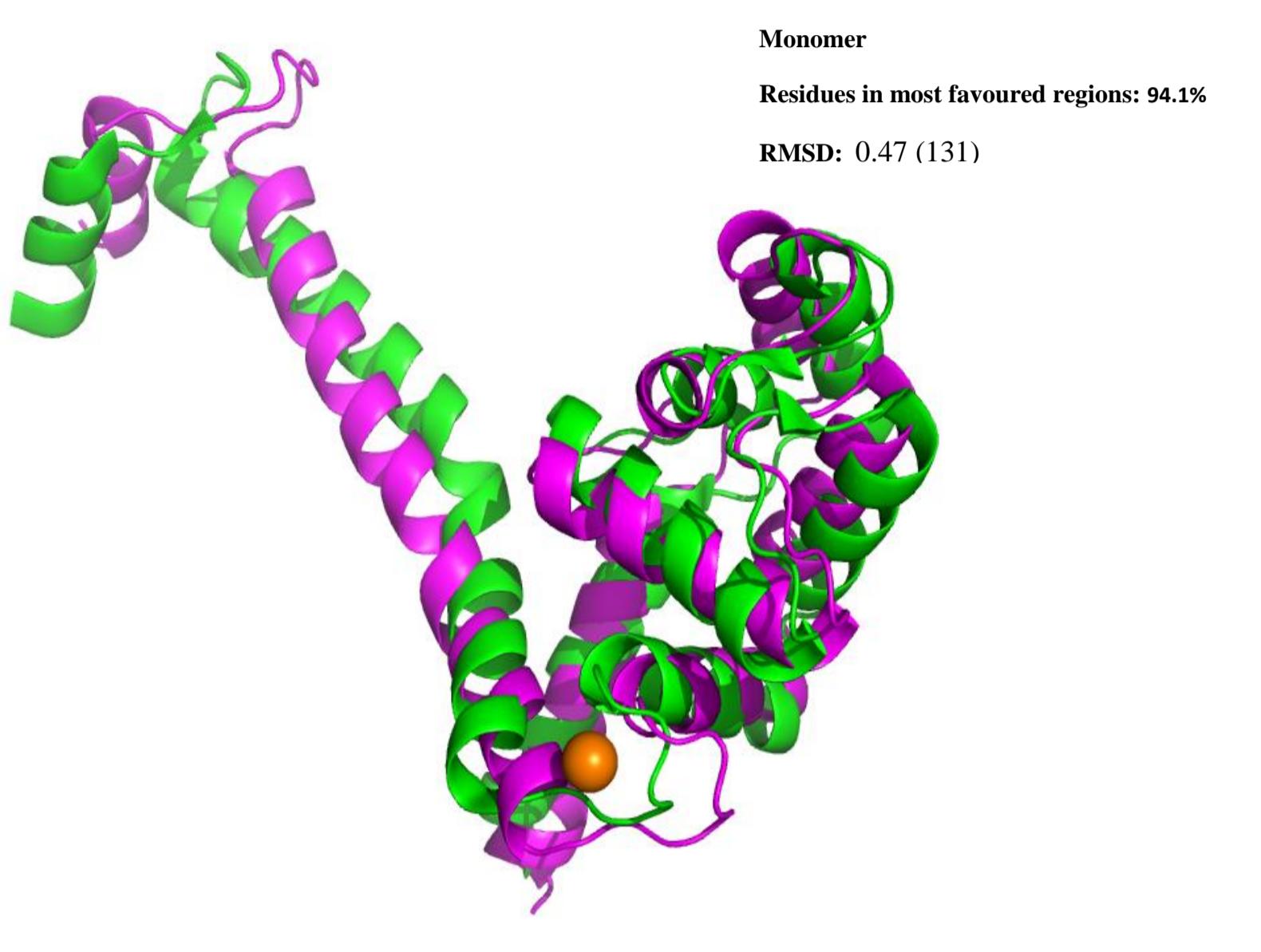
- Sequence alignment of AtRbohB with template using **Modeler9v8** is given as follows:

3A8RA	138	TKS-SAAVALKGLQFVTAKVGN	D-GWA	AVEKRFNQLQVDGVLLRSRG	KCIGMDGSDEF	AVQMFDSLARKRGIVKQVL	TKDELKDFYEQLTDQGF	DNRLRTFFDMV	[K]A[GRLTAE]	VKEIIALSASANKLSK	IKERADEYTALIMEELDPT	NLGYIEMEDLEALL	-----	303				
AtRbohB	78	SKSGAMFALRGLRFIAKND	AVG	WDEVAMRF	FDKLAVEGKLP	SKFGH	CIGMVE	SSEEVNLFEALVRRG	TTSSSITKTEL	FEFWEQITGNSF	DDRLQIFFDMV	[K]L[GRI	TGDV	KEIIALSASANKLSK	IKENVDEYALIMEELDR	DNLYIELHNLET	LLLQVPSQSNNSP	255
consrvd		F-81	R-100															

Model: AtRbohB.B99990001.pdb

- Edited alignment

3A8RA	138	TKS-SAAVALKGLQFVTAKVGN	D-GWA	AVEKRFNQLQVDGVLLRSRG	KCIGMDGSDEF	AVQMFDSLARKRGIVKQVL	TKDELKDFYEQLTDQGF	DNRLRTFFDMV	[K]A[GRLTAE]	VKEIIALSASANKLSK	IKERADEYTALIMEELDPT	NLGYIEMEDLEALL	-----	303				
AtRbohB	78	SKSGAMFALRGLRFIAKND	AVG	WDEVAMRF	FDKLAVEGKLP	SKFGH	CIGMVE	SSEEVNLFEALVRRG	TTSSSITKTEL	FEFWEQITGNSF	DDRLQIFFDMV	[K]L[GRI	TGDV	KEIIALSASANKLSK	IKENVDEYALIMEELDR	DNLYIELHNLET	LLLQVPSQSNNSP	255
consrvd																		



11. AtRbohC (AAC39477- 140 aa)

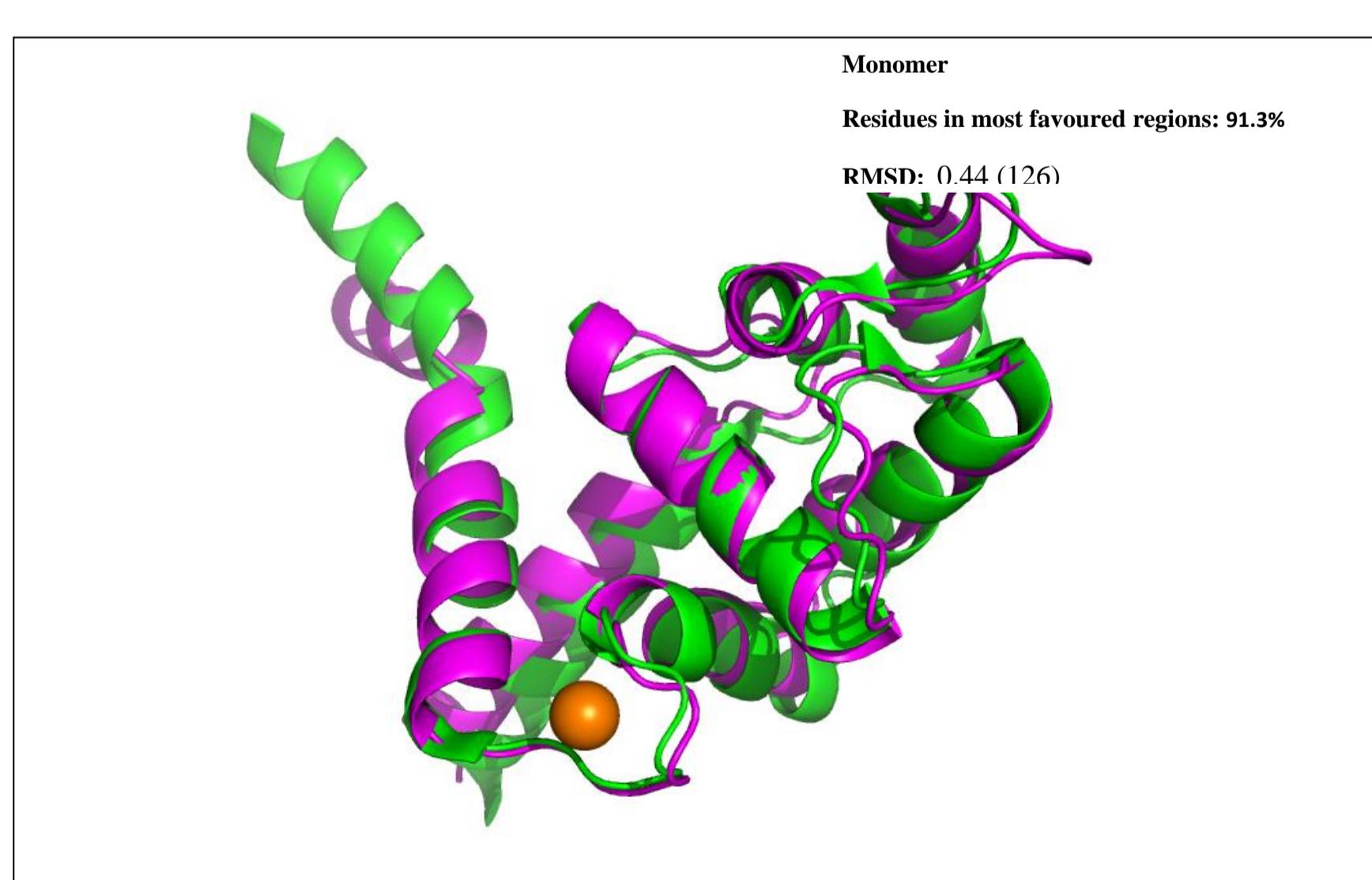
- Sequence alignment of AtRbohC with template using **Modeler9v8** is given as follows:

3A8RA	138	146	156	166	76	186	196	206	216	226	236	246	256	266	276	286	
AtRbohC	134	TKSSAVALKGLQFVTAKVGN	D-GWA	AVEKRFNQLQVD	--GVLL	RSRG	KCIGMDGSDEF	AVQMFDSLARKRGIVKQVL	TKDELKDFYEQLTDQGF	DNRLRTFFDMV	[K]A[GRLTAE]	VKEIIALSASANKLSK	IKERADEYTALIMEELDPT	NLGYIEMEDLEALL	-----	303	
consrvd		T-171	T-187														

Model: AtRbohC.B99990001.pdb

Mutations suggested for Ca-binding site in following Rbohs : Mutate D to N in AtRbohC (because N is replaced by D)

3A8RA	138	TKSSAVALKGLQFVTAKVGN	D-GWA	AVEKRFNQLQVD	--GVLL	RSRG	KCIGMDGSDEF	AVQMFDSLARKRGIVKQVL	TKDELKDFYEQLTDQGF	DNRLRTFFDMV	[K]A[GRLTAE]	VKEIIALSASANKLSK	IKERADEYTALIMEELDPT	NLGYIEMEDLEALL	-----	303
AtRbohC	134	TKSAASQALKGLKFISKT	DGAGWSAVEKRFNQI	TTGG	LRTKFGECIGMT	-SKDF	FALELF	DALARRRNITGEVID	GDQLKEFWEQINDQSF	DSRLKTFDMV	[K]A[GCLTED]	VRELESLETLL	--LQAATQSVITST	-----	273	
consrvd																



Clustal W alignment

Modeller 9v8 alignment

3A8R	138	TKSSAAVALKGLQFVTAKVGNDGWA AVEKRFNQLQVD--GVILLRSRGKCIGMDGSDEF AVQMFDSLARKRGIVKQVLTKDELKDFYEQLTDQ GFDNRRLRTFFDMVIEKNA DGRLTAEHVKEIIALSASANKLS KIKERADEYTALIMEELDPTNLGYIE MEDLEALL-----*	303
AtRbohC	134	TKSAASQALKGLKFISKT DGGAGWSAVEKRFNQITATTGG LLLRTKFGE CIGMT-SKDFALELF DALARRNITGE VIDGDQLKEFW EQINDQS FDSRLKT FFDMVIEKD ADGRLT EDVREIISLS ASANNL STIQKRA DEYAAL IMEELDP DNIGYIM LESLET LLQAAT QSVITST*	311

Edited Modeller 9v8 alignment (use for modeling) [G1]

3A8R	138	TKSSAAVALKGLQFVTAKVGNDGWA AVEKRFNQLQVD--GVLLRSRGK CIGMDGSDEF AVQMFDSLARKRGIVK QVLTKDELKDFY EQ LTDQGF DNRLRTFFDMV DKNA DGR LTAE FVKE II ALSASANKL SKIKERADEY TALIMEELDPTNLGYI EMEDLE ALLL*	303
AtRbohC	134	TKSAASQALKGLKFISKT DGGAGW SAVEKRFNQITATTGGLLLRTKFGECIGMT-SKDFALELF DALARRNITGEVIDGDQLKEFWEQINDQSFD SRLKT FFDMV DKDA DGR LTEDEVREI IISLSASAN NLSTI QKRADEYA ALIMEELDPDNIGYIMLESLETLLL*	300

12. AtRbohD (AAC39479 – 177 aa) 1.429215 over 160 residue

Sequence alignment of AtRbohD with template using **Modeller9v8** is given as follow

Sequence alignment showing conservation across four proteins: 3A8RA, AtRbohD, and two conserved regions (consrvd). The alignment highlights conserved regions with colored boxes and mutated positions with asterisks (*).

	146	156	166	176	186	196	206	216	226	236	246	256	266	276	286	296	303
3A8RA	TKSSAAVALKGLQFVTAKVGNDGWA 138			GVLRSRGKCI 176	GSDFAVQMFDLARKRGIVKQVL 186	KDELKDFYEQLTDQGF 196	DNRLLRTFFDMVK 206	NADGHLTAEEVKE 216	IALSASANKLS 226	SKIKERADEYTALIMEELDPTNLGYI 236	EMEDLEALLL----- 246	MEEDLEALLL----- 256	266	276	286	296	303
AtRbohD	TSSAAIAHALKGLKFIATKTA-A-WPA 161			VDQRFKLSADS 176	NGLLLSAKFWCLGN 186	NEKSKDFADQLFRA 196	LARRNNVSGDAIT 206	KEQLRIFWEQ 216	ISDESFDAKLQV 226	FDMDV 236	DKEDGHVTEEE 246	VAEISLSASANKLS 256	NIQQAKEYA 266	ALIMEELDPDNAGF 276	IMIENLEM 286	LLQAPNQS 296	VRMG 337
consrvd	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*

Key positions highlighted in the sequence alignment:

- A-180:** Located at position 156, highlighted in black.
- S-196:** Located at position 196, highlighted in purple.
- K-213:** Located at position 213, highlighted in blue.
- D-266:** Located at position 266, highlighted in green.

Model: Atkbind.B99990001.pdt

Mutations suggested for Ca-binding site in following Rbohs : Mutate D to N in AtRbohD (because N is replaced by D)

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGNQWAAVEKRFNQLQVD--GVLLRSRGKCIGMD-GSDEFQVQMFDSLARKRKGIVKQVLTKDELKDFYEQLTDQGFNRLRTFFDMVKNA
AtRbohD 161 TSSAAIHALKGLKFIATKTA-A-WPAVDQRFDKLSADSNGLLSAFKWECLGMNKESKDFADQLFRALARRNNVSGDAITKEQLRIFWEQISDESFDAKLQVFFDMVKNDGHLTAEEVKEIIALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDEALLI
TSSAAIHALKGLKFIATKTA-A-WPAVDQRFDKLSADSNGLLSAFKWECLGMNKESKDFADQLFRALARRNNVSGDAITKEQLRIFWEQISDESFDAKLQVFFDMVKNDGHLTAEEVKEIIALSASANKLSNIQKQAKEYAALIMEELDPTNLGYIEMEDEALLI



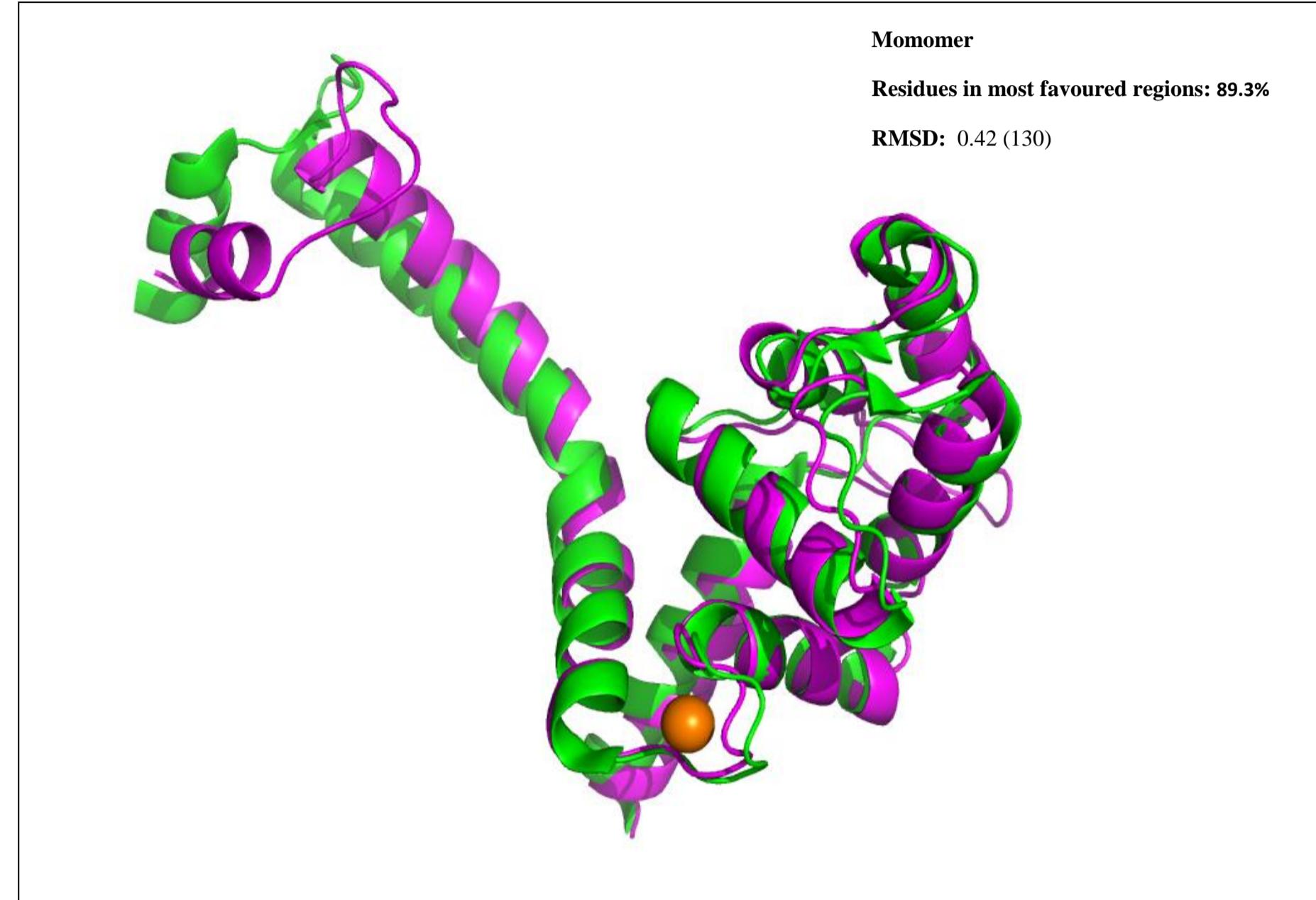
13. AtRbohE (AAC39478 – 190 aa)

- Sequence alignment of AtRbohE with template using **Modeller9v8** is given as follow:

Model: AtRbohE.B99990001.pdb

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKV-GN---D----GWAAYEKRNFQLQVDGVLLRSRGKCIGMDGSDEFAVQMFDLARKRQIVKQVLTKDELKDFYEQLTDQGFDNRLRTFFDMVKNADGHLTAAEVKEIIALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDIEALLI
AtRbohE 165 STSSAQRALKGLQFINKTRGNSCVCDWDCDCDQMWKVEKFESLSKNGLLARDDFGEVGMVDSKDFAVSVFDALARRRQKLEKITKDELHDFWLQISDQSFDARLQIFFDMASNEDGKITREEIKELLMLSASANKLAKLKEQAEEYASLIMEELDPENFGYIELWQLETLLI



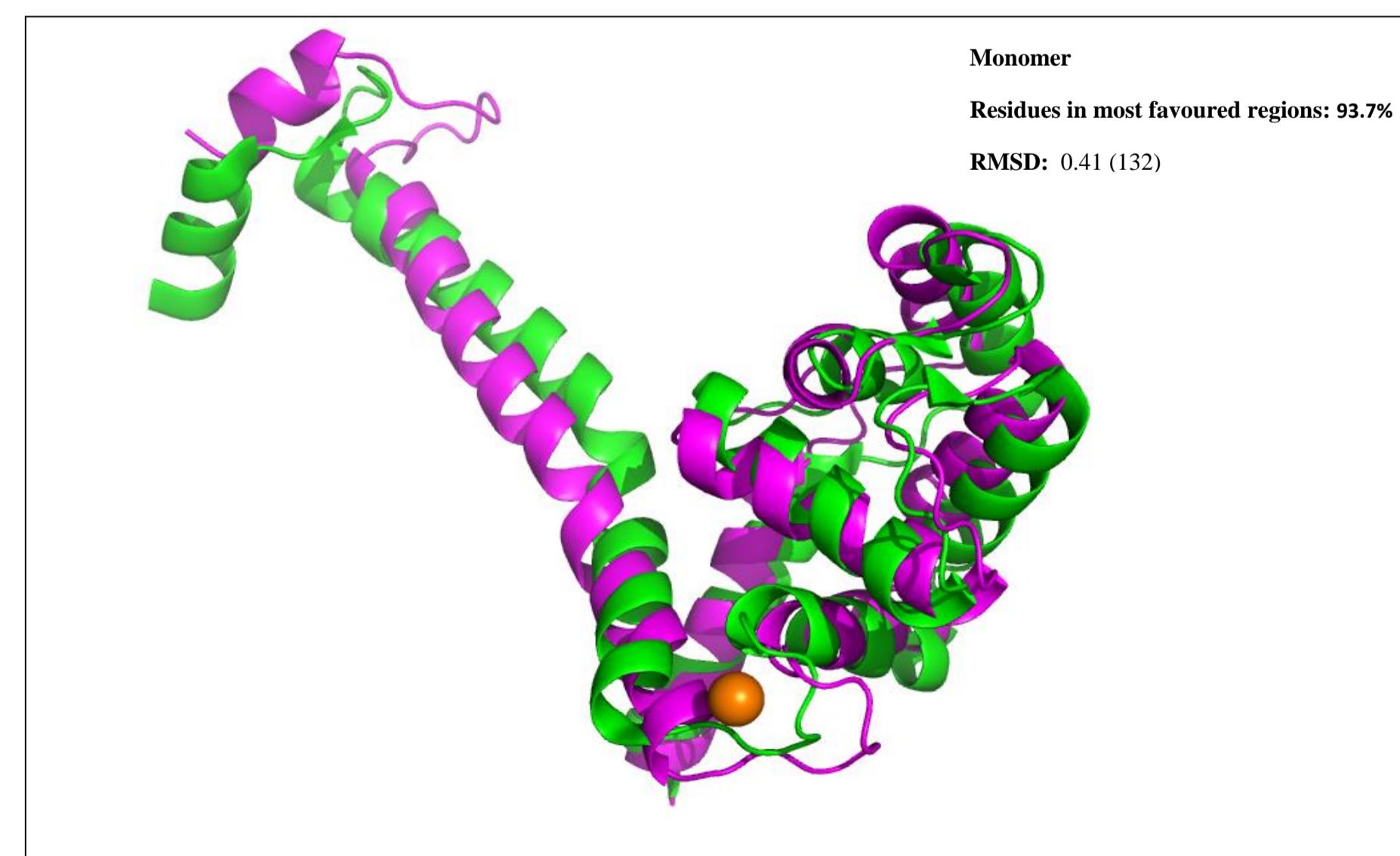
14. AtRbohF (BAA28953 – 178 aa)

- Sequence alignment of AtRbohF with template using **Modeller9v8** is given as follows:

Model: AtRbohF.B99990001.pdb

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- Edited alignment
3A8RA 138 TKSSAAVALKGLQFVTAKVGN-DGWAABEKRNFNQLQVDGVLLRSRGKCIIGMDGSDEFAVQMFDLARKRGIVKQVLTKDELKDFYEQLTDQGFDNRLRTFFDMV**I****K****N****A****D****G****R****L****T****A****E****F****V****K****E****I****I****A****L****S****A****S****A****N****K****L****S****K****I****K****E****A****D****E****Y****T****A****L****I****M****E****E****L****D****P****T****N****L****G****Y****I****E****M****D****L****E****A****L****L**
ATrbobE 172 TRSSAQAPALRGIRETSNKOKNVDCWNDVOSNEEFKEEKNGTYIYRSDEAOCTGMKDSKEFAELIEDAISSRRRIKVEKINHDFIYEXWSOINDESFSRBIQIFFDIV**K****E****G****H****I****T****E****E****F****V****K****E****I****I****M****I****S****A****S****A****N****K****L****S****K****I****K****E****A****D****E****Y****T****A****L****I****M****E****E****L****D****P****T****N****L****G****Y****I****E****M****D****L****E****A****L****L**



15. AtRbohG (NP_194239 - 178 aa)

- Sequence alignment of AtRbohG with template using **Modeler9v8** is given as follows:

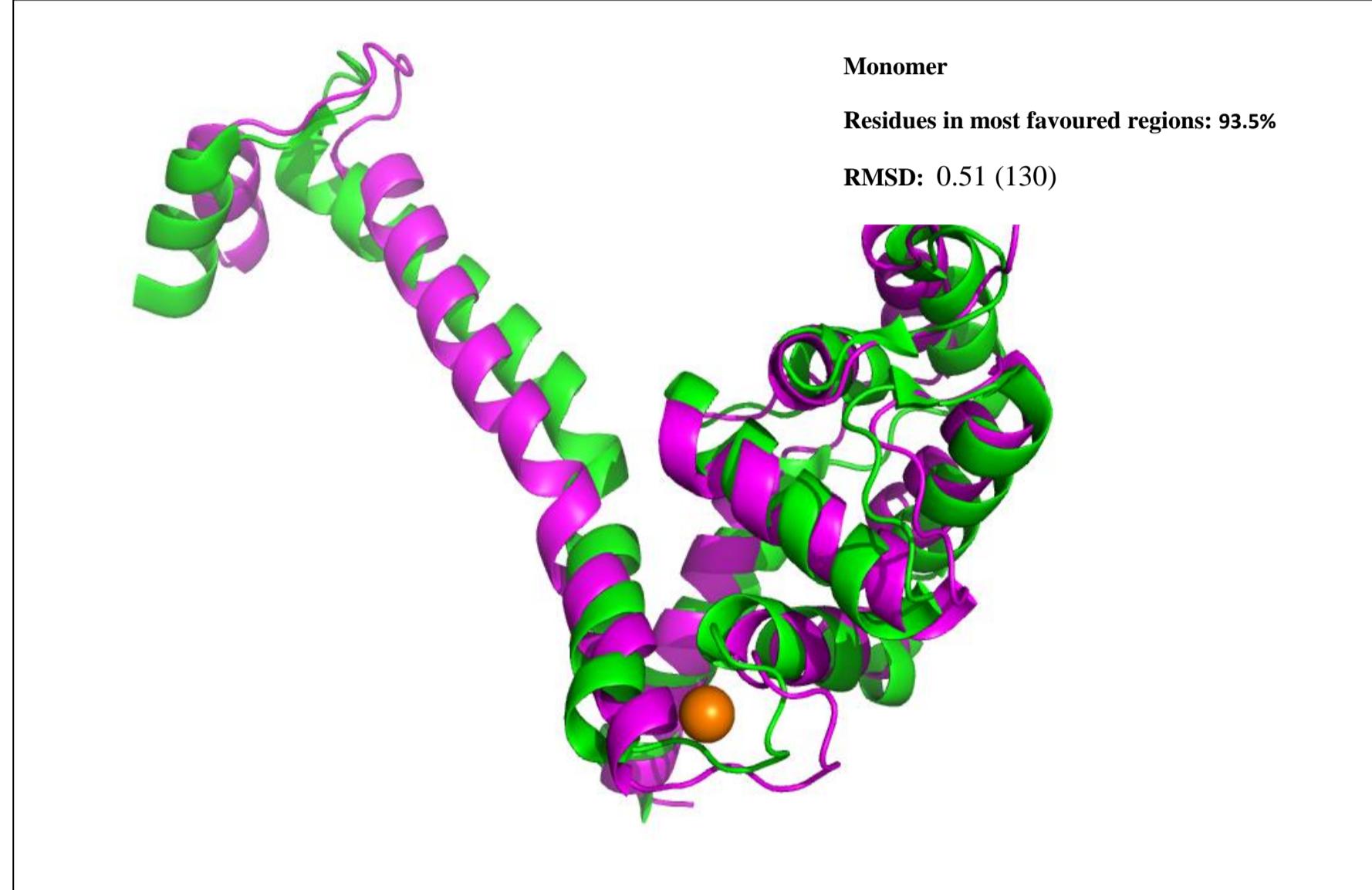
3A8RA 138 TKSSAAVALKGLQFVTAKVGNNDGWAABEKRNFQQLQV--DGVLRLRSRGKCGIGMDGSDEFQVQMFDSLARKRGIVKQVLTKEDELKDFYEQLTDQGFDNRLRTFFDMV[KAGGLTAEVKEIIIALSASANKLSKIKERADEYTALEIMELDPTNLGYIEMEDLEALLL----- 303 AtRbohG 84 SKSTAGQALKGLKIIISKTDGNAAWTVVEKRYLKITANTDGLLLRSKFGECIGMN-SKEFALELFDALARKSHLKGDVITETELKKFWEQINDKSFDSRLITFFDLM[KESIGGLTEEVREIIIKLSSSANHLSCIQNKADEYAAMIMEELDPDHMGYIMMESLKLLLQAEKSVSTDI 261 consrvd	146 156 166 176 186 196 206 216 226 236 246 256 266 276 286 296 N-120 N-137 D-189
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Model: AtRbohG.B99990001.pdb

Mutations suggested for Ca-binding site in following Rbohs : Mutate D to N in AtRbohG (because N is replaced by D)

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGNNDGWAABEKRNFQQLQV--DGVLRLRSRGKCGIGMDGSDEFQVQMFDSLARKRGIVKQVLTKEDELKDFYEQLTDQGFDNRLRTFFDMV[KAGGLTAEVKEIIIALSASANKLSKIKERADEYTALEIMELDPTNLGYIEMEDLEALLL----- 303 AtRbohG 84 SKSTAGQALKGLKIIISKTDGNAAWTVVEKRYLKITANTDGLLLRSKFGECIGMN-SKEFALELFDALARKSHLKGDVITETELKKFWEQINDKSFDSRLITFFDLM[KESIGGLTEEVREIIIKLSSSANHLSCIQNKADEYAAMIMEELDPDHMGYIMMESLKLLL
--



16. AtRbohH (NP_200809 - 180 aa)

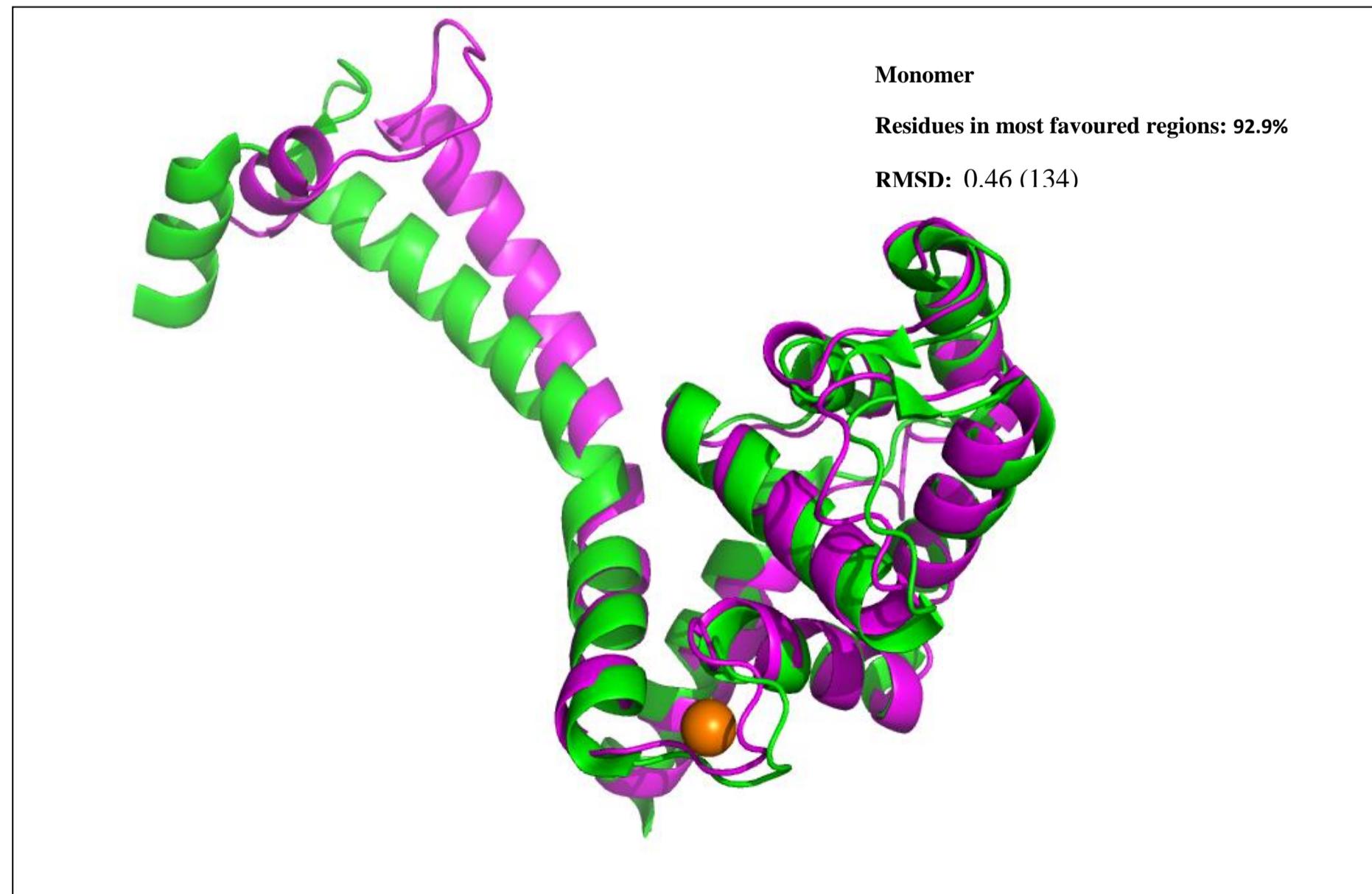
- Sequence alignment of AtRbohH with template using **Modeler9v8** is given as follows:

3A8RA 138 TKSSAAVALKGLQFVTAKVGN--DGWAABEKRNFQQLQVDGVLLRSRGKCGIGMDGSDEFQVQMFDSLARKRGIVKQVLTKEDELKDFYEQLTDQGFDNRLRTFFDMV[KAGGLTAEVKEIIIALSASANKLSKIKERADEYTALEIMELDPTNLGYIEMEDLEALLL----- 303 AtRbohH 100 TTSSAARGLQSLRFLDRTVTGRERDAWRSIENRFNQFSVDGKLPKEKFVGVCIGMGTMEFAAEVYEAALGRRQIETENGIDKEQLKLFWEDMIKKDLCRLQIFFDMC[KAGGLTEEVKEVIVLVSASANRLGNLKKNAAYASLIMEELDPDHKGYIEMWQLEILLTGMVTNADTEK 279 consrvd	146 156 166 176 186 196 206 216 226 236 246 256 266 276 286 296 R-121 E-174 D-208
--	--

Model: AtRbohH.B99990001.pdb

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGN--DGWAABEKRNFQQLQVDGVLLRSRGKCGIGMDGSDEFQVQMFDSLARKRGIVKQVLTKEDELKDFYEQLTDQGFDNRLRTFFDMV[KAGGLTAEVKEIIIALSASANKLSKIKERADEYTALEIMELDPTNLGYIEMEDLEALLL----- 303 AtRbohH 100 TTSSAARGLQSLRFLDRTVTGRERDAWRSIENRFNQFSVDGKLPKEKFVGVCIGMGTMEFAAEVYEAALGRRQIETENGIDKEQLKLFWEDMIKKDLCRLQIFFDMC[KAGGLTEEVKEVIVLVSASANRLGNLKKNAAYASLIMEELDPDHKGYIEMWQLEILLTGMVTNADTEK



17. AtRbohI (NP_192862 – 181 aa)

- Sequence alignment of AtRboH1 with template using **Modeller9v8** is given as follows

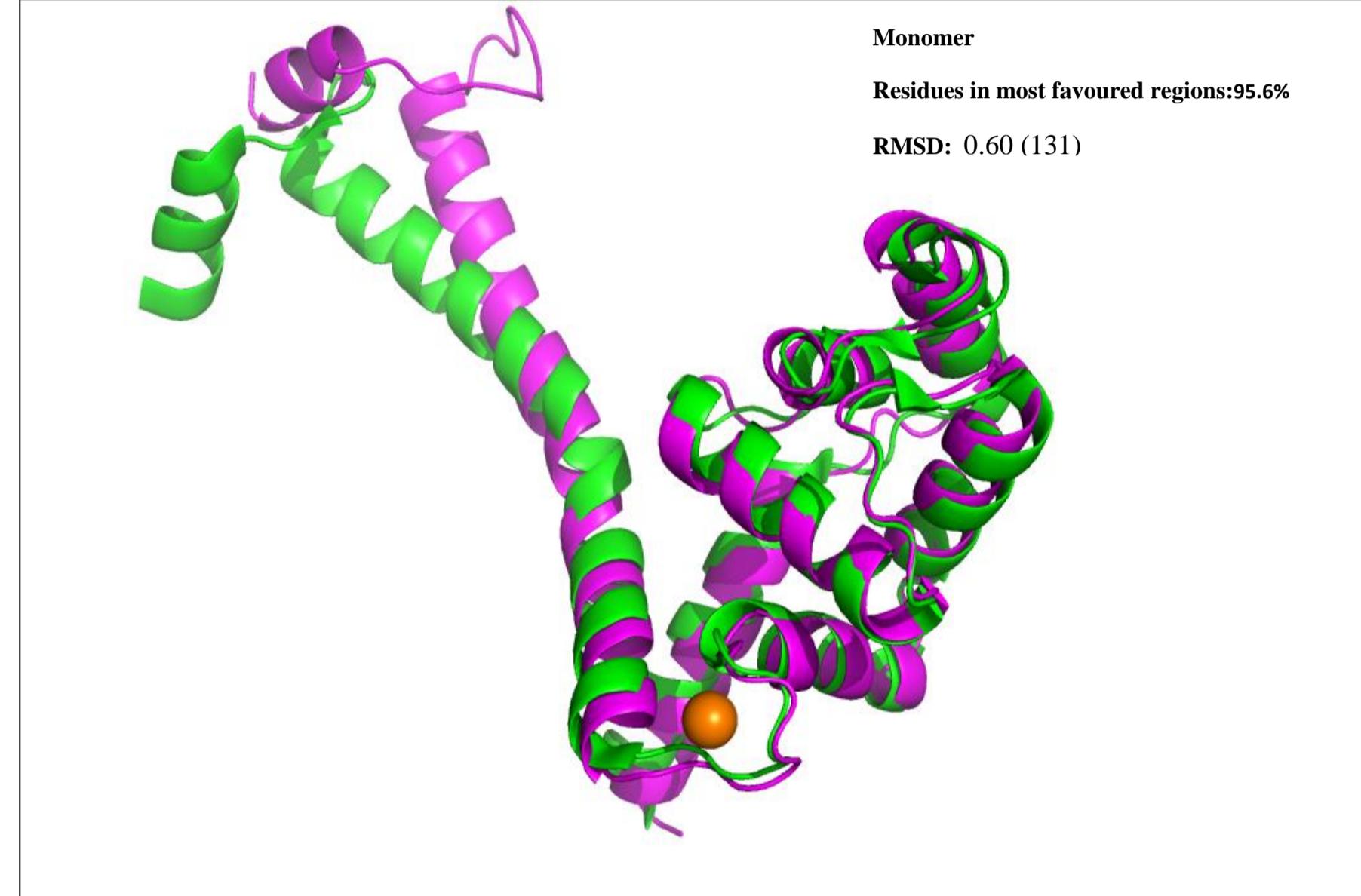
Sequence alignment of 3A8RA and AtRbohI showing conservation across the N-terminus. The sequence starts at residue 138 and ends at 303. Conserved residues are marked with asterisks (*). Insertions are shown as purple boxes above the sequence, and deletions are shown as red boxes below the sequence. Secondary structure elements I-182, N-214, V-267, and Y-316 are indicated by colored boxes below the sequence.

Model: AtRbohI.B99990001.pdb

Deletion associated with Ca-binding site : D-242 is absent in AtRboH1 (Minor deletion)

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGN-DGWAAVEKRFNQLQVDGVLLRSRGKICGMD--GSDEFAVQMFDSLARKRGIVKQVLTKDELKDFYEQLTDQGFNRLRTFFDMVDKNAIGTAEEVKEIIALSASANKLSKIKERADEYTALIMEELDPTNL--GYIEMEDLEALLL
AtRbohI 161 DGSGTERAIHGLKFISSKENGIVDWNDVQNNFAHLSKDGYLFKSDFAHIGLENENSKEFADELFDALCRRRIMVDKINLQELYEFWYQITDESFDTRLQIFNMV-KNGUGITENEVKEIIILSASANNLSRLRERAEEYAALIMEELAPDGLYSQYIELKDLEILL



18. AtRbohJ (NP_190167 – 180 aa)

- Sequence alignment of AtRbohJ with template using **Modeller9v8** is given as follows

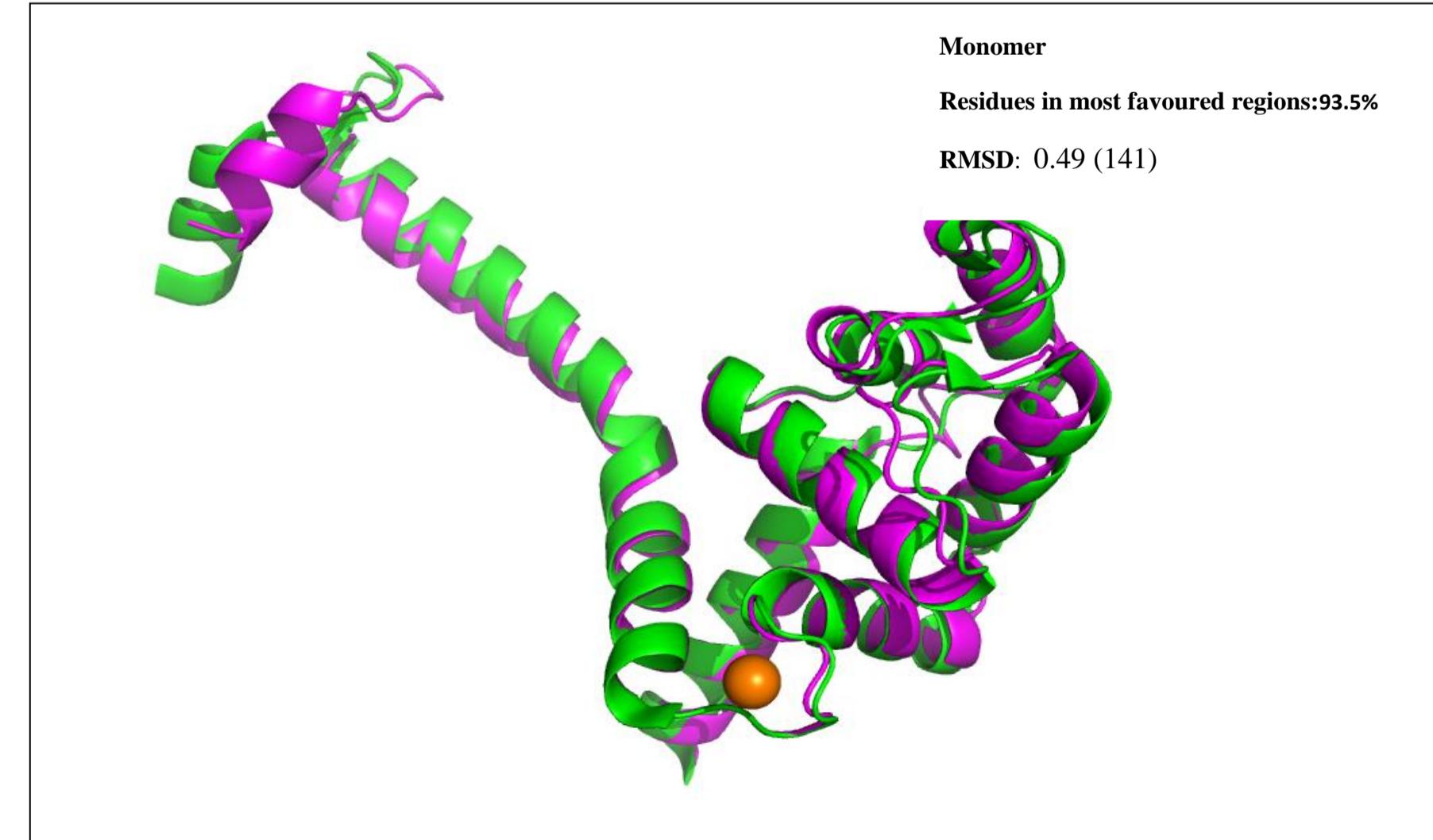
Sequence alignment of 3A8RA and AtRbohJ. The alignment shows conserved regions (consrvd) and mutations. Key residues highlighted include R-131 (purple box), N-187 (green box), and D-218 (blue box). The sequence starts at position 138 for 3A8RA and 110 for AtRbohJ.

Model: AtRbohJ.B99990001.pdb

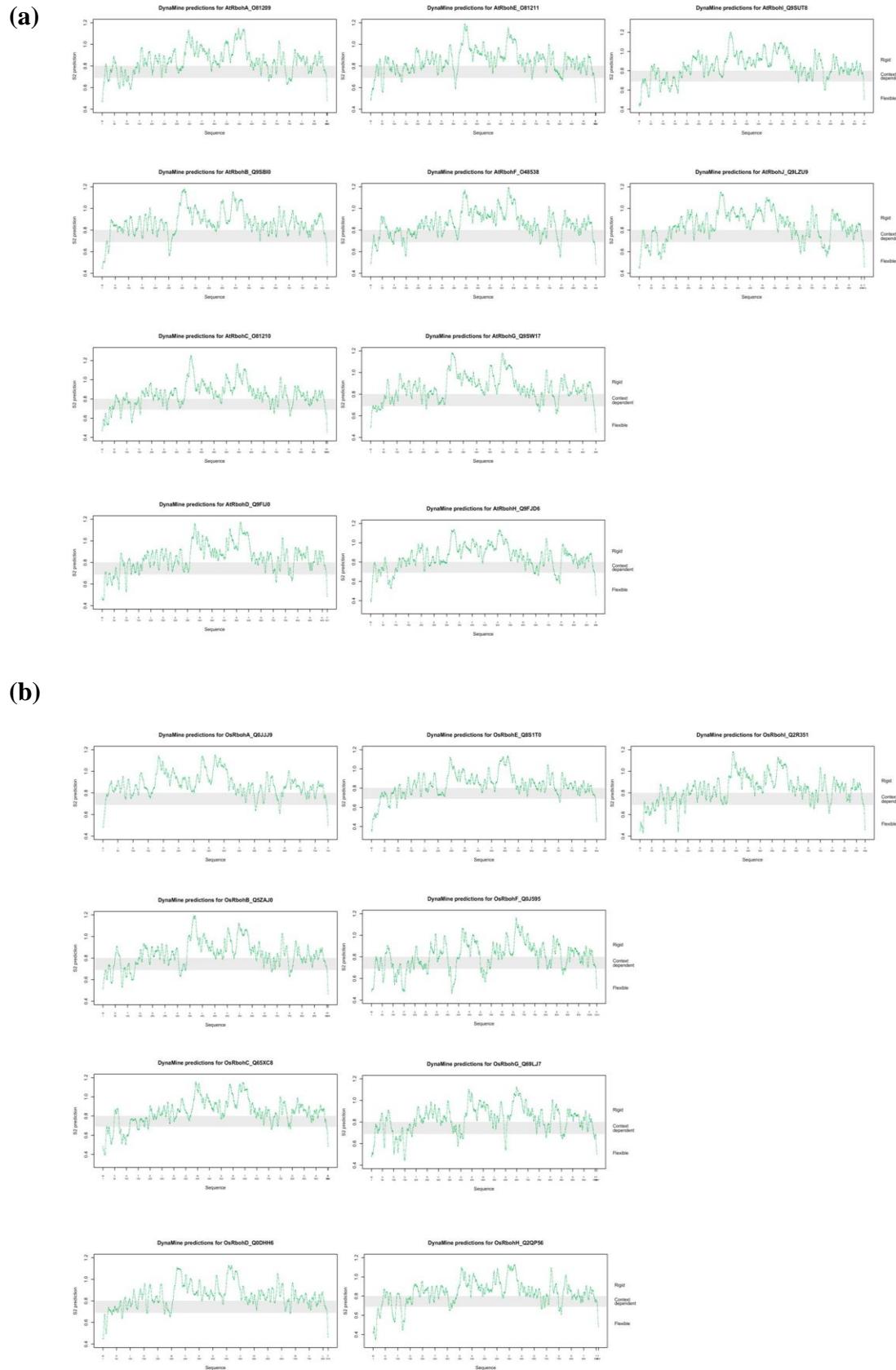
Mutations suggested for Ca-binding site in following Rbohs : Mutate D to N in AtRbohJ (because N is replaced by D)

- Edited alignment

3A8RA 138 TKSSAAVALKGLQFVTAKVGN---DGWAAVEKRFNQLQVDGVLLRSRGKCIQMDGSDEFAVQMFDSLARKRGIVKQ-VLTKEDELKDFYEQLTDQGFDNRRTFFDMVDKNAIGRLTAEHVKEIIALSASANKLSKIKERADEYTALIMEELDPTNLGYIEMEDLEALLIA
AtRbohJ 110 TTSSAARGLQSLRFLDRTVTGRERDSWRSIENRFNQFAVDGRLPKDKFGVCIGMGDTLEFAAKVYEALGRRQIKTENGIDKEQLKLFEDMIKKDLDTRLQIFFDMCOKDGUGKLTEEVKEIVLVSASANRLVNLKNAASYASLIMEELDPNEQGYIEMWQLEVLLTA



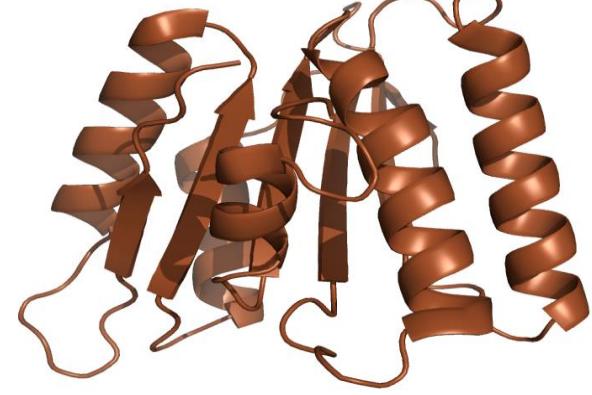
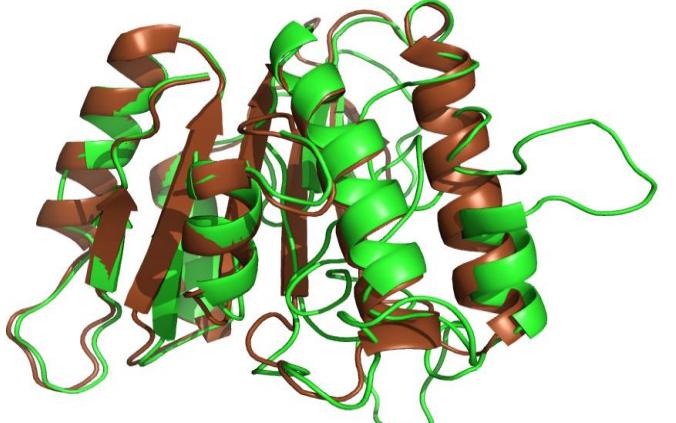
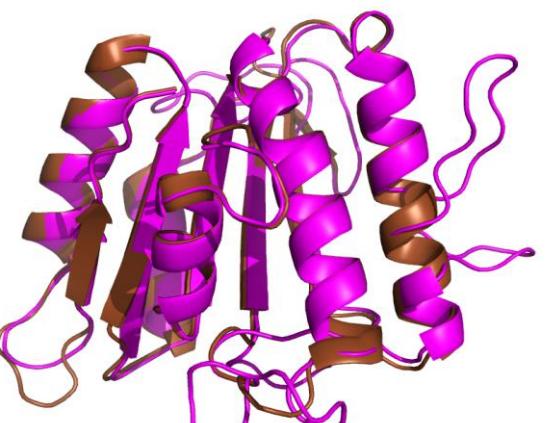
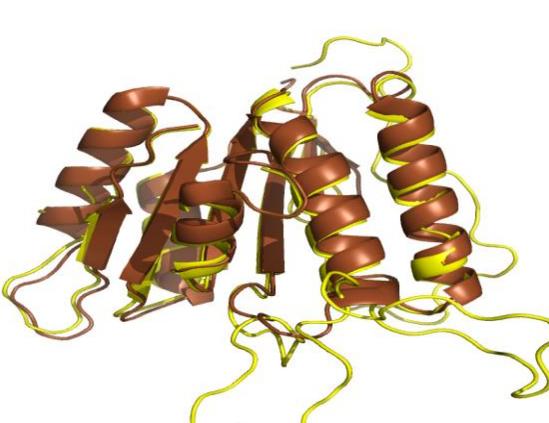
S7 File

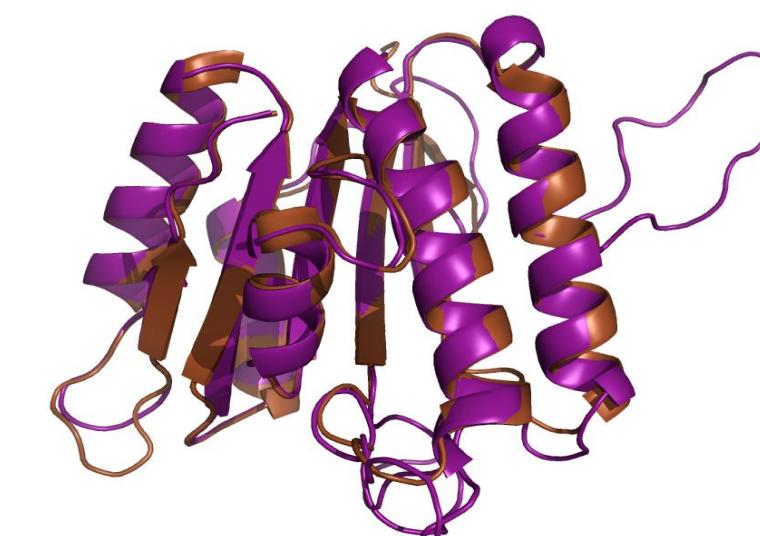
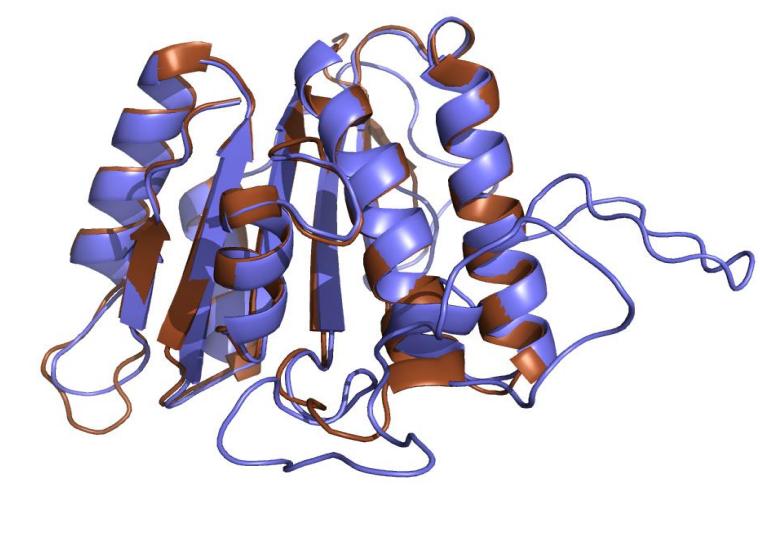
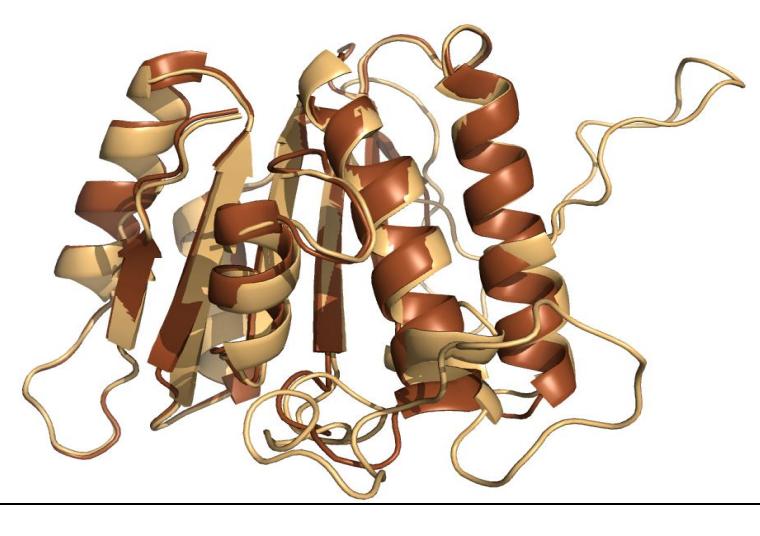


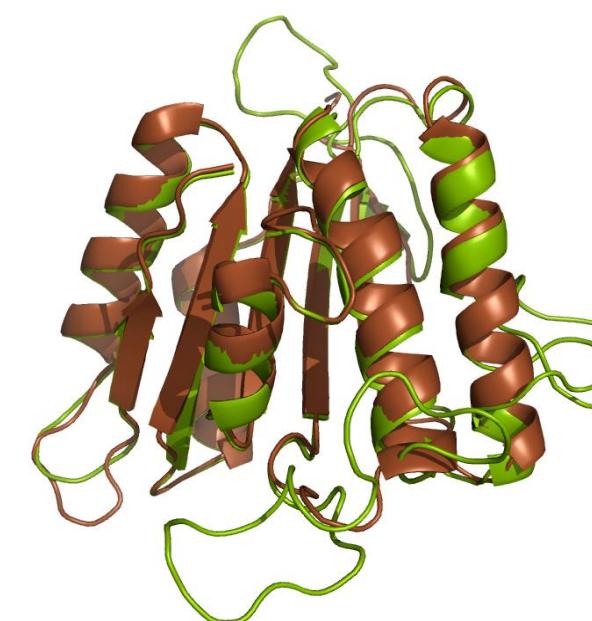
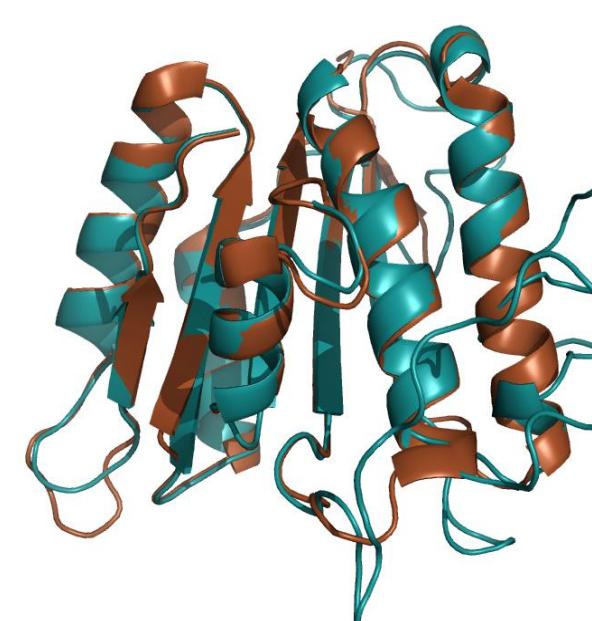
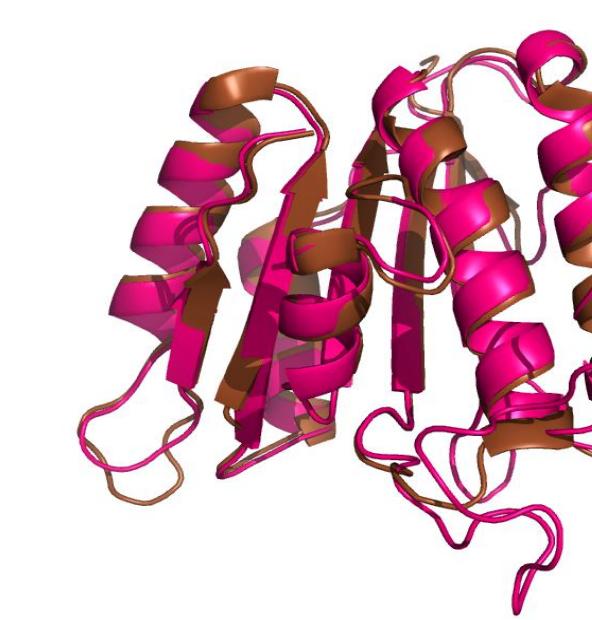
4 NADPH binding sites in 3A1F (target)

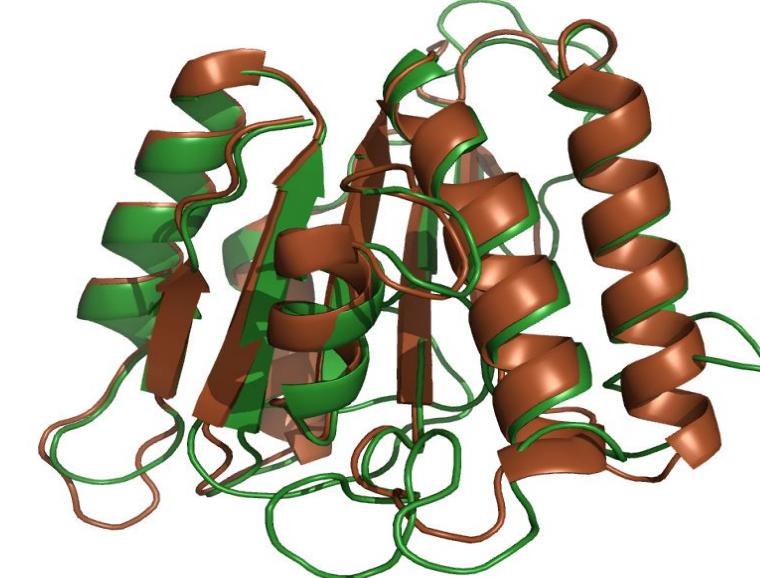
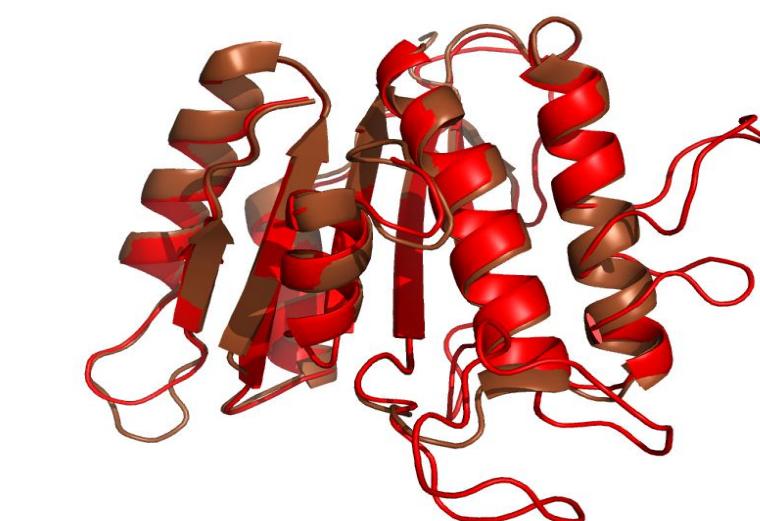
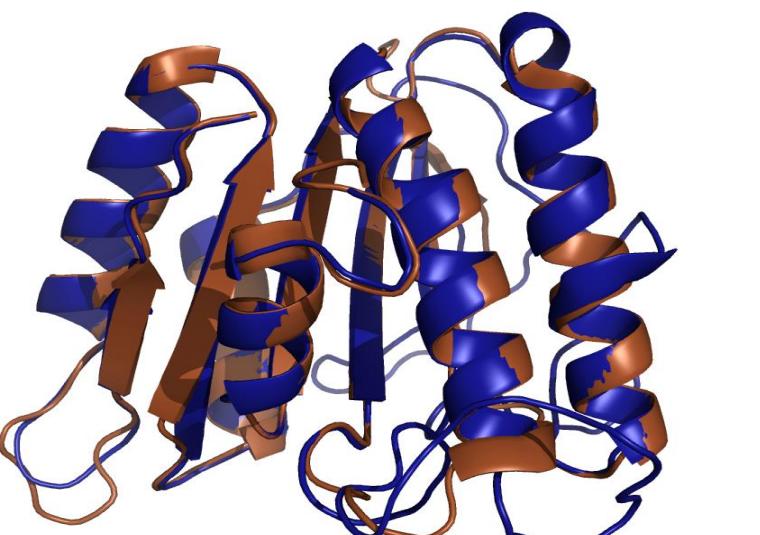
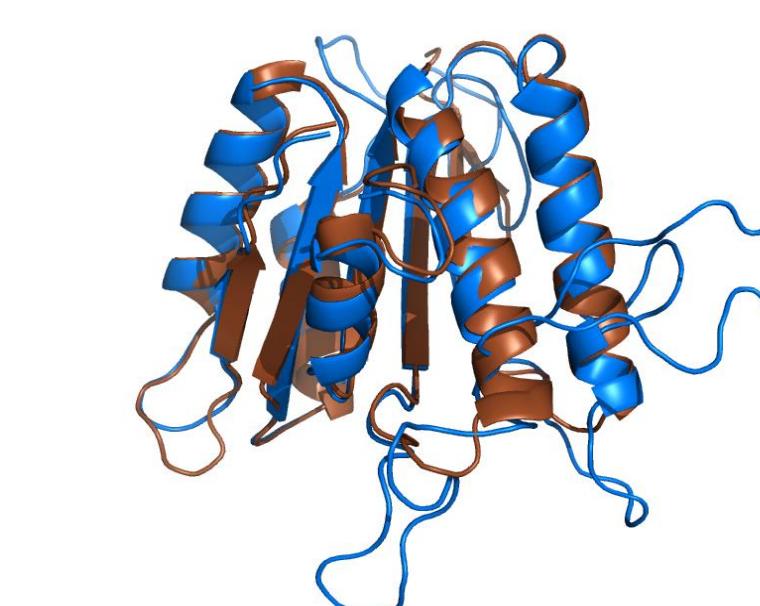
W-99, GLKQ-123 (GL coordinates missing from pdb)

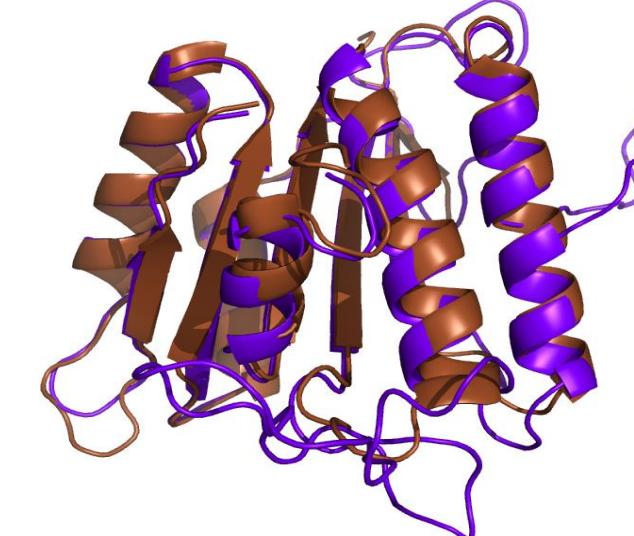
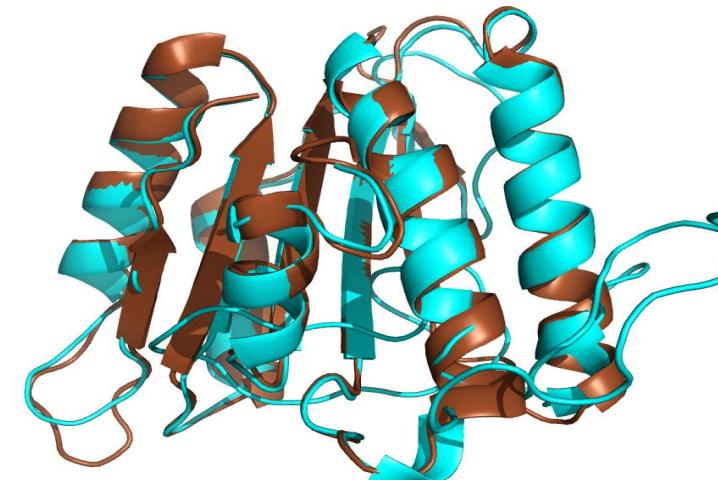
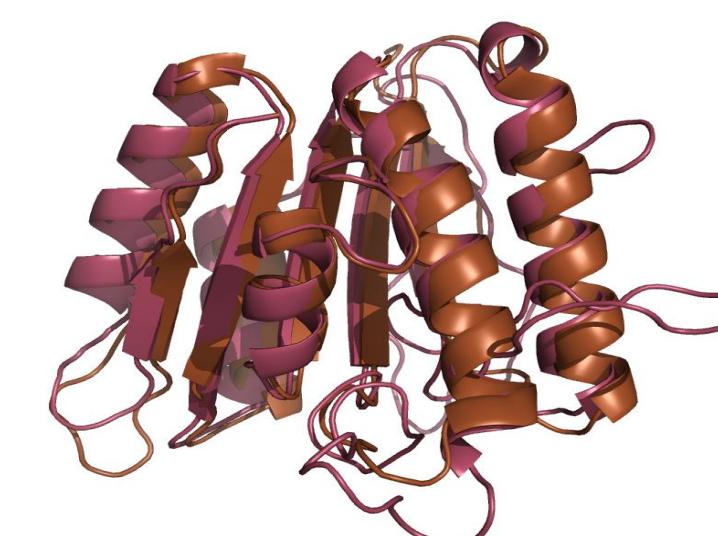
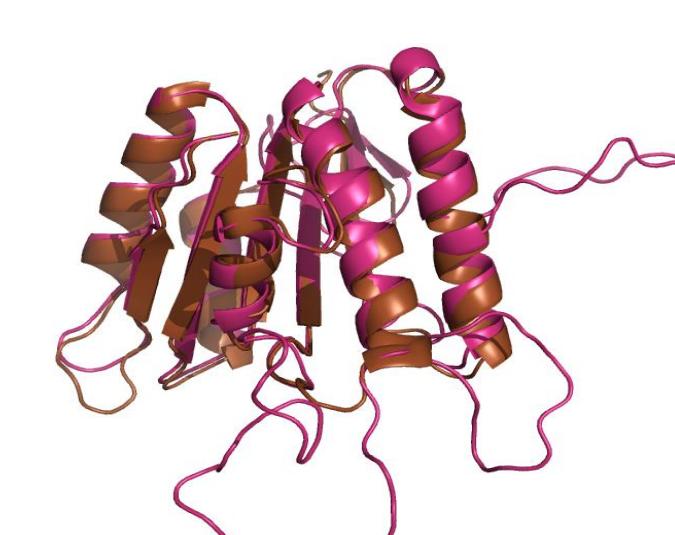
Good models of 5 Rbohs

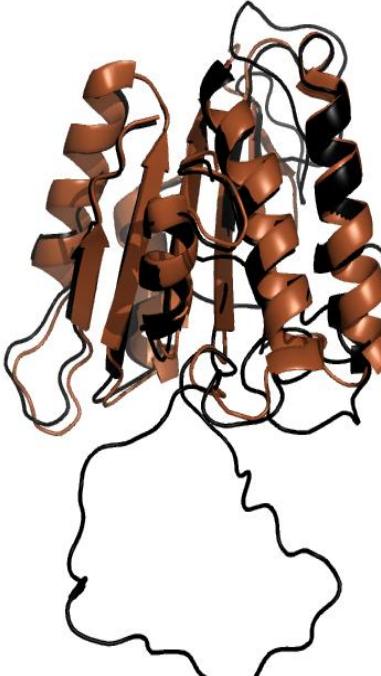
Template	3A1F The crystal structure of NADPH binding domain of gp91(phox)	570 aa (Full Nox2)	186 (coordinates from 100-122 absent = 164 aa)		NADPH-binding sites = 4 (i) MLVGAGIGVTPF = 21-32 (ii) YWLCRD = 58-63 (iii) GLKQ = (iv) FLCGPE					
S.No.	Rbohs	No. of amino acid residues in C-terminal (Clustal W alignment w.r.t. OsRbohB-Uniprot annotation)	Modelled residues	%age seq id	Superimposed 3D-Models with the template (3A1F)	Ramachandran values (%age allowed)	RMSD (C-alpha a)	Verify 3-D	Position of NADPH-binding residues	Mutations in NADPH-binding sites w.r.t. 3A1F
1.	OsRbohA	330 (R-414:F-743)	218 (D-526:F-743)	43.75		72.3	0.83 (143)	58.90% of the residues had an averaged 3D-1D score > 0.2	L-543:F-554	M→L-543, A→L-547, V→A-551
								Y-613:E-618	L→V-615, C→T-616, D→E-618	
								T-680	Q→T-680	
								F-710:P-715	L→Y-611, P→A-714, E→P-715	
2.	OsRbohB	316	201 (V-705:F-905)	39.751999		85.7	0.44 (152)	75.25% of the residues had an averaged 3D-1D score > 0.2	L-723:L-734	M→L-723, V→I-725, A→L-727, V→A-731, F→L-734,
								Y-775:E-780	L→V-777, C→T-778, D→E-780	
								V-844	Q→V-844	
								F-872:P-877	L→Y-873, P→E-876, E→P-877	
3.	OsRbohC	330	218 (D-734:951)	40.000000		84.9	0.52 (151)	59.82% of the residues had an averaged 3D-1D score > 0.2	L-751:F-762	M→L-751, A→L-755, V→A-759
								Y-821:E-826	L→V-823, C→T-824, D→E-826	
								Q-873	None	

S8 File									F-918:P-923	L→Y-919, P→A-922, E→P-923
4.	OsRbohD	320	200 (I-620:F-819)	37.888000		85.8	0.59 (149)	72.64% of the residues had an averaged 3D-1D score > 0.2	L-638:F-649	M→L-638, V→I-640, A→L-642, V→A-646
								Y-688:E-694	L→V-690, C→T-691, D→E-693	
								S-756	Q→S-756	
								F-786:P-791	L→Y-787, P→S-790, E→P-791	
5.	OsRbohE	319	199 (I-645:F-843)	37.266998		84.6	0.53 (152)	69.00% of the residues had an averaged 3D-1D score > 0.2	L-663:F-674	M→L-663, V→I-665, A→L-667, V→A-671
								Y-713:E-718	L→V-715, C→T-716, D→E-718	
								D-775	Q→D-775	
								F-810:P-815	L→Y-811, P→S-814, E→P-815	
6.	OsRbohF	327	215 (V-819:F-1033)	41.615002		83.0	0.63 (153)	70.83% of the residues had an averaged 3D-1D score > 0.2	L-837:F-848	M→L-837, A→L-841, V→A-845
								Y-903:E-908	L→V-905, C→T-906, D→E-908	
								K-961	Q→K-961	
								F-1000:P-1005	L→Y-1001, P→K-1004, E→P-1005	
7.	OsRbohG	327	215 (V-793:F-1007)	42.236000		83.5	0.61 (151)	61.57% of the residues had an averaged 3D-1D score > 0.2	L-811:F-822	M→L-811, A→L-815, V→A-819
								Y-877:E-882	L→V-879, C→T-880, D→E-882	
								K-935	Q→K-935	

S8 File									F-974:P-979	L→Y-975, P→K-978, E→P-979
8.	OsRboH	281	206 (I-687:F-892)	37.888000		81.1	0.53 (150)	91.79% of the residues had an averaged 3D-1D score > 0.2	L-705:L-716	M→L-705, V→I-707, A→L-709, V→A-713, F→L-716
								Y-761:E-766	L→C-763, C→T-764, D→E-766	
								V-831	Q→V-831	
								F-859:Q-864	L→F-860, P→D-863, E→Q-864	
9.	OsRbohI	319	202 (D-735:F-936)	38.750000		86.6	0.53 (150)	81.28% of the residues had an averaged 3D-1D score > 0.2	L-752:L-763	M→L-752, A→L-756, V→A-760, F→M-763
								Y-806:E-811	L→V-808, C→T-809, D→E-811	
								V-875	Q→V-875	
								F-903:P-908	L→Y-904, P→A-907, E→P-908	
10.	AtRbohA	324	209 (D-694:F-902)	39.375000		86.4	0.36 (150)	74.29% of the residues had an averaged 3D-1D score > 0.2	L-711:M-722	M→L-711, A→L-715, V→A-719, F→M-722
								Y-772:E-777	L→V-774, C→T-775, D→E-777	
								T-839	Q→T-839	
								F-869:A-874	L→Y-870, P→A-873, E→A-874	

S8 File	11.	AtRbohB	311	197 (I-647:F-843)	37.888000		80.8	0.65 (147)	83.33% of the residues had an averaged 3D-1D score > 0.2	L-665:L-676	M→L-665, A→L-669, V→A-673, F→L-676
										Y-713:E-718	L→V-715, C→T-716, D→E-718
										V-782	Q→V-782
										F-810, T-815	L→Y-811, P→N-814, E→T-815
12.	AtRbohC	319	204 (D-664:F-867)	38.125000		82.5	0.43 (151)	71.22% of the residues had an averaged 3D-1D score > 0.2	L-681, M-692	M→L-681, A→L-685, V→A-689, F→M-692	
										F-736, E-742	L→V-738, C→T-739, D→E-741
										T-804	Q→T-804
										F-834, P-839	L→Y-835, P→A-838, E→P-839
13.	AtRbohD	312	199 (D-723:F-921)	40.625000		81.5	0.55 (149)	68.00% of the residues had an averaged 3D-1D score > 0.2	L-740:M-751	M→L-740, A→L-744, V→A-748, F→M-751	
										Y-791:E-796	L→V-793, C→T-794, D→E-796
										Q-846, K-861	None
										F-888:P-893	L→Y-889, P→M-892, E→P-893
14.	AtRbohE	328	215 (V-734:F-948)	40.993999		84.3	0.53 (148)	68.06% of the residues had an averaged 3D-1D score > 0.2	L-752:F-763	M→L-752, V→I-754, A→L-756, V→A-760	
										Y-818:E-823	L→V-820, C→T-821, D→E-823
										V-887	Q→V-887
										F-915:Q-920	L→Y-916, P→I-919, E→Q-920

S8 File											
15.	AtRbohF	324	212 (D-733:F-944)	39.375000		82.9	0.49 (147)	59.15% of the residues had an averaged 3D-1D score > 0.2	L-750:761	M→L-750, A→L-754, V→A-758	
									Y-814:E-819	L→V-816, C→T-817, D→E-819	
									V-883	Q→V-883	
									F-911:P-916	L→Y-912, P→V-915, E→P-916	
16.	AtRbohG	310	202 (D-648:F-849)	36.250000		81.0	0.48 (148)	84.73% of the residues had an averaged 3D-1D score > 0.2	L-665:M-676	M→L-665, V→I-667, A→L-669, V→A-673, F→M-676	
									Y-719:E-724	L→V-721, C→T-722, R→K-723, D→E-724	
									T-786	Q→T-786	
									F-816:P-821	L→Y-817, P→A-820, E→P-821	
17.	AtRbohH	337	213 (I-674:F-886)	37.423000		84.5%	0.74 (150)	82.24% of the residues had an averaged 3D-1D score > 0.2	L-694:F-705	M→L-694, A→L-698, V→A-702	
									F-756:E-761	V→F-756, L→V-758, C→T-759, D→E-761	
									Q-811	None	
									F-853:P-858	L→Y-854, P→S-857, E→P-858	
18.	AtRbohI	334	223 (I-719:F-941)	39.130001		83.4	0.53 (150)	61.16% of the residues had an averaged 3D-1D score > 0.2	L-737:F-748	M→L-737, A→L-741, V→A-745	
									Y-811:E-816	L→V-813, C→T-814, D→E-816	
									V-880	Q→V-880	
									F-908:P-913	L→Y-909, P→V-912, E→P-913	

S8 File	19.	AtRbohJ	353	230 (I-683:F-912)	36.810001		79.1%	0.72 (145)	63.64% of the residues had an averaged 3D-1D score > 0.2	L-703:F-714	M→L-703, V→I-705, A→L-707, V→A-711
									Y-782:E-787	L→V-784, C→T-785, D→E-787	
									Q-837	None	
									F-879:P-884	L→Y-880, P→S-883, E→P-884	