wwPDB EM Validation Summary Report (i)

Oct 12, 2026 – 04:57 PM EDT

PDB ID	:	9ZNZ / pdb_00009znz
EMDB ID	:	EMD-74462
Title	:	Dimer of tubulin cofactors D,E, and Arl2 bound to beta tubulin in a back to back orientation
Authors	:	Taheri, A.; Al-bassam, J.
Deposited on	:	2025-12-14
Resolution	:	6.30 Å(reported)

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

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

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

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

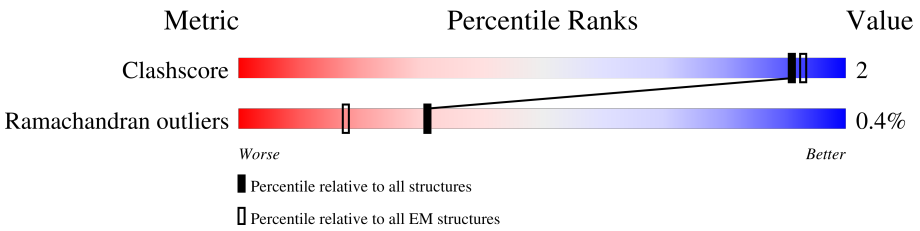
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.51

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 6.30 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)
Clashscore	229148	23984
Ramachandran outliers	224038	23583

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	C	527	8% 16% • 83%
1	E	527	10% 16% • 83%
2	B	184	52% 83% 9% • 8%
2	G	184	51% 84% 8% • 8%
3	A	1205	45% 90% • 8%
3	H	1205	43% 90% • 8%
4	D	447	27% 90% • 8%
4	I	447	37% 90% • 8%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 17650 atoms, of which 24 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 Tubulin-specific chaperone E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	C	89	441	263	89	89	0	0
1	E	89	441	263	89	89	0	0

- Molecule 2 is a protein called ADP-ribosylation factor-like protein 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	170	838	498	170	170	0	0
2	G	170	838	498	170	170	0	0

- Molecule 3 is a protein called Tubulin-specific chaperone D.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	A	1110	5486	3266	1110	1110	0	0
3	H	1110	5486	3266	1110	1110	0	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	initiating methionine	UNP Q9BTW9
A	-11	TRP	-	expression tag	UNP Q9BTW9
A	-10	SER	-	expression tag	UNP Q9BTW9
A	-9	HIS	-	expression tag	UNP Q9BTW9
A	-8	PRO	-	expression tag	UNP Q9BTW9
A	-7	GLN	-	expression tag	UNP Q9BTW9
A	-6	PHE	-	expression tag	UNP Q9BTW9
A	-5	GLU	-	expression tag	UNP Q9BTW9
A	-4	LYS	-	expression tag	UNP Q9BTW9

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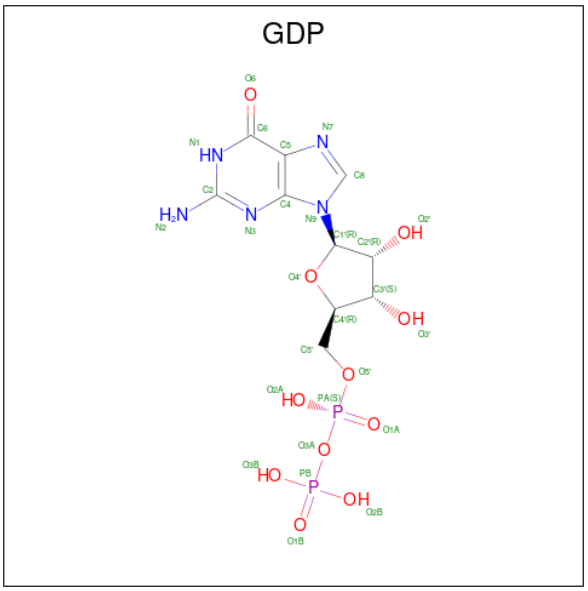
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q9BTW9
A	-2	SER	-	expression tag	UNP Q9BTW9
A	-1	GLY	-	expression tag	UNP Q9BTW9
A	0	SER	-	expression tag	UNP Q9BTW9
H	-12	MET	-	initiating methionine	UNP Q9BTW9
H	-11	TRP	-	expression tag	UNP Q9BTW9
H	-10	SER	-	expression tag	UNP Q9BTW9
H	-9	HIS	-	expression tag	UNP Q9BTW9
H	-8	PRO	-	expression tag	UNP Q9BTW9
H	-7	GLN	-	expression tag	UNP Q9BTW9
H	-6	PHE	-	expression tag	UNP Q9BTW9
H	-5	GLU	-	expression tag	UNP Q9BTW9
H	-4	LYS	-	expression tag	UNP Q9BTW9
H	-3	GLY	-	expression tag	UNP Q9BTW9
H	-2	SER	-	expression tag	UNP Q9BTW9
H	-1	GLY	-	expression tag	UNP Q9BTW9
H	0	SER	-	expression tag	UNP Q9BTW9

- Molecule 4 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	411	2020	1198	411	411	0	0
			Total	C	N	O		
4	I	411	2020	1198	411	411	0	0

- Molecule 5 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



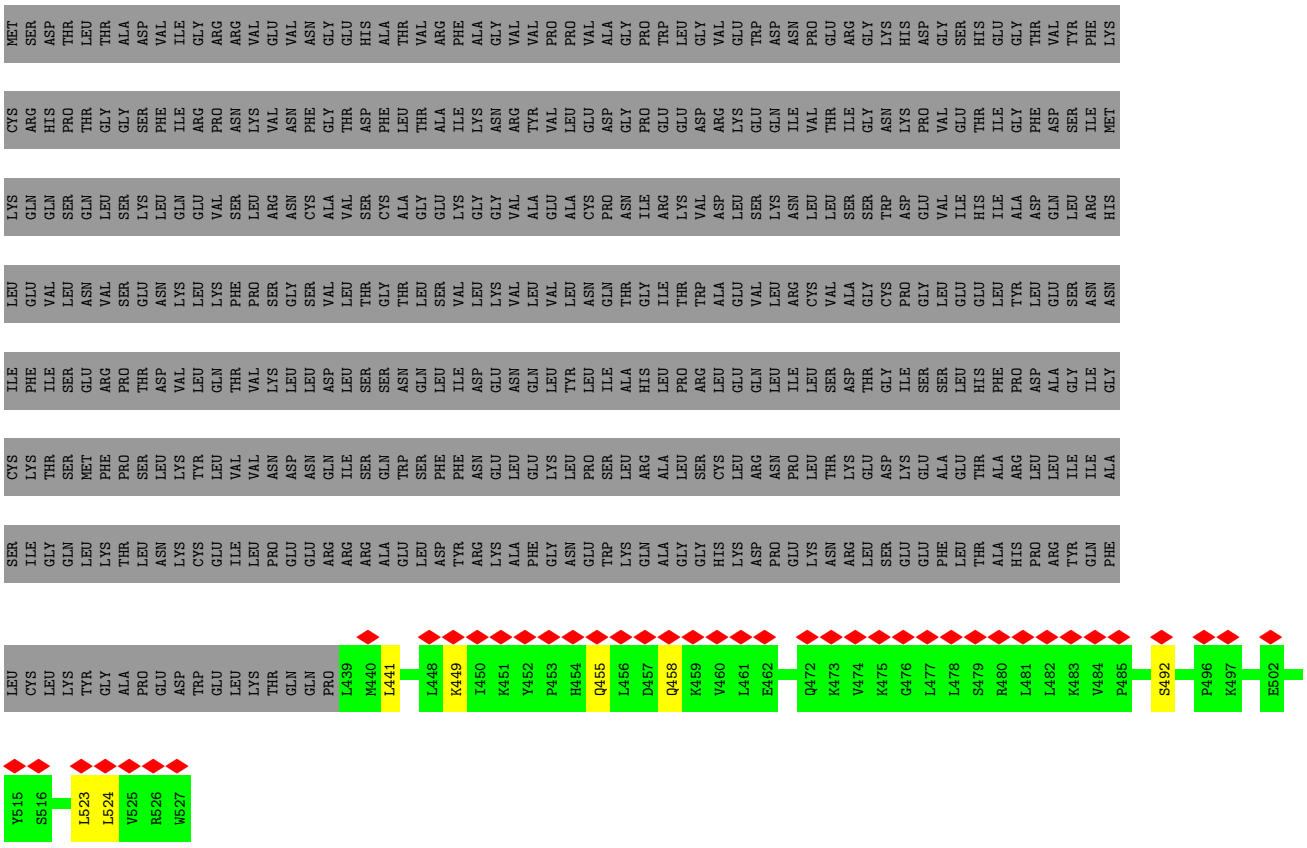
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
5	D	1	40	10	12	5	11	2	0
			Total	C	H	N	O	P	
5	I	1	40	10	12	5	11	2	0

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.

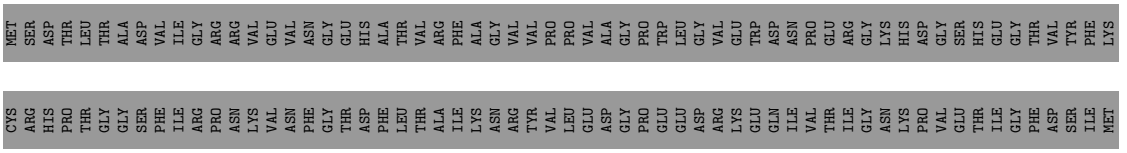
- Molecule 1: Tubulin-specific chaperone E

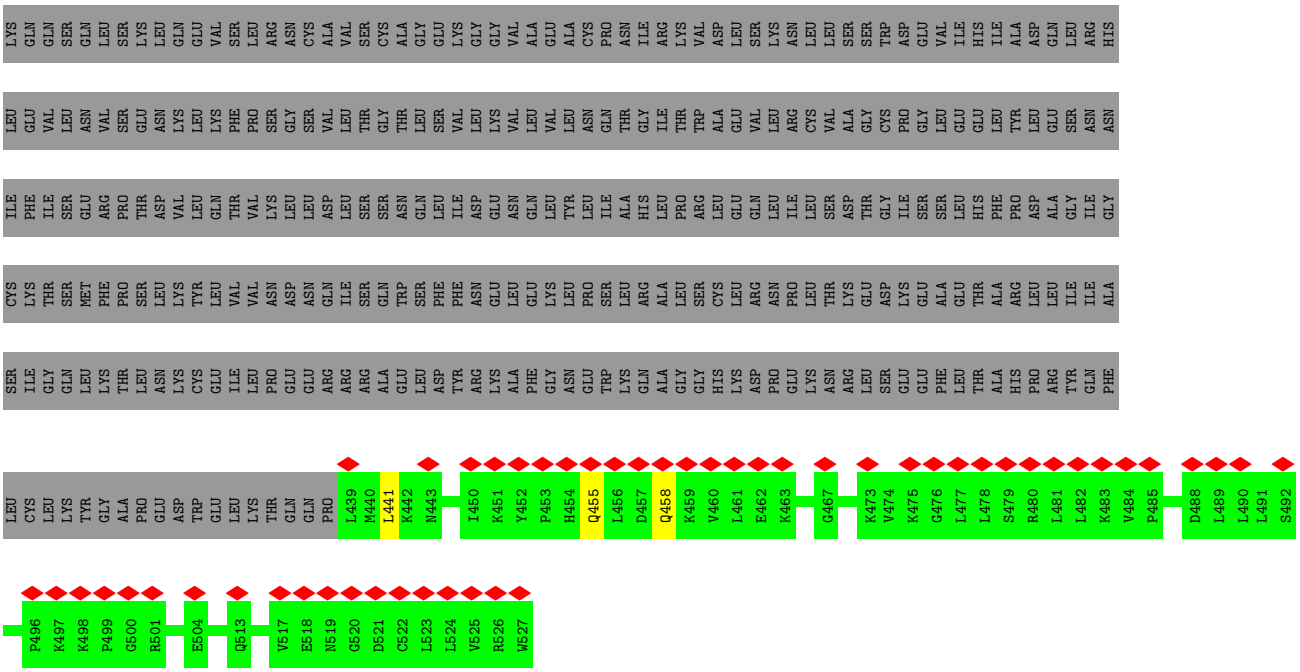
Chain C:



- Molecule 1: Tubulin-specific chaperone E

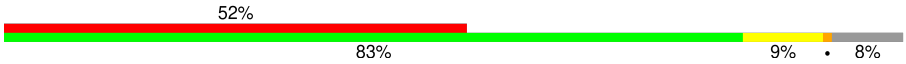
Chain E:

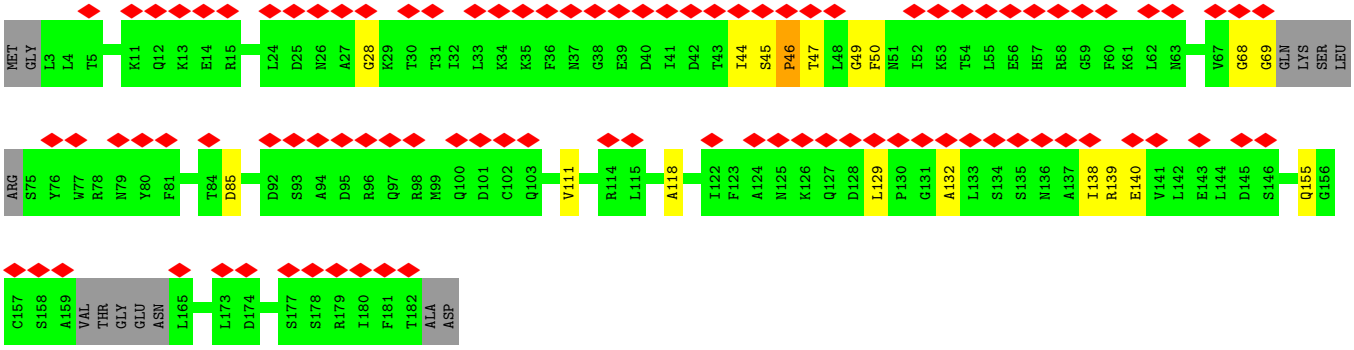




- Molecule 2: ADP-ribosylation factor-like protein 2

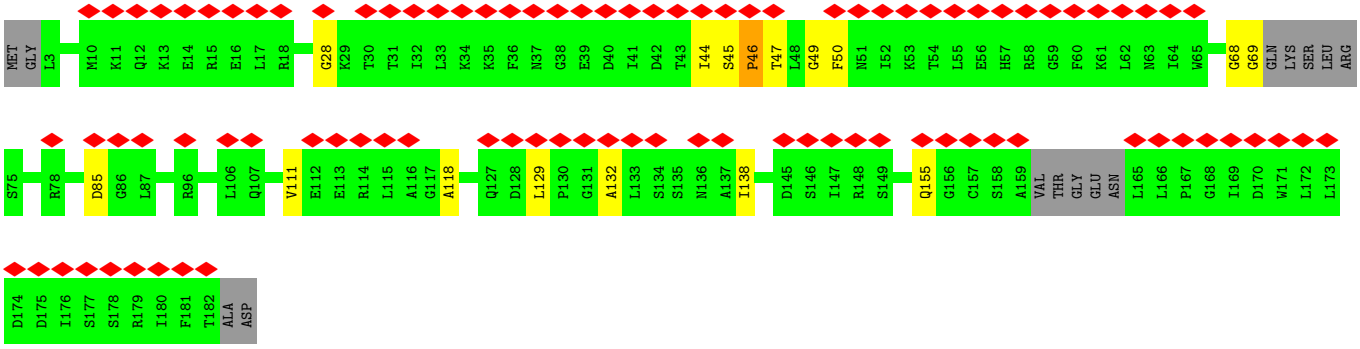
Chain B:





- Molecule 2: ADP-ribosylation factor-like protein 2

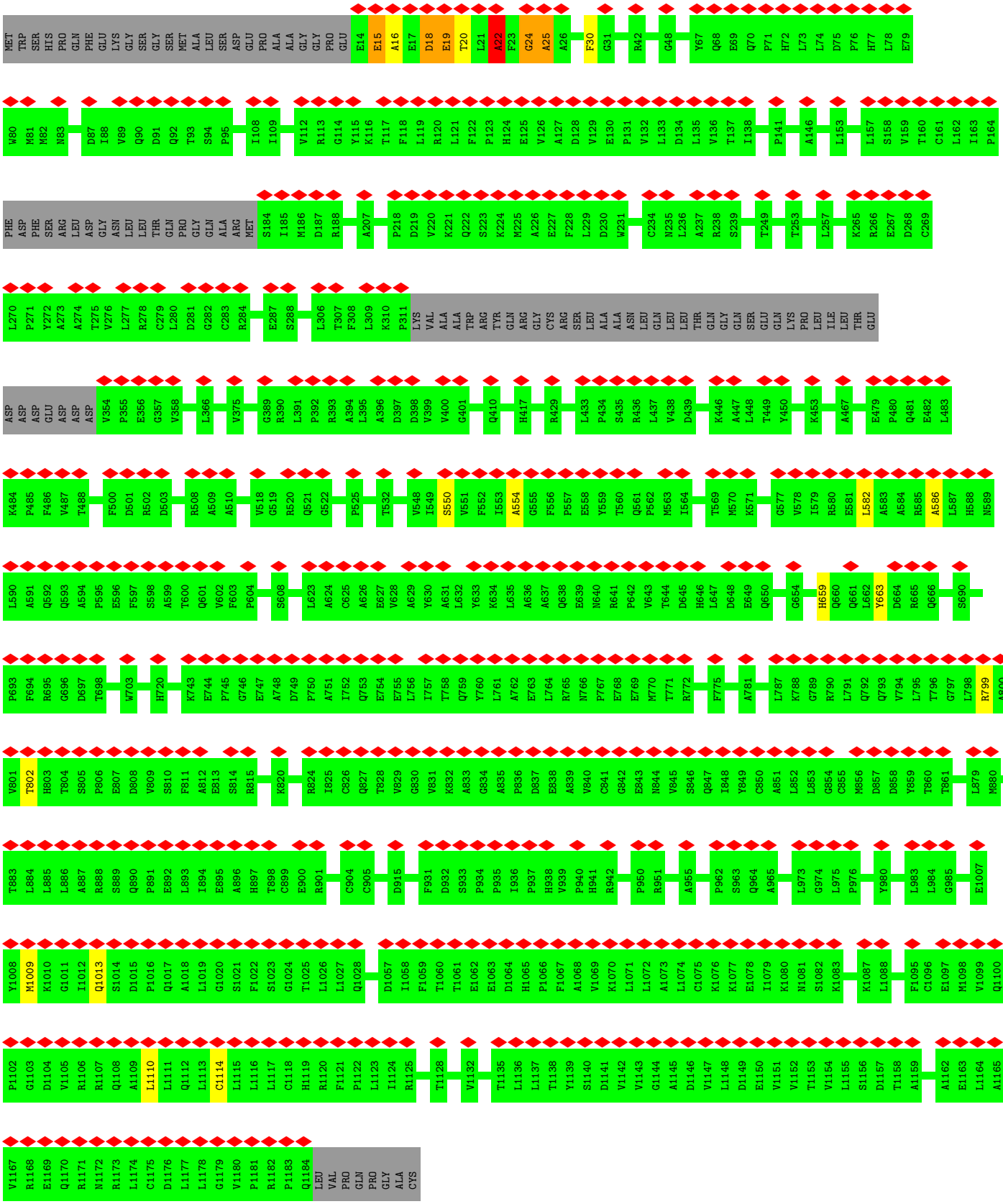
Chain G:



- Molecule 3: Tubulin-specific chaperone D

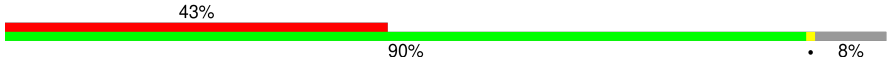
Chain A:

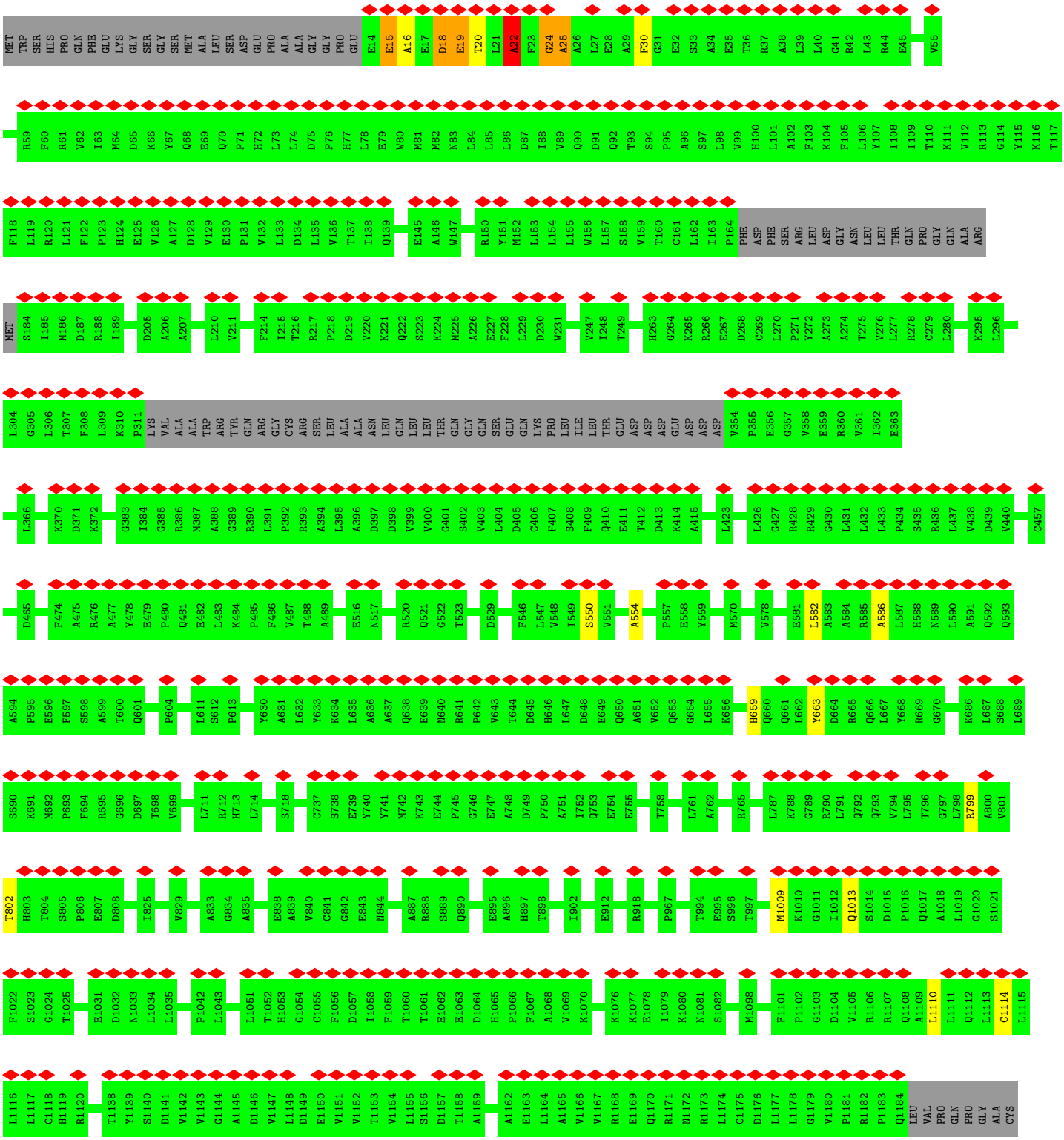
45%
90%
8%


MET TRP SER HIS PRO GLN PHE GLU LYS GLY SER GLY SER MET ALA LEU SER ASP GLU PRO ALA ALA GLY GLY PRO GLU E14 E15 A16 E17 D18 E19 T20 L21 A22 F23 G24 A25 A26 F30 G31 R42 G48 Y67 Q68 E69 Q70 P71 H72 L73 L74 D75 P76 H77 L78 E79
W80 M81 M82 N83 D87 I88 V89 Q90 D91 Q92 T93 S94 P95 I108 I109 V112 R113 G114 Y115 K116 T117 F118 L119 R120 L121 F122 P123 H124 E125 V126 A127 D128 V129 E130 P131 V132 L133 D134 L135 V136 T137 I138 P141 A146 L153 L157 S158 V159 T160 C161 L162 I163 P164
PHE ASP PHE SER ARG LEU ASP GLY ASN LEU LEU THR GLN PRO GLY GLN ALA ARG MET S184 I185 M186 D187 R188 A207 P218 D219 V220 K221 Q222 S223 K224 M225 A226 E227 F228 L229 D230 W231 C234 N235 L236 A237 R238 S239 T249 T253 L257 K265 R266 E267 D268 C269
L270 P271 Y272 A273 A274 T275 V276 L277 R278 C279 L280 D281 G282 C283 R284 E287 S288 L306 T307 F308 L309 K310 P311 LYS VAL ALA ALA TRP ARG TYR GLN ARG GLY CYS ARG SER LEU ALA ALA ASN LEU GLN LEU LEU THR GLN GLY GLN SER GLU GLN LYS PRO LEU ILE LEU THR GLU
ASP ASP ASP GLU ASP ASP ASP V354 P355 E356 G357 V358 L366 V375 G389 R390 L391 P392 R393 A394 L395 A396 D397 D398 V399 V400 G401 Q410 H417 R429 L433 P434 S435 R436 L437 V438 D439 K446 A447 L448 T449 Y450 K453 A467 E479 P480 Q481 E482 L483
K484 P485 F486 V487 T488 F500 D501 R502 D503 R508 A509 A510 V518 G519 R520 Q521 G522 P525 T532 V548 I549 S550 V551 F552 I553 A554 G555 F556 P557 E558 Y559 T560 Q561 P562 M563 I564 T569 M570 K571 G577 V578 I579 R580 E581 L582 A583 A584 R585 A586 L587 H588 N589
L590 A591 Q592 Q593 A594 P595 E596 F597 S598 A599 T600 Q601 V602 F603 P604 S608 L623 A624 C625 A626 E627 V628 A629 Y630 A631 L632 Y633 K634 L635 A636 A637 Q638 E639 N640 R641 P642 E643 T644 D645 H646 L647 D648 E649 Q650 G654 H659 Q660 Q661 L662 Y663 D664 R665 Q666 S690
P693 F694 R695 G696 D697 T698 W703 H720 K743 E744 P745 G746 E747 A748 D749 P750 A751 I752 Q753 E754 E755 L756 I757 T758 Q759 Y760 L761 A762 E763 L764 R765 N766 P767 E768 E769 M770 T771 R772 F775 A781 L787 K788 G789 R790 L791 Q792 Q793 V794 L795 T796 G797 L798 R799 A800
V801 T802 H803 T804 S805 P806 E807 D808 V809 S810 F811 A812 E813 S814 R815 K820 R824 I825 C826 Q827 T828 V829 G830 V831 K832 A833 G834 A835 P836 D837 E838 A839 V840 C841 G842 E843 N844 V845 S846 Q847 I848 Y849 C850 A851 L852 L853 G854 C855 M856 D857 D858 Y859 T860 T861 L879 M880
T883 L884 L885 L886 A887 R888 S889 Q890 P891 E892 L893 I894 E895 A896 H897 T898 C899 E900 R901 C904 C905 D915 F931 D932 S933 P934 P935 I936 P937 H938 V939 P940 H941 R942 P950 R951 A955 P962 S963 Q964 A965 L973 G974 L975 P976 Y980 L983 L984 G985 E1007
Y1008 M1009 K1010 G1011 I1012 Q1013 S1014 D1015 P1016 Q1017 A1018 L1019 G1020 S1021 F1022 S1023 G1024 T1025 L1026 L1027 Q1028 D1057 I1058 F1059 T1060 T1061 E1062 E1063 D1064 H1065 P1066 F1067 A1068 V1069 K1070 L1071 L1072 A1073 L1074 C1075 K1076 K1077 E1078 I1079 K1080 N1081 S1082 K1083 K1087 L1088 F1095 C1096 E1097 M1098 V1099 Q1100 F1101
P1102 G1103 D1104 V1105 R1106 R1107 Q1108 A1109 L1110 L1111 Q1112 L1113 C1114 L1115 L1116 L1117 C1118 H1119 R1120 F1121 P1122 L1123 I1124 R1125 T1128 V1132 T1135 L1136 L1137 T1138 Y1139 S1140 D1141 V1142 V1143 G1144 A1145 D1146 V1147 L1148 D1149 E1150 V1151 V1152 T1153 V1154 L1155 S1156 D1157 T1158 A1159 A1162 E1163 L1164 A1165 V1166
V1167 R1168 E1169 Q1170 R1171 N1172 R1173 L1174 C1175 D1176 L1177 L1178 G1179 V1180 P1181 R1182 P1183 Q1184 LEU VAL PRO GLN PRO GLY ALA CYS

- Molecule 3: Tubulin-specific chaperone D

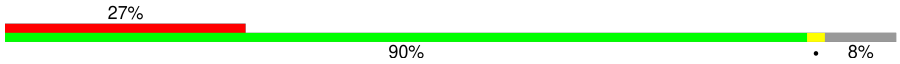
Chain H:

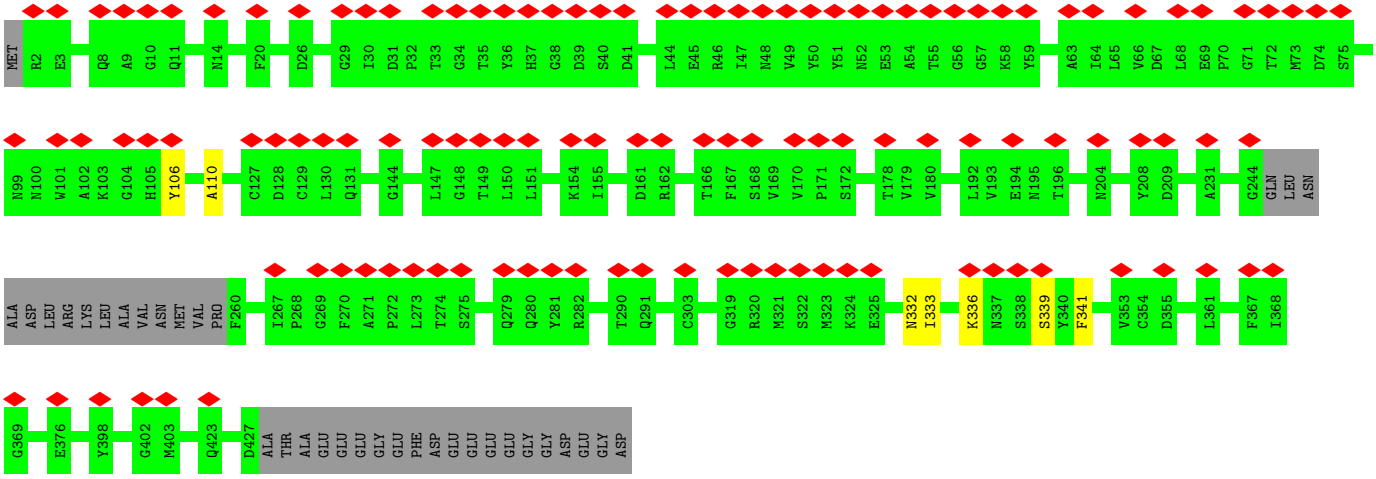




- Molecule 4: Tubulin beta chain

Chain D:





- Molecule 4: Tubulin beta chain

Chain I:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75072	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.276	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.0352	Depositor
Map size (Å)	328.0, 328.0, 328.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.64, 1.64, 1.64	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: GDP

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	C	0.25	0/440	0.58	1/612 (0.2%)
1	E	0.25	0/440	0.58	1/612 (0.2%)
2	B	0.78	0/835	1.31	7/1157 (0.6%)
2	G	0.78	0/835	1.31	7/1157 (0.6%)
3	A	0.22	1/5483 (0.0%)	0.46	8/7633 (0.1%)
3	H	0.22	1/5483 (0.0%)	0.46	8/7633 (0.1%)
4	D	0.34	0/2018	0.61	1/2801 (0.0%)
4	I	0.34	0/2018	0.61	1/2801 (0.0%)
All	All	0.34	2/17552 (0.0%)	0.63	34/24406 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	16	ALA	CA-C	5.30	1.59	1.52
3	H	16	ALA	CA-C	5.25	1.59	1.52

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	H	15	GLU	N-CA-C	-9.97	100.53	112.89
3	A	15	GLU	N-CA-C	-9.95	100.55	112.89
3	A	30	PHE	N-CA-C	-9.16	96.45	110.10
3	H	30	PHE	N-CA-C	-9.14	96.48	110.10
3	A	24	GLY	N-CA-C	-8.88	102.08	112.73

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	C	441	0	176	3	0
1	E	441	0	176	1	0
2	B	838	0	370	4	0
2	G	838	0	370	3	0
3	A	5486	0	2550	12	0
3	H	5486	0	2550	11	0
4	D	2020	0	911	3	0
4	I	2020	0	911	3	0
5	D	28	12	12	0	0
5	I	28	12	12	0	0
All	All	17626	24	8038	40	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 2.

The worst 5 of 40 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:15:GLU:HA	3:H:18:ASP:CB	1.98	0.94
3:A:15:GLU:HA	3:A:18:ASP:CB	1.98	0.93
2:G:85:ASP:O	2:G:118:ALA:HB1	2.01	0.61
2:B:85:ASP:O	2:B:118:ALA:HB1	2.01	0.60
3:H:15:GLU:CA	3:H:18:ASP:CB	2.78	0.58

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	C	87/527 (16%)	85 (98%)	2 (2%)	0	100	100
1	E	87/527 (16%)	85 (98%)	2 (2%)	0	100	100
2	B	164/184 (89%)	146 (89%)	13 (8%)	5 (3%)	3	22
2	G	164/184 (89%)	146 (89%)	13 (8%)	5 (3%)	3	22
3	A	1104/1205 (92%)	1070 (97%)	32 (3%)	2 (0%)	43	77
3	H	1104/1205 (92%)	1070 (97%)	32 (3%)	2 (0%)	43	77
4	D	407/447 (91%)	391 (96%)	16 (4%)	0	100	100
4	I	407/447 (91%)	391 (96%)	16 (4%)	0	100	100
All	All	3524/4726 (75%)	3384 (96%)	126 (4%)	14 (0%)	31	67

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	44	ILE
2	B	46	PRO
2	B	50	PHE
2	G	44	ILE
2	G	46	PRO

5.3.2 Protein sidechains (i)

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

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)

2 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	$\#\|Z\| > 2$
5	GDP	I	501	-	29,30,30	1.65	5 (17%)	45,47,47	1.54	6 (13%)
5	GDP	D	501	-	29,30,30	1.65	5 (17%)	45,47,47	1.54	6 (13%)

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
5	GDP	I	501	-	-	7/16/32/32	0/3/3/3
5	GDP	D	501	-	-	7/16/32/32	0/3/3/3

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	501	GDP	PA-O3A	-4.52	1.54	1.59
5	D	501	GDP	PA-O3A	-4.45	1.54	1.59
5	D	501	GDP	PA-O5'	4.16	1.75	1.59
5	I	501	GDP	PA-O5'	4.16	1.75	1.59
5	I	501	GDP	C4-N3	2.48	1.39	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	501	GDP	O2A-PA-O3A	5.79	122.92	107.27
5	I	501	GDP	O2A-PA-O3A	5.79	122.91	107.27
5	D	501	GDP	O3A-PB-O1B	-2.95	95.51	111.04
5	I	501	GDP	O3A-PB-O1B	-2.95	95.53	111.04
5	D	501	GDP	O6-C6-N1	-2.34	115.70	120.11

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

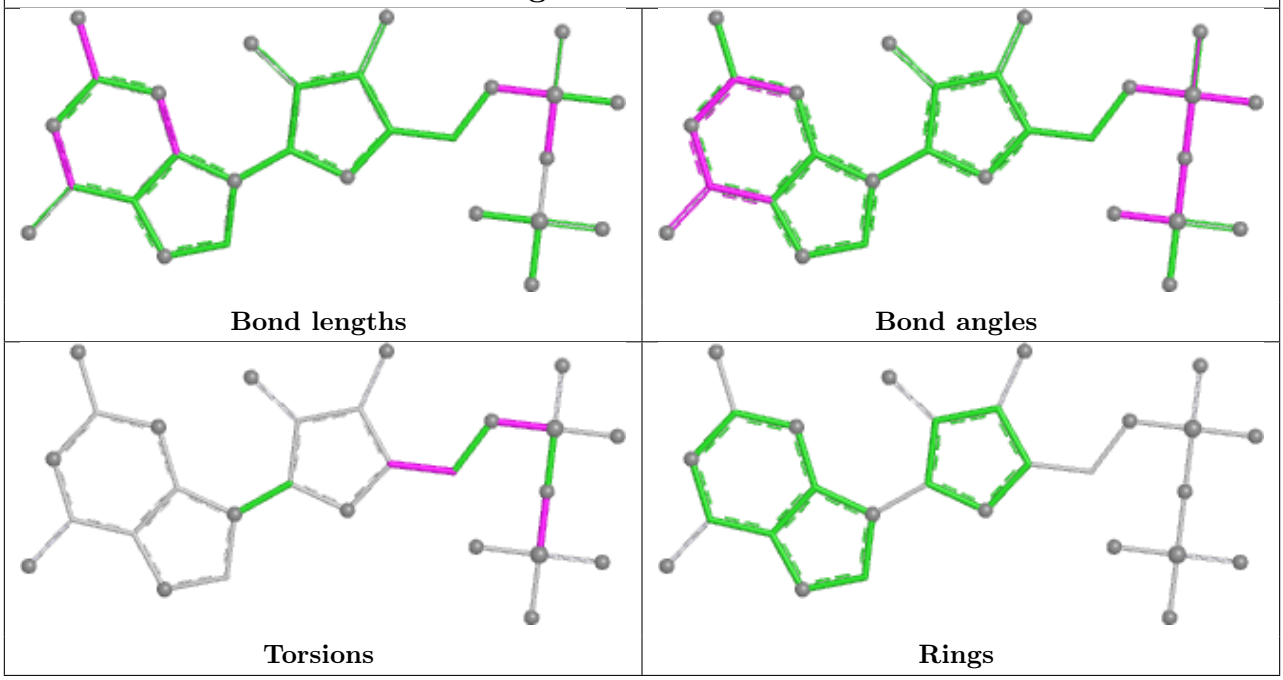
Mol	Chain	Res	Type	Atoms
5	D	501	GDP	PA-O3A-PB-O2B
5	D	501	GDP	C5'-O5'-PA-O3A
5	D	501	GDP	C5'-O5'-PA-O1A
5	I	501	GDP	PA-O3A-PB-O2B
5	I	501	GDP	C5'-O5'-PA-O3A

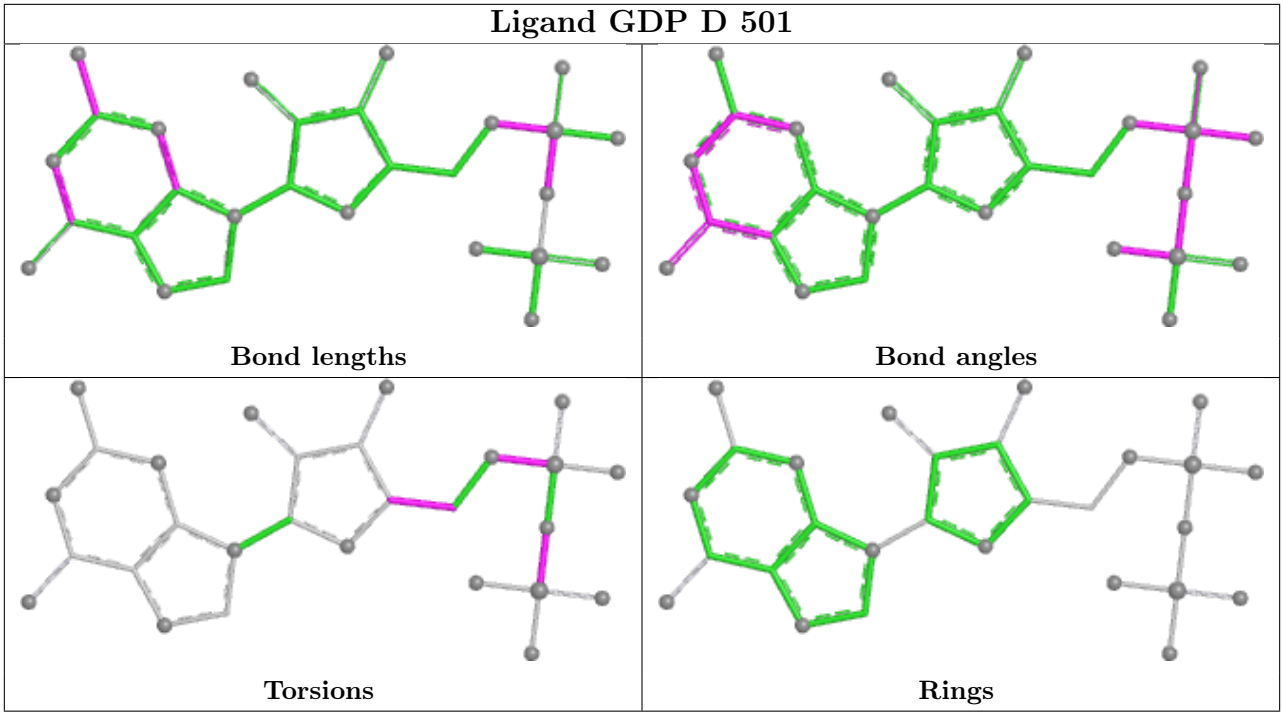
There are no ring outliers.

No monomer is involved in short contacts.

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 GDP I 501





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

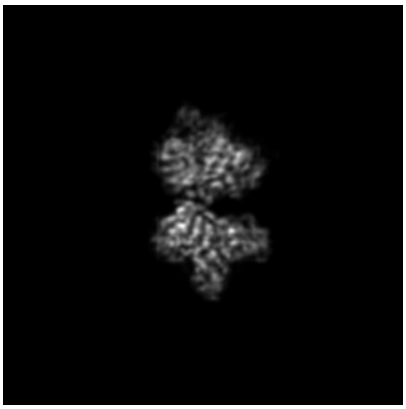
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-74462. These allow visual inspection of the internal detail of the map and identification of artifacts.

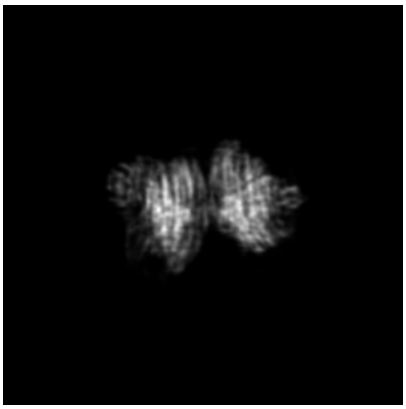
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

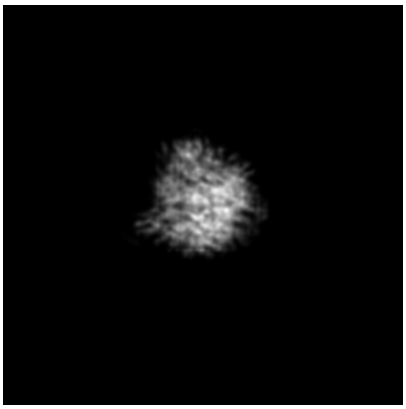
6.1.1 Primary map



X

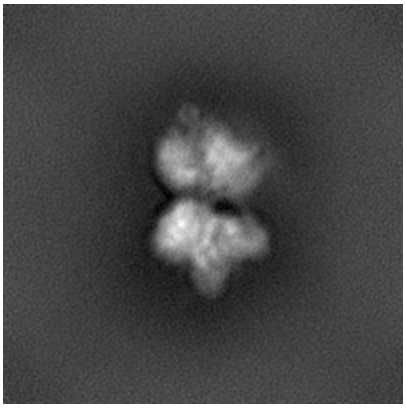


Y

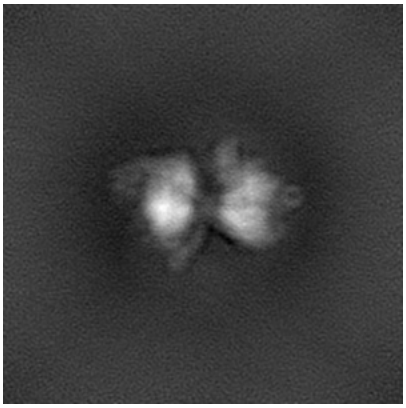


Z

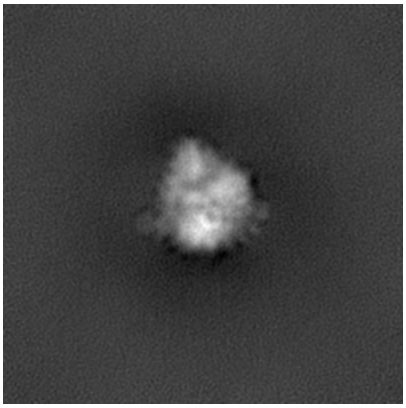
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

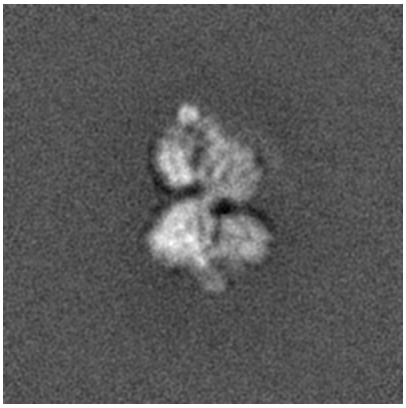
6.2.1 Primary map

X Index: 100

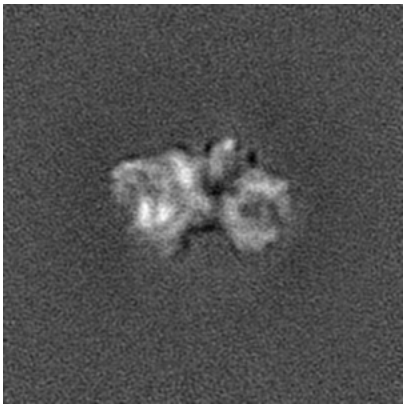
Y Index: 100

Z Index: 100

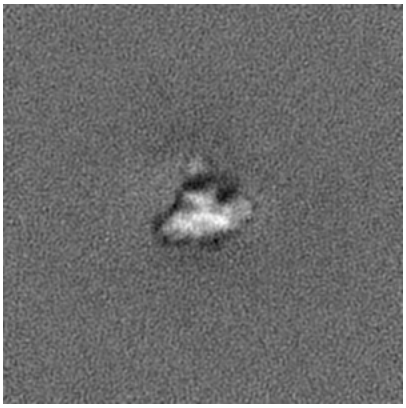
6.2.2 Raw map



X Index: 100



Y Index: 100



Z Index: 100

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

6.3 Largest variance slices (i)

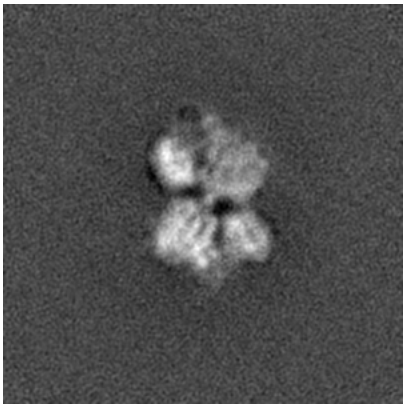
6.3.1 Primary map

X Index: 96

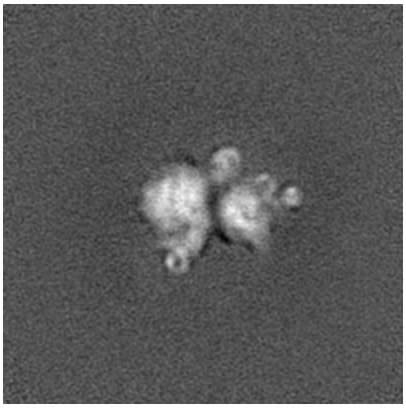
Y Index: 97

Z Index: 86

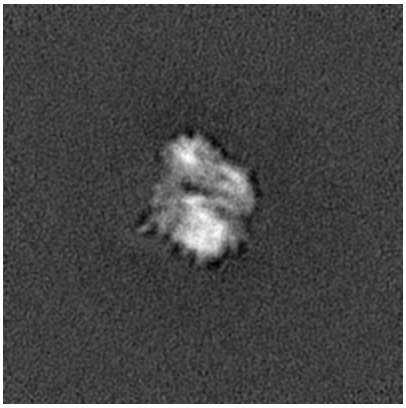
6.3.2 Raw map



X Index: 96



Y Index: 88

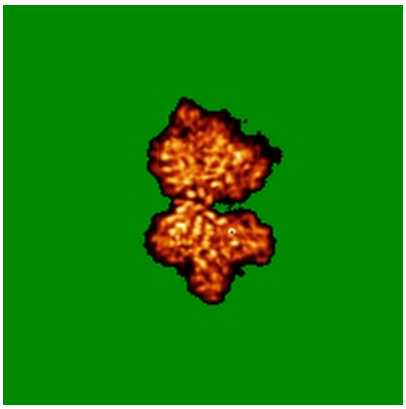


Z Index: 81

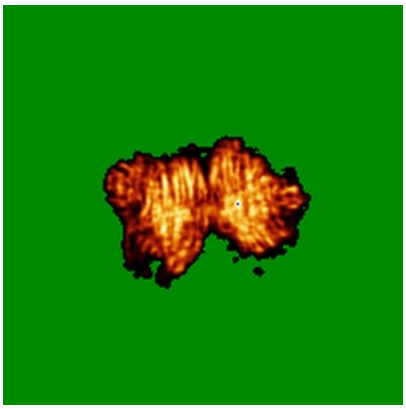
The images above show the largest variance slices of the map in three orthogonal directions.

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

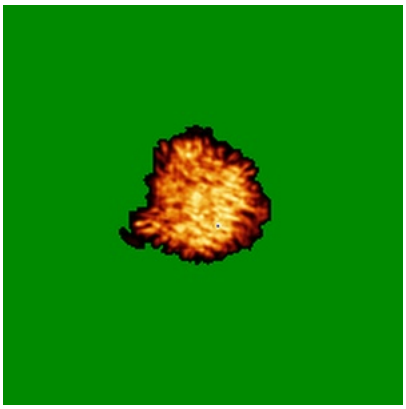
6.4.1 Primary map



X

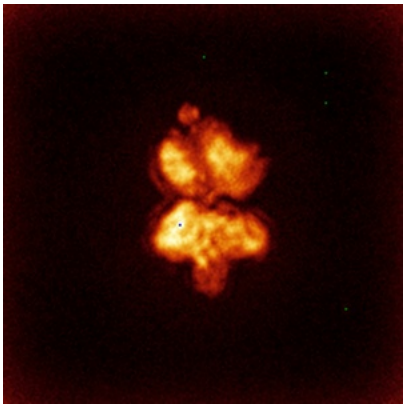


Y



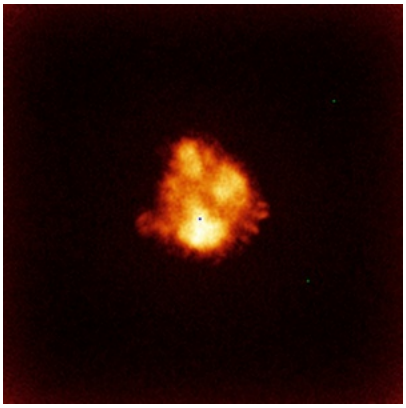
Z

6.4.2 Raw map



X

Y

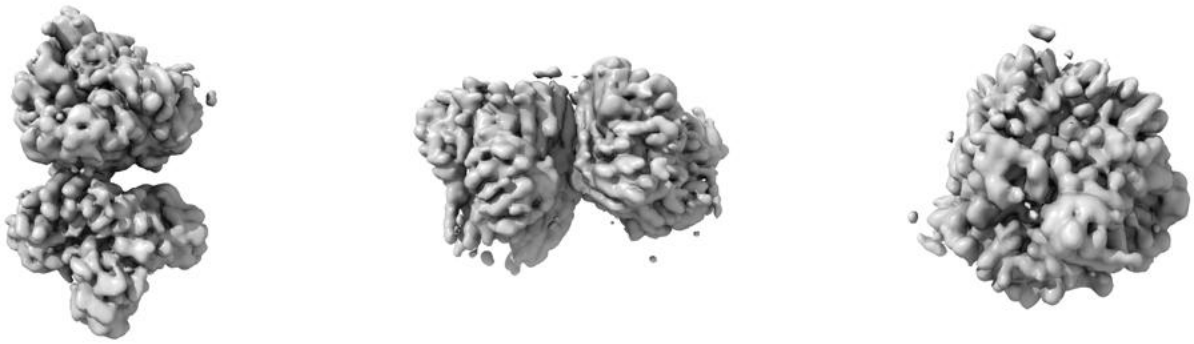


Z

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 0.0352. 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.

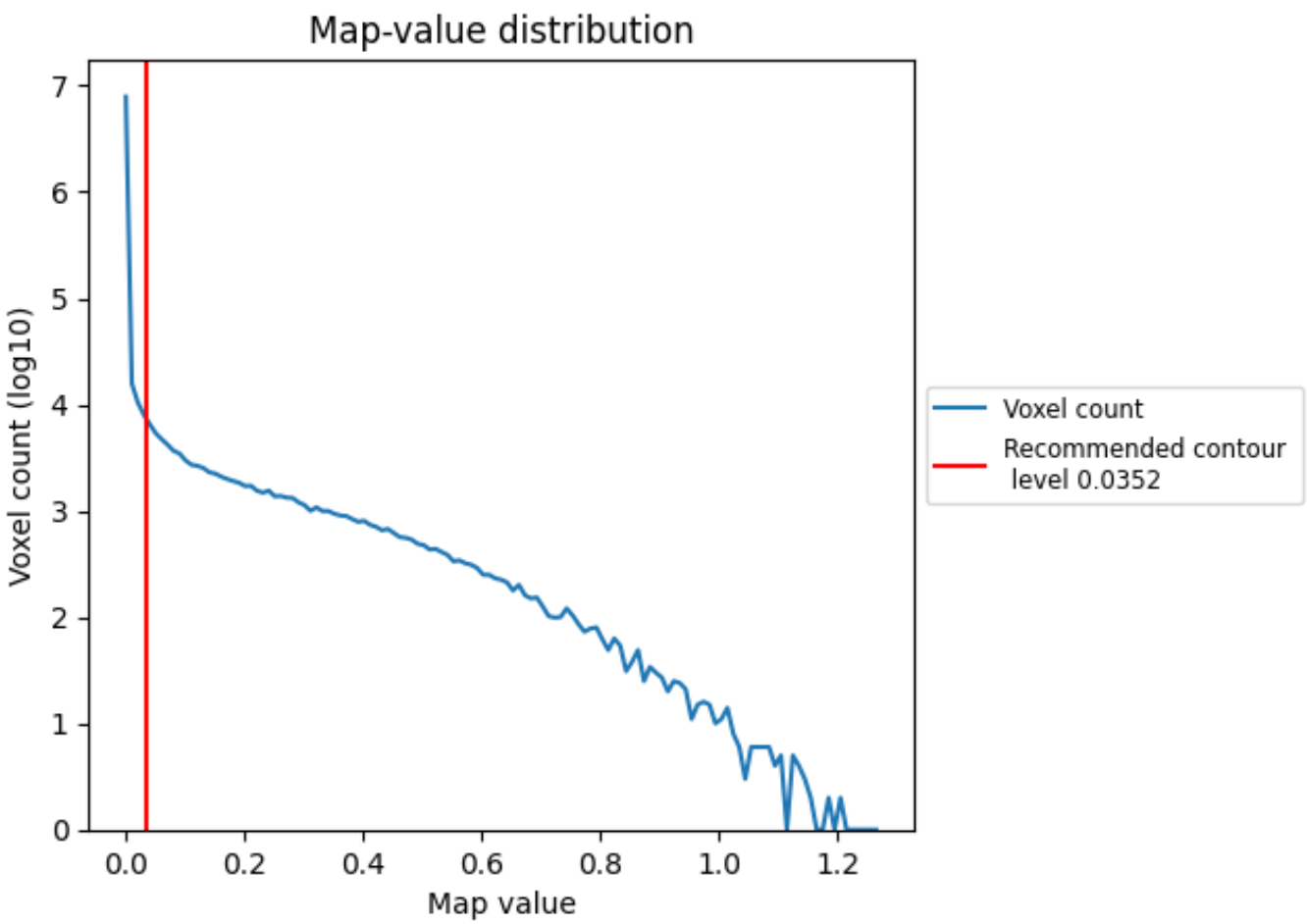
6.6 Mask visualisation (i)

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

7 Map analysis (i)

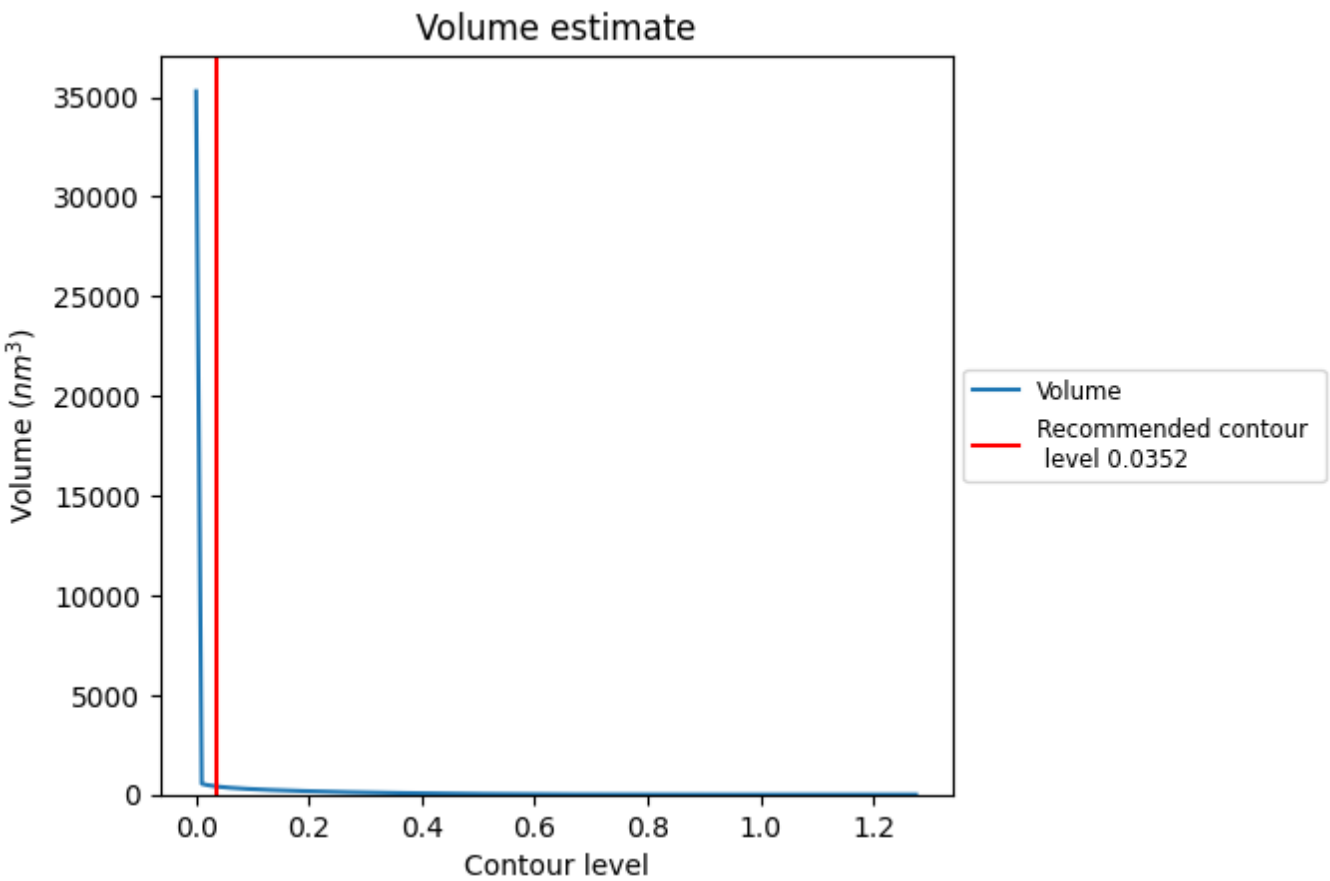
This section contains the results of statistical analysis of the map.

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.

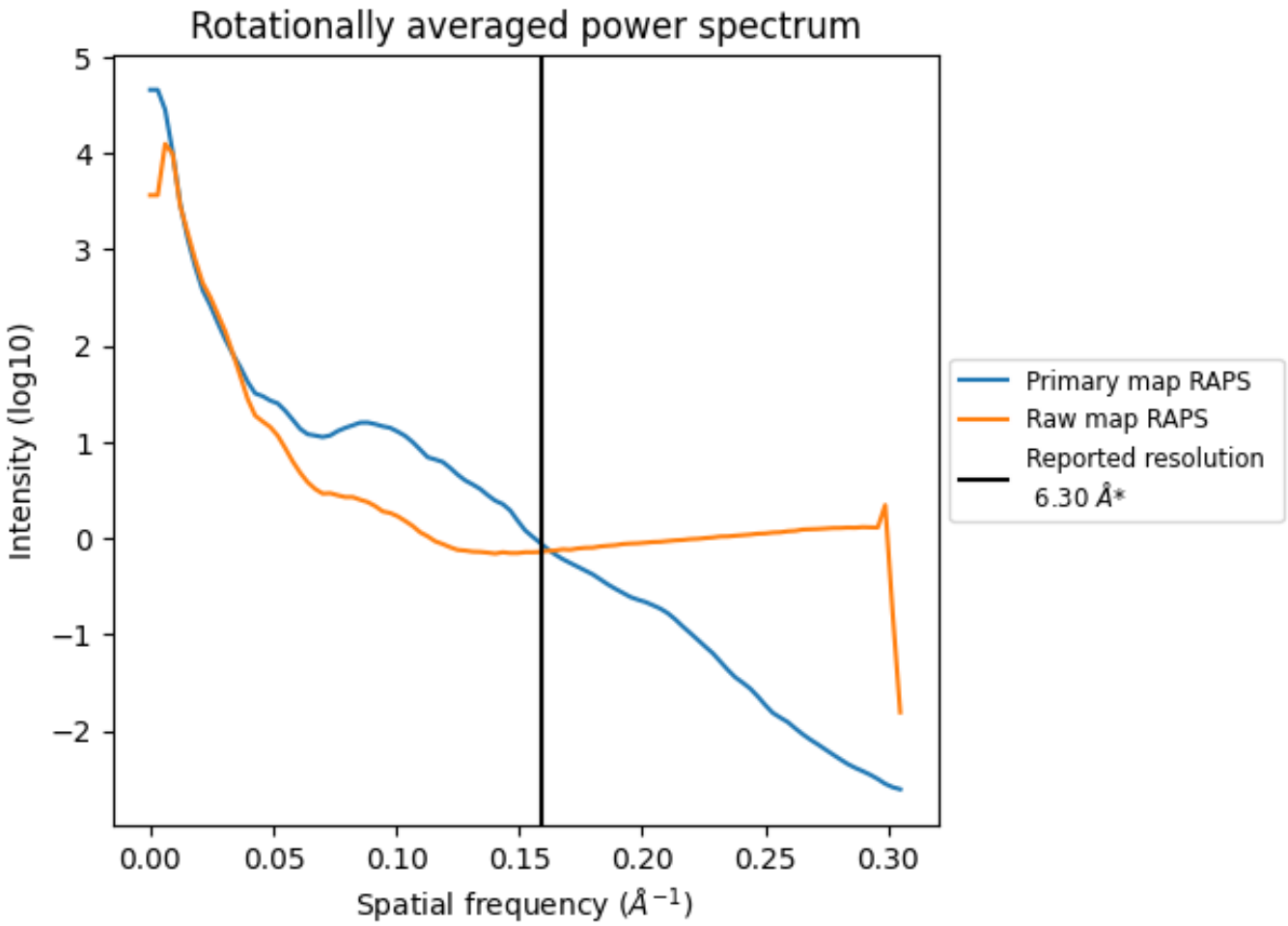
7.2 Volume estimate (i)



The volume at the recommended contour level is 410 nm^3; this corresponds to an approximate mass of 370 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)

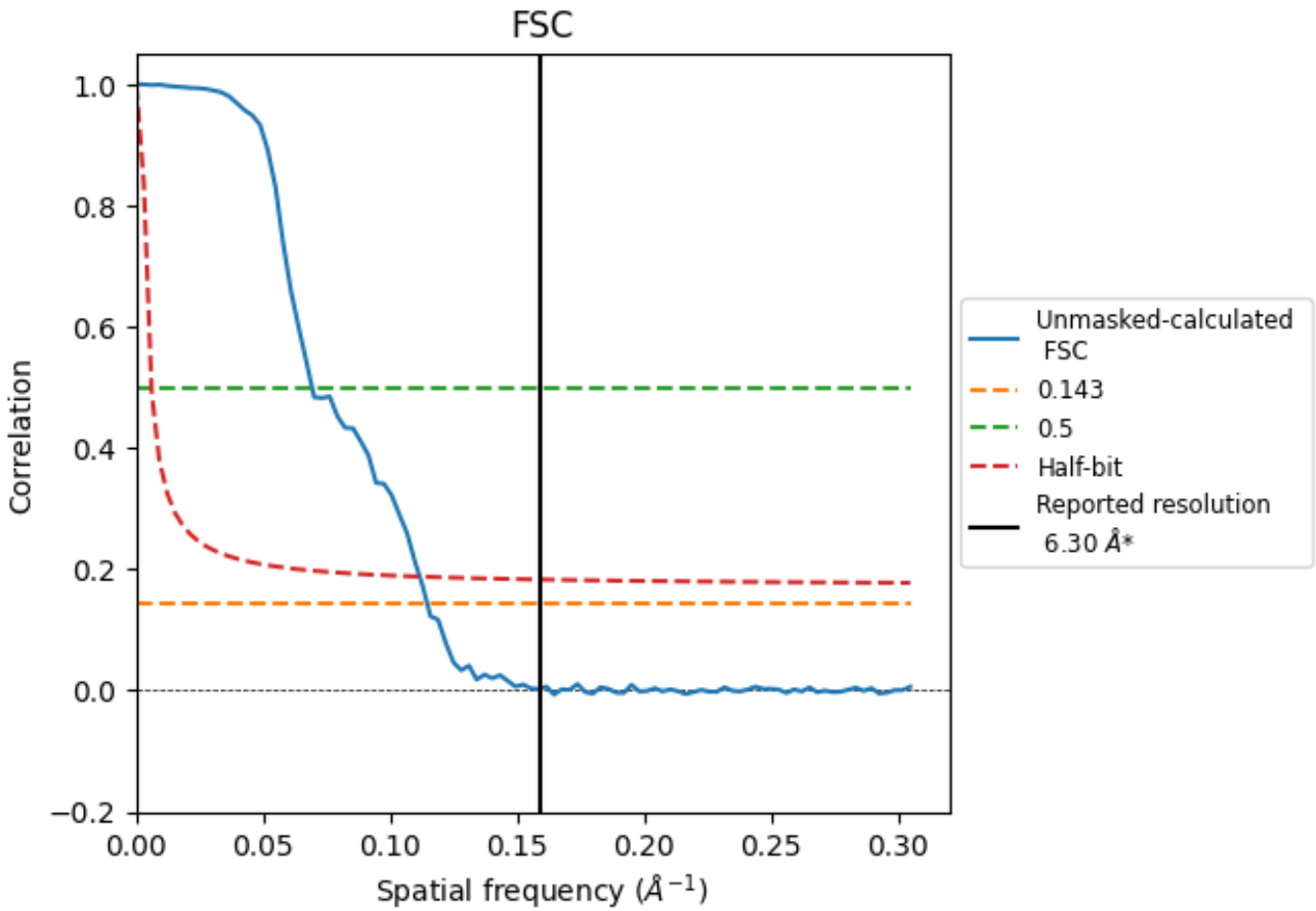


*Reported resolution corresponds to spatial frequency of 0.159 Å^{-1}

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 0.159 Å^{-1}

8.2 Resolution estimates (i)

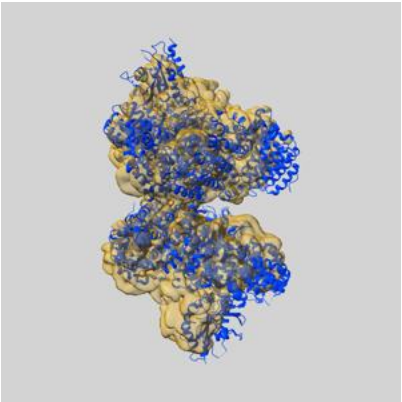
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.73	14.45	8.95

*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 8.73 differs from the reported value 6.3 by more than 10 %

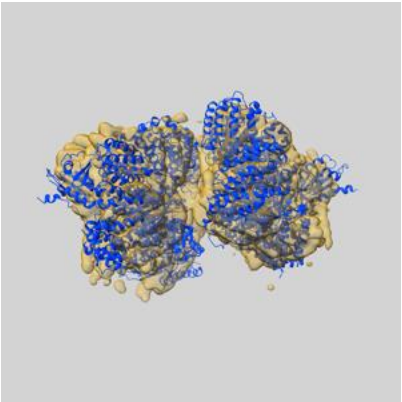
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-74462 and PDB model 9ZNZ. Per-residue inclusion information can be found in section 3 on page 6.

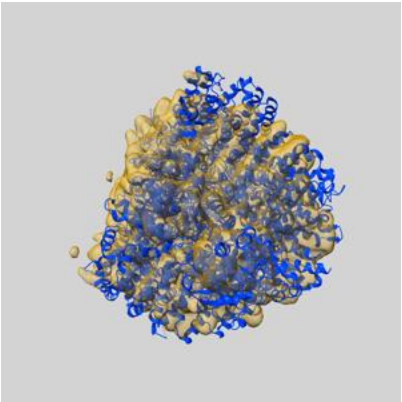
9.1 Map-model overlay (i)



X



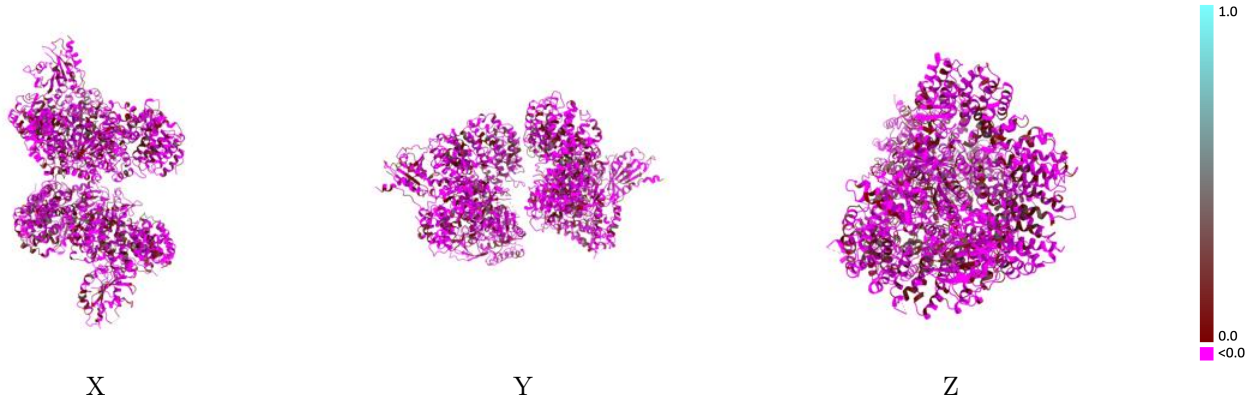
Y



Z

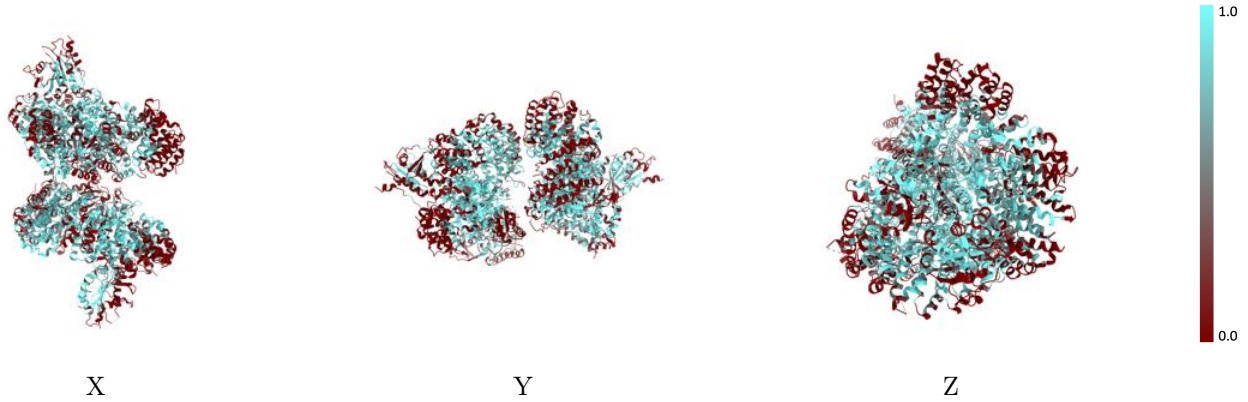
The images above show the 3D surface view of the map at the recommended contour level 0.0352 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



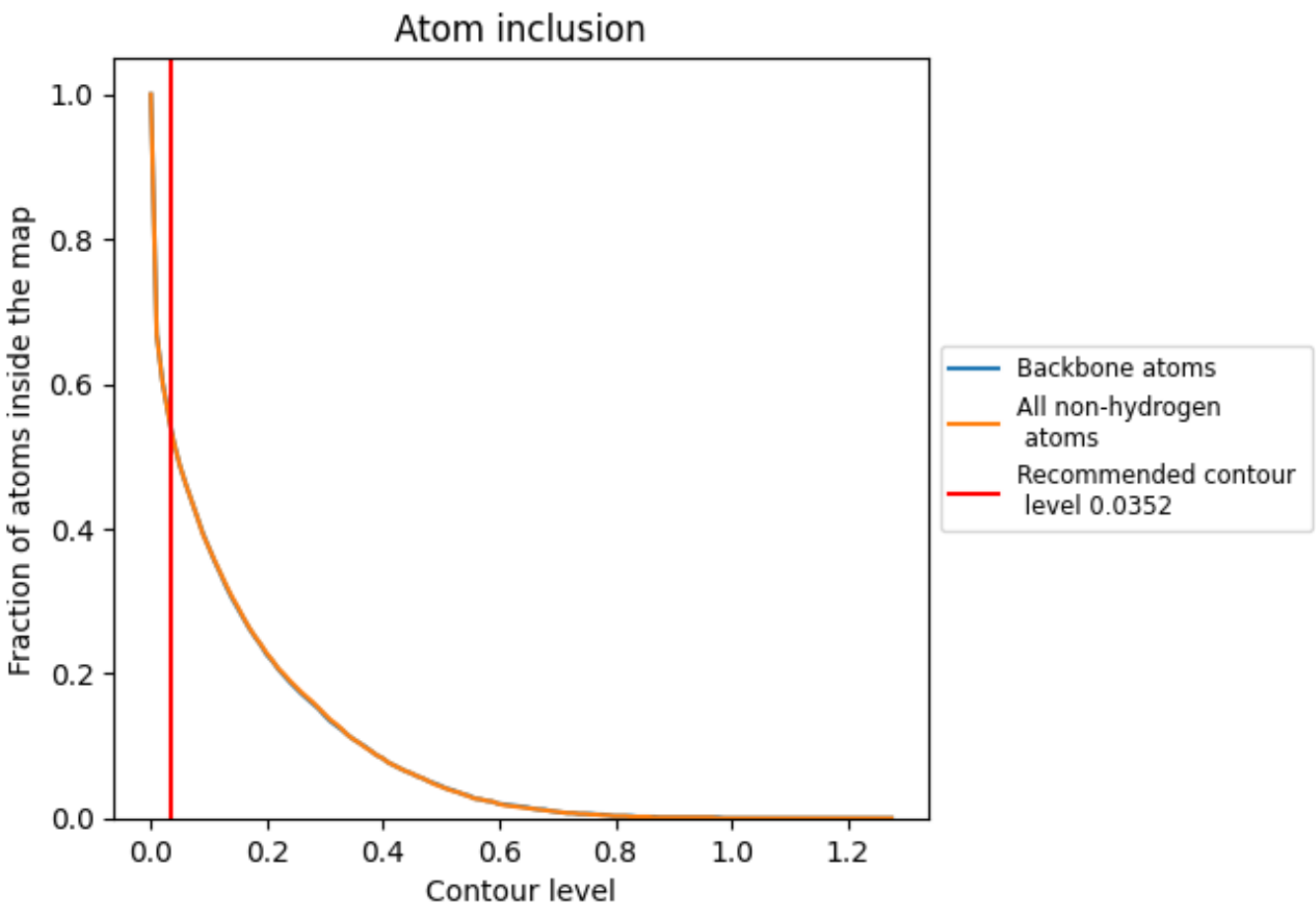
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0352).

9.4 Atom inclusion (i)



At the recommended contour level, 53% of all backbone atoms, 53% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0352) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5330	-0.0640
A	0.5000	-0.0630
B	0.4340	-0.0960
C	0.5400	-0.0680
D	0.6990	-0.0590
E	0.4040	-0.1110
G	0.4650	-0.0400
H	0.5210	-0.0590
I	0.5860	-0.0710