wwPDB EM Validation Summary Report (i)

May 11, 2024 – 07:48 pm BST

PDB ID	:	6R9G
EMDB ID	:	EMD-4770
Title	:	Structural basis of transcription inhibition by the DNA mimic Ocr protein of bacteriophage T7
Authors	:	Ye, F.Z.; Zhang, X.D.
Deposited on	:	2019-04-03
Resolution	:	3.70 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

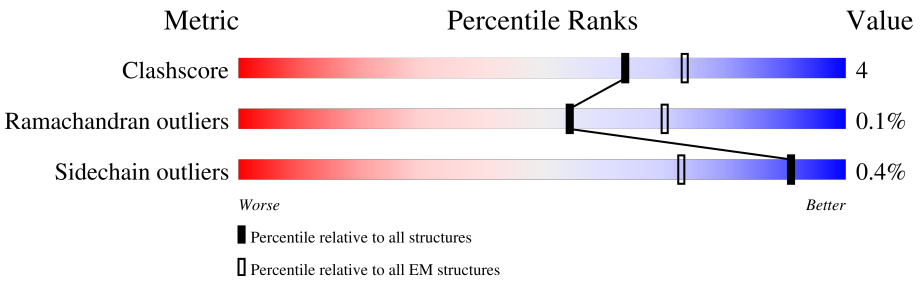
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	329	70% 61% 9% 30%
1	B	329	70% 63% 7% • 30%
2	C	1342	99% 86% 13%
3	D	1407	94% 86% 9% 5%
4	E	80	94% 88% 6% 6%
5	F	117	91% 79% 12% 9%
5	G	117	89% 79% 10% 11%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 25944 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	230	1765	1100	308	351	6	0	0
1	B	231	1743	1090	301	346	6	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	1341	10112	6334	1735	2006	37	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	1334	10051	6297	1777	1934	43	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	75	572	351	110	109	2	0	0

- Molecule 5 is a protein called Overcome classical restriction gp0.3.

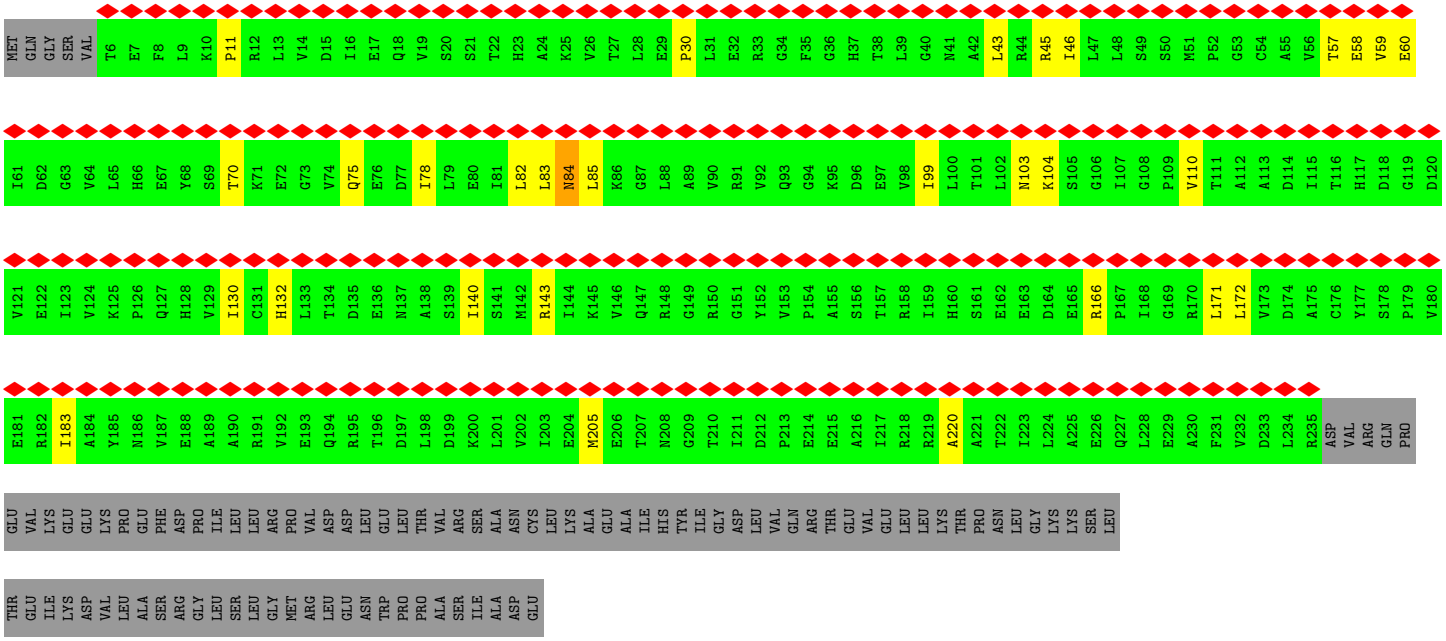
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	104	849	534	131	179	5	0	0
5	F	106	852	530	136	182	4	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

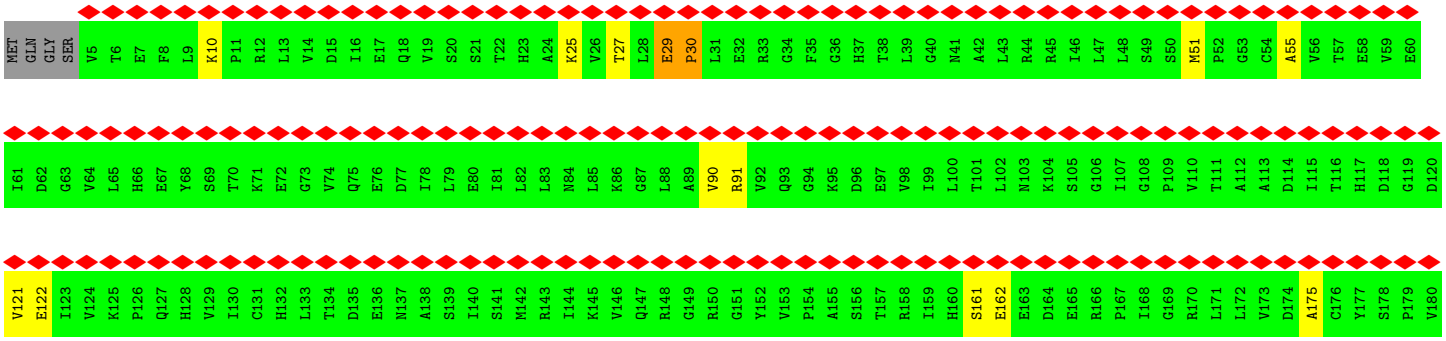
- Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain A:



- Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain B:



E181 R182 I183 A184 Y185 N186 V187 E188 A189 A190 R191 V192 E193 Q194 R195 T196 D197 L198 D199 K200 L201 V202 I203 E204 M205 E206 T207 N208 G209 T210 I211 D212 P213 E214 E215 A216 I217 R218 R219 A220 A221 T222 I223 L224 A225 E226 Q227 L228 E229 A230 F231 V232 D233 L234 R235 ASP VAL ARG GLN PRO

GLU VAL LYS GLU GLU LYS PRO GLU PHE ASP PRO ILE LEU LEU ARG PRO VAL ASP ASP LEU GLU LEU THR VAL ARG SER ALA ASN CYS LEU LYS ALA GLU ALA ILE HIS TYR ILE GLY ASP LEU VAL GLN ARG THR GLU VAL GLU LEU LEU LYS THR PRO ASN LEU GLY LYS LYS SER LEU

THR GLU ILE LYS ASP VAL LEU ALA SER ARG GLY LEU SER LEU GLY MET ARG LEU GLU ASN TRP PRO PRO ALA SER ILE ALA ASP GLU

- Molecule 2: DNA-directed RNA polymerase subunit beta

Chain C: 99% 86% 13%

M1 V2 Y3 S4 Y5 T6 E7 K8 K9 R10 I11 R12 K13 D14 F15 G16 K17 R18 P19 Q20 V21 L22 D23 V24 P25 Y26 L27 L28 S29 I30 Q31 L32 D33 S34 F35 Q36 K37 F38 I39 E40 Q41 D42 P43 E44 G45 Q46 Y47 G48 L49 E50 A51 A52 F53 R54 S55 V56 F57 P58 I59 Q60

S61 Y62 S63 G64 N65 S66 E67 L68 Q69 Y70 V71 S72 Y73 R74 L75 G76 E77 P78 V79 F80 D81 V82 Q83 E84 C85 Q86 I87 R88 G89 V90 T91 Y92 S93 A94 P95 L96 R97 V98 K99 L100 R101 L102 V103 I104 Y105 E106 R107 E108 A109 P110 E111 G112 T113 V114 K115 D116 I117 K118 E119 Q120

E121 V122 Y123 M124 G125 E126 I127 P128 L129 M130 T131 D132 N133 G134 T135 F136 V137 I138 N139 G140 T141 E142 R143 V144 I145 V146 S147 Q148 L149 H150 R151 S152 P153 G154 V155 F156 F157 D158 S159 D160 K161 G162 K163 T164 H165 S166 S167 G168 K169 V170 L171 Y172 N173 A174 R175 I176 I177 P178 Y179 R180

G181 S182 W183 L184 D185 F186 E187 F188 D189 P190 K191 D192 N193 L194 F195 V196 R197 I198 D199 R200 R201 R202 K203 L204 P205 A206 T207 I208 I209 L210 R211 A212 L213 N214 Y215 T216 T217 E218 Q219 I220 L221 D222 L223 F224 F225 E226 K227 V228 I229 F230 E231 I232 R233 D234 N235 K236 L237 Q238 M239 E240

L241 V242 P243 E244 R245 L246 R247 G248 E249 T250 A251 S252 F253 D254 I255 E256 A257 N258 G259 K260 V261 Y262 V263 E264 K265 G266 R267 R268 I269 T270 A271 R272 H273 I274 R275 Q276 L277 E278 K279 D280 D281 V282 K283 L284 I285 E286 V287 P288 V289 E290 Y291 I292 A293 G294 K295 V296 V297 A298 K299 D300

Y301 I302 D303 E304 S305 T306 G307 E308 L309 I310 C311 A312 A313 N314 M315 E316 L317 S318 L319 D320 L321 L322 A323 K324 L325 S326 Q327 S328 G329 H330 K331 R332 I333 E334 T335 L336 F337 T338 N339 D340 L341 D342 H343 G344 P345 Y346 I347 S348 E349 T350 L351 R352 V353 D354 P355 T356 N357 D358 R359 L360

S361 A362 L363 V364 E365 I366 Y367 R368 M369 M370 R371 P372 G373 E374 P375 P376 T377 R378 E379 A380 A381 E382 S383 I384 F385 E386 N387 L388 F389 F390 S391 E392 D393 R394 Y395 D396 L397 S398 A399 V400 G401 R402 M403 K404 F405 N406 R407 S408 L409 L410 R411 E412 E413 I414 E415 G416 S417 G418 I419 L420

S421 K422 D423 D424 I425 I426 D427 V428 M429 K430 K431 L432 I433 D434 I435 R436 N437 G438 K439 G440 E441 V442 D443 D444 I445 D446 H447 L448 G449 N450 R451 R452 I453 R454 S455 V456 G457 E458 M459 A460 E461 N462 Q463 F464 R465 V466 G467 L468 V469 R470 V471 E472 R473 A474 V475 K476 E477 R478 L479 S480

L481 G482 D483 L484 D485 T486 L487 M488 P489 Q490 D491 M492 I493 N494 A495 K496 P497 I498 S499 A500 A501 V502 K503 E504 F505 F506 G507 S508 S509 Q510 L511 S512 Q513 F514 M515 D516 Q517 N518 N519 P520 L521 S522 E523 I524 T525 H526 K527 R528 R529 I530 S531 A532 L533 G534 P535 G536 G537 L538 T539 R540

E541 R542 A543 G544 F545 E546 V547 R548 D549 V550 H551 P552 T553 H554 Y555 G556 R557 V558 C559 P560 I561 E562 T563 P564 E565 G566 P567 N568 I569 G570 L571 I572 N573 S574 L575 S576 V577 Y578 A579 Q580 T581 N582 E583 Y584 G585 F586 L587 E588 T589 P590 Y591 R592 K593 V594 T595 D596 G597 V598 V599 T600

D601 E602 I603 H604 Y605 L606 S607 A608 I609 E610 E611 G612 N613 Y614 V615 I616 A617 Q618 A619 N620 S621 N622 L623 D624 E625 E626 G627 H628 F629 V630 E631 D632 L633 V634 T635 C636 R637 S638 K639 G640 E641 S642 S643 L644 F645 S646 R647 D648 Q649 V650 D651 Y652 M653 D654 V655 S656 T657 Q658 Q659 V660

V661 S662 V663 G664 A665 S666 L667 I668 P669 F670 L671 E672 H673 D674 D675 A676 N677 R678 A679 L680 M681 G682 A683 N684 M685 Q686 R687 Q688 A689 V690 P691 T692 L693 R694 A695 D696 K697 P698 L699 V700 G701 T702 G703 M704 E705 R706 A707 V708 A709 V710 D711 S712 G713 V714 T715 A716 V717 A718 K719 R720

G721 G722 V723 V724 Q725 Y726 V727 D728 A729 S730 R731 I732 V733 I734 K735 V736 N737 E738 D739 E740 M741 Y742 P743 G744 E745 A746 G747 I748 D749 I750 Y751 N752 L753 T754 K755 Y756 T757 R758 S759 N760 Q761 N762 T763 C764 I765 N766 Q767 M768 P769 C770 V771 S772 L773 G774 E775 P776 V777 E778 R779 G780

D781 V782 L783 A784 D785 G786 P787 S788 T789 D790 L791 G792 E793 L794 A795 L796 G797 Q798 N799 M800 R801 V802 A803 F804 M805 P806 W807 N808 G809 Y810 N811 F812 E813 D814 S815 I816 L817 V818 S819 E820 R821 V822 V823 Q824 E825 D826 R827 F828 T829 T830 I831 H832 I833 Q834 E835 L836 A837 C838 V839 S840

R841 D842 T843 K844 L845 G846 P847 E848 E849 I850 T851 A852 D853 I854 P855 N856 V857 G858 E859 A860 A861 L862 S863 K864 L865 D866 E867 S868 G869 I870 V871 Y872 I873 G874 A875 E876 V877 T878 G879 G880 D881 I882 L883 V884 G885 K886 V887 T888 P889 K890 G891 E892 T893 Q894 L895 T896 P897 E898 E899 K900

L901 L902 R903 A904 I905 F906 G907 E908 K909 A910 S911 D912 V913 K914 D915 S916 S917 L918 R919 V920 P921 N922 G923 V924 S925 G926 T927 V928 I929 D930 V931 Q932 V933 F934 T935 R936 D937 G938 V939 E940 K941 D942 K943 R944 A945 L946 E947 I948 E949 E950 M951 Q952 L953 K954 Q955 A956 K957 K958 D959 L960

S961 E962 E963 L964 Q965 I966 L967 E968 A969 G970 L971 F972 S973 R974 I975 R976 A977 V978 L979 V980 A981 G982 G983 V984 E985 A986 E987 K988 L989 D990 K991 L992 P993 R994 D995 R996 W997 L998 E999 L1000 G1001 L1002 T1003 D1004 E1005 E1006 K1007 Q1008 N1009 Q1010 L1011 E1012 Q1013 L1014 A1015 E1016 Q1017 Y1018 D1019 E1020

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E1083 D1084 M1085 P1086 Y1087 D1088 E1089 N1090 G1091 T1092 P1093 V1094 D1095 I1096 V1097 L1098 N1099 P1100 L1101 G1102 V1103 P1104 S1105 R1106 M1107 N1108 I1109 G1110 Q1111 I1112 L1113 E1114 T1115 H1116 L1117 G1118 M1119 A1120 A1121 K1122 G1123 I1124 G1125 D1126 K1127 I1128 N1129 A1130 M1131 L1132 K1133 Q1134 Q1135 Q1136 E1137 V1138 A1139 K1140 L1141 R1142

E1143 F1144 I1145 Q1146 R1147 A1148 Y1149 D1150 L1151 G1152 A1153 D1154 V1155 R1156 Q1157 K1158 V1159 D1160 L1161 S1162 T1163 F1164 S1165 D1166 E1167 E1168 V1169 M1170 R1171 L1172 A1173 E1174 N1175 L1176 R1177 K1178 G1179 M1180 P1181 I1182 A1183 T1184 P1185 V1186 F1187 D1188 G1189 A1190 K1191 E1192 A1193 E1194 I1195 K1196 E1197 L1198 L1199 K1200 L1201 G1202

D1203 L1204 P1205 T1206 S1207 G1208 Q1209 I1210 R1211 L1212 Y1213 D1214 G1215 R1216 T1217 G1218 E1219 Q1220 F1221 E1222 R1223 P1224 V1225 T1226 V1227 G1228 Y1229 M1230 Y1231 M1232 L1233 K1234 L1235 N1236 H1237 L1238 V1239 D1240 D1241 K1242 M1243 H1244 A1245 R1246 S1247 T1248 G1249 S1250 Y1251 S1252 L1253 V1254 T1255 Q1256 Q1257 P1258 L1259 G1260 G1261 K1262

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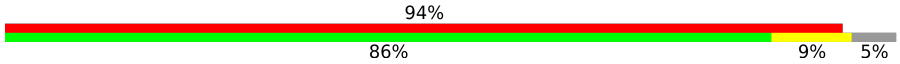
F1323 N1324 V1325 L1326 L1327 K1328 E1329 I1330 R1331 S1332 L1333 G1334 I1335 N1336 I1337 E1338 L1339 E1340 D1341 GLU

- Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain D:



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I61 F62 G63 P64 V65 K66 D67 Y68 E69 C70 L71 C72 G73 K74 Y75 K76 R77 L78 K79 H80 R81 G82 V83 I84 C85 E86 K87 C88 G89 V90 E91 V92 T93 Q94 T95 K96 V97 R98 R99 E100 R101 M102 G103 H104 I105 E106 L107 A108 S109 P110 T111 A112 H113 I114 W115 F116 L117 K118 S119 L120

P121 S122 R123 I124 G125 L126 L127 L128 D129 M130 P131 L132 R133 D134 I135 E136 R137 V138 L139 Y140 F141 E142 S143 Y144 V145 V146 I147 E148 G149 G150 M151 T152 N153 L154 E155 R156 Q157 Q158 I159 L160 T161 E162 E163 Q164 Y165 L166 D167 A168 L169 E170 E171 F172 G173 D174 E175 F176 D177 A178 K179 M180

G181 A182 E183 A184 I185 Q186 A187 L188 L189 K190 S191 M192 D193 L194 E195 Q196 E197 C198 E199 Q200 L201 R202 E203 E204 L205 N206 E207 T208 N209 S210 E211 T212 K213 R214 K215 K216 L217 T218 K219 R220 I221 K222 L223 L224 E225 A226 F227 V228 Q229 S230 G231 N232 K233 P234 E235 W236 M237 I238 L239 T240

V241 L242 P243 V244 L245 P246 P247 D248 L249 R250 P251 L252 V253 P254 L255 D256 G257 G258 R259 F260 A261 T262 S263 D264 L265 N266 D267 L268 Y269 R270 R271 V272 I273 N274 R275 N276 N277 R278 L279 K280 R281 L282 L283 D284 L285 A286 A287 P288 D289 I290 I291 V292 R293 N294 E295 K296 R297 M298 L299 Q300

E301 A302 V303 D304 A305 L306 L307 D308 N309 G310 R311 R312 G313 R314 A315 I316 T317 G318 S319 N320 K321 R322 P323 L324 K325 S326 L327 A328 D329 M330 I331 K332 G333 K334 Q335 G336 R337 F338 R339 Q340 N341 L342 L343 G344 K345 R346 V347 D348 Y349 R352 S353 V354 I355 T356 V357 G358 P359 Y360 L361

R362 L363 H364 Q365 C366 G367 L368 P369 K370 K371 M372 A373 L374 E375 L376 F377 K378 P379 F380 I381 Y382 G383 K384 L385 E386 L387 R388 G389 L390 A391 T392 T393 I394 K395 A396 A397 K398 K399 M400 V401 E402 R403 E404 E405 A406 V407 V408 W409 D410 I411 L412 D413 E414 V415 I416 R417 E418 H419 P420 V421

L422 L423 N424 R425 A426 P427 T428 L429 H430 R431 L432 G433 I434 Q435 A436 F437 E438 P439 V440 L441 I442 E443 G444 K445 A446 I447 Q448 L449 H450 P451 L452 V453 C454 A455 A456 Y457 N458 A459 D460 F461 D462 G463 D464 Q465 M466 A467 V468 H469 V470 P471 L472 T473 L474 E475 A476 Q477 L478 E479 A480 R481

A482 L483 M484 M485 S486 T487 N488 N489 I490 L491 S492 P493 A494 N495 G496 E497 P498 I499 I500 V501 P502 S503 Q504 D505 V506 V507 L508 G509 L510 Y511 V512 M513 T514 R515 D516 C517 V518 N519 A520 K521 G522 E523 G524 M525 V526 L527 T528 G529 P530 K531 E532 A533 E534 R535 L536 Y537 R538 S539 G540 L541

A542 S543 L544 H545 A546 R547 V548 K549 V550 R551 I552 T553 E554 Y555 E556 K557 D558 A559 N560 G561 E562 L563 V564 A565 K566 T567 S568 L569 K570 D571 T572 T573 V574 G575 R576 A577 I578 L579 W580 M581 I582 V583 P584 K585 G586 L587 P588 Y589 S590 I591 V592 N593 Q594 A595 L596 G597 K598 K599 A600 I601

S602 K603 M604 L605 N606 T607 C608 Y609 R610 I611 I612 G613 L614 K615 P616 T617 V618 I619 F620 A621 D622 Q623 I624 M625 Y626 T627 G628 F629 A630 Y631 A632 A633 R634 S635 G636 A637 S638 V639 G640 I641 D642 D643 M644 V645 I646 P647 E648 K649 K650 H651 E652 I653 I654 S655 E656 A657 E658 A659 E660 V661

A662 E663 I664 Q665 E666 Q667 F668 Q669 S670 G671 L672 V673 T674 A675 G676 E677 R678 Y679 N680 K681 V682 I683 D684 I685 W686 A687 A688 A689 N690 D691 R692 V693 S694 K695 A696 M697 M698 D699 N700 L701 Q702 T703 E704 T705 V706 I707 N708 R709 D710 G711 Q712 E713 E714 K715 Q716 V717 S718 F719 N720 S721

I722 Y723 M724 M725 A726 D727 S728 G729 A730 R731 G732 S733 A734 A735 Q736 I737 R738 Q739 L740 A741 G742 M743 R744 G745 L746 M747 A748 K749 P750 D751 G752 S753 I754 I755 E756 T757 P758 I759 T760 A761 N762 F763 R764 E765 G766 L767 N768 V769 L770 Q771 Y772 F773 I774 S775 T776 H777 G778 A779 R780 K781

G782 L783 A784 D785 T786 A787 L788 K789 T790 A791 N792 S793 G794 Y795 L796 T797 R798 R799 L800 V801 D802 V803 A804 Q805 D806 L807 V808 V809 T810 E811 D812 D813 C814 G815 T816 H817 E818 G819 I820 M821 M822 T823 P824 V825 I826 E827 G828 G829 D830 V831 K832 E833 P834 L835 R836 D837 R838 V839 L840 G841

R842 V843 T844 A845 E846 D847 V848 L849 K850 P851 G852 T853 A854 D855 I856 L857 V858 P859 R860 N861 T862 L863 L864 H865 E866 Q867 W868 C869 D870 L871 L872 E873 E874 N875 S876 V877 D878 A879 V880 K881 V882 R883 S884 V885 V886 S887 C888 D889 T890 D891 F892 G893 V894 C895 A896 H897 C898 Y899 G900 R901

D902 L903 A904 R905 G906 H907 I908 I909 N910 K911 G912 E913 A914 I915 G916 V917 I918 A919 A920 Q921 S922 I923 G924 E925 P926 G927 T928 Q929 L930 T931 M932 R933 T934 F935 H936 I937 G938 G939 A940 A941 S942 R943 A944 A945 A946 E947 S948 S949 I950 Q951 V952 K953 N954 K955 G956 S957 I958 K959 L960 S961

N962 V963 K964 S965 V966 V967 N968 S969 S970 G971 K972 L973 V974 I975 T976 S977 R978 N979 T980 E981 I982 K983 L984 I985 D986 E987 F988 G989 R990 T991 K992 E993 S994 Y995 K996 V997 P998 Y999 G1000 A1001 V1002 L1003 A1004 K1005 G1006 D1007 G1008 E1009 Q1010 V1011 A1012 G1013 G1014 E1015 T1016 V1017 A1018 N1019 W1020 D1021

P1022 H1023 T1024 M1025 P1026 V1027 I1028 T1029 E1030 V1031 S1032 G1033 F1034 V1035 R1036 F1037 T1038 D1039 M1040 I1041 D1042 G1043 Q1044 T1045 I1046 T1047 R1048 Q1049 THR ASP GLU LEU THR GLY LEU SER S1058 L1059 V1060 V1061 L1062 D1063 S1064 A1065 E1066 R1067 THR ALA GLY GLY LYS ASP LEU R1075 P1076 A1077 L1078 K1079 I1080 V1081

D1082 A1083 Q1084 G1085 N1086 D1087 V1088 LEU ILE PRO GLY THR ASP MET PRO A1097 Q1098 Y1099 F1100 L1101 P1102 G1103 K1104 A1105 I1106 V1107 Q1108 L1109 E1110 D1111 G1112 V1113 Q1114 I1115 S1116 S1117 G1118 D1119 T1120 L1121 A1122 R1123 I1124 P1125 Q1126 GLU SER GLY GLY THR LYS D1133 I1134 T1135 G1136 G1137 L1138 P1139 R1140 V1141

A1142 D1143 L1144 F1145 E1146 A1147 R1148 R1149 P1150 K1151 E1152 P1153 A1154 I1155 L1156 A1157 E1158 I1159 S1160 G1161 I1162 V1163 S1164 F1165 G1166 K1167 E1168 T1169 K1170 G1171 K1172 R1173 R1174 L1175 V1176 I1177 T1178 P1179 V1180 D1181 G1182 S1183 D1184 P1185 Y1186 E1187 E1188 M1189 I1190 P1191 K1192 W1193 R1194 Q1195 L1196 N1197 V1198 F1199 E1200 G1201

E1202 R1203 V1204 E1205 R1206 G1207 D1208 V1209 I1210 S1211 D1212 G1213 P1214 E1215 A1216 P1217 H1218 D1219 I1220 L1221 R1222 L1223 R1224 G1225 V1226 H1227 A1228 V1229 T1230 R1231 Y1232 I1233 V1234 M1235 E1236 V1237 Q1238 D1239 V1240 Y1241 R1242 L1243 Q1244 G1245 V1246 K1247 I1248 M1249 D1250 K1251 H1252 I1253 E1254 V1255 I1256 V1257 R1258 Q1259 M1260 L1261

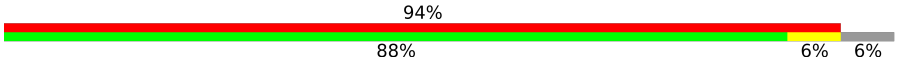
R1262 K1263 A1264 T1265 I1266 V1267 N1268 A1269 G1270 S1271 S1272 D1273 F1274 L1275 E1276 G1277 E1278 Q1279 V1280 E1281 Y1282 S1283 R1284 V1285 K1286 I1287 A1288 N1289 R1290 E1291 L1292 E1293 A1294 N1295 G1296 K1297 V1298 G1299 A1300 T1301 Y1302 S1303 R1304 D1305 L1306 L1307 G1308 I1309 T1310 K1311 A1312 S1313 L1314 A1315 T1316 E1317 S1318 F1319 I1320 S1321

A1322 A1323 S1324 F1325 Q1326 E1327 T1328 T1329 R1330 V1331 L1332 T1333 E1334 A1335 A1336 V1337 A1338 G1339 K1340 R1341 D1342 E1343 L1344 R1345 G1346 L1347 K1348 E1349 N1350 V1351 I1352 V1353 G1354 R1355 L1356 I1357 P1358 A1359 G1360 T1361 G1362 Y1363 A1364 Y1365 H1366 Q1367 D1368 R1369 M1370 R1371 R1372 R1373 A1374 A1375 G1376 GLU ALA PRO ALA ALA

PRO GLN VAL THR ALA GLU ASP ALA SER ALA SER LEU ALA GLU LEU LEU ASN ALA GLY LEU GLY GLY SER ASP ASN GLU

- Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:

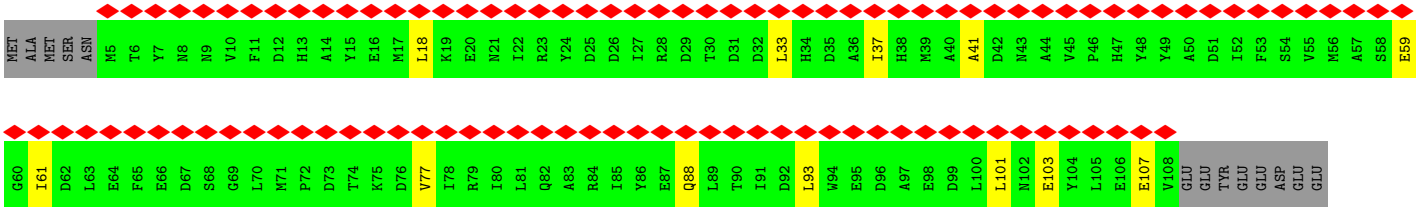


M1 A2 R3 V4 T5 V6 Q7 D8 A9 V10 E11 K12 I13 G14 N15 R16 F17 D18 L19 V20 L21 V22 A23 A24 R25 R26 A27 R28 Q29 M30 Q31 V32 G33 G34 K35 D36 P37 L38 V39 P40 E41 E42 N43 D44 K45 T46 T47 V48 I49 A50 L51 R52 E53 I54 E55 E56 G57 L58 I59 N60

N61 Q62 I63 L64 D65 V66 R67 E68 R69 Q70 E71 Q72 Q73 E74 Q75 GLU ALA ALA GLU LEU

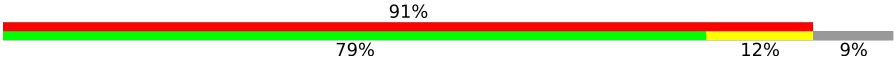
• Molecule 5: Overcome classical restriction gp0.3

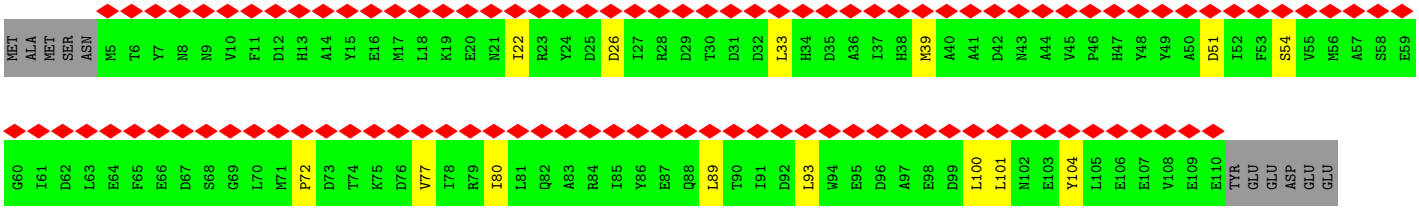
Chain G:



• Molecule 5: Overcome classical restriction gp0.3

Chain F:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	33646	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	49.53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.220	Depositor
Minimum map value	-0.151	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	270.08, 270.08, 270.08	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| >5$	RMSZ	$\#\|Z\| >5$
1	A	0.26	0/1786	0.52	0/2424
1	B	0.26	0/1764	0.57	0/2398
2	C	0.26	0/10263	0.53	0/13922
3	D	0.26	0/10187	0.51	0/13803
4	E	0.25	0/574	0.49	0/775
5	F	0.25	0/866	0.50	1/1177 (0.1%)
5	G	0.24	0/866	0.42	0/1178
All	All	0.26	0/26306	0.52	1/35677 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	F	26	ASP	CB-CG-OD1	5.19	122.97	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1765	0	1775	21	0
1	B	1743	0	1741	13	0
2	C	10112	0	9785	112	0
3	D	10051	0	10034	81	0
4	E	572	0	574	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	852	0	772	8	0
5	G	849	0	768	7	0
All	All	25944	0	25449	219	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 219 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:121:PRO:HD2	5:G:59:GLU:HG3	1.66	0.75
5:F:100:LEU:O	5:F:104:TYR:HB2	1.87	0.74
3:D:189:LEU:HD21	3:D:234:PRO:HB2	1.76	0.67
3:D:707:ILE:H	3:D:716:GLN:HG2	1.60	0.65
2:C:205:PRO:HG2	2:C:208:ILE:HG12	1.79	0.65

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	228/329 (69%)	220 (96%)	8 (4%)	0	100	100
1	B	229/329 (70%)	214 (93%)	13 (6%)	2 (1%)	17	54
2	C	1339/1342 (100%)	1226 (92%)	113 (8%)	0	100	100
3	D	1324/1407 (94%)	1198 (90%)	124 (9%)	2 (0%)	47	78
4	E	73/80 (91%)	66 (90%)	7 (10%)	0	100	100
5	F	104/117 (89%)	100 (96%)	4 (4%)	0	100	100
5	G	102/117 (87%)	100 (98%)	2 (2%)	0	100	100
All	All	3399/3721 (91%)	3124 (92%)	271 (8%)	4 (0%)	54	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	30	PRO
3	D	886	VAL
3	D	1183	SER
1	B	29	GLU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	194/286 (68%)	193 (100%)	1 (0%)	88	94
1	B	189/286 (66%)	188 (100%)	1 (0%)	88	94
2	C	1057/1157 (91%)	1053 (100%)	4 (0%)	91	95
3	D	1048/1168 (90%)	1043 (100%)	5 (0%)	88	94
4	E	58/68 (85%)	58 (100%)	0	100	100
5	F	91/105 (87%)	91 (100%)	0	100	100
5	G	91/105 (87%)	91 (100%)	0	100	100
All	All	2728/3175 (86%)	2717 (100%)	11 (0%)	91	95

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	128	LEU
3	D	314	ARG
3	D	1268	ASN
3	D	320	ASN
2	C	1175	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	1023	HIS
3	D	1268	ASN

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Mol	Chain	Res	Type
3	D	320	ASN
3	D	341	ASN
3	D	504	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

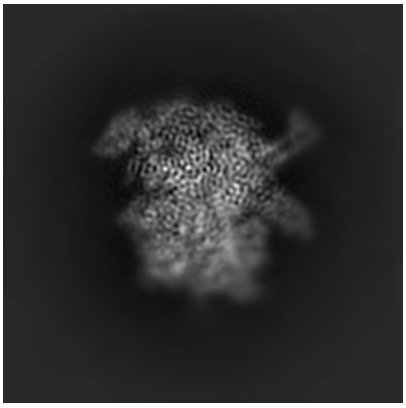
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4770. These allow visual inspection of the internal detail of the map and identification of artifacts.

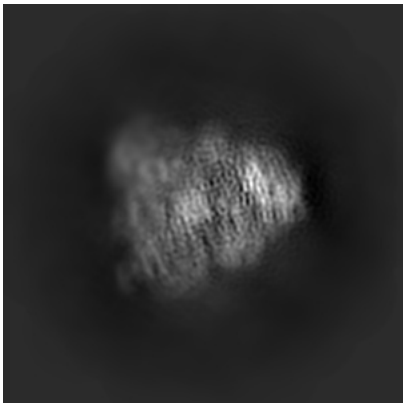
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

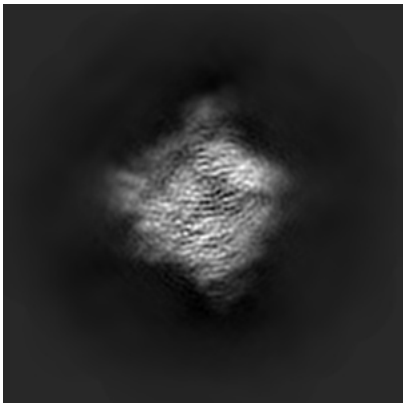
6.1.1 Primary map



X



Y

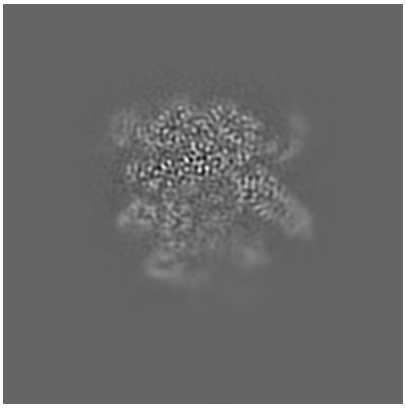


Z

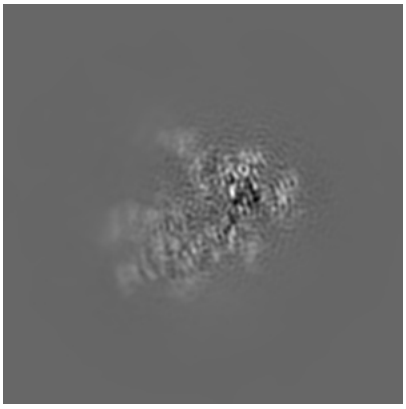
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

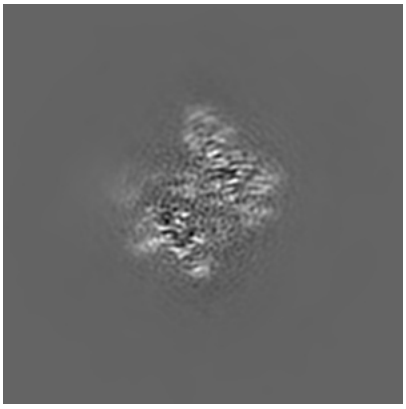
6.2.1 Primary map



X Index: 128



Y Index: 128

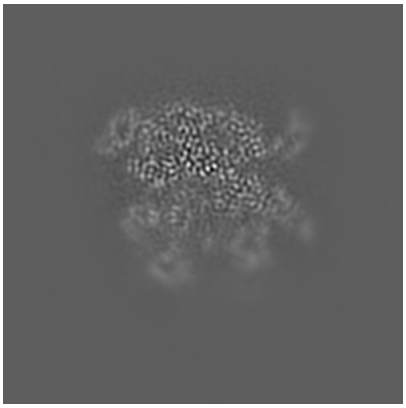


Z Index: 128

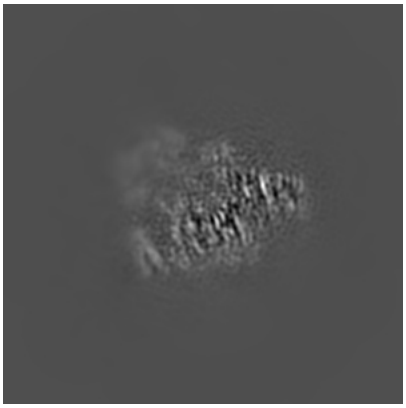
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

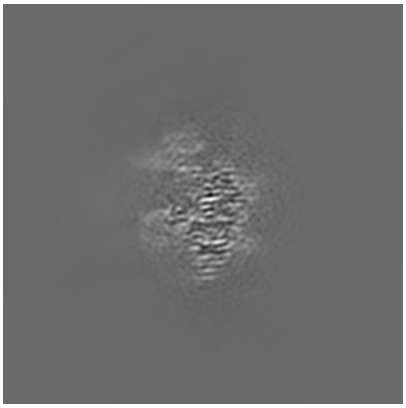
6.3.1 Primary map



X Index: 133



Y Index: 115

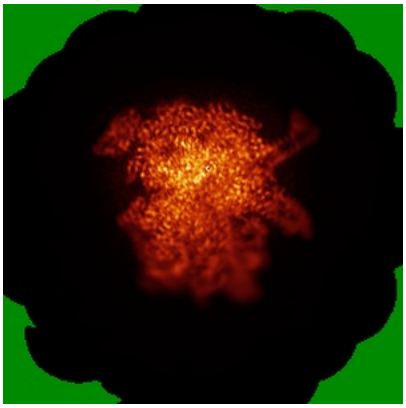


Z Index: 150

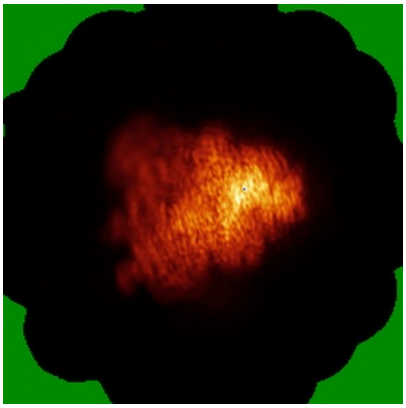
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

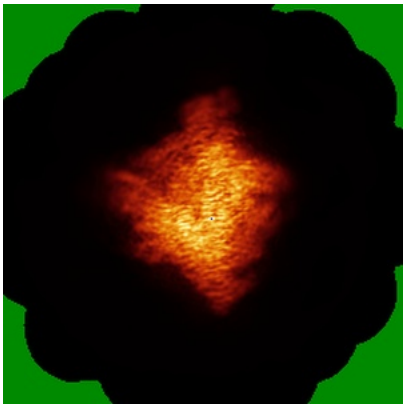
6.4.1 Primary map



X



Y

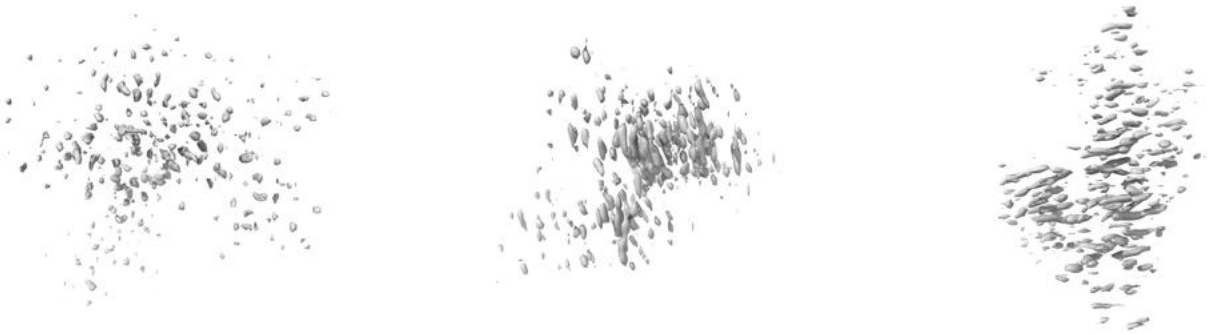


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

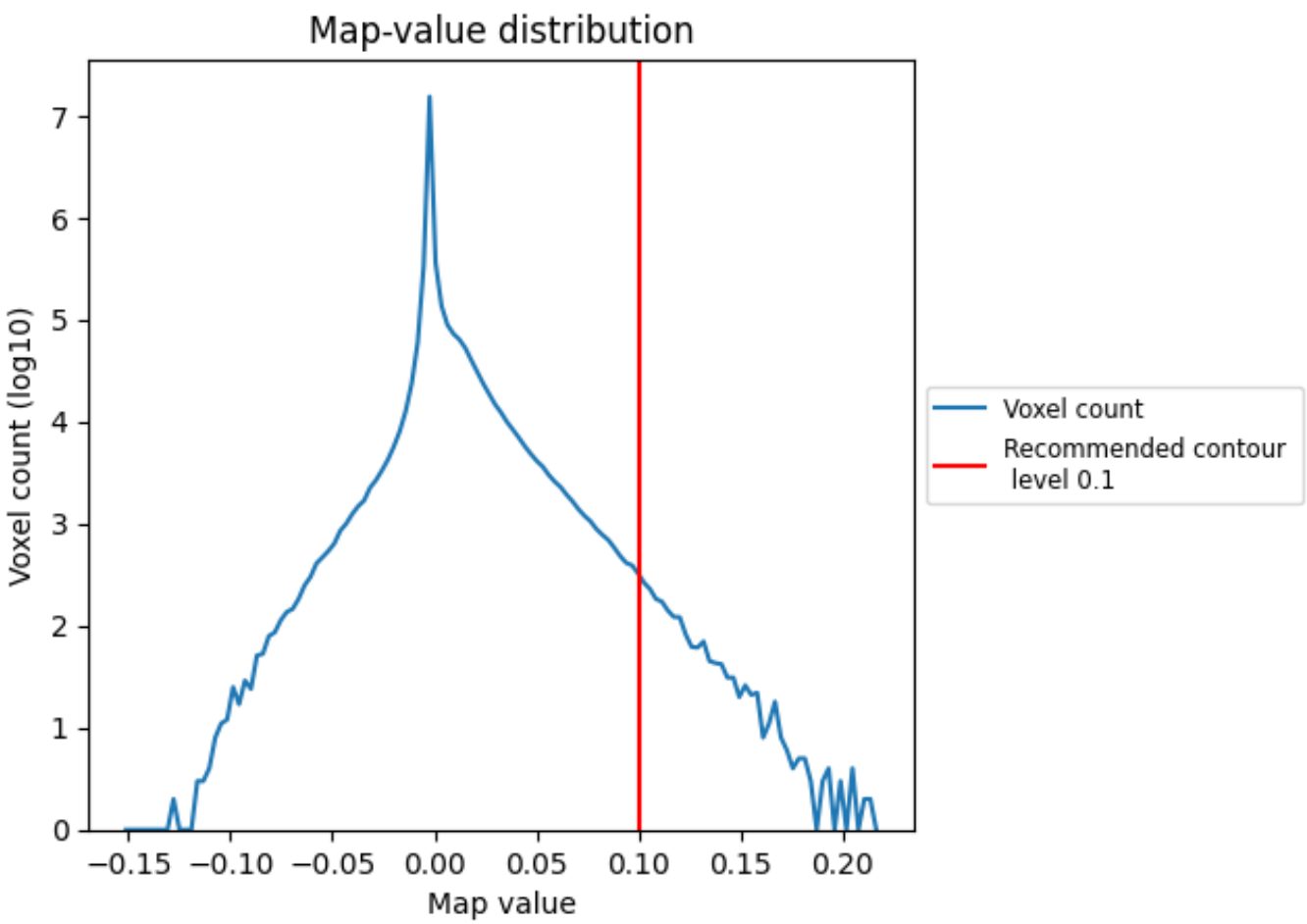
6.6 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

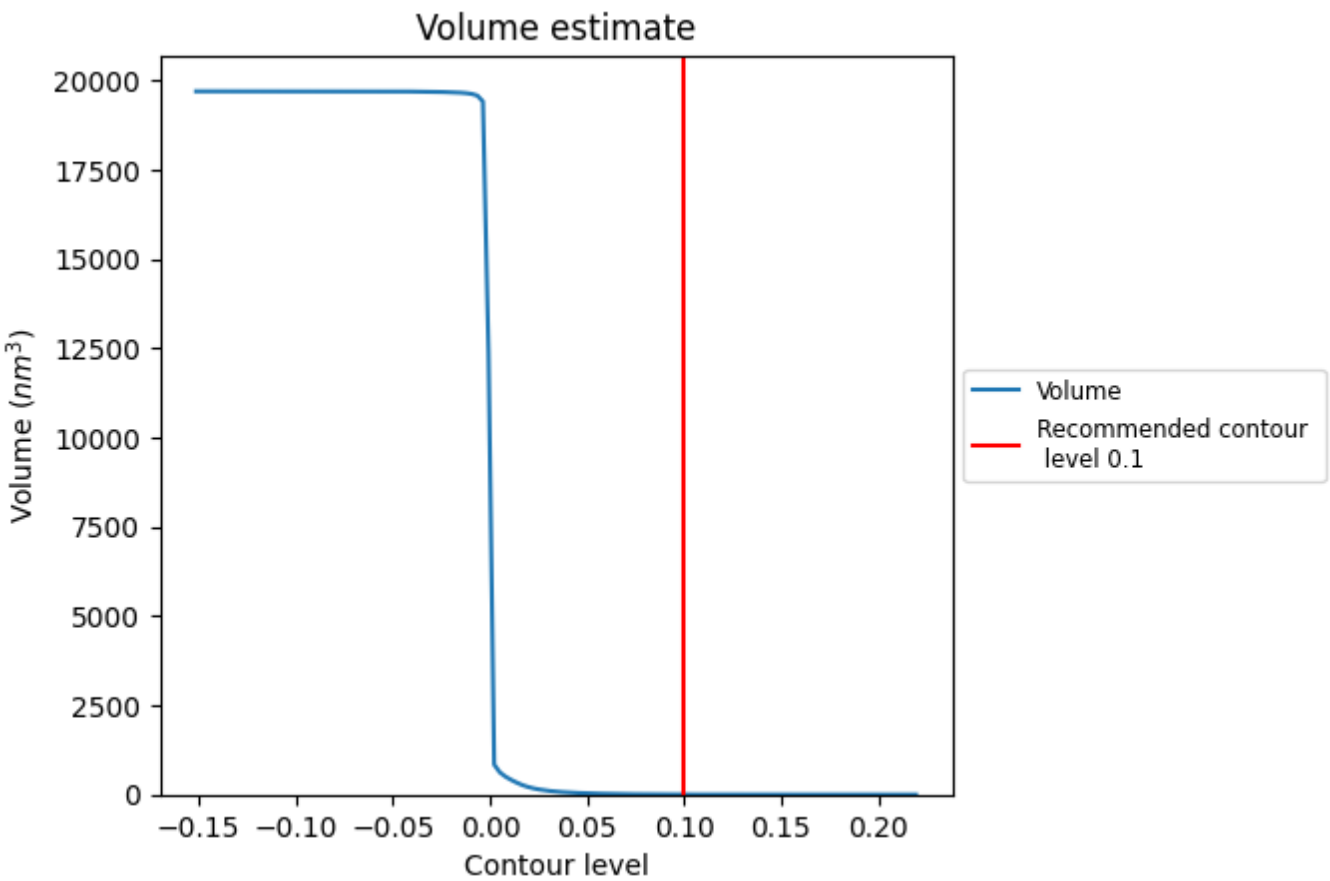
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

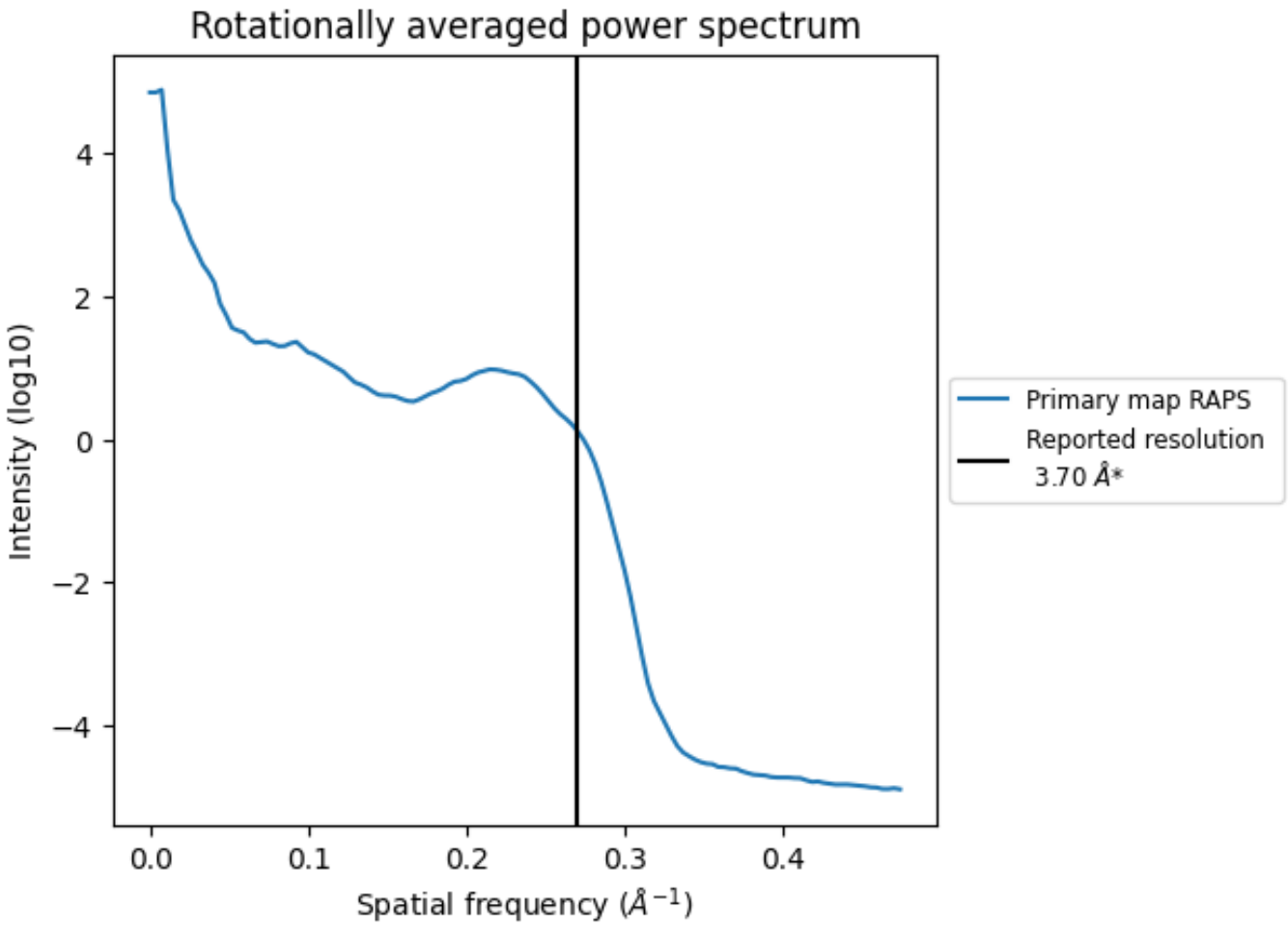
7.2 Volume estimate (i)



The volume at the recommended contour level is 3 nm^3; this corresponds to an approximate mass of 2 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

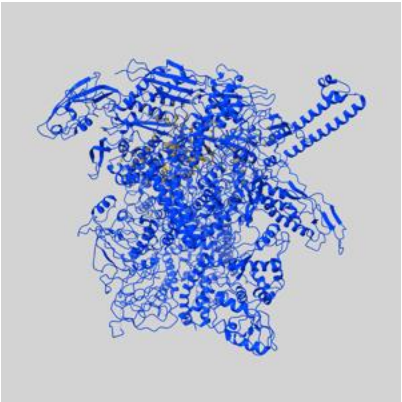
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

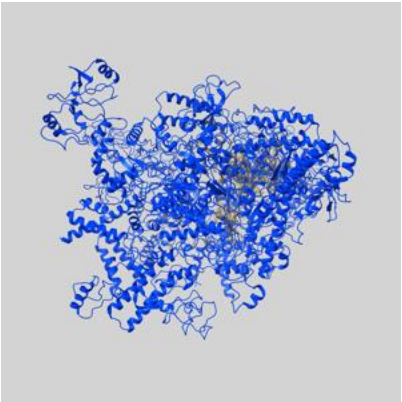
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4770 and PDB model 6R9G. Per-residue inclusion information can be found in section 3 on page 4.

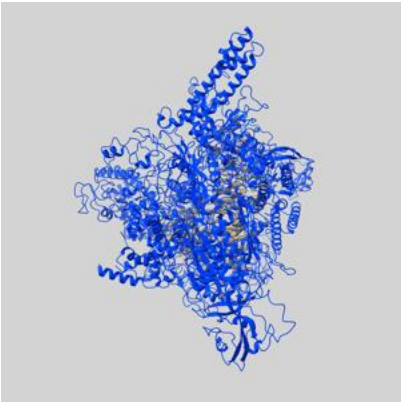
9.1 Map-model overlay (i)



X



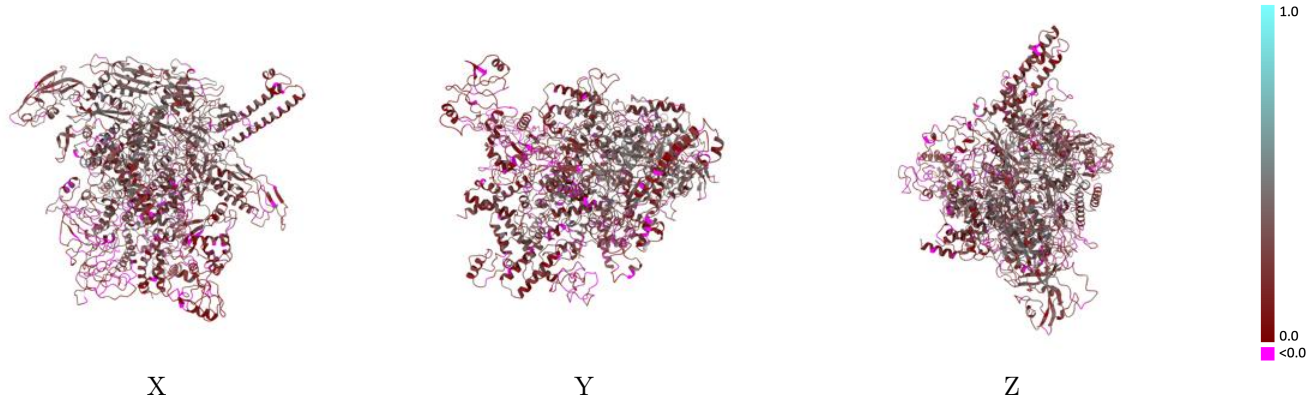
Y



Z

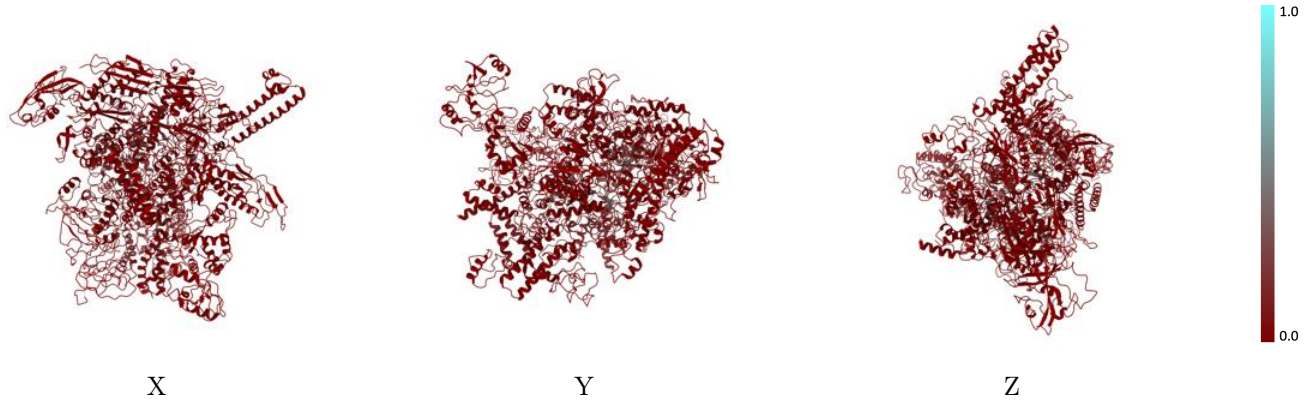
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



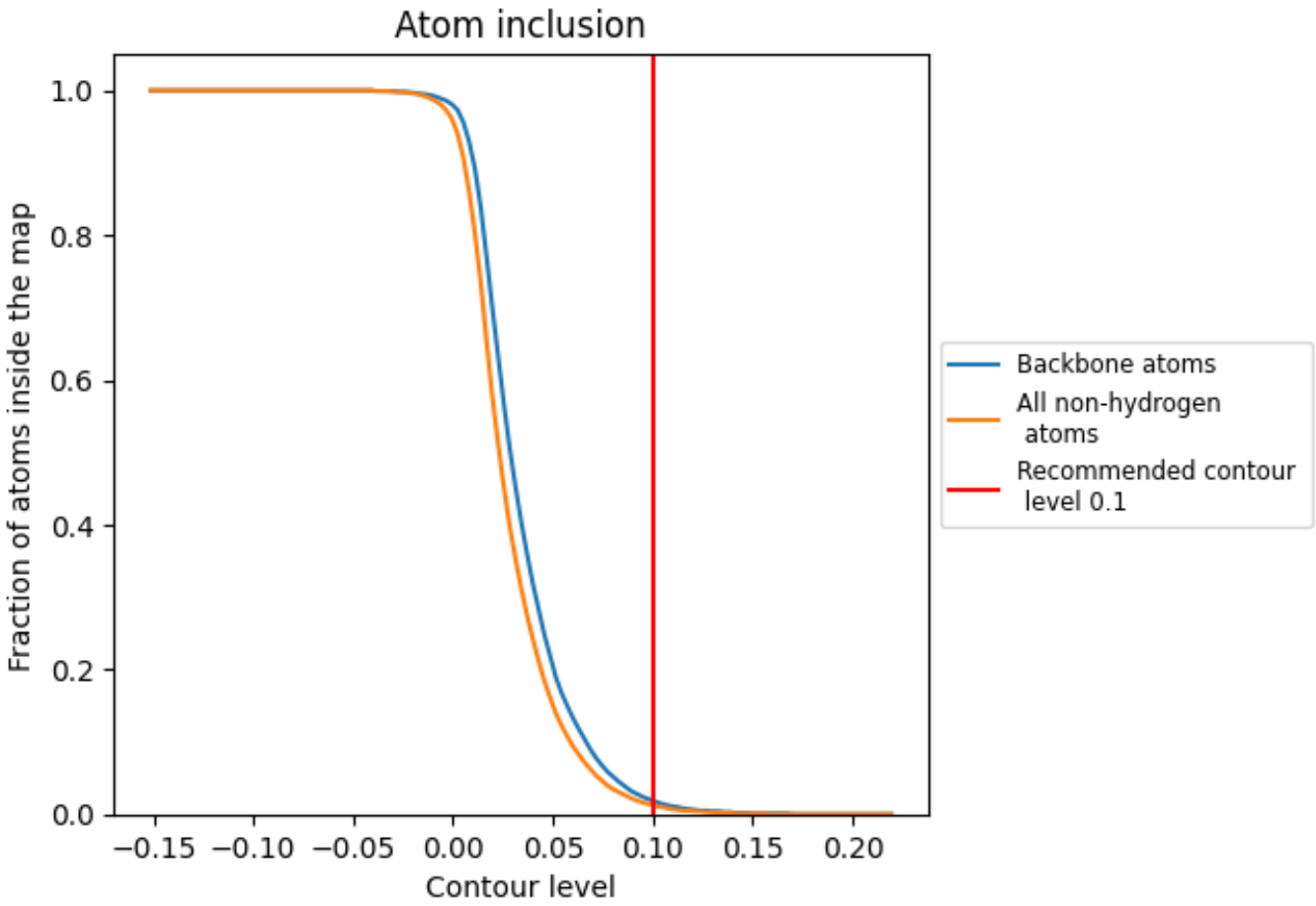
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 2% of all backbone atoms, 1% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.0130	0.2250
A	0.0060	0.3070
B	0.0030	0.2760
C	0.0170	0.2340
D	0.0140	0.2030
E	0.0000	0.1290
F	0.0000	0.2230
G	0.0000	0.1720