



wwPDB EM Validation Summary Report ⓘ

Nov 16, 2022 – 03:09 PM EST

PDB ID : 6WGG
EMDB ID : EMD-21665
Title : Atomic model of pre-insertion mutant OCCM-DNA complex(ORC-Cdc6-Cdt1-Mcm2-7 with Mcm6 WHD truncation)
Authors : Yuan, Z.; Schneider, S.; Dodd, T.; Riera, A.; Bai, L.; Yan, C.; Magdalou, I.; Ivanov, I.; Stillman, B.; Li, H.; Speck, C.
Deposited on : 2020-04-05
Resolution : 8.10 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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

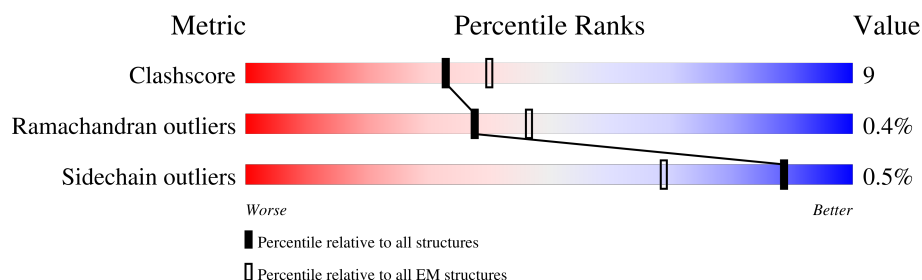
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.10 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	8	604	<div> <div>61%</div> <div> <div>41%</div> <div>23%</div> <div>36%</div> </div> </div>
2	9	513	<div> <div>46%</div> <div> <div>50%</div> <div>22%</div> <div>27%</div> </div> </div>
3	A	913	<div> <div>23%</div> <div> <div>38%</div> <div>9%</div> <div>54%</div> </div> </div>
4	B	620	<div> <div>31%</div> <div> <div>40%</div> <div>13%</div> <div>47%</div> </div> </div>
5	C	616	<div> <div>41%</div> <div> <div>71%</div> <div>17%</div> <div>12%</div> </div> </div>
6	E	479	<div> <div>45%</div> <div> <div>68%</div> <div>20%</div> <div>12%</div> </div> </div>
7	D	529	<div> <div>40%</div> <div> <div>62%</div> <div>20%</div> <div>18%</div> </div> </div>
8	F	435	<div> <div>26%</div> <div> <div>28%</div> <div>8%</div> <div>64%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
9	G	41	<div> <div>46%</div> <div>98%</div> </div>
10	H	41	<div> <div>29%</div> <div>98%</div> </div>
11	2	868	<div> <div>45%</div> <div>56%</div> <div>10%</div> <div>33%</div> </div>
12	3	971	<div> <div>43%</div> <div>53%</div> <div>13%</div> <div>34%</div> </div>
13	4	933	<div> <div>48%</div> <div>57%</div> <div>14%</div> <div>29%</div> </div>
14	5	775	<div> <div>62%</div> <div>65%</div> <div>12%</div> <div>23%</div> </div>
15	6	1017	<div> <div>34%</div> <div>48%</div> <div>9%</div> <div>43%</div> </div>
16	7	845	<div> <div>54%</div> <div>64%</div> <div>12%</div> <div>24%</div> </div>

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 54601 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 cycle protein CDT1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	388	Total	C	N	O	S	0	0
			3011	1916	518	566	11		

- Molecule 2 is a protein called Cell division control protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	9	373	Total	C	N	O	S	0	0
			2972	1907	495	553	17		

- Molecule 3 is a protein called Origin recognition complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	424	Total	C	N	O	S	0	0
			3368	2151	566	633	18		

- Molecule 4 is a protein called Origin recognition complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	326	Total	C	N	O	S	0	0
			2663	1721	442	484	16		

- Molecule 5 is a protein called Origin recognition complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	544	Total	C	N	O	S	0	0
			4505	2909	743	838	15		

- Molecule 6 is a protein called Origin recognition complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	422	Total	C	N	O	S	0	0
			3425	2226	545	641	13		

- Molecule 7 is a protein called Origin recognition complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	436	Total	C	N	O	S	0	0
			3551	2275	603	660	13		

- Molecule 8 is a protein called Origin recognition complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	157	Total	C	N	O	S	0	0
			1315	846	222	235	12		

- Molecule 9 is a DNA chain called DNA (41-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	41	Total	C	N	O	P	0	0
			831	407	118	266	40		

- Molecule 10 is a DNA chain called DNA (41-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	41	Total	C	N	O	P	0	0
			847	404	178	224	41		

- Molecule 11 is a protein called DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2	581	Total	C	N	O	S	0	0
			4478	2824	786	849	19		

- Molecule 12 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	3	642	Total	C	N	O	S	0	0
			4866	3073	837	942	14		

- Molecule 13 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	4	665	Total	C	N	O	S	0	0
			4995	3126	864	981	24		

- Molecule 14 is a protein called Minichromosome maintenance protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	5	599	Total	C	N	O	S	0	0
			4317	2699	750	849	19		

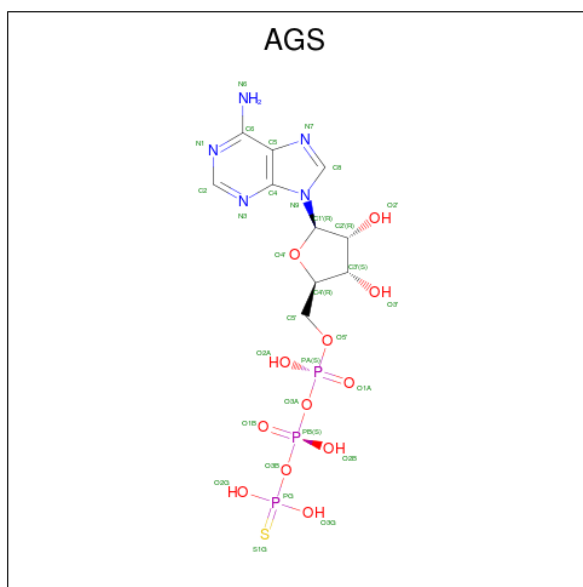
- Molecule 15 is a protein called DNA replication licensing factor MCM6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	6	576	Total	C	N	O	S	0	0
			4475	2825	782	845	23		

- Molecule 16 is a protein called DNA replication licensing factor MCM7.

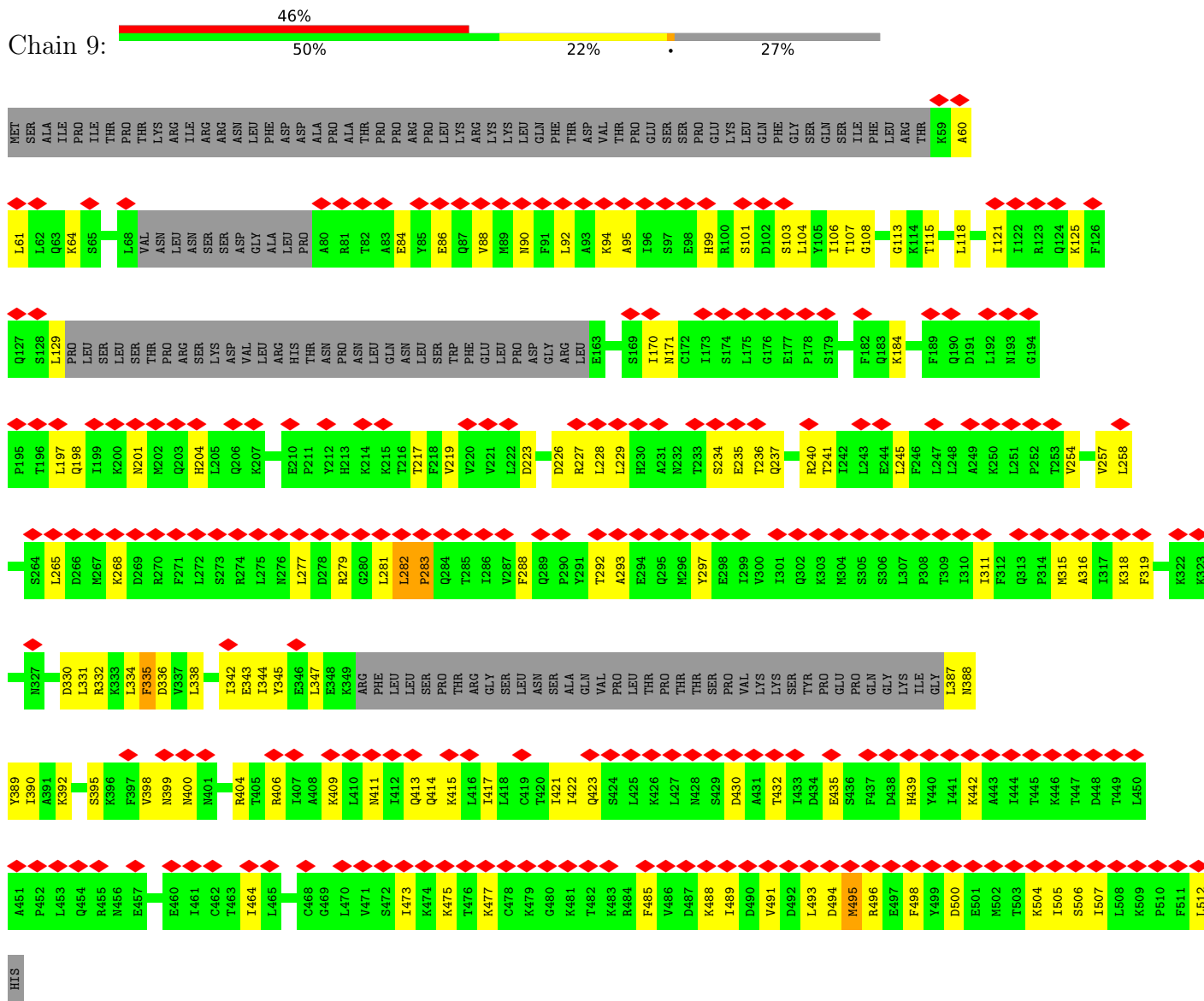
Mol	Chain	Residues	Atoms					AltConf	Trace
16	7	641	Total	C	N	O	S	0	0
			4858	3053	834	943	28		

- Molecule 17 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).

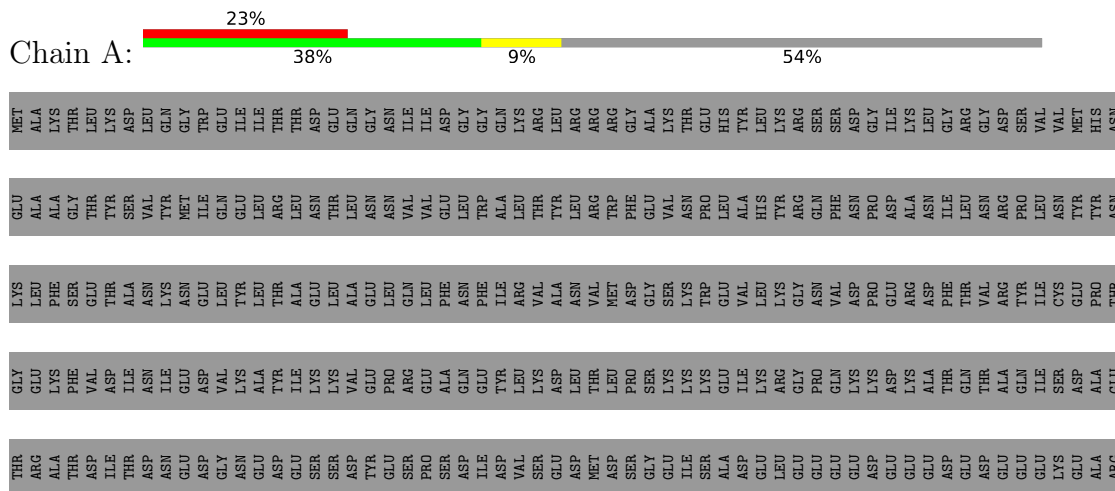


Mol	Chain	Residues	Atoms						AltConf
17	9	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
17	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
17	E	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
17	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

- Molecule 2: Cell division control protein 6



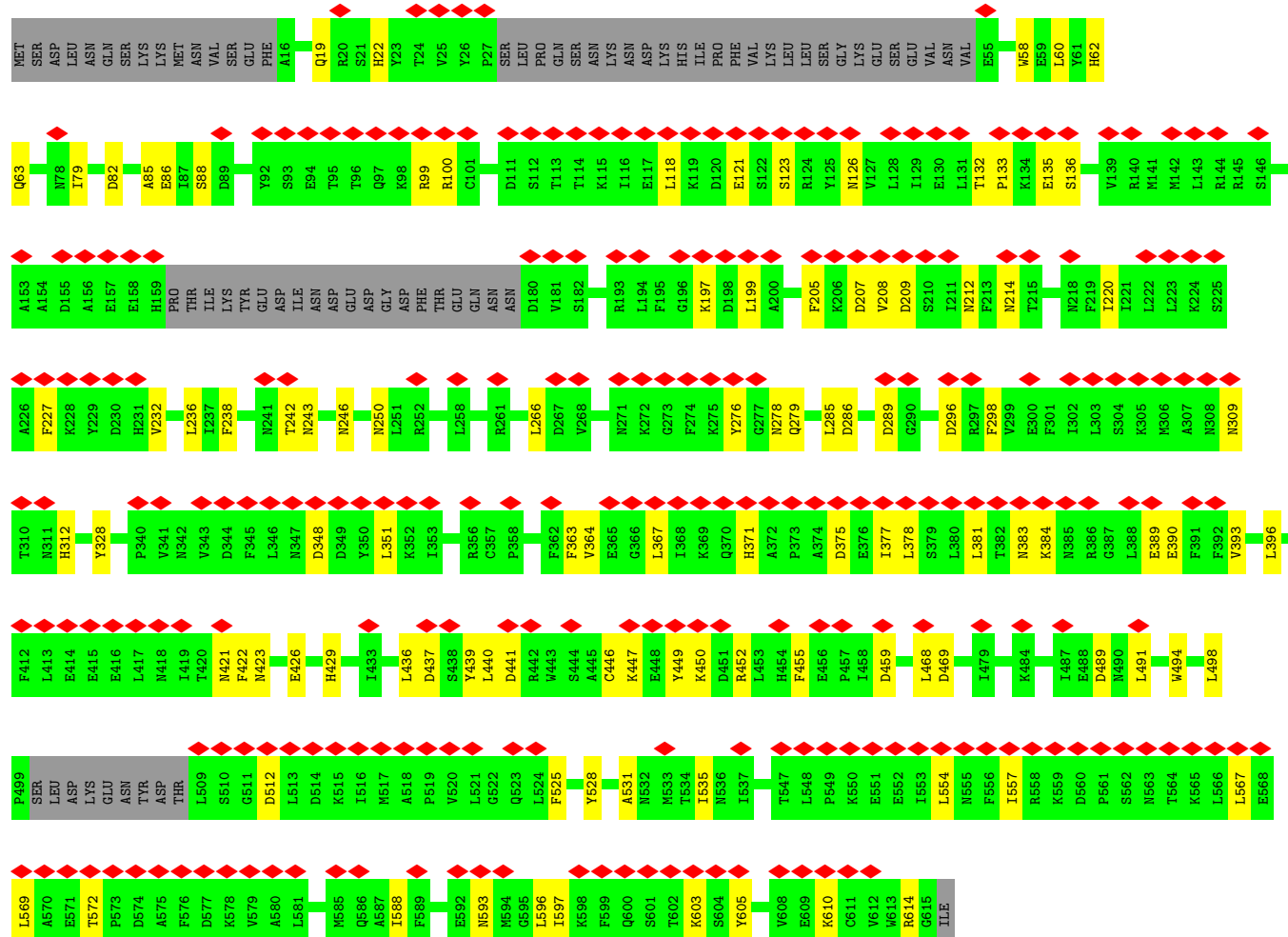
- Molecule 3: Origin recognition complex subunit 1





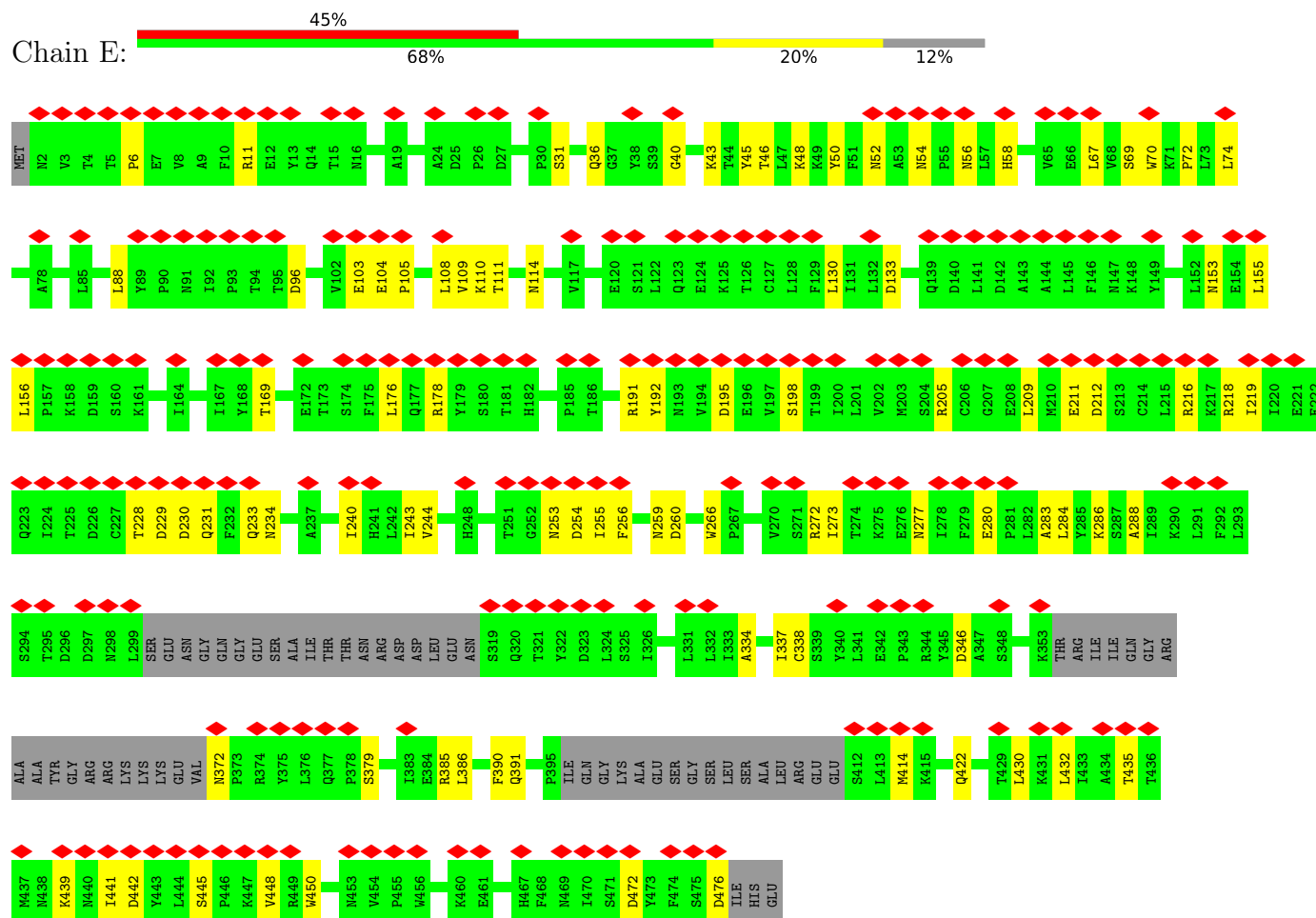
Government	Percentage
Current government	31%
Previous government	40%
Current government	13%
Previous government	47%





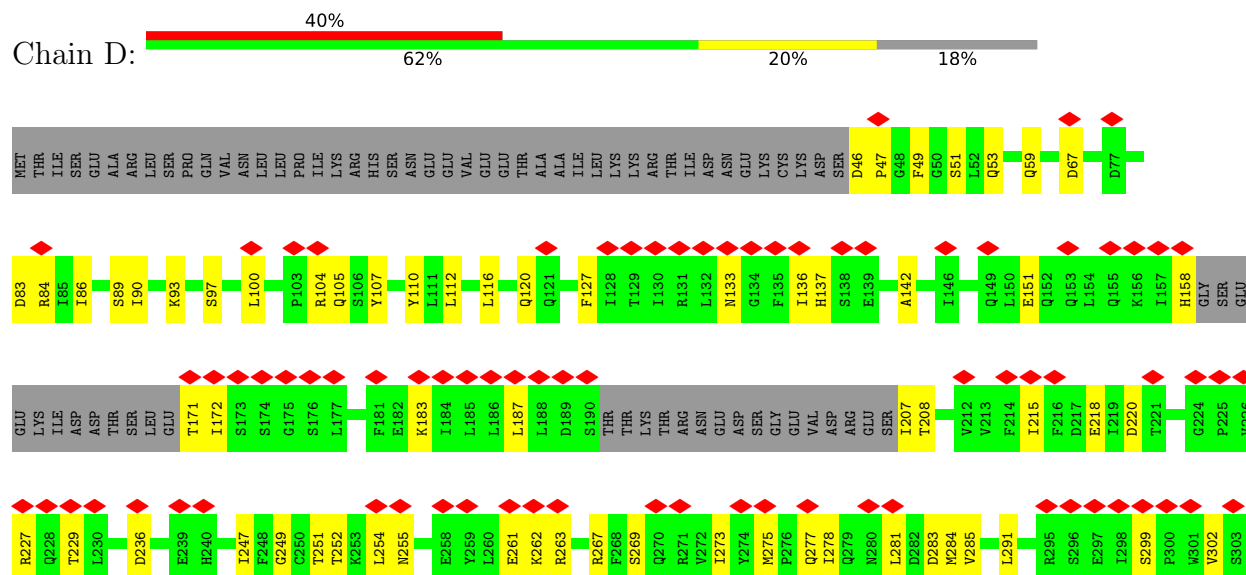
• Molecule 6: Origin recognition complex subunit 5

Chain E:

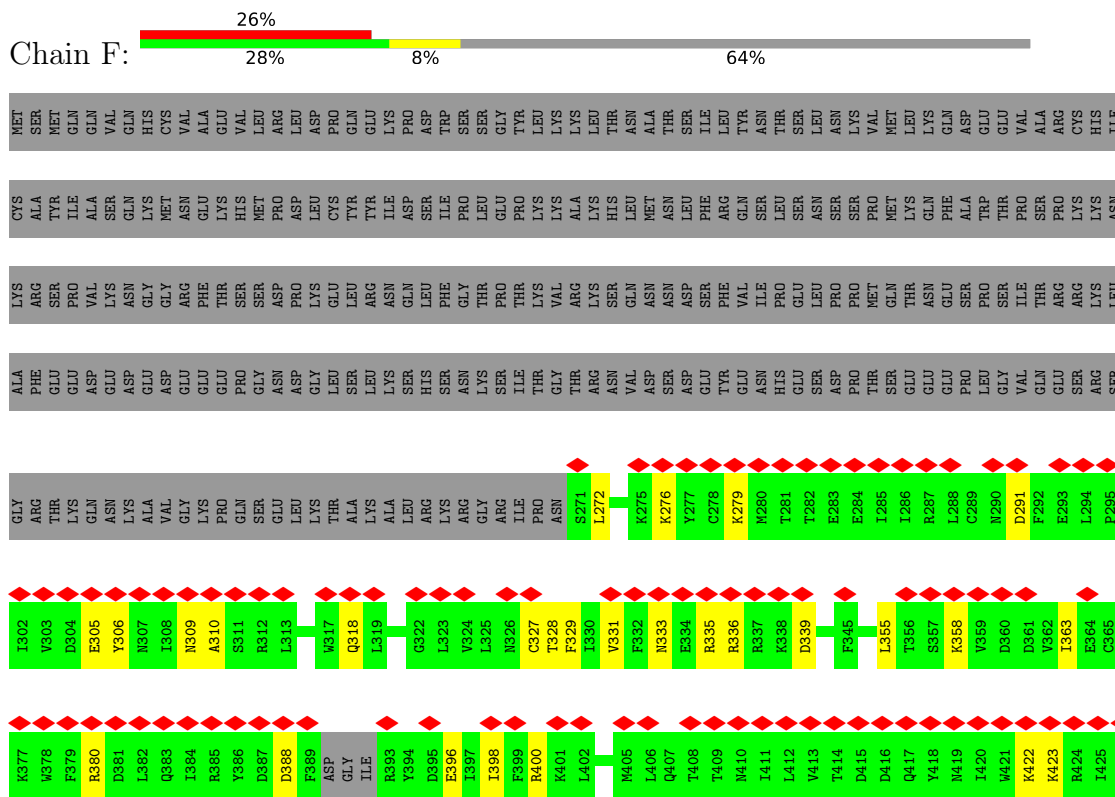


• Molecule 7: Origin recognition complex subunit 4

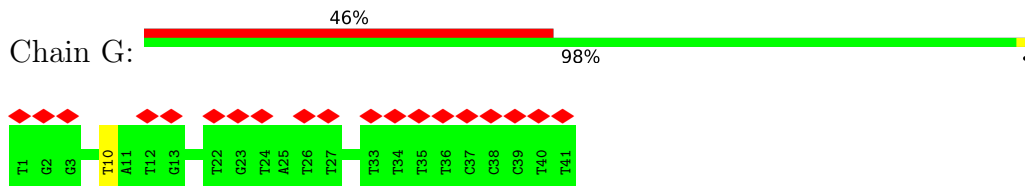
Chain D:



- Molecule 8: Origin recognition complex subunit 6



- Molecule 9: DNA (41-MER)

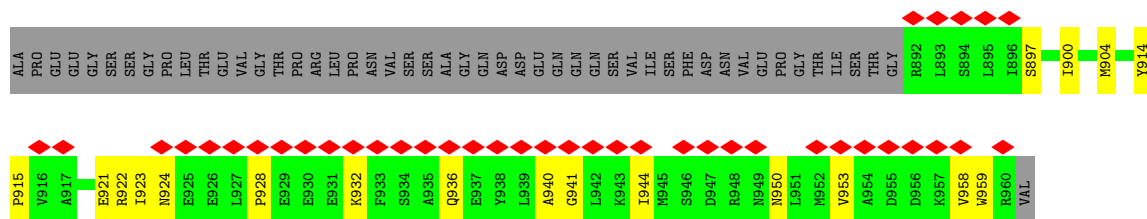


- Molecule 10: DNA (41-MER)

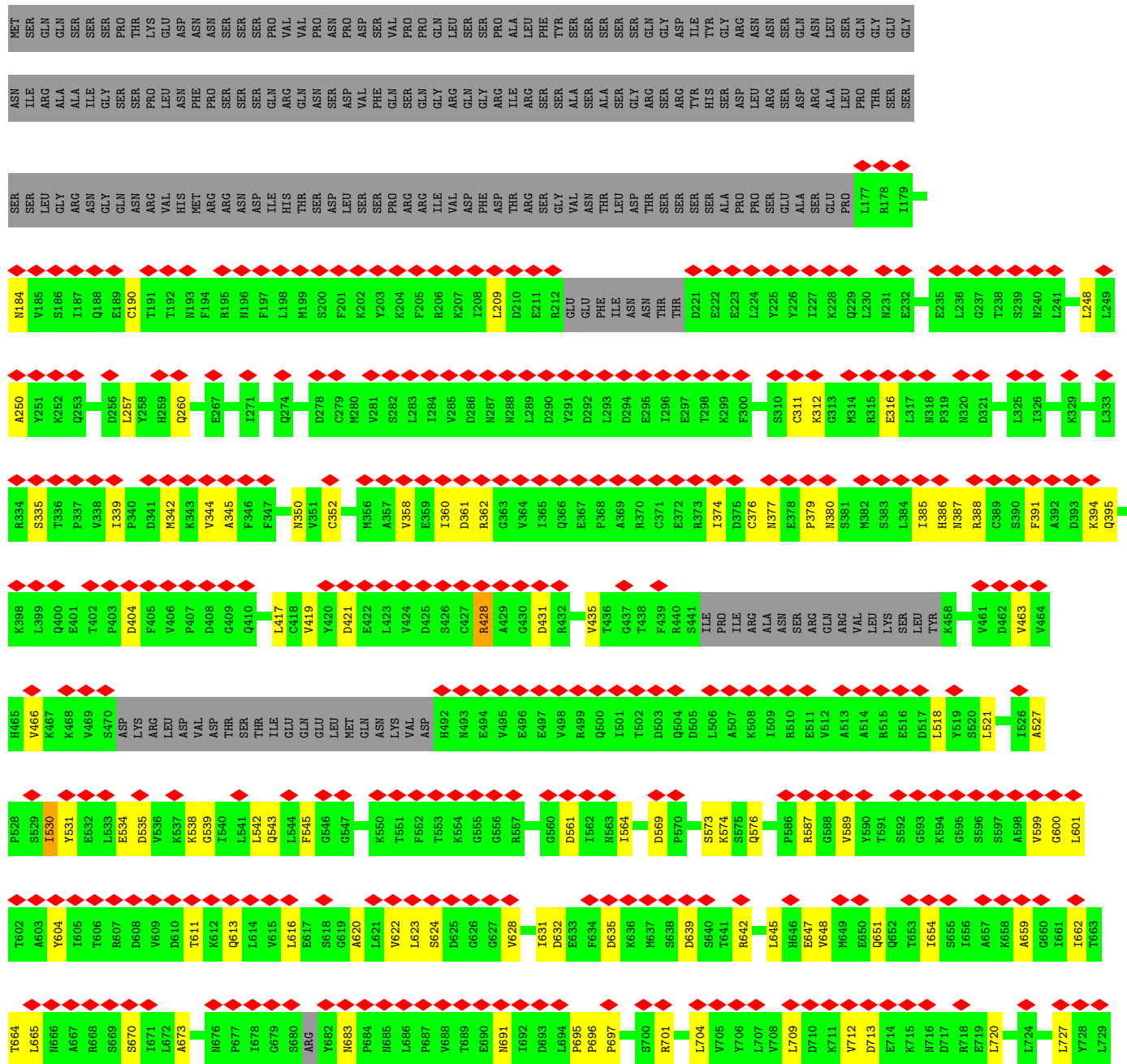


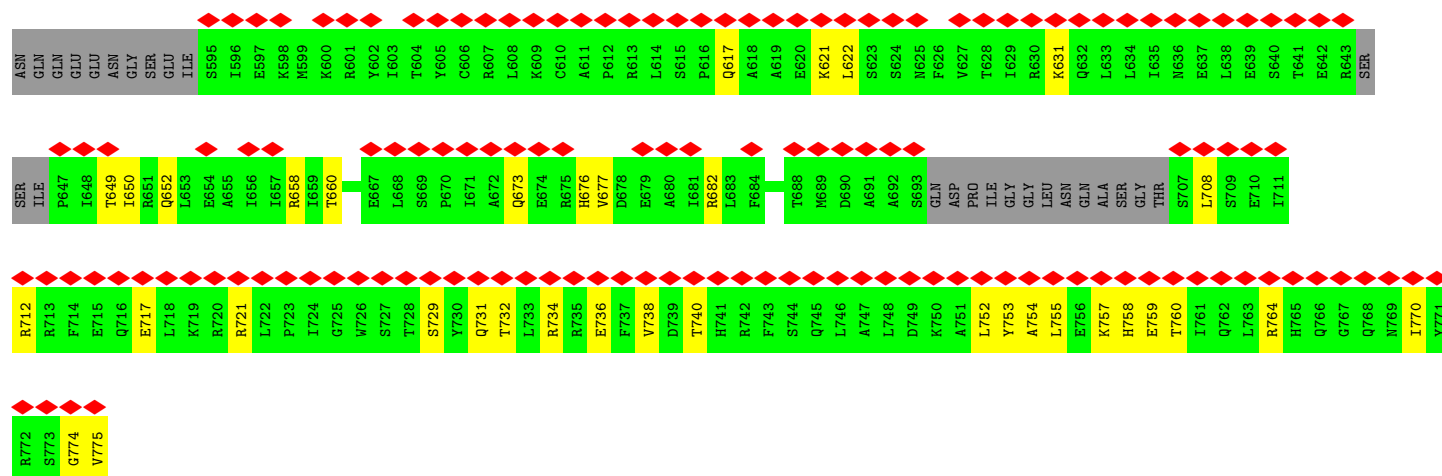
Chain 3:



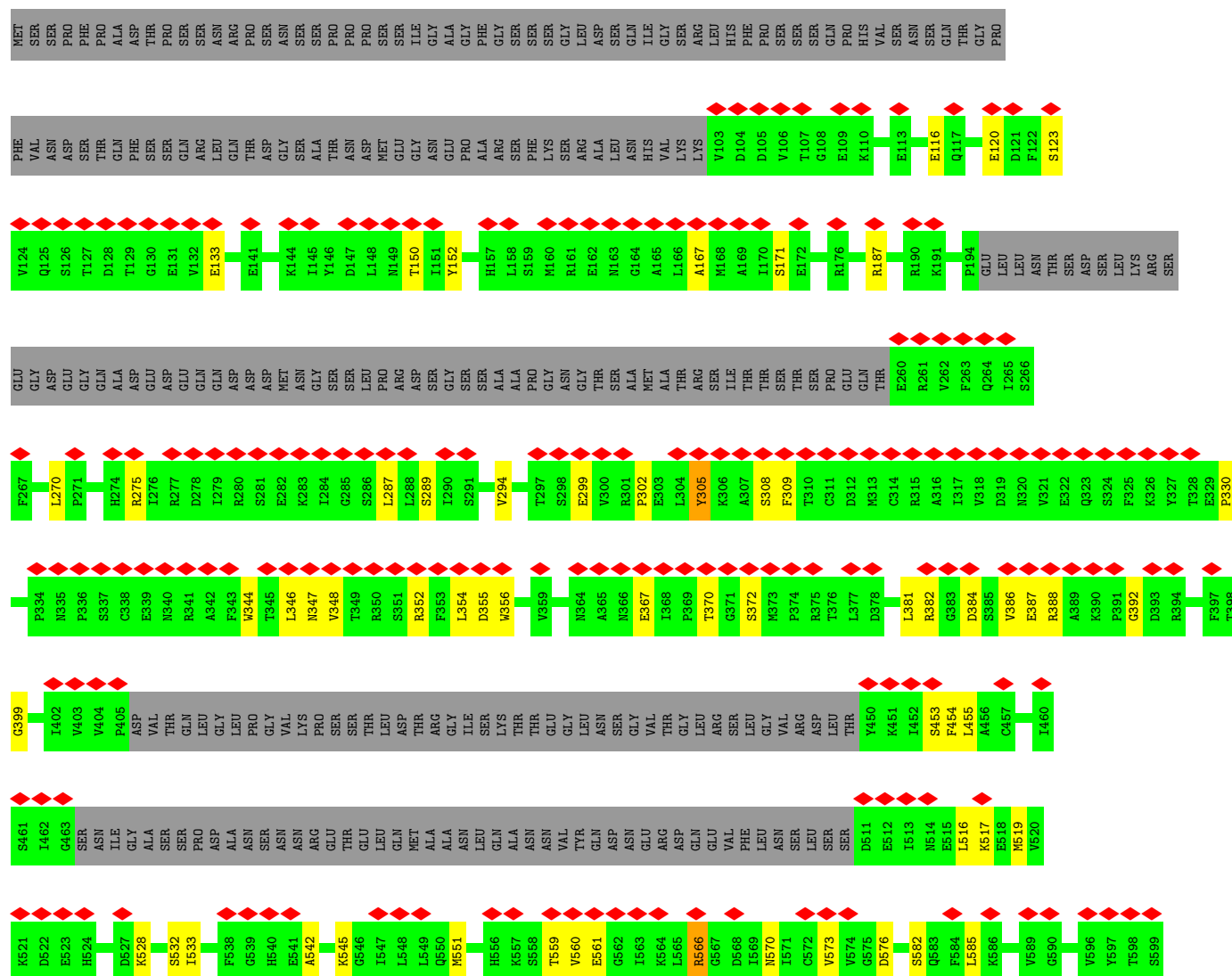


• Molecule 13: DNA replication licensing factor MCM4





• Molecule 15: DNA replication licensing factor MCM6



LEU	ILE	ASN	GLU	GLY	ASN	THR	LEU	LYS	PHE	VAL	ASP	ASP	GLN	GLU	ASP	THR	ASP	GLN	GLU	ASP	SER	LEU	VAL	SER	THR	PRO	LYS	LEU	ALA	SER	ALA	ASN	VAL	SER	ALA	GLN	ASP	SER	ASP	ILE	ASP	LEU	GLN	ASP	ALA																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	25126	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)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.060	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	335.36, 335.36, 335.36	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.31, 1.31, 1.31	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: 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	8	0.25	0/3070	0.52	0/4175
2	9	0.32	0/3014	0.58	0/4055
3	A	0.35	0/3415	0.56	1/4596 (0.0%)
4	B	0.34	0/2717	0.53	0/3662
5	C	0.34	0/4602	0.55	0/6212
6	E	0.38	0/3505	0.55	0/4767
7	D	0.36	0/3612	0.52	0/4879
8	F	0.29	0/1336	0.50	0/1798
9	G	0.78	0/923	1.16	0/1425
10	H	0.76	0/958	0.94	0/1474
11	2	0.38	0/4552	0.66	1/6152 (0.0%)
12	3	0.39	0/4944	0.67	1/6718 (0.0%)
13	4	0.39	0/5060	0.68	2/6863 (0.0%)
14	5	0.38	0/4362	0.65	0/5924
15	6	0.39	0/4550	0.65	1/6148 (0.0%)
16	7	0.39	0/4918	0.64	1/6653 (0.0%)
All	All	0.39	0/55538	0.63	7/75501 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	3	717	LEU	CA-CB-CG	6.48	130.20	115.30
3	A	538	THR	C-N-CA	-6.33	105.88	121.70
13	4	804	LEU	CA-CB-CG	5.74	128.51	115.30
16	7	238	LEU	CA-CB-CG	5.49	127.93	115.30
11	2	211	LEU	CA-CB-CG	5.08	126.98	115.30

There are no chirality outliers.

There are no planarity outliers.

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	8	3011	0	2969	111	0
2	9	2972	0	3082	85	0
3	A	3368	0	3420	66	0
4	B	2663	0	2673	51	0
5	C	4505	0	4458	72	0
6	E	3425	0	3402	67	0
7	D	3551	0	3615	82	0
8	F	1315	0	1353	23	0
9	G	831	0	480	3	0
10	H	847	0	457	7	0
11	2	4478	0	4424	77	0
12	3	4866	0	4733	93	0
13	4	4995	0	4751	106	0
14	5	4317	0	4060	72	0
15	6	4475	0	4414	71	0
16	7	4858	0	4803	73	0
17	9	31	0	12	4	0
17	A	31	0	12	7	0
17	D	31	0	12	4	0
17	E	31	0	12	5	0
All	All	54601	0	53142	990	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 9.

The worst 5 of 990 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)
12:3:534:ALA:HB1	14:5:757:LYS:O	1.52	1.08
13:4:601:LEU:HA	13:4:620:ALA:HB3	1.29	1.08
1:8:338:PRO:HG2	1:8:383:MET:O	1.55	1.07
3:A:541:ALA:HB2	9:G:10:DT:OP1	1.57	1.05
12:3:246:GLY:HA3	16:7:109:ASN:HA	1.05	1.04

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	8	380/604 (63%)	340 (90%)	36 (10%)	4 (1%)	14	52
2	9	363/513 (71%)	319 (88%)	42 (12%)	2 (1%)	25	66
3	A	410/913 (45%)	378 (92%)	32 (8%)	0	100	100
4	B	314/620 (51%)	292 (93%)	22 (7%)	0	100	100
5	C	536/616 (87%)	505 (94%)	30 (6%)	1 (0%)	47	81
6	E	414/479 (86%)	385 (93%)	28 (7%)	1 (0%)	47	81
7	D	428/529 (81%)	403 (94%)	25 (6%)	0	100	100
8	F	153/435 (35%)	146 (95%)	7 (5%)	0	100	100
11	2	569/868 (66%)	545 (96%)	20 (4%)	4 (1%)	22	63
12	3	626/971 (64%)	582 (93%)	40 (6%)	4 (1%)	25	66
13	4	651/933 (70%)	603 (93%)	45 (7%)	3 (0%)	29	69
14	5	579/775 (75%)	552 (95%)	24 (4%)	3 (0%)	29	69
15	6	568/1017 (56%)	538 (95%)	28 (5%)	2 (0%)	34	72
16	7	623/845 (74%)	595 (96%)	25 (4%)	3 (0%)	29	69
All	All	6614/10118 (65%)	6183 (94%)	404 (6%)	27 (0%)	38	72

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	C	605	TYR
6	E	445	SER
11	2	350	PRO
1	8	303	SER
2	9	282	LEU

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	8	329/545 (60%)	326 (99%)	3 (1%)	78	87
2	9	338/470 (72%)	333 (98%)	5 (2%)	65	80
3	A	370/812 (46%)	370 (100%)	0	100	100
4	B	298/573 (52%)	296 (99%)	2 (1%)	84	90
5	C	505/576 (88%)	505 (100%)	0	100	100
6	E	387/440 (88%)	387 (100%)	0	100	100
7	D	402/488 (82%)	401 (100%)	1 (0%)	93	96
8	F	151/406 (37%)	151 (100%)	0	100	100
11	2	479/770 (62%)	475 (99%)	4 (1%)	81	89
12	3	512/835 (61%)	510 (100%)	2 (0%)	91	94
13	4	519/848 (61%)	516 (99%)	3 (1%)	86	92
14	5	431/688 (63%)	427 (99%)	4 (1%)	78	87
15	6	475/886 (54%)	474 (100%)	1 (0%)	93	96
16	7	525/753 (70%)	523 (100%)	2 (0%)	91	94
All	All	5721/9090 (63%)	5694 (100%)	27 (0%)	89	93

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	2	794	ARG
13	4	190	CYS
15	6	566	ARG
12	3	527	ARG
13	4	428	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 71 such sidechains are listed below:

Mol	Chain	Res	Type
13	4	380	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	4	543	GLN
14	5	411	ASN
5	C	243	ASN
5	C	78	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
17	AGS	A	2001	-	26,33,33	0.72	1 (3%)	26,52,52	1.08	2 (7%)
17	AGS	E	2001	-	26,33,33	0.68	0	26,52,52	1.33	2 (7%)
17	AGS	9	2001	-	26,33,33	0.73	1 (3%)	26,52,52	1.30	2 (7%)
17	AGS	D	2001	-	26,33,33	0.76	0	26,52,52	1.41	2 (7%)

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
17	AGS	A	2001	-	-	7/17/38/38	0/3/3/3
17	AGS	E	2001	-	-	7/17/38/38	0/3/3/3
17	AGS	9	2001	-	-	7/17/38/38	0/3/3/3
17	AGS	D	2001	-	-	2/17/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	9	2001	AGS	C8-N7	-2.02	1.31	1.34
17	A	2001	AGS	C8-N7	-2.01	1.31	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	D	2001	AGS	PA-O3A-PB	-5.96	112.37	132.83
17	9	2001	AGS	PA-O3A-PB	-5.46	114.08	132.83
17	E	2001	AGS	PA-O3A-PB	-5.21	114.94	132.83
17	A	2001	AGS	PA-O3A-PB	-3.84	119.66	132.83
17	D	2001	AGS	C5-C6-N6	2.31	123.87	120.35

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	9	2001	AGS	C5'-O5'-PA-O2A
17	9	2001	AGS	C5'-O5'-PA-O3A
17	A	2001	AGS	C5'-O5'-PA-O1A
17	A	2001	AGS	C5'-O5'-PA-O2A
17	A	2001	AGS	O4'-C4'-C5'-O5'

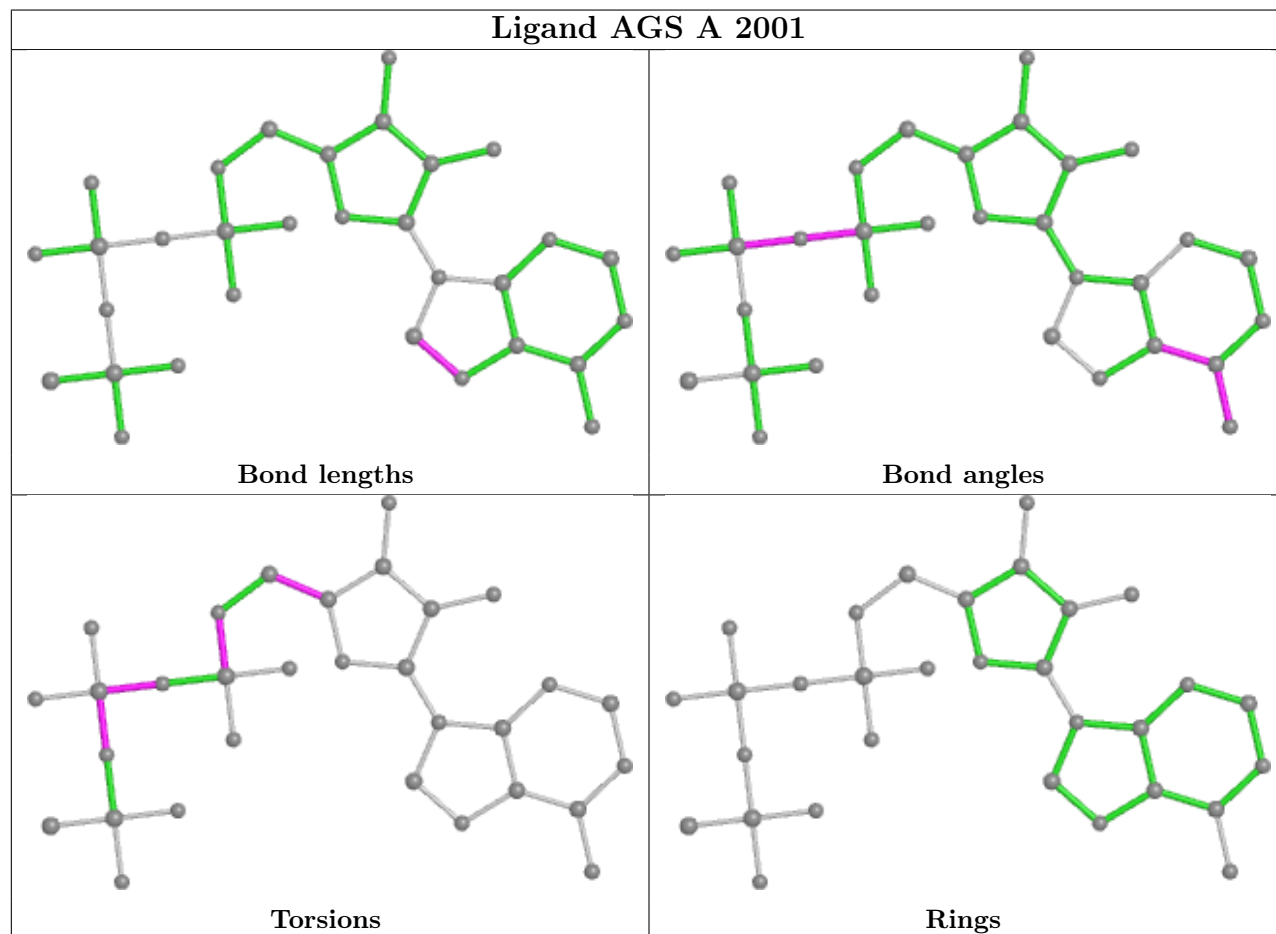
There are no ring outliers.

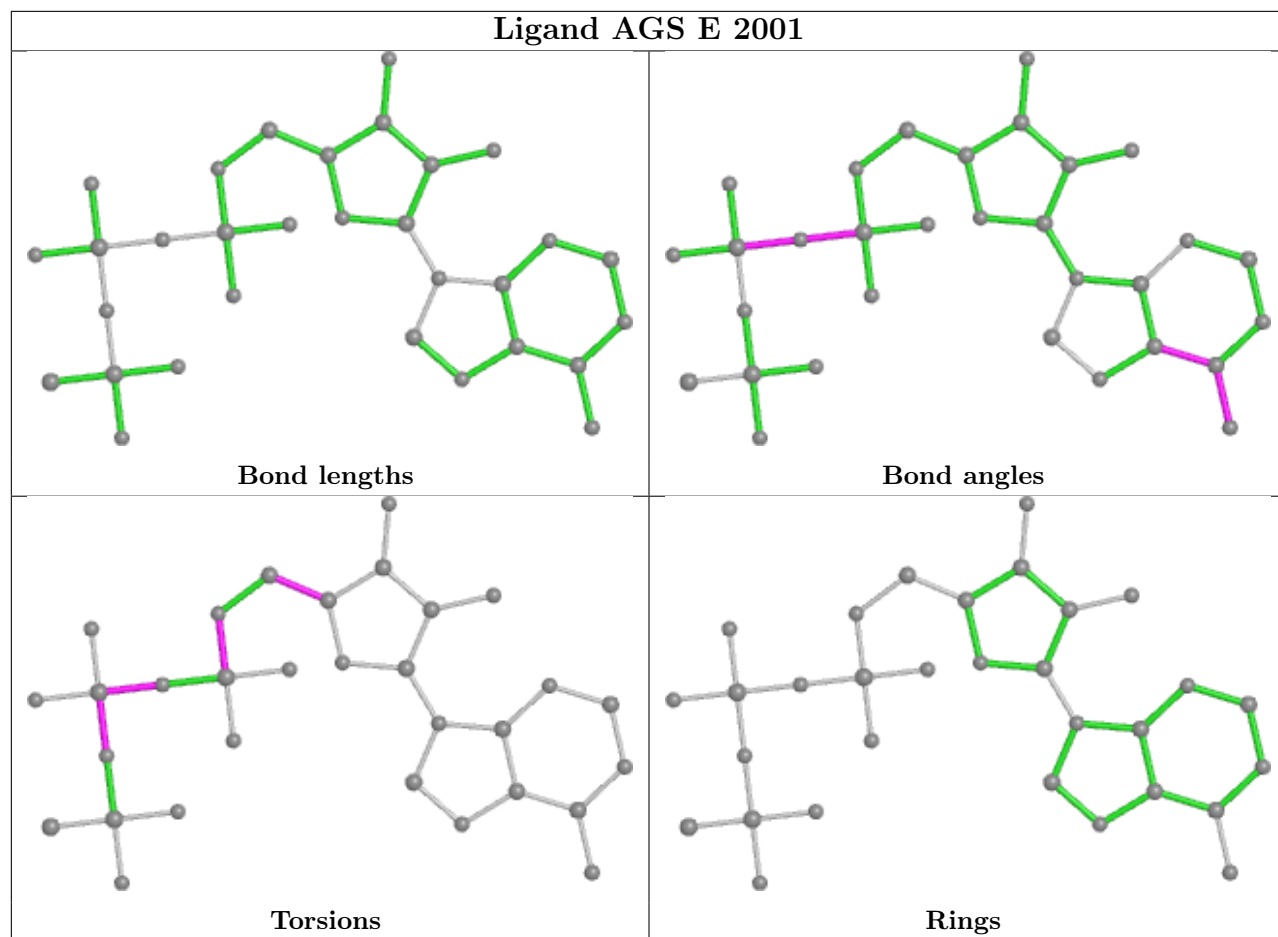
4 monomers are involved in 20 short contacts:

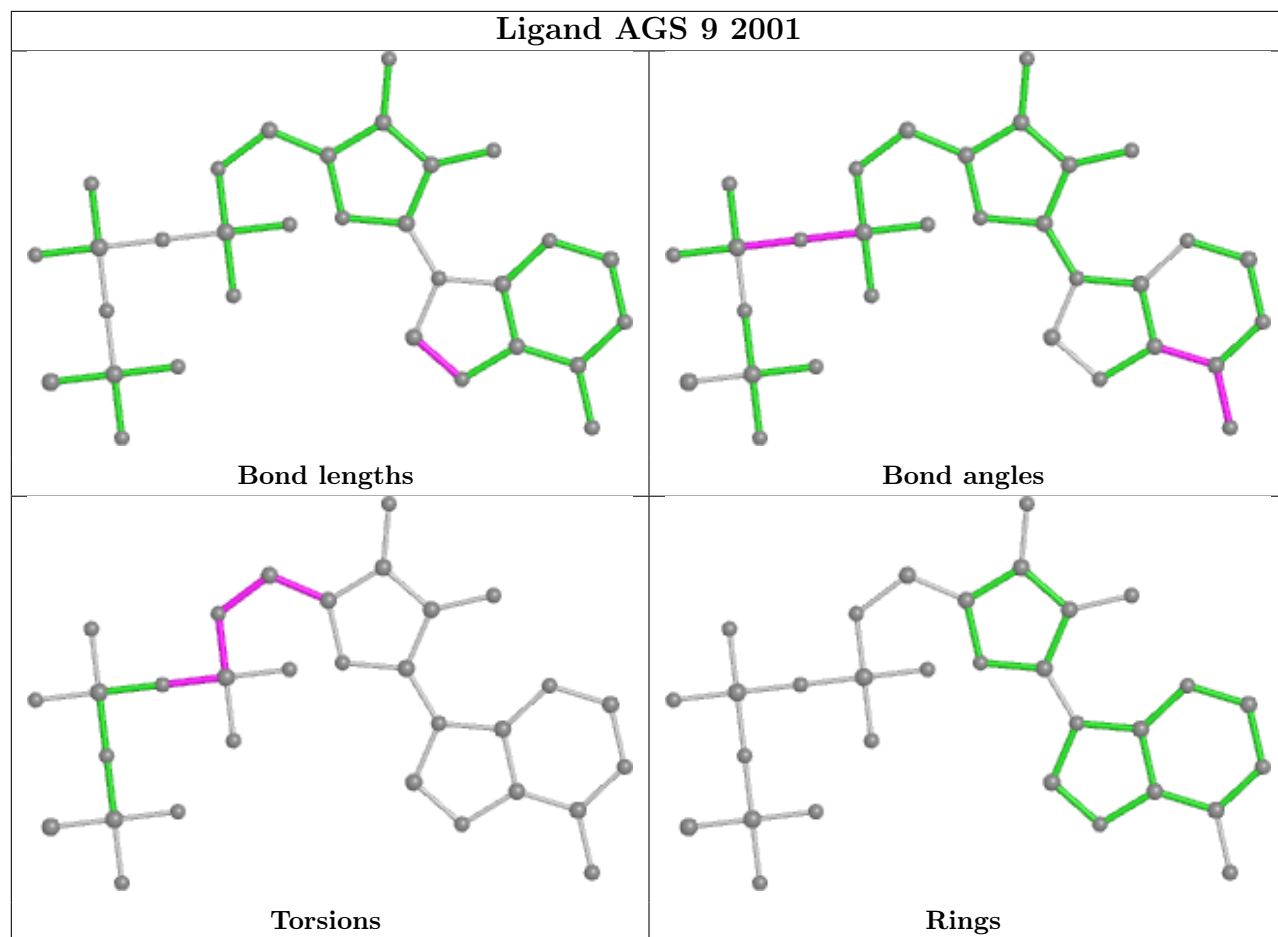
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	A	2001	AGS	7	0
17	E	2001	AGS	5	0
17	9	2001	AGS	4	0
17	D	2001	AGS	4	0

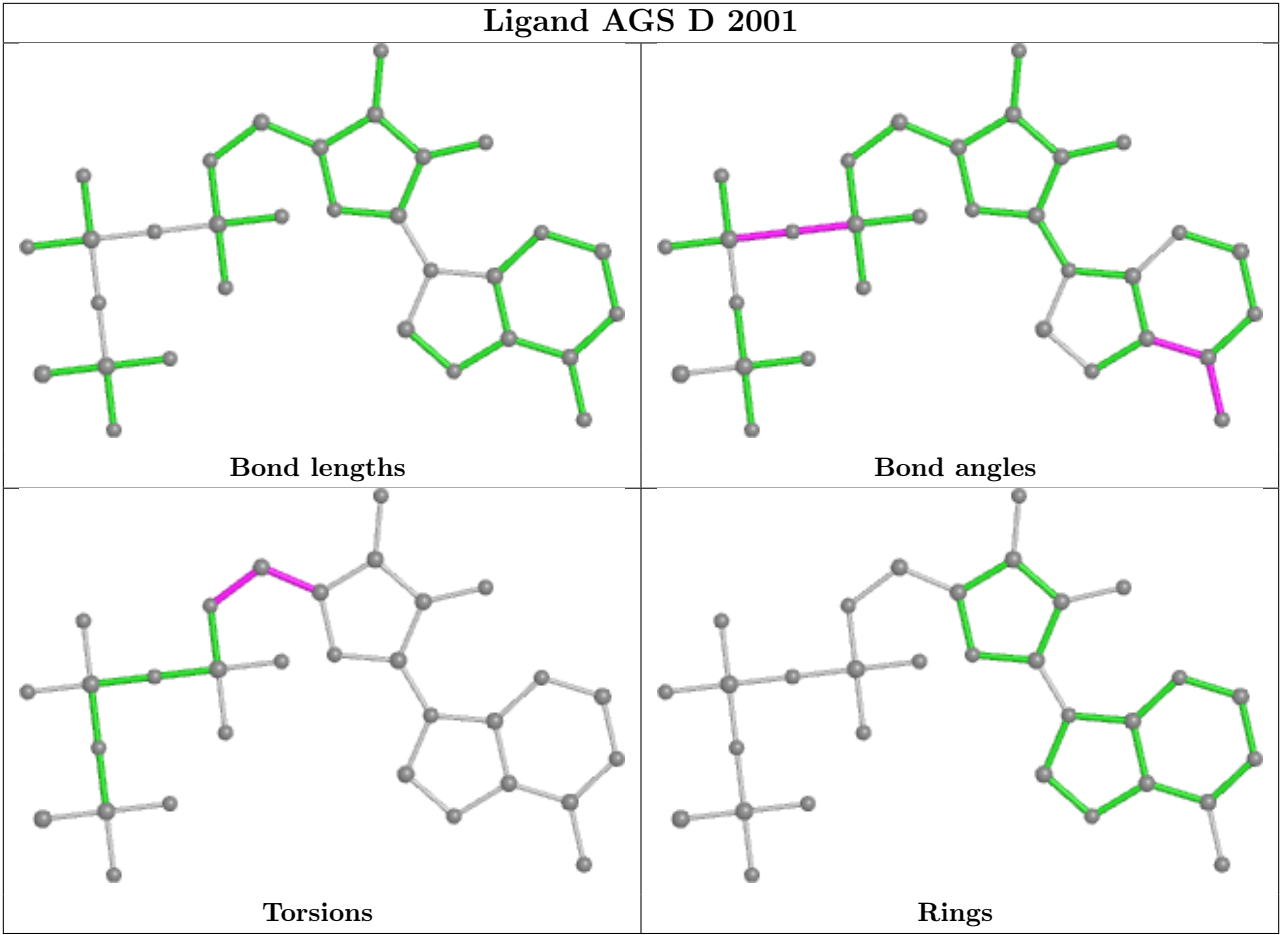
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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.









5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	9	1
16	7	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	9	399:ASN	C	400:ASN	N	3.97
1	7	785:GLU	C	786:TYR	N	3.65

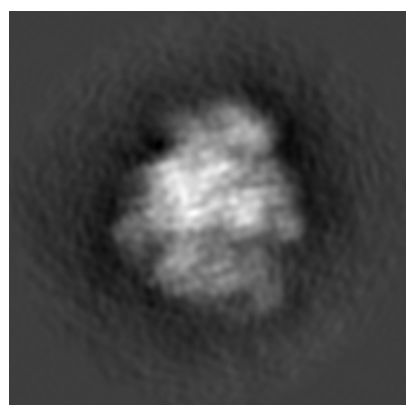
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21665. These allow visual inspection of the internal detail of the map and identification of artifacts.

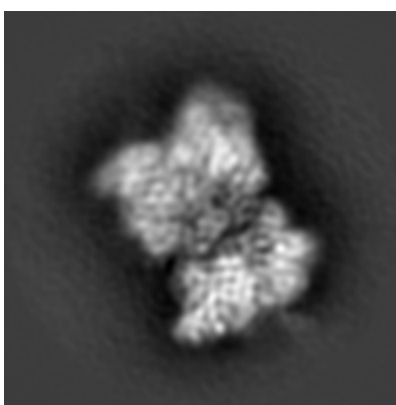
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

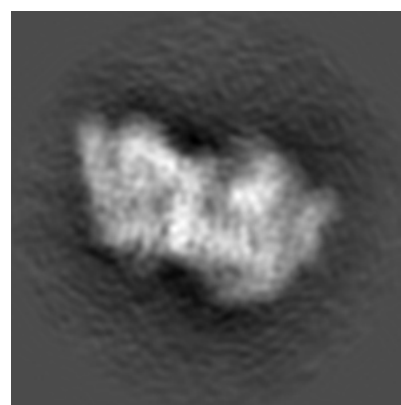
6.1.1 Primary map



X



Y

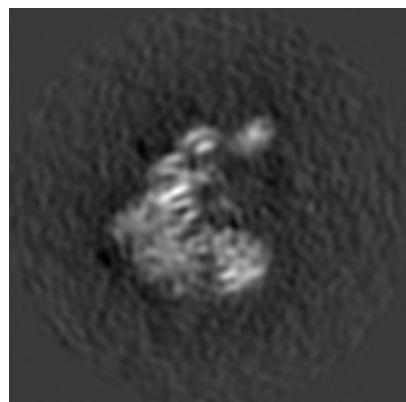


Z

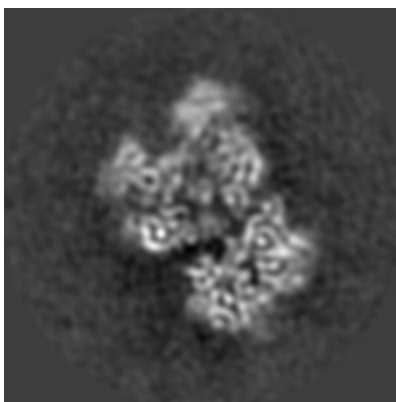
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

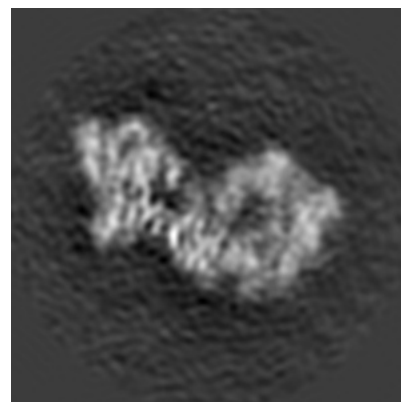
6.2.1 Primary map



X Index: 128



Y Index: 128

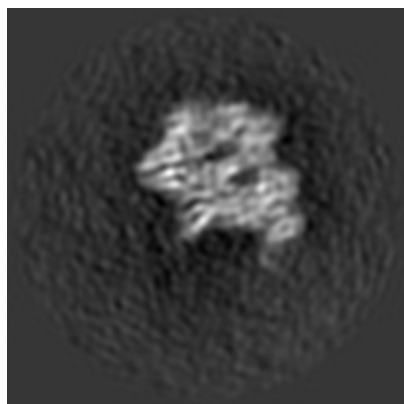


Z Index: 128

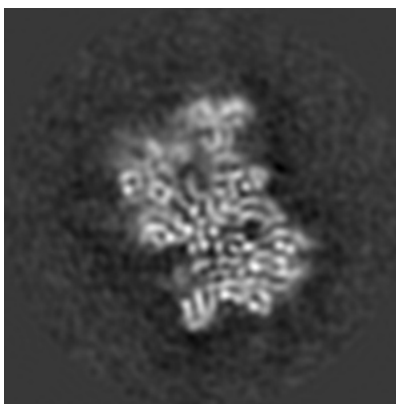
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

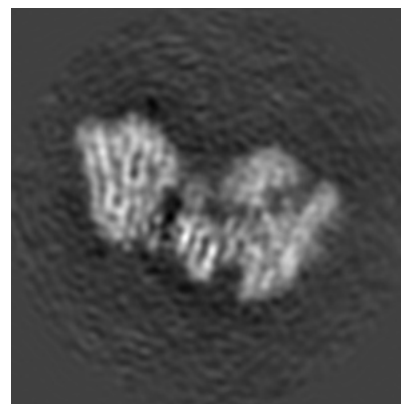
6.3.1 Primary map



X Index: 86



Y Index: 113

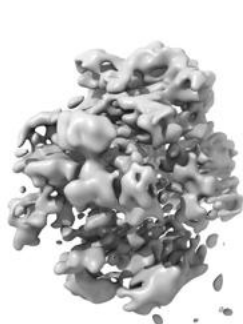


Z Index: 134

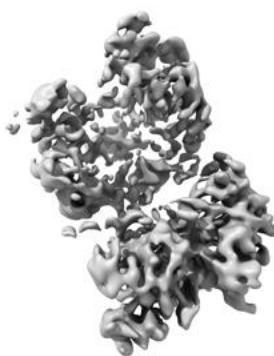
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

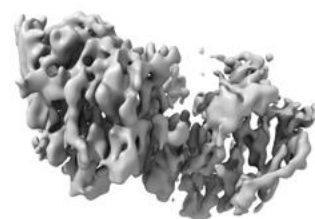
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

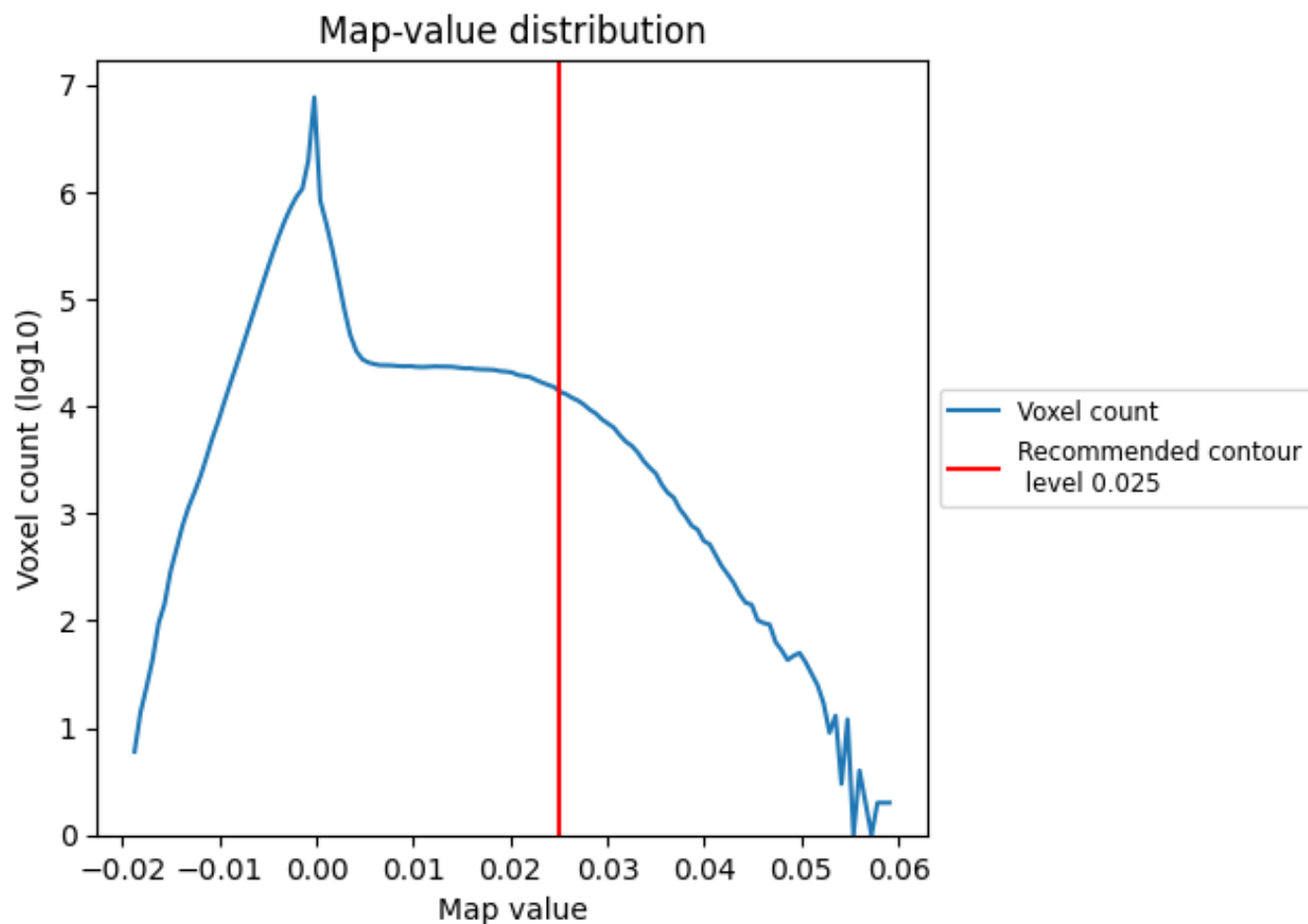
6.5 Mask visualisation

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

7 Map analysis [i](#)

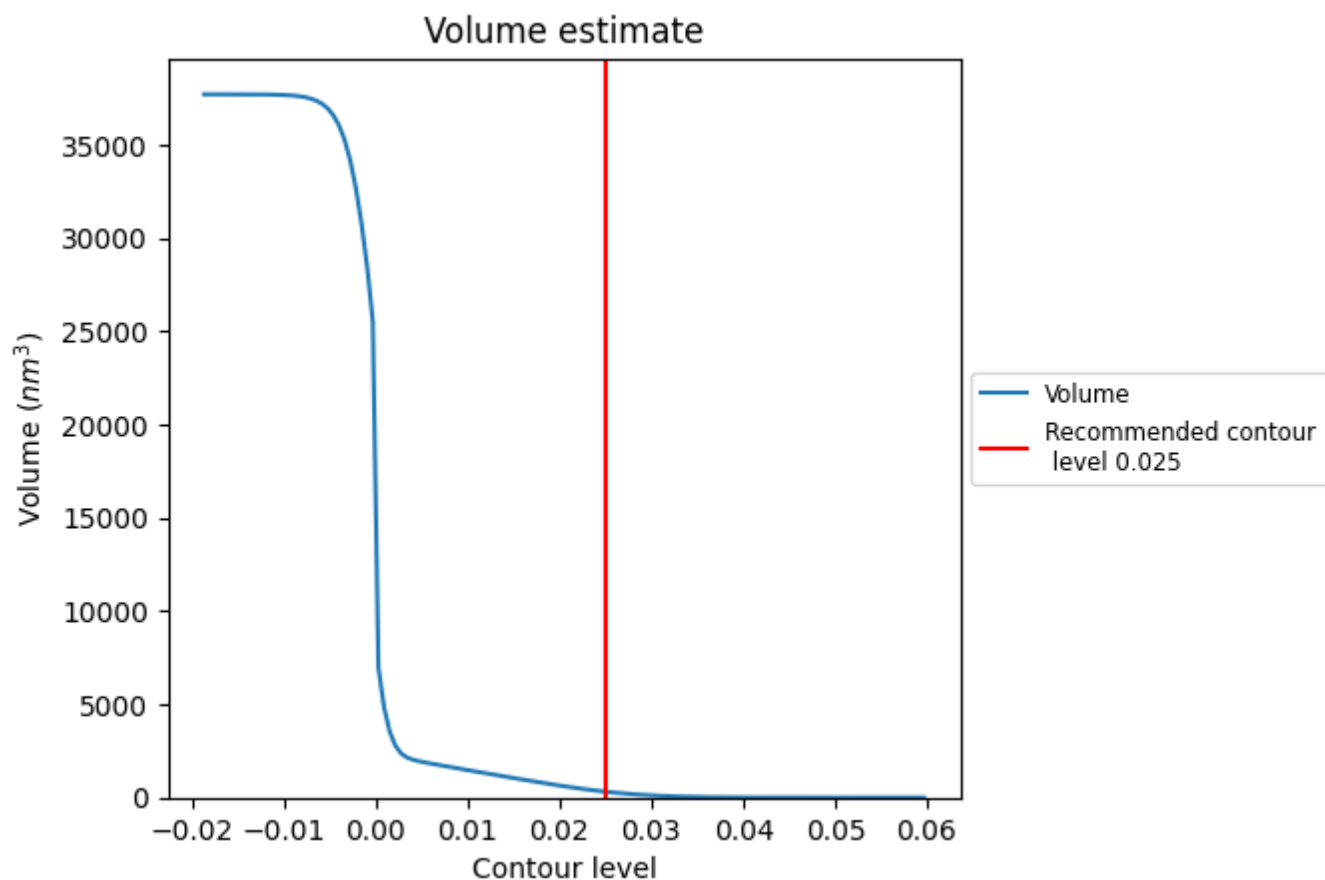
This section contains the results of statistical analysis of the map.

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.

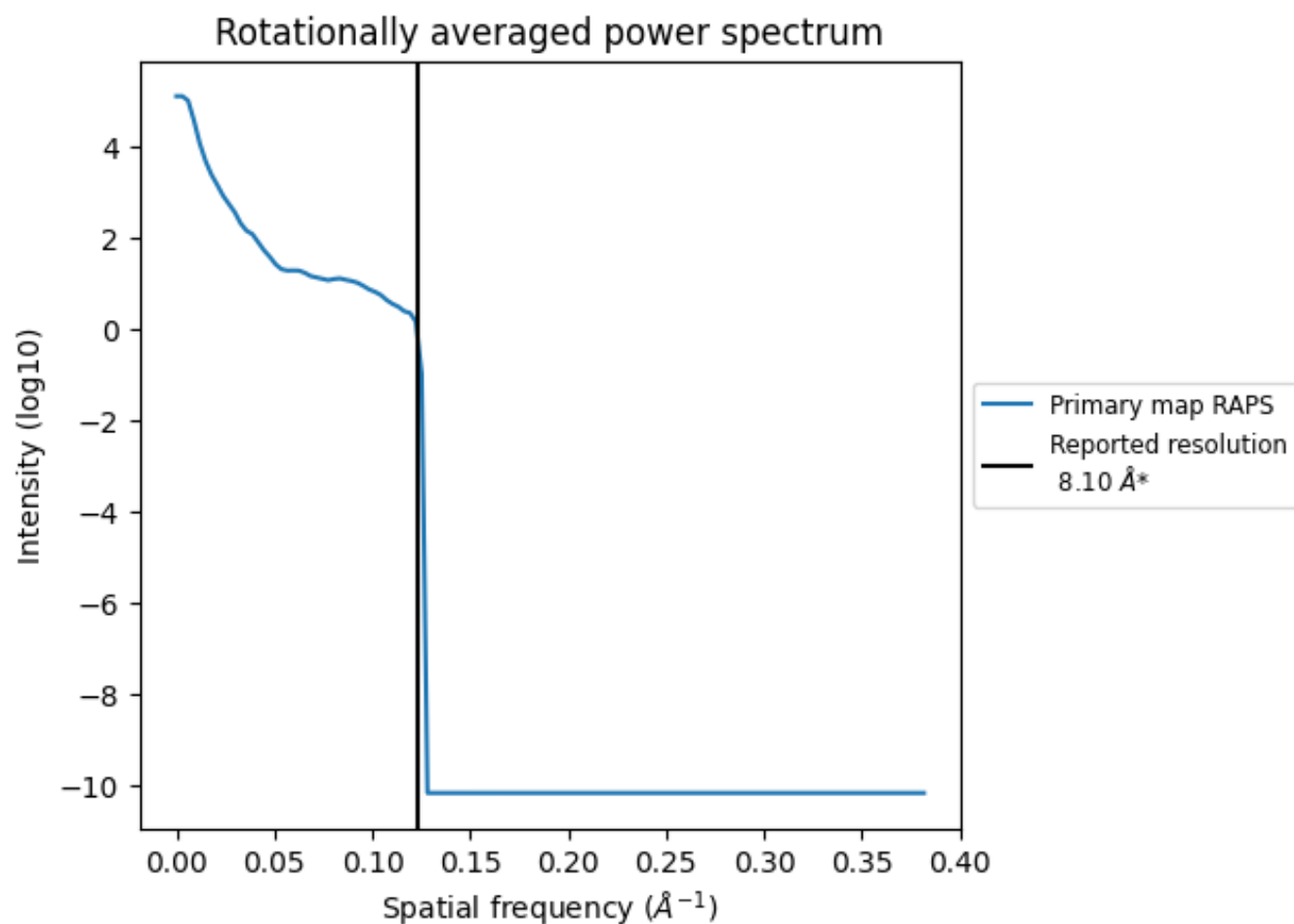
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 315 nm³; this corresponds to an approximate mass of 284 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 0.123 \AA^{-1}

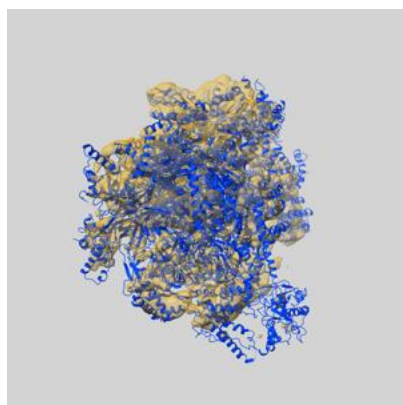
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

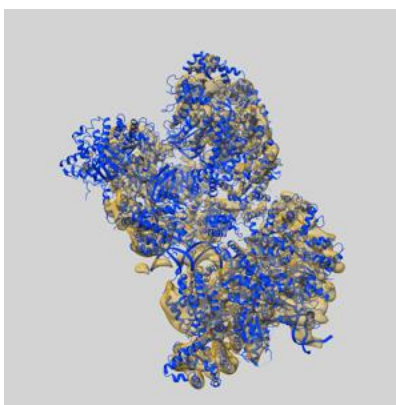
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21665 and PDB model 6WGG. Per-residue inclusion information can be found in section 3 on page 7.

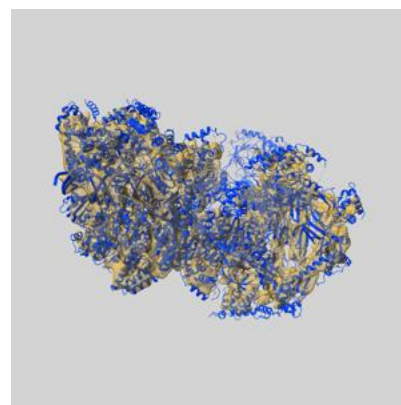
9.1 Map-model overlay [i](#)



X



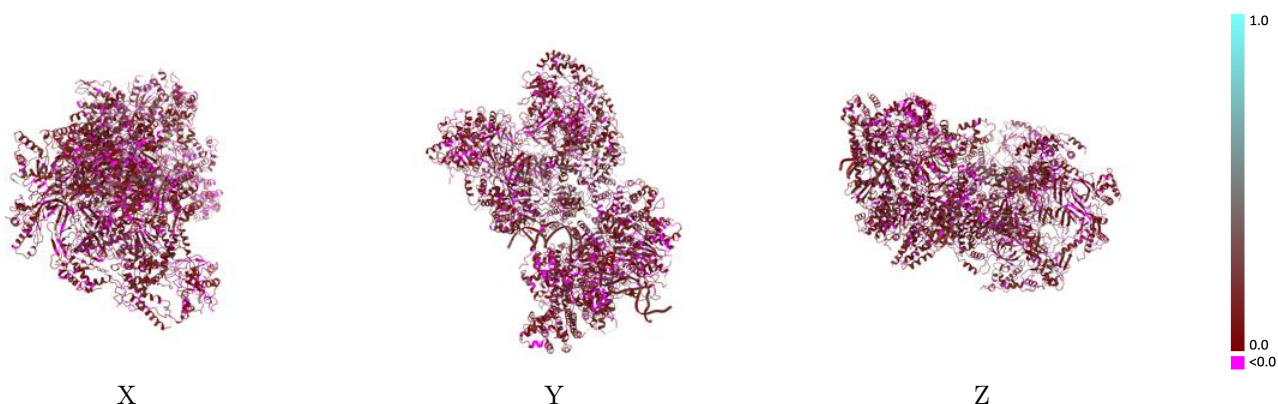
Y



Z

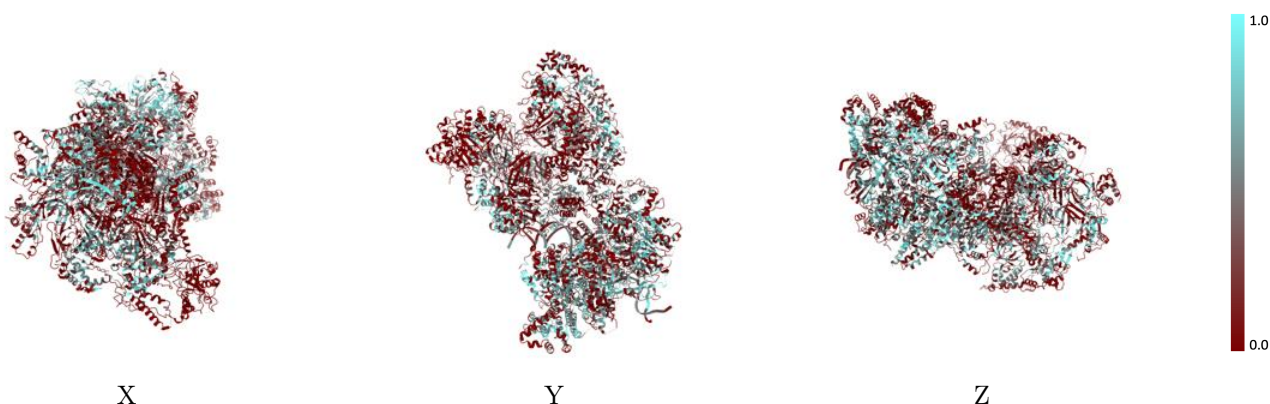
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



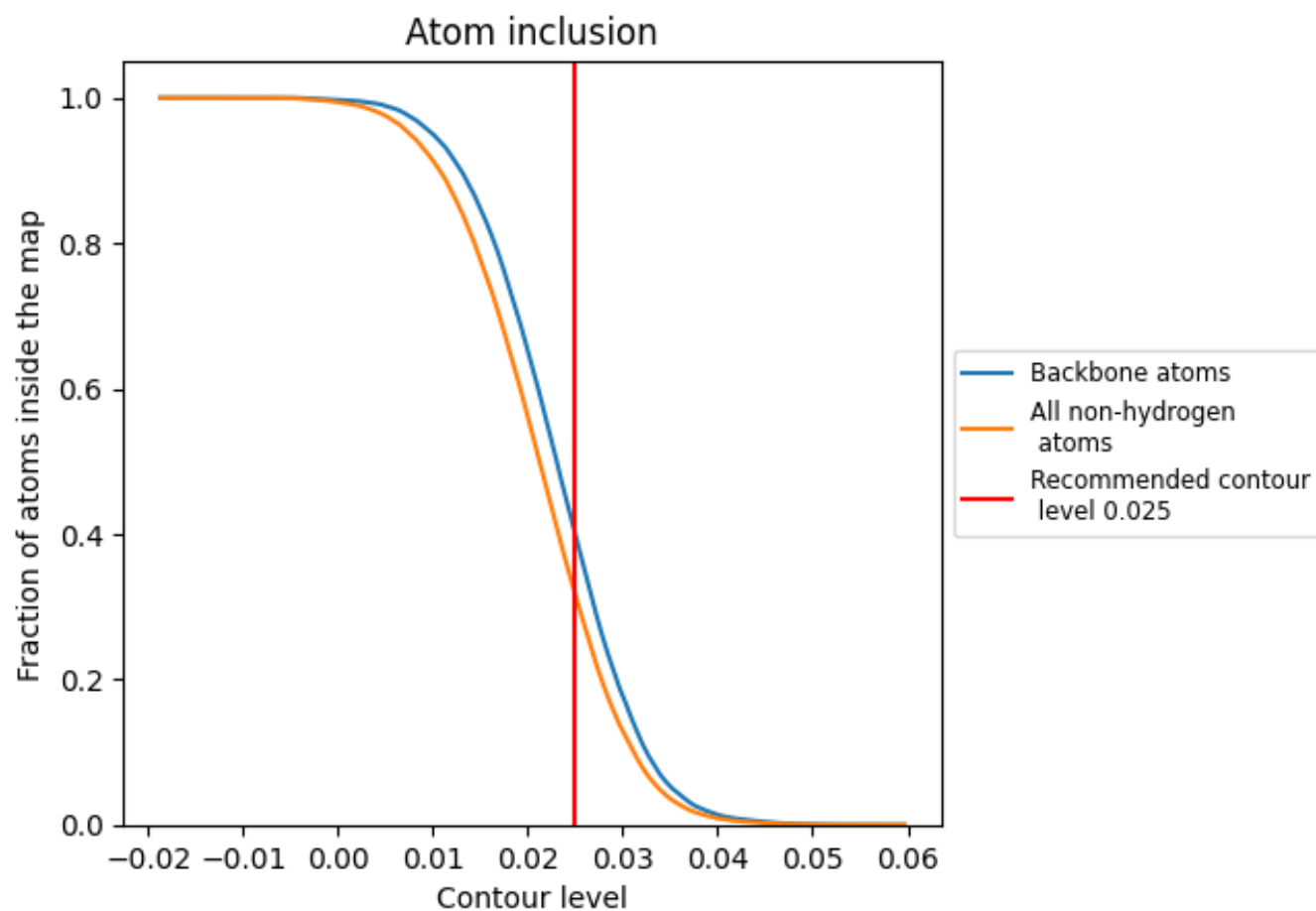
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).



































9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 32% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3162	 0.1040
2	 0.2791	 0.1060
3	 0.3103	 0.1010
4	 0.2853	 0.1110
5	 0.1860	 0.0970
6	 0.3390	 0.1010
7	 0.2474	 0.1150
8	 0.0376	 0.0690
9	 0.3418	 0.0670
A	 0.4343	 0.1060
B	 0.3385	 0.0930
C	 0.4401	 0.1060
D	 0.4253	 0.1220
E	 0.4012	 0.1230
F	 0.2363	 0.0540
G	 0.4320	 0.1780
H	 0.5573	 0.2000

