



Full wwPDB EM Validation Report ⓘ

Aug 4, 2026 – 05:22 PM EDT

PDB ID : 8U7T / pdb_00008u7t
EMDB ID : EMD-41992
Title : Substrate-bound Cdc48, Class 1
Authors : Cooney, I.; Schubert, H.L.; Cedeno, K.; Lin, H.J.L.; Fisher, O.N.; Price, J.C.; Hill, C.P.; Shen, P.S.
Deposited on : 2023-09-15
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation 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.dev133
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) : 2.50

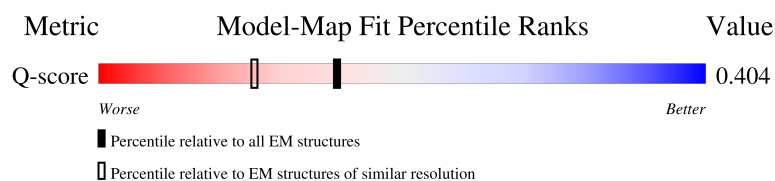
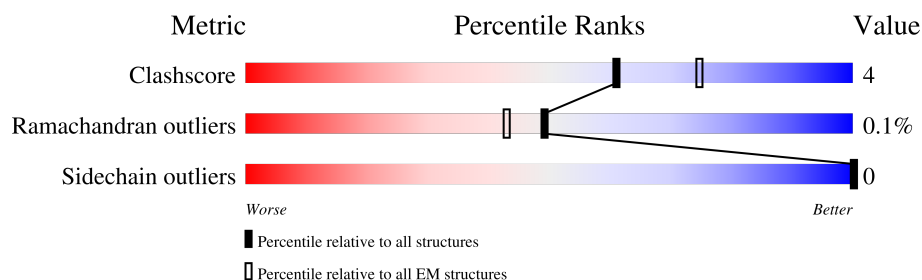
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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 $\leq 5\%$. 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	835	 5% 55% 8% 37%
1	B	835	 60% 6% 34%
1	C	835	 58% 8% 34%
1	D	835	 57% 7% 35%

Continued on next page...

Mol	Chain	Length	Quality of chain
1	E	835	
1	F	835	
2	G	23	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22540 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.

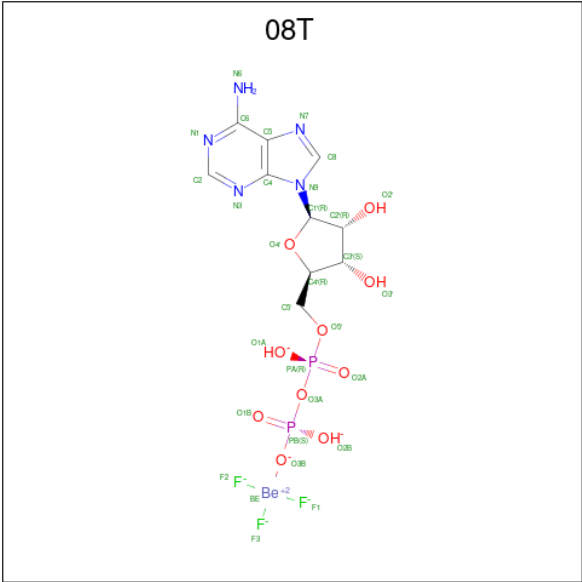
- Molecule 1 is a protein called Cell division control protein 48.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	459	Total	C	N	O		0	0
			2264	1346	459	459			
1	A	523	Total	C	N	O	S	0	0
			3789	2381	669	728	11		
1	B	549	Total	C	N	O	S	0	0
			4096	2569	725	786	16		
1	C	552	Total	C	N	O	S	0	0
			4163	2610	732	804	17		
1	D	542	Total	C	N	O	S	0	0
			3987	2508	703	759	17		
1	E	514	Total	C	N	O	S	0	0
			3808	2399	674	717	18		

- Molecule 2 is a protein called Substrate.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	23	Total	C	N	O	0	0
			123	77	23	23		

- Molecule 3 is [[[(2R,3S,4R,5R)-5-(6-aminopurin-9-yl)-3,4-bis(oxidanyl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl]oxy-oxidanyl-phosphoryl]oxy-tris(fluoranyl)beryllium (CCD ID: 08T) (formula: C₁₀H₁₄BeF₃N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

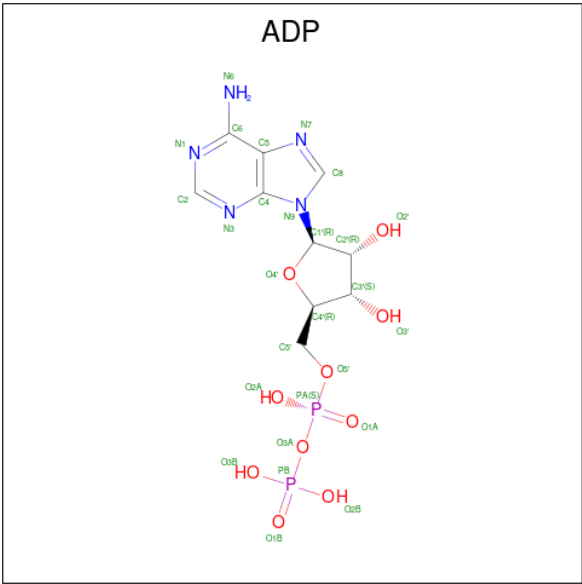


Mol	Chain	Residues	Atoms							AltConf
3	A	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	A	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	B	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	B	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	C	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	C	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	D	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	
3	D	1	Total	Be	C	F	N	O	P	0
			31	1	10	3	5	10	2	

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
4	A	2	Total	Mg	0
			2	2	
4	B	2	Total	Mg	0
			2	2	
4	C	2	Total	Mg	0
			2	2	
4	D	2	Total	Mg	0
			2	2	

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).



GLY
ALA
GLY
ALA
ALA
PHE
GLY
SER
GLY
ASN
ALA
GLU
GLY
ASP
ASP
ASP
TYR
SER

• Molecule 1: Cell division control protein 48



MET
GLY
GLU
GLU
GLY
HIS
LYS
PRO
LEU
LEU
ASP
ASP
ALA
GLY
SER
GLY
VAL
ASP
PRO
THR
GLU
GLU
GLY
ASP
LYS
LYS
PHE
ASP
ASP
ASP
TYR
SER

LEU
PHE
ARG
GLY
ILE
SER
THR
VAL
LEU
LEU
VAL
VAL
GLY
ASP
LYS
ARG
GLY
ASP
THR
THR
GLU
VAL
LEU
ILE
VAL
VAL
LEU
THR
ALA
ILE
THR
ASP
ASP
ASP
TYR
TYR

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

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

K536
M537
A538
S543
M544
A552
I562
I565
D566
S567
I568
A569
P570
D573
K574
T575
M576
G577
E578
V579
E580
R581
V584
T589
D592
G593
M594
K595
A596
R597
T603
A604
A605
T606
I612
D613
P614
F622
R636
L637
E638
A650
ASP
ASP
VAL
ASP
LEU

GLU
ALA
I658
T662
C674
S675
M686
ASP
LEU
LYS
ILE
ASP
LEU
ASP
ASP
GLU
ASP
GLY
ILE
ASP
ASP
GLY
VAL
T707
N710
F711
L723
R724
V727
V728
E729
S730
V731
D742
E743
I744
S768
F775
K788
S800
A828
V833

E837
G846
SER
LEU
GLY
D851
A852
G853
V860
R861
L864
G869
A872
V878
M883
I892
R897
L898
D899
I902
F903
V904
P907
D908
F909
N910
A911
R912
L916
N917
R921
E930
L931
T938
L946
I949
E973
V974
LYS
VAL
GLU

GLY
GLU
ASP
VAL
GLY
MET
THR
ASP
GLY
GLY
ALA
LYS
GLY
GLU
GLN
P994
M1011
R1016
S1017
Q1032
MET
LYS
ALA
SER
ARG
GLY
GLN
PHE
SER
ASN
PHE
ASN
PHE
ASN
ASP
ALA
PRO
LEU
ILE
GLY
THR
THR
ALA
ASN
SER
SER
PRO
SER
GLY
ALA

GLY
ALA
PHE
SER
ASN
ALA
GLU
ASP
ASP
GLY
LEU
TYR
SER

• Molecule 1: Cell division control protein 48

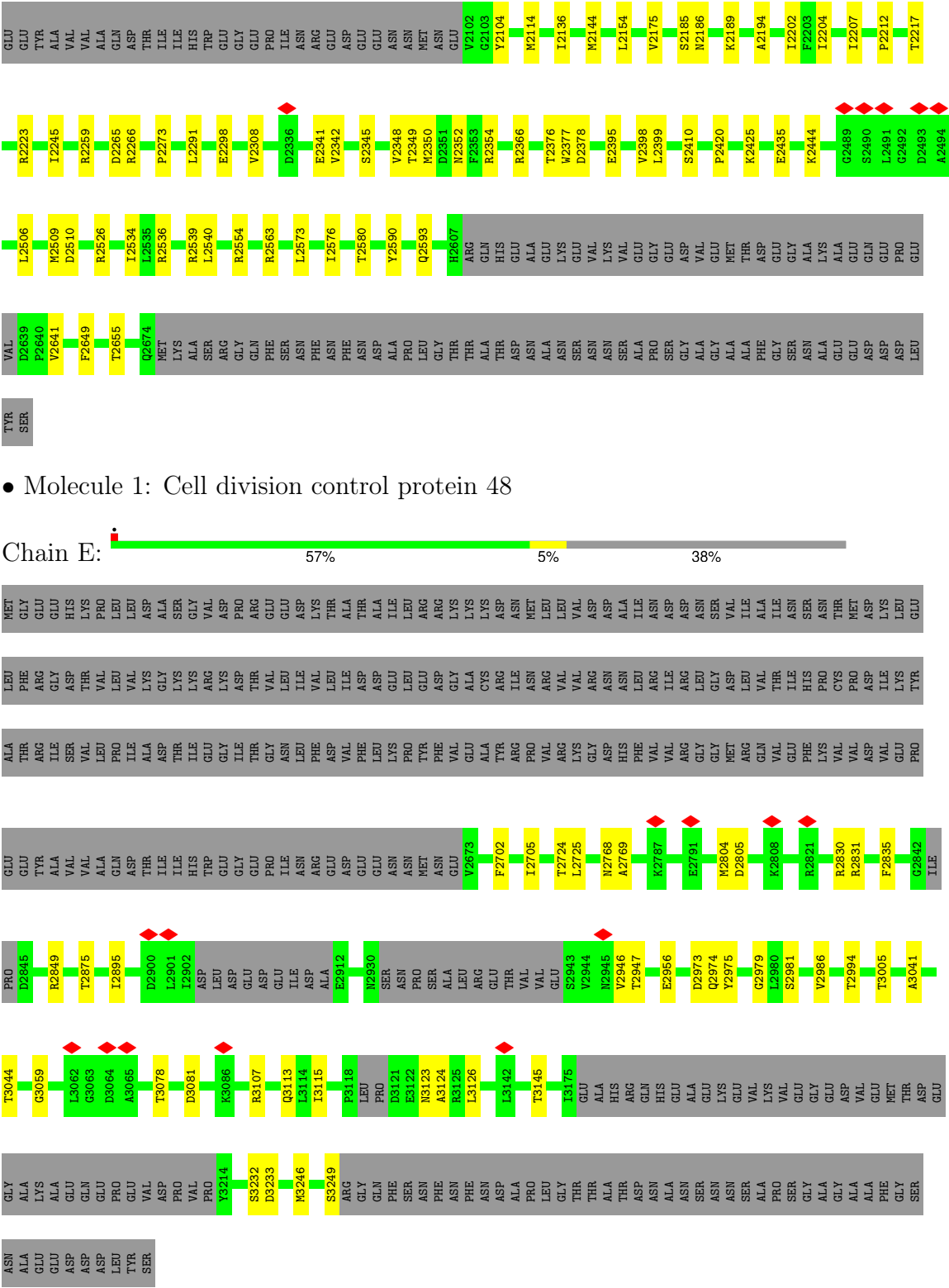


MET
GLU
GLU
GLY
HIS
LYS
PRO
LEU
LEU
ASP
ASP
ALA
GLY
SER
GLY
VAL
ASP
PRO
THR
GLU
GLU
GLY
ASP
LYS
LYS
PHE
ASP
ASP
ASP
TYR
SER

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

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

GLU
GLU
TYR
ALA
VAL
VAL
ALA
GLN
ASP
THR
THR
ILE
HIS
TRP
GLY
GLY
GLU
PRO
ILE
ILE
ASN
ASN
ARG
GLU
V989
T1037
V1046
T1050
M1058
E1061
V1062
E1071
S1072
M1073
K1076
A1081
M1084
A1085
I1089
E1109
R1110
R1111

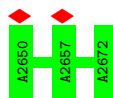


• Molecule 1: Cell division control protein 48



• Molecule 2: Substrate





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41227	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 ($e^-/\text{\AA}^2$)	33	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.833	Depositor
Minimum map value	-0.368	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	311.04, 311.04, 311.04	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, 08T, MG

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	0.16	0/3840	0.43	0/5204
1	B	0.17	0/4158	0.33	0/5628
1	C	0.15	0/4229	0.36	0/5725
1	D	0.15	0/4049	0.36	0/5492
1	E	0.14	0/3863	0.34	0/5224
1	F	0.42	1/2253 (0.0%)	0.63	2/3118 (0.1%)
2	G	0.18	0/122	0.28	0/170
All	All	0.20	1/22514 (0.0%)	0.40	2/30561 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	333	GLN	C-N	-5.48	1.26	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	23	ILE	CA-C-N	5.03	128.78	122.00
1	F	23	ILE	C-N-CA	5.03	128.78	122.00

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	3789	0	3590	47	0
1	B	4096	0	4023	34	0
1	C	4163	0	4100	46	0
1	D	3987	0	3909	48	0
1	E	3808	0	3755	27	0
1	F	2264	0	1076	4	0
2	G	123	0	130	0	0
3	A	62	0	26	2	0
3	B	62	0	26	1	0
3	C	62	0	26	3	0
3	D	62	0	26	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	E	54	0	24	3	0
All	All	22540	0	20711	188	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.

All (188) 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:528:ILE:HD11	1:A:562:ILE:HG22	1.39	1.05
1:A:562:ILE:HD12	1:A:565:ILE:HD11	1.40	1.03
1:D:2350:MET:SD	1:D:2354:ARG:NH1	2.57	0.77
1:B:1229:THR:OG1	1:B:1231:ASP:OD1	2.03	0.77
1:A:724:ARG:NH1	1:B:1146:ARG:O	2.18	0.76
1:B:1177:LYS:NZ	1:C:1575:ALA:O	2.21	0.74
1:C:2036:ARG:NH2	1:C:2040:TYR:OH	2.21	0.73
1:C:2051:GLN:NE2	1:C:2055:GLU:OE2	2.22	0.73
1:A:566:ASP:OD1	1:A:606:THR:OG1	2.07	0.72
1:B:1121:ASP:OD2	1:B:1147:ARG:NH2	2.22	0.72
1:B:1046:VAL:O	1:B:1050:THR:OG1	2.05	0.72
1:A:480:GLU:OE2	1:A:521:THR:OG1	2.08	0.71
1:A:469:ARG:NH2	1:A:638:GLU:OE2	2.22	0.71
1:D:2349:THR:OG1	1:D:2352:ASN:OD1	2.08	0.70
1:B:1210:GLN:NE2	1:B:1226:LEU:O	2.26	0.69
1:D:2526:ARG:NH1	1:E:3059:GLY:O	2.26	0.69
1:D:2398:VAL:HG13	1:D:2399:LEU:HD12	1.74	0.68
1:C:1923:ASP:OD1	1:C:1966:THR:OG1	2.12	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:23:ILE:CB	1:E:2895:ILE:HD11	2.23	0.67
1:B:1247:GLU:OE2	1:C:1701:ARG:NH1	2.28	0.67
1:D:2576:ILE:HG21	1:D:2649:PHE:HE2	1.59	0.66
1:A:949:ILE:HD11	1:A:1011:MET:HE1	1.78	0.66
1:D:2377:TRP:N	1:D:2435:GLU:OE2	2.30	0.65
1:D:2185:SER:OG	1:D:2189:LYS:NZ	2.30	0.65
1:A:917:ASN:O	1:A:921:ARG:NE	2.30	0.65
1:E:2805:ASP:OD2	1:E:2831:ARG:NH2	2.30	0.65
1:B:1324:LYS:NZ	1:C:1949:THR:O	2.28	0.65
1:B:1292:SER:OG	1:B:1421:ASP:OD2	2.14	0.64
1:B:1071:GLU:OE2	1:B:1111:ARG:NH1	2.31	0.63
1:B:1072:SER:OG	1:B:1076:LYS:NZ	2.32	0.62
1:B:1058:ASN:ND2	1:B:1061:GLU:OE2	2.32	0.62
1:D:2376:THR:OG1	1:D:2378:ASP:OD1	2.09	0.62
1:B:1282:ASP:OD1	1:B:1283:GLN:N	2.33	0.62
1:A:833:VAL:CG2	1:A:878:VAL:HG12	2.30	0.61
1:A:731:VAL:HG21	1:A:788:LYS:HD2	1.82	0.61
1:A:907:PRO:O	1:A:908:ASP:N	2.34	0.61
1:E:3081:ASP:OD2	1:E:3107:ARG:NH2	2.32	0.61
1:B:1434:ARG:NH2	1:B:1461:GLN:O	2.33	0.60
1:A:949:ILE:HD11	1:A:1011:MET:SD	2.41	0.60
1:A:949:ILE:HD11	1:A:1011:MET:CE	2.31	0.60
1:A:916:LEU:HB3	1:A:931:LEU:HD23	1.81	0.60
1:C:1720:ARG:NH1	1:C:1747:HIS:O	2.34	0.60
1:E:3041:ALA:O	1:E:3044:THR:OG1	2.18	0.60
1:C:1808:ARG:NH1	1:D:2259:ARG:O	2.36	0.59
1:A:1016:ARG:O	1:A:1017:SER:N	2.36	0.58
1:D:2506:LEU:HD12	1:D:2534:ILE:HD11	1.86	0.57
1:C:1661:GLY:N	1:C:1664:GLU:OE2	2.38	0.57
1:B:1084:ASN:OD1	1:B:1085:ALA:N	2.38	0.57
1:D:2576:ILE:HD13	1:D:2649:PHE:CE2	2.40	0.57
1:B:1109:GLU:OE1	1:B:1109:GLU:N	2.39	0.56
1:B:1245:LEU:HD22	1:B:1321:ILE:HD11	1.87	0.56
1:A:562:ILE:HD11	1:A:604:ALA:HB2	1.87	0.56
1:B:1185:GLU:N	1:B:1185:GLU:OE1	2.38	0.55
1:F:203:ILE:CB	1:A:488:LEU:HD21	2.37	0.55
1:D:2194:ALA:HB2	1:D:2202:ILE:HD11	1.88	0.55
1:D:2194:ALA:CB	1:D:2202:ILE:HD11	2.37	0.54
1:D:2539:ARG:O	1:D:2540:LEU:HD23	2.08	0.54
1:A:636:ARG:NE	1:A:662:THR:O	2.40	0.54
1:A:775:PHE:CE1	1:A:902:ILE:HD11	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1599:ARG:O	1:C:1603:ASN:ND2	2.41	0.54
1:A:724:ARG:O	1:A:727:VAL:HG13	2.08	0.54
1:D:2204:ILE:HG21	1:D:2207:ILE:HD12	1.90	0.54
1:C:1640:ALA:HB1	1:C:1641:PRO:HD2	1.91	0.53
1:C:1797:PHE:O	1:C:1801:ASN:ND2	2.42	0.53
1:A:710:ASN:OD1	1:A:711:PHE:N	2.42	0.52
1:C:1546:TYR:O	1:C:1556:MET:HE1	2.09	0.52
1:B:1419:ARG:C	1:B:1420:LEU:HD12	2.34	0.52
1:C:1978:ARG:NH1	1:C:1979:PRO:O	2.42	0.52
3:C:2201:08T:F3	1:D:2536:ARG:NH1	2.32	0.52
1:E:3123:ASN:OD1	1:E:3124:ALA:N	2.42	0.52
1:D:2366:ARG:NH1	1:E:2830:ARG:O	2.42	0.51
1:E:2725:LEU:HD22	5:E:3302:ADP:H2'	1.92	0.51
1:A:930:GLU:OE1	1:A:930:GLU:N	2.43	0.51
1:C:1699:ALA:O	1:C:1705:ARG:NH1	2.40	0.51
1:A:916:LEU:HD21	1:A:946:LEU:HD12	1.92	0.51
1:D:2398:VAL:HG13	1:D:2399:LEU:CD1	2.38	0.51
1:C:1844:ASP:OD1	1:C:1845:GLN:N	2.45	0.50
1:E:2849:ARG:NE	1:E:2875:THR:O	2.44	0.50
1:A:573:ASP:OD2	1:A:574:LYS:NZ	2.45	0.50
1:C:1993:GLU:N	1:C:1993:GLU:OE1	2.43	0.50
1:B:1211:ILE:HD11	1:C:1576:ILE:HD13	1.93	0.50
1:D:2378:ASP:OD2	1:D:2563:ARG:NH2	2.42	0.50
1:C:1621:MET:SD	1:C:1621:MET:N	2.85	0.50
1:A:860:VAL:O	1:A:864:LEU:HD23	2.12	0.50
1:B:1120:MET:O	1:B:1126:ARG:NH1	2.44	0.50
1:B:1473:GLN:NE2	1:C:1852:SER:O	2.44	0.50
1:D:2154:LEU:N	3:D:2803:08T:O1A	2.40	0.50
1:C:1765:GLN:NE2	1:C:1788:LEU:O	2.45	0.50
1:B:1062:VAL:O	1:B:1073:ASN:ND2	2.45	0.49
1:D:2298:GLU:OE1	1:D:2298:GLU:N	2.44	0.49
1:A:916:LEU:CD2	1:A:946:LEU:HD12	2.43	0.49
1:B:1089:ILE:O	1:B:1132:ILE:N	2.41	0.49
1:E:2804:MET:HE1	1:E:2835:PHE:CZ	2.48	0.49
1:E:3246:MET:O	1:E:3249:SER:OG	2.30	0.49
1:C:1724:LEU:HB3	1:C:1739:LEU:HD12	1.95	0.49
1:D:2341:GLU:OE1	1:D:2341:GLU:N	2.44	0.49
1:A:910:ASN:OD1	1:A:911:ALA:N	2.46	0.49
1:B:1081:ALA:CB	1:B:1089:ILE:HD11	2.43	0.49
1:B:1207:ALA:O	1:B:1211:ILE:HD12	2.12	0.49
1:E:2946:VAL:O	1:E:3005:THR:HG21	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1855:LYS:NZ	1:C:1958:LYS:O	2.42	0.48
1:D:2212:PRO:HB2	1:D:2217:THR:HG21	1.95	0.48
1:E:3232:SER:OG	1:E:3233:ASP:N	2.46	0.48
1:F:23:ILE:CB	1:E:2895:ILE:CD1	2.92	0.48
1:C:2081:GLU:OE1	1:C:2081:GLU:N	2.46	0.48
1:D:2342:VAL:O	1:D:2345:SER:OG	2.25	0.48
1:A:837:GLU:OE2	1:A:883:ASN:ND2	2.46	0.48
1:B:1288:GLY:C	1:B:1289:LEU:HD12	2.38	0.48
1:D:2509:MET:HE1	1:D:2534:ILE:HD12	1.95	0.48
1:C:1951:MET:CE	1:C:1976:ILE:HD11	2.43	0.48
1:D:2204:ILE:HG21	1:D:2207:ILE:CD1	2.44	0.48
1:D:2104:TYR:O	1:D:2114:MET:HE1	2.14	0.48
1:E:2768:ASN:OD1	1:E:2769:ALA:N	2.46	0.48
1:C:1967:ASN:O	1:C:2085:TYR:OH	2.26	0.48
1:D:2420:PRO:O	1:D:2425:LYS:NZ	2.46	0.48
1:D:2510:ASP:OD2	1:D:2536:ARG:NH2	2.46	0.48
1:A:949:ILE:CG1	1:A:1011:MET:HE1	2.44	0.47
1:C:2008:PRO:O	1:C:2009:LEU:HD12	2.14	0.47
1:E:2986:VAL:CG1	1:E:3115:ILE:HD12	2.44	0.47
1:C:1636:ALA:HB2	1:C:1644:ILE:HD11	1.97	0.47
1:E:2994:THR:N	5:E:3301:ADP:O1B	2.48	0.46
1:A:949:ILE:CD1	1:A:1011:MET:HE1	2.43	0.46
1:C:1664:GLU:O	1:C:1668:VAL:HG23	2.16	0.46
1:D:2573:LEU:HD23	1:D:2576:ILE:HD11	1.97	0.46
1:A:509:GLY:N	3:A:1103:08T:O1B	2.44	0.46
1:D:2144:MET:HE1	1:D:2245:ILE:HG21	1.97	0.46
1:E:2956:GLU:OE1	1:E:2956:GLU:N	2.43	0.46
1:B:1165:ARG:NH1	1:B:1191:THR:O	2.49	0.46
1:D:2590:TYR:OH	1:E:3113:GLN:OE1	2.28	0.46
1:D:2291:LEU:HA	1:D:2348:VAL:HG22	1.98	0.46
1:D:2291:LEU:H	1:D:2291:LEU:HD23	1.81	0.46
1:D:2175:VAL:O	1:D:2186:ASN:ND2	2.46	0.45
1:A:534:MET:HE3	1:B:1111:ARG:HD2	1.98	0.45
1:E:2975:TYR:O	1:E:2979:GLY:N	2.50	0.45
1:D:2655:THR:O	1:D:2655:THR:HG23	2.17	0.45
1:C:1560:ARG:HA	1:C:1563:VAL:HG22	1.98	0.44
3:B:1601:08T:F3	1:C:1981:ARG:NH1	2.36	0.44
1:B:1231:ASP:OD1	1:B:1232:ASN:N	2.51	0.44
1:C:1601:VAL:O	1:C:1605:THR:HG22	2.17	0.44
1:A:521:THR:HG22	1:A:523:ALA:H	1.82	0.44
1:E:2973:ASP:OD1	1:E:2974:GLN:N	2.50	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2576:ILE:HD13	1:D:2649:PHE:CZ	2.52	0.43
1:C:1731:MET:HB3	1:D:2136:ILE:HD11	1.99	0.43
1:A:912:ARG:NH1	1:A:938:THR:O	2.51	0.43
1:A:674:CYS:SG	1:A:675:SER:N	2.91	0.43
1:E:2724:THR:HG22	5:E:3302:ADP:O2B	2.17	0.43
1:C:1626:GLU:OE2	1:C:1666:ARG:NH1	2.52	0.43
1:D:2444:LYS:HB3	1:E:3078:THR:HG21	2.01	0.43
1:A:562:ILE:HD12	1:A:565:ILE:CD1	2.30	0.43
1:A:742:ASP:N	1:A:742:ASP:OD1	2.50	0.43
1:C:1596:LEU:HD22	3:C:2203:08T:H6	2.00	0.43
1:F:228:GLU:O	1:F:232:GLU:CB	2.67	0.43
1:A:568:ILE:HG22	1:A:568:ILE:O	2.18	0.43
1:E:2702:PHE:HA	1:E:2705:ILE:HG22	2.00	0.43
1:E:2947:THR:O	1:E:2947:THR:HG23	2.19	0.43
1:A:580:GLU:O	1:A:584:VAL:HG12	2.19	0.42
1:D:2554:ARG:NH1	1:D:2580:THR:O	2.52	0.42
1:C:2014:GLU:OE2	1:C:2016:THR:N	2.47	0.42
1:A:723:LEU:HD11	1:A:828:ALA:HB3	2.00	0.42
1:C:1592:THR:HG22	1:C:1712:ILE:HG22	2.00	0.42
1:C:2035:GLN:NE2	1:D:2410:SER:O	2.47	0.42
1:E:3126:LEU:HD21	1:E:3145:THR:HA	2.02	0.42
1:A:904:VAL:HG23	1:A:904:VAL:O	2.20	0.42
1:C:1912:ALA:O	1:C:1915:THR:OG1	2.37	0.42
1:D:2593:GLN:NE2	1:E:2981:SER:O	2.53	0.42
1:C:1594:LYS:NZ	3:C:2203:08T:F2	2.41	0.42
1:A:512:LEU:HD11	3:A:1103:08T:H6	2.00	0.42
1:D:2217:THR:O	1:D:2223:ARG:NH2	2.53	0.41
1:B:1037:THR:HG22	1:B:1157:ILE:HG22	2.02	0.41
1:C:1952:ASP:OD2	1:C:1978:ARG:NH2	2.49	0.41
1:B:1265:GLU:OE1	1:B:1265:GLU:N	2.47	0.41
1:D:2641:VAL:HG23	1:D:2641:VAL:O	2.21	0.41
1:A:534:MET:N	1:A:534:MET:SD	2.93	0.41
1:A:479:VAL:HG21	1:A:517:VAL:HG11	2.02	0.41
1:C:2014:GLU:HG3	1:C:2016:THR:HG22	2.02	0.41
1:C:1857:VAL:CG2	1:C:1986:ILE:HD12	2.50	0.41
1:C:1951:MET:HE1	1:C:1976:ILE:HD11	2.02	0.41
1:A:897:ARG:O	1:A:898:LEU:HD12	2.21	0.41
1:D:2265:ASP:OD1	1:D:2266:ARG:N	2.54	0.41
1:D:2395:GLU:HA	1:D:2398:VAL:HG12	2.03	0.41
1:C:1592:THR:CG2	1:C:1712:ILE:HG22	2.52	0.41
1:D:2273:PRO:HD3	1:D:2308:VAL:HG23	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1506:GLU:O	1:B:1509:LYS:NZ	2.54	0.40
1:B:1211:ILE:HD12	1:B:1211:ILE:H	1.86	0.40
1:A:892:ILE:HG23	1:A:898:LEU:HD13	2.04	0.40
1:C:1750:VAL:HG22	1:C:1750:VAL:O	2.21	0.40
1:A:744:ILE:HD11	1:A:902:ILE:HD12	2.04	0.40
1:D:2573:LEU:CD2	1:D:2576:ILE:HD11	2.51	0.40

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	509/835 (61%)	488 (96%)	21 (4%)	0	100	100
1	B	543/835 (65%)	516 (95%)	27 (5%)	0	100	100
1	C	548/835 (66%)	521 (95%)	27 (5%)	0	100	100
1	D	538/835 (64%)	512 (95%)	26 (5%)	0	100	100
1	E	502/835 (60%)	482 (96%)	20 (4%)	0	100	100
1	F	437/835 (52%)	399 (91%)	35 (8%)	3 (1%)	18	49
2	G	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
All	All	3098/5033 (62%)	2936 (95%)	159 (5%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	27	PRO
1	F	29	ARG
1	F	250	VAL

5.3.2 Protein sidechains ⓘ

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	355/695 (51%)	355 (100%)	0	100	100
1	B	412/695 (59%)	412 (100%)	0	100	100
1	C	426/695 (61%)	426 (100%)	0	100	100
1	D	396/695 (57%)	396 (100%)	0	100	100
1	E	379/695 (54%)	379 (100%)	0	100	100
2	G	4/4 (100%)	4 (100%)	0	100	100
All	All	1972/3479 (57%)	1972 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	883	ASN
1	B	1136	ASN
1	B	1172	HIS
1	B	1439	ASN
1	B	1489	GLN
1	B	1503	HIS
1	C	1628	ASN
1	C	1691	ASN
1	C	1881	ASN
1	C	1967	ASN
1	C	2065	HIS
1	D	2249	ASN
1	D	2361	ASN
1	D	2525	ASN
1	E	2971	HIS

5.3.3 RNA ⓘ

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](#)

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
3	08T	A	1103	4	31,33,33	0.46	0	41,52,52	0.63	1 (2%)
3	08T	D	2803	4	31,33,33	0.47	0	41,52,52	0.60	1 (2%)
3	08T	C	2203	4	31,33,33	0.53	0	41,52,52	0.57	0
3	08T	D	2801	4	31,33,33	0.55	0	41,52,52	0.61	1 (2%)
5	ADP	E	3301	-	28,29,29	1.37	4 (14%)	43,45,45	1.89	11 (25%)
3	08T	C	2201	4	31,33,33	0.52	0	41,52,52	0.51	0
5	ADP	E	3302	-	28,29,29	1.40	4 (14%)	43,45,45	1.89	10 (23%)
3	08T	B	1601	4	31,33,33	0.46	0	41,52,52	0.73	1 (2%)
3	08T	B	1603	4	31,33,33	0.54	0	41,52,52	0.68	0
3	08T	A	1101	4	31,33,33	0.48	0	41,52,52	0.64	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
3	08T	A	1103	4	-	6/16/38/38	0/3/3/3
3	08T	D	2803	4	-	5/16/38/38	0/3/3/3
3	08T	C	2203	4	-	5/16/38/38	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	08T	D	2801	4	-	3/16/38/38	0/3/3/3
5	ADP	E	3301	-	-	0/16/32/32	0/3/3/3
3	08T	C	2201	4	-	5/16/38/38	0/3/3/3
5	ADP	E	3302	-	-	5/16/32/32	0/3/3/3
3	08T	B	1601	4	-	4/16/38/38	0/3/3/3
3	08T	B	1603	4	-	6/16/38/38	0/3/3/3
3	08T	A	1101	4	-	1/16/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	3302	ADP	C5-C4	4.52	1.47	1.39
5	E	3301	ADP	C5-C4	4.49	1.47	1.39
5	E	3301	ADP	C5-C6	2.62	1.48	1.41
5	E	3302	ADP	C5-C6	2.62	1.48	1.41
5	E	3302	ADP	C8-N7	2.44	1.36	1.31
5	E	3302	ADP	C5-N7	-2.44	1.34	1.39
5	E	3301	ADP	C5-N7	-2.38	1.34	1.39
5	E	3301	ADP	C8-N7	2.30	1.36	1.31

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	3302	ADP	C5-C4-N3	-5.94	118.54	126.72
5	E	3301	ADP	C5-C4-N3	-5.77	118.77	126.72
5	E	3302	ADP	N3-C4-N9	4.71	135.18	127.17
5	E	3301	ADP	N3-C4-N9	4.65	135.08	127.17
5	E	3302	ADP	C2-N3-C4	3.90	121.35	111.83
5	E	3301	ADP	C2-N3-C4	3.83	121.17	111.83
3	B	1601	08T	O2B-PB-O3A	3.78	117.50	107.27
5	E	3302	ADP	N3-C2-N1	-3.66	123.05	128.58
5	E	3301	ADP	N3-C2-N1	-3.65	123.06	128.58
5	E	3302	ADP	C4-C5-N7	-3.45	106.64	110.58
5	E	3301	ADP	C4-C5-N7	-3.32	106.79	110.58
5	E	3301	ADP	C4-N9-C8	2.83	108.71	105.74
5	E	3302	ADP	C4-N9-C8	2.75	108.63	105.74
5	E	3302	ADP	C3'-C2'-C1'	2.70	106.57	101.46
5	E	3302	ADP	C5-N7-C8	2.69	107.68	103.45
5	E	3301	ADP	C5-N7-C8	2.62	107.56	103.45
5	E	3301	ADP	C3'-C2'-C1'	2.49	106.18	101.46
3	D	2803	08T	O3B-PB-O1B	-2.26	105.19	111.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	3302	ADP	N9-C8-N7	-2.23	110.78	113.94
5	E	3301	ADP	N9-C8-N7	-2.22	110.79	113.94
3	A	1103	08T	O3B-PB-O1B	-2.22	105.31	111.52
3	D	2801	08T	O3B-PB-O1B	-2.15	105.49	111.52
5	E	3302	ADP	C6-C5-N7	2.09	136.11	132.09
5	E	3301	ADP	C2-N1-C6	2.06	122.11	118.73
5	E	3301	ADP	C6-C5-N7	2.01	135.97	132.09

There are no chirality outliers.

All (40) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1103	08T	O4'-C4'-C5'-O5'
3	B	1603	08T	C5'-O5'-PA-O1A
3	B	1603	08T	C5'-O5'-PA-O2A
3	B	1603	08T	C5'-O5'-PA-O3A
3	B	1603	08T	O4'-C4'-C5'-O5'
3	C	2203	08T	C5'-O5'-PA-O1A
3	C	2203	08T	C5'-O5'-PA-O2A
3	C	2203	08T	C5'-O5'-PA-O3A
3	C	2203	08T	O4'-C4'-C5'-O5'
3	D	2801	08T	C5'-O5'-PA-O1A
3	D	2803	08T	C5'-O5'-PA-O2A
5	E	3302	ADP	C5'-O5'-PA-O1A
5	E	3302	ADP	C5'-O5'-PA-O2A
5	E	3302	ADP	C5'-O5'-PA-O3A
3	A	1103	08T	C3'-C4'-C5'-O5'
5	E	3302	ADP	O4'-C4'-C5'-O5'
3	B	1601	08T	O4'-C4'-C5'-O5'
3	B	1601	08T	C3'-C4'-C5'-O5'
3	C	2203	08T	C3'-C4'-C5'-O5'
3	B	1603	08T	C3'-C4'-C5'-O5'
5	E	3302	ADP	C3'-C4'-C5'-O5'
3	C	2201	08T	O4'-C4'-C5'-O5'
3	D	2803	08T	O4'-C4'-C5'-O5'
3	D	2803	08T	C3'-C4'-C5'-O5'
3	C	2201	08T	C3'-C4'-C5'-O5'
3	A	1103	08T	C4'-C5'-O5'-PA
3	B	1601	08T	C4'-C5'-O5'-PA
3	B	1601	08T	PB-O3A-PA-O1A
3	A	1103	08T	C5'-O5'-PA-O2A
3	D	2801	08T	C5'-O5'-PA-O2A

Continued on next page...

Continued from previous page...

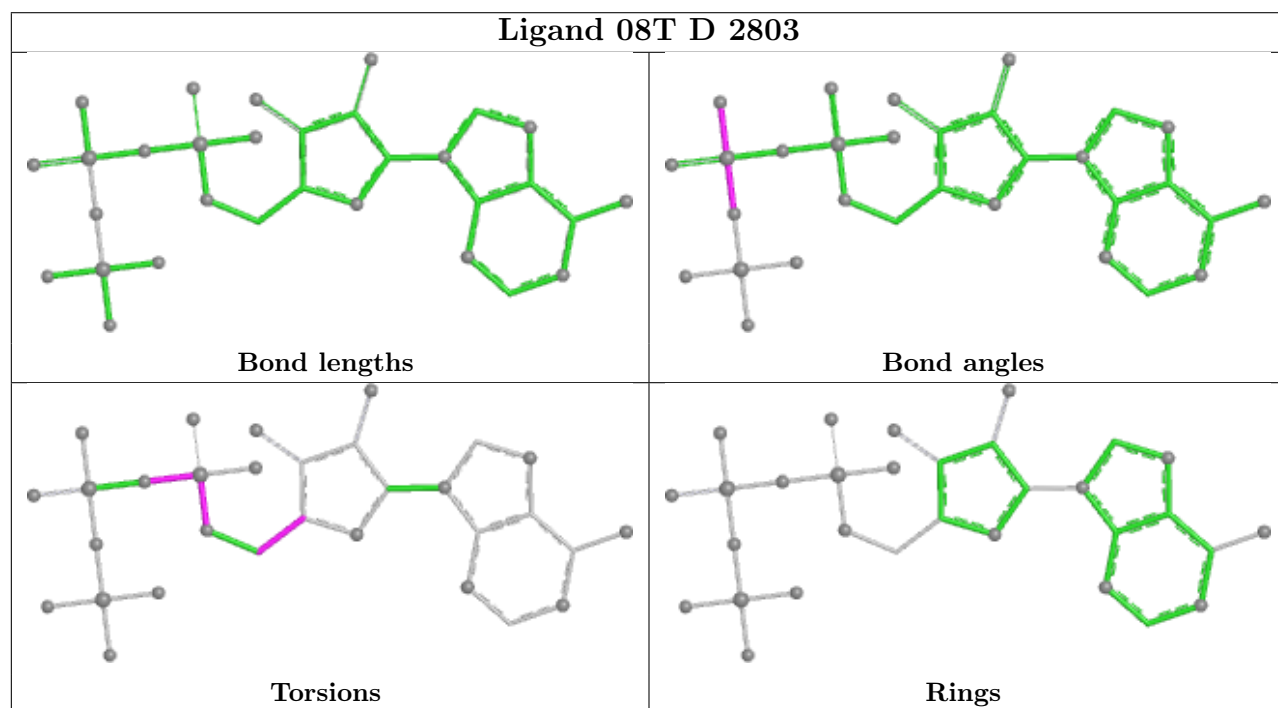
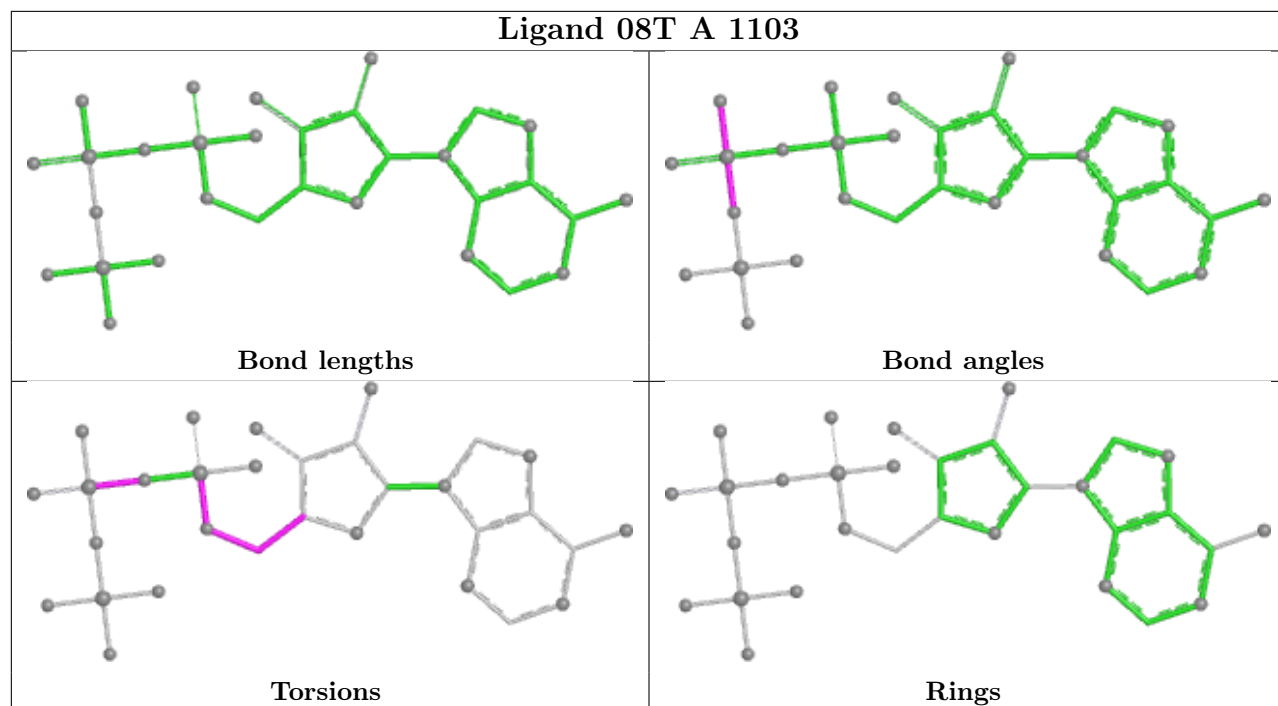
Mol	Chain	Res	Type	Atoms
3	D	2801	08T	C5'-O5'-PA-O3A
3	C	2201	08T	C4'-C5'-O5'-PA
3	C	2201	08T	PB-O3A-PA-O2A
3	A	1103	08T	PA-O3A-PB-O1B
3	C	2201	08T	PB-O3A-PA-O1A
3	A	1103	08T	PA-O3A-PB-O2B
3	D	2803	08T	PB-O3A-PA-O1A
3	D	2803	08T	PB-O3A-PA-O2A
3	B	1603	08T	C2'-C1'-N9-C8
3	A	1101	08T	PA-O3A-PB-O2B

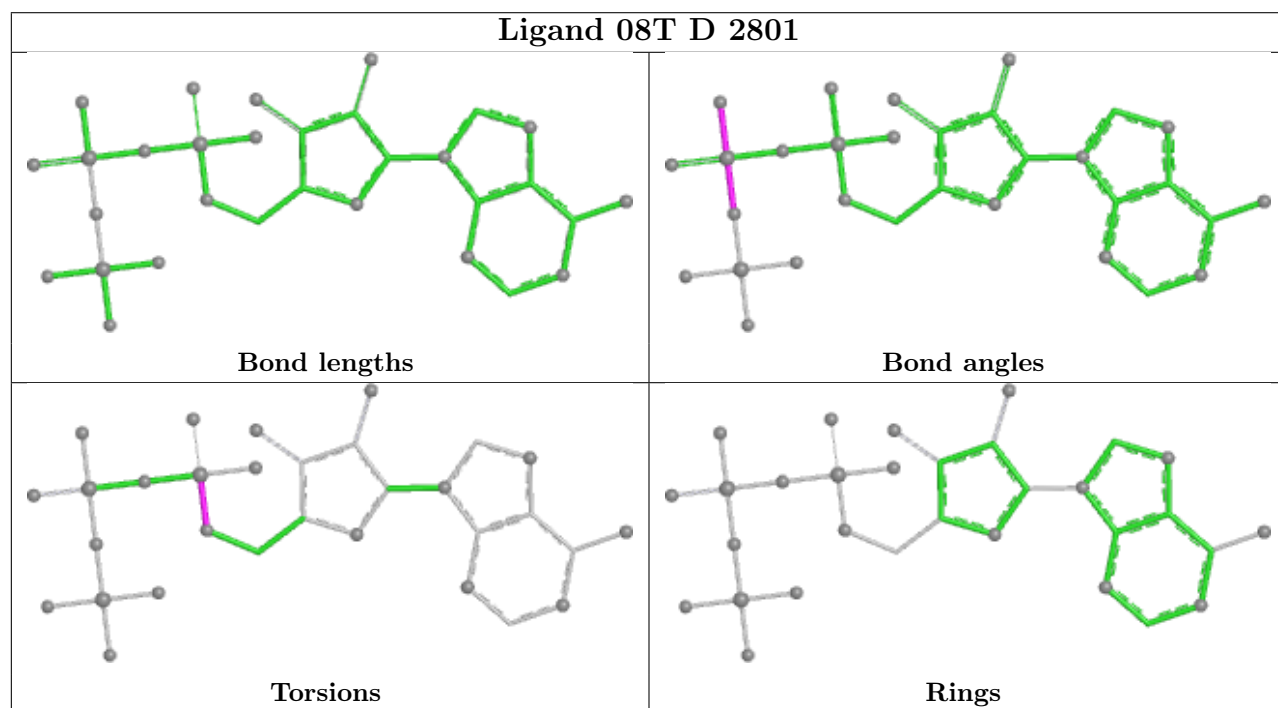
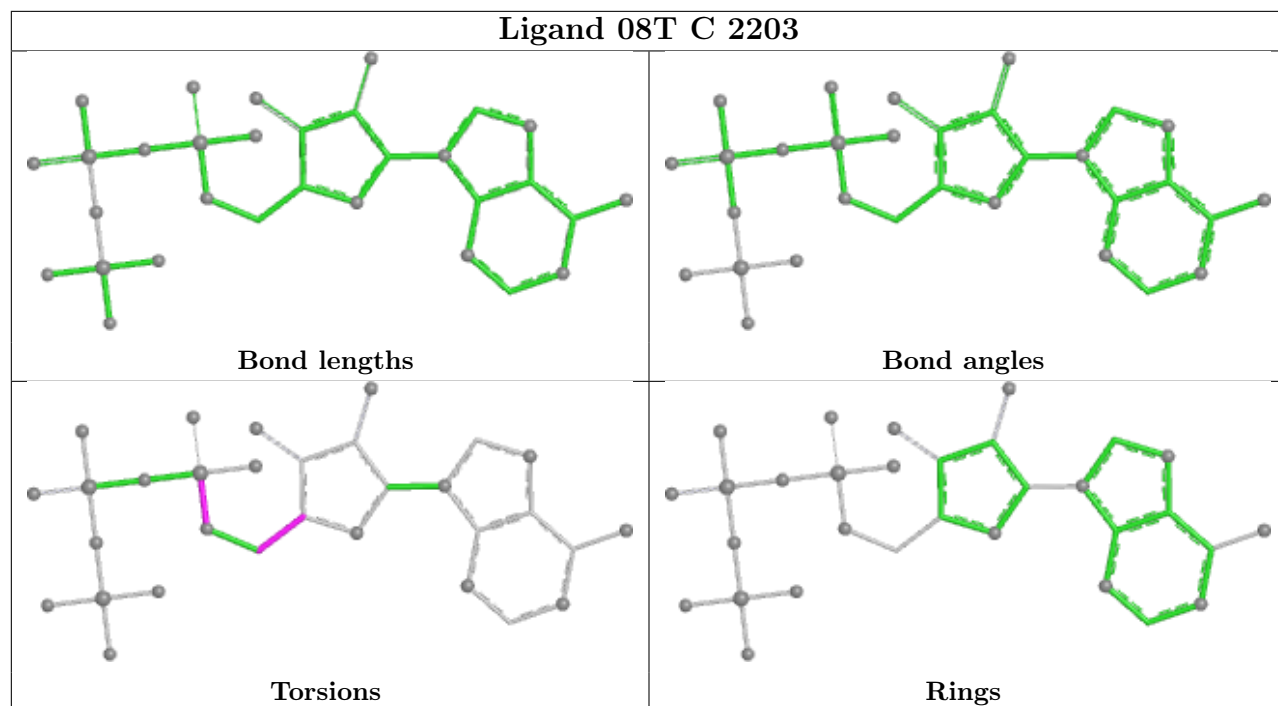
There are no ring outliers.

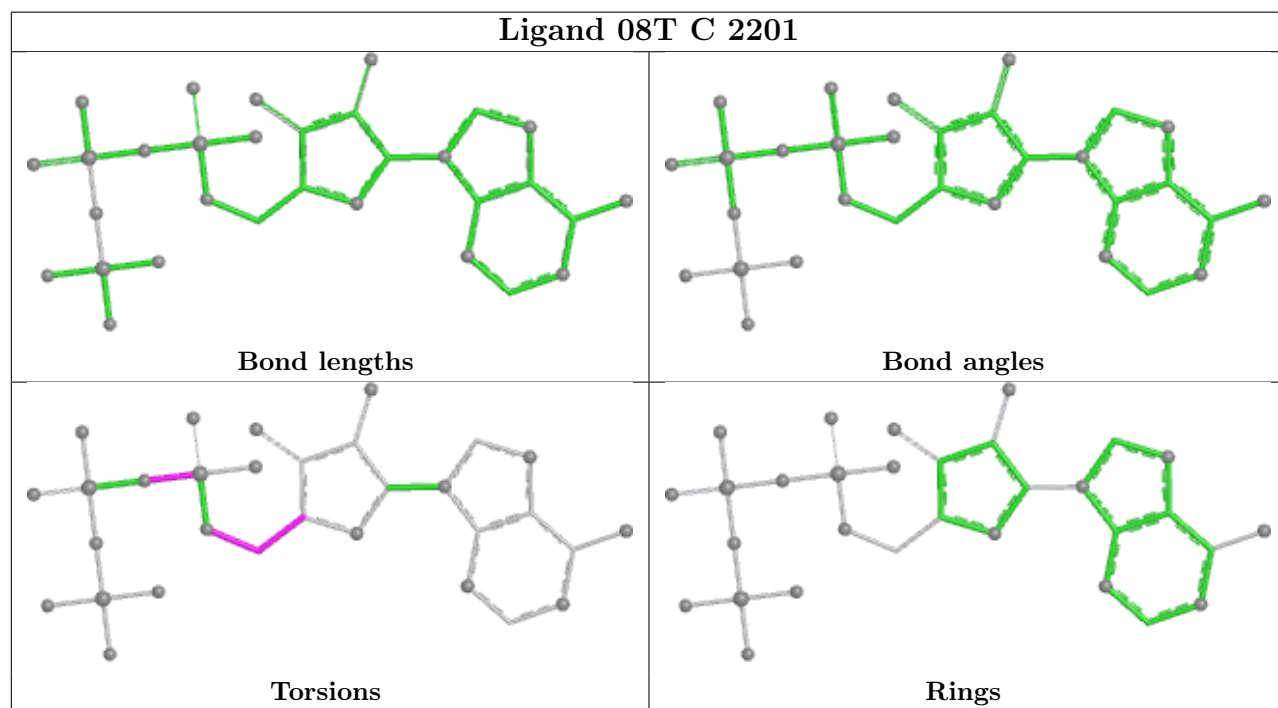
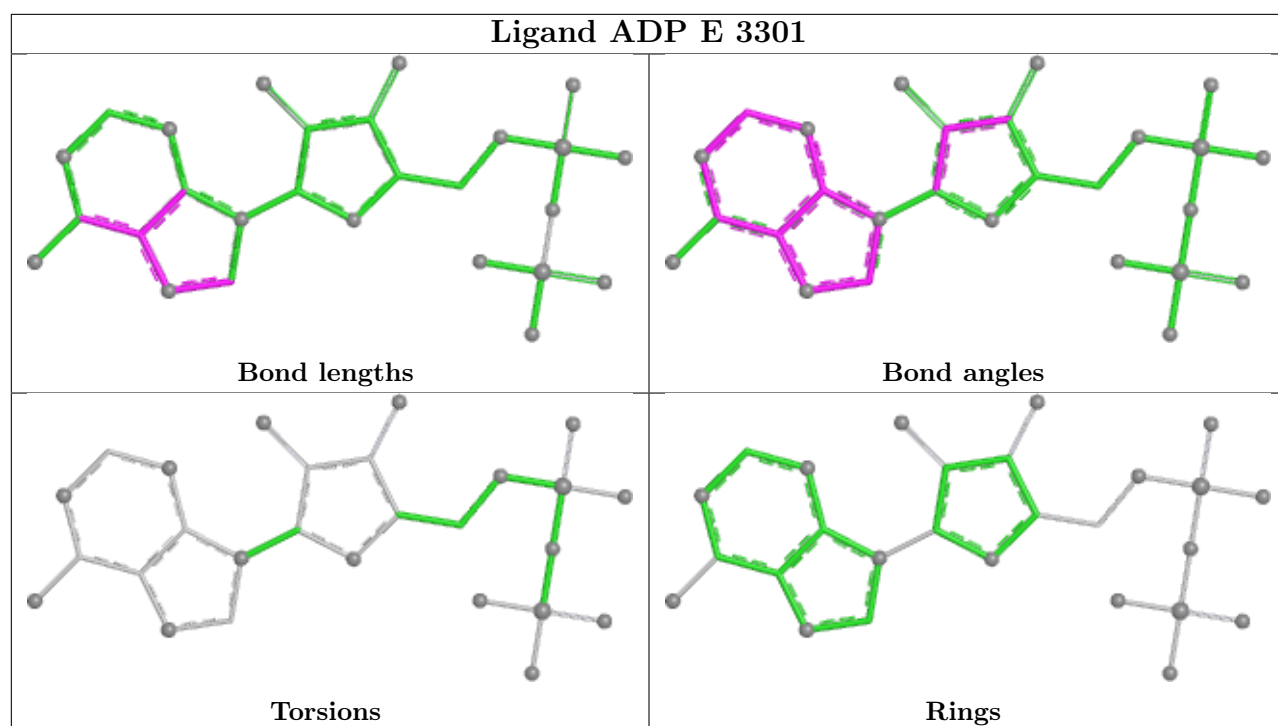
7 monomers are involved in 10 short contacts:

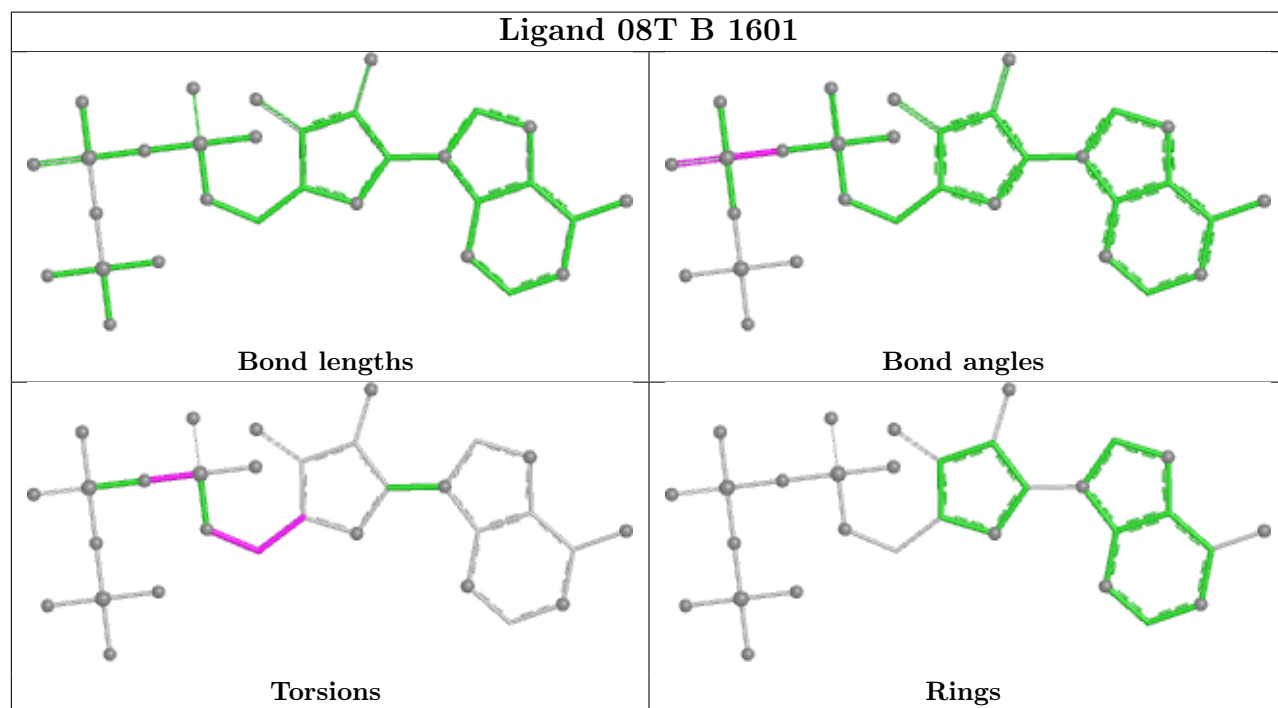
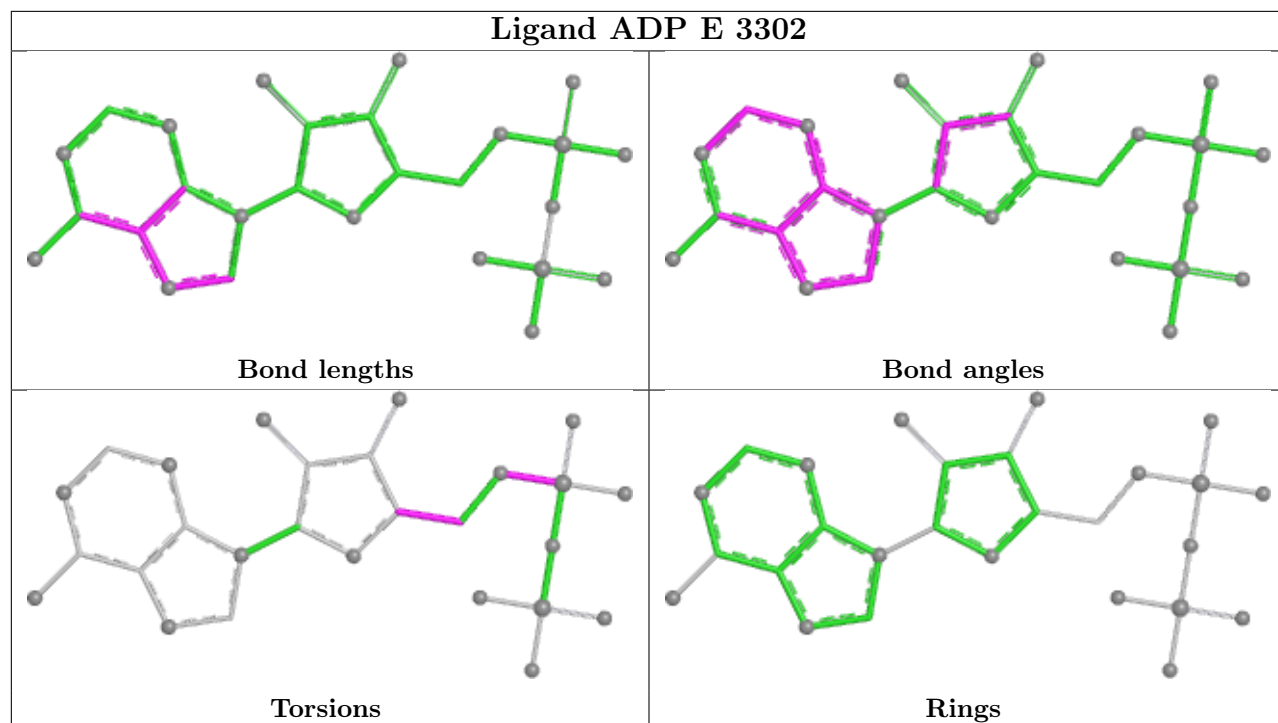
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1103	08T	2	0
3	D	2803	08T	1	0
3	C	2203	08T	2	0
5	E	3301	ADP	1	0
3	C	2201	08T	1	0
5	E	3302	ADP	2	0
3	B	1601	08T	1	0

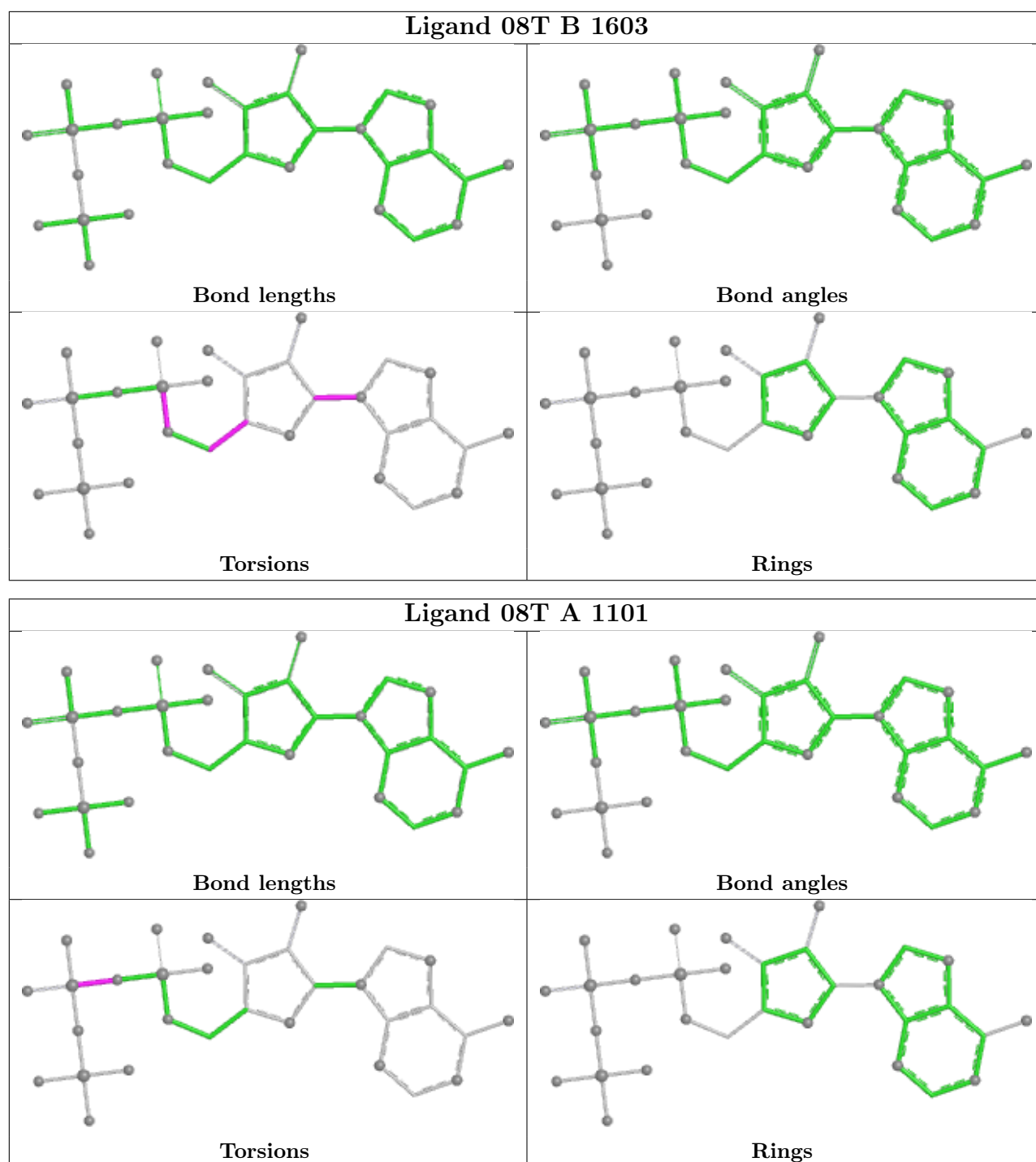
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 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.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1016:ARG	C	1017:SER	N	3.14
1	A	907:PRO	C	908:ASP	N	3.11

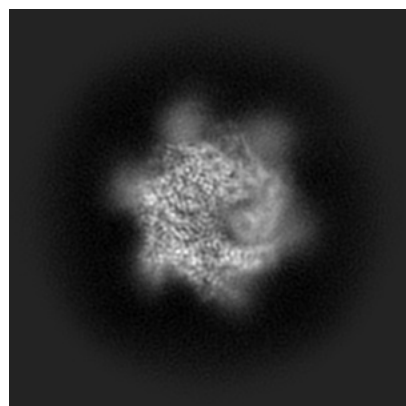
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41992. These allow visual inspection of the internal detail of the map and identification of artifacts.

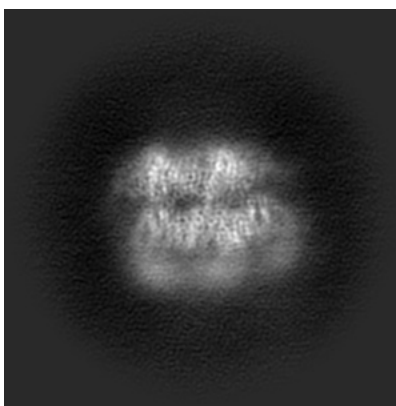
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

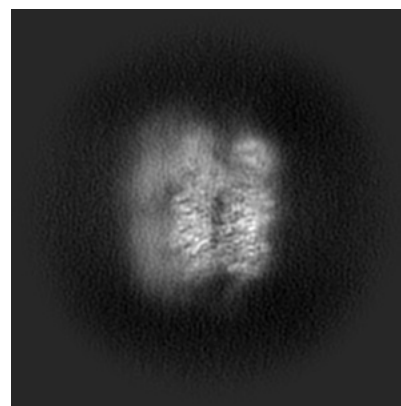
6.1.1 Primary map



X

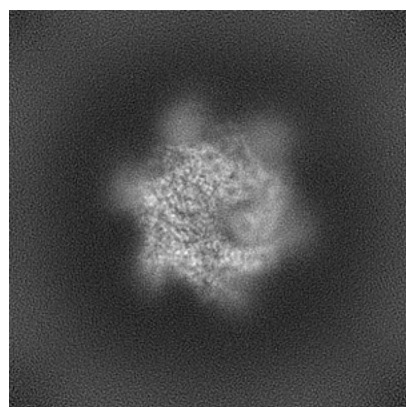


Y

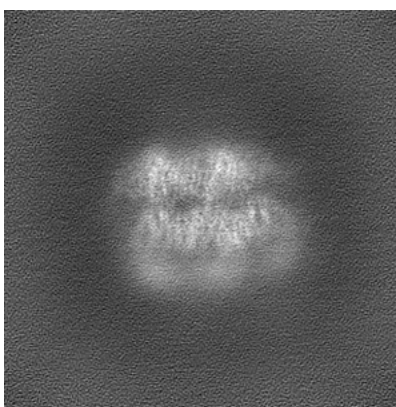


Z

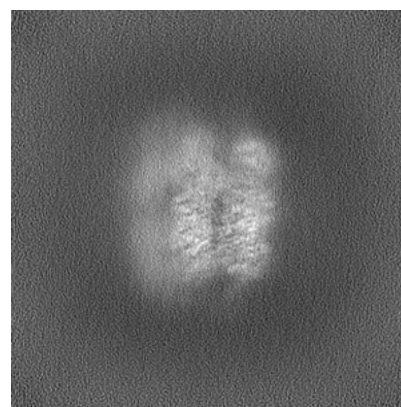
6.1.2 Raw map



X



Y

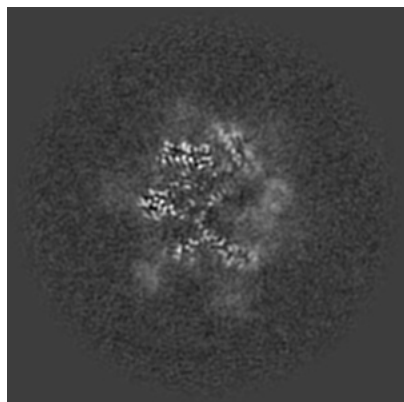


Z

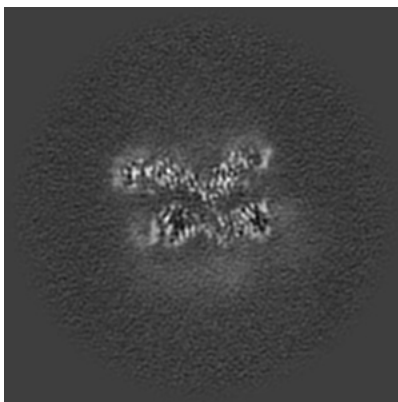
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

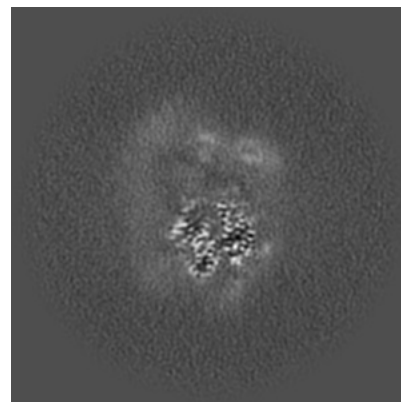
6.2.1 Primary map



X Index: 144

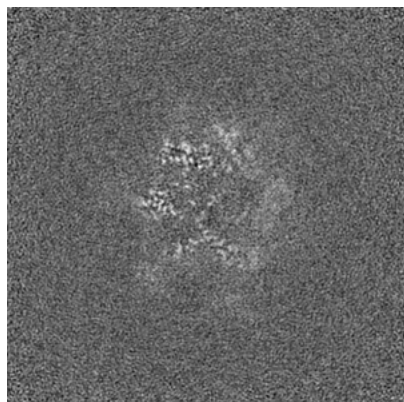


Y Index: 144

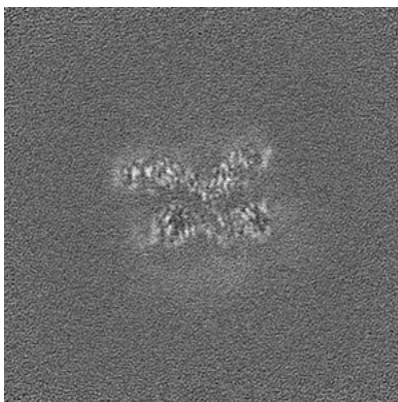


Z Index: 144

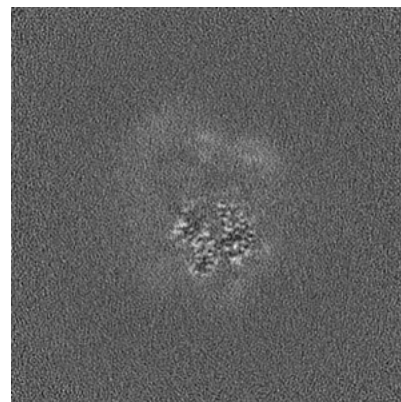
6.2.2 Raw map



X Index: 144



Y Index: 144

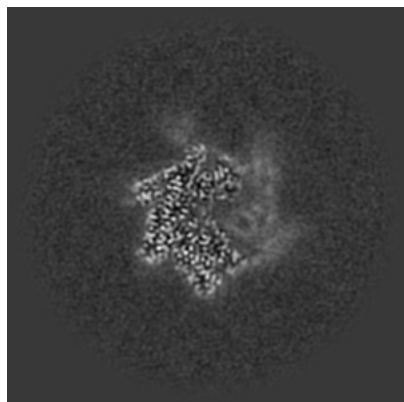


Z Index: 144

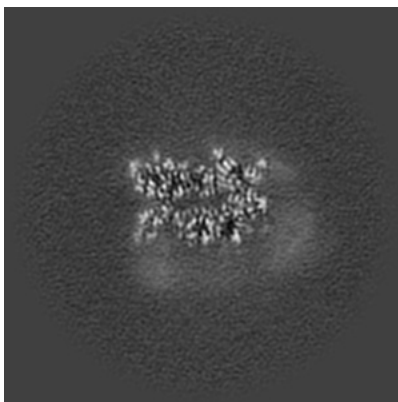
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

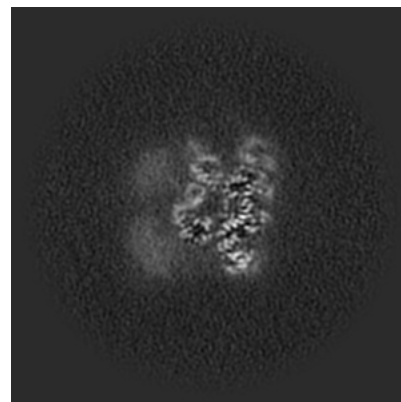
6.3.1 Primary map



X Index: 168

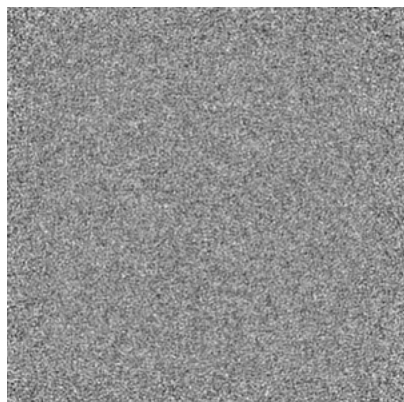


Y Index: 130

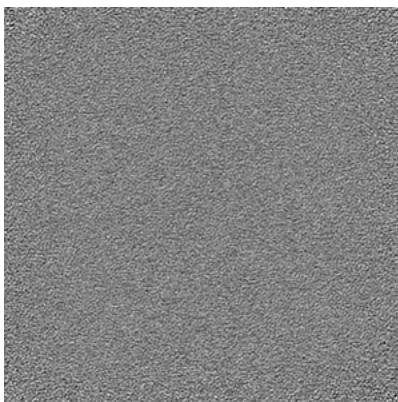


Z Index: 106

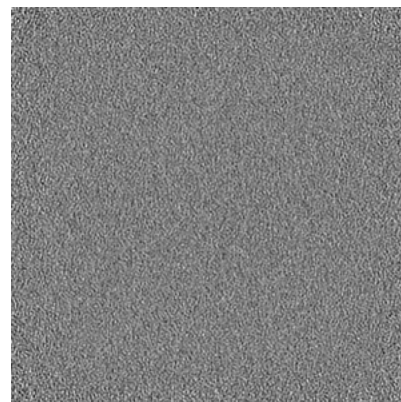
6.3.2 Raw map



X Index: 0



Y Index: 1

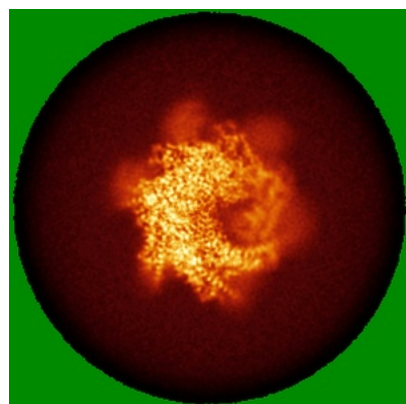


Z Index: 0

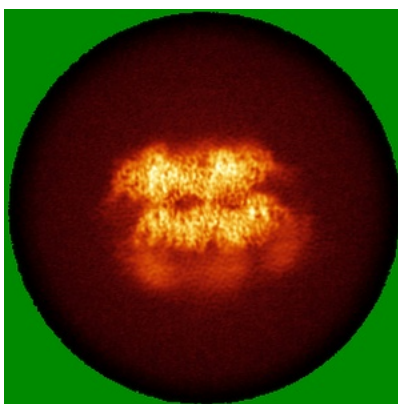
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

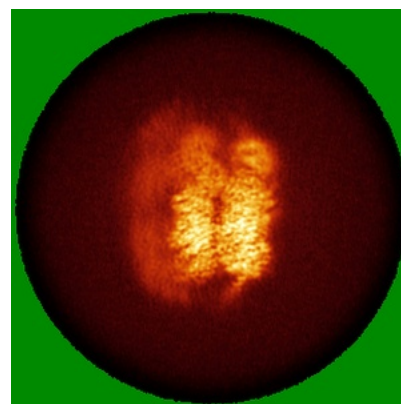
6.4.1 Primary map



X

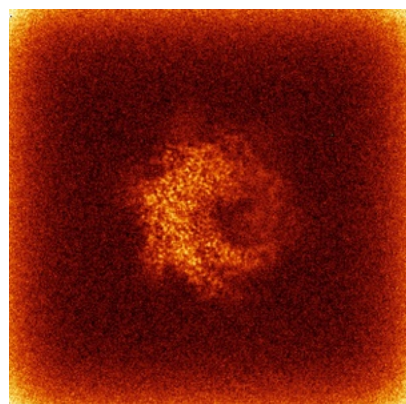


Y

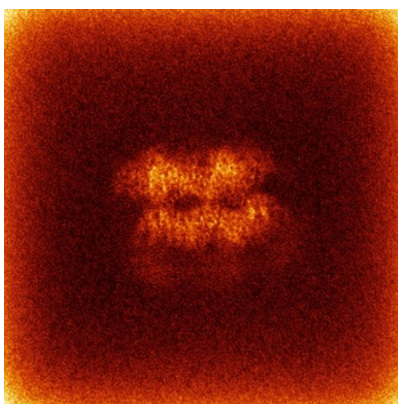


Z

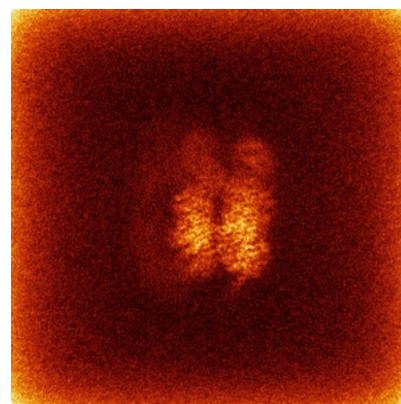
6.4.2 Raw map



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.

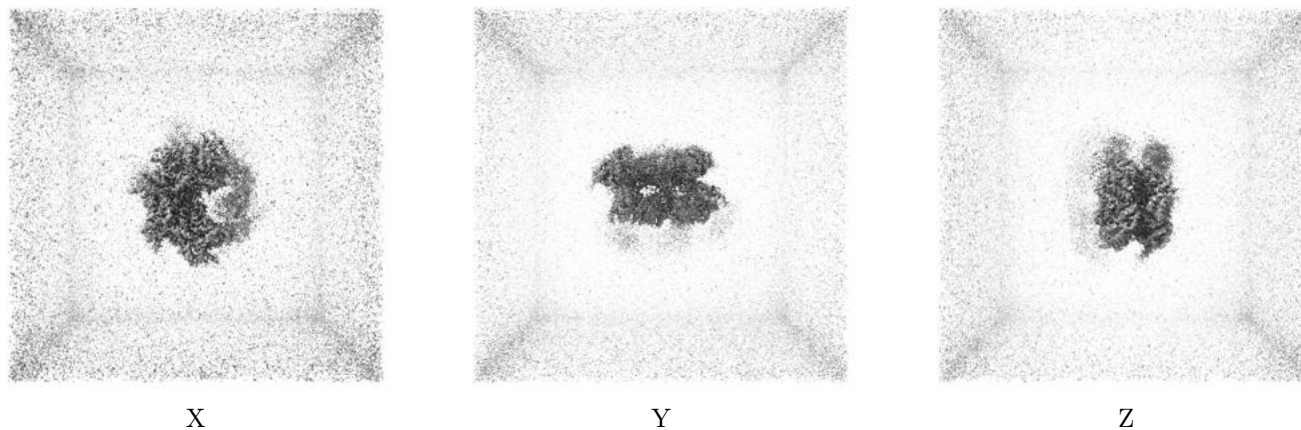
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.14. 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



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.

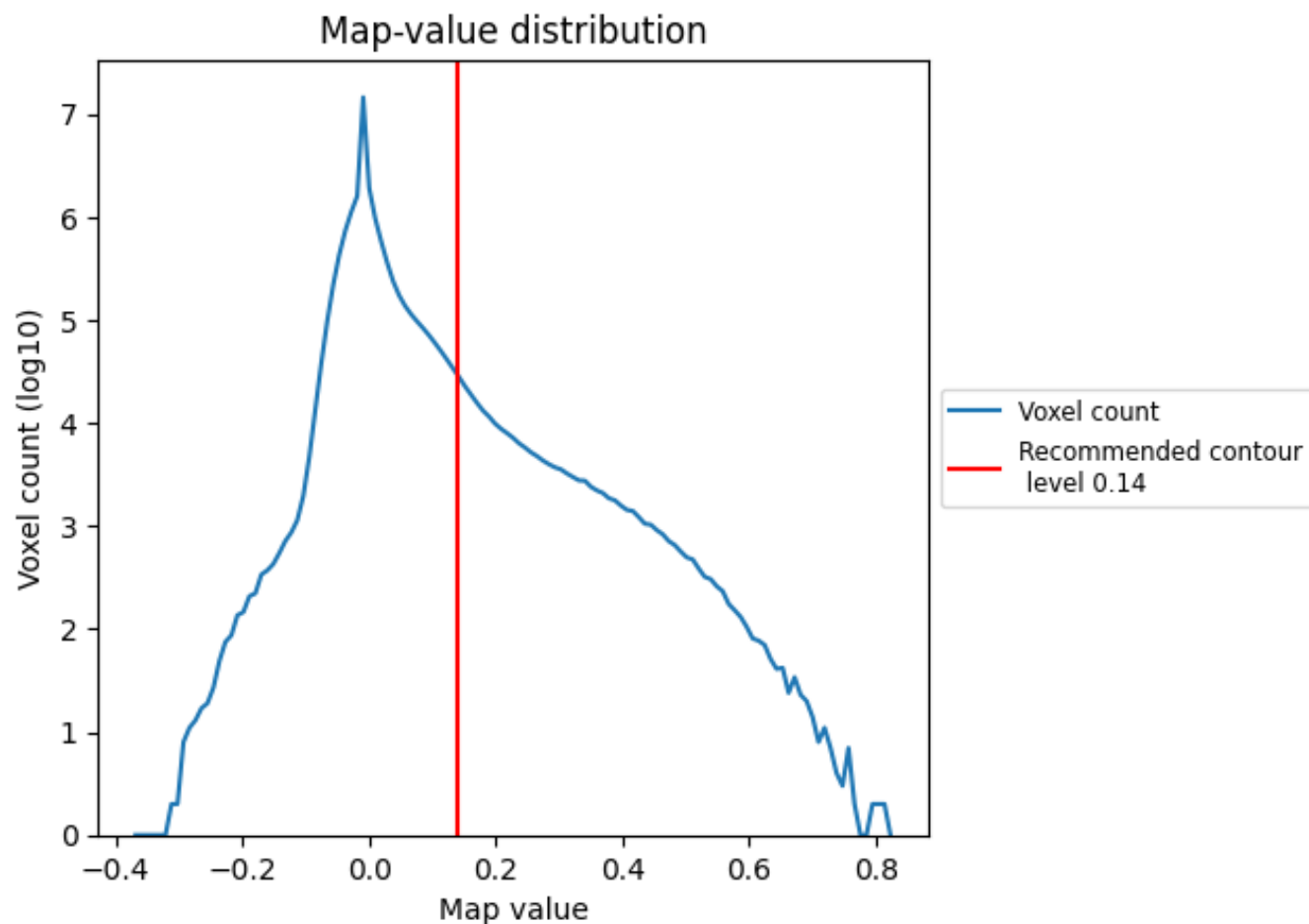
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

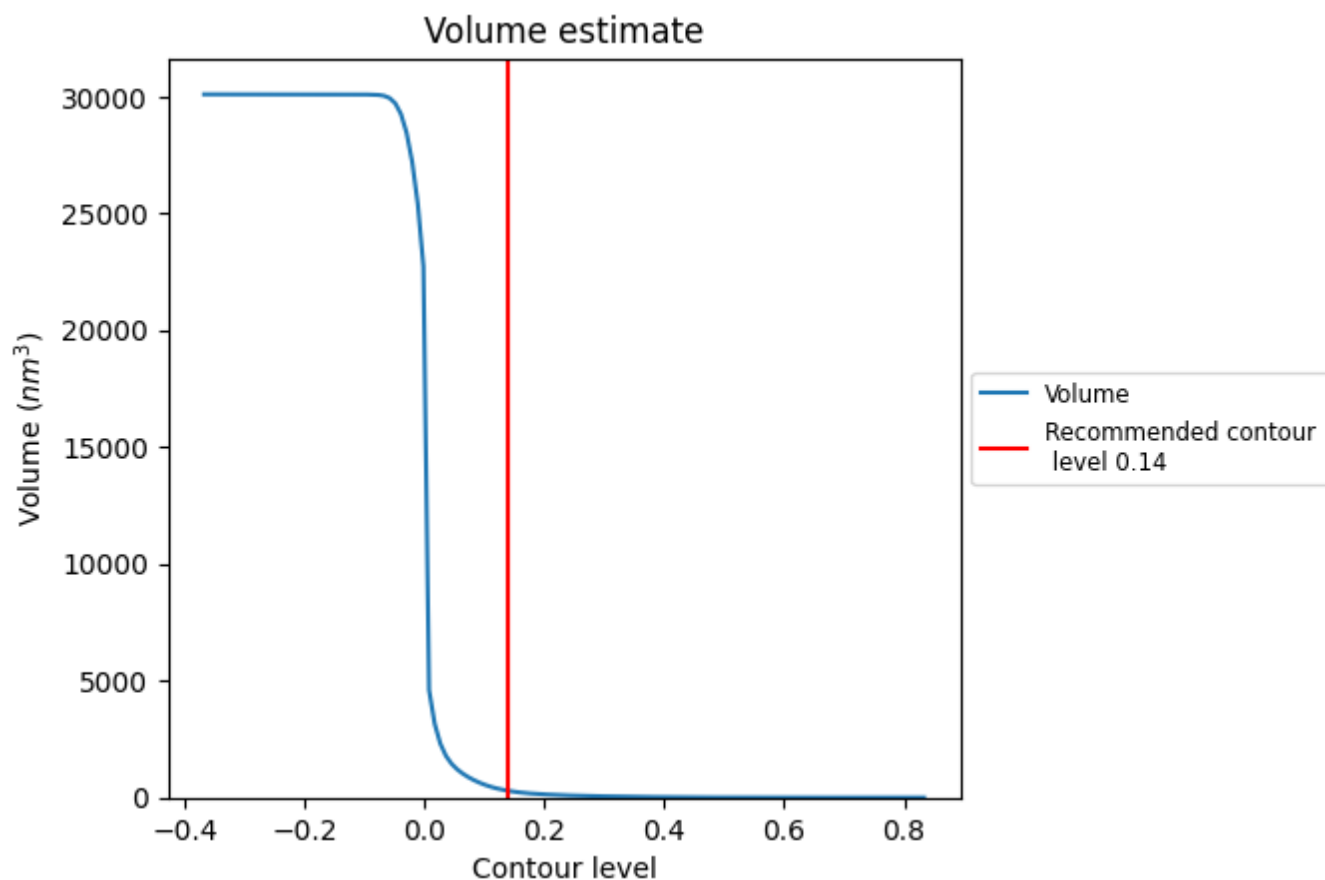
This section contains the results of statistical analysis of the map.

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.

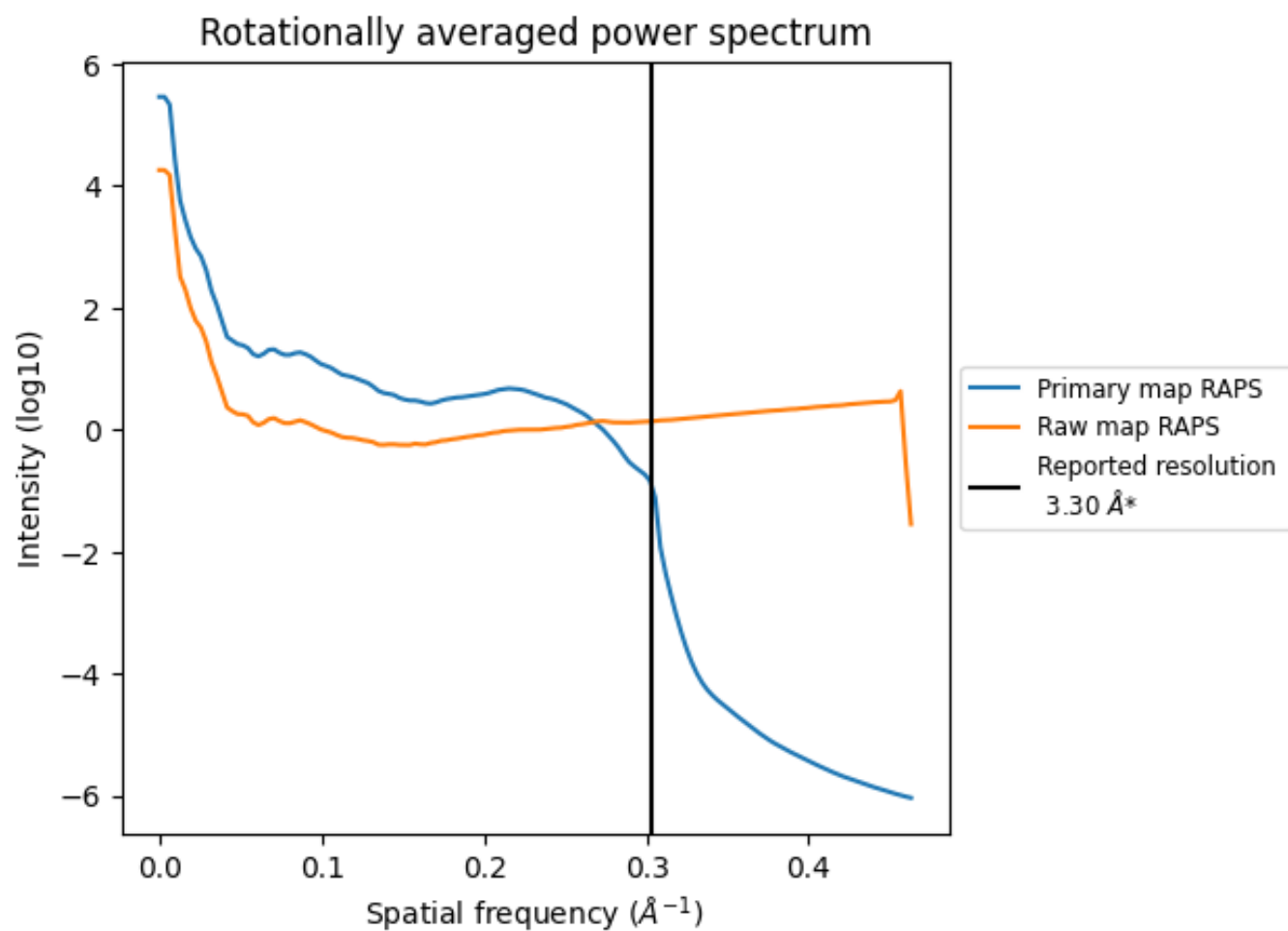
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 286 nm³; this corresponds to an approximate mass of 259 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 ⓘ

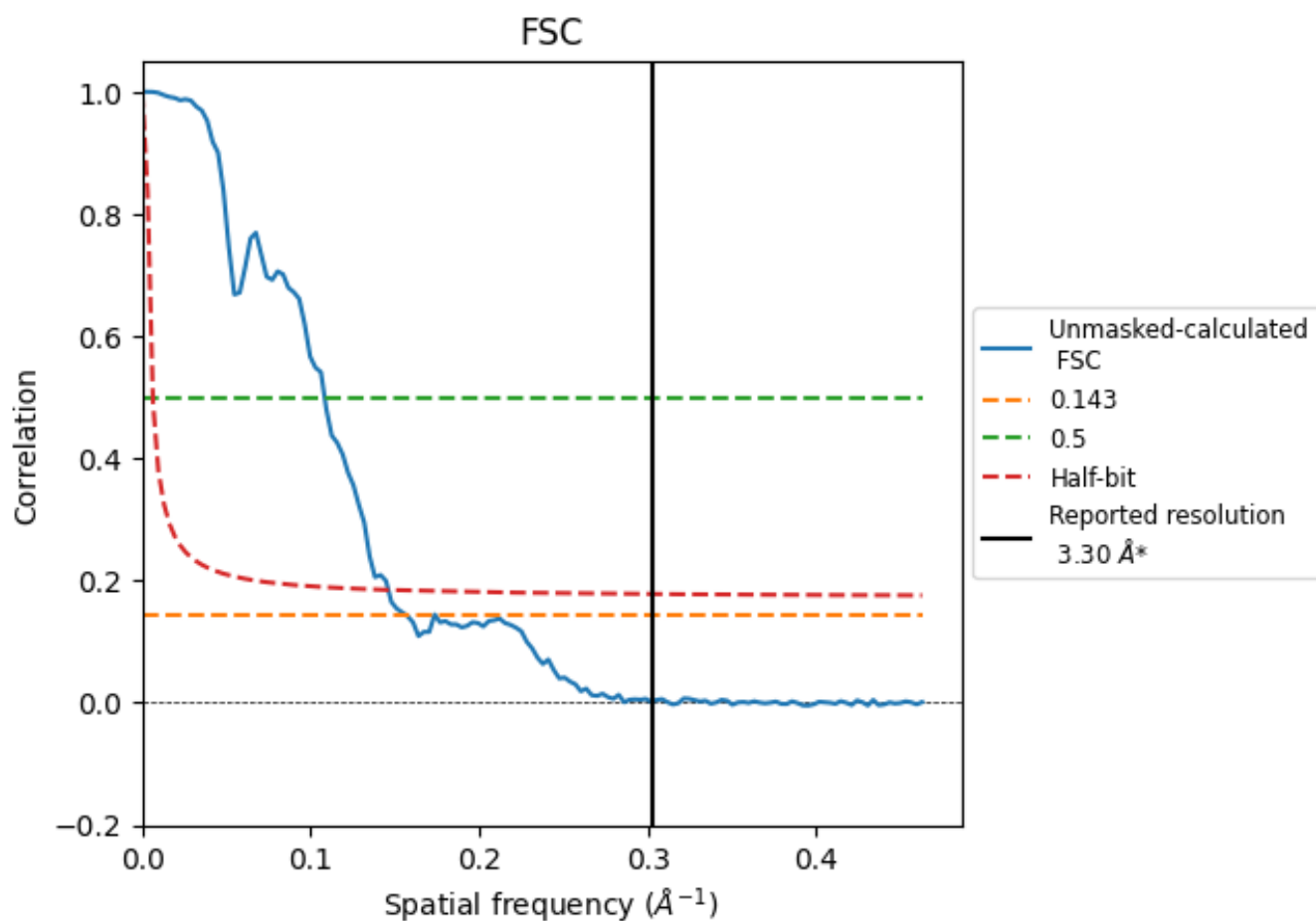


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

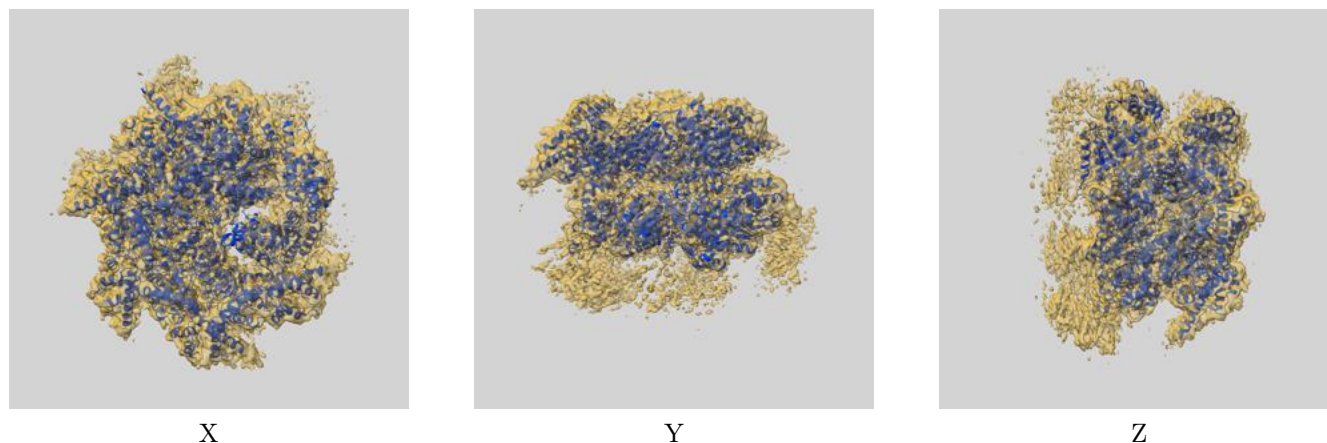
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.38	9.23	6.84

*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 6.38 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

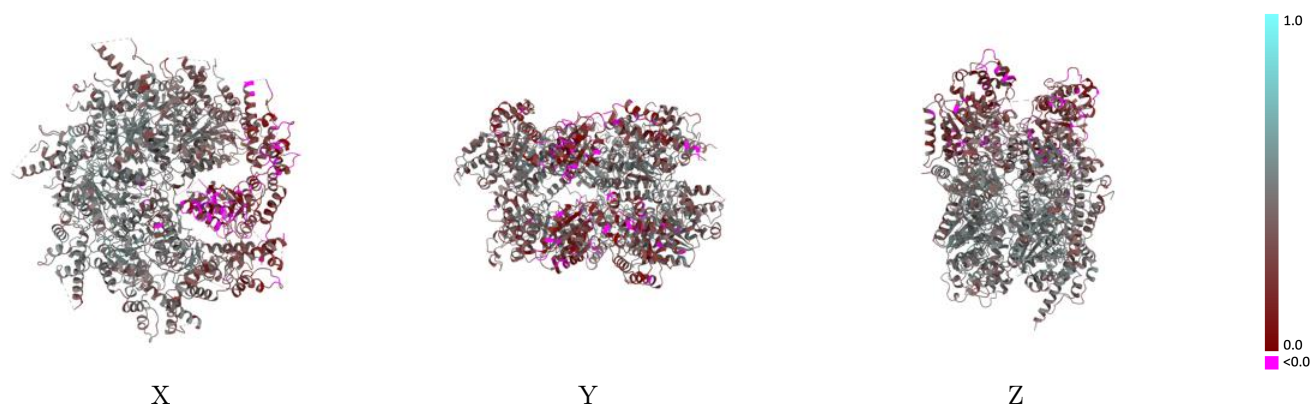
This section contains information regarding the fit between EMDB map EMD-41992 and PDB model 8U7T. Per-residue inclusion information can be found in [section 3](#) on [page 7](#).

9.1 Map-model overlay [i](#)



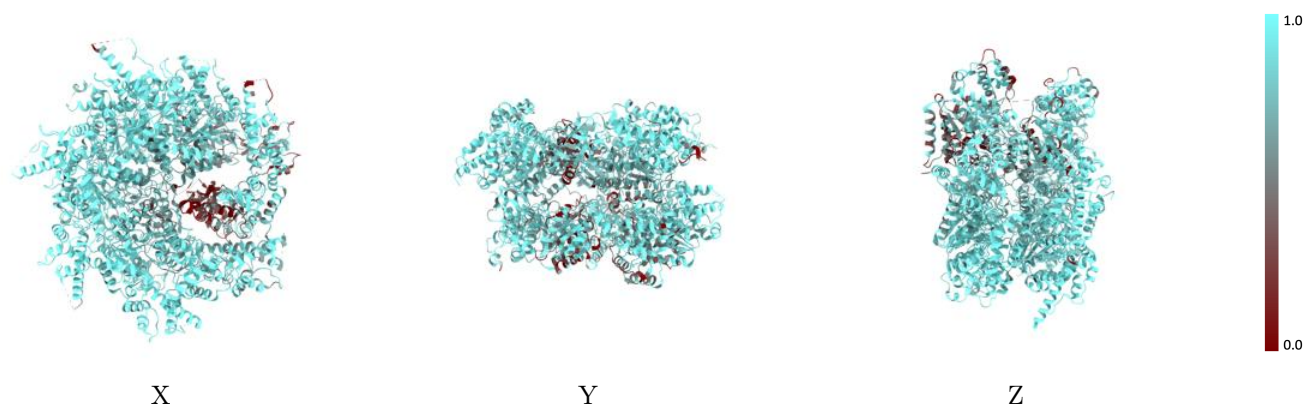
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



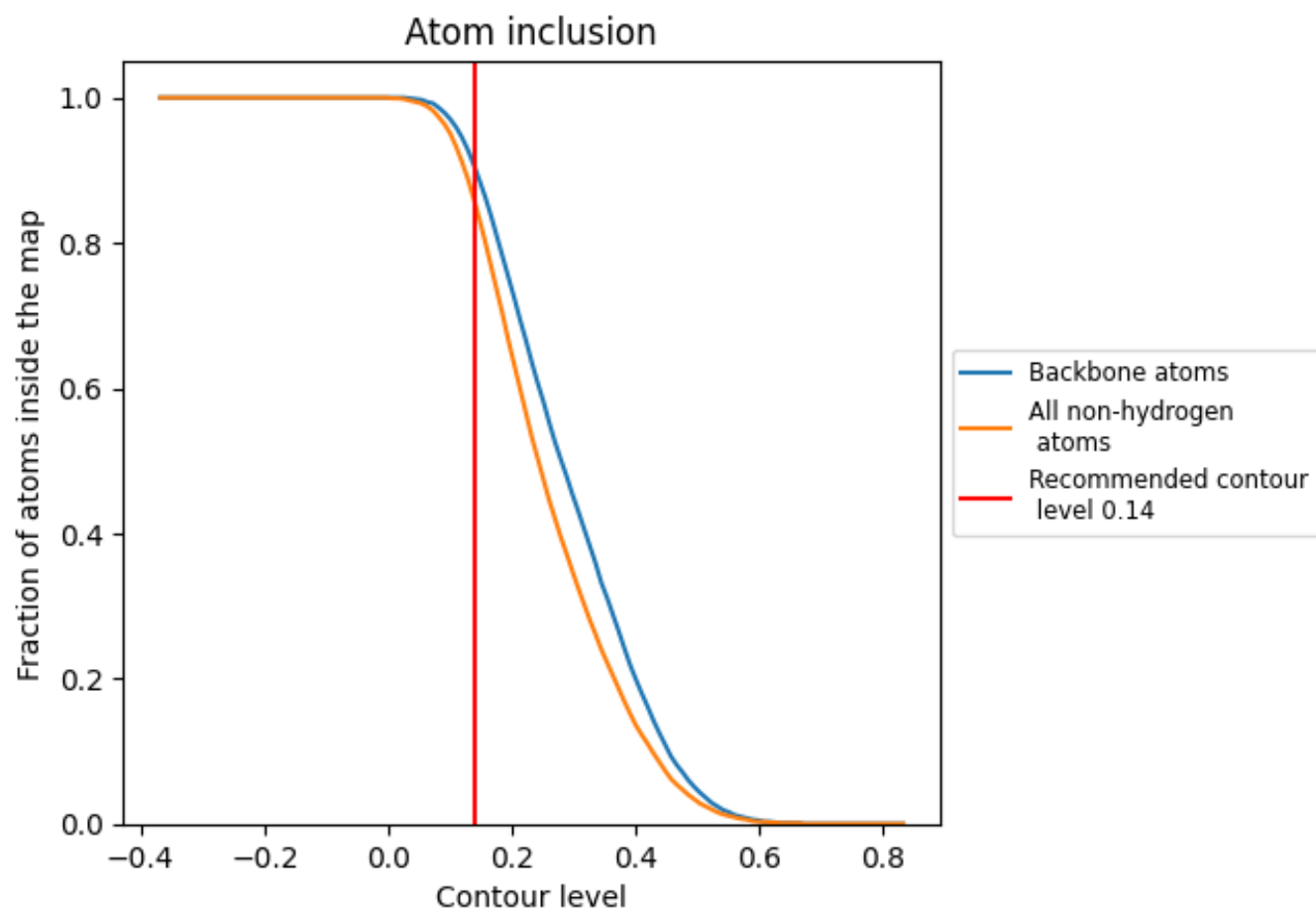
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8570	0.4040
A	0.8090	0.3710
B	0.9180	0.4630
C	0.9240	0.4760
D	0.9240	0.4690
E	0.8410	0.3790
F	0.6110	0.1360
G	0.8290	0.4880

1.0

0.0

<0.0