wwPDB EM Validation Summary Report

Mar 26, 2026 – 05:08 PM UTC

PDB ID	:	9O81 / pdb_00009o81
EMDB ID	:	EMD-70214
Title	:	Cryo-EM structure of apo rabbit TRPM3 having 2 resting and 2 activated subunits (ortho position) at 37 degrees Celsius
Authors	:	Kumar, S.; Lu, W.; Du, J.
Deposited on	:	2025-04-15
Resolution	:	3.96 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 ⓘ 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 ⓘ) were used in the production of this report:

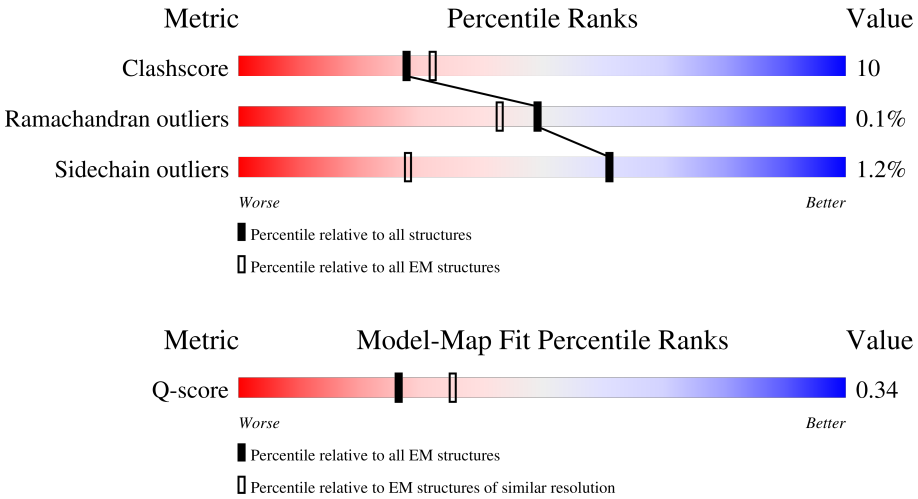
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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 3.96 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	7646 (3.46 - 4.46)

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	1306	22% 63% 15% • 21%
1	B	1306	17% 63% 16% 21%
1	C	1306	15% 61% 17% 21%
1	D	1306	23% 64% 14% • 20%

2 Entry composition

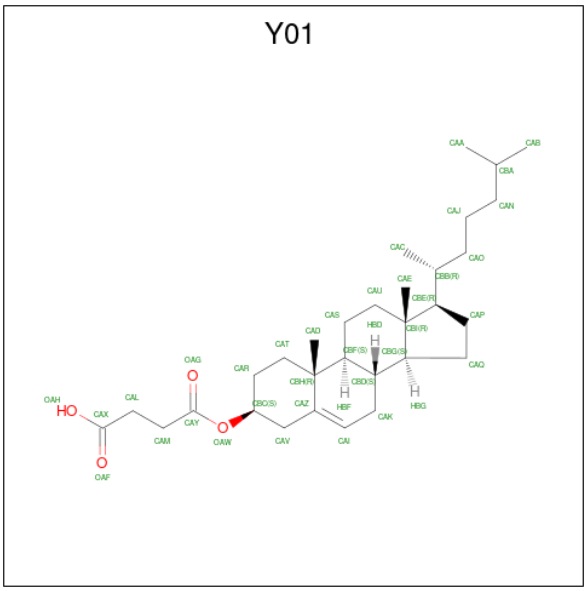
There are 2 unique types of molecules in this entry. The entry contains 31676 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 TRPM3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	1033	Total	C	N	O	S	0	0
			7863	5094	1329	1384	56		
1	B	1032	Total	C	N	O	S	0	0
			7835	5060	1334	1387	54		
1	A	1038	Total	C	N	O	S	0	0
			7818	5068	1328	1366	56		
1	D	1039	Total	C	N	O	S	1	0
			7740	5012	1313	1359	56		

- Molecule 2 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: $C_{31}H_{50}O_4$).



Mol	Chain	Residues	Atoms			AltConf
2	C	1	Total	C	O	0
			35	31	4	
2	C	1	Total	C	O	0
			35	31	4	
2	C	1	Total	C	O	0
			35	31	4	

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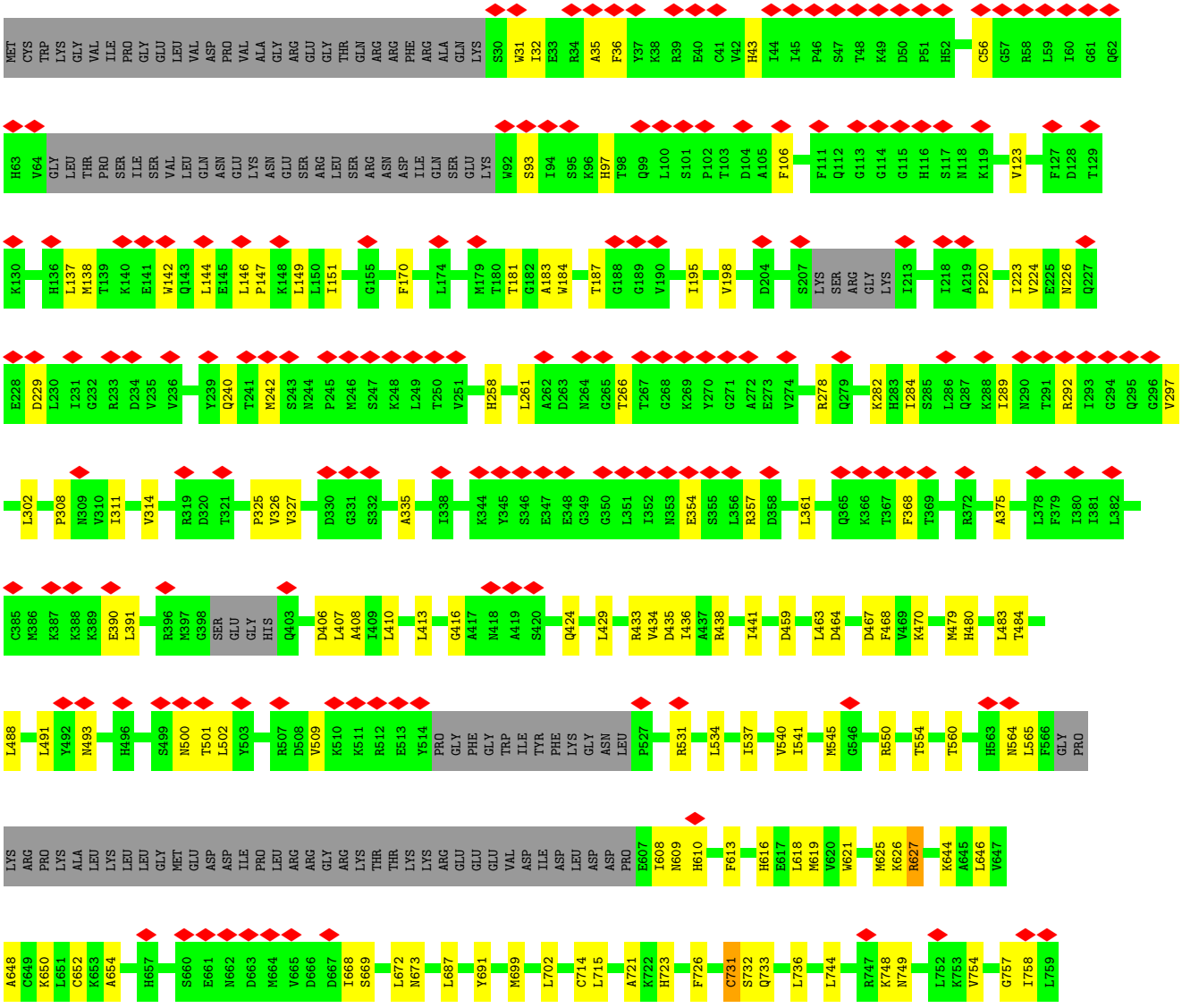
Mol	Chain	Residues	Atoms	AltConf
2	B	1	Total C O 35 31 4	0
2	B	1	Total C O 35 31 4	0
2	B	1	Total C O 35 31 4	0
2	A	1	Total C O 35 31 4	0
2	A	1	Total C O 35 31 4	0
2	A	1	Total C O 35 31 4	0
2	D	1	Total C O 35 31 4	0
2	D	1	Total C O 35 31 4	0
2	D	1	Total C O 35 31 4	0

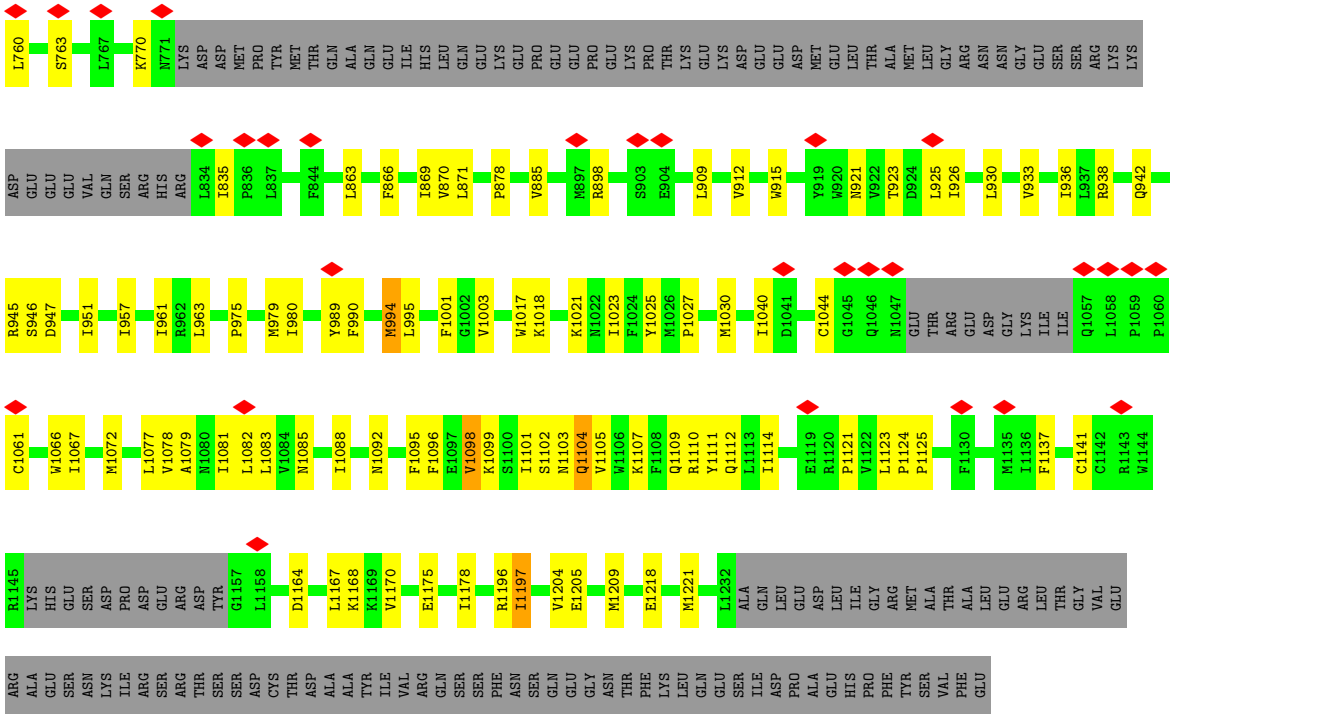
3 Residue-property plots (i)

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: TRPM3

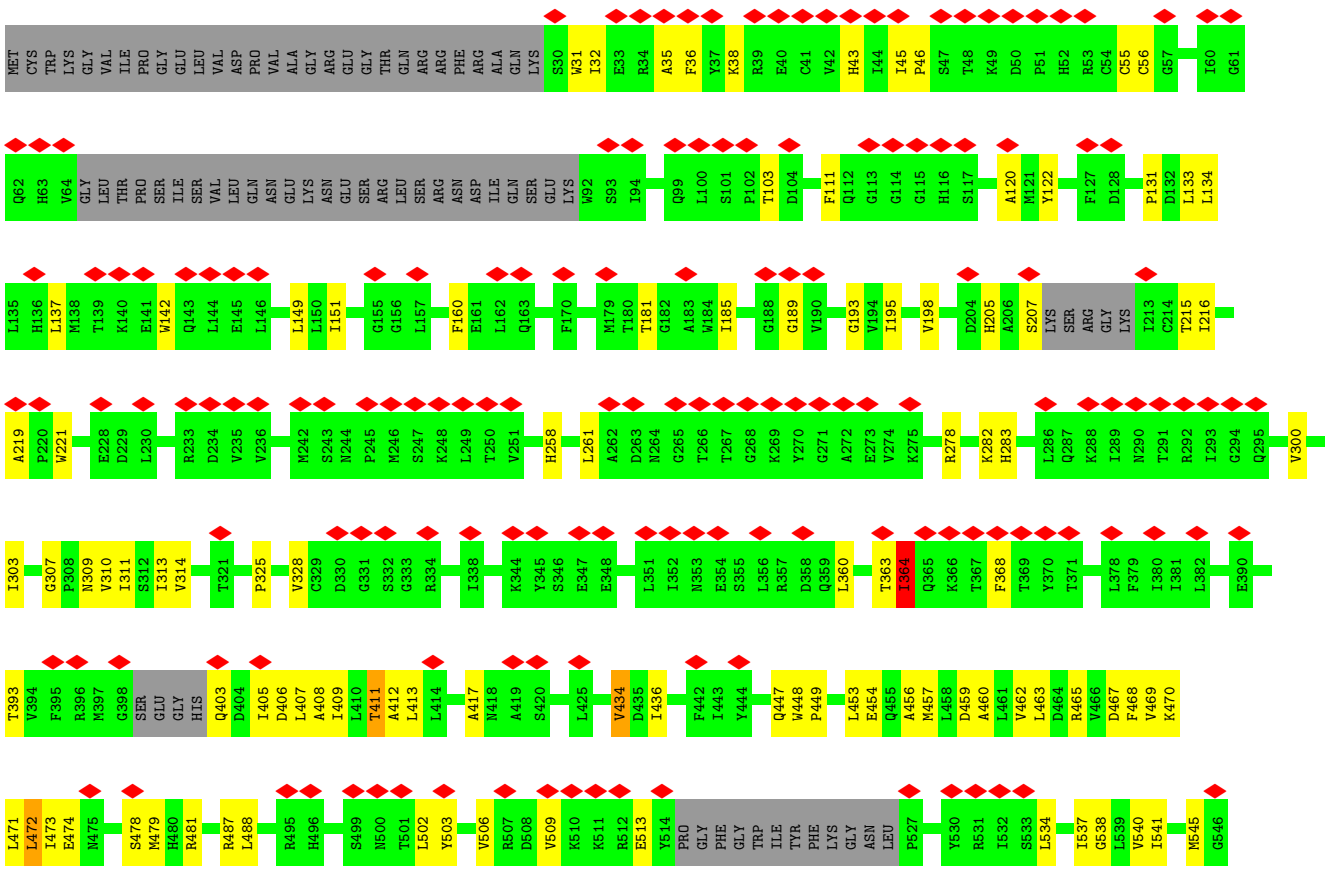
Chain C:

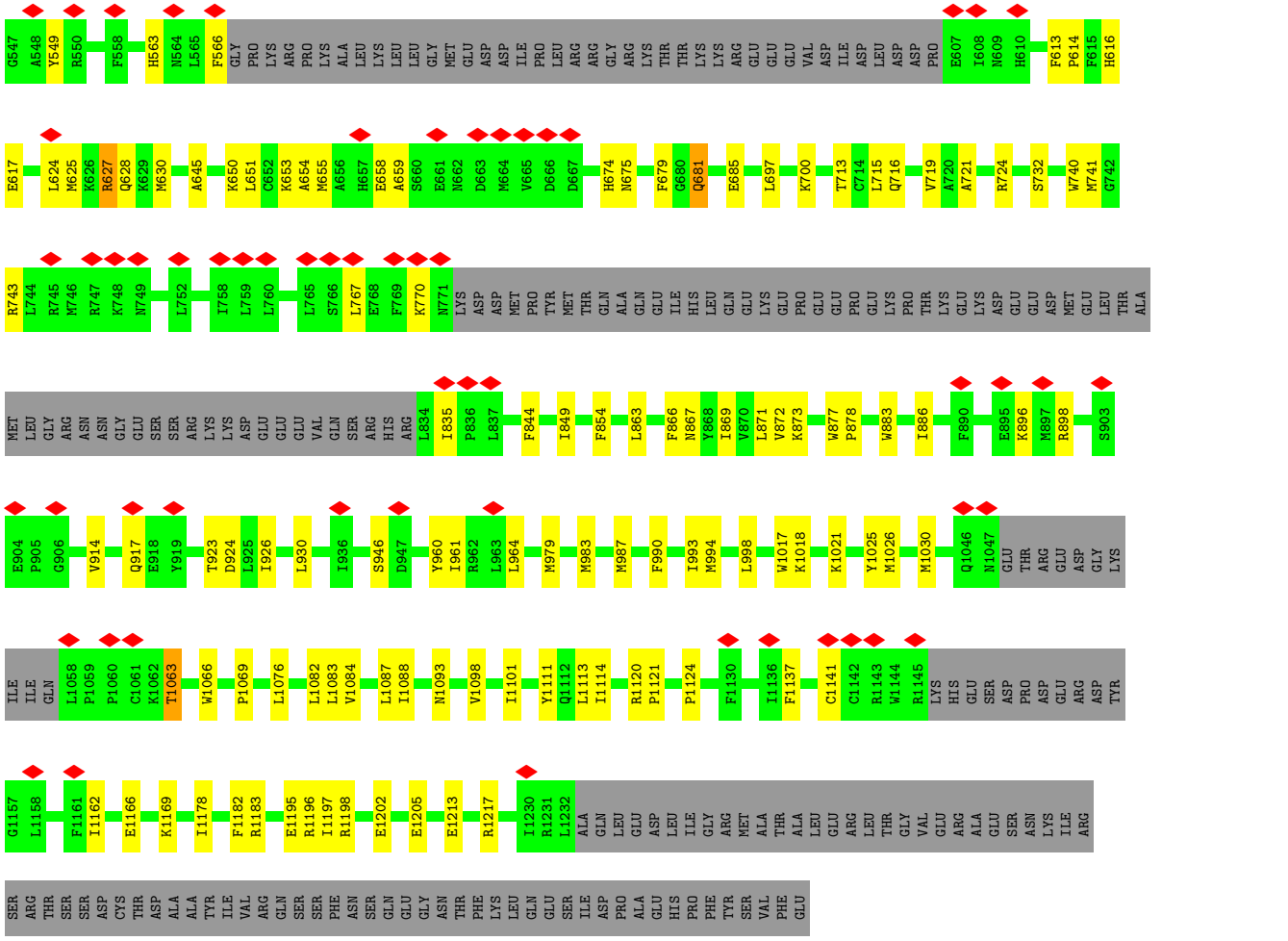




• Molecule 1: TRPM3

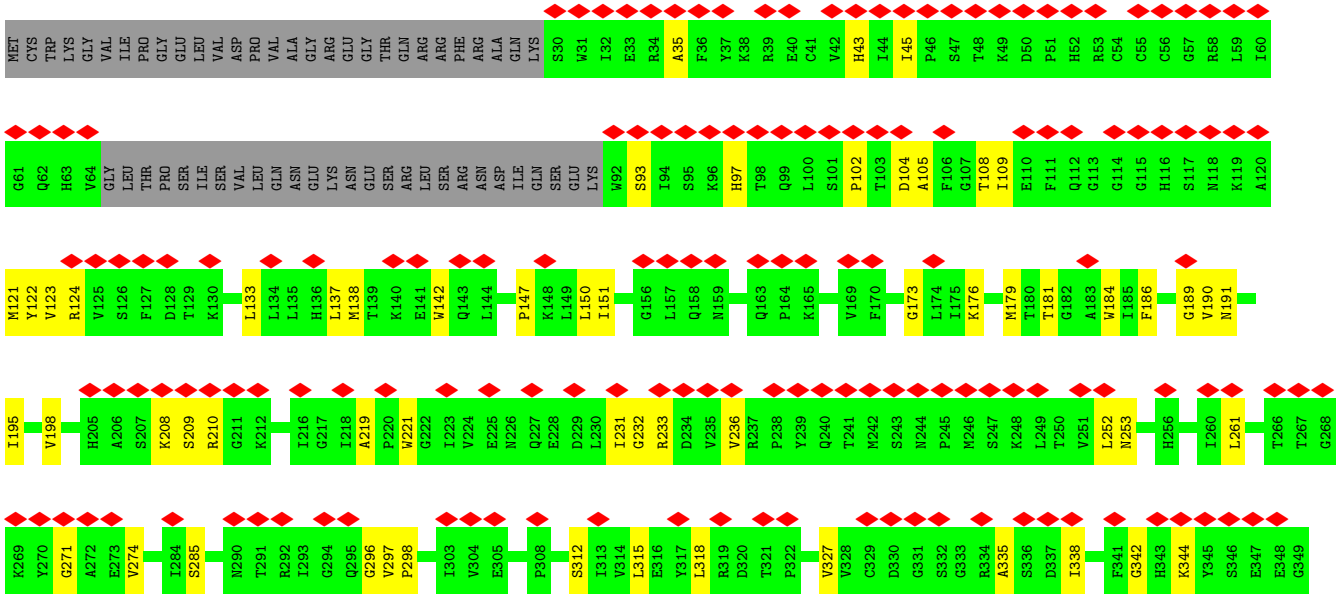
Chain B:

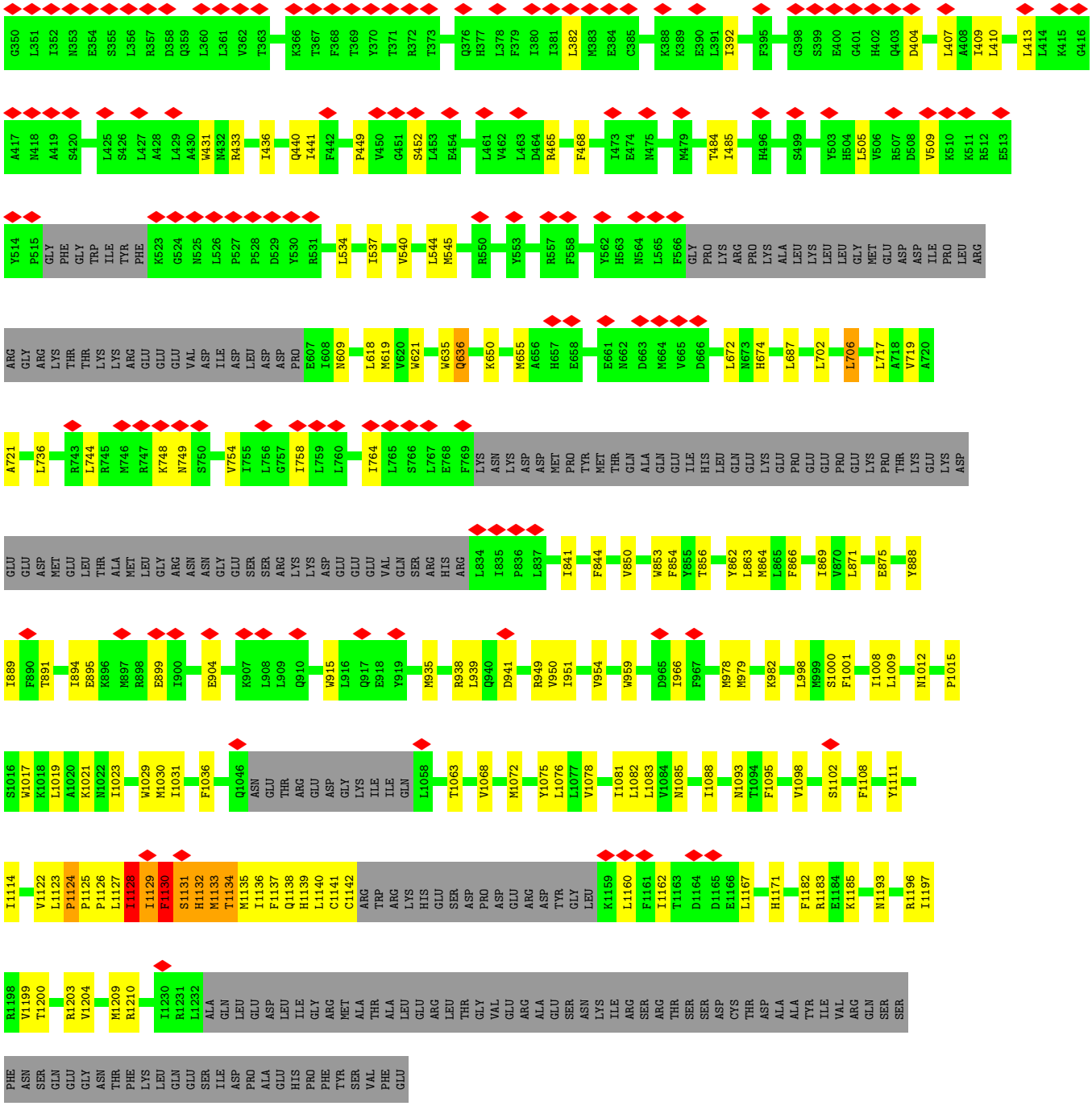




• Molecule 1: TRPM3

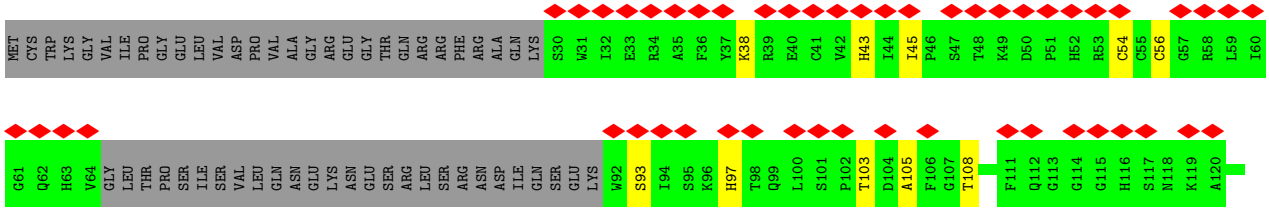
Chain A:

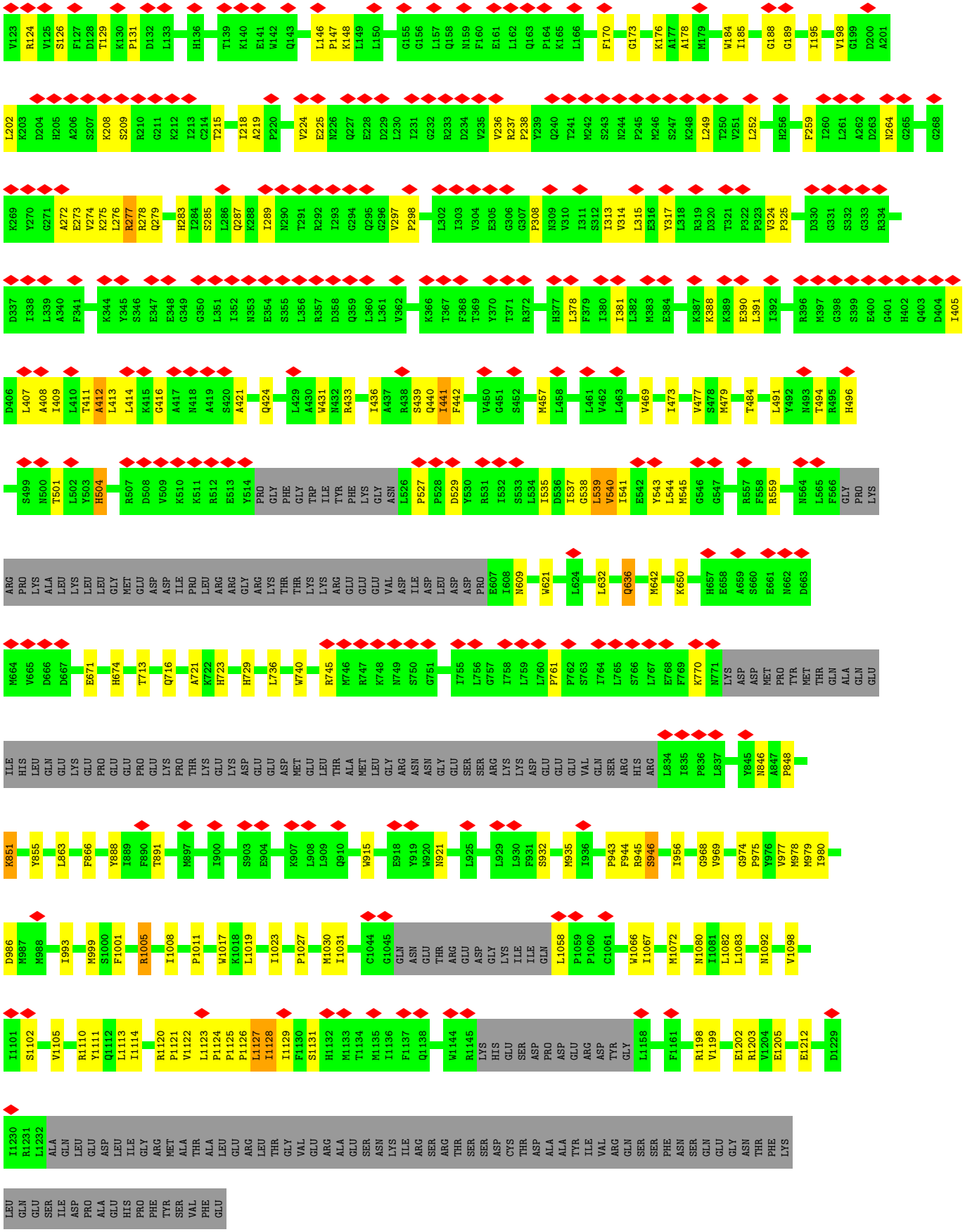




• Molecule 1: TRPM3

Chain D:




V123 R124 V125 S126 F127 D128 T129 K130 P131 D132 L133 H136 T139 K140 E141 W142 Q143 L146 P147 K148 L149 L150 G155 G156 L157 Q158 N159 F160 E161 L162 Q163 P164 K165 L166 F170 G173 K176 A177 A178 M179 W184 I185 G188 G189 I195 V198 G199 D200 A201
L202 K203 D204 H205 A206 S207 K208 S209 R210 G211 K212 I213 C214 T215 I218 A219 P220 V224 E225 N226 Q227 E228 D229 L230 I231 G232 R233 D234 V235 V236 R237 P238 Y239 Q240 T241 M242 S243 N244 P245 M246 S247 K248 L249 T250 V251 L252 H256 F259 I260 L261 A262 D263 N264 G265 G268
K269 Y270 G271 A272 E273 V274 K275 L276 R277 R278 Q279 H283 I284 S285 L286 Q287 K288 I289 N290 T291 R292 I293 G294 Q295 G296 V297 P298 L302 I303 V304 E305 G306 G307 P308 N309 V310 I311 S312 I313 V314 L315 E316 Y317 L318 R319 D320 T321 P322 P323 V324 P325 D330 G331 S332 G333 R334
D337 I338 L339 A340 F341 K344 Y345 S346 E347 E348 G349 G350 L351 I352 N353 E354 S355 L356 R357 D358 Q359 L360 L361 V362 K366 T367 F368 T369 Y370 T371 R372 H377 L378 F379 I380 I381 L382 M383 E384 K387 K388 K389 E390 L391 I392 R396 M397 G398 S399 E400 G401 H402 Q403 D404 I405
D406 L407 A408 I409 L410 T411 A412 L413 L414 K415 G416 A417 N418 A419 S420 A421 Q424 L429 A430 W431 N432 R433 I436 A437 R438 S439 Q440 I441 F442 V450 G451 S452 M457 L458 L461 V462 L463 V469 I473 V477 S478 M479 T484 L491 Y492 N493 T494 R495 H496
S499 N500 T501 L502 Y503 H504 R507 D508 V509 K510 K511 R512 E513 Y514 PRO GLY PHE GLY TRP ILE TYR PHE LYS GLY ASN L526 P527 P528 D529 Y530 R531 I532 S533 L534 I535 D536 I537 G538 L539 V540 I541 E542 Y543 L544 M545 G546 G547 R557 F558 R559 N564 L565 F566 GLY PRO LYS
ARG PRO LYS ALA LEU LYS LEU LEU GLY MET GLU ASP ASP ILE PRO LEU ARG ARG GLY ARG LYS THR THR LYS LYS ARG GLU GLU GLU VAL ASP ILE ASP LEU ASP ASP PRO E607 I608 N609 W621 L624 L632 Q636 M642 K650 H657 E658 A659 S660 E661 N662 D663
M664 V665 D666 D667 E671 H674 T713 Q716 A721 K722 H723 H729 L736 W740 R745 M746 R747 K748 N749 S750 G751 I755 L756 G757 I758 L759 L760 P761 P762 S763 I764 L765 S766 L767 E768 F769 K770 N771 LYS ASP ASP MET PRO TYR MET THR GLN ALA GLN GLU
ILE HIS LEU GLN GLU LYS GLU PRO GLU GLU PRO GLU LYS PRO THR LYS GLU LYS ASP GLU GLU ASP MET GLU LEU THR ALA MET LEU GLY ARG ASN ASN GLY GLU SER SER ARG LYS LYS ASP GLU GLU GLU VAL GLN SER ARG HIS ARG L834 I835 P836 L837 Y845 N846 A847 P848
K851 Y855 L863 F866 Y888 I889 F890 T891 M897 I900 S903 E904 K907 L908 L909 Q910 W915 E918 Y919 W920 N921 L925 L929 L930 F931 S932 M935 I936 P943 F944 R945 S946 I956 G968 V969 G974 P975 Y976 V977 M978 M979 I980
D986 M987 M988 I993 M999 S1000 F1001 R1005 I1008 P1011 W1017 K1018 L1019 I1023 P1027 M1030 I1031 C1044 G1045 GLN ASN GLU THR ARG GLU ASP GLY LYS ILE ILE GLN L1058 P1059 P1060 C1061 W1066 I1067 M1072 N1080 I1081 L1082 L1083 N1092 V1098
I1101 S1102 V1105 R1110 Y1111 Q1112 L1113 I1114 R1120 P1121 V1122 L1123 P1124 P1125 P1126 L1127 I1128 I1129 F1130 S1131 H1132 M1133 T1134 M1135 I1136 F1137 Q1138 W1144 R1145 LYS HIS GLU SER ASP PRO ASP GLU ARG ASP TYR GLY L1158 F1161 R1198 V1199 E1202 R1203 V1204 E1205 E1212 D1229
I1230 R1231 L1232 ALA GLN LEU GLU ASP LEU ILE GLY ARG MET ALA THR ALA LEU GLU ARG LEU THR GLY VAL GLU ARG ALA GLU SER ASN LYS ILE ARG SER ARG THR SER SER ASP CYS THR ASP ALA ALA TYR ILE VAL ARG GLN SER SER PHE ASN SER GLN GLU GLY ASN THR PHE LYS
LEU GLN GLU SER ILE ASP PRO ALA GLU HIS PRO PHE TYR SER VAL PHE GLU

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84256	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 ($e^-/Å^2$)	58	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.004	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0025	Depositor
Map size (Å)	317.184, 317.184, 317.184	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.826, 0.826, 0.826	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: Y01

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	0.44	1/8000 (0.0%)	0.91	8/10896 (0.1%)
1	B	0.50	2/8009 (0.0%)	0.97	13/10891 (0.1%)
1	C	0.49	1/8039 (0.0%)	0.95	9/10932 (0.1%)
1	D	0.49	1/7919 (0.0%)	0.95	14/10793 (0.1%)
All	All	0.48	5/31967 (0.0%)	0.95	44/43512 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	835	ILE	C-N	6.55	1.43	1.33
1	D	761	PRO	C-N	6.22	1.41	1.34
1	B	1026	MET	C-N	5.53	1.42	1.33
1	A	904	GLU	C-N	5.49	1.40	1.33
1	C	835	ILE	C-N	5.32	1.41	1.33

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1031	ILE	N-CA-C	-7.60	105.31	112.83
1	A	441	ILE	N-CA-C	-7.50	105.40	112.83
1	A	941	ASP	N-CA-C	7.48	120.18	110.53
1	D	1067	ILE	CA-C-N	7.20	124.78	120.24
1	D	1067	ILE	C-N-CA	7.20	124.78	120.24

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	7818	0	7458	155	0
1	B	7835	0	7473	163	0
1	C	7863	0	7557	169	0
1	D	7740	0	7291	145	0
2	A	105	0	147	8	0
2	B	105	0	147	5	0
2	C	105	0	147	5	0
2	D	105	0	147	9	0
All	All	31676	0	30367	603	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 10.

The worst 5 of 603 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:B:434:VAL:CG2	1:B:471:LEU:HD11	1.67	1.24
1:D:237:ARG:CD	1:D:238:PRO:HD2	1.75	1.17
1:D:237:ARG:HD3	1:D:238:PRO:HD2	1.23	1.14
1:D:1124:PRO:HB2	1:D:1127:LEU:HB2	1.40	1.02
1:D:440:GLN:HG3	1:D:441:ILE:H	1.21	1.02

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	1024/1306 (78%)	947 (92%)	75 (7%)	2 (0%)	43 75
1	B	1014/1306 (78%)	936 (92%)	78 (8%)	0	100 100
1	C	1015/1306 (78%)	944 (93%)	71 (7%)	0	100 100
1	D	1026/1306 (79%)	954 (93%)	71 (7%)	1 (0%)	48 81
All	All	4079/5224 (78%)	3781 (93%)	295 (7%)	3 (0%)	49 81

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1130	PHE
1	A	1128	ILE
1	D	441	ILE

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	771/1162 (66%)	756 (98%)	15 (2%)	50 67
1	B	779/1162 (67%)	774 (99%)	5 (1%)	78 81
1	C	788/1162 (68%)	779 (99%)	9 (1%)	65 74
1	D	749/1162 (64%)	740 (99%)	9 (1%)	63 73
All	All	3087/4648 (66%)	3049 (99%)	38 (1%)	61 73

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1162	ILE
1	D	1005	ARG
1	D	277	ARG
1	D	636	GLN
1	D	1128	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	723	HIS
1	D	610	HIS
1	A	1006	GLN
1	D	253	ASN
1	D	1138	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	Y01	A	1401	-	38,38,38	0.41	0	57,57,57	0.82	1 (1%)
2	Y01	D	1401	-	38,38,38	0.40	0	57,57,57	0.48	0
2	Y01	B	1402	-	38,38,38	0.44	0	57,57,57	0.65	0
2	Y01	D	1402	-	38,38,38	0.40	0	57,57,57	0.48	0
2	Y01	D	1403	-	38,38,38	0.39	0	57,57,57	0.65	0
2	Y01	C	1402	-	38,38,38	0.37	0	57,57,57	0.57	0
2	Y01	C	1401	-	38,38,38	0.42	0	57,57,57	0.67	0
2	Y01	A	1402	-	38,38,38	0.40	0	57,57,57	0.52	0
2	Y01	A	1403	-	38,38,38	0.40	0	57,57,57	0.43	0
2	Y01	C	1403	-	38,38,38	0.41	0	57,57,57	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	Y01	B	1401	-	38,38,38	0.37	0	57,57,57	0.66	1 (1%)
2	Y01	B	1403	-	38,38,38	0.40	0	57,57,57	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	Y01	A	1401	-	-	7/19/77/77	0/4/4/4
2	Y01	D	1401	-	-	10/19/77/77	0/4/4/4
2	Y01	B	1402	-	-	1/19/77/77	0/4/4/4
2	Y01	D	1402	-	-	9/19/77/77	0/4/4/4
2	Y01	D	1403	-	-	10/19/77/77	0/4/4/4
2	Y01	C	1402	-	-	9/19/77/77	0/4/4/4
2	Y01	C	1401	-	-	3/19/77/77	0/4/4/4
2	Y01	A	1402	-	-	9/19/77/77	0/4/4/4
2	Y01	A	1403	-	-	9/19/77/77	0/4/4/4
2	Y01	C	1403	-	-	8/19/77/77	0/4/4/4
2	Y01	B	1401	-	-	8/19/77/77	0/4/4/4
2	Y01	B	1403	-	-	9/19/77/77	0/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1401	Y01	CBD-CAK-CAI	-2.44	109.38	112.76
2	B	1401	Y01	OAW-CBC-CAV	-2.19	103.52	108.04

There are no chirality outliers.

5 of 92 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1401	Y01	CAO-CBB-CBE-CBI
2	C	1401	Y01	CAJ-CAO-CBB-CAC
2	C	1402	Y01	CAJ-CAO-CBB-CAC
2	B	1401	Y01	CAJ-CAO-CBB-CAC
2	B	1403	Y01	CAJ-CAO-CBB-CAC

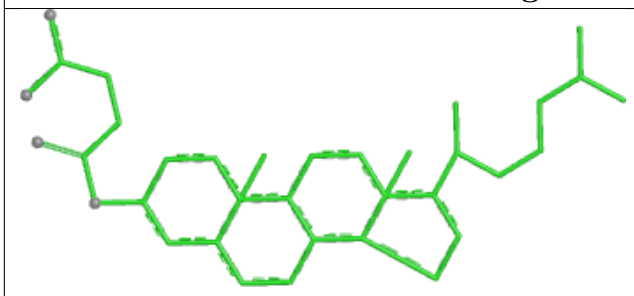
There are no ring outliers.

10 monomers are involved in 24 short contacts:

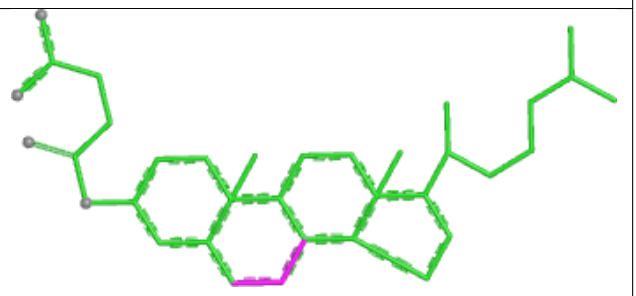
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1401	Y01	1	0
2	D	1401	Y01	2	0
2	B	1402	Y01	3	0
2	D	1402	Y01	4	0
2	D	1403	Y01	3	0
2	C	1401	Y01	2	0
2	A	1402	Y01	2	0
2	A	1403	Y01	5	0
2	C	1403	Y01	3	0
2	B	1401	Y01	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

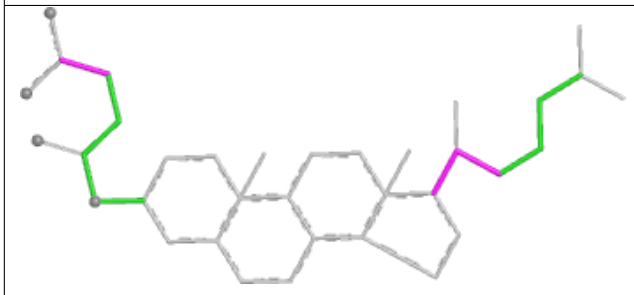
Ligand Y01 A 1401



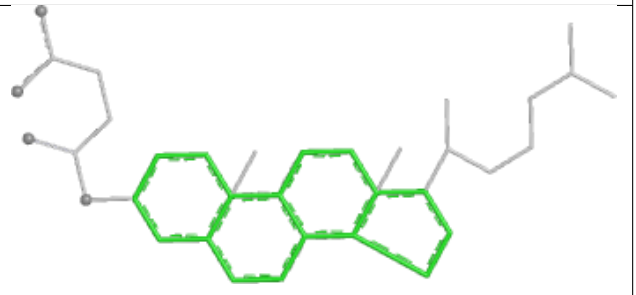
Bond lengths



Bond angles

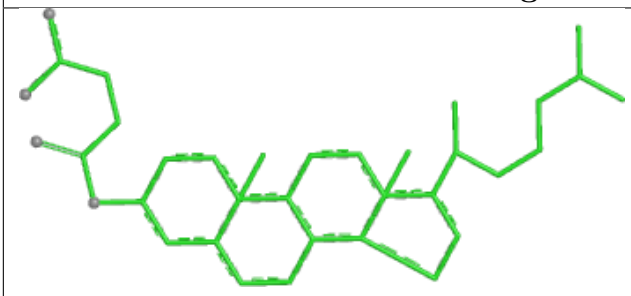


Torsions



Rings

Ligand Y01 D 1401



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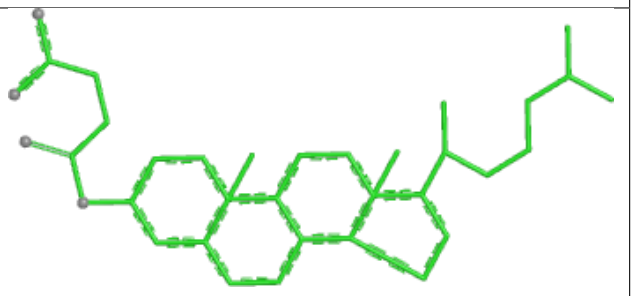
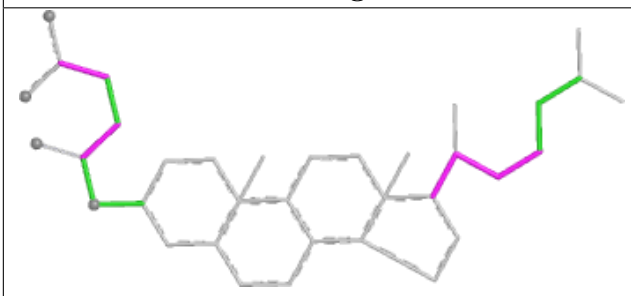


Bond angles



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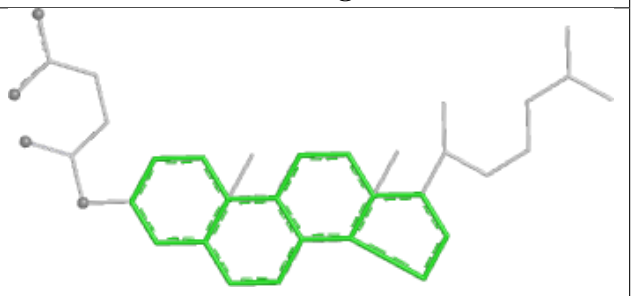
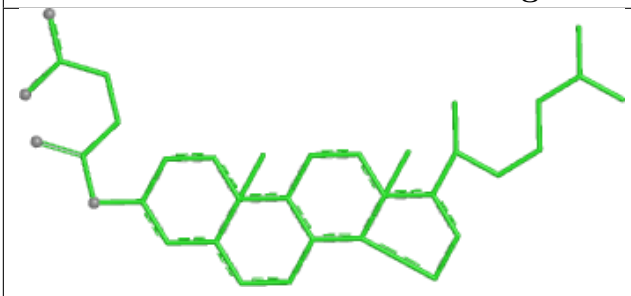


Rings

Ligand Y01 B 1402



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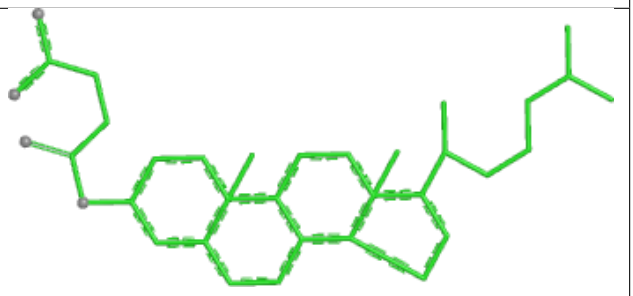
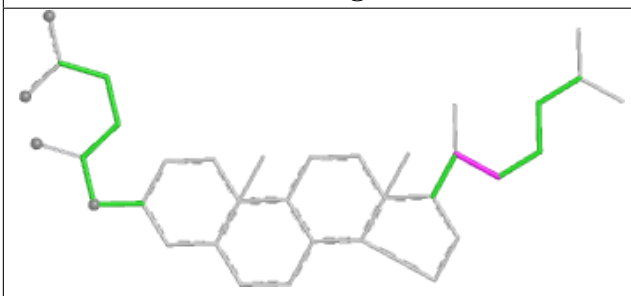
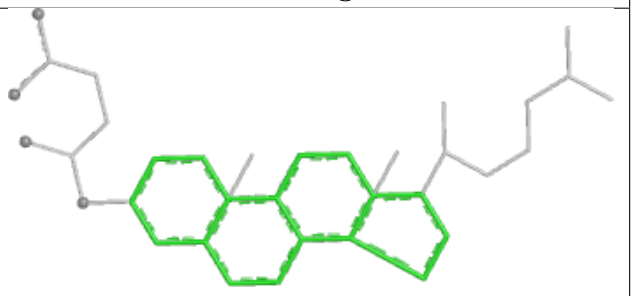


Bond angles

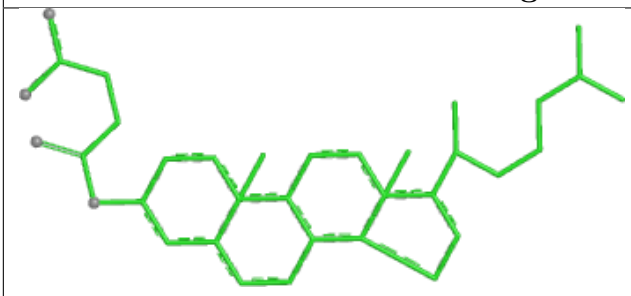


Torsions



Rings

Ligand Y01 D 1402



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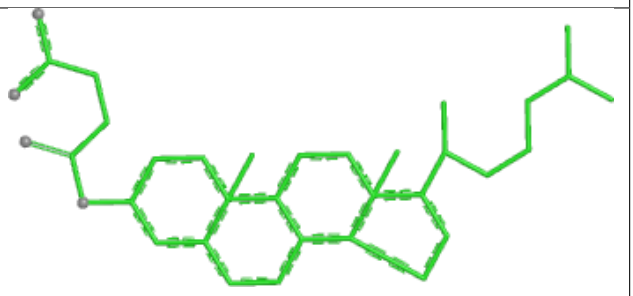

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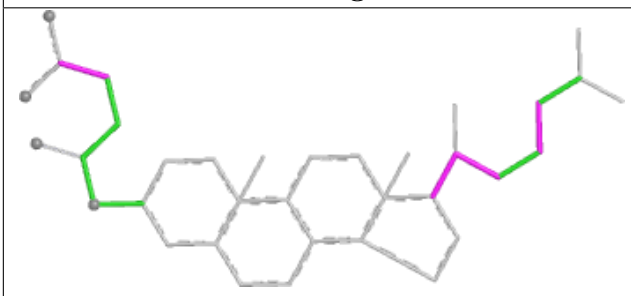

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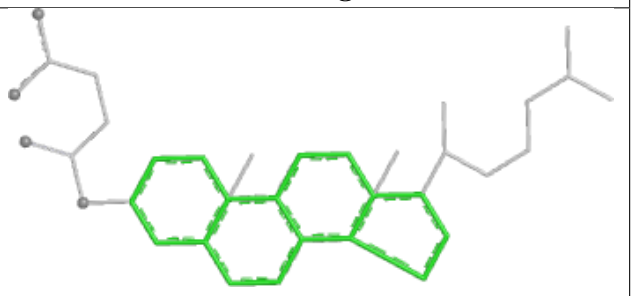
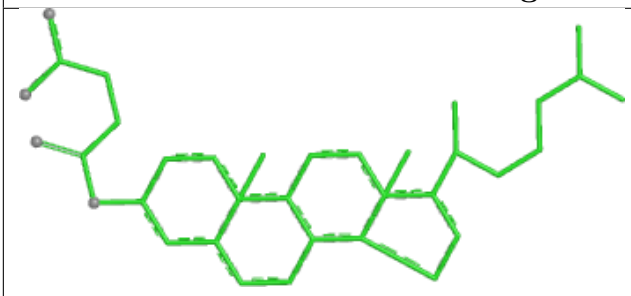


Rings

Ligand Y01 D 1403



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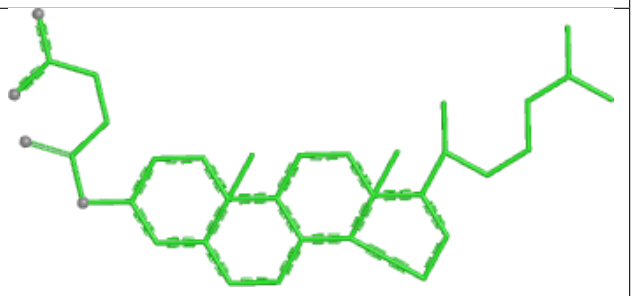

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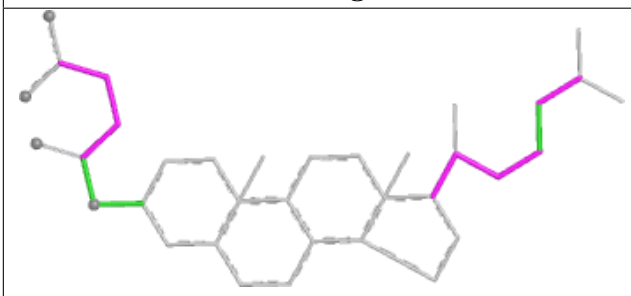

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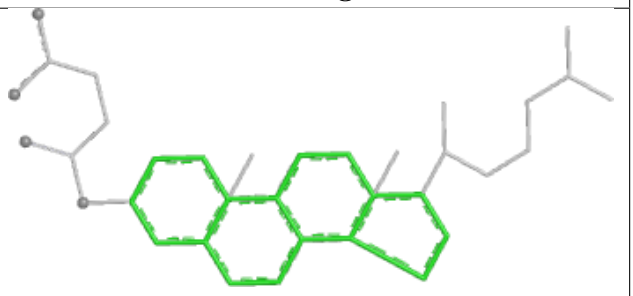
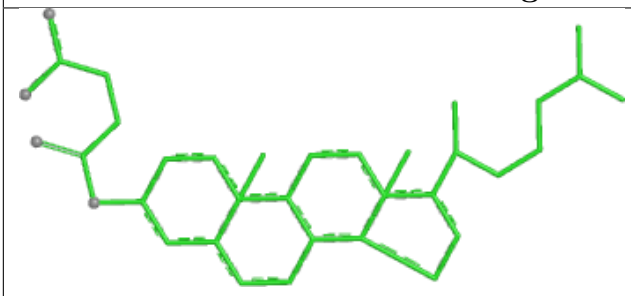


Rings

Ligand Y01 C 1402



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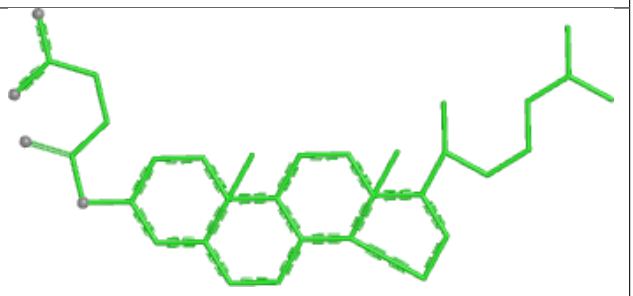

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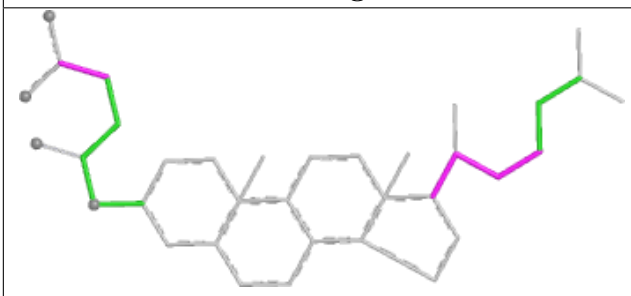

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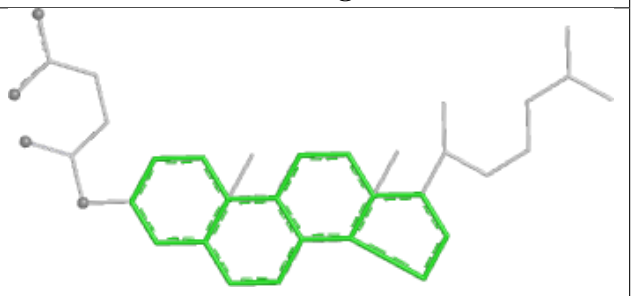
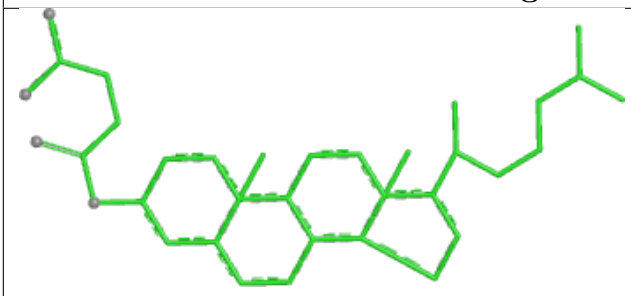


Rings

Ligand Y01 C 1401



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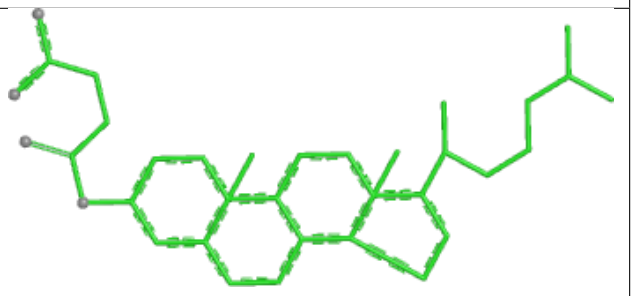

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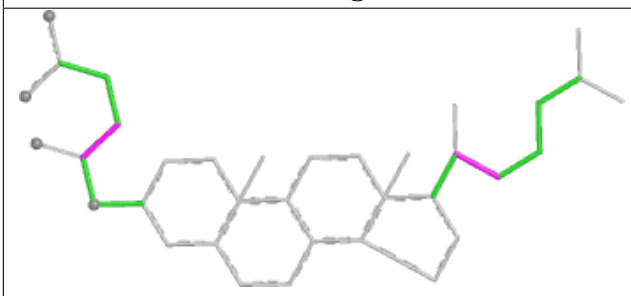

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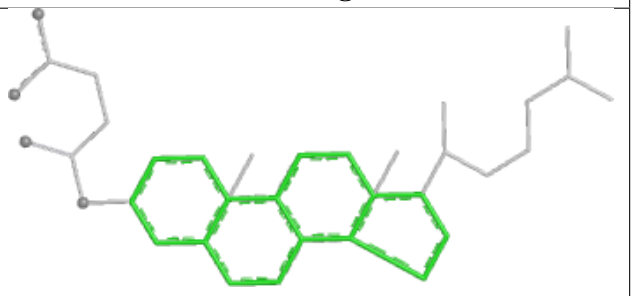
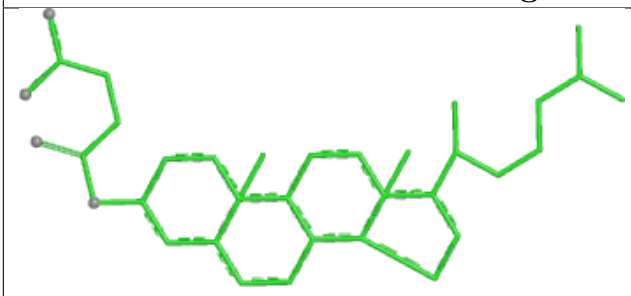


Rings

Ligand Y01 A 1402



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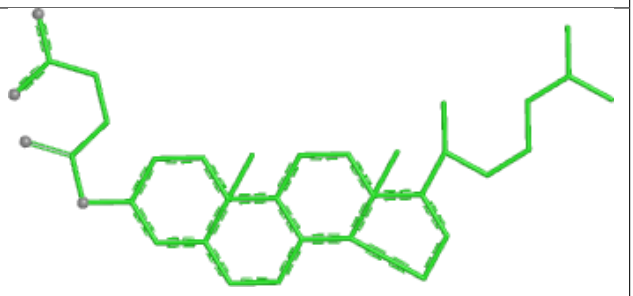

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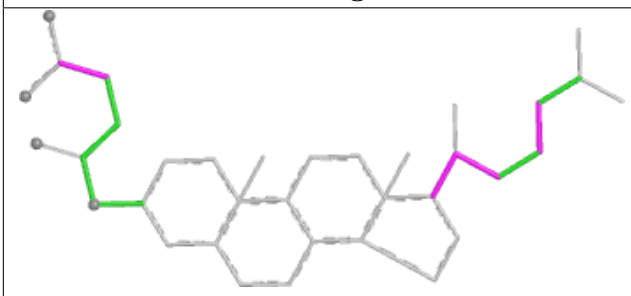

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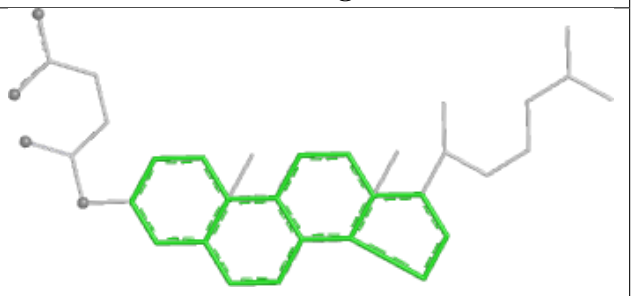
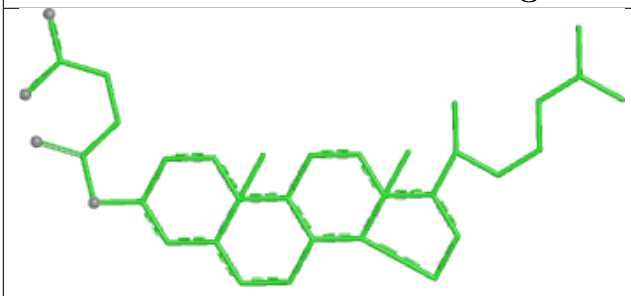


Rings

Ligand Y01 A 1403



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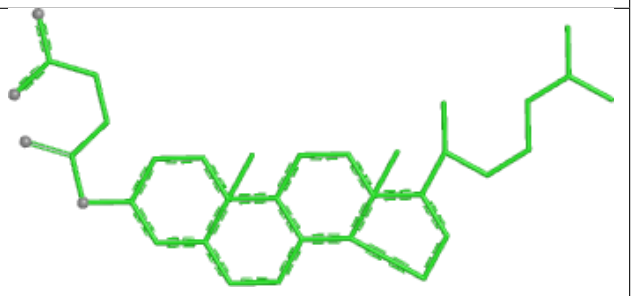
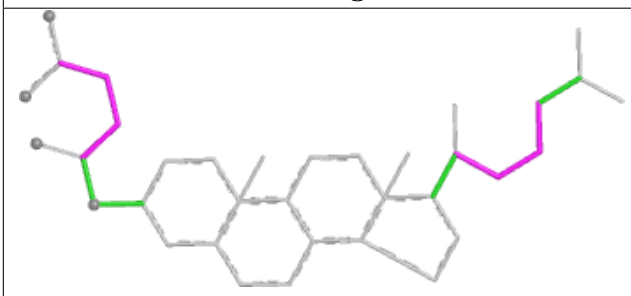


Bond angles



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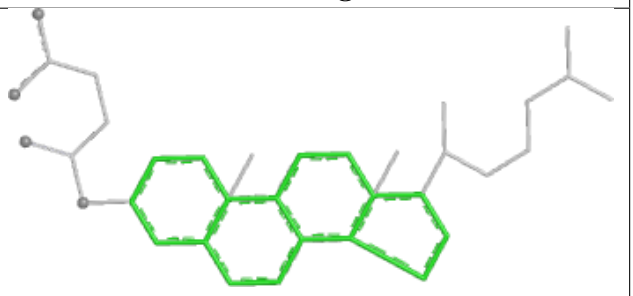
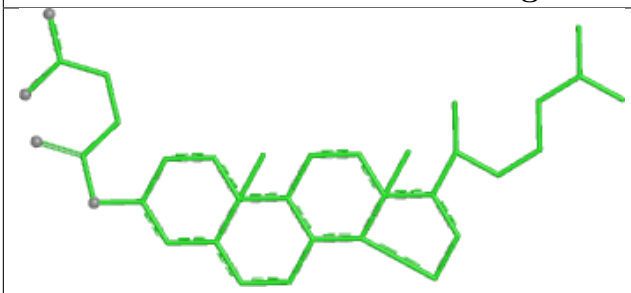


Rings

Ligand Y01 C 1403



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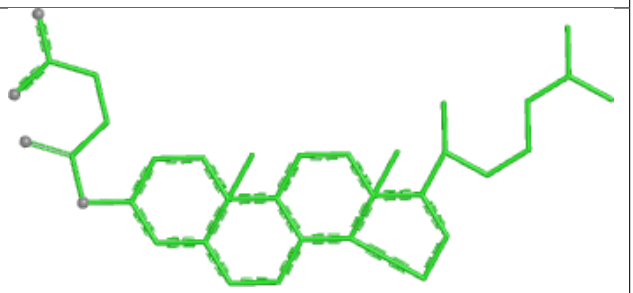

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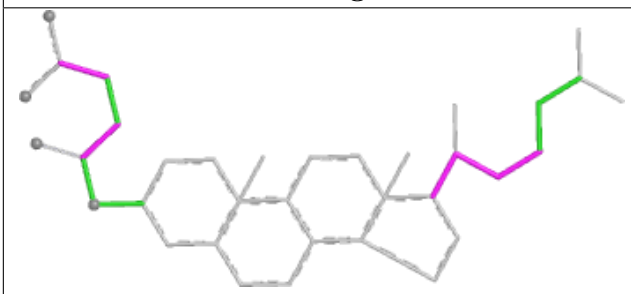

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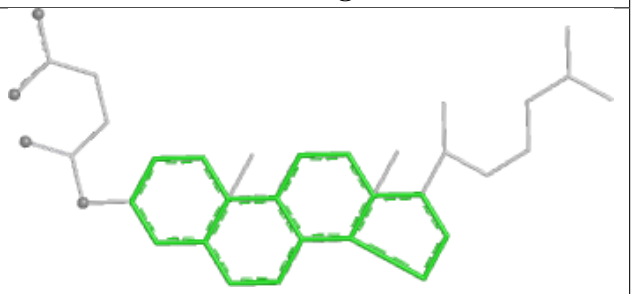
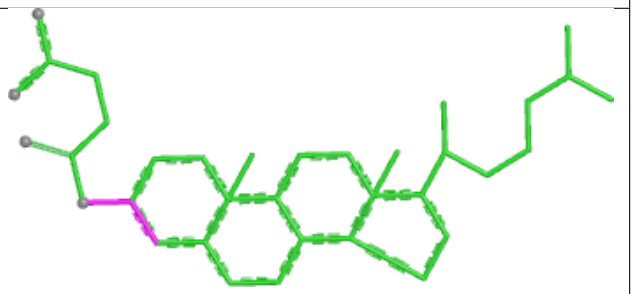


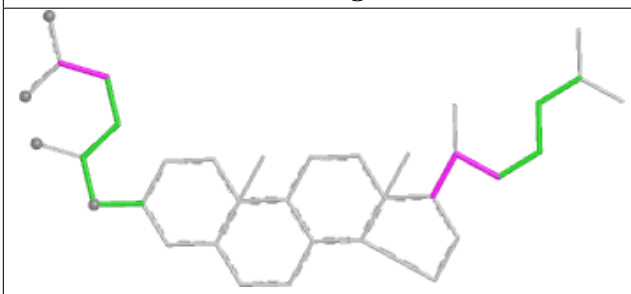
Rings

Ligand Y01 B 1401

Bond lengths



Bond angles



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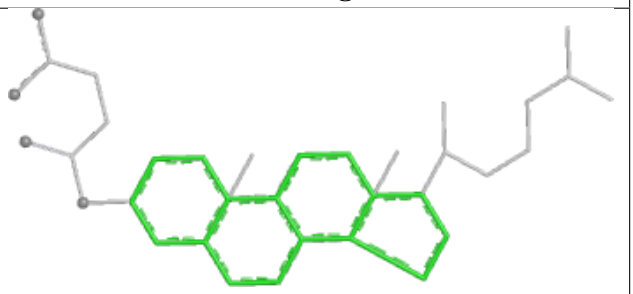
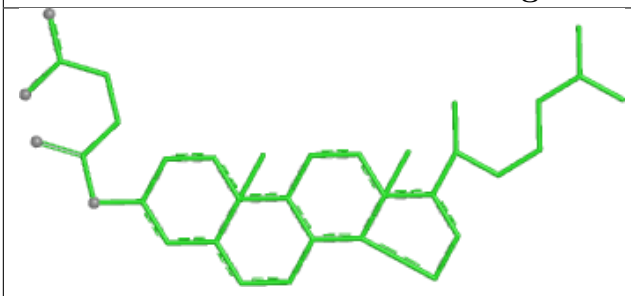
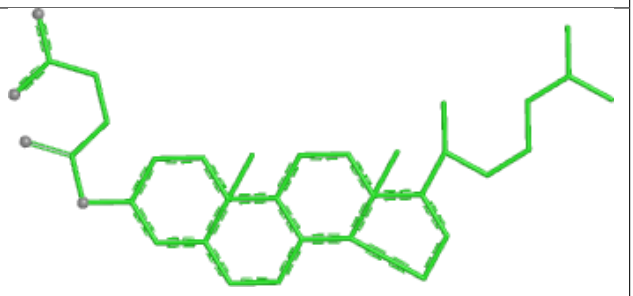
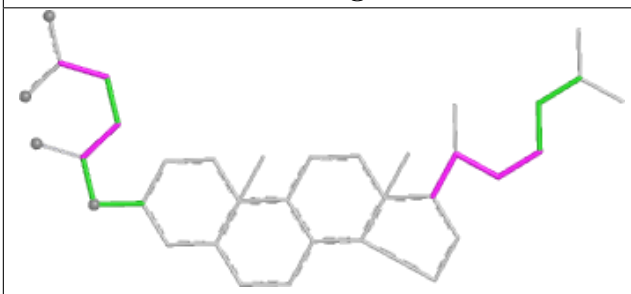
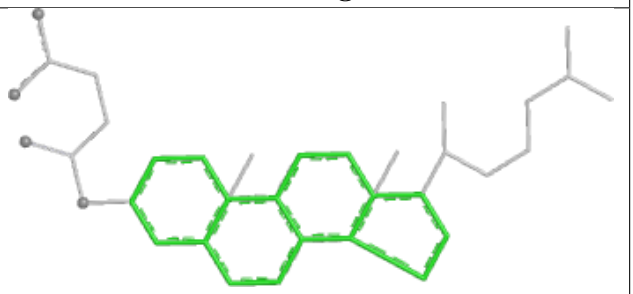


Rings

Ligand Y01 B 1403	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.

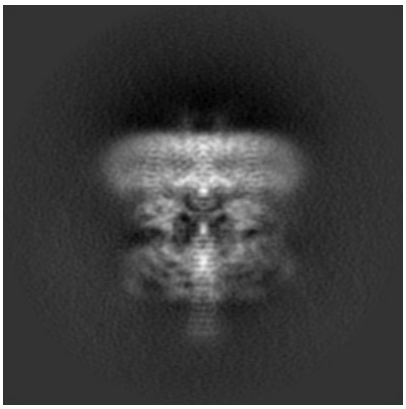
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-70214. These allow visual inspection of the internal detail of the map and identification of artifacts.

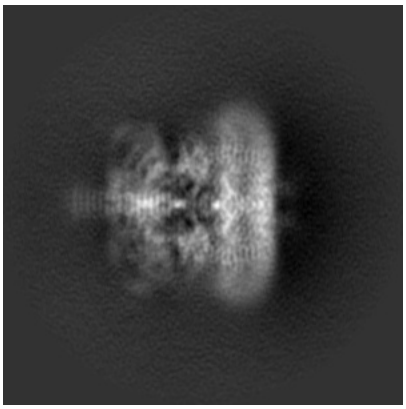
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

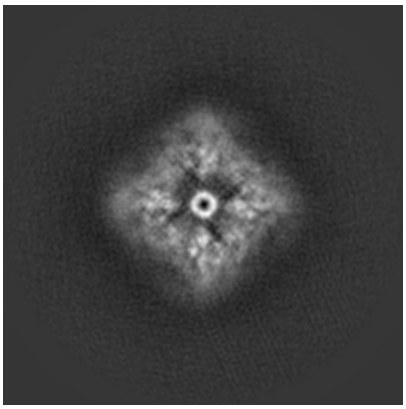
6.1.1 Primary map



X

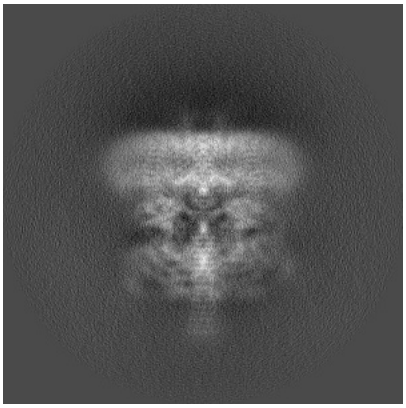


Y

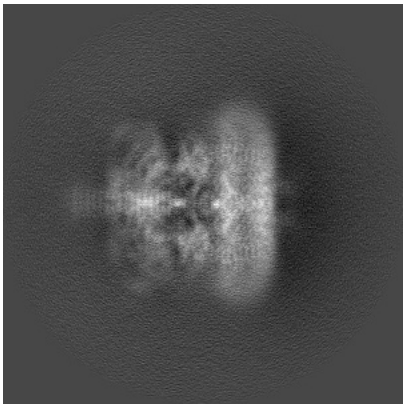


Z

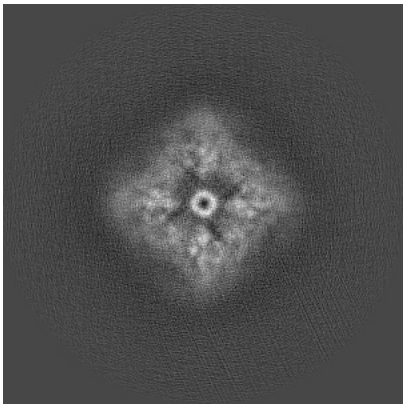
6.1.2 Raw map



X



Y

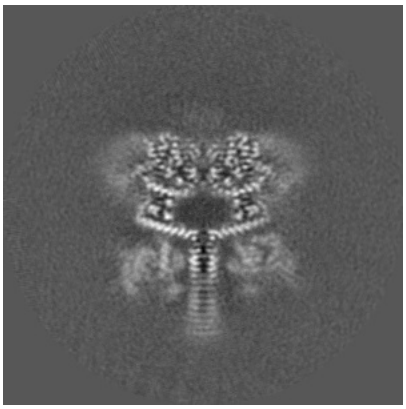


Z

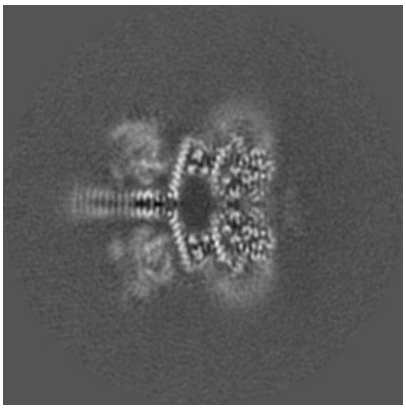
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

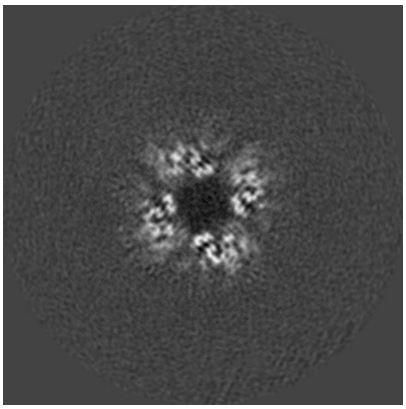
6.2.1 Primary map



X Index: 192

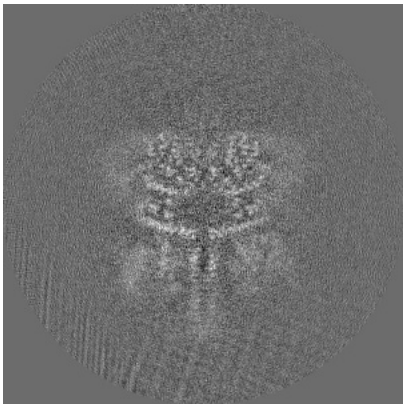


Y Index: 192

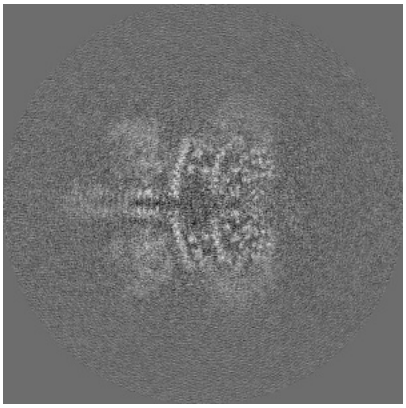


Z Index: 192

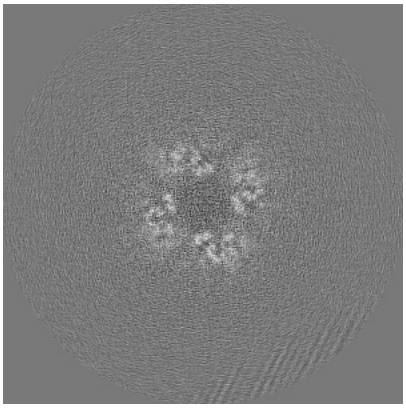
6.2.2 Raw map



X Index: 192



Y Index: 192

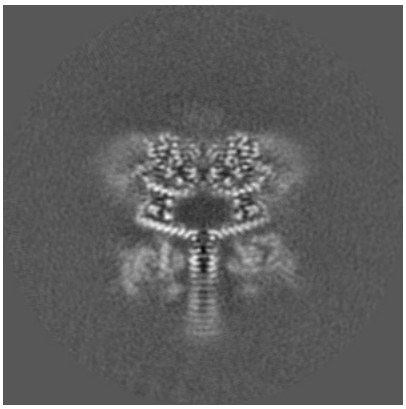


Z Index: 192

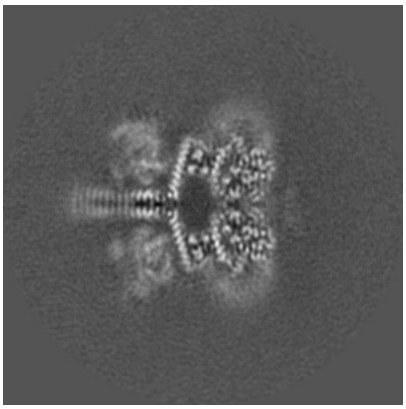
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

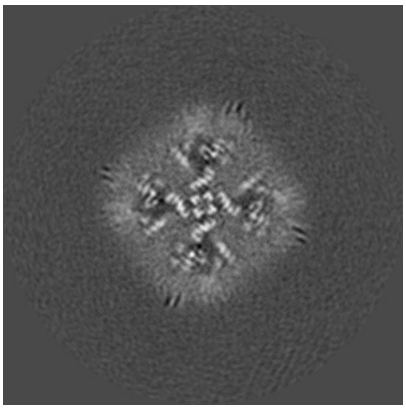
6.3.1 Primary map



X Index: 192

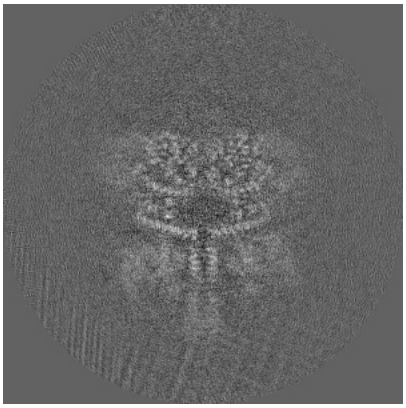


Y Index: 192

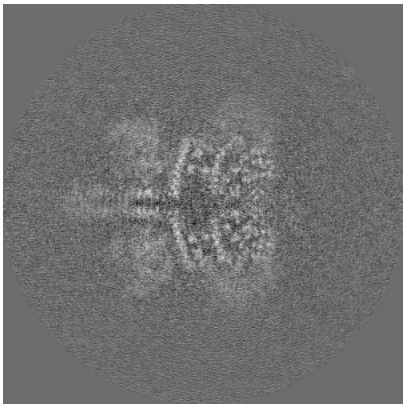


Z Index: 214

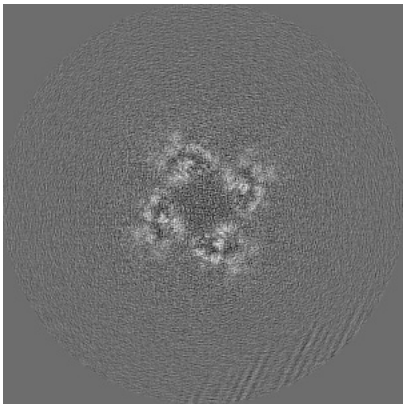
6.3.2 Raw map



X Index: 193



Y Index: 192

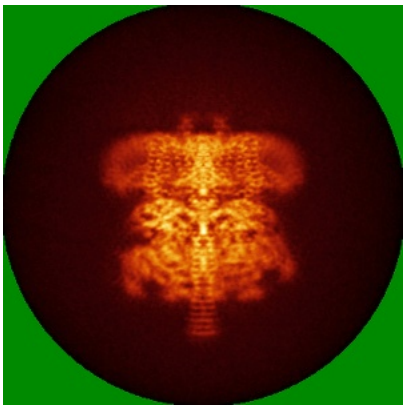


Z Index: 186

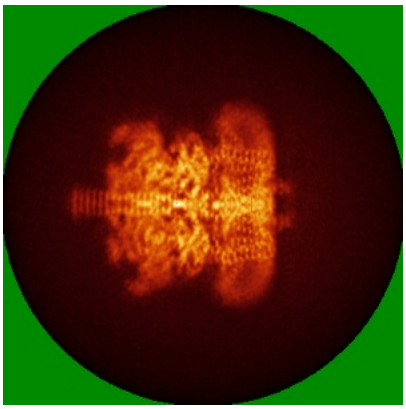
The images above show the largest variance slices of the map in three orthogonal directions.

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

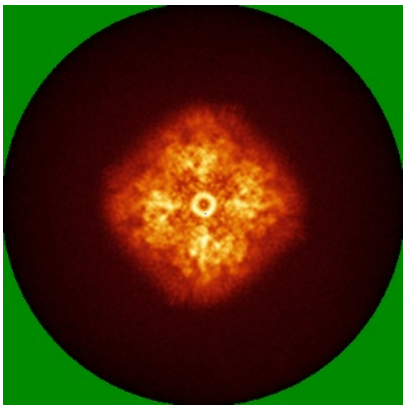
6.4.1 Primary map



X

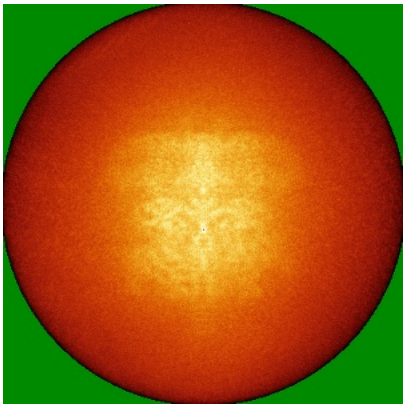


Y

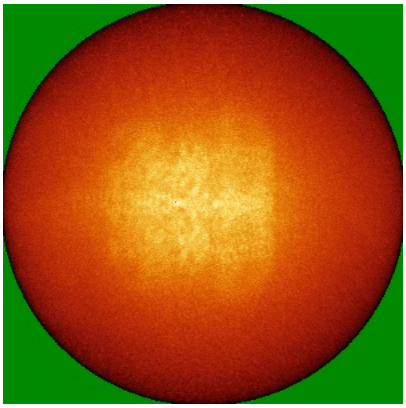


Z

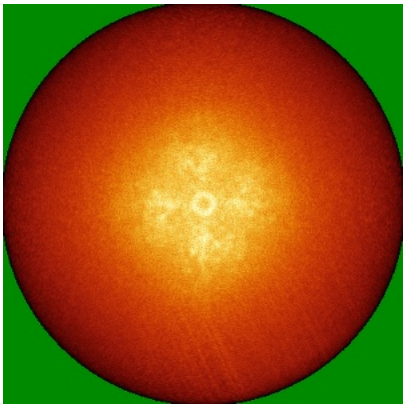
6.4.2 Raw map



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.

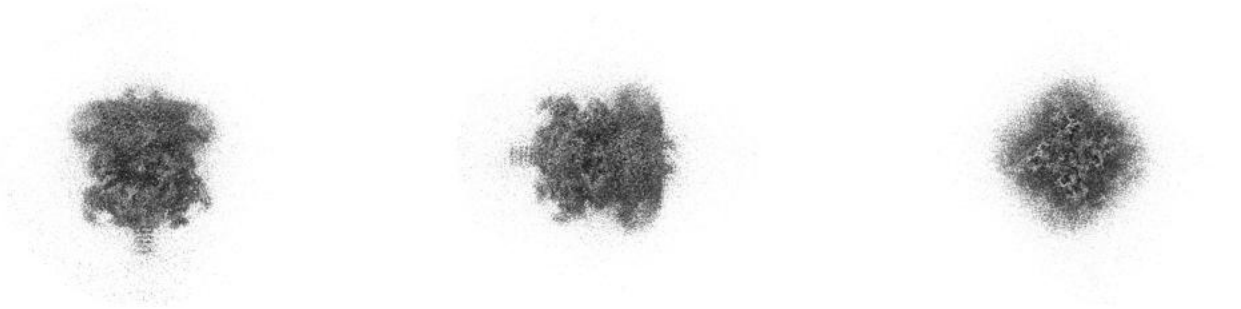
6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0025. 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.

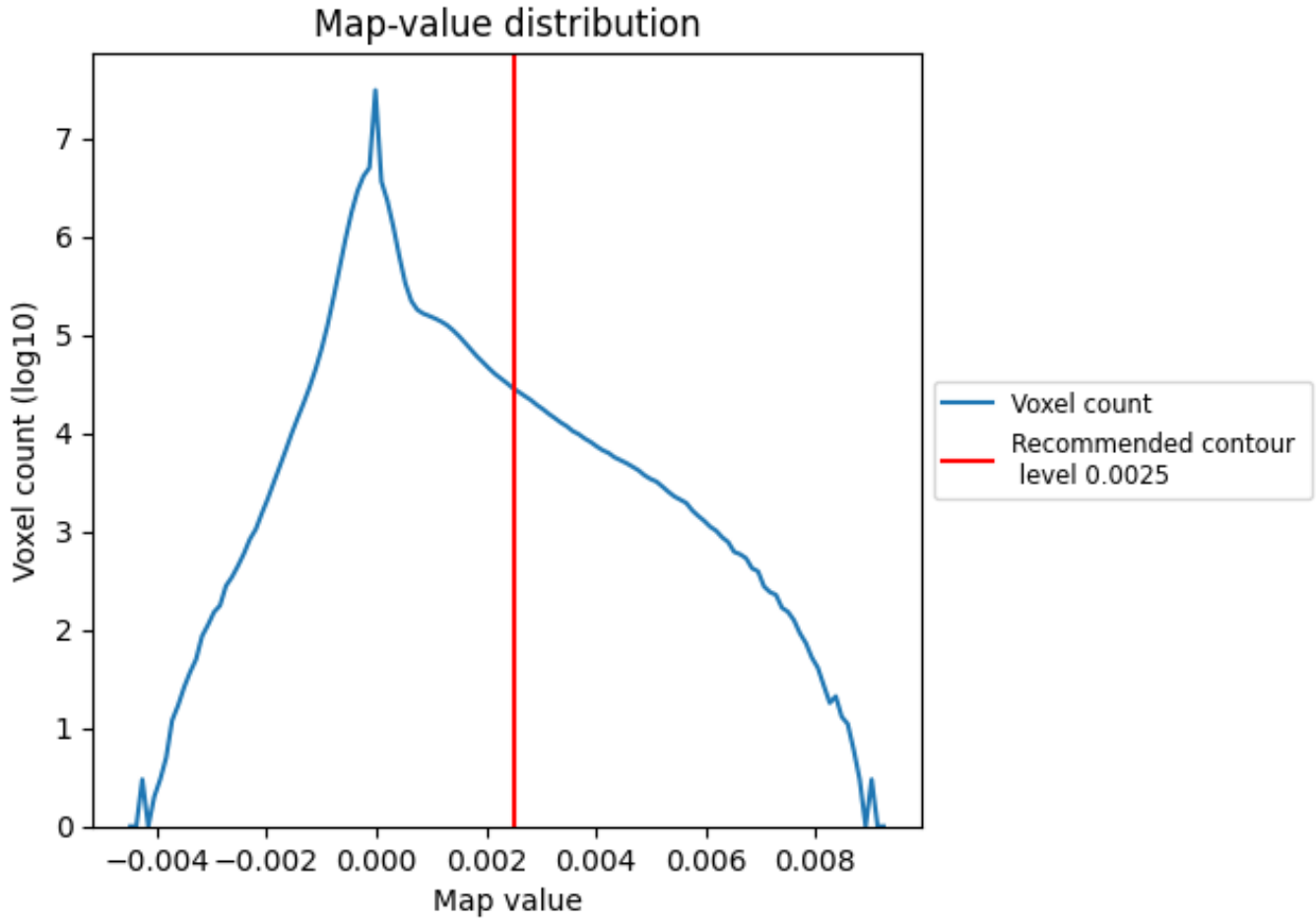
6.6 Mask visualisation (i)

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

7 Map analysis

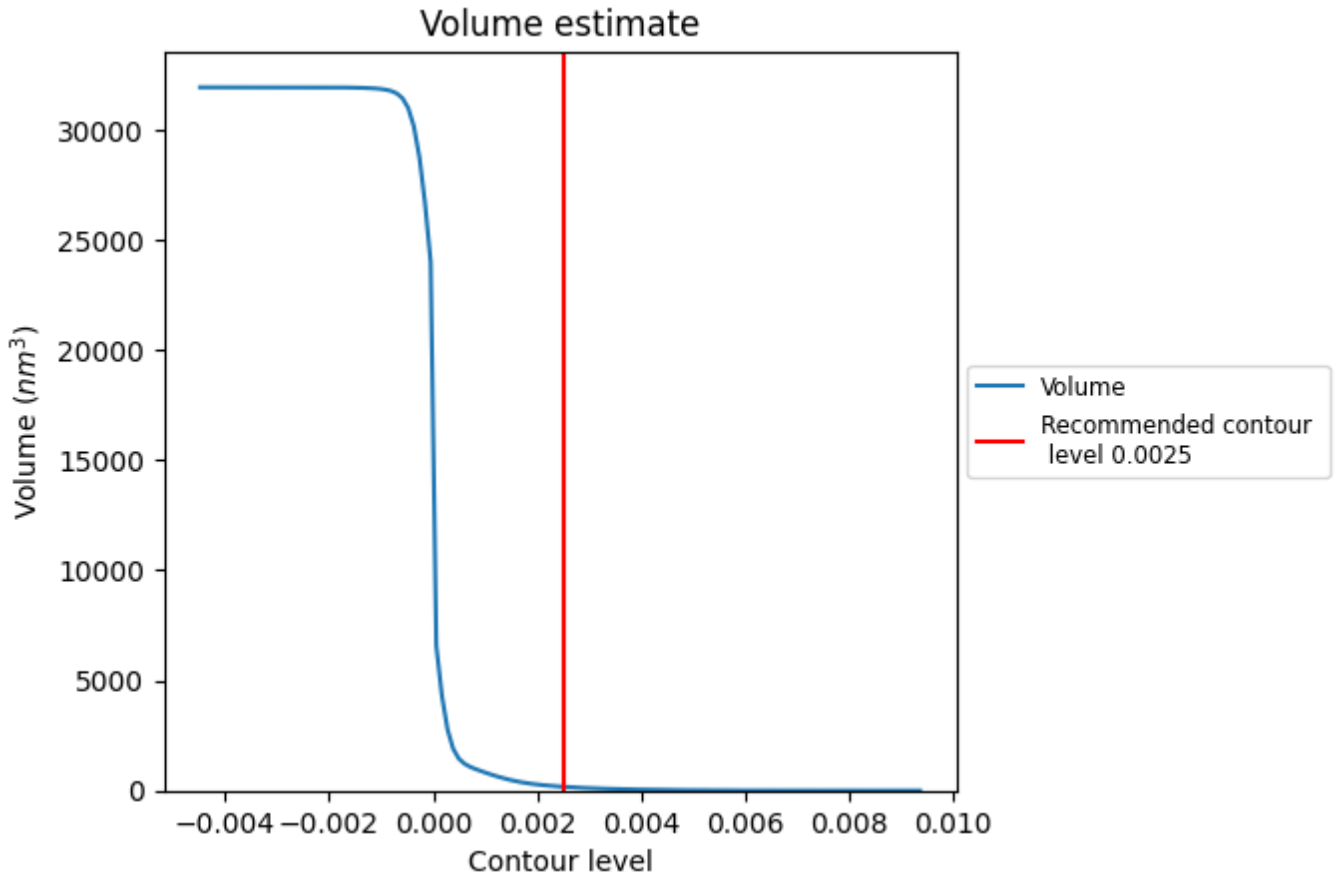
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

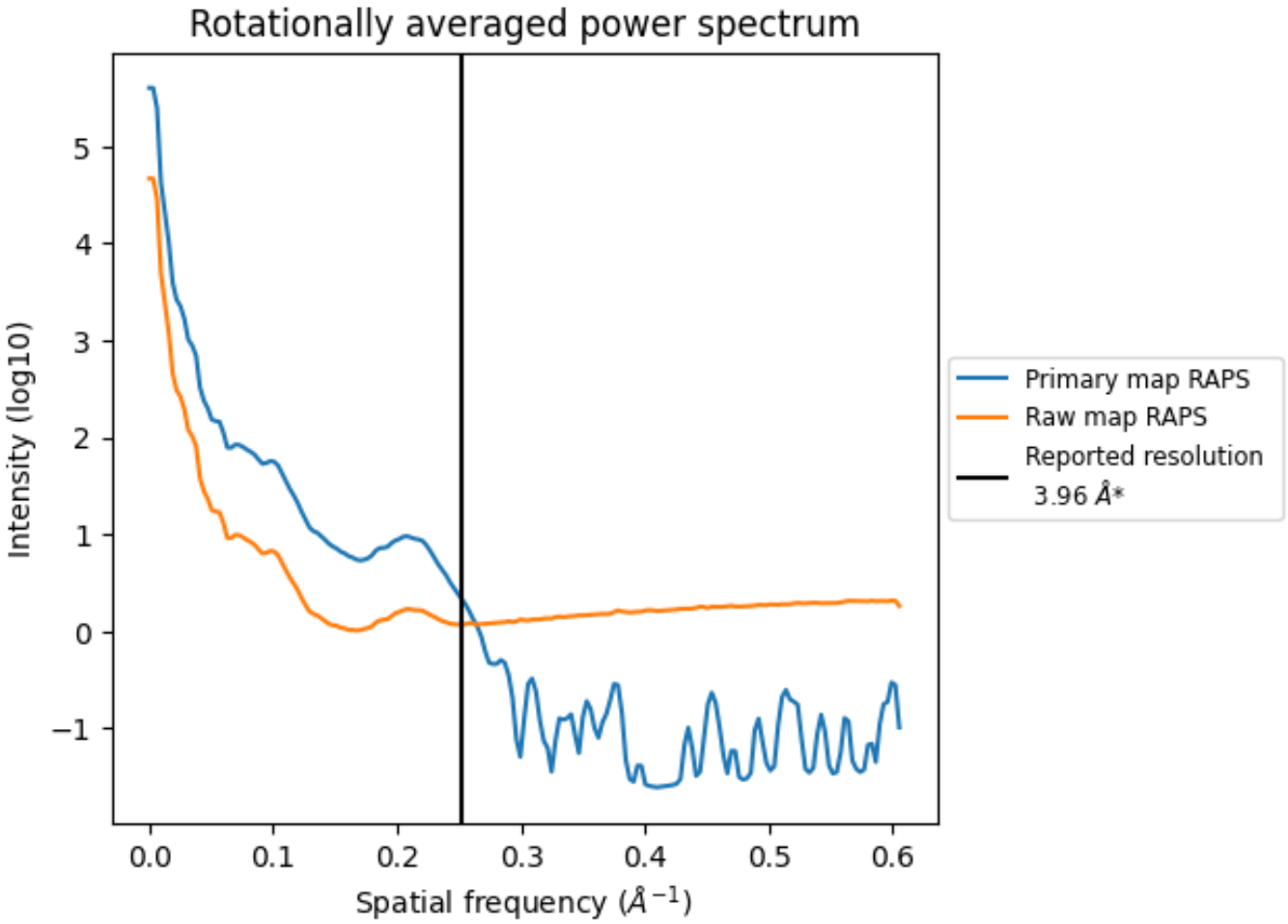
7.2 Volume estimate (i)



The volume at the recommended contour level is 172 nm^3; this corresponds to an approximate mass of 155 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)

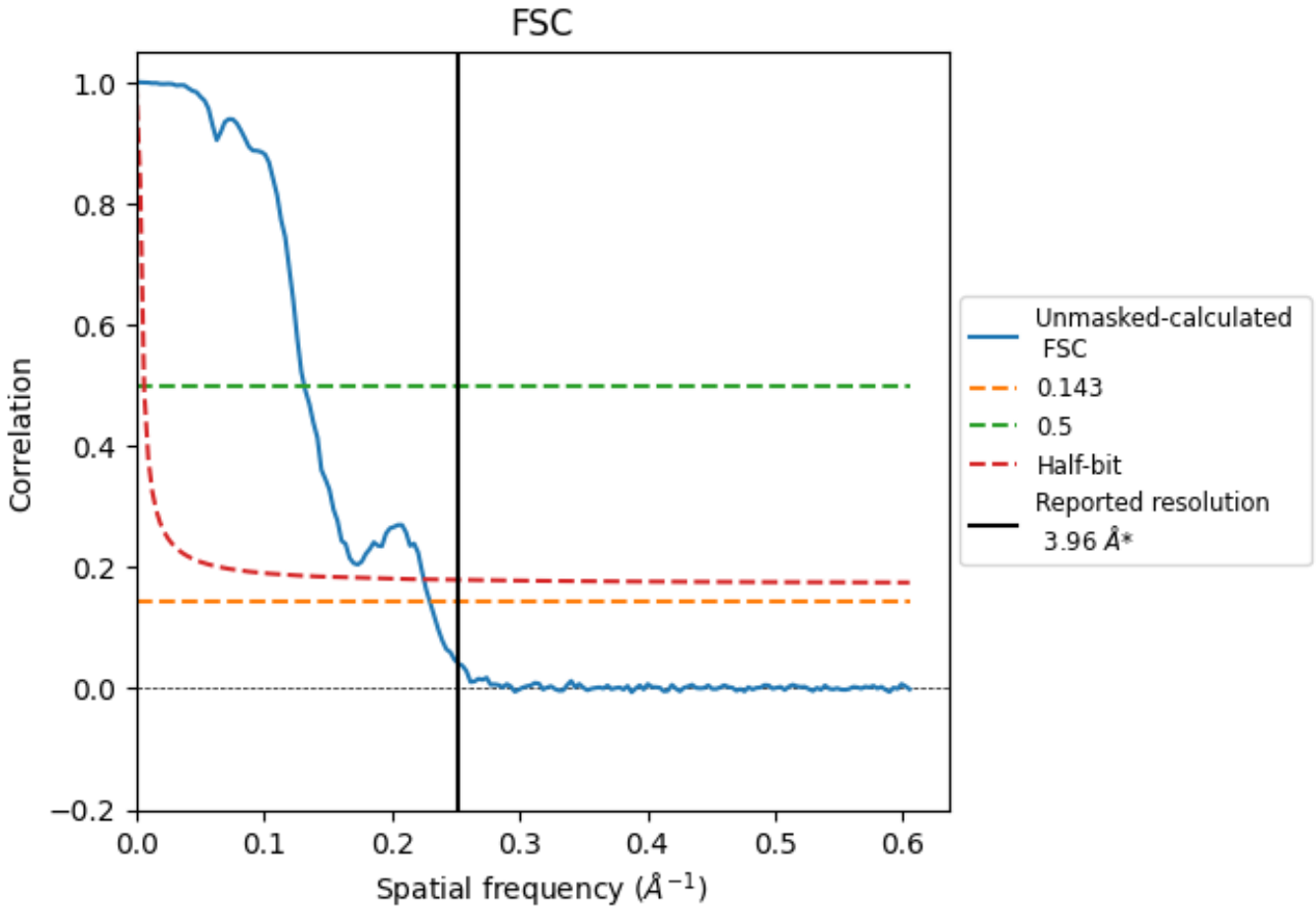


*Reported resolution corresponds to spatial frequency of 0.253 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.253 Å^{-1}

8.2 Resolution estimates (i)

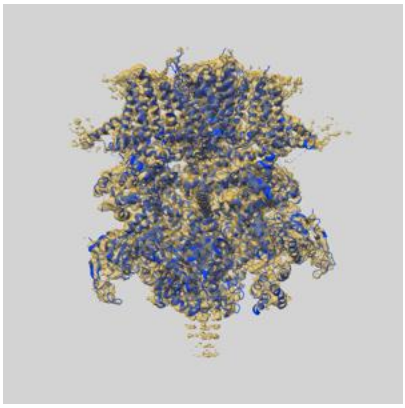
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.96	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.35	7.60	4.44

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

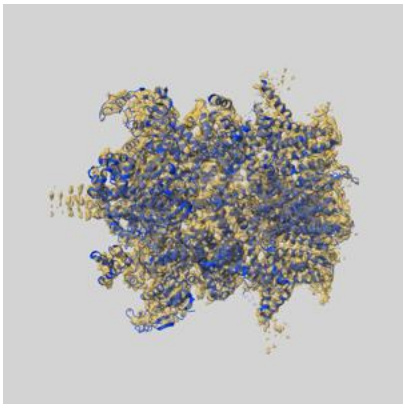
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-70214 and PDB model 9O81. Per-residue inclusion information can be found in section 3 on page 5.

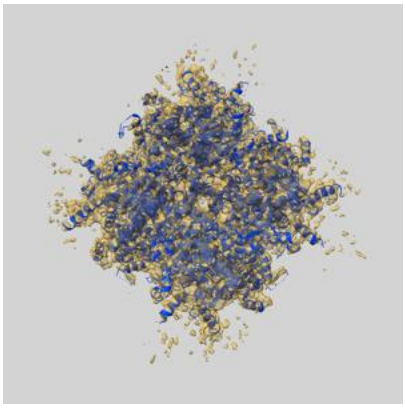
9.1 Map-model overlay



X



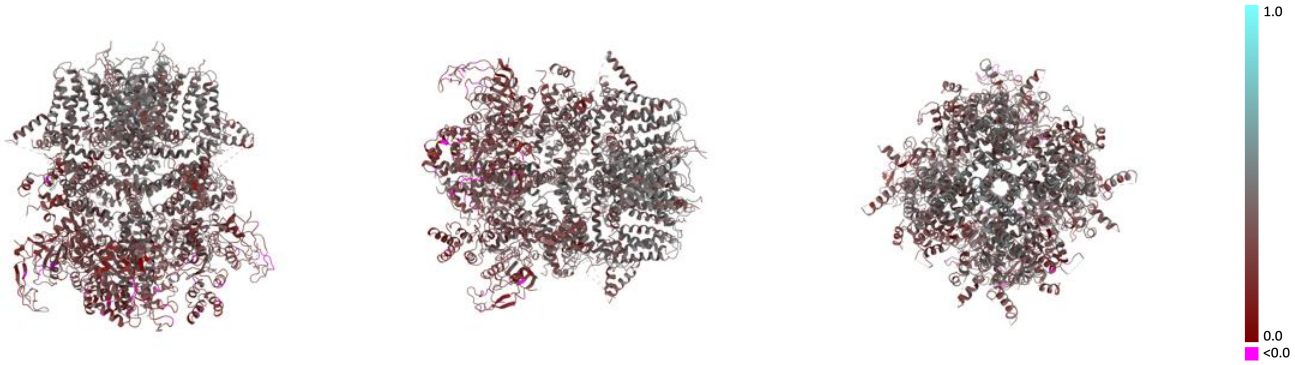
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0025 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.

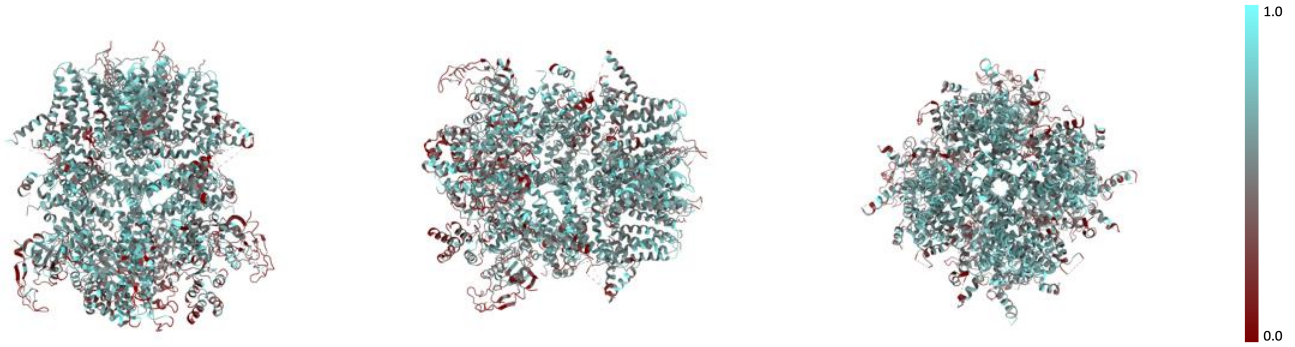
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

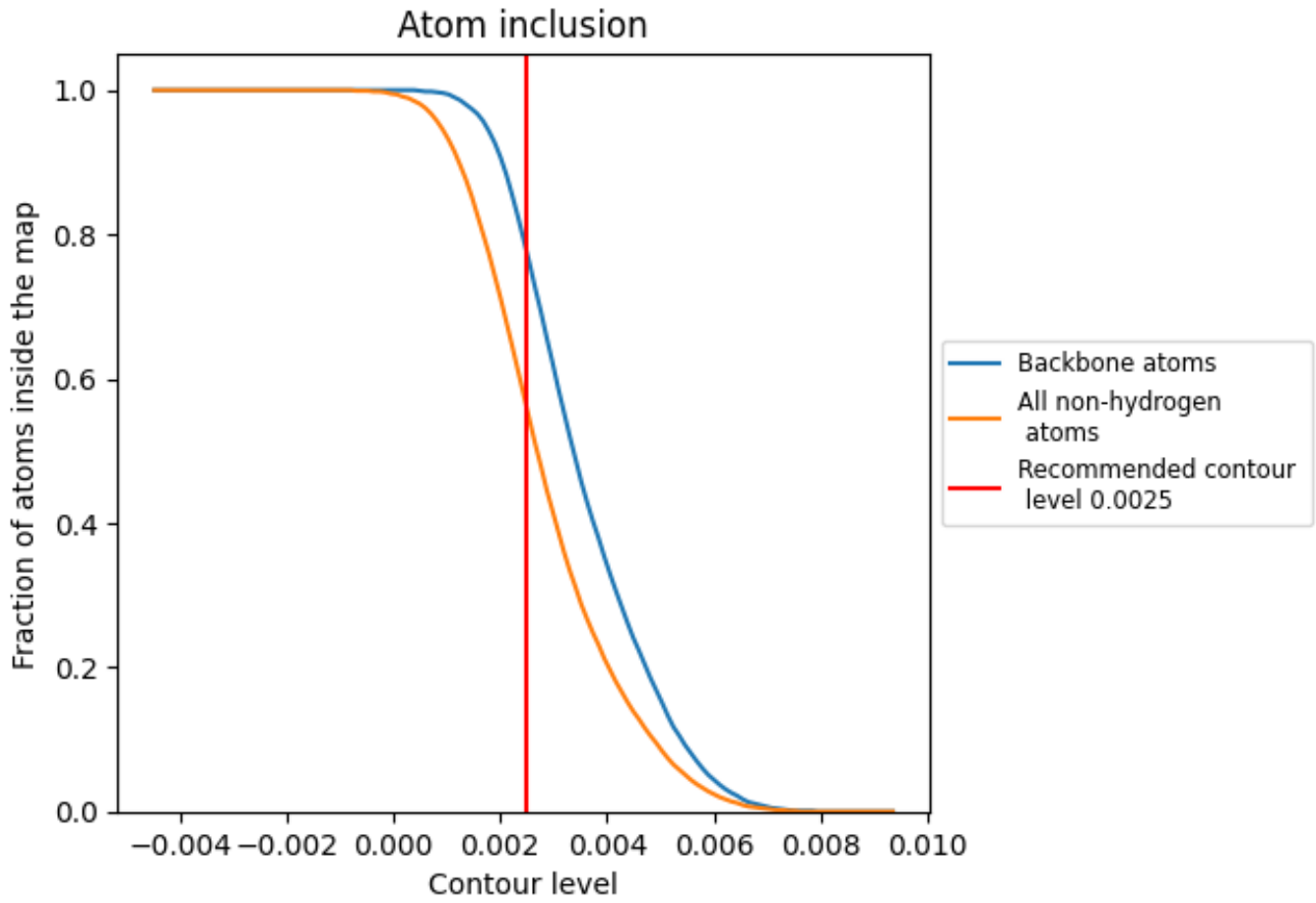
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0025).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5580	0.3400
A	0.5350	0.3480
B	0.5760	0.3350
C	0.5800	0.3380
D	0.5390	0.3390