wwPDB EM Validation Summary Report (i)

Mar 12, 2026 – 03:58 PM UTC

PDB ID	:	7T8C / pdb_00007t8c
EMDB ID	:	EMD-25744
Title	:	Heptameric Human Twinkle Helicase Clinical Variant W315L
Authors	:	Riccio, A.A.; Bouvette, J.; Krahn, J.; Borgnia, M.J.; Copeland, W.C.
Deposited on	:	2021-12-16
Resolution	:	4.50 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:

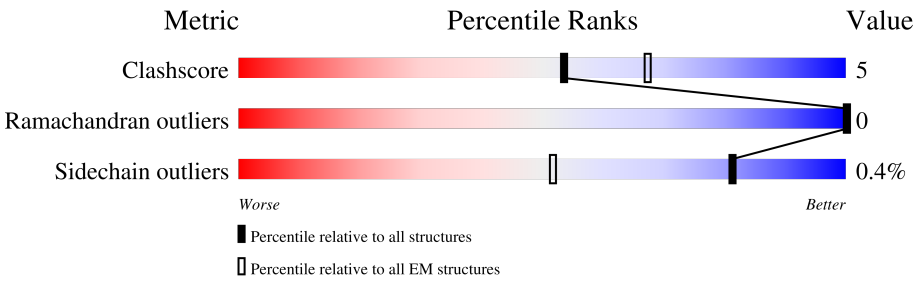
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

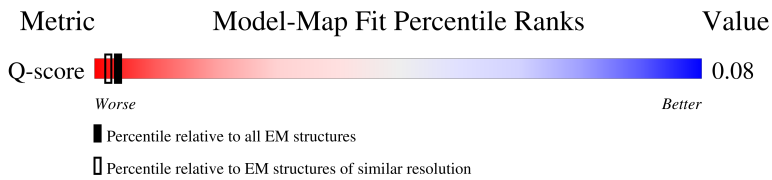
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	695	27% 63% 12% 25%
1	B	695	25% 63% 11% 25%
1	C	695	27% 63% 11% 25%
1	D	695	32% 64% 11% 25%

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Mol	Chain	Length	Quality of chain
1	E	695	31% 63% 11% 25%
1	F	695	27% 63% 11% 25%
1	G	695	27% 63% 11% 25%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 28952 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 Twinkle mtDNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	518	4136	2640	725	756	15	0	1
1	B	518	4136	2640	725	756	15	0	1
1	C	518	4136	2640	725	756	15	0	1
1	D	518	4136	2640	725	756	15	0	1
1	E	518	4136	2640	725	756	15	0	1
1	F	518	4136	2640	725	756	15	0	1
1	G	518	4136	2640	725	756	15	0	1

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	315	LEU	TRP	variant	UNP Q96RR1
A	685	ALA	-	expression tag	UNP Q96RR1
A	686	ALA	-	expression tag	UNP Q96RR1
A	687	ALA	-	expression tag	UNP Q96RR1
A	688	LEU	-	expression tag	UNP Q96RR1
A	689	GLU	-	expression tag	UNP Q96RR1
A	690	HIS	-	expression tag	UNP Q96RR1
A	691	HIS	-	expression tag	UNP Q96RR1
A	692	HIS	-	expression tag	UNP Q96RR1
A	693	HIS	-	expression tag	UNP Q96RR1
A	694	HIS	-	expression tag	UNP Q96RR1
A	695	HIS	-	expression tag	UNP Q96RR1
B	315	LEU	TRP	variant	UNP Q96RR1
B	685	ALA	-	expression tag	UNP Q96RR1
B	686	ALA	-	expression tag	UNP Q96RR1
B	687	ALA	-	expression tag	UNP Q96RR1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	688	LEU	-	expression tag	UNP Q96RR1
B	689	GLU	-	expression tag	UNP Q96RR1
B	690	HIS	-	expression tag	UNP Q96RR1
B	691	HIS	-	expression tag	UNP Q96RR1
B	692	HIS	-	expression tag	UNP Q96RR1
B	693	HIS	-	expression tag	UNP Q96RR1
B	694	HIS	-	expression tag	UNP Q96RR1
B	695	HIS	-	expression tag	UNP Q96RR1
C	315	LEU	TRP	variant	UNP Q96RR1
C	685	ALA	-	expression tag	UNP Q96RR1
C	686	ALA	-	expression tag	UNP Q96RR1
C	687	ALA	-	expression tag	UNP Q96RR1
C	688	LEU	-	expression tag	UNP Q96RR1
C	689	GLU	-	expression tag	UNP Q96RR1
C	690	HIS	-	expression tag	UNP Q96RR1
C	691	HIS	-	expression tag	UNP Q96RR1
C	692	HIS	-	expression tag	UNP Q96RR1
C	693	HIS	-	expression tag	UNP Q96RR1
C	694	HIS	-	expression tag	UNP Q96RR1
C	695	HIS	-	expression tag	UNP Q96RR1
D	315	LEU	TRP	variant	UNP Q96RR1
D	685	ALA	-	expression tag	UNP Q96RR1
D	686	ALA	-	expression tag	UNP Q96RR1
D	687	ALA	-	expression tag	UNP Q96RR1
D	688	LEU	-	expression tag	UNP Q96RR1
D	689	GLU	-	expression tag	UNP Q96RR1
D	690	HIS	-	expression tag	UNP Q96RR1
D	691	HIS	-	expression tag	UNP Q96RR1
D	692	HIS	-	expression tag	UNP Q96RR1
D	693	HIS	-	expression tag	UNP Q96RR1
D	694	HIS	-	expression tag	UNP Q96RR1
D	695	HIS	-	expression tag	UNP Q96RR1
E	315	LEU	TRP	variant	UNP Q96RR1
E	685	ALA	-	expression tag	UNP Q96RR1
E	686	ALA	-	expression tag	UNP Q96RR1
E	687	ALA	-	expression tag	UNP Q96RR1
E	688	LEU	-	expression tag	UNP Q96RR1
E	689	GLU	-	expression tag	UNP Q96RR1
E	690	HIS	-	expression tag	UNP Q96RR1
E	691	HIS	-	expression tag	UNP Q96RR1
E	692	HIS	-	expression tag	UNP Q96RR1
E	693	HIS	-	expression tag	UNP Q96RR1

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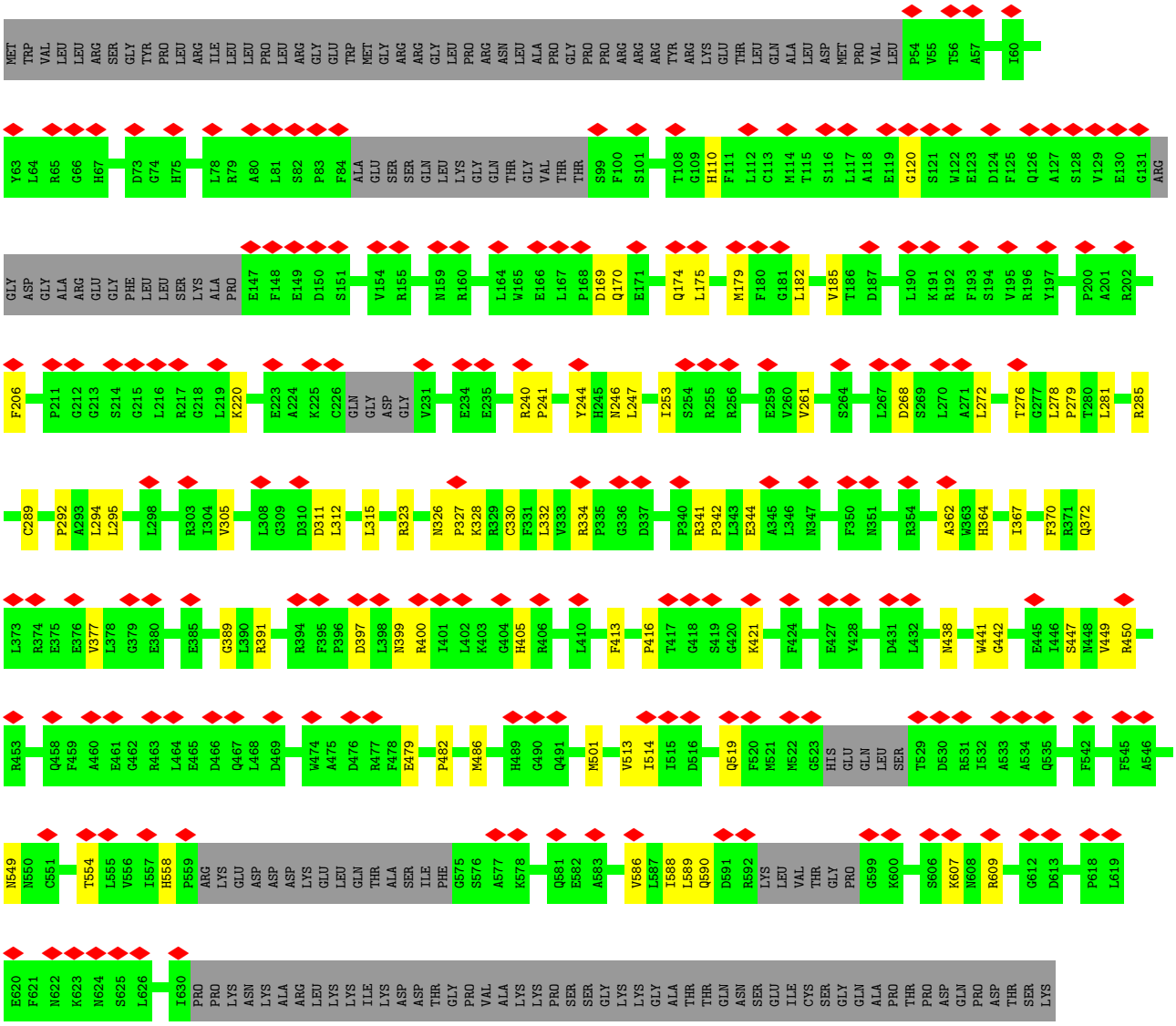
Chain	Residue	Modelled	Actual	Comment	Reference
E	694	HIS	-	expression tag	UNP Q96RR1
E	695	HIS	-	expression tag	UNP Q96RR1
F	315	LEU	TRP	variant	UNP Q96RR1
F	685	ALA	-	expression tag	UNP Q96RR1
F	686	ALA	-	expression tag	UNP Q96RR1
F	687	ALA	-	expression tag	UNP Q96RR1
F	688	LEU	-	expression tag	UNP Q96RR1
F	689	GLU	-	expression tag	UNP Q96RR1
F	690	HIS	-	expression tag	UNP Q96RR1
F	691	HIS	-	expression tag	UNP Q96RR1
F	692	HIS	-	expression tag	UNP Q96RR1
F	693	HIS	-	expression tag	UNP Q96RR1
F	694	HIS	-	expression tag	UNP Q96RR1
F	695	HIS	-	expression tag	UNP Q96RR1
G	315	LEU	TRP	variant	UNP Q96RR1
G	685	ALA	-	expression tag	UNP Q96RR1
G	686	ALA	-	expression tag	UNP Q96RR1
G	687	ALA	-	expression tag	UNP Q96RR1
G	688	LEU	-	expression tag	UNP Q96RR1
G	689	GLU	-	expression tag	UNP Q96RR1
G	690	HIS	-	expression tag	UNP Q96RR1
G	691	HIS	-	expression tag	UNP Q96RR1
G	692	HIS	-	expression tag	UNP Q96RR1
G	693	HIS	-	expression tag	UNP Q96RR1
G	694	HIS	-	expression tag	UNP Q96RR1
G	695	HIS	-	expression tag	UNP Q96RR1

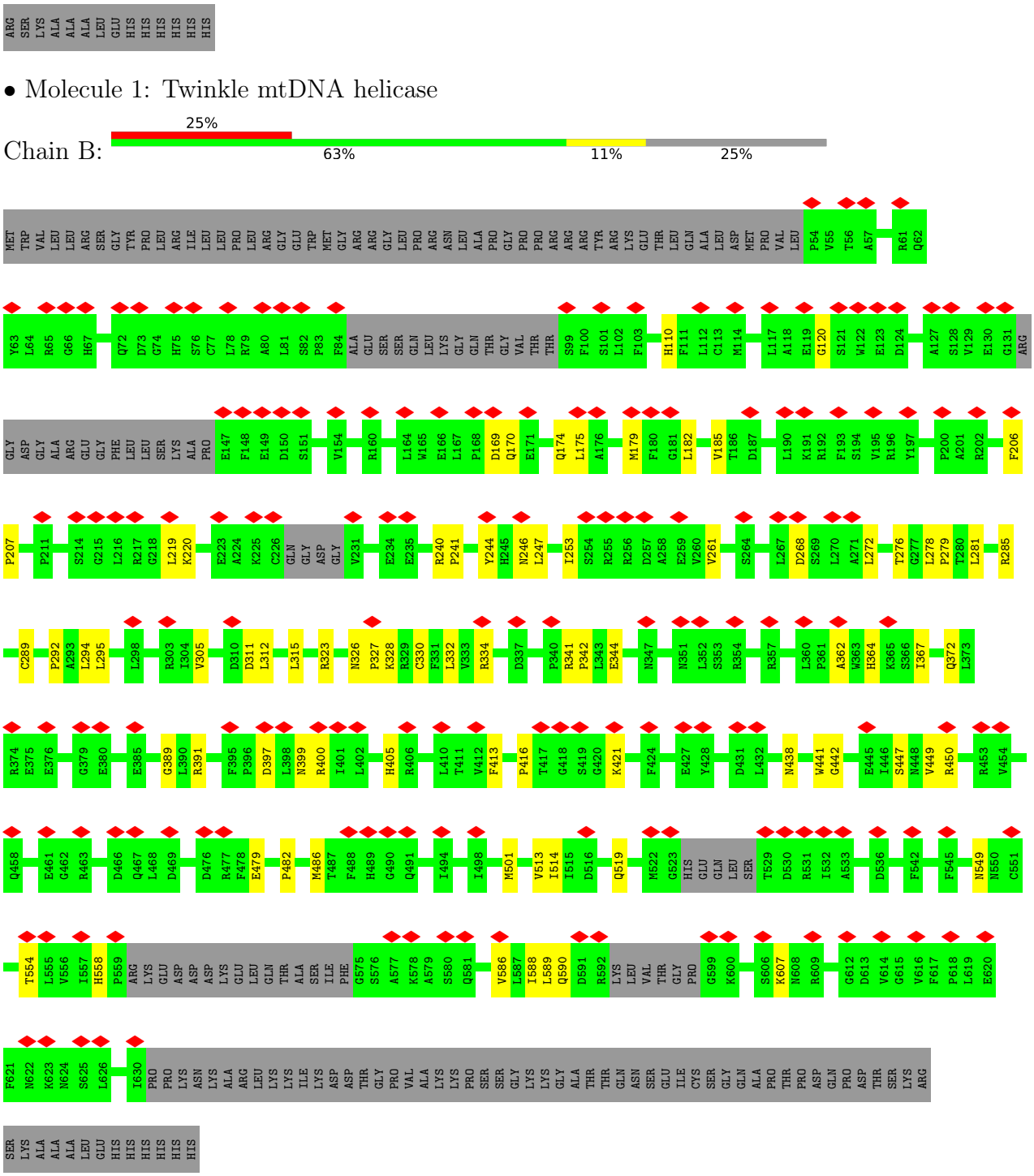
3 Residue-property plots (i)

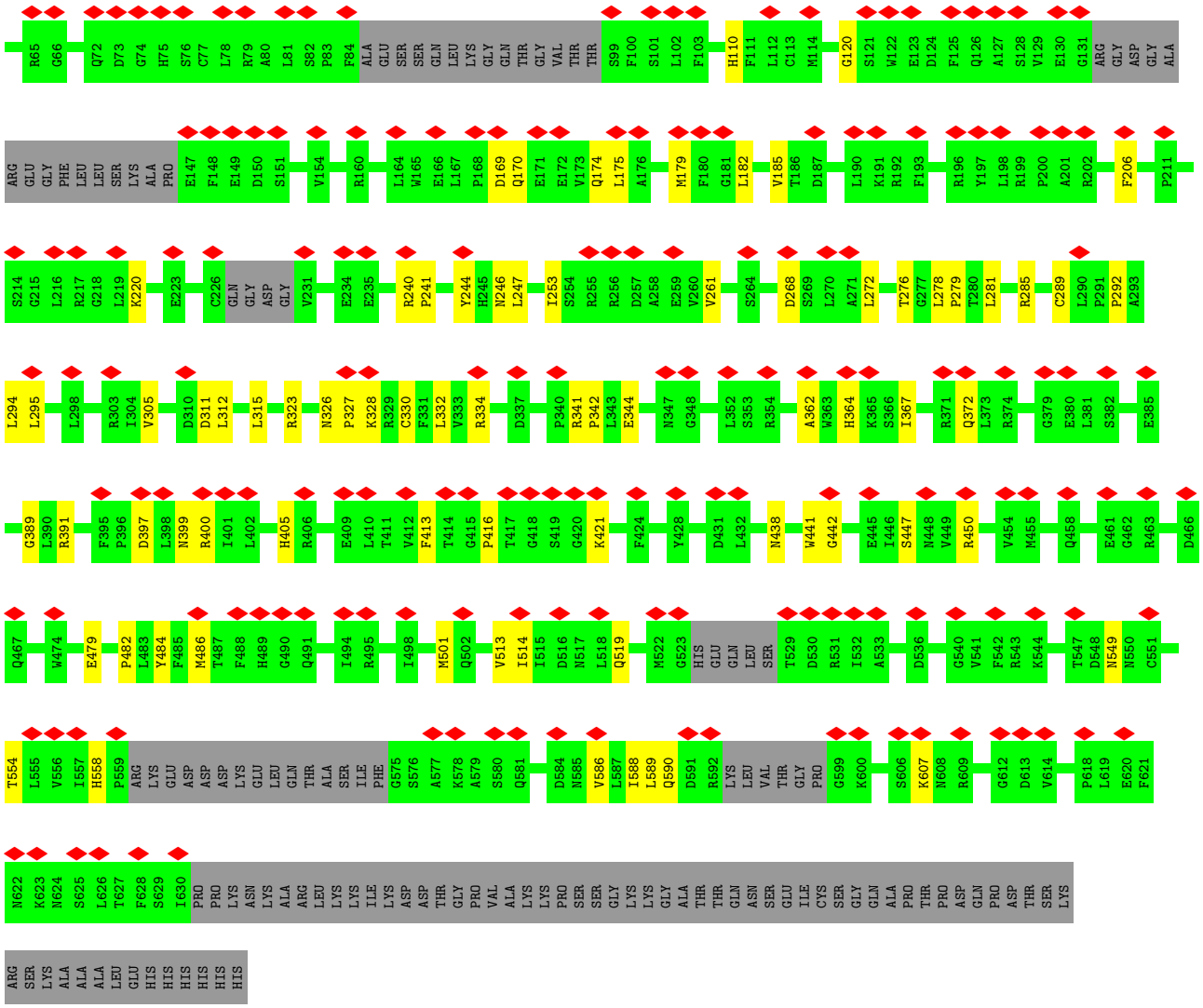
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Twinkle mtDNA helicase

Chain A:

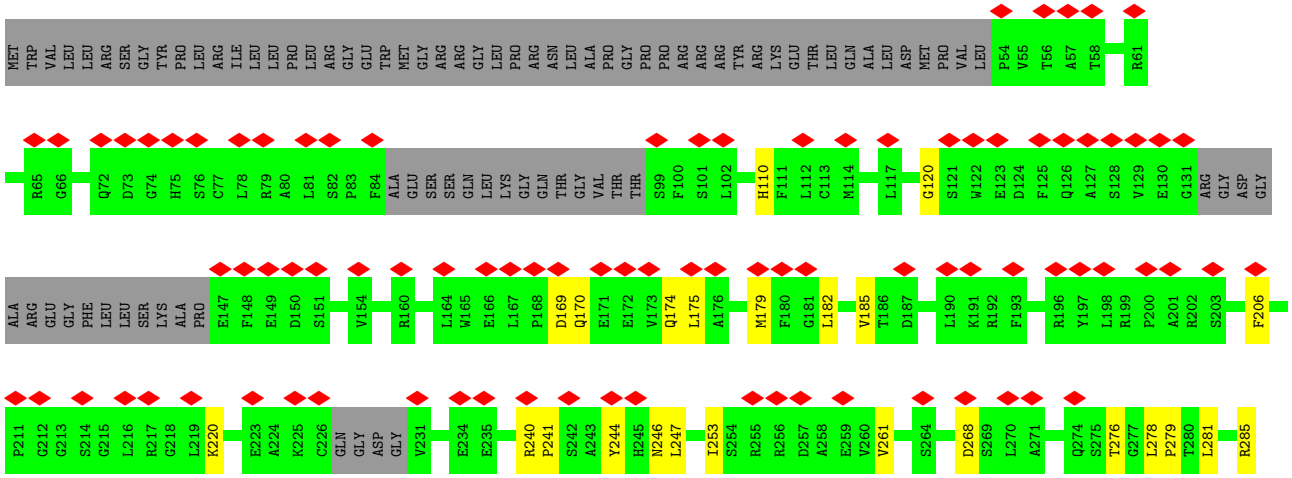


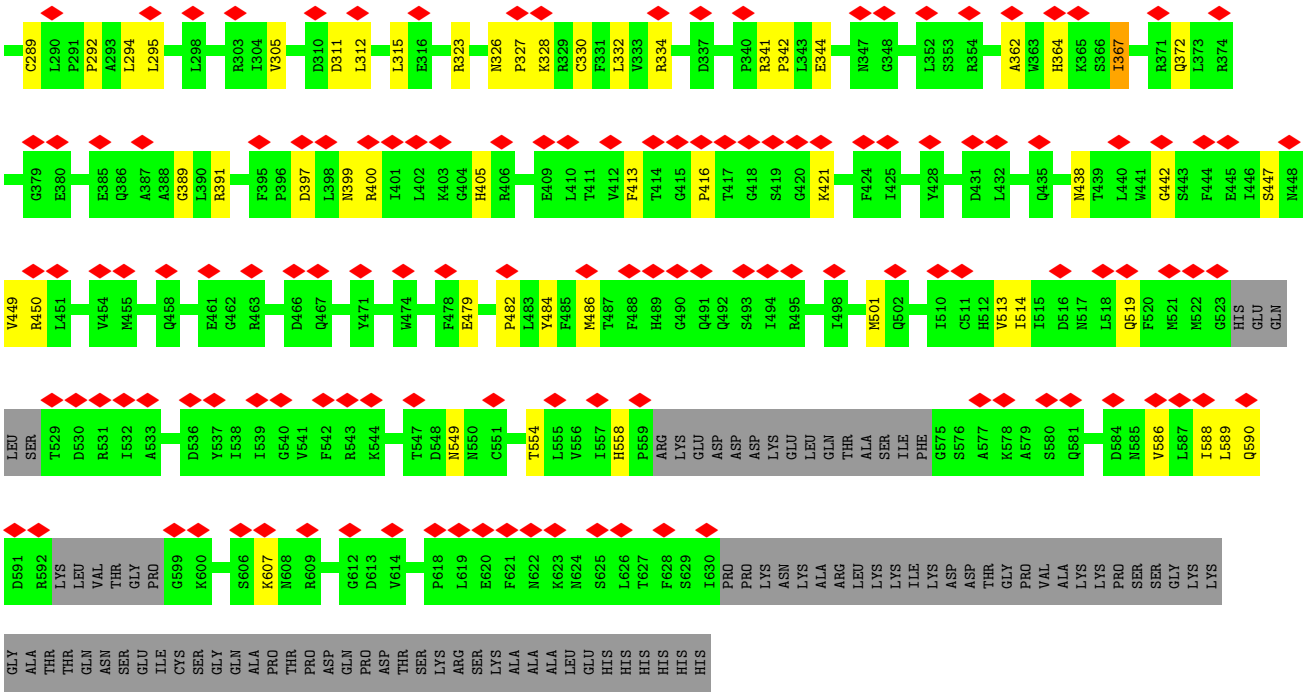

ARG SER LYS ALA ALA ALA LEU GLU HIS HIS HIS HIS HIS HIS
• Molecule 1: Twinkle mtDNA helicase
Chain B:
25%
63%
11%
25%
MET TRP VAL LEU LEU ARG SER GLY TYR PRO LEU ARG ILE LEU LEU LEU PRO LEU ARG GLY GLU TRP MET GLY ARG ARG GLY LEU PRO ARG ASN LEU ALA PRO GLY PRO PRO ARG ARG ARG TYR ARG LYS GLU THR LEU GLN ALA LEU ASP MET PRO VAL LEU P54 V55 T56 A57 R61 Q62
Y63 L64 R65 G66 H67 Q72 D73 G74 H75 S76 C77 L78 R79 A80 L81 S82 P83 F84 ALA GLU SER SER GLN LEU LYS GLY GLN THR GLY VAL THR THR S99 F100 S101 L102 F103 H110 F111 L112 C113 M114 L117 A118 E119 G120 S121 W122 E123 D124 A127 S128 V129 E130 G131 ARG
GLY ASP GLY ALA ARG GLU GLY PHE LEU LEU SER LYS ALA PRO E147 F148 E149 D150 S151 V154 R160 L164 W165 E166 L167 P168 D169 Q170 E171 Q174 L175 A176 M179 F180 G181 L182 V185 T186 D187 L190 K191 R192 F193 S194 V195 R196 Y197 P200 A201 R202 F206
P207 P211 S214 G215 L216 R217 G218 L219 K220 E223 A224 K225 C226 GLN GLY ASP GLY V231 E234 E235 R240 P241 Y244 H245 N246 L247 I253 S254 R255 R256 D257 A258 E259 V260 V261 S264 L267 D268 S269 L270 A271 L272 T276 G277 L278 P279 T280 L281 R285
C289 P292 A293 L294 L295 L298 R303 I304 V305 D310 D311 L312 L315 R323 N326 P327 K328 R329 C330 F331 L332 V333 R334 D337 P340 R341 P342 L343 E344 N347 N351 L352 S353 R354 R357 L360 P361 A362 W363 H364 K365 S366 I367 Q372 L373
R374 E375 E376 G379 E380 E385 G389 L390 R391 F395 P396 D397 L398 N399 R400 I401 L402 H405 R406 L410 T411 V412 F413 P416 T417 G418 S419 G420 K421 F424 E427 Y428 D431 L432 N438 W441 G442 E445 I446 S447 N448 V449 R450 R453 V454
Q458 E461 G462 R463 D466 Q467 L468 D469 D476 R477 F478 E479 P482 M486 T487 F488 H489 G490 Q491 I494 I498 M501 V513 I514 I515 D516 Q519 M522 G523 HIS GLU GLN LEU SER T529 D530 R531 I532 A533 D536 F542 F545 N549 N550 C551
T554 L555 V556 I557 H558 P559 ARG LYS GLU ASP ASP ASP LYS GLU LEU GLN THR ALA SER ILE PHE G575 S576 A577 K578 A579 S580 Q581 V586 L587 I588 L589 Q590 D591 R592 LYS LEU VAL THR GLY PRO G599 K600 S606 K607 N608 R609 G612 D613 V614 G615 V616 F617 P618 L619 E620
F621 N622 K623 N624 S625 L626 I630 PRO PRO LYS ASN LYS ALA ARG LEU LYS LYS ILE LYS ASP ASP THR GLY PRO VAL ALA LYS LYS PRO SER SER GLY LYS LYS GLY ALA THR THR GLN ASN SER GLU ILE CYS SER GLY GLN ALA PRO THR PRO ASP GLN PRO ASP THR SER LYS ARG
SER LYS ALA ALA ALA LEU GLU HIS HIS HIS HIS HIS HIS
• Molecule 1: Twinkle mtDNA helicase
Chain C:
27%
63%
11%
25%
MET TRP VAL LEU LEU ARG SER GLY TYR PRO LEU ARG ILE LEU LEU LEU PRO LEU ARG GLY GLU TRP MET GLY ARG ARG GLY LEU PRO ARG ASN LEU ALA PRO GLY PRO PRO ARG ARG ARG TYR ARG LYS GLU THR LEU GLN ALA LEU ASP MET PRO VAL LEU P54 V55 T56 A57 T58 R61



- Molecule 1: Twinkle mtDNA helicase

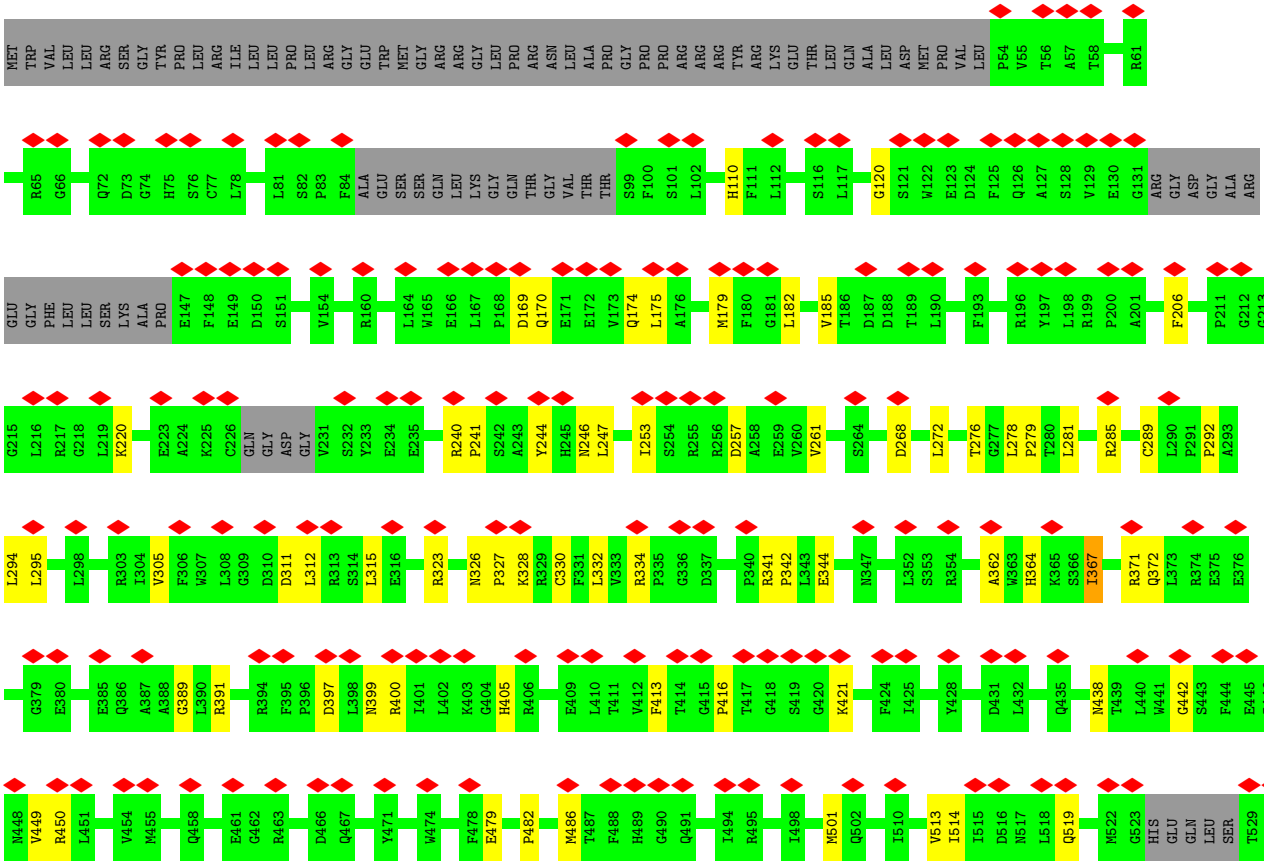
Chain D:

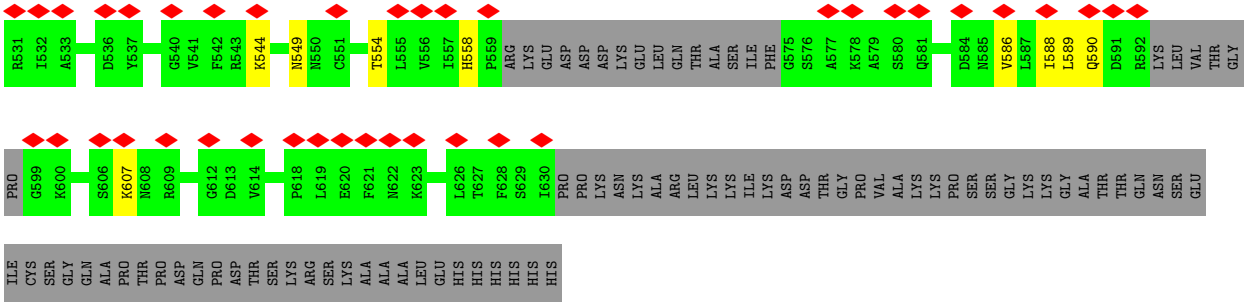




- Molecule 1: Twinkle mtDNA helicase

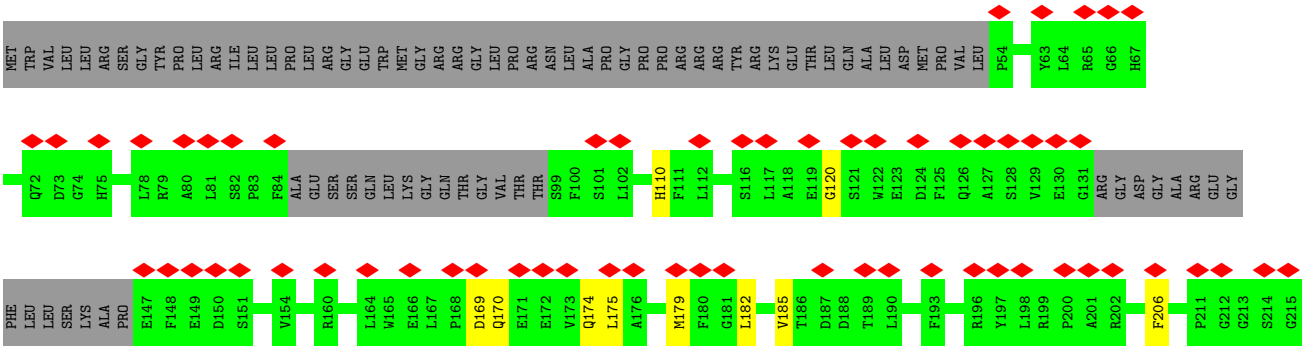
Chain E: 31% 63% 11% 25%





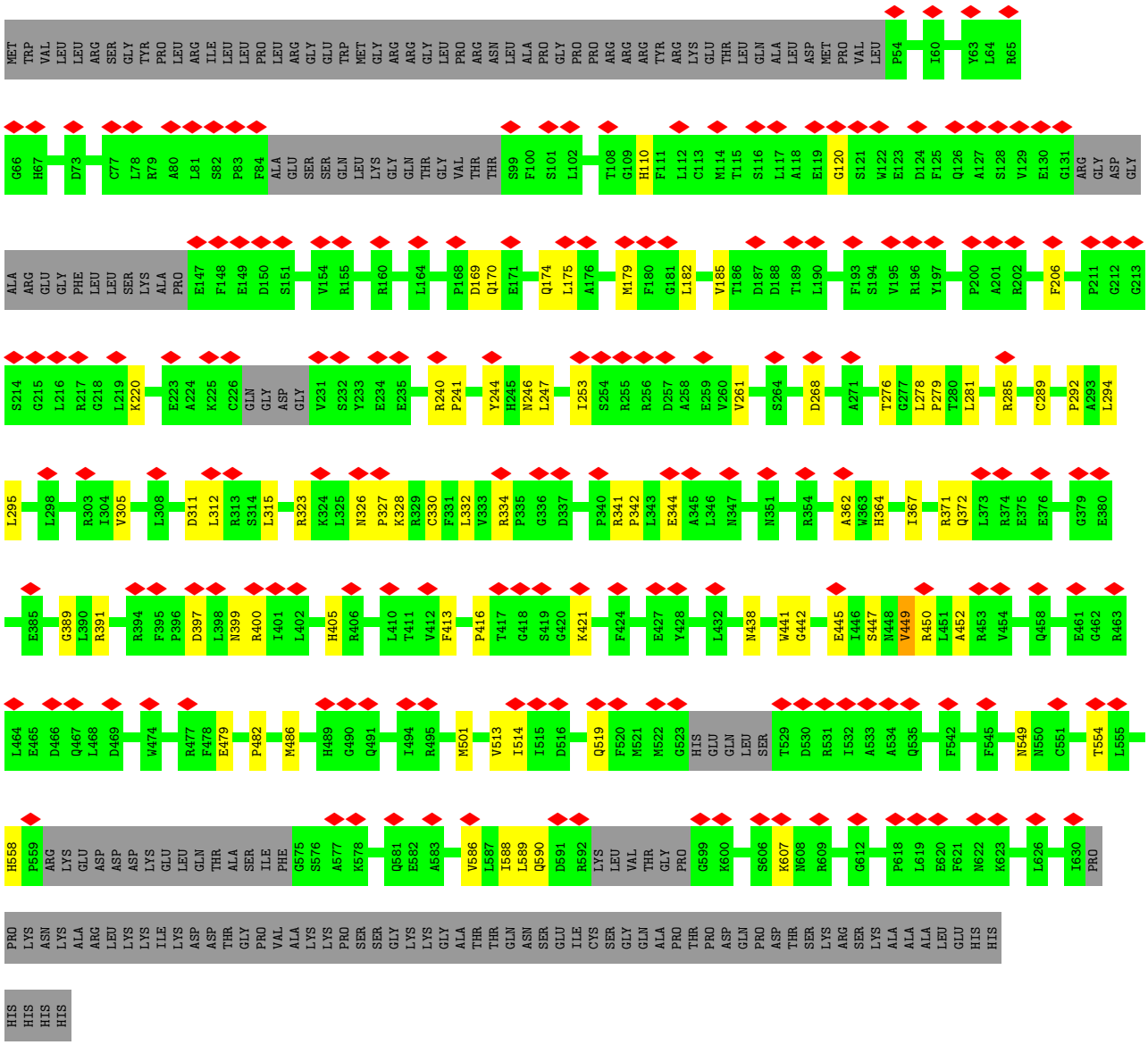
- Molecule 1: Twinkle mtDNA helicase

Chain F:



- Molecule 1: Twinkle mtDNA helicase

Chain G:


MET TRP VAL LEU LEU ARG SER GLY TYR PRO LEU ARG ILE LEU LEU PRO LEU ARG GLY GLU TRP MET GLY ARG ARG GLY LEU PRO ARG ASN LEU ALA PRO GLY PRO PRO ARG ARG ARG TYR ARG LYS GLU THR LEU GLN ALA LEU ASP MET PRO VAL LEU P54 I60 Y63 L64 R65
G66 H67 D73 C77 L78 R79 A80 L81 S82 P83 P84 ALA GLU SER SER GLN LEU LYS GLY GLN THR GLY VAL THR THR S99 F100 S101 L102 T108 G109 H110 F111 L112 C113 M114 T115 S116 L117 A118 E119 G120 S121 W122 E123 D124 F125 Q126 A127 S128 V129 E130 G131 ARG GLY ASP GLY
ALA ARG GLU GLY PHE LEU LEU SER LYS ALA PRO E147 F148 E149 D150 S151 V154 R155 R160 L164 P168 D169 Q170 E171 Q174 L175 A176 M179 F180 G181 L182 V185 T186 D187 D188 T189 L190 F193 S194 V195 R196 Y197 P200 A201 R202 F206 P211 G212 G213
S214 G215 L216 R217 G218 L219 K220 E223 A224 K225 C226 GLN GLY ASP GLY V231 S232 Y233 E234 E235 R240 P241 Y244 H245 N246 L247 I253 S254 R255 R256 D257 A258 E259 V260 V261 S264 D268 A271 T276 G277 L278 P279 T280 L281 R285 C289 P292 A293 L294
L295 L298 R303 I304 V305 L308 D311 L312 R313 S314 L315 R323 K324 L325 N326 P327 K328 R329 C330 F331 L332 V333 R334 P335 G336 D337 P340 R341 P342 L343 E344 A345 L346 N347 N351 R354 A362 W363 H364 I367 R371 Q372 L373 R374 E375 E376 G379 E380
E385 G389 L390 R391 R394 F395 P396 D397 I398 N399 R400 I401 L402 H405 R406 L410 T411 V412 F413 P416 T417 G418 S419 G420 K421 F424 E427 Y428 L432 N438 W441 G442 E445 T446 S447 N448 V449 R450 L451 A452 R453 V454 Q458 E461 G462 R463
L464 E465 D466 Q467 L468 D469 W474 R477 F478 E479 P482 M486 H489 G490 Q491 T494 R495 M501 V513 I514 I515 D516 Q519 F520 M521 M522 G523 HIS GLU GLN LEU SER T529 D530 R531 I532 A533 A534 Q535 F542 F545 N549 N550 C551 T554 L555
H558 P559 ARG LYS GLU ASP ASP ASP LYS GLU LEU GLN THR ALA SER ILE PHE G575 S576 A577 K578 Q581 E582 A583 V586 L587 I588 L589 Q590 D591 R592 LYS LEU VAL THR GLY PRO G599 K600 S606 K607 N608 R609 G612 P618 L619 E620 F621 K622 K623 L626 I630 PRO
PRO LYS ASN LYS ALA ARG LEU LYS LYS ILE LYS ASP ASP THR GLY PRO VAL ALA LYS LYS PRO SER SER GLY LYS LYS GLY ALA THR THR GLN ASN SER GLU ILE CYS SER GLY GLN ALA PRO THR PRO ASP GLN PRO ASP THR SER LYS ARG SER LYS ALA ALA ALA LEU GLU HIS HIS
HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	55655	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.915	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.159	Depositor
Map size (Å)	423.19998, 423.19998, 423.19998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.058, 1.058, 1.058	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	0.08	0/4230	0.23	0/5729
1	B	0.08	0/4230	0.23	0/5729
1	C	0.08	0/4230	0.23	0/5729
1	D	0.08	0/4230	0.23	0/5729
1	E	0.08	0/4230	0.23	0/5729
1	F	0.08	0/4230	0.23	0/5729
1	G	0.08	0/4230	0.23	0/5729
All	All	0.08	0/29610	0.23	0/40103

There are no bond length outliers.

There are no bond angle outliers.

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	4136	0	4076	45	0
1	B	4136	0	4076	42	0
1	C	4136	0	4076	43	0
1	D	4136	0	4076	43	0
1	E	4136	0	4076	44	0
1	F	4136	0	4076	44	0
1	G	4136	0	4076	45	0
All	All	28952	0	28532	297	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 5.

The worst 5 of 297 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)
1:A:285:ARG:NH2	1:A:289:CYS:SG	2.68	0.67
1:G:285:ARG:NH2	1:G:289:CYS:SG	2.68	0.67
1:F:285:ARG:NH2	1:F:289:CYS:SG	2.68	0.67
1:B:285:ARG:NH2	1:B:289:CYS:SG	2.68	0.66
1:D:285:ARG:NH2	1:D:289:CYS:SG	2.68	0.66

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	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
1	B	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
1	C	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
1	D	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
1	E	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
1	F	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
1	G	504/695 (72%)	486 (96%)	18 (4%)	0	100	100
All	All	3528/4865 (72%)	3402 (96%)	126 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	448/599 (75%)	446 (100%)	2 (0%)	84	82
1	B	448/599 (75%)	446 (100%)	2 (0%)	84	82
1	C	448/599 (75%)	447 (100%)	1 (0%)	87	85
1	D	448/599 (75%)	446 (100%)	2 (0%)	84	82
1	E	448/599 (75%)	446 (100%)	2 (0%)	84	82
1	F	448/599 (75%)	446 (100%)	2 (0%)	84	82
1	G	448/599 (75%)	446 (100%)	2 (0%)	84	82
All	All	3136/4193 (75%)	3123 (100%)	13 (0%)	81	82

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	367	ILE
1	E	449	VAL
1	G	449	VAL
1	F	449	VAL
1	G	367	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	624	ASN
1	F	624	ASN
1	F	273	ASN
1	F	519	GLN
1	G	503	HIS

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 oligosaccharides 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.

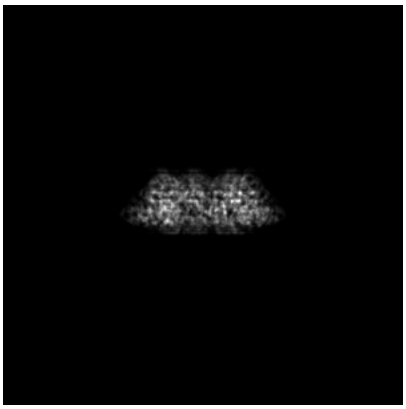
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-25744. These allow visual inspection of the internal detail of the map and identification of artifacts.

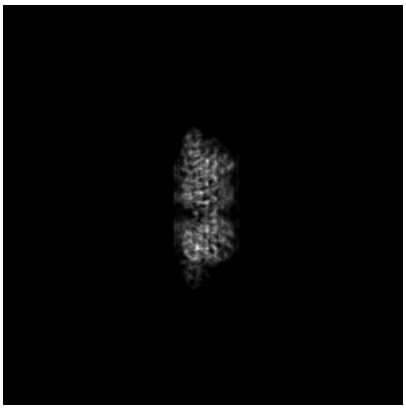
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

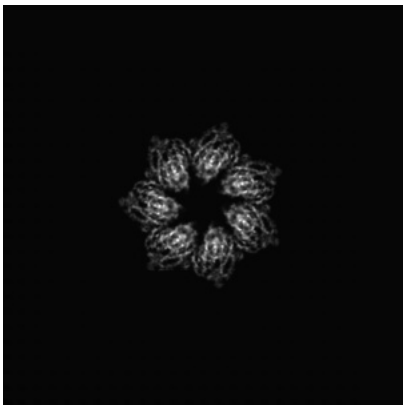
6.1.1 Primary map



X

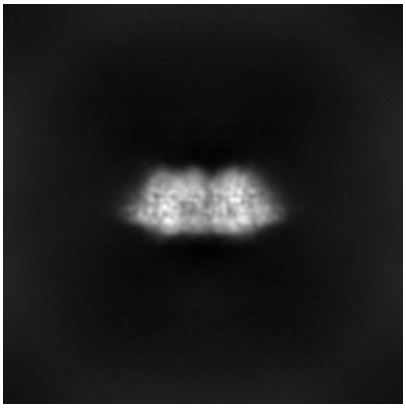


Y

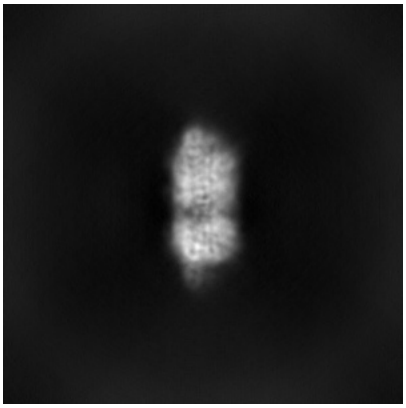


Z

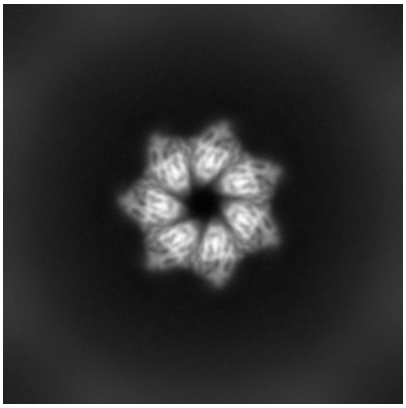
6.1.2 Raw map



X



Y



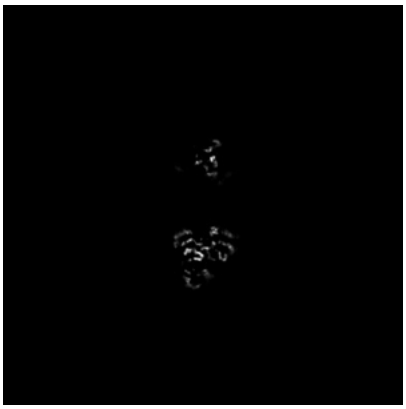
Z

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

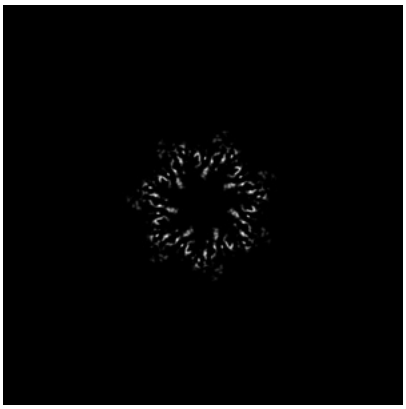
6.2 Central slices (i)

6.2.1 Primary map

X Index: 200

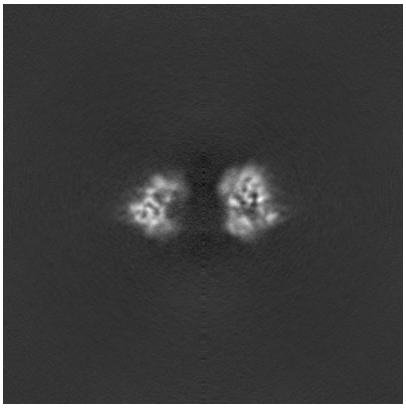


Y Index: 200

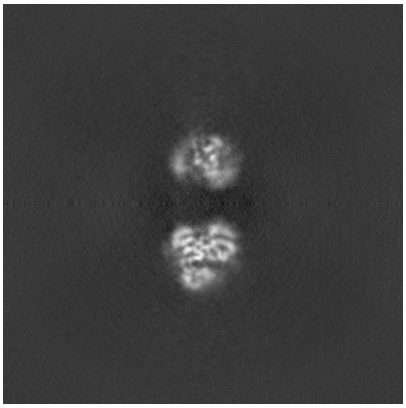


Z Index: 200

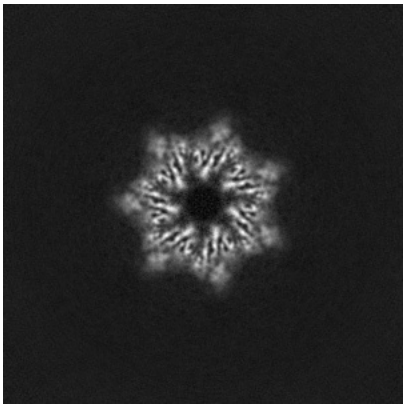
6.2.2 Raw map



X Index: 200



Y Index: 200



Z Index: 200

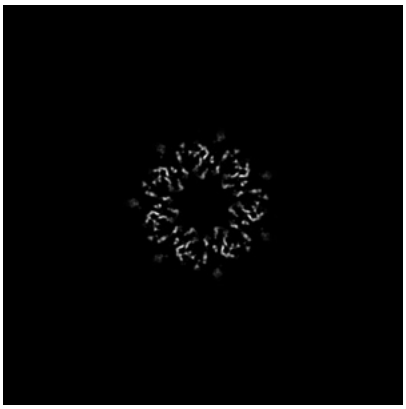
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

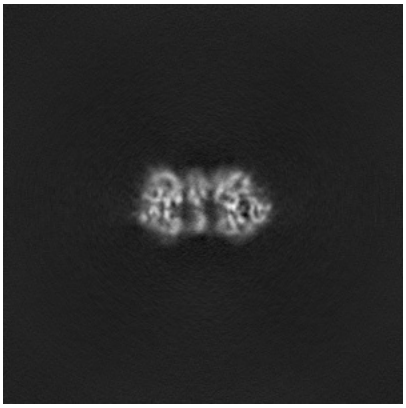
X Index: 156

Y Index: 158



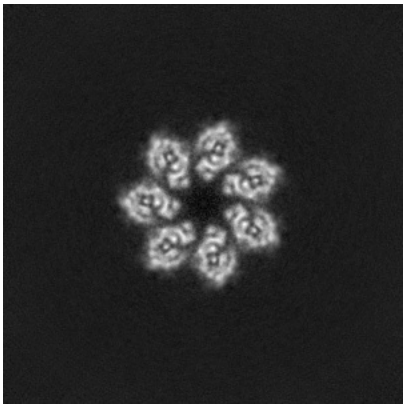
Z Index: 203

6.3.2 Raw map



X Index: 173

Y Index: 236

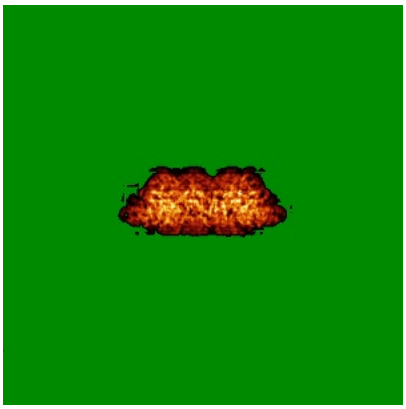


Z Index: 184

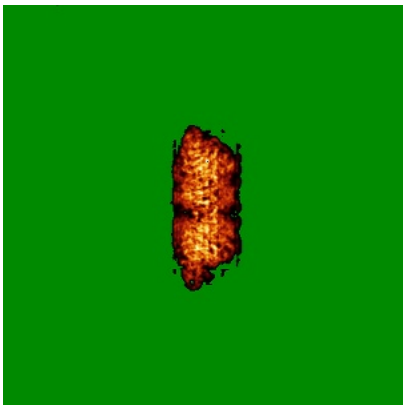
The images above show the largest variance slices of the map in three orthogonal directions.

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

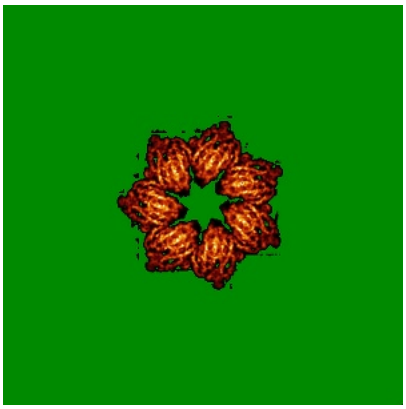
6.4.1 Primary map



X

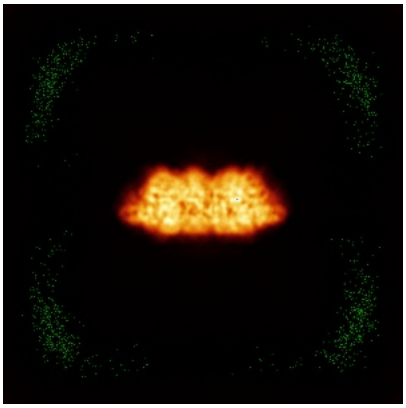


Y

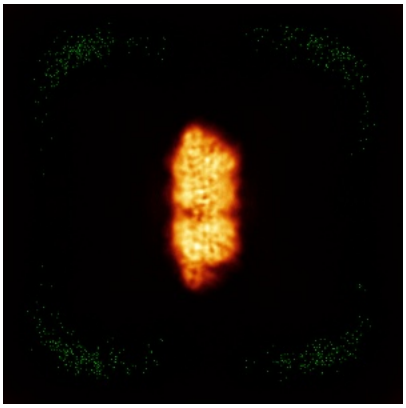


Z

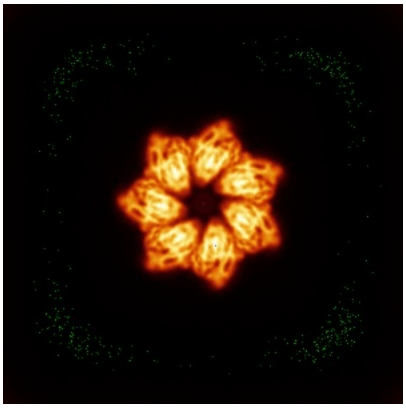
6.4.2 Raw map



X



Y

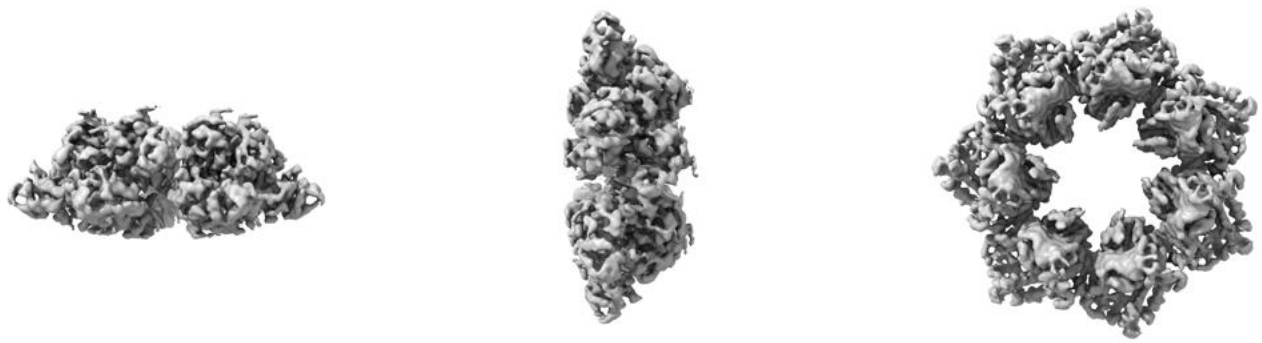


Z

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 0.159. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

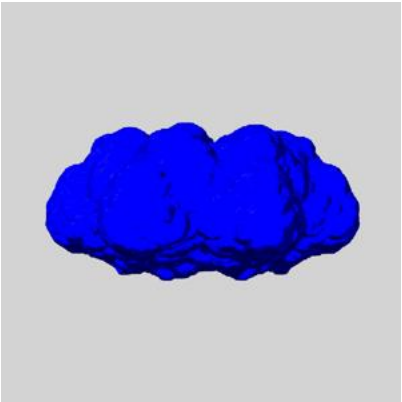
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

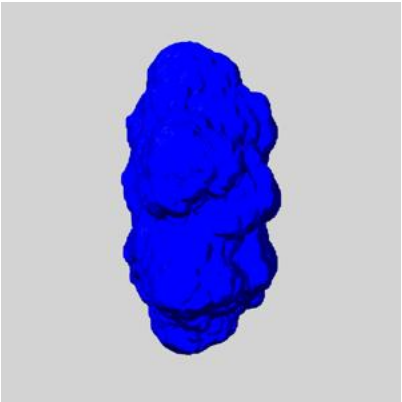
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

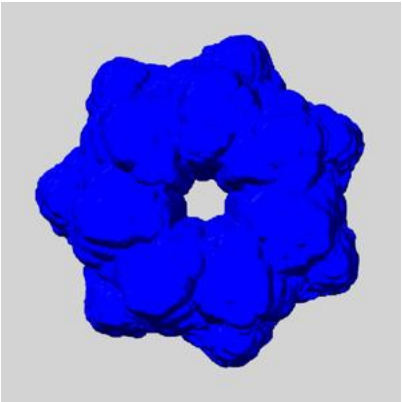
6.6.1 emd_25744_msk_1.map (i)



X



Y

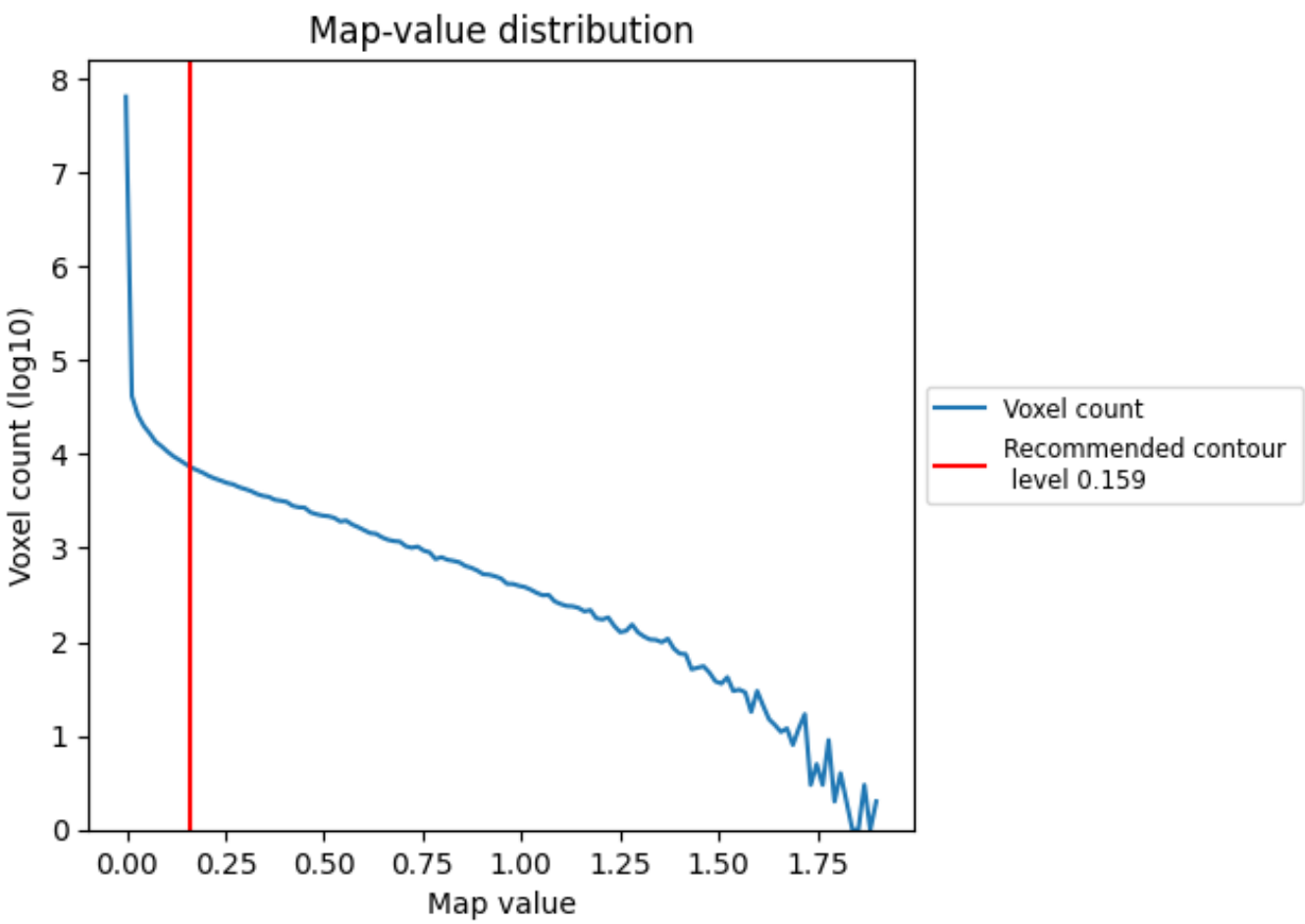


Z

7 Map analysis (i)

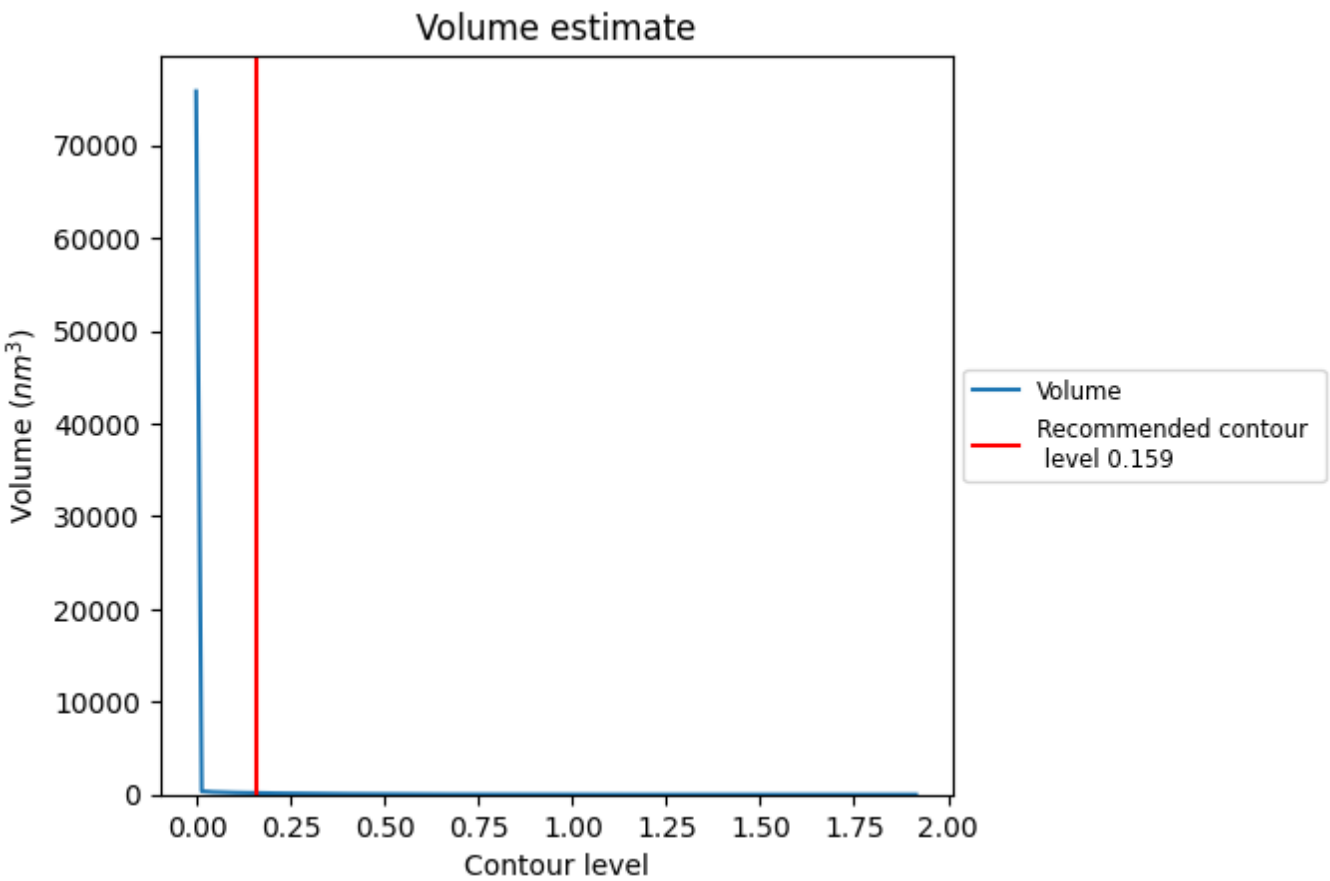
This section contains the results of statistical analysis of the map.

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.

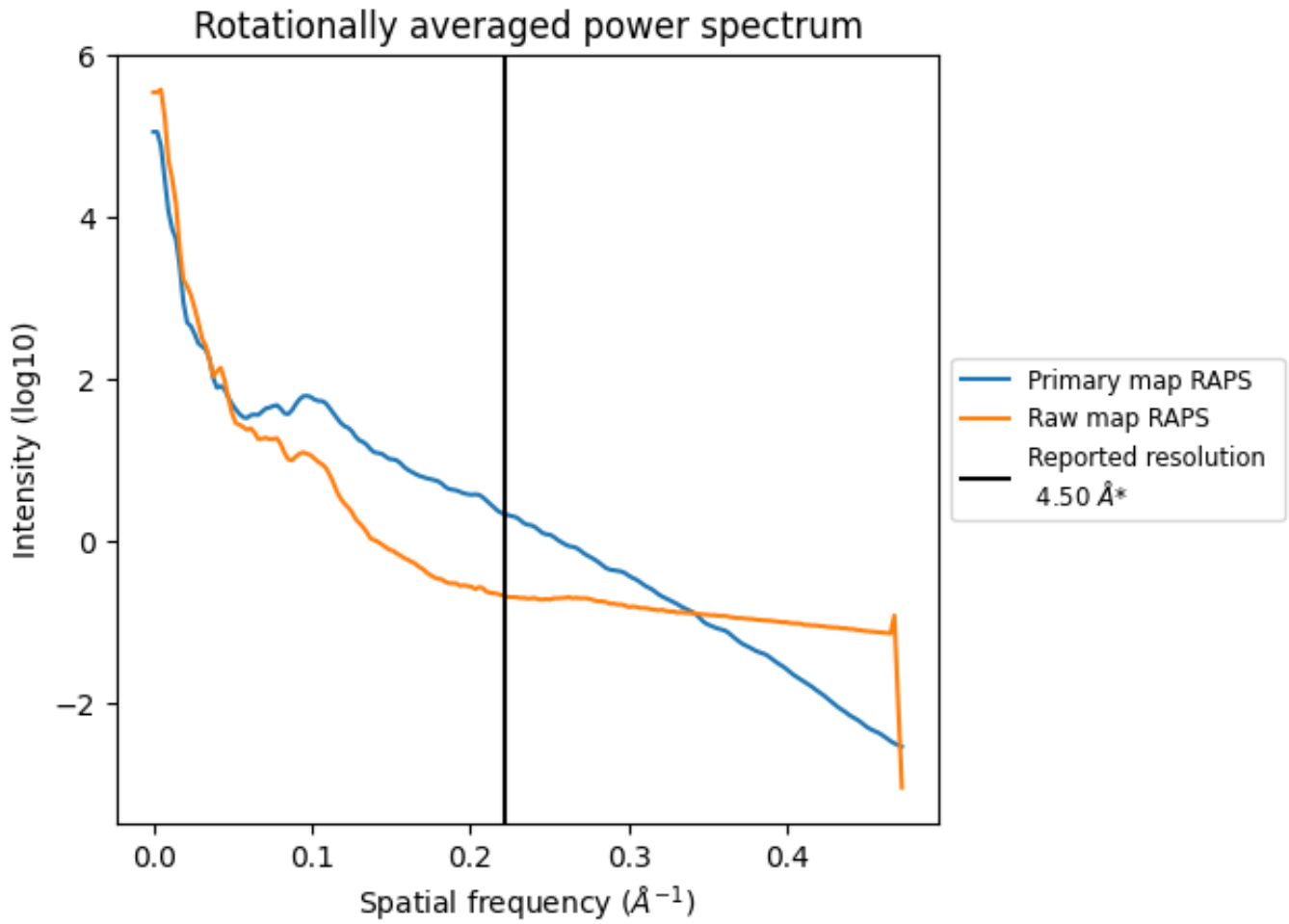
7.2 Volume estimate (i)



The volume at the recommended contour level is 163 nm^3; this corresponds to an approximate mass of 147 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)

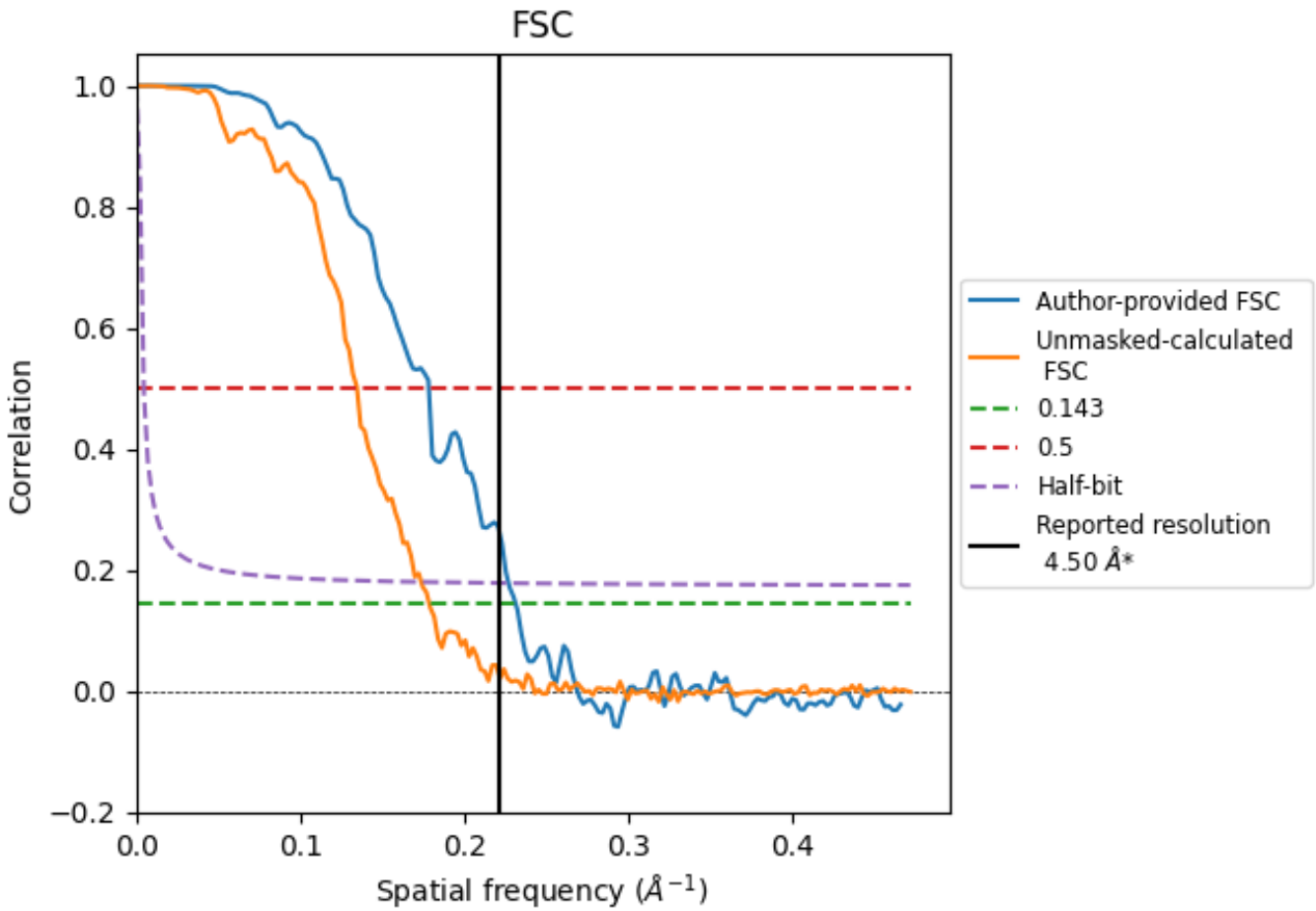


*Reported resolution corresponds to spatial frequency of 0.222 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.222 Å^{-1}

8.2 Resolution estimates (i)

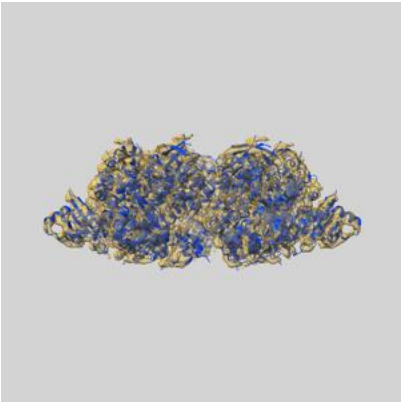
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.50	-	-
Author-provided FSC curve	4.32	5.60	4.40
Unmasked-calculated*	5.59	7.42	5.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.59 differs from the reported value 4.5 by more than 10 %

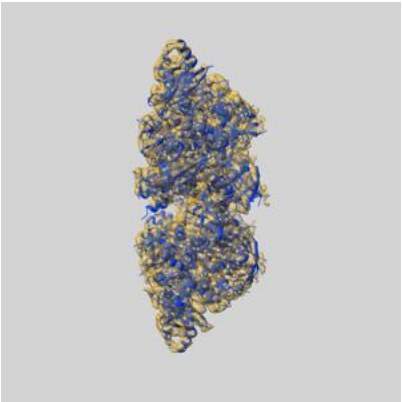
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-25744 and PDB model 7T8C. Per-residue inclusion information can be found in section 3 on page 7.

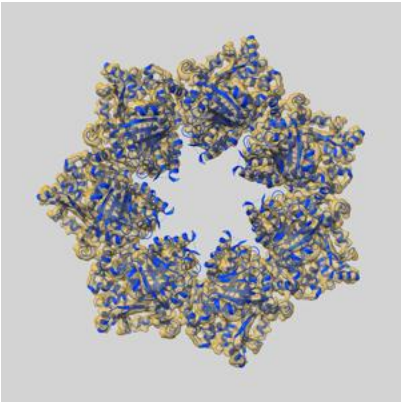
9.1 Map-model overlay (i)



X



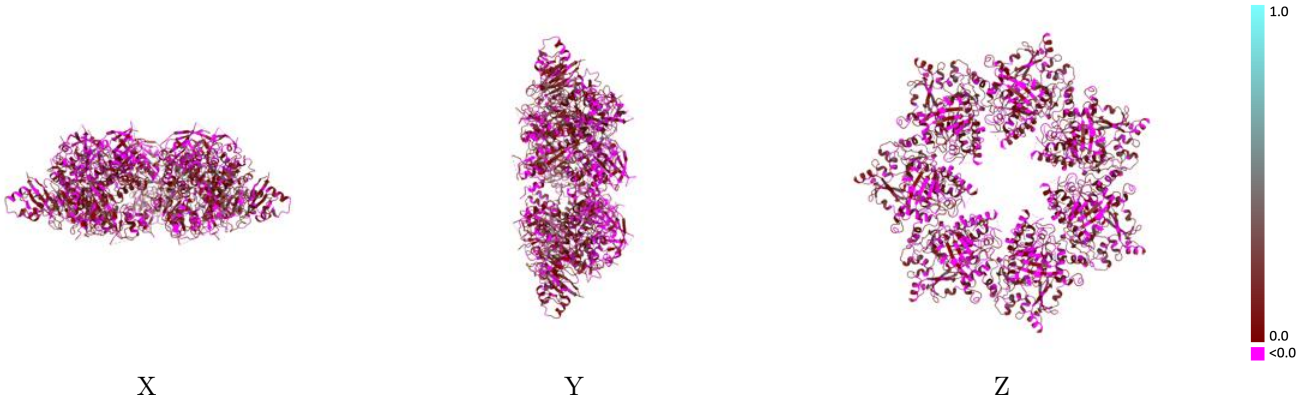
Y



Z

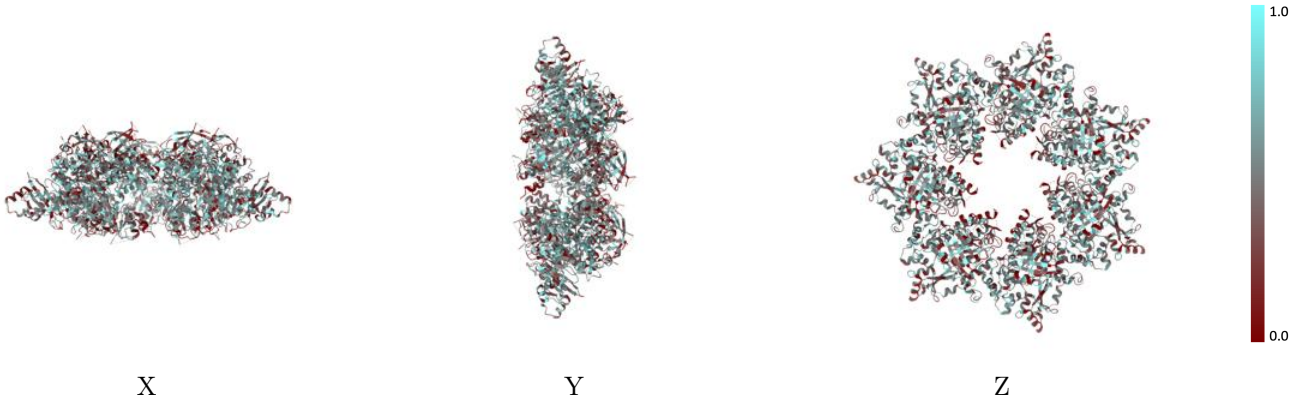
The images above show the 3D surface view of the map at the recommended contour level 0.159 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



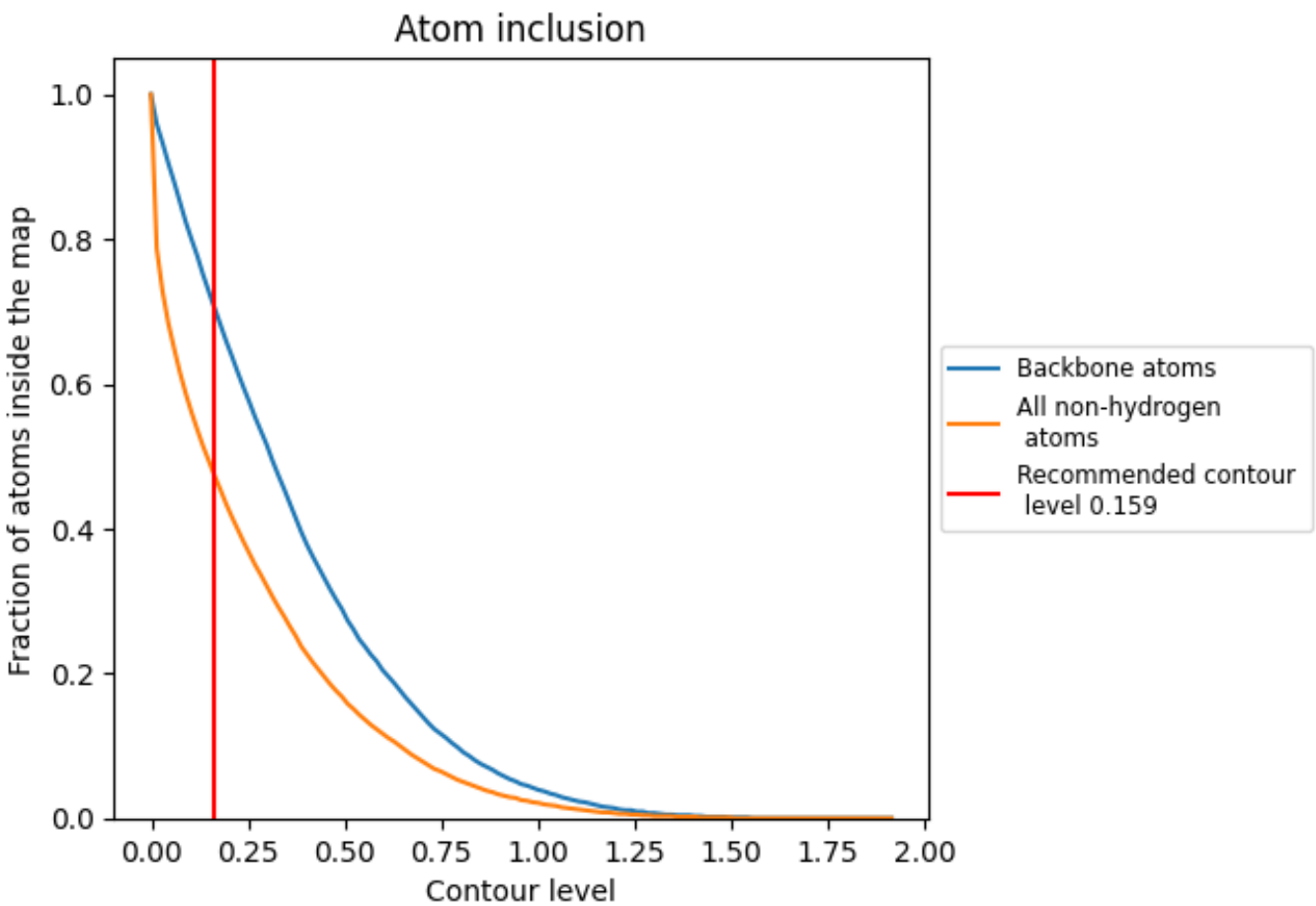
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.159).

9.4 Atom inclusion (i)



At the recommended contour level, 71% of all backbone atoms, 48% 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 (0.159) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4780	0.0800
A	0.4820	0.0870
B	0.4930	0.0930
C	0.4820	0.0790
D	0.4620	0.0670
E	0.4600	0.0690
F	0.4790	0.0810
G	0.4860	0.0850