



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:18 PM UTC

PDB ID : 9C57 / pdb_00009c57
EMDB ID : EMD-45206
Title : Reconstituted P400 Subcomplex of the human TIP60 complex
Authors : Yang, Z.; Mameri, A.; Florez Ariza, A.J.; Cote, J.; Nogales, E.
Deposited on : 2024-06-05
Resolution : 2.75 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:

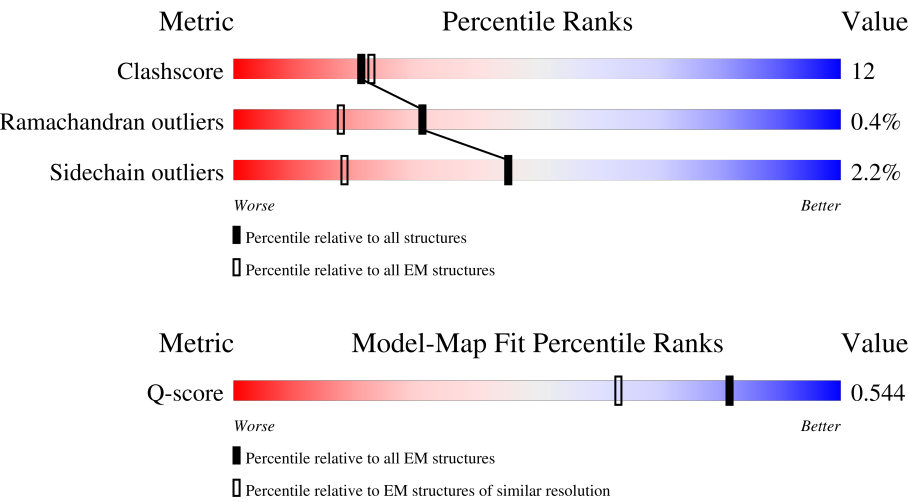
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.75 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.



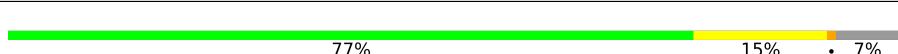
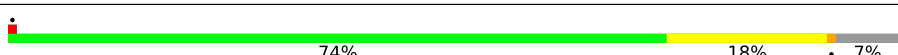
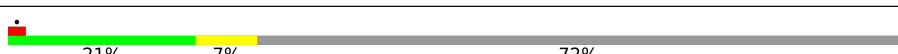
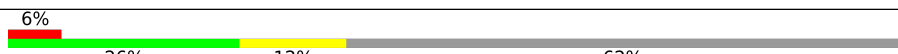
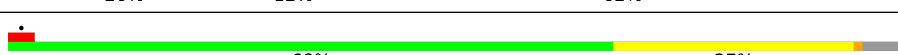
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10570 (2.25 - 3.25)

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	456	
1	C	456	
1	E	456	
2	H	836	

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Mol	Chain	Length	Quality of chain
3	L	429	
3	M	429	
4	B	463	
4	D	463	
4	F	463	
5	G	3159	
6	I	467	
7	J	375	
8	K	364	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	AGS	D	501	-	-	X	-
9	AGS	F	501	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 77055 atoms, of which 38687 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 RuvB-like 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	E	437	Total	C	H	N	O	S	0	0
			6781	2111	3433	575	645	17		
1	C	425	Total	C	H	N	O	S	0	0
			6659	2064	3386	562	631	16		
1	A	416	Total	C	H	N	O	S	0	0
			6522	2017	3323	553	613	16		

- Molecule 2 is a protein called Enhancer of polycomb homolog 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	H	48	Total	C	H	N	O	S	0	0
			774	240	387	80	65	2		

- Molecule 3 is a protein called Actin-like protein 6A.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	M	324	Total	C	H	N	O	S	0	0
			5021	1608	2487	431	474	21		
3	L	404	Total	C	H	N	O	S	0	0
			6246	1990	3096	536	600	24		

- Molecule 4 is a protein called RuvB-like 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	B	389	Total	C	H	N	O	S	0	0
			6140	1899	3109	528	590	14		
4	D	431	Total	C	H	N	O	S	0	0
			6699	2082	3374	581	647	15		
4	F	431	Total	C	H	N	O	S	0	0
			6736	2085	3402	582	651	16		

- Molecule 5 is a protein called E1A-binding protein p400.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	G	878	Total	C	H	N	O	S	0	0
			14464	4555	7287	1291	1296	35		

- Molecule 6 is a protein called DNA methyltransferase 1-associated protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	I	179	Total	C	H	N	O	S	0	0
			3012	972	1484	280	273	3		

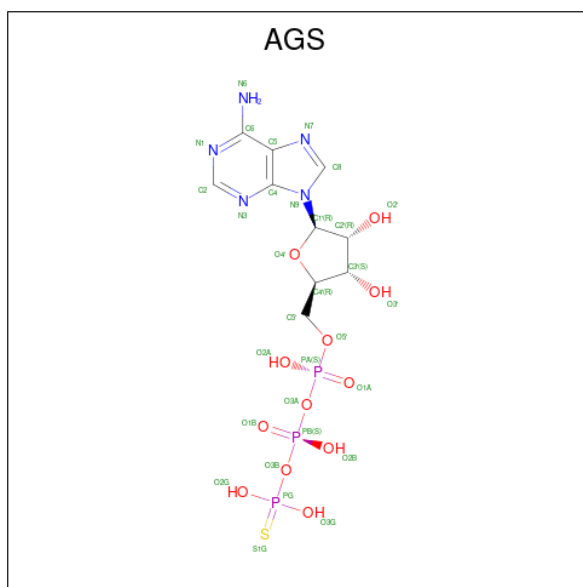
- Molecule 7 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	J	360	Total	C	H	N	O	S	0	0
			5602	1785	2788	471	538	20		

- Molecule 8 is a protein called Vacuolar protein sorting-associated protein 72 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	K	123	Total	C	H	N	O	S	0	0
			2055	651	1035	183	183	3		

- Molecule 9 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S) (labeled as "Ligand of Interest" by depositor).



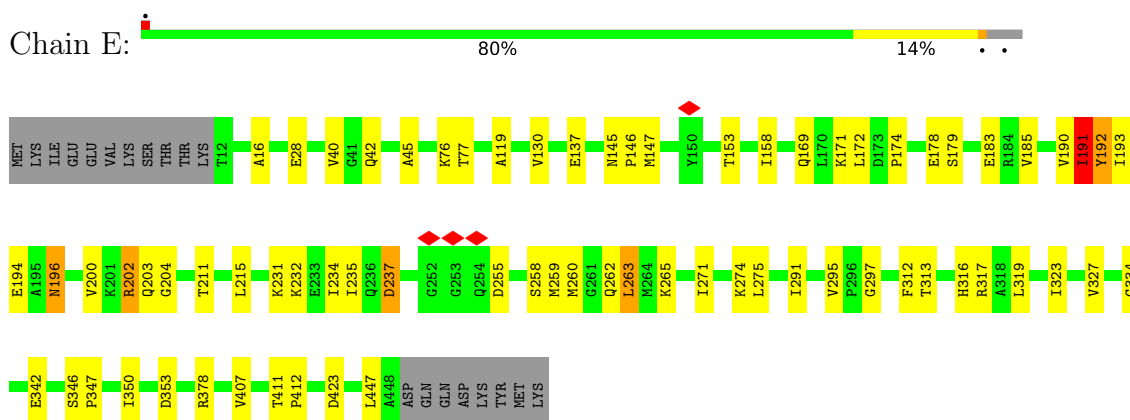
Mol	Chain	Residues	Atoms							AltConf
9	E	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	

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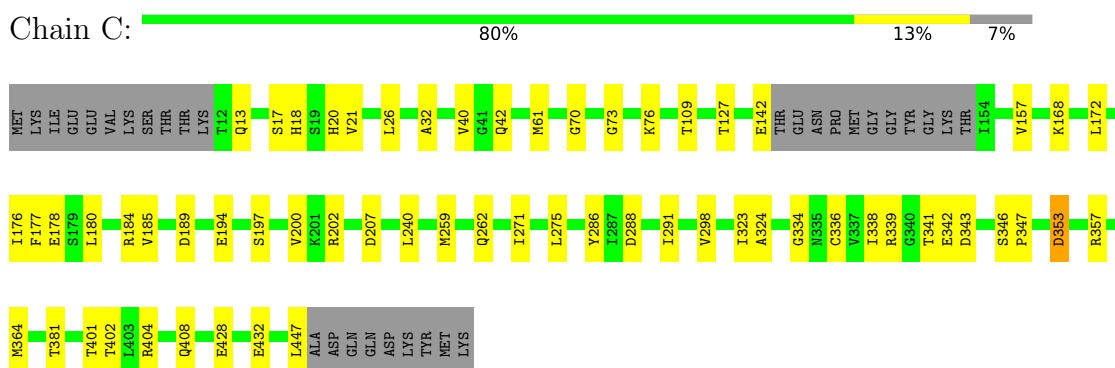
3 Residue-property plots

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.

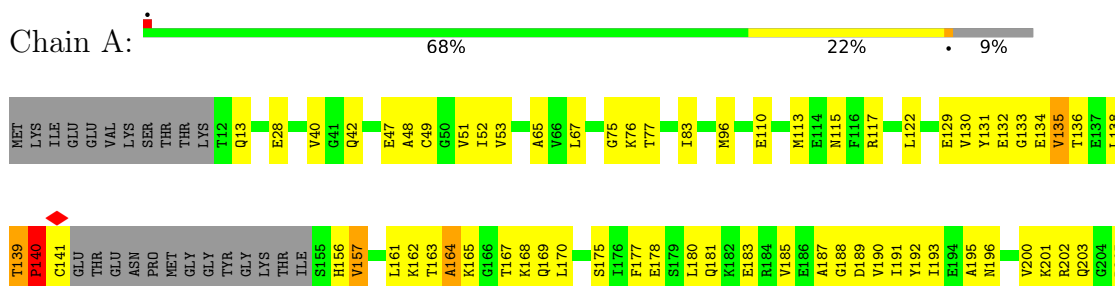
• Molecule 1: RuvB-like 1

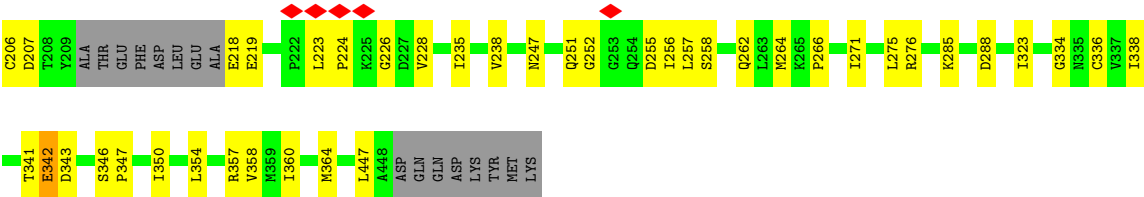


• Molecule 1: RuvB-like 1

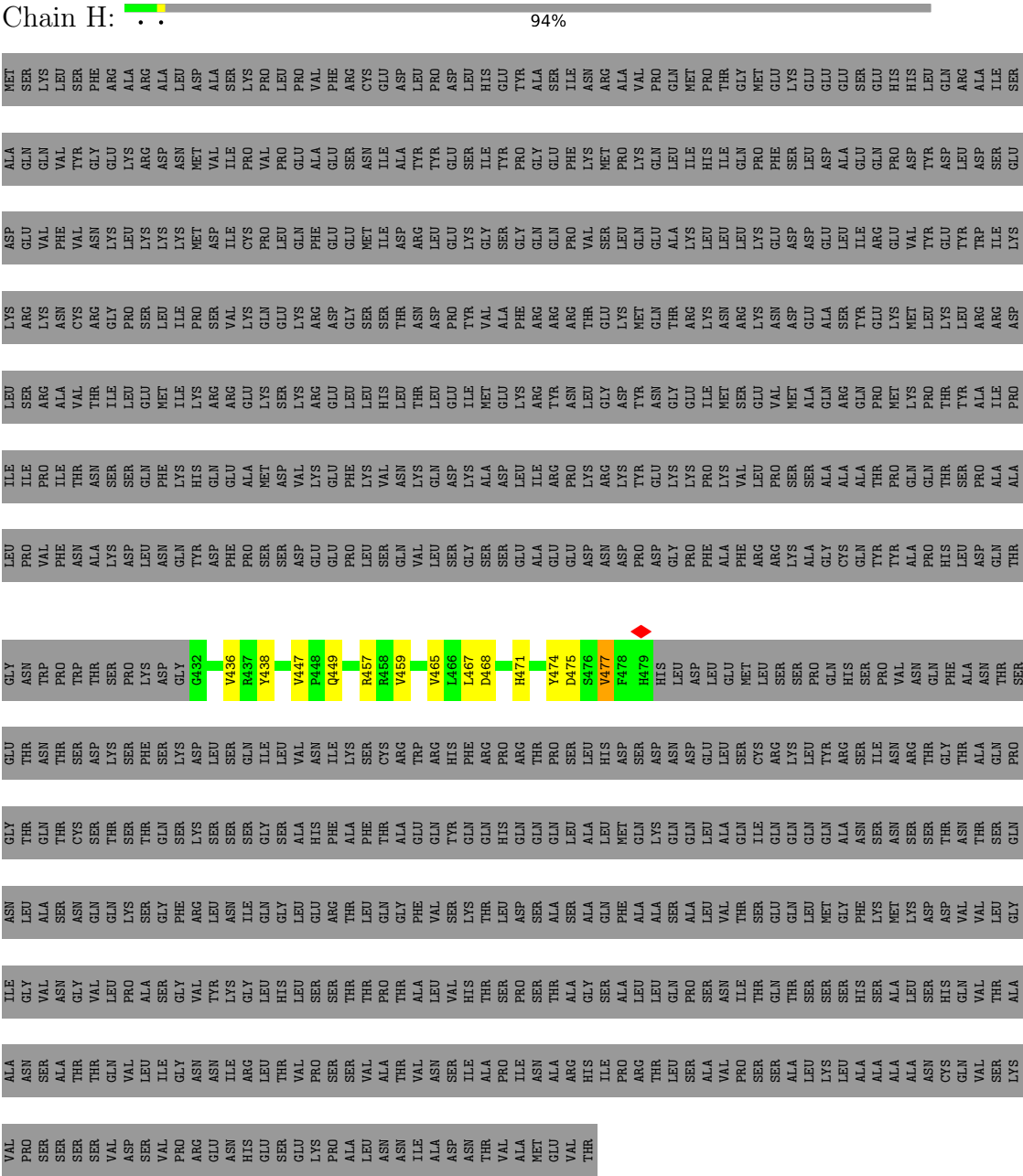


• Molecule 1: RuvB-like 1



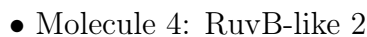
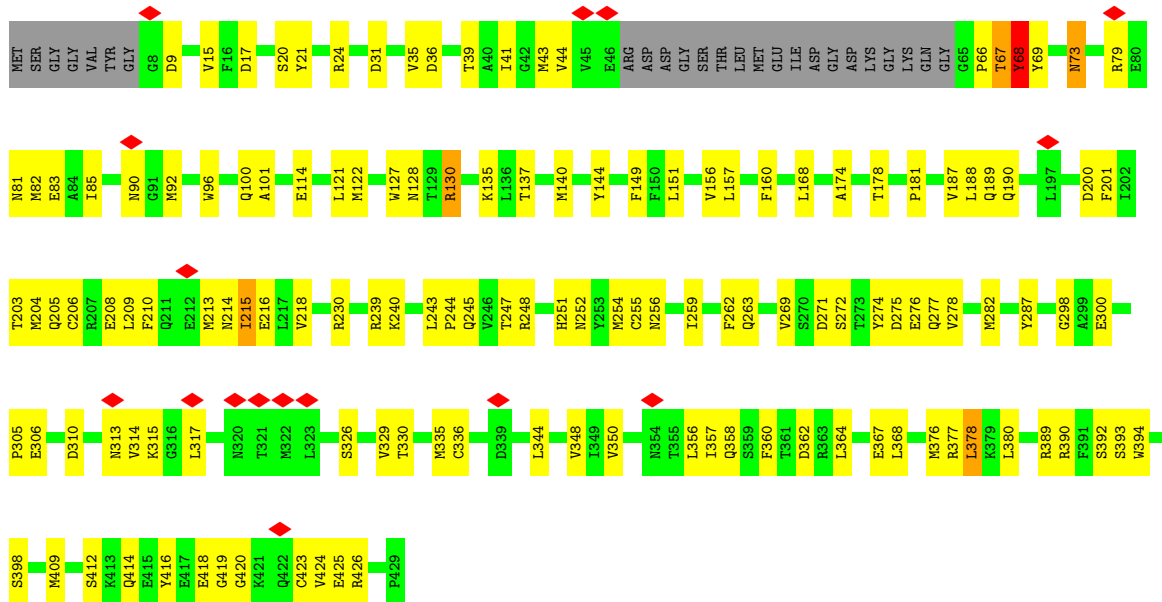
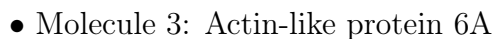


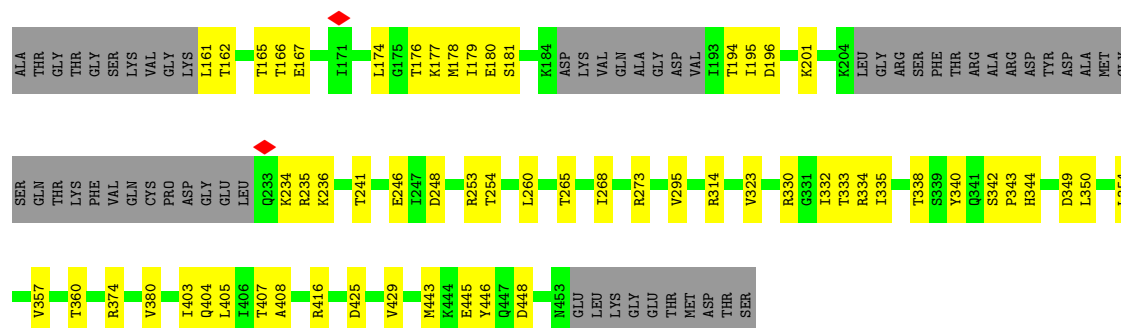
● Molecule 2: Enhancer of polycomb homolog 1



● Molecule 3: Actin-like protein 6A

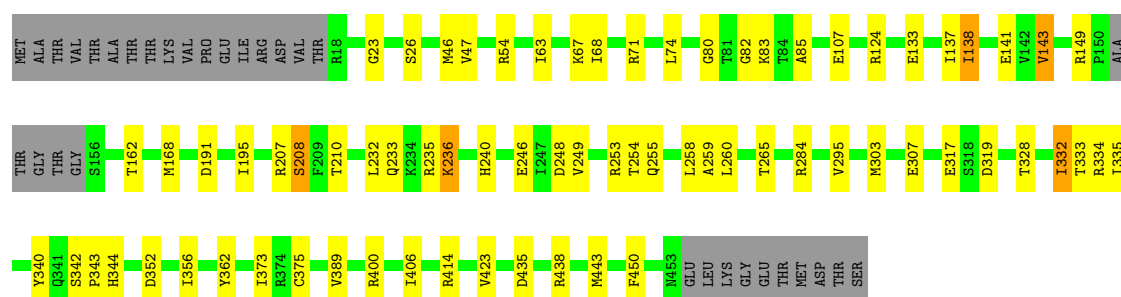






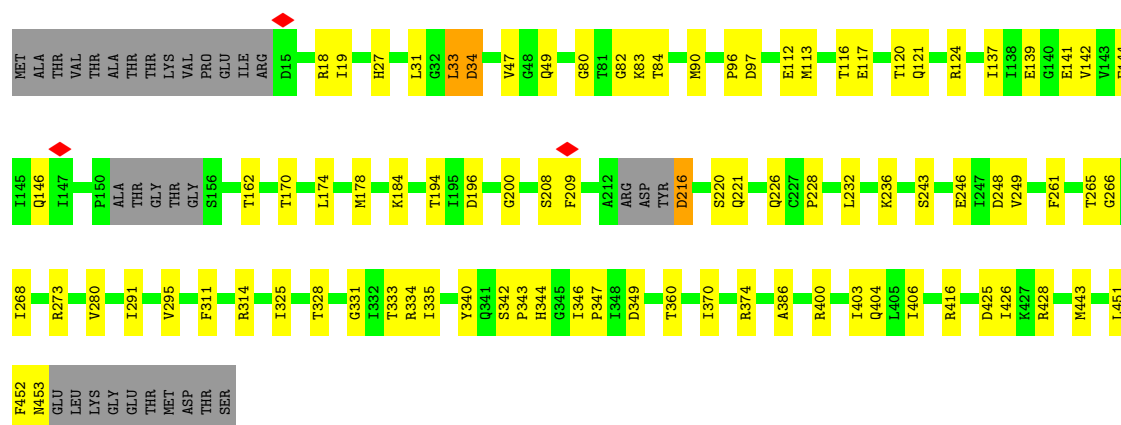
• Molecule 4: RuvB-like 2

Chain D: 77% 15% 7%



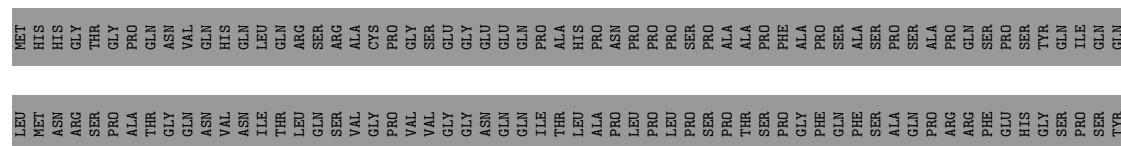
• Molecule 4: RuvB-like 2

Chain F: 74% 18% 7%



• Molecule 5: E1A-binding protein p400

Chain G: 21% 7% 72%







[illegible]

- Molecule 6: DNA methyltransferase 1-associated protein 1

[illegible]

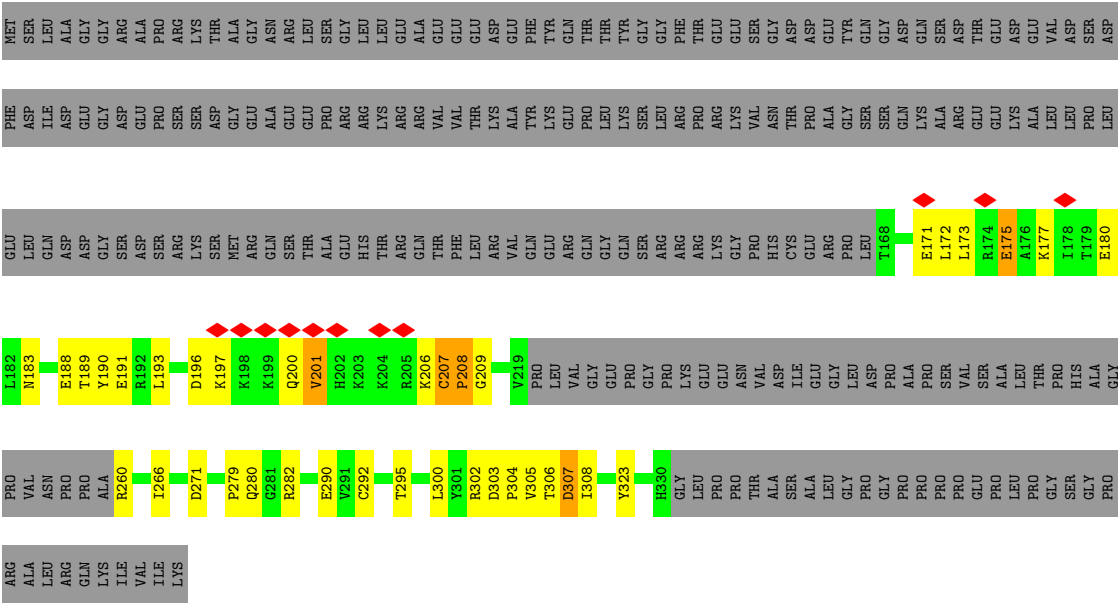
- Molecule 7: Actin, cytoplasmic 1



NET	ASP	ASP	ASP	I5		D11	M12	G13	S14	M15	M16		F31		I34	V35	G36	R37	F38	R39	HIS	GLN	GLY	VAL	VAL	VAL	GLY	NET	NET	NET	GLY	GLN	GLN	LYS	D51	V54	G55	D56		Q59	S60	K61	R62	G63	G64	L65	T66	L67	K68		I71		N78		D81	M82		H88	T89		V93
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● Molecule 8: Vacuolar protein sorting-associated protein 72 homolog



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	166442	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	21.007	Depositor
Minimum map value	-0.821	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.569	Depositor
Recommended contour level	2.4	Depositor
Map size ($\text{\AA}$)	377.0, 377.0, 377.0	wwPDB
Map dimensions	377, 377, 377	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0, 1.0, 1.0	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: ATP, AGS

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	0.25	1/3239 (0.0%)	0.47	5/4363 (0.1%)
1	C	0.18	0/3315	0.31	0/4468
1	E	0.68	7/3393 (0.2%)	0.55	9/4575 (0.2%)
2	H	0.19	0/394	0.36	0/529
3	L	0.18	0/3221	0.45	1/4367 (0.0%)
3	M	0.14	0/2590	0.37	0/3504
4	B	0.17	0/3063	0.31	0/4121
4	D	0.18	0/3364	0.34	0/4531
4	F	0.17	0/3371	0.33	0/4538
5	G	0.18	0/7314	0.40	2/9868 (0.0%)
6	I	0.18	0/1570	0.46	0/2114
7	J	0.18	0/2875	0.39	0/3894
8	K	0.20	0/1045	0.46	0/1414
All	All	0.27	8/38754 (0.0%)	0.40	17/52286 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	E	0	1
3	L	0	1
All	All	0	3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	191	ILE	C-O	-23.57	1.00	1.24
1	E	204	GLY	C-O	-21.40	0.95	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	204	GLY	CA-C	-9.67	1.39	1.52
1	E	191	ILE	C-N	-9.10	1.21	1.33
1	A	140	PRO	CG-CD	-6.98	1.27	1.50

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	204	GLY	CA-C-O	-12.14	112.53	120.91
1	A	140	PRO	N-CD-CG	-11.58	85.83	103.20
1	A	140	PRO	CA-CB-CG	-11.01	83.58	104.50
1	E	192	TYR	CA-C-O	10.88	131.78	120.24
1	A	140	PRO	N-CA-CB	-9.15	93.64	103.25

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	139	THR	Peptide
1	E	202	ARG	Sidechain
3	L	67	THR	Peptide

5.2 Too-close contacts ⓘ

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	3199	3323	3317	97	0
1	C	3273	3386	3383	49	0
1	E	3348	3433	3449	62	0
2	H	387	387	386	13	0
3	L	3150	3096	3089	126	0
3	M	2534	2487	2482	82	0
4	B	3031	3109	3103	57	0
4	D	3325	3374	3370	66	0
4	F	3334	3402	3394	74	0
5	G	7177	7287	7306	209	0
6	I	1528	1484	1481	61	0
7	J	2814	2788	2785	88	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	K	1020	1035	1033	46	0
9	A	31	12	12	5	0
9	B	31	12	12	3	0
9	C	31	12	12	7	0
9	D	31	12	12	11	0
9	E	31	12	12	3	0
9	F	31	12	12	12	0
9	G	31	12	12	4	0
10	L	31	12	12	2	0
All	All	38368	38687	38674	917	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 12.

The worst 5 of 917 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:M:337:ASP:OD1	3:M:338:ILE:N	2.02	0.90
5:G:1984:GLU:OE1	5:G:1984:GLU:N	2.05	0.90
1:C:76:LYS:NZ	9:C:501:AGS:S1G	2.43	0.90
5:G:800:PRO:O	6:I:226:ARG:NH2	2.05	0.89
3:L:114:GLU:N	3:L:114:GLU:OE1	2.05	0.89

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	410/456 (90%)	386 (94%)	21 (5%)	3 (1%)	18	34
1	C	421/456 (92%)	407 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	435/456 (95%)	412 (95%)	22 (5%)	1 (0%)	43	64
2	H	46/836 (6%)	44 (96%)	2 (4%)	0	100	100
3	L	400/429 (93%)	384 (96%)	15 (4%)	1 (0%)	36	56
3	M	314/429 (73%)	297 (95%)	16 (5%)	1 (0%)	36	56
4	B	381/463 (82%)	364 (96%)	16 (4%)	1 (0%)	36	56
4	D	427/463 (92%)	402 (94%)	24 (6%)	1 (0%)	43	64
4	F	425/463 (92%)	407 (96%)	18 (4%)	0	100	100
5	G	862/3159 (27%)	807 (94%)	50 (6%)	5 (1%)	21	38
6	I	175/467 (38%)	161 (92%)	14 (8%)	0	100	100
7	J	356/375 (95%)	334 (94%)	22 (6%)	0	100	100
8	K	119/364 (33%)	99 (83%)	15 (13%)	5 (4%)	2	3
All	All	4771/8816 (54%)	4504 (94%)	249 (5%)	18 (0%)	31	50

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	G	2014	LYS
8	K	201	VAL
8	K	207	CYS
8	K	208	PRO
8	K	280	GLN

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	352/387 (91%)	344 (98%)	8 (2%)	44	66
1	C	360/387 (93%)	353 (98%)	7 (2%)	50	70
1	E	365/387 (94%)	352 (96%)	13 (4%)	31	55
2	H	40/738 (5%)	37 (92%)	3 (8%)	12	24
3	L	346/364 (95%)	335 (97%)	11 (3%)	34	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	M	278/364 (76%)	275 (99%)	3 (1%)	65	79
4	B	330/390 (85%)	323 (98%)	7 (2%)	47	67
4	D	356/390 (91%)	350 (98%)	6 (2%)	53	71
4	F	361/390 (93%)	354 (98%)	7 (2%)	50	70
5	G	779/2663 (29%)	763 (98%)	16 (2%)	47	67
6	I	159/400 (40%)	156 (98%)	3 (2%)	50	70
7	J	306/318 (96%)	301 (98%)	5 (2%)	55	73
8	K	112/312 (36%)	108 (96%)	4 (4%)	31	55
All	All	4144/7490 (55%)	4051 (98%)	93 (2%)	45	67

5 of 93 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	G	1968	CYS
8	K	193	LEU
5	G	2169	TYR
7	J	14	SER
3	L	68	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	143	HIS
3	L	236	ASN
4	D	404	GLN
4	D	369	GLN
3	L	414	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

8 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
9	AGS	C	501	-	32,33,33	0.76	3 (9%)	45,52,52	1.12	3 (6%)
9	AGS	F	501	-	32,33,33	0.54	1 (3%)	45,52,52	0.72	1 (2%)
10	ATP	L	501	-	32,33,33	0.34	0	48,52,52	0.72	1 (2%)
9	AGS	B	501	-	32,33,33	0.51	1 (3%)	45,52,52	0.60	1 (2%)
9	AGS	D	501	-	32,33,33	0.69	2 (6%)	45,52,52	0.76	1 (2%)
9	AGS	E	501	-	32,33,33	0.61	1 (3%)	45,52,52	0.71	1 (2%)
9	AGS	A	501	-	32,33,33	0.71	1 (3%)	45,52,52	0.78	1 (2%)
9	AGS	G	3201	-	32,33,33	0.46	1 (3%)	45,52,52	0.71	1 (2%)

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
9	AGS	C	501	-	-	4/21/38/38	0/3/3/3
9	AGS	F	501	-	-	6/21/38/38	0/3/3/3
10	ATP	L	501	-	-	9/22/38/38	0/3/3/3
9	AGS	B	501	-	-	4/21/38/38	0/3/3/3
9	AGS	D	501	-	-	11/21/38/38	0/3/3/3
9	AGS	E	501	-	-	4/21/38/38	0/3/3/3
9	AGS	A	501	-	-	5/21/38/38	0/3/3/3
9	AGS	G	3201	-	-	11/21/38/38	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)
9	C	501	AGS	PA-O3A	-2.33	1.57	1.59
9	E	501	AGS	PG-S1G	2.16	1.95	1.90
9	A	501	AGS	PG-S1G	2.15	1.95	1.90
9	B	501	AGS	PG-S1G	2.15	1.95	1.90
9	C	501	AGS	PB-O3A	-2.13	1.57	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	501	AGS	PB-O3B-PG	-4.59	116.36	133.17
9	C	501	AGS	PB-O3B-PG	-4.19	117.83	133.17
9	E	501	AGS	PB-O3B-PG	-4.10	118.15	133.17
9	C	501	AGS	C2'-C1'-N9	4.04	123.35	113.30
9	F	501	AGS	PB-O3B-PG	-3.92	118.84	133.17

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	E	501	AGS	PB-O3B-PG-O3G
9	B	501	AGS	PB-O3B-PG-O3G
9	C	501	AGS	PB-O3B-PG-O3G
9	D	501	AGS	PB-O3B-PG-O2G
9	D	501	AGS	PB-O3B-PG-O3G

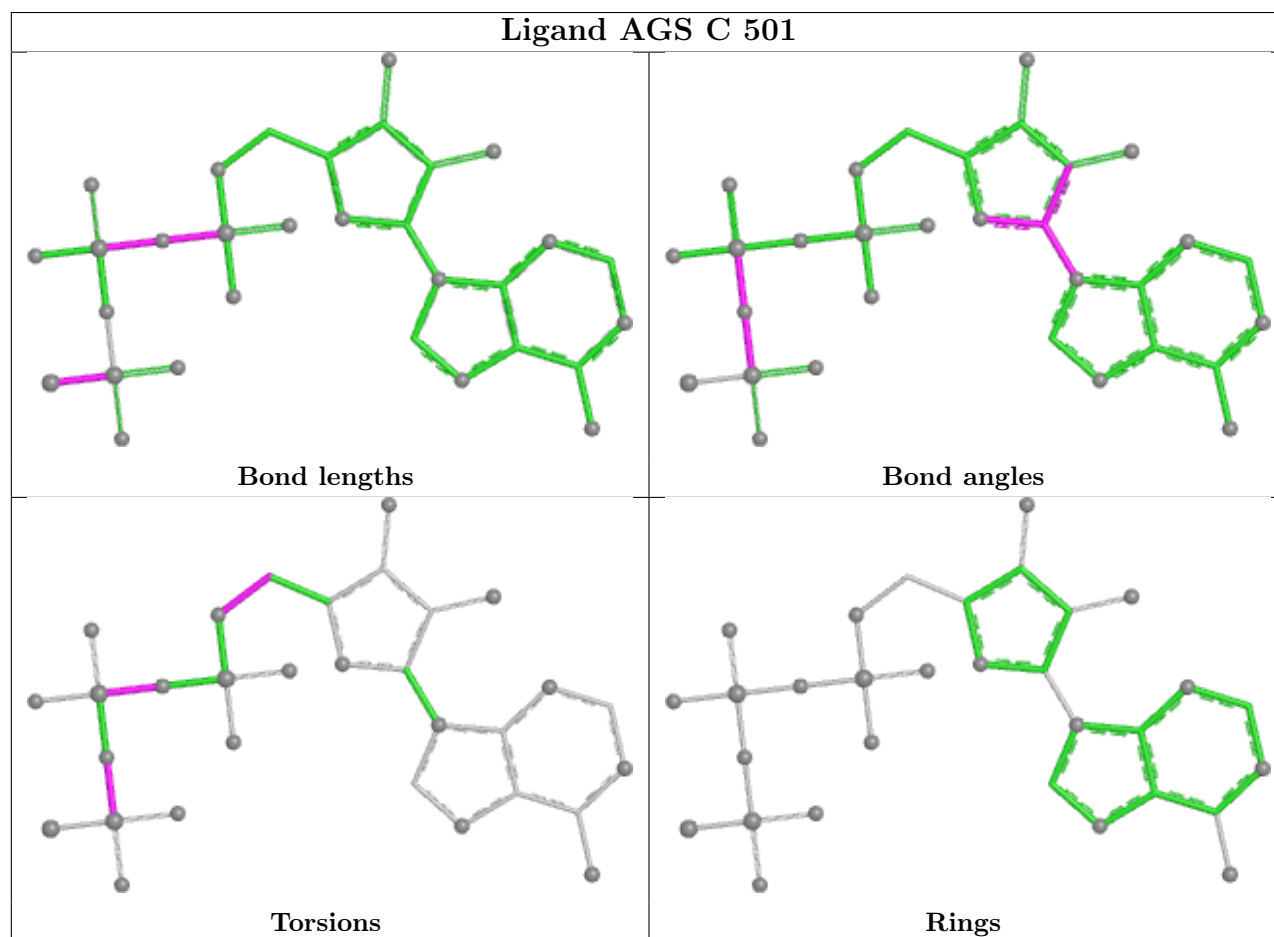
There are no ring outliers.

8 monomers are involved in 47 short contacts:

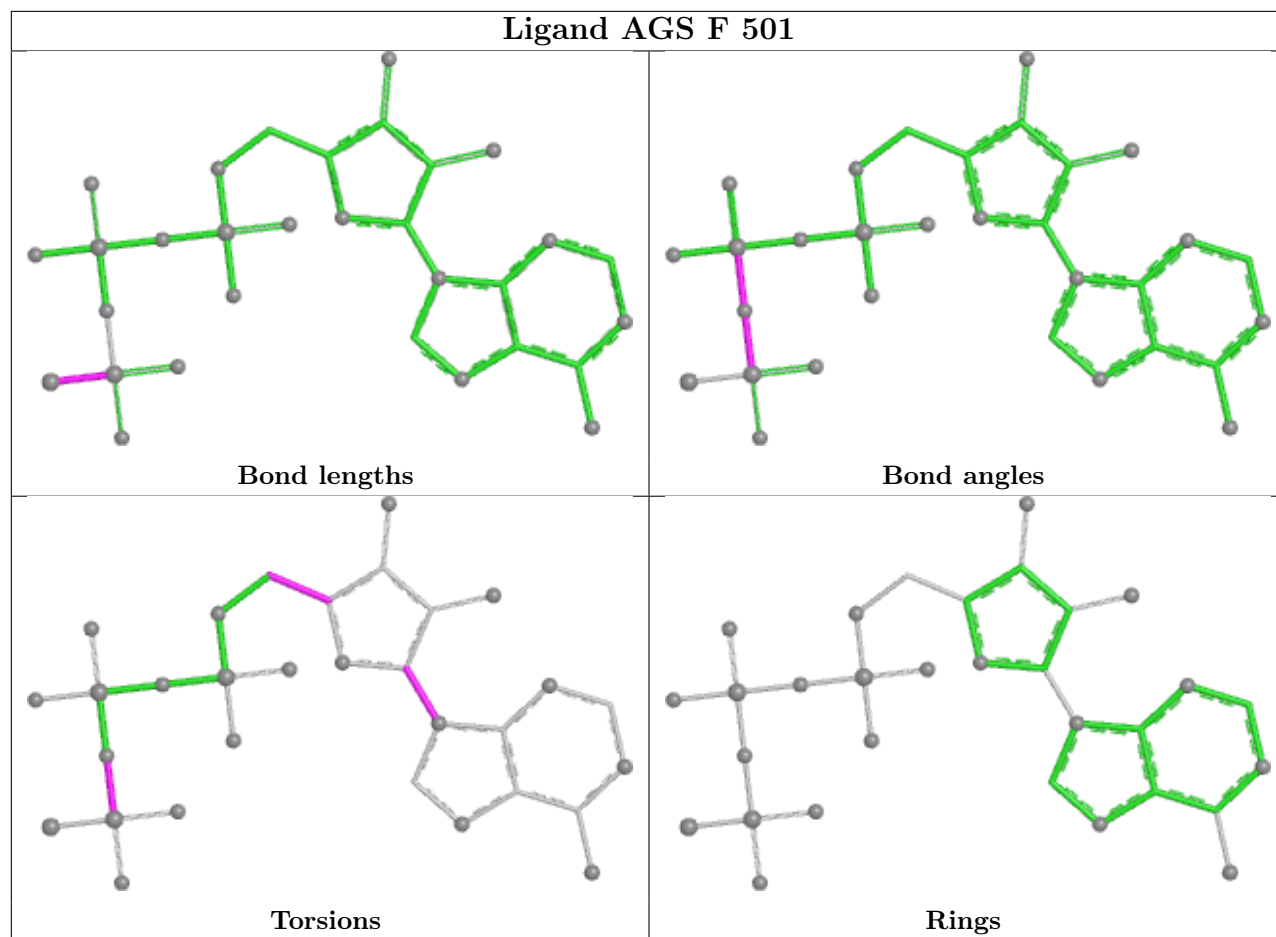
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	C	501	AGS	7	0
9	F	501	AGS	12	0
10	L	501	ATP	2	0
9	B	501	AGS	3	0
9	D	501	AGS	11	0
9	E	501	AGS	3	0
9	A	501	AGS	5	0
9	G	3201	AGS	4	0

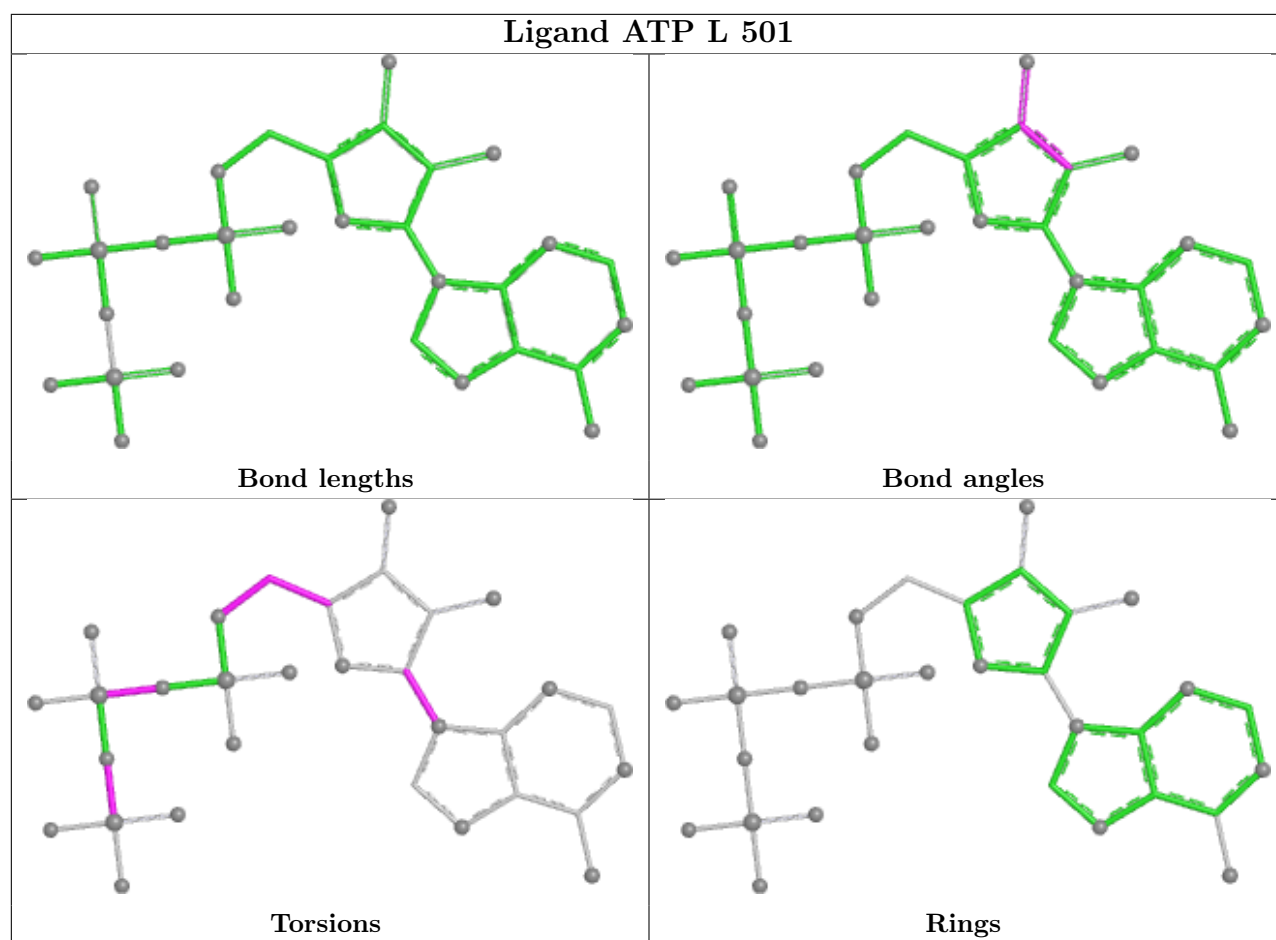
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

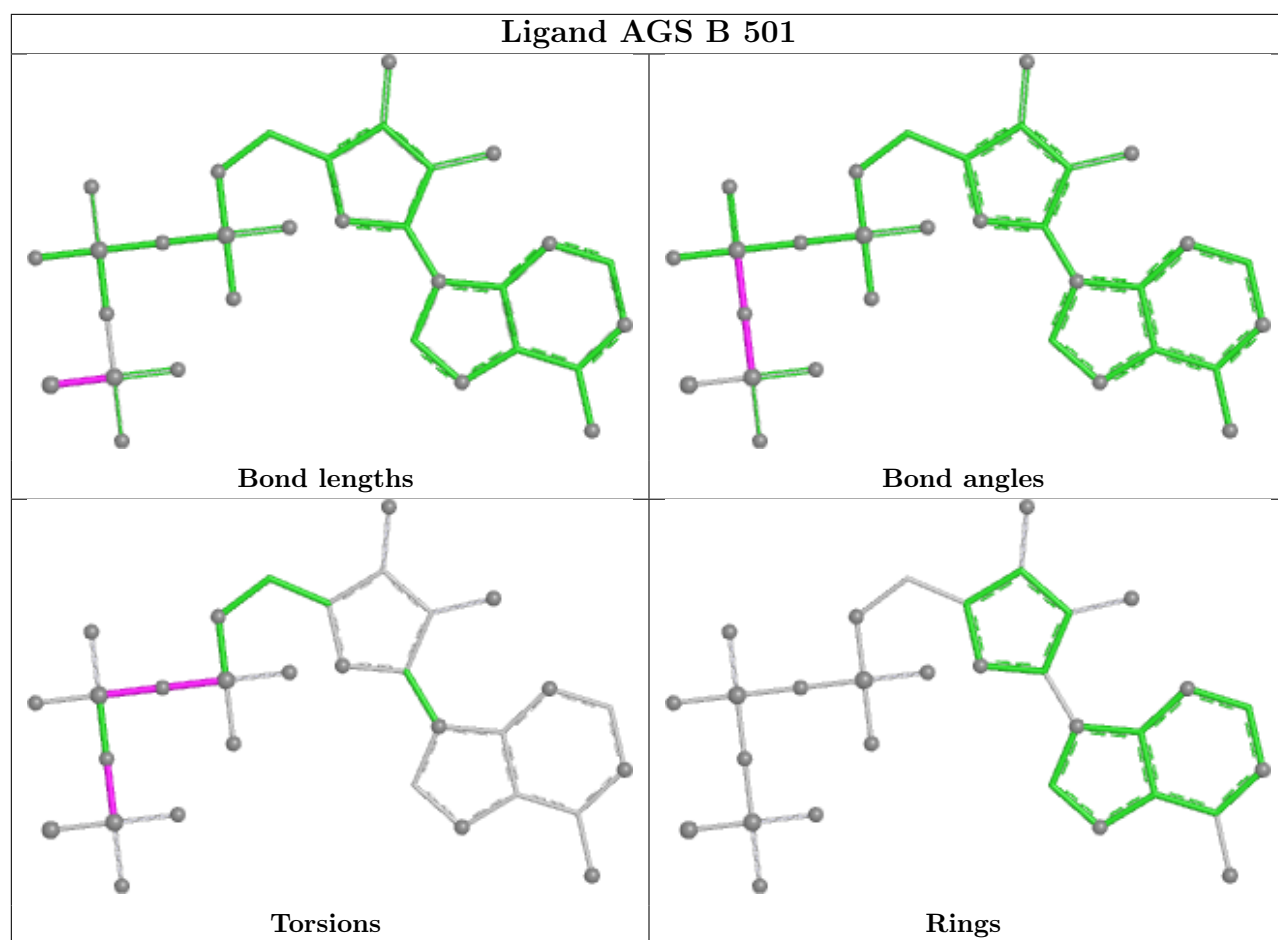
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.



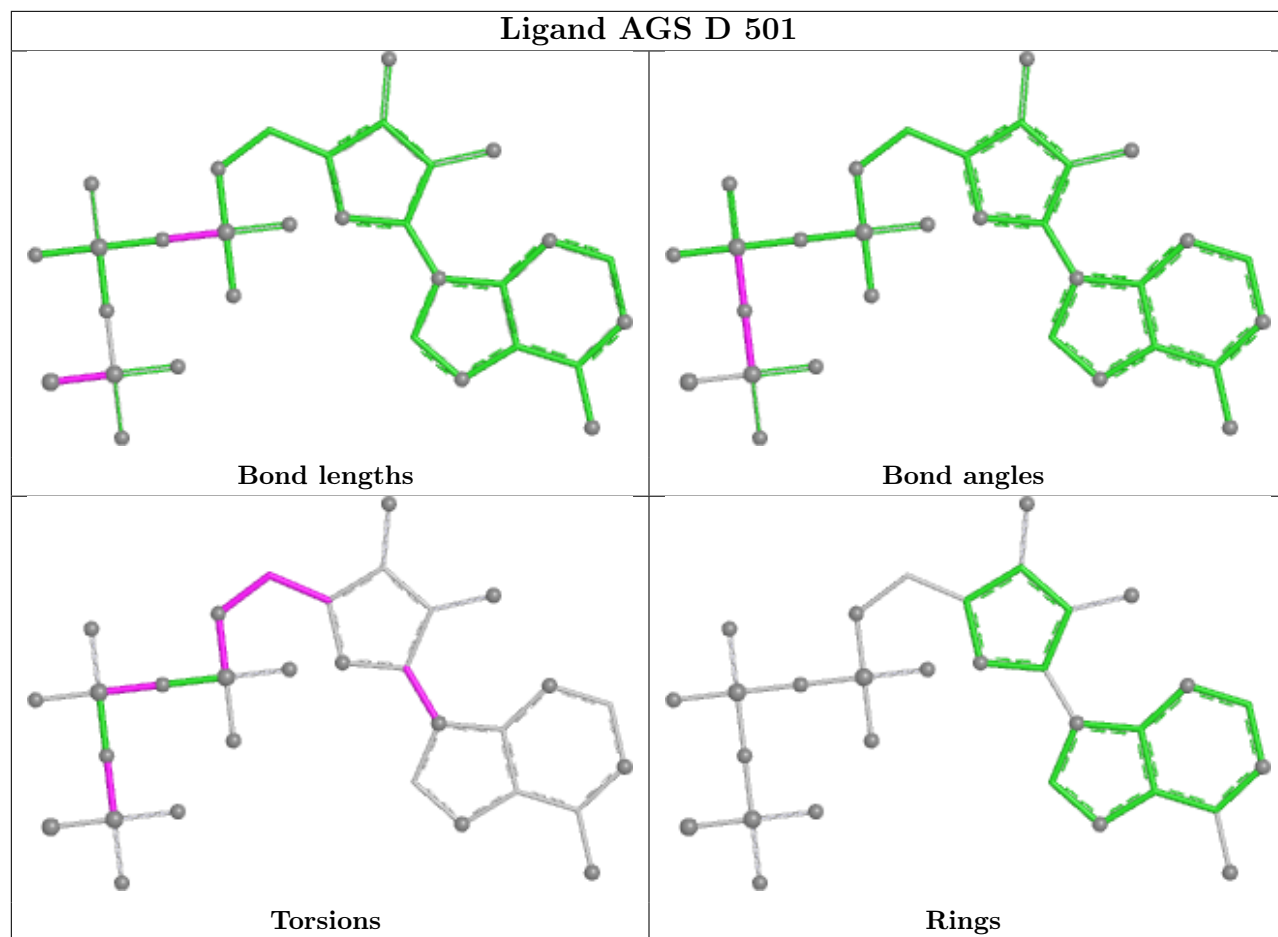
Ligand AGS F 501



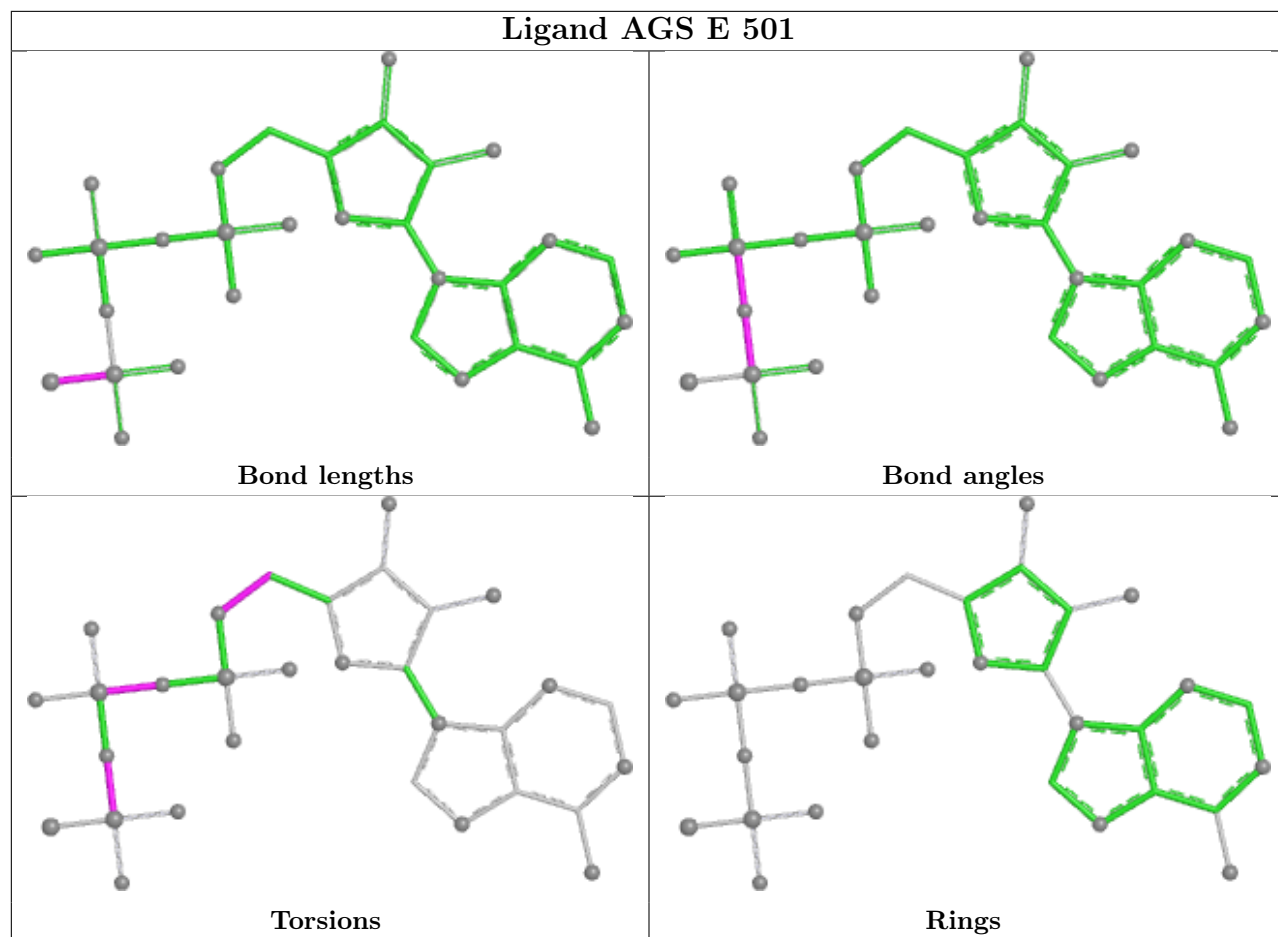




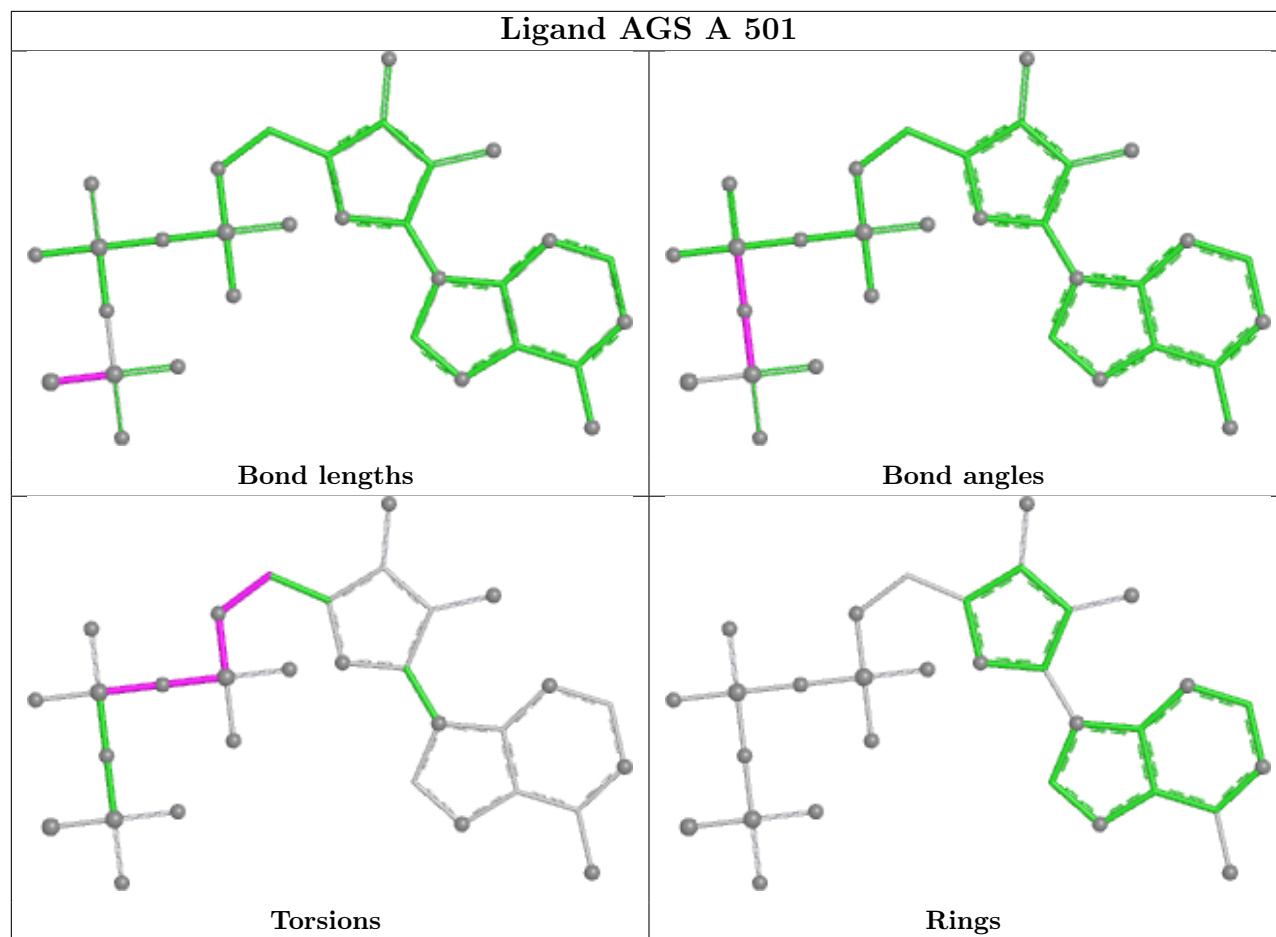
Ligand AGS D 501

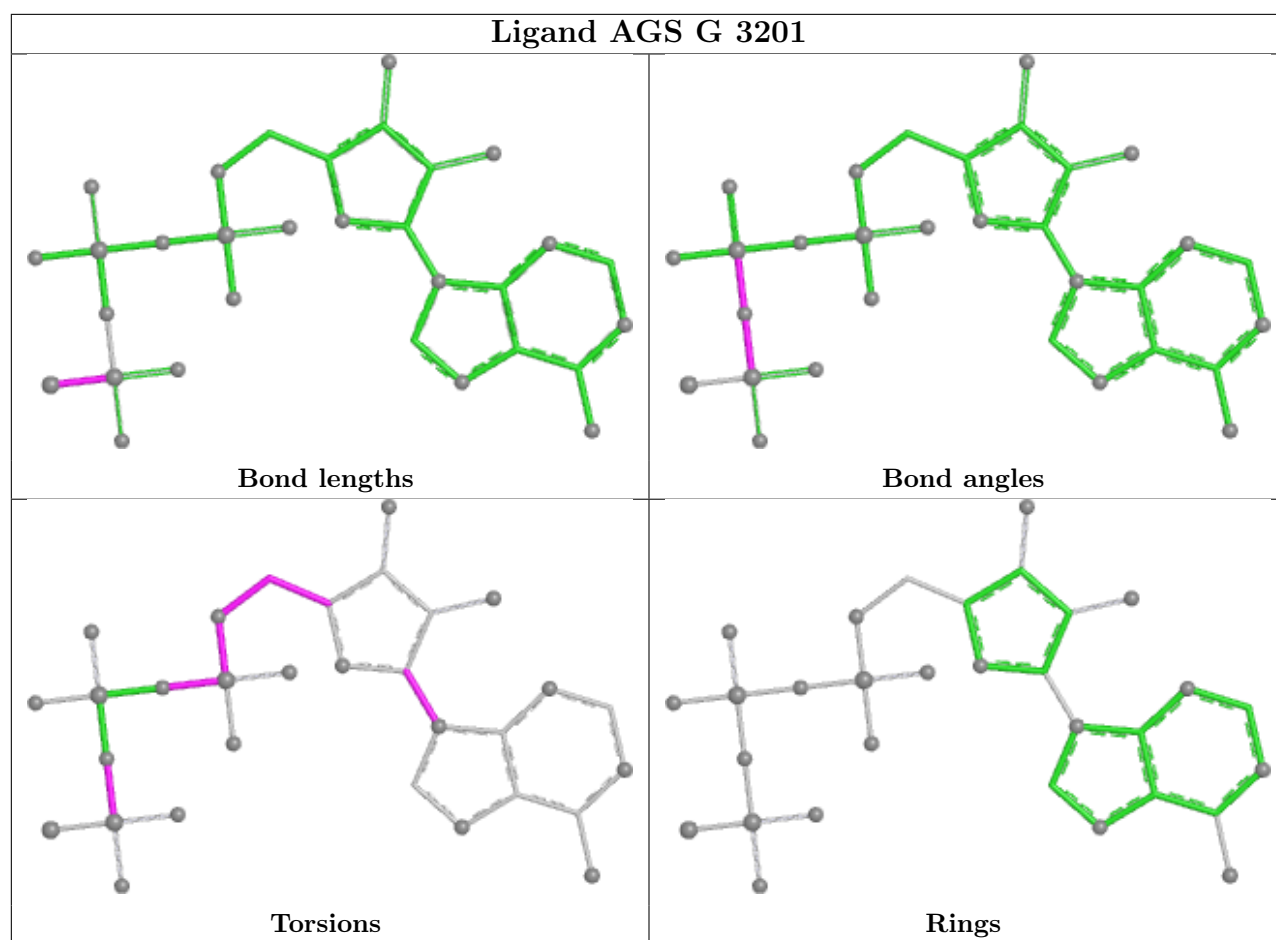


Ligand AGS E 501



Ligand AGS A 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.

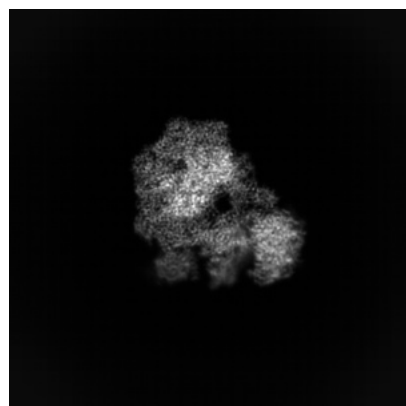
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-45206. These allow visual inspection of the internal detail of the map and identification of artifacts.

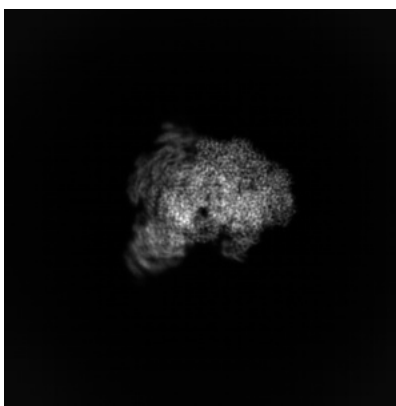
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

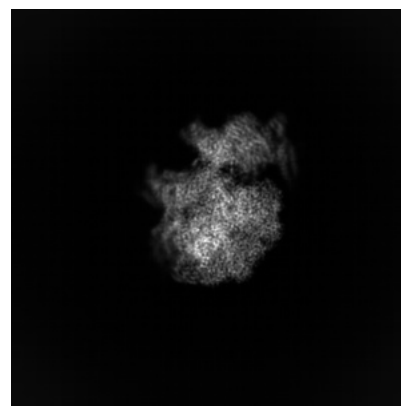
6.1.1 Primary map



X

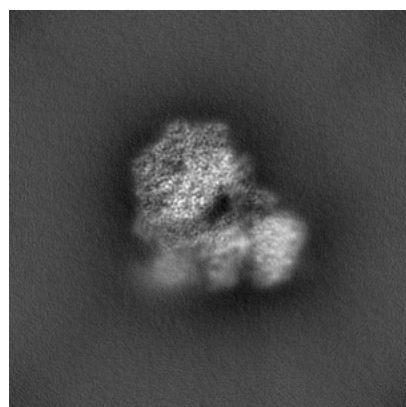


Y

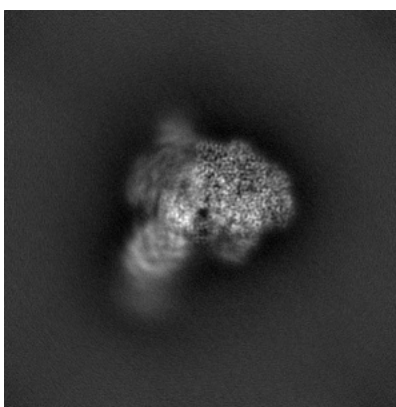


Z

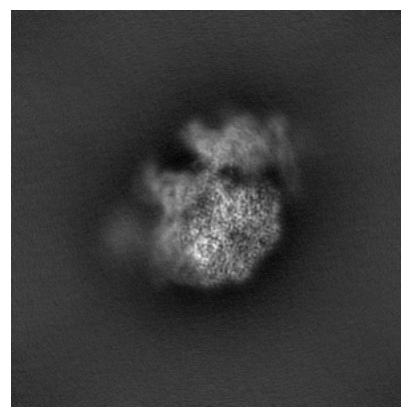
6.1.2 Raw map



X



Y

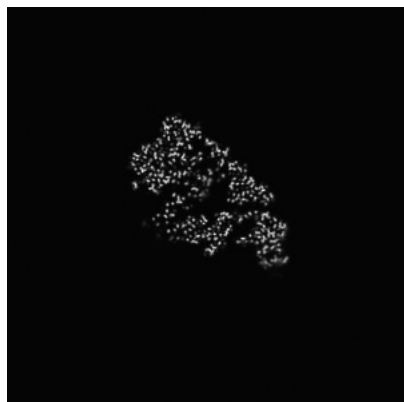


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 188

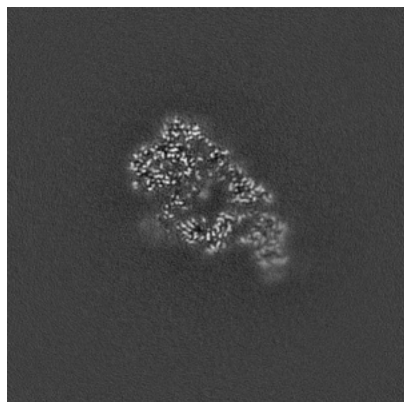


Y Index: 188

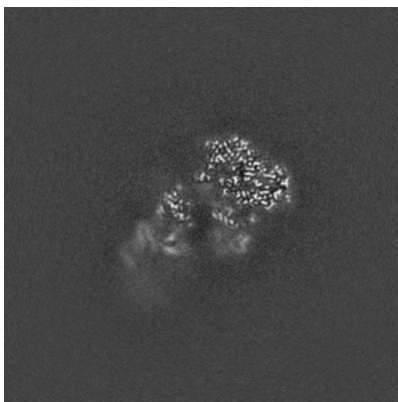


Z Index: 188

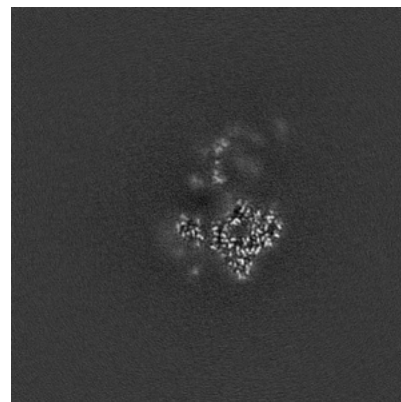
6.2.2 Raw map



X Index: 180



Y Index: 180

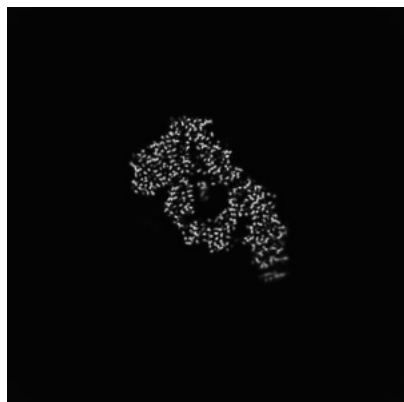


Z Index: 180

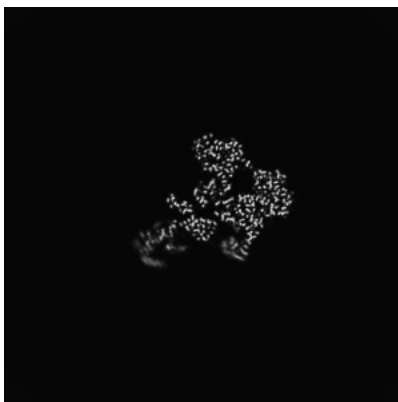
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

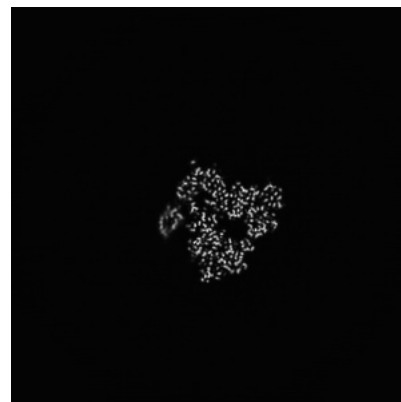
6.3.1 Primary map



X Index: 194

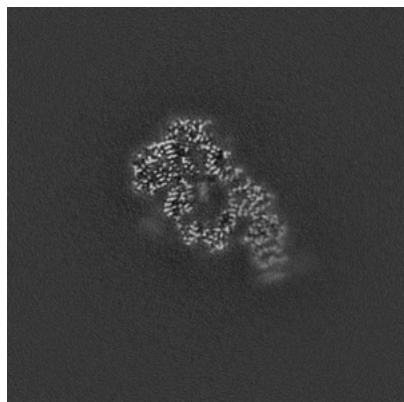


Y Index: 169

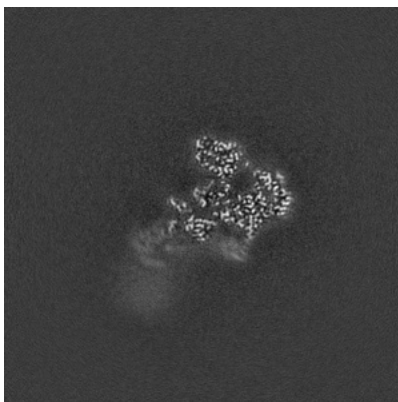


Z Index: 219

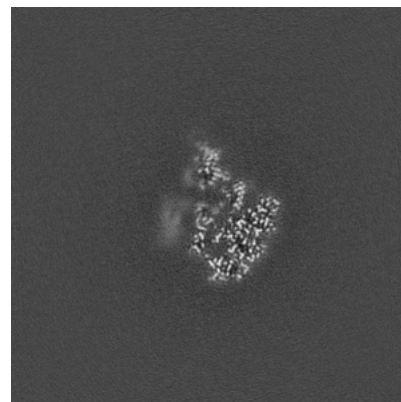
6.3.2 Raw map



X Index: 184



Y Index: 160

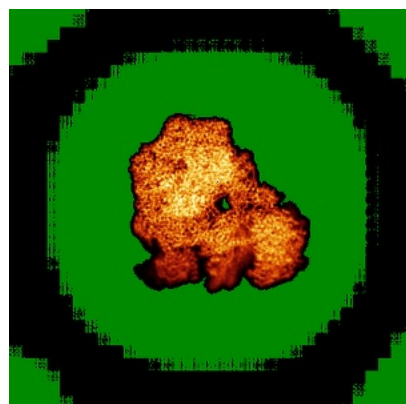


Z Index: 196

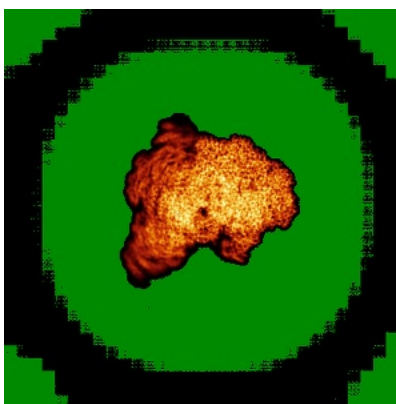
The images above show the largest variance slices of the map in three orthogonal directions.

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

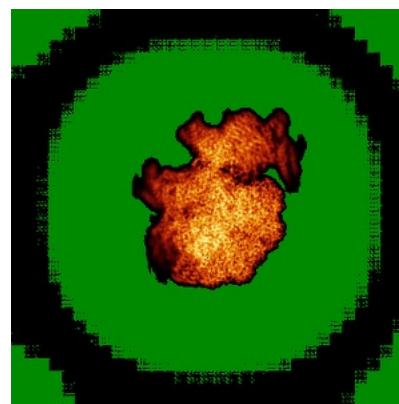
6.4.1 Primary map



X

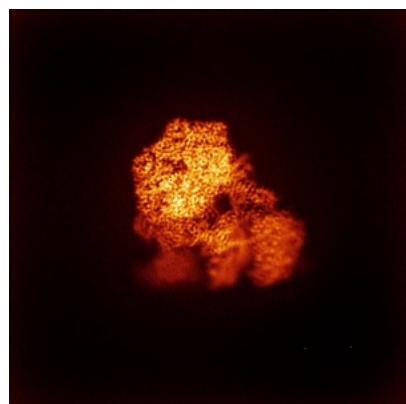


Y

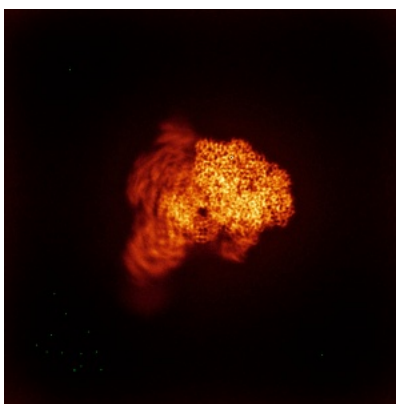


Z

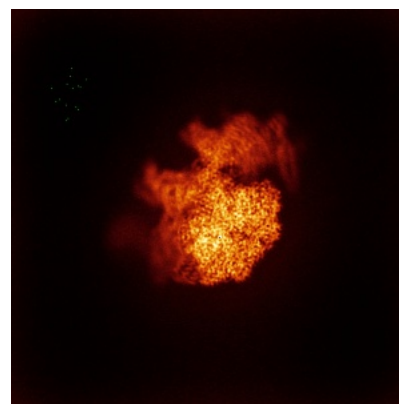
6.4.2 Raw map



X



Y

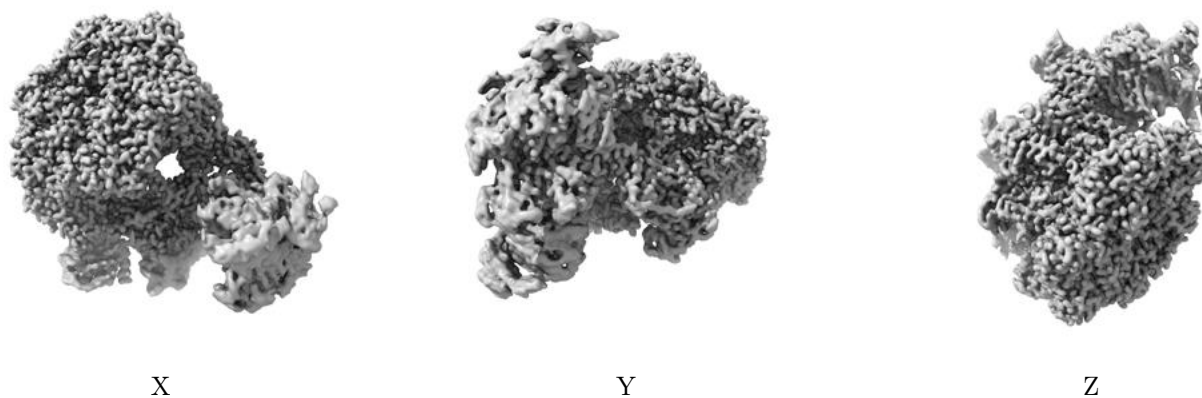


Z

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.

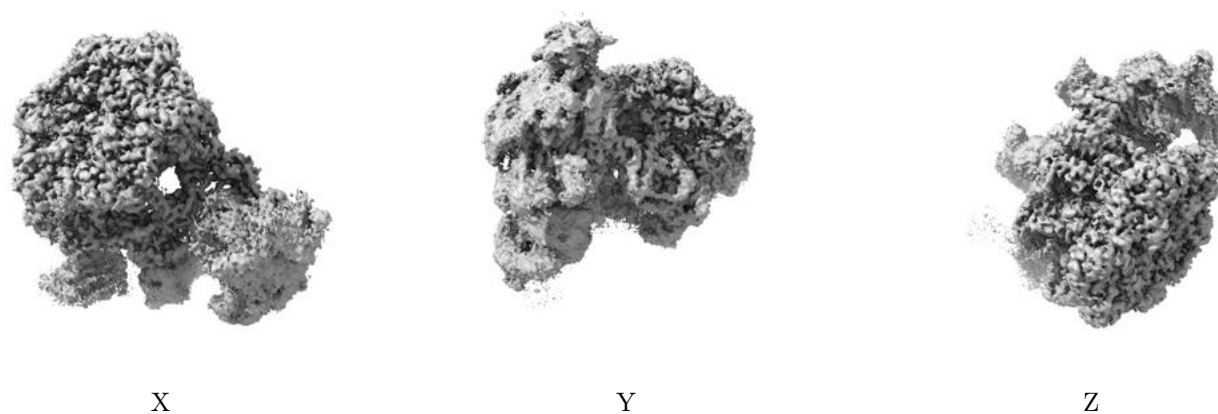
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.4. 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.

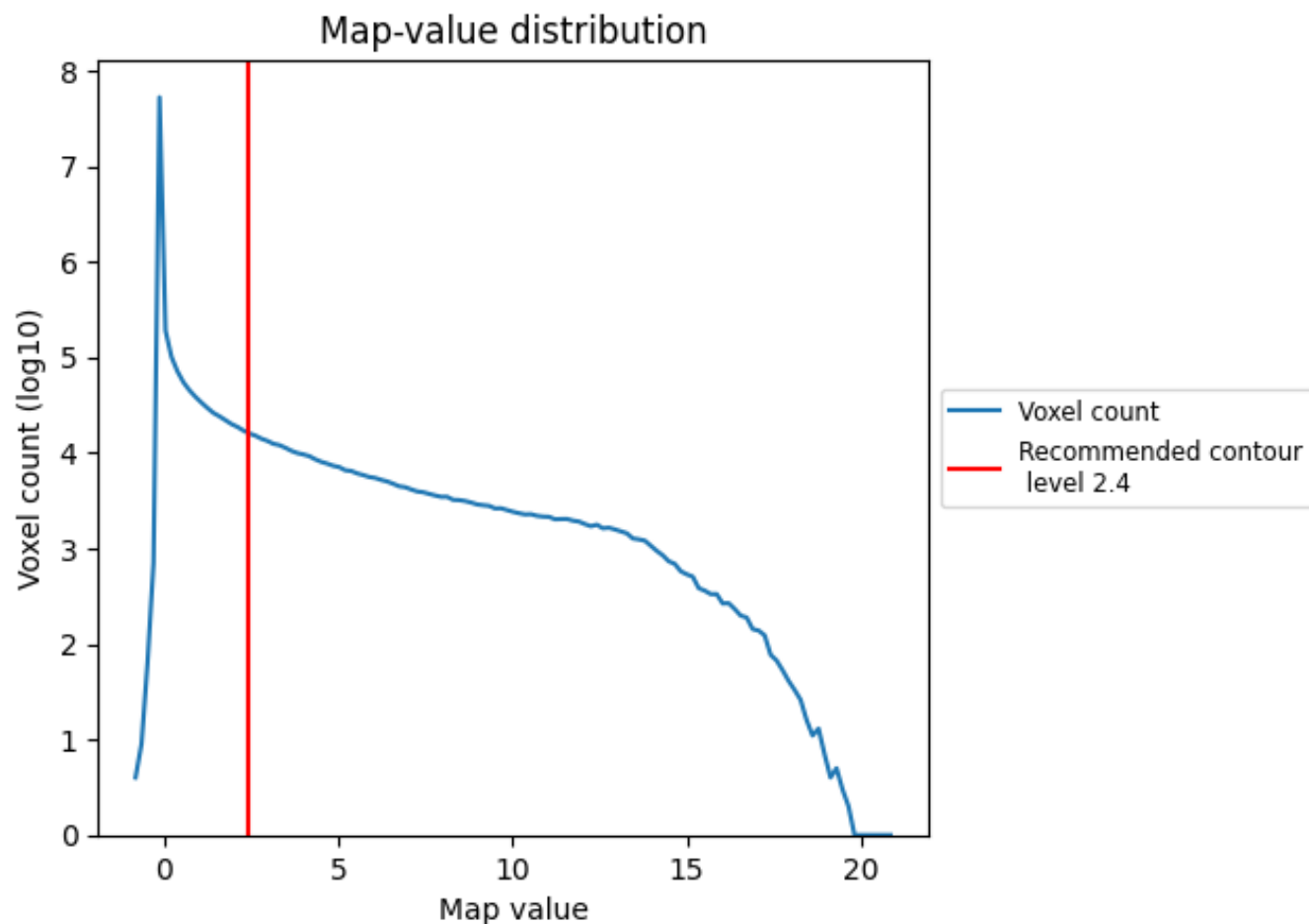
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

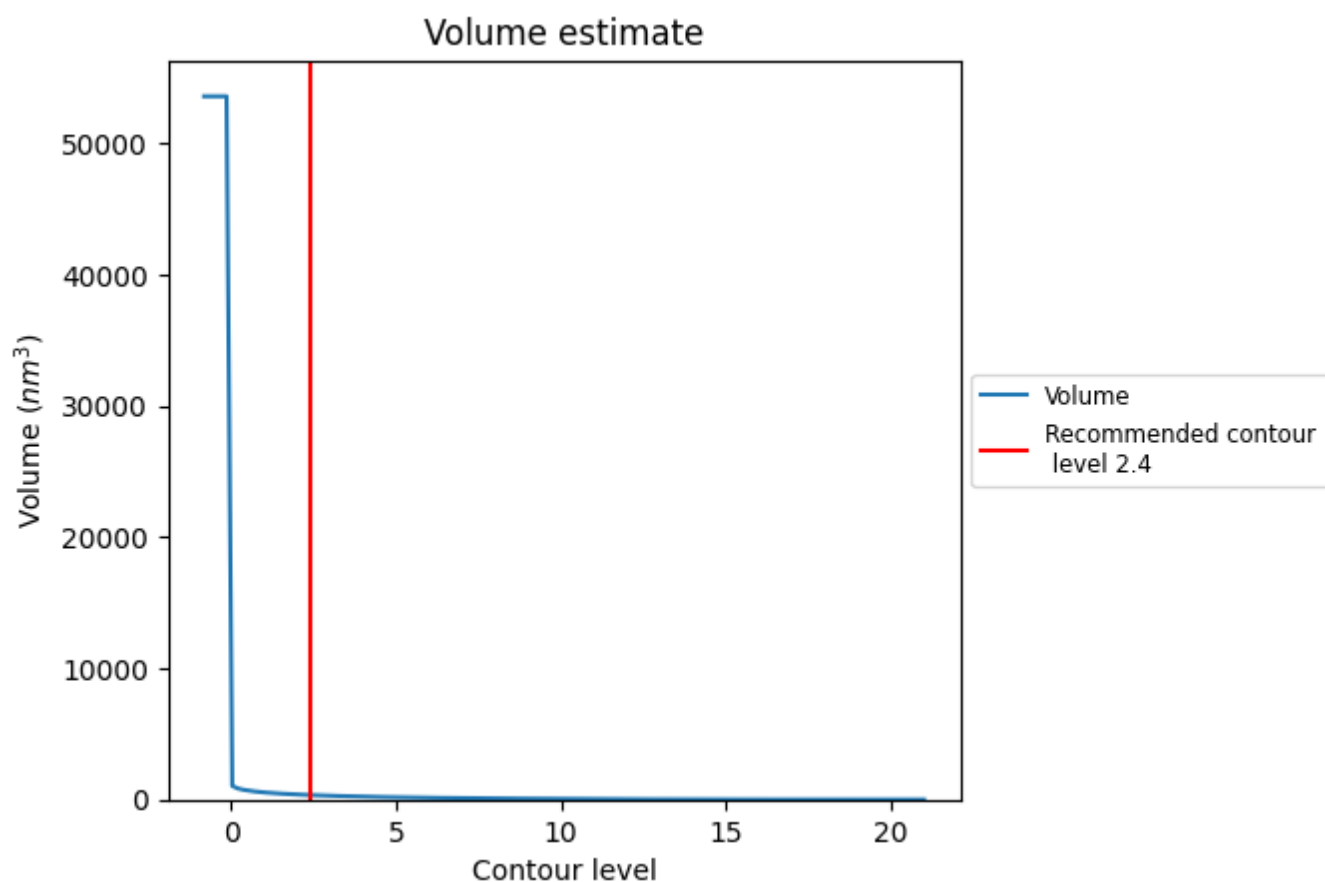
This section contains the results of statistical analysis of the map.

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.

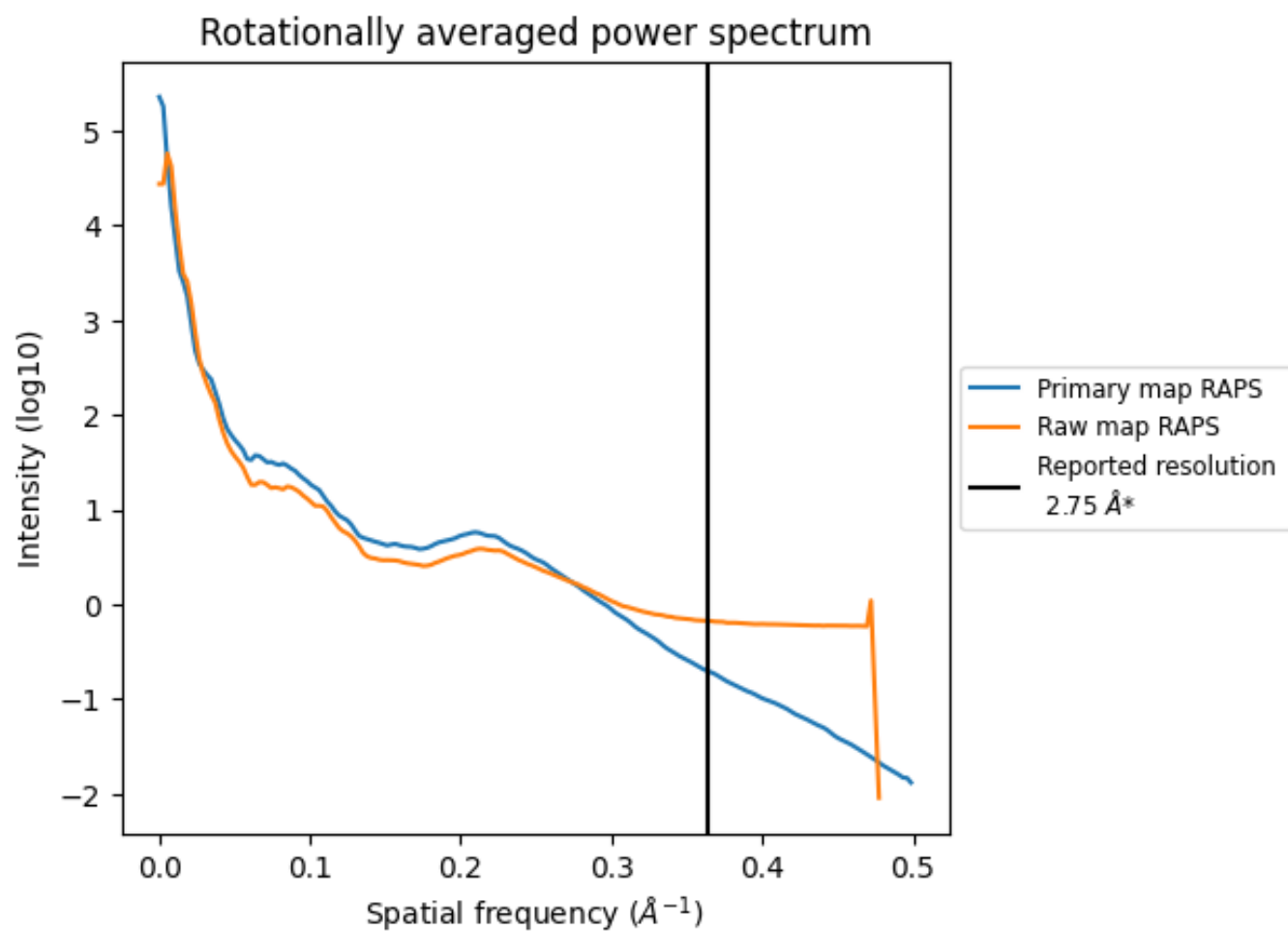
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 343 nm³; this corresponds to an approximate mass of 310 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 ⓘ

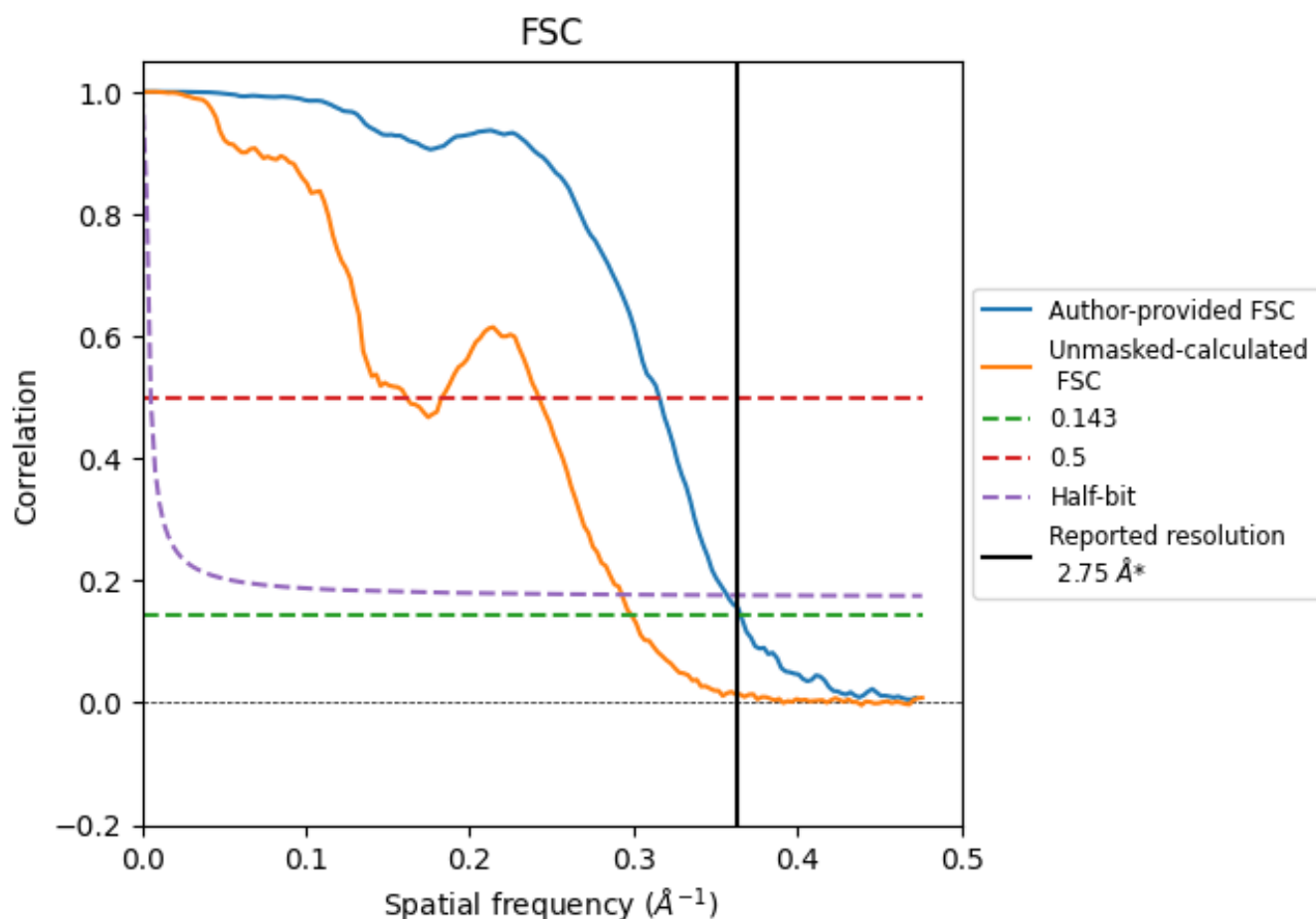


*Reported resolution corresponds to spatial frequency of 0.364 Å⁻¹

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 0.364 $\text{\AA}^{-1}$

8.2 Resolution estimates

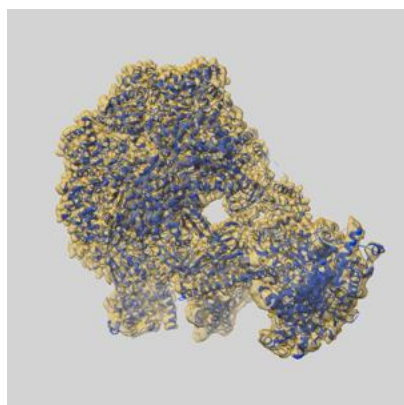
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.75	-	-
Author-provided FSC curve	2.74	3.17	2.80
Unmasked-calculated*	3.35	6.20	3.42

*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 3.35 differs from the reported value 2.75 by more than 10 %

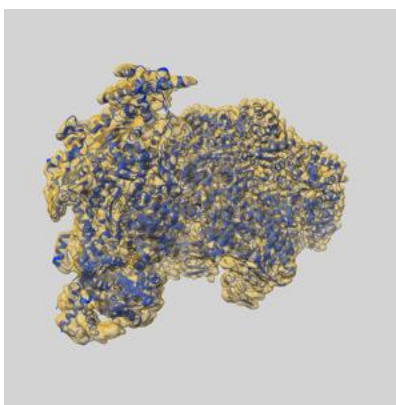
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-45206 and PDB model 9C57. Per-residue inclusion information can be found in section [3](#) on page [7](#).

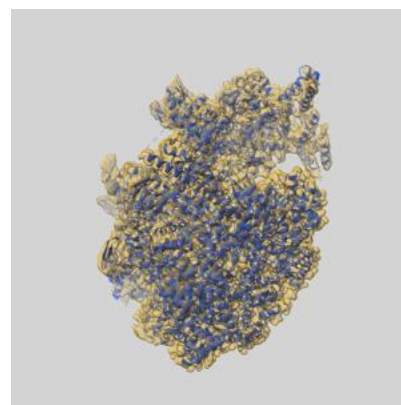
9.1 Map-model overlay [i](#)



X



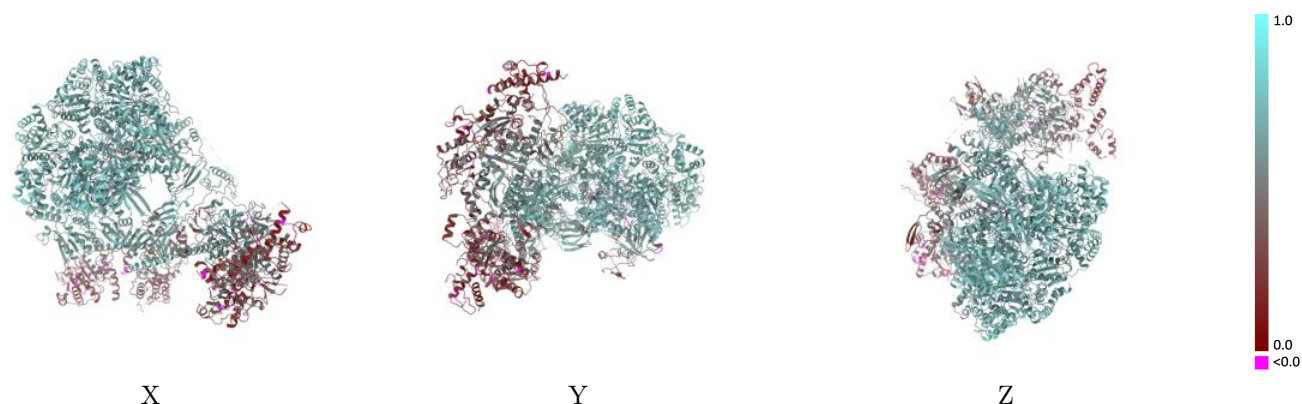
Y



Z

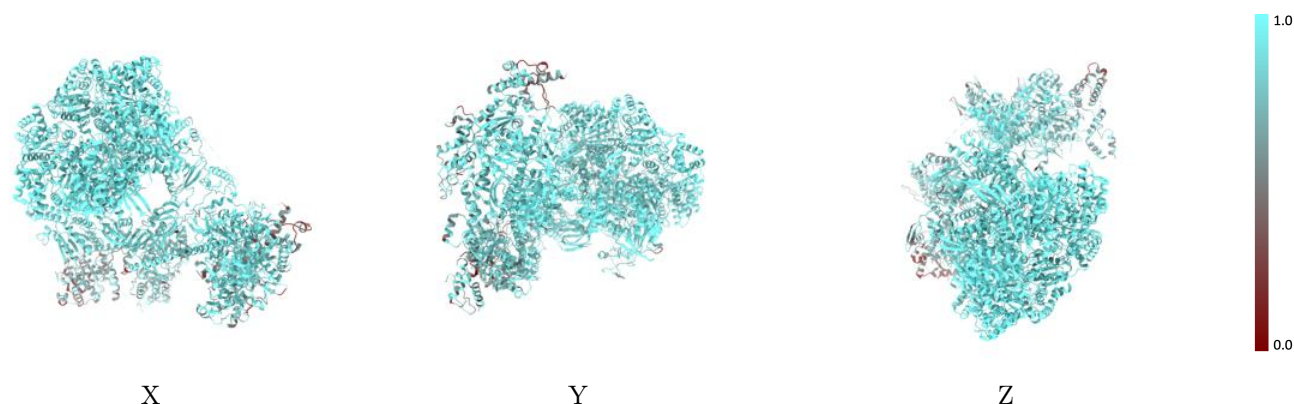
The images above show the 3D surface view of the map at the recommended contour level 2.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



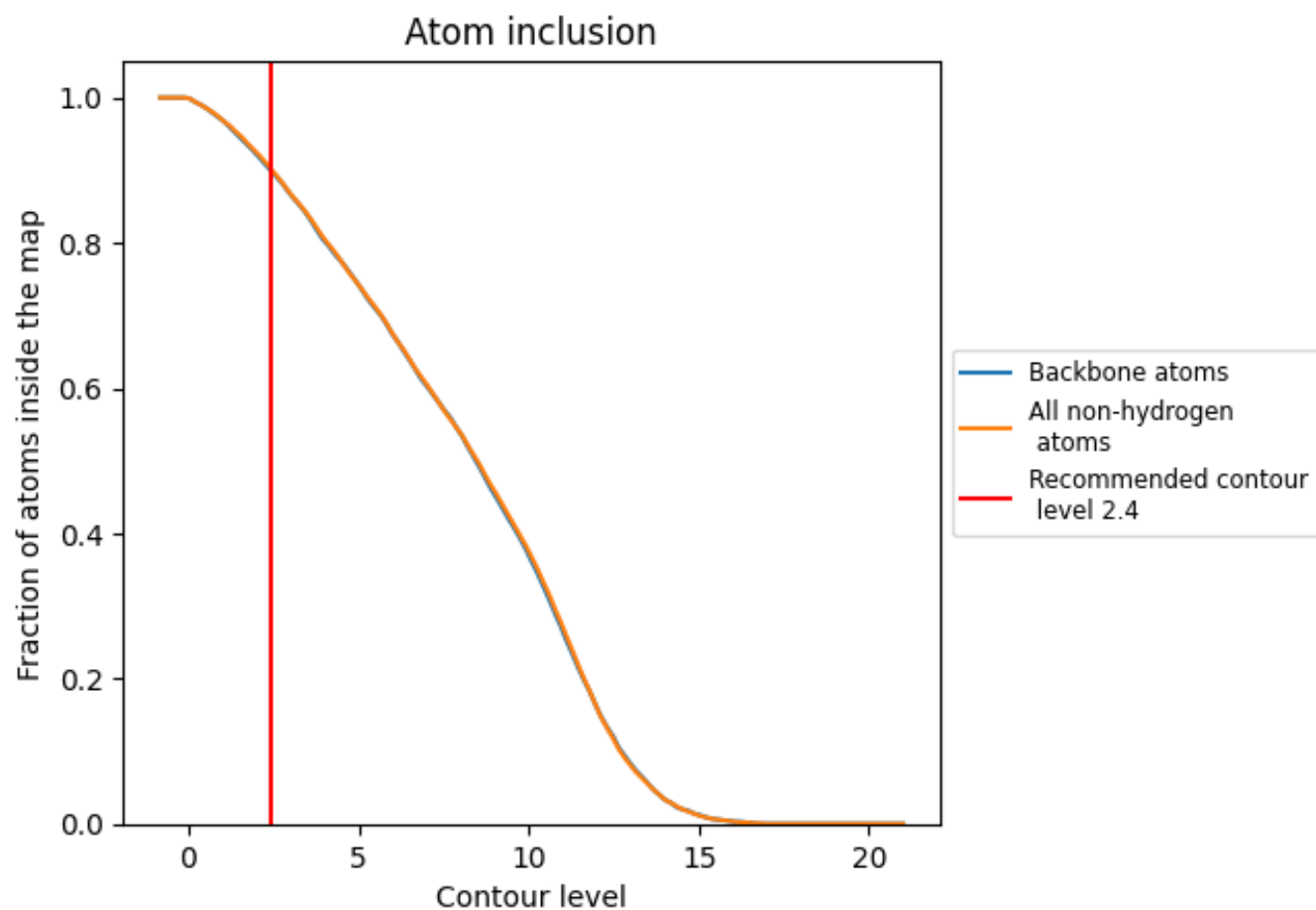
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 90% 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 (2.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9040	 0.5440
A	 0.9640	 0.6300
B	 0.9690	 0.6320
C	 0.9920	 0.6730
D	 0.9870	 0.6710
E	 0.9680	 0.6490
F	 0.9800	 0.6550
G	 0.8340	 0.4810
H	 0.8960	 0.4590
I	 0.7380	 0.3360
J	 0.8920	 0.4850
K	 0.8500	 0.5190
L	 0.8550	 0.3810
M	 0.7880	 0.3070

