



wwPDB EM Validation Summary Report ⓘ

Aug 2, 2026 – 04:35 PM EDT

PDB ID : 9NFZ / pdb_00009nfz
EMDB ID : EMD-49378
Title : Human SRCAP-nucleosome complex in the fully inserted state of the H2A.Z histone exchange reaction (composite structure)
Authors : Louder, R.K.; Park, G.
Deposited on : 2025-02-21
Resolution : 3.80 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:

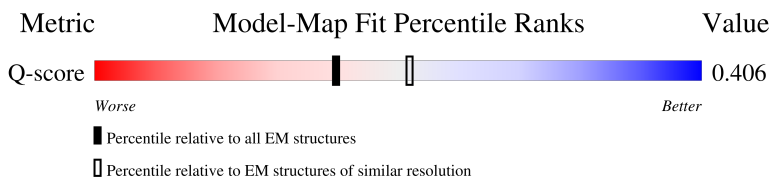
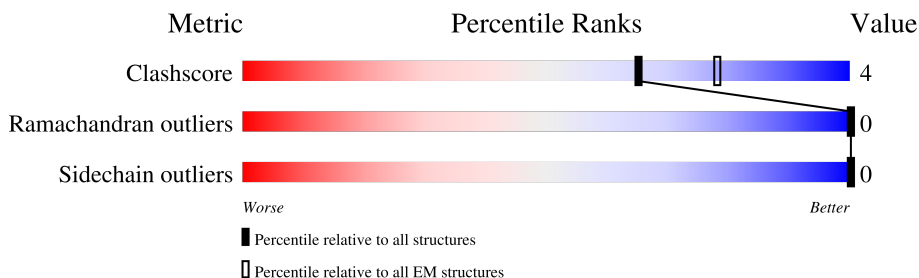
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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.



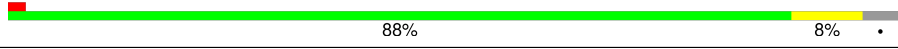
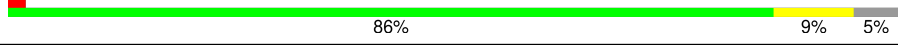
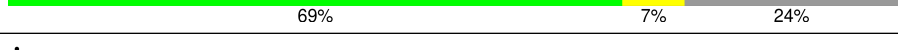
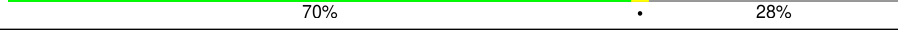
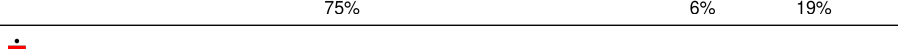
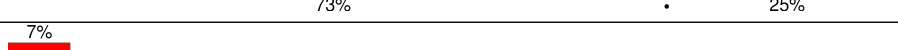
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	3230	 19% 78%
2	B	364	 20% 47% 48%
3	C	396	 9% 89% 11%
4	D	154	 9% 63% 5% 32%

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Mol	Chain	Length	Quality of chain
5	E	456	
5	G	456	
5	I	456	
6	F	463	
6	H	463	
6	J	463	
7	Q	127	
8	R	125	
9	S	128	
10	T	125	
11	U	135	
11	W	135	
12	V	102	
12	X	102	
13	Y	285	
14	Z	285	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 42020 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 Helicase SRCAP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	703	Total	C	N	O	S	0	0
			5767	3689	1049	994	35		

- Molecule 2 is a protein called Vacuolar protein sorting-associated protein 72 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	188	Total	C	N	O	S	0	0
			1508	937	269	298	4		

- Molecule 3 is a protein called Actin-related protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	396	Total	C	N	O	S	0	0
			3226	2064	528	616	18		

- Molecule 4 is a protein called Zinc finger HIT domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	105	Total	C	N	O	S	0	0
			831	508	164	151	8		

- Molecule 5 is a protein called RuvB-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	433	Total	C	N	O	S	0	0
			3344	2107	574	646	17		
5	G	445	Total	C	N	O	S	0	0
			3430	2159	588	665	18		
5	I	436	Total	C	N	O	S	0	0
			3365	2119	577	652	17		

- Molecule 6 is a protein called RuvB-like 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	438	Total	C	N	O	S	0	0
			3395	2121	596	662	16		
6	H	432	Total	C	N	O	S	0	0
			3361	2101	590	654	16		
6	J	418	Total	C	N	O	S	0	0
			3254	2039	568	632	15		

- Molecule 7 is a protein called Histone H2A.Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q	97	Total	C	N	O		0	0
			732	457	143	132			

- Molecule 8 is a protein called Histone H2B type 1-C/E/F/G/I.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	R	90	Total	C	N	O	S	0	0
			700	441	124	133	2		

- Molecule 9 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	S	104	Total	C	N	O		0	0
			800	504	156	140			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	99	ARG	GLY	conflict	UNP P06897
S	123	SER	-	expression tag	UNP P06897
S	124	LYS	-	expression tag	UNP P06897
S	125	SER	-	expression tag	UNP P06897
S	126	LYS	-	expression tag	UNP P06897
S	127	SER	-	expression tag	UNP P06897
S	128	LYS	-	expression tag	UNP P06897

- Molecule 10 is a protein called Histone H2B 1.1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	T	94	Total	C	N	O	S	0	0
			736	463	132	139	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	32	THR	SER	conflict	UNP P02281

- Molecule 11 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	U	90	Total	C	N	O	S	0	0
			740	467	140	130	3		
11	W	96	Total	C	N	O	S	0	0
			795	501	154	137	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	102	ALA	GLY	conflict	UNP Q71DI3
W	102	ALA	GLY	conflict	UNP Q71DI3

- Molecule 12 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	V	79	Total	C	N	O	S	0	0
			627	395	121	110	1		
12	X	79	Total	C	N	O	S	0	0
			627	395	121	110	1		

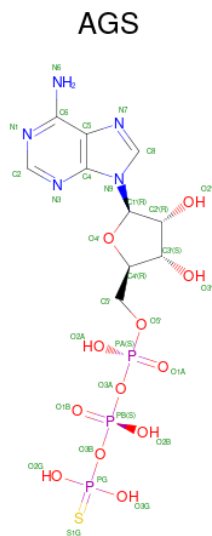
- Molecule 13 is a DNA chain called DNA (285-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Y	111	Total	C	N	O	P	0	0
			2266	1074	414	667	111		

- Molecule 14 is a DNA chain called DNA (285-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Z	111	Total	C	N	O	P	0	0
			2285	1080	429	665	111		

- Molecule 15 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms					AltConf	
15	A	1	Total 31	C 10	N 5	O 12	P 3	S 1	0
15	C	1	Total 31	C 10	N 5	O 12	P 3	S 1	0

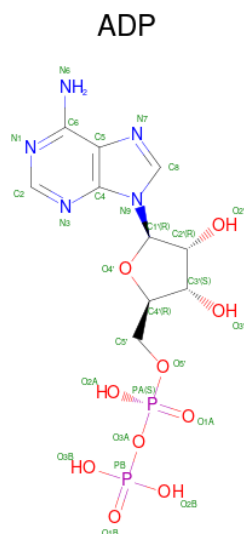
- Molecule 16 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
16	A	1	Total Mg 1 1	0
16	C	1	Total Mg 1 1	0
16	F	1	Total Mg 1 1	0
16	H	1	Total Mg 1 1	0
16	J	1	Total Mg 1 1	0

- Molecule 17 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
17	D	2	Total Zn 2 2	0

- Molecule 18 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

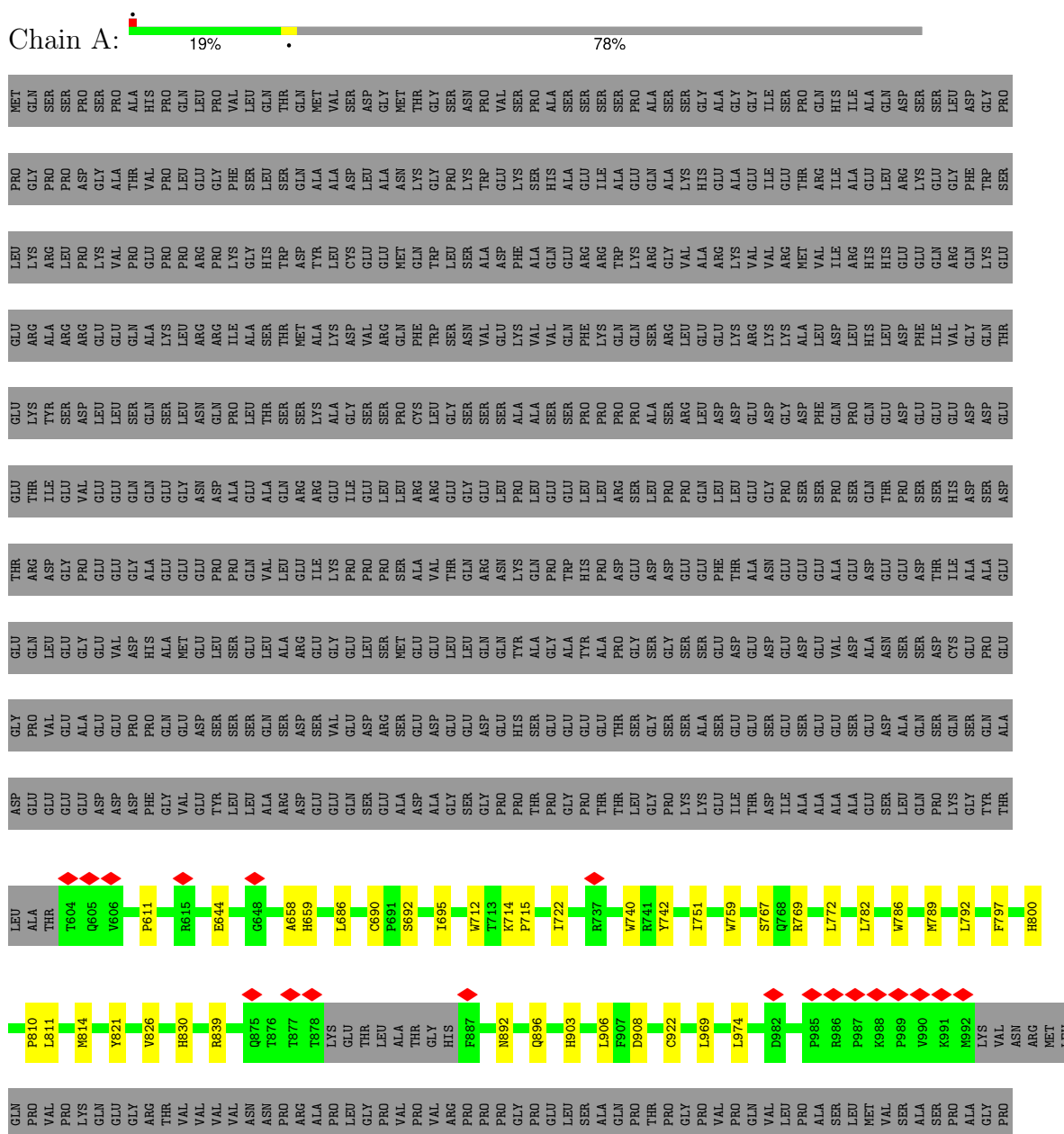


Mol	Chain	Residues	Atoms					AltConf
18	E	1	Total 27	C 10	N 5	O 10	P 2	0
18	F	1	Total 27	C 10	N 5	O 10	P 2	0
18	G	1	Total 27	C 10	N 5	O 10	P 2	0
18	H	1	Total 27	C 10	N 5	O 10	P 2	0
18	I	1	Total 27	C 10	N 5	O 10	P 2	0
18	J	1	Total 27	C 10	N 5	O 10	P 2	0

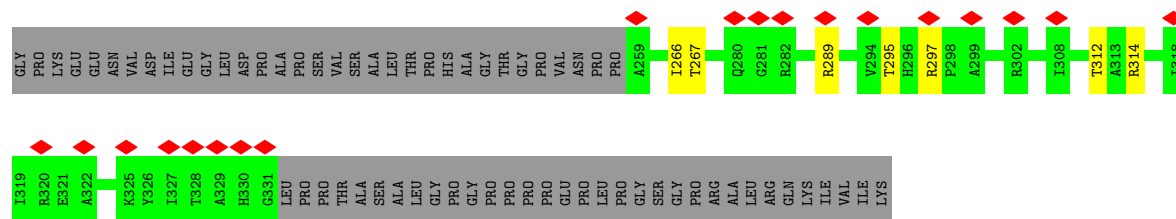
3 Residue-property plots

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.

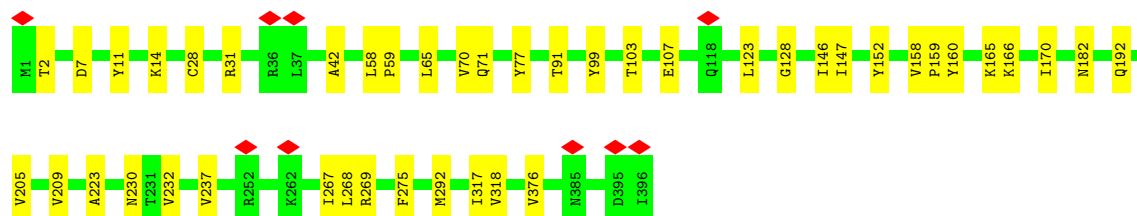
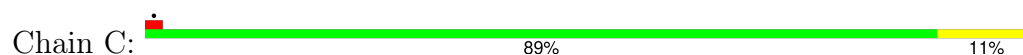
• Molecule 1: Helicase SRCAP



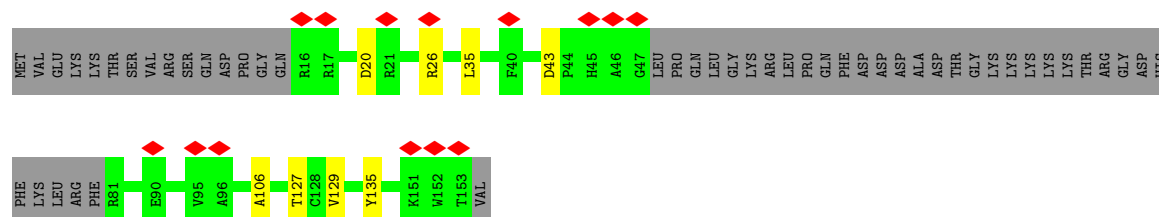




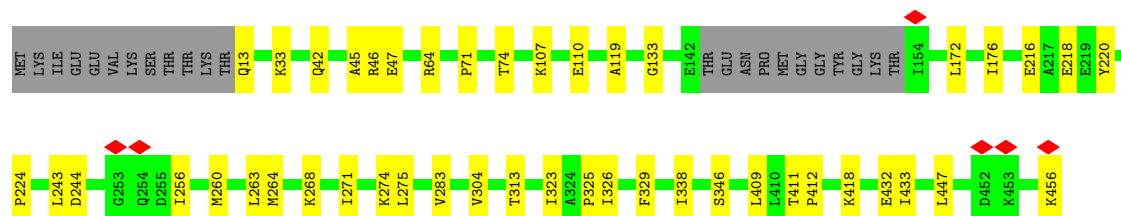
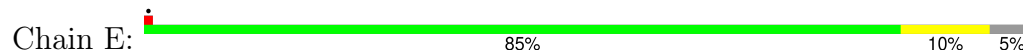
• Molecule 3: Actin-related protein 6



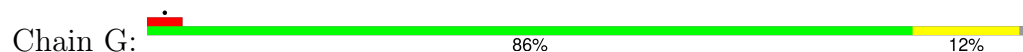
• Molecule 4: Zinc finger HIT domain-containing protein 1



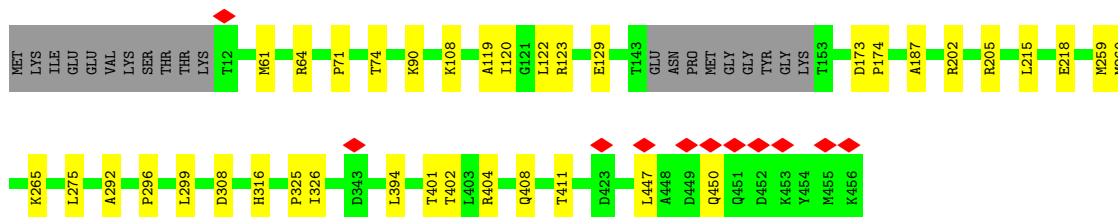
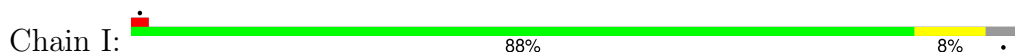
• Molecule 5: RuvB-like 1



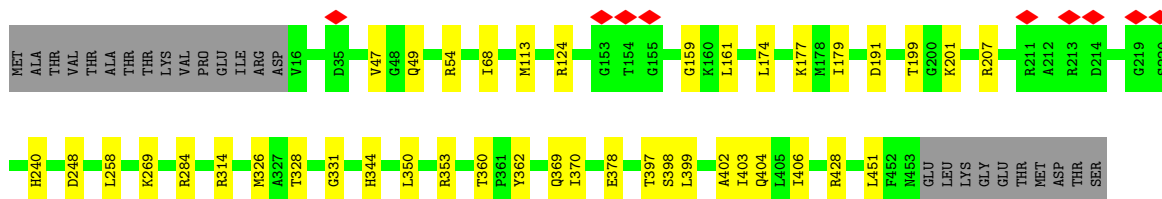
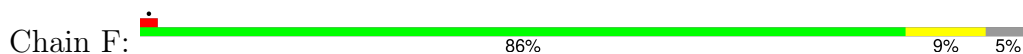
• Molecule 5: RuvB-like 1



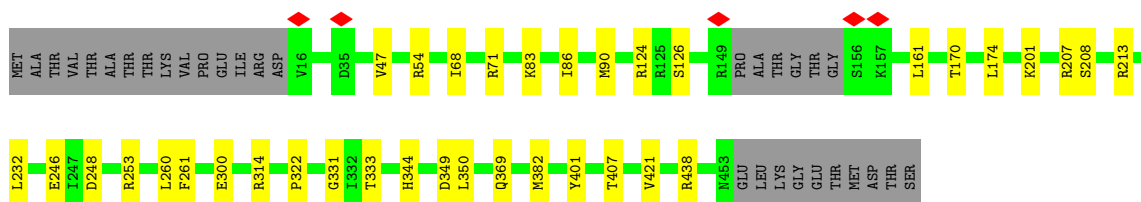
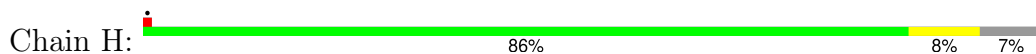
- Molecule 5: RuvB-like 1



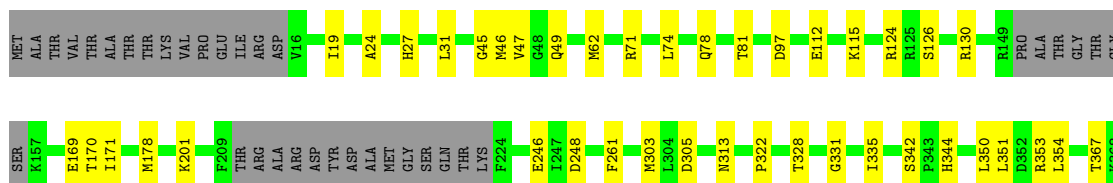
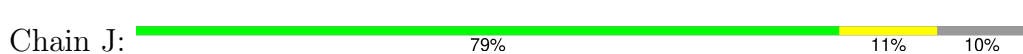
- Molecule 6: RuvB-like 2



- Molecule 6: RuvB-like 2

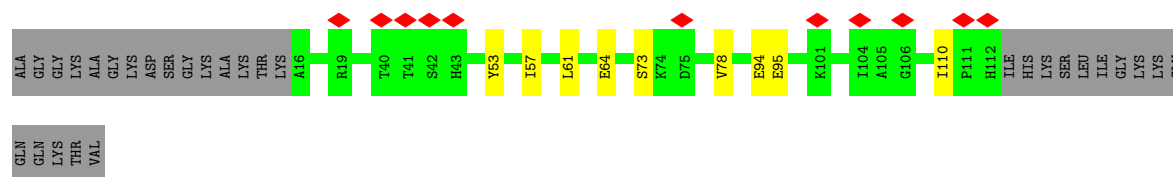


- Molecule 6: RuvB-like 2

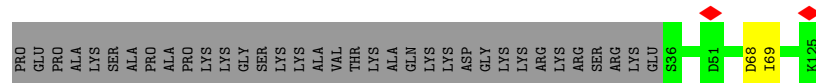




• Molecule 7: Histone H2A.Z



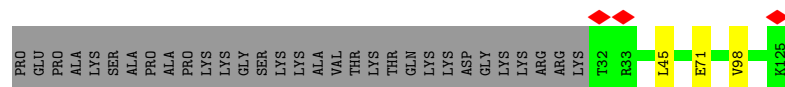
• Molecule 8: Histone H2B type 1-C/E/F/G/I



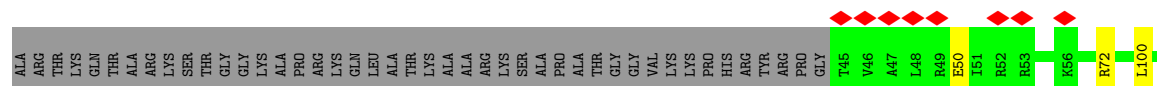
• Molecule 9: Histone H2A type 1



• Molecule 10: Histone H2B 1.1



• Molecule 11: Histone H3.2



• Molecule 11: Histone H3.2



DT DC DG DA DT

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24589	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.419	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	393.59998, 393.59998, 393.59998	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.025, 1.025, 1.025	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, ZN, 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	0.11	0/5914	0.28	0/8005
2	B	0.12	0/1536	0.35	0/2070
3	C	0.10	0/3300	0.24	0/4467
4	D	0.10	0/848	0.28	0/1147
5	E	0.12	0/3387	0.26	0/4561
5	G	0.11	0/3476	0.24	0/4683
5	I	0.11	0/3408	0.23	0/4591
6	F	0.11	0/3435	0.24	0/4625
6	H	0.11	0/3399	0.24	0/4573
6	J	0.12	0/3290	0.24	0/4426
7	Q	0.15	0/742	0.49	1/1001 (0.1%)
8	R	0.14	0/711	0.41	0/956
9	S	0.10	0/810	0.22	0/1095
10	T	0.10	0/747	0.21	0/1004
11	U	0.12	0/748	0.24	0/1003
11	W	0.11	0/806	0.23	0/1081
12	V	0.11	0/634	0.23	0/848
12	X	0.15	0/634	0.31	0/848
13	Y	0.25	0/2539	0.52	0/3914
14	Z	0.24	0/2565	0.49	0/3959
All	All	0.14	0/42929	0.31	1/58857 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	Q	110	ILE	N-CA-C	6.12	113.89	108.63

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	A	5767	0	5844	48	0
2	B	1508	0	1473	11	0
3	C	3226	0	3147	26	0
4	D	831	0	798	10	0
5	E	3344	0	3449	33	0
5	G	3430	0	3530	43	0
5	I	3365	0	3470	30	0
6	F	3395	0	3467	28	0
6	H	3361	0	3435	25	0
6	J	3254	0	3330	38	0
7	Q	732	0	766	7	0
8	R	700	0	719	2	0
9	S	800	0	851	6	0
10	T	736	0	760	3	0
11	U	740	0	781	10	0
11	W	795	0	833	7	0
12	V	627	0	663	5	0
12	X	627	0	663	10	0
13	Y	2266	0	1245	36	0
14	Z	2285	0	1244	38	0
15	A	31	0	12	0	0
15	C	31	0	12	0	0
16	A	1	0	0	0	0
16	C	1	0	0	0	0
16	F	1	0	0	0	0
16	H	1	0	0	0	0
16	J	1	0	0	0	0
17	D	2	0	0	0	0
18	E	27	0	12	0	0
18	F	27	0	12	1	0
18	G	27	0	12	3	0
18	H	27	0	12	1	0
18	I	27	0	12	0	0
18	J	27	0	12	1	0
All	All	42020	0	40564	333	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 333 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)
14:Z:49:DC:H2'	14:Z:50:DG:C8	2.22	0.75
5:G:411:THR:HG21	6:H:68:ILE:HG13	1.69	0.74
1:A:692:SER:HB2	2:B:176:ALA:HB1	1.71	0.71
13:Y:25:DG:H2'	13:Y:26:DG:C8	2.26	0.71
6:H:207:ARG:NH1	5:I:173:ASP:OD1	2.24	0.70

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	697/3230 (22%)	686 (98%)	11 (2%)	0	100	100
2	B	178/364 (49%)	174 (98%)	4 (2%)	0	100	100
3	C	394/396 (100%)	381 (97%)	13 (3%)	0	100	100
4	D	101/154 (66%)	99 (98%)	2 (2%)	0	100	100
5	E	429/456 (94%)	423 (99%)	6 (1%)	0	100	100
5	G	443/456 (97%)	440 (99%)	3 (1%)	0	100	100
5	I	432/456 (95%)	423 (98%)	9 (2%)	0	100	100
6	F	436/463 (94%)	428 (98%)	8 (2%)	0	100	100
6	H	428/463 (92%)	419 (98%)	9 (2%)	0	100	100
6	J	412/463 (89%)	404 (98%)	8 (2%)	0	100	100
7	Q	95/127 (75%)	94 (99%)	1 (1%)	0	100	100
8	R	88/125 (70%)	87 (99%)	1 (1%)	0	100	100
9	S	102/128 (80%)	101 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	T	92/125 (74%)	90 (98%)	2 (2%)	0	100	100
11	U	88/135 (65%)	88 (100%)	0	0	100	100
11	W	94/135 (70%)	92 (98%)	2 (2%)	0	100	100
12	V	77/102 (76%)	75 (97%)	2 (3%)	0	100	100
12	X	77/102 (76%)	76 (99%)	1 (1%)	0	100	100
All	All	4663/7880 (59%)	4580 (98%)	83 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	633/2721 (23%)	633 (100%)	0	100	100
2	B	166/312 (53%)	166 (100%)	0	100	100
3	C	361/361 (100%)	361 (100%)	0	100	100
4	D	89/133 (67%)	89 (100%)	0	100	100
5	E	367/387 (95%)	367 (100%)	0	100	100
5	G	376/387 (97%)	376 (100%)	0	100	100
5	I	370/387 (96%)	370 (100%)	0	100	100
6	F	368/390 (94%)	368 (100%)	0	100	100
6	H	365/390 (94%)	365 (100%)	0	100	100
6	J	354/390 (91%)	354 (100%)	0	100	100
7	Q	75/96 (78%)	75 (100%)	0	100	100
8	R	77/105 (73%)	77 (100%)	0	100	100
9	S	82/101 (81%)	82 (100%)	0	100	100
10	T	80/105 (76%)	80 (100%)	0	100	100
11	U	79/110 (72%)	79 (100%)	0	100	100
11	W	84/110 (76%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	V	64/78 (82%)	64 (100%)	0	100	100
12	X	64/78 (82%)	64 (100%)	0	100	100
All	All	4054/6641 (61%)	4054 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
5	I	393	HIS
11	U	85	GLN
12	X	93	GLN
12	V	93	GLN
6	J	255	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	ADP	G	501	-	28,29,29	1.38	4 (14%)	43,45,45	1.74	8 (18%)
15	AGS	C	401	16	32,33,33	0.65	1 (3%)	45,52,52	0.70	1 (2%)
18	ADP	J	501	16	28,29,29	1.37	4 (14%)	43,45,45	1.74	8 (18%)
18	ADP	E	501	-	28,29,29	1.38	4 (14%)	43,45,45	1.76	8 (18%)
18	ADP	I	501	-	28,29,29	1.38	5 (17%)	43,45,45	1.76	8 (18%)
18	ADP	F	501	16	28,29,29	1.37	4 (14%)	43,45,45	1.75	8 (18%)
15	AGS	A	3301	16	32,33,33	0.58	0	45,52,52	0.73	1 (2%)
18	ADP	H	501	16	28,29,29	1.38	4 (14%)	43,45,45	1.77	7 (16%)

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
18	ADP	G	501	-	-	5/16/32/32	0/3/3/3
15	AGS	C	401	16	-	4/21/38/38	0/3/3/3
18	ADP	J	501	16	-	7/16/32/32	0/3/3/3
18	ADP	E	501	-	-	3/16/32/32	0/3/3/3
18	ADP	I	501	-	-	3/16/32/32	0/3/3/3
18	ADP	F	501	16	-	4/16/32/32	0/3/3/3
15	AGS	A	3301	16	-	2/21/38/38	0/3/3/3
18	ADP	H	501	16	-	0/16/32/32	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	H	501	ADP	C5-C4	4.51	1.47	1.39
18	G	501	ADP	C5-C4	4.48	1.47	1.39
18	J	501	ADP	C5-C4	4.47	1.47	1.39
18	E	501	ADP	C5-C4	4.46	1.47	1.39
18	I	501	ADP	C5-C4	4.45	1.47	1.39

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	H	501	ADP	C5-C4-N3	-5.89	118.61	126.72
18	J	501	ADP	C5-C4-N3	-5.83	118.69	126.72
18	E	501	ADP	C5-C4-N3	-5.82	118.71	126.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	I	501	ADP	C5-C4-N3	-5.80	118.73	126.72
18	F	501	ADP	C5-C4-N3	-5.79	118.74	126.72

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

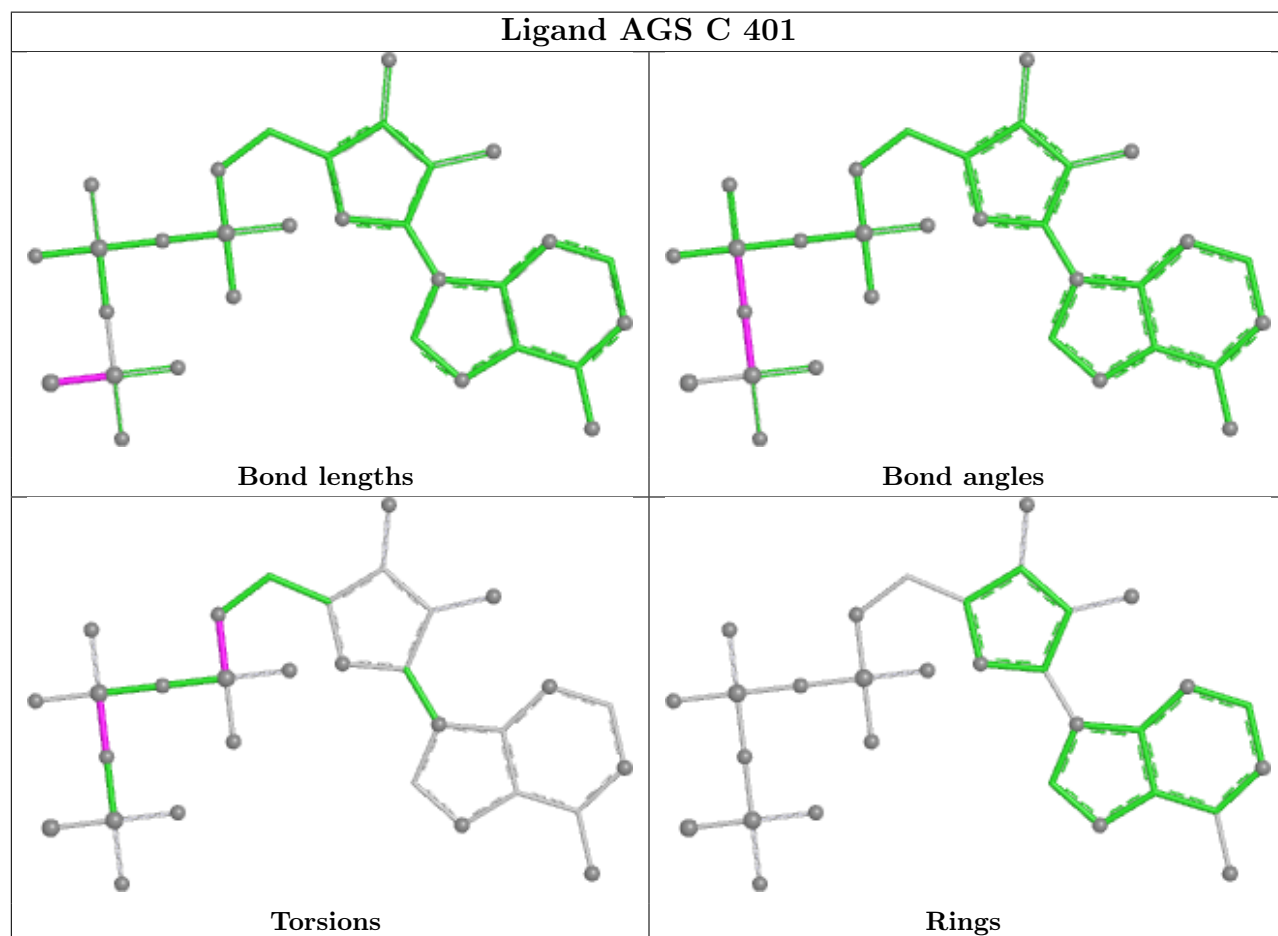
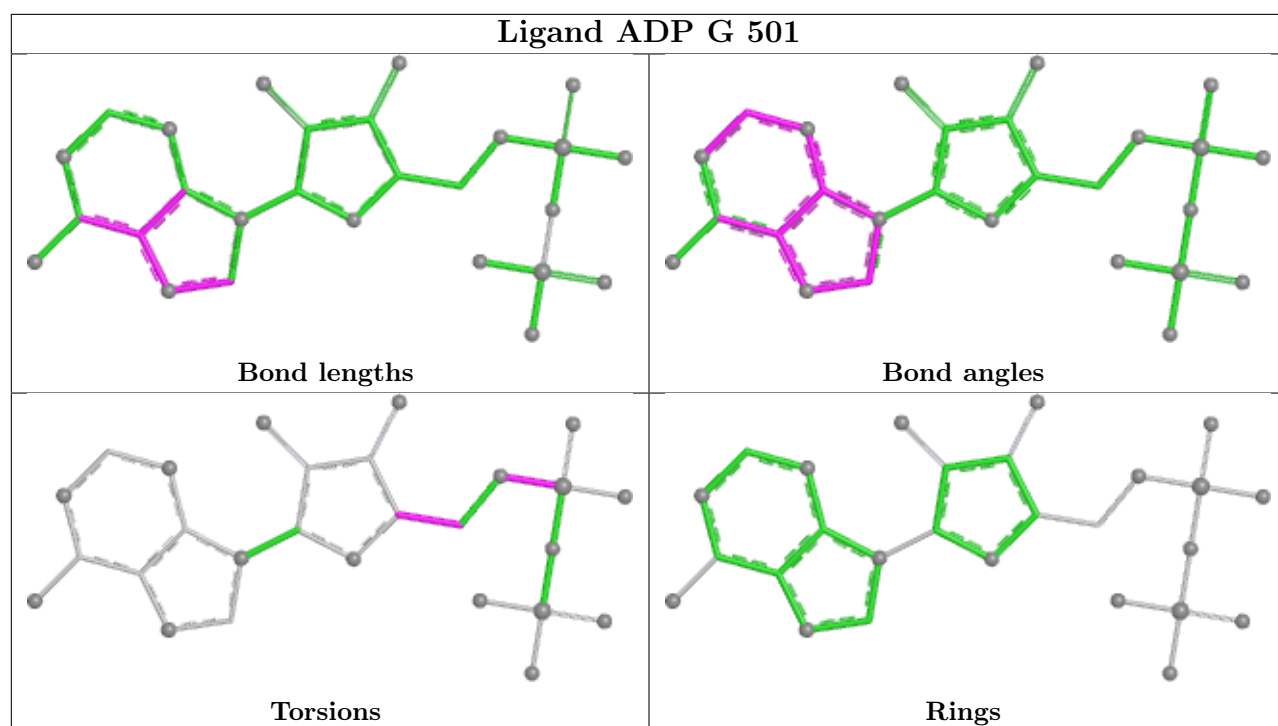
Mol	Chain	Res	Type	Atoms
15	C	401	AGS	C5'-O5'-PA-O1A
18	F	501	ADP	PA-O3A-PB-O2B
18	G	501	ADP	C5'-O5'-PA-O1A
18	G	501	ADP	O4'-C4'-C5'-O5'
18	J	501	ADP	C5'-O5'-PA-O1A

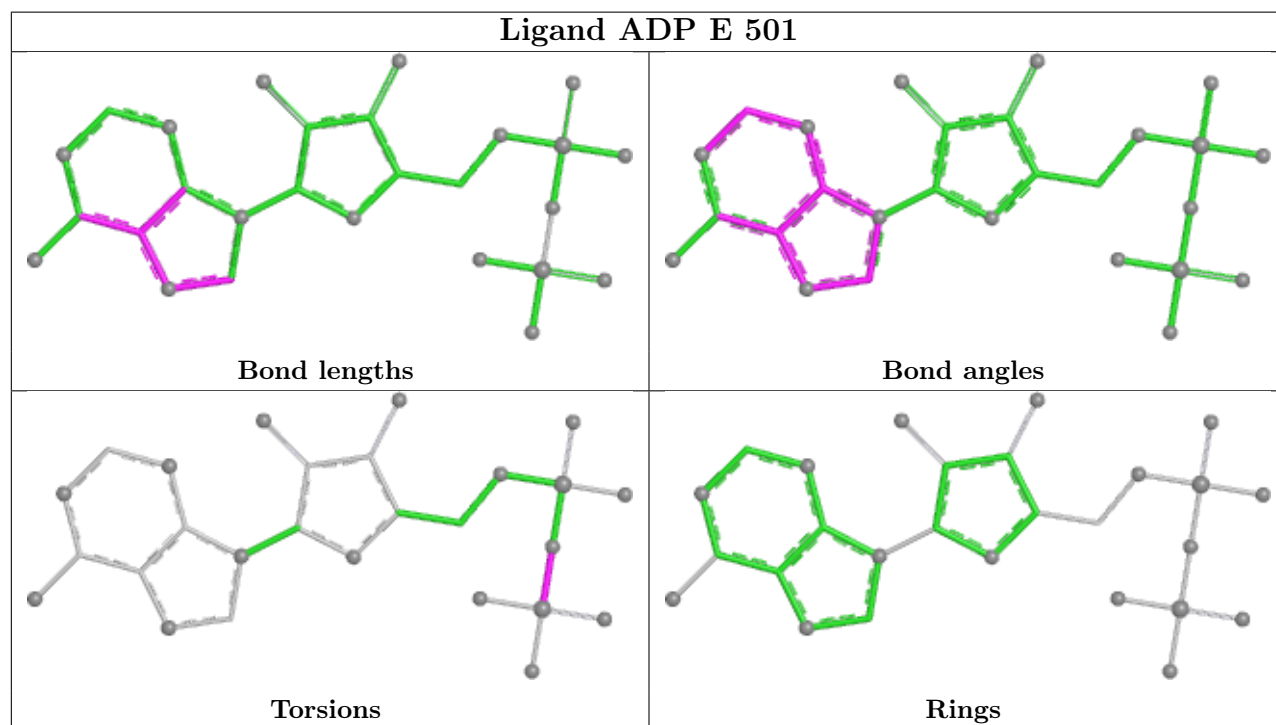
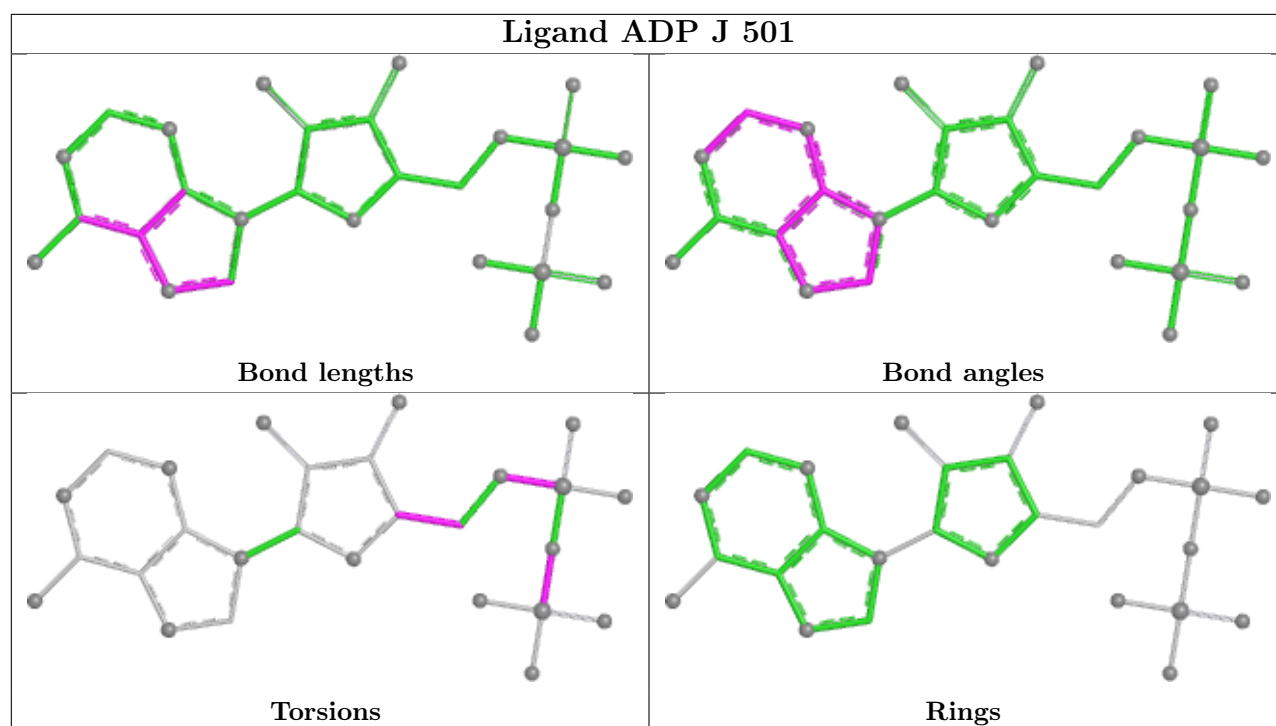
There are no ring outliers.

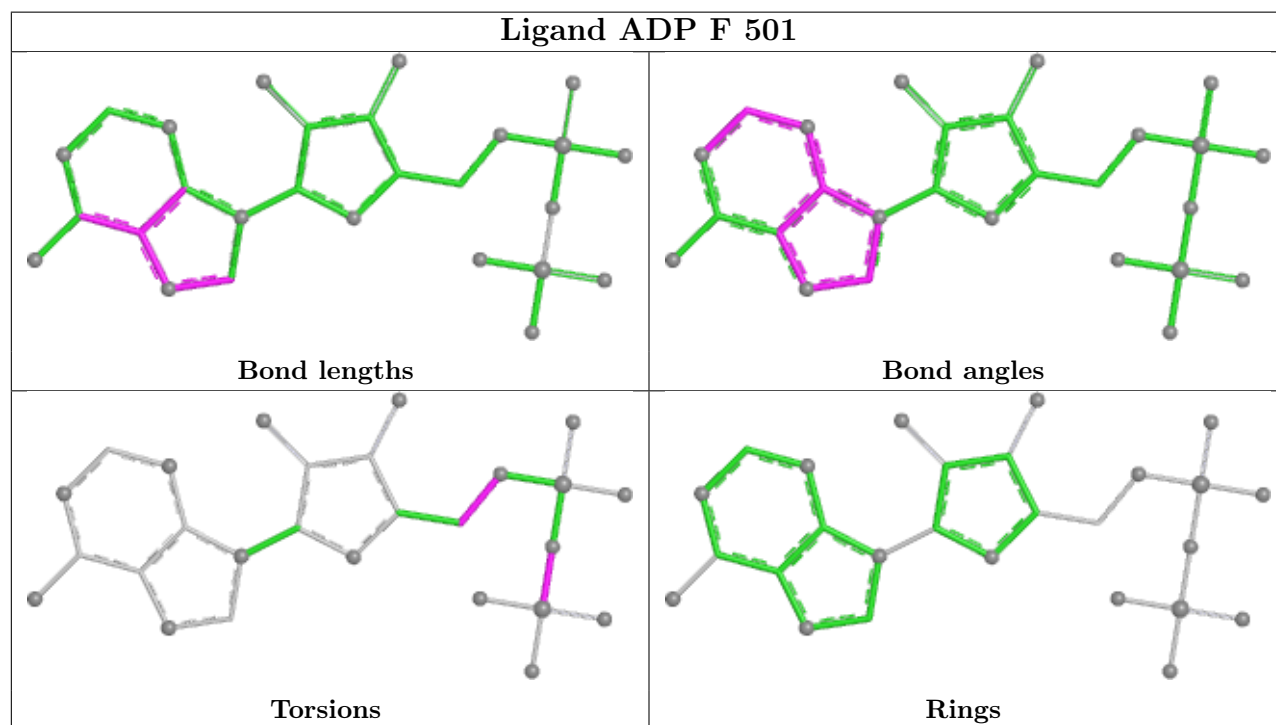
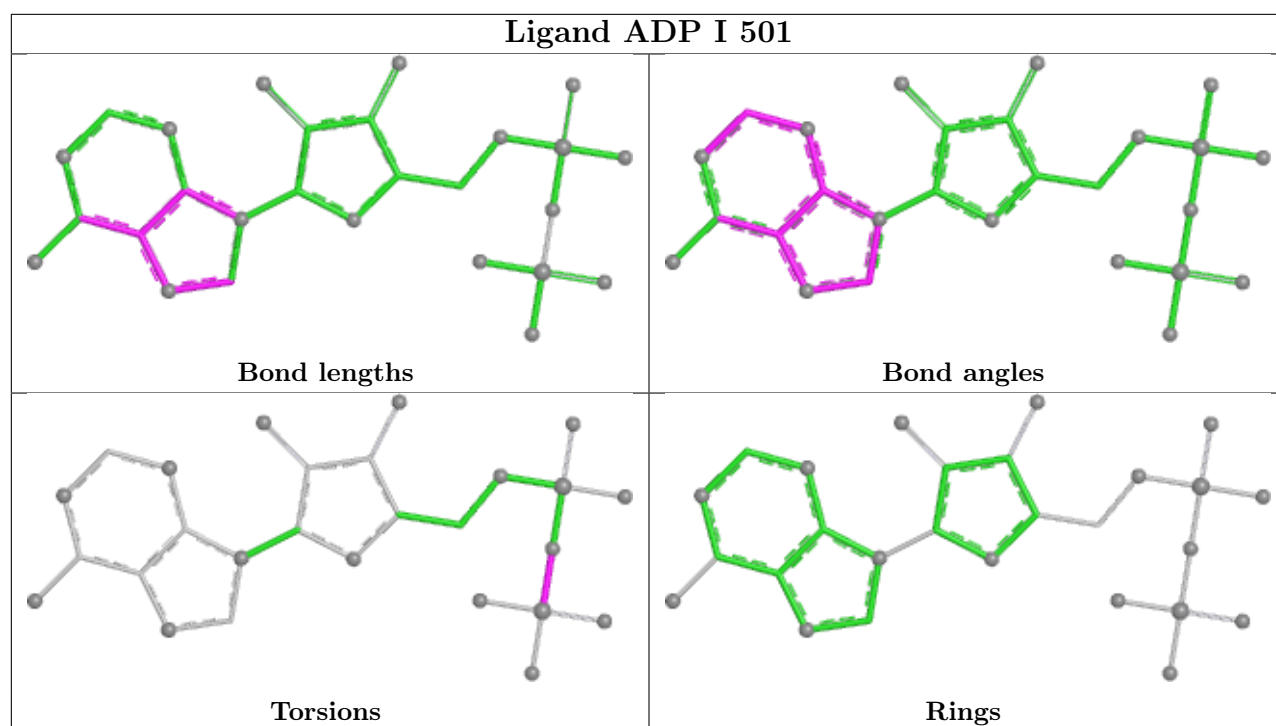
4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
18	G	501	ADP	3	0
18	J	501	ADP	1	0
18	F	501	ADP	1	0
18	H	501	ADP	1	0

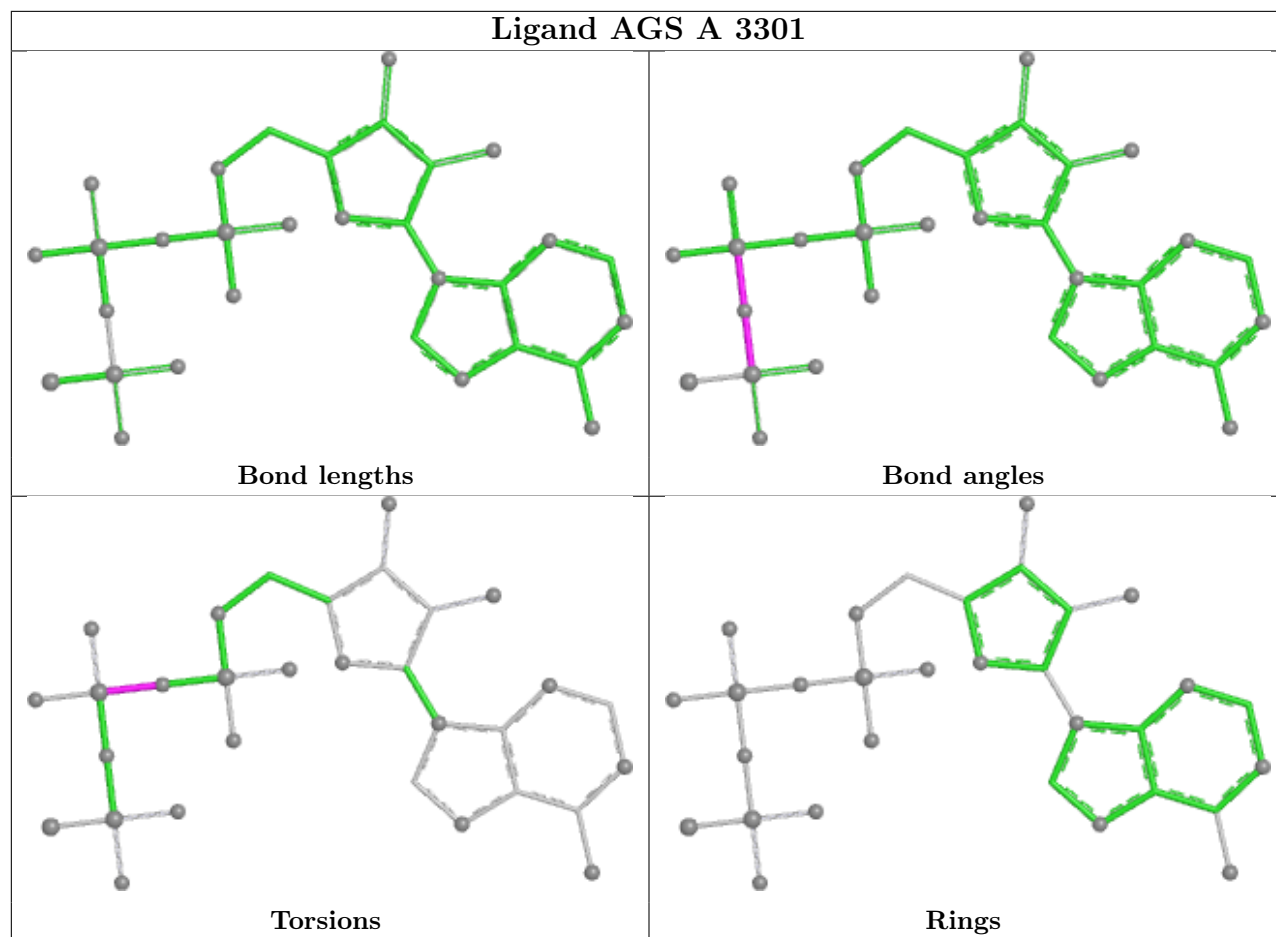
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



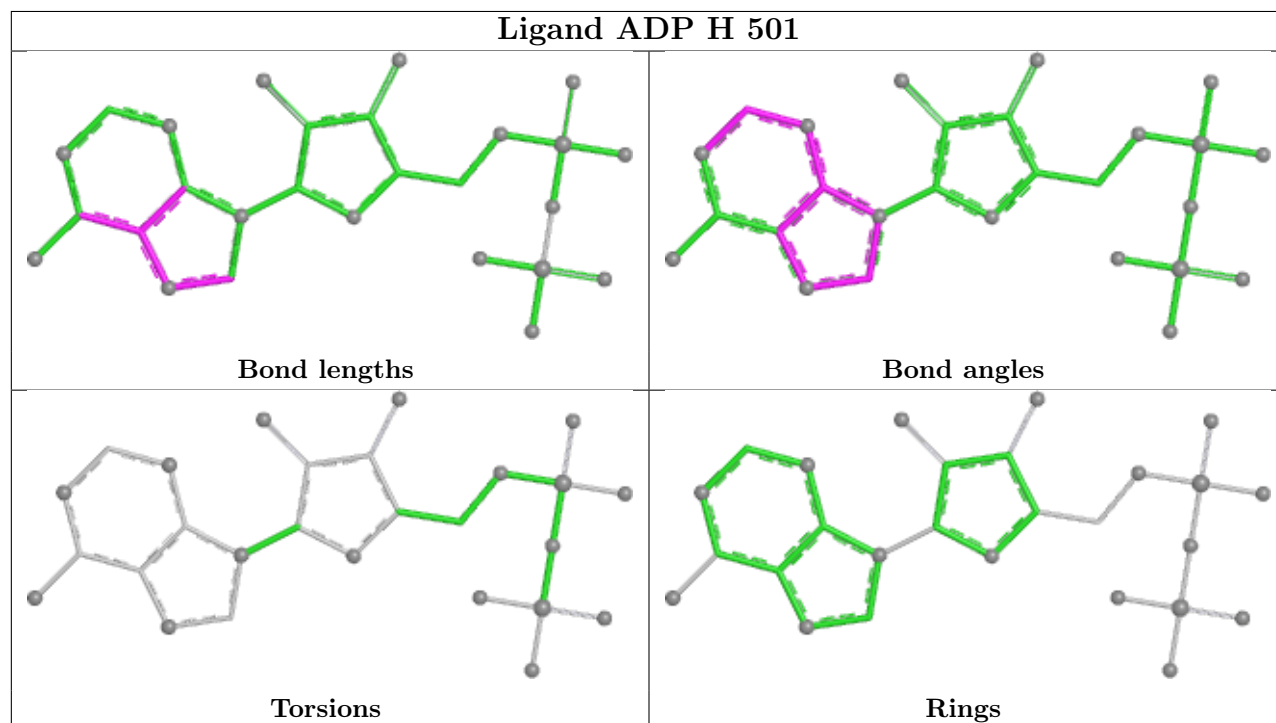




Ligand AGS A 3301



Ligand ADP H 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.

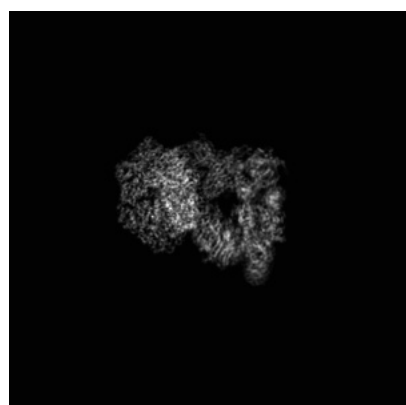
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49378. These allow visual inspection of the internal detail of the map and identification of artifacts.

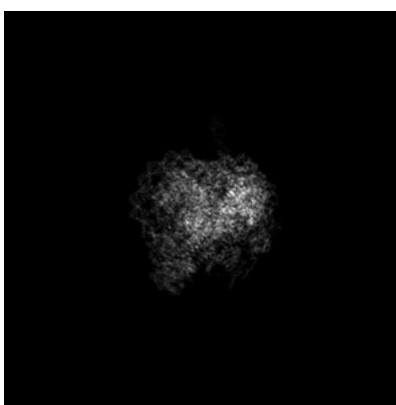
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

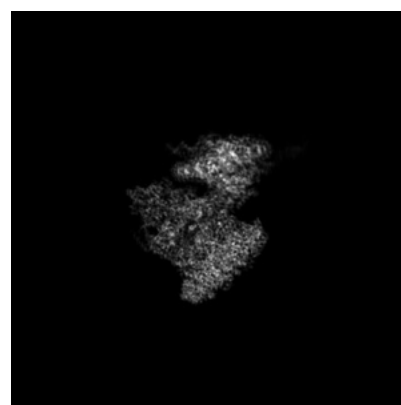
6.1.1 Primary map



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: 192



Y Index: 192



Z Index: 192

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

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 193



Y Index: 161

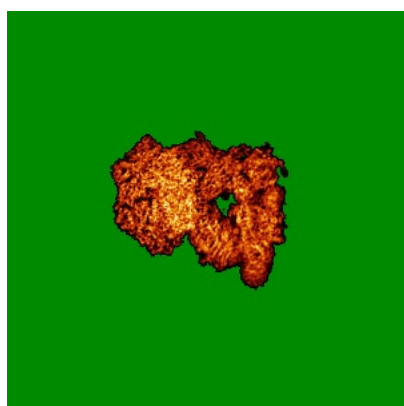


Z Index: 219

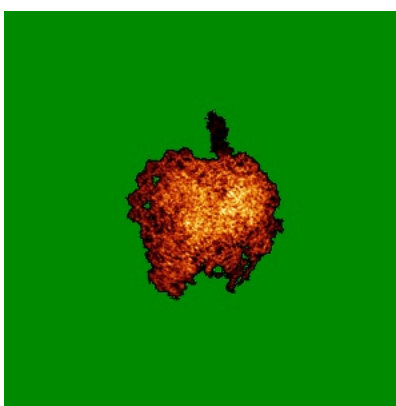
The images above show the largest variance slices of the map in three orthogonal directions.

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

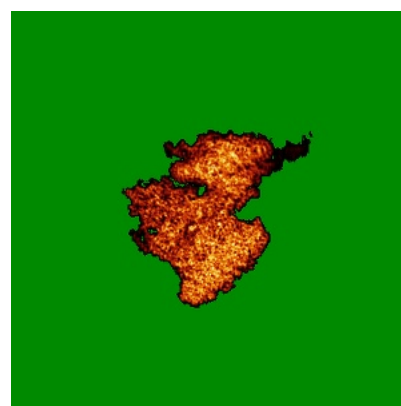
6.4.1 Primary map



X



Y

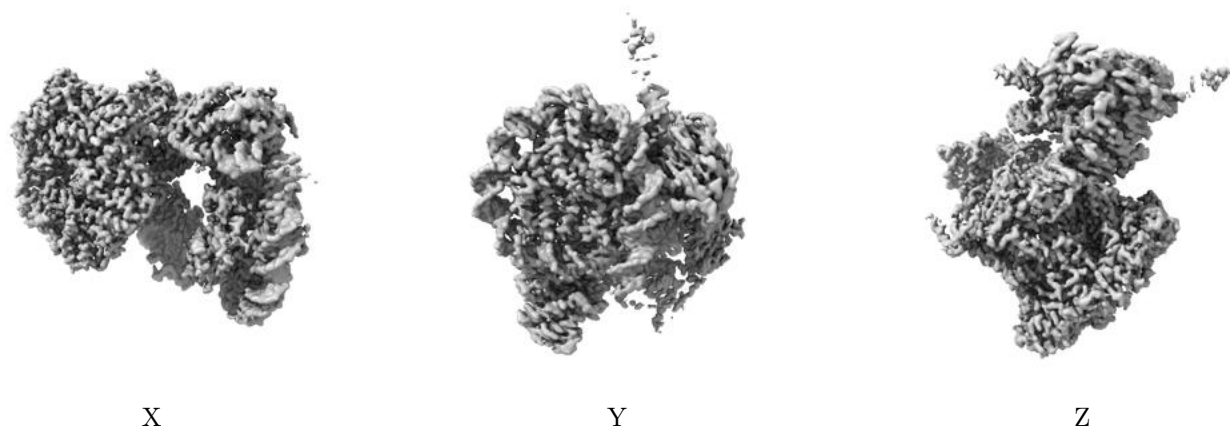


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

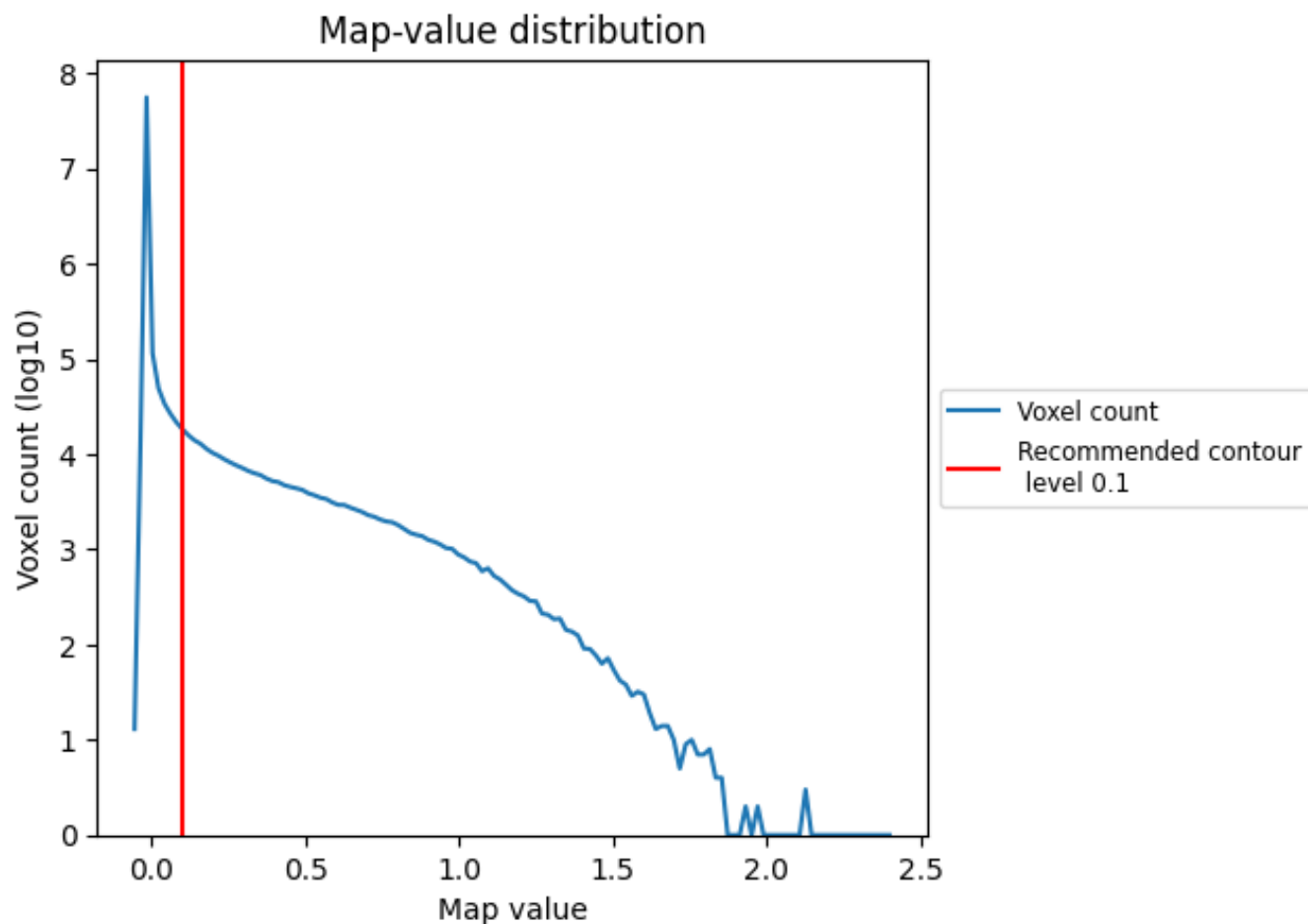
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

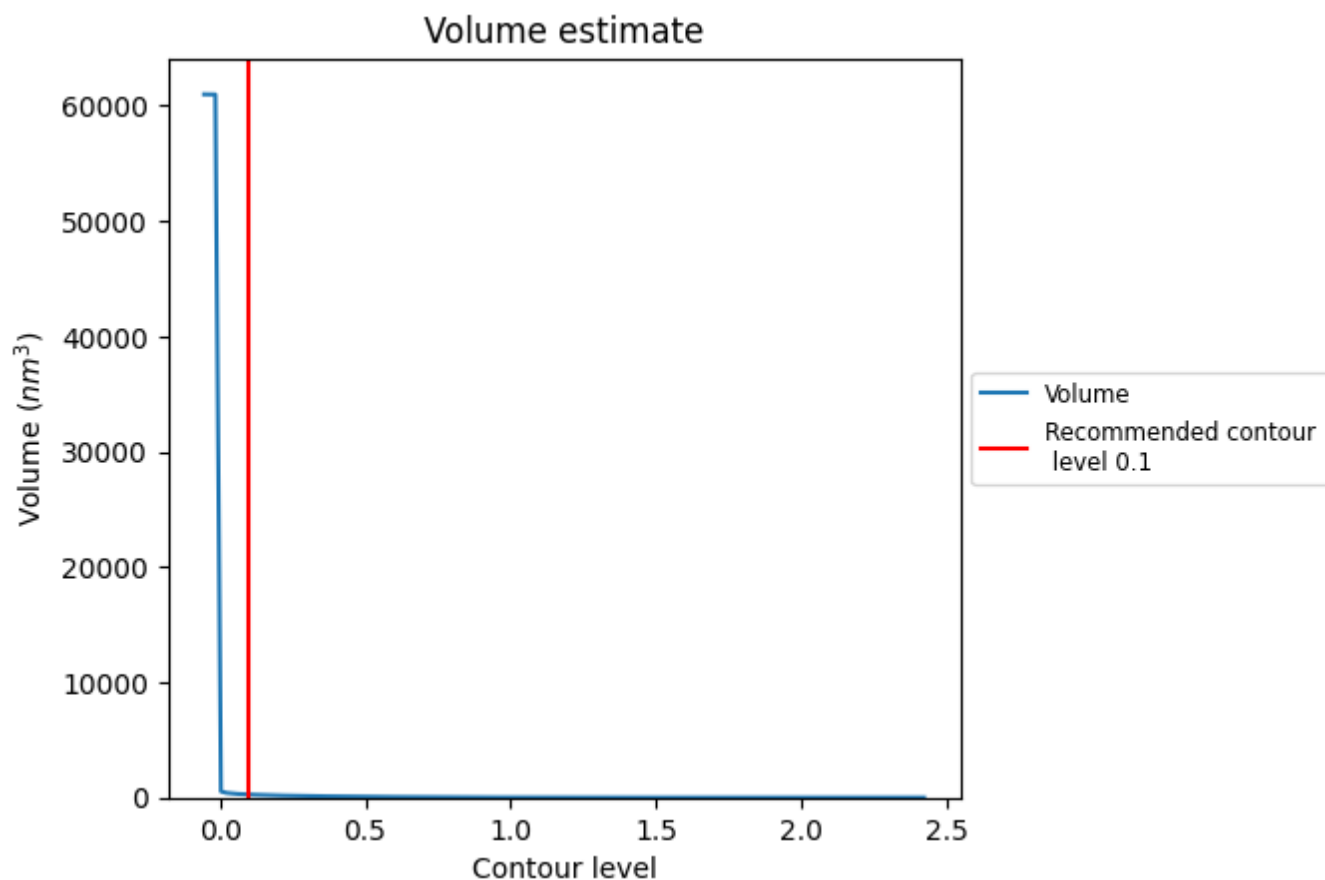
This section contains the results of statistical analysis of the map.

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.

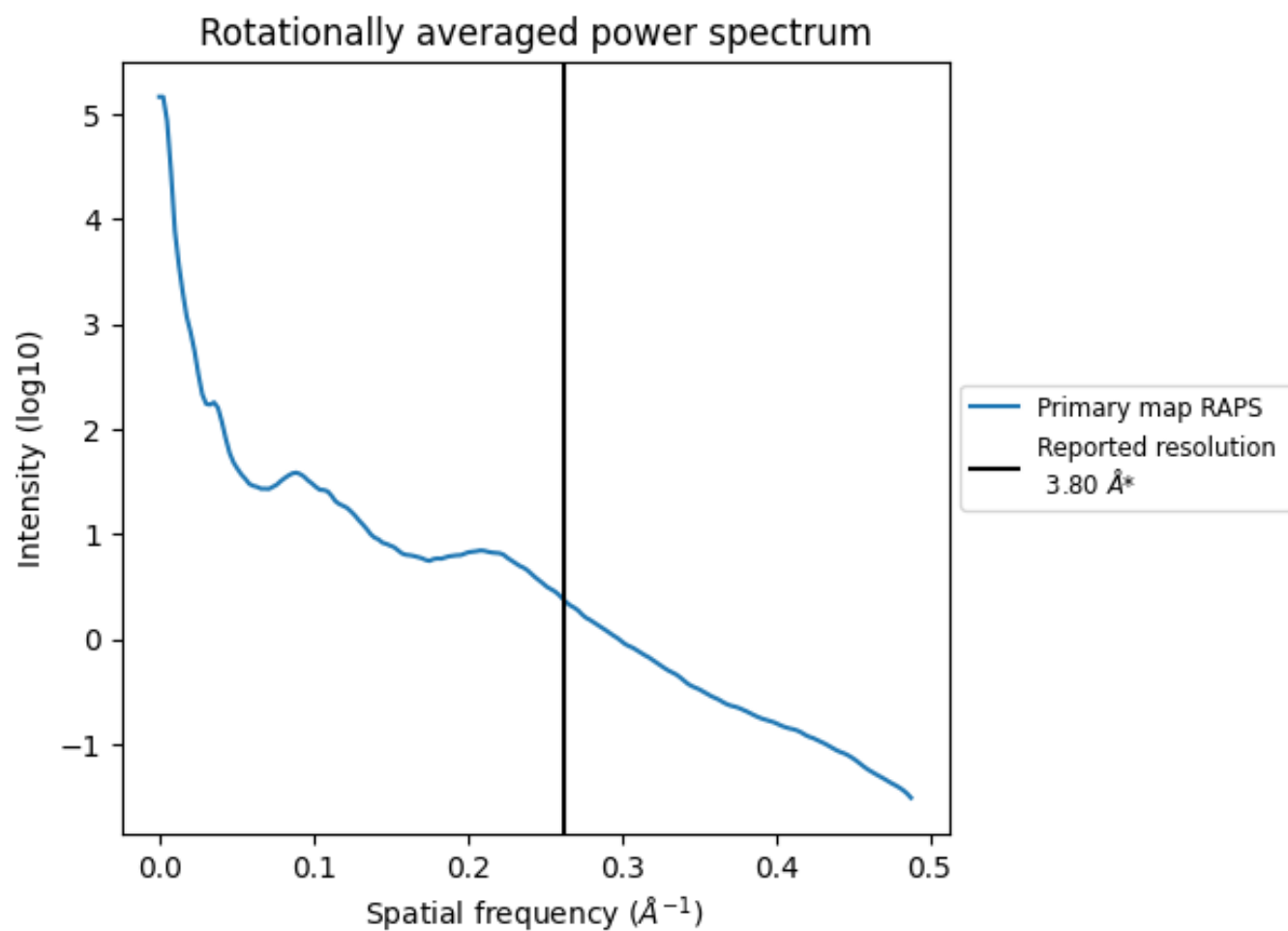
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 263 nm^3 ; this corresponds to an approximate mass of 237 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 0.263 Å⁻¹

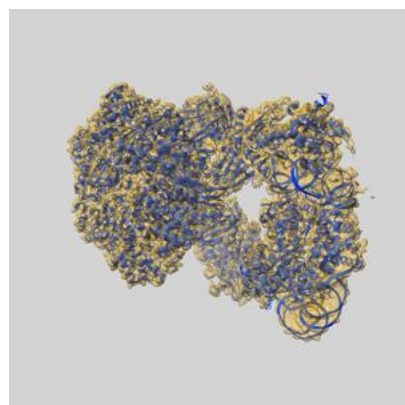
8 Fourier-Shell correlation

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

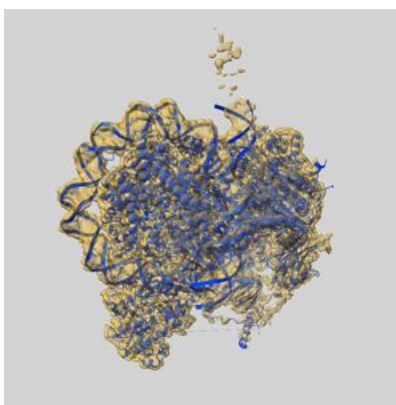
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-49378 and PDB model 9NFZ. Per-residue inclusion information can be found in section [3](#) on page [9](#).

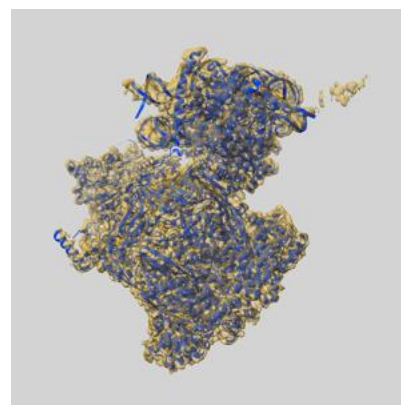
9.1 Map-model overlay [i](#)



X



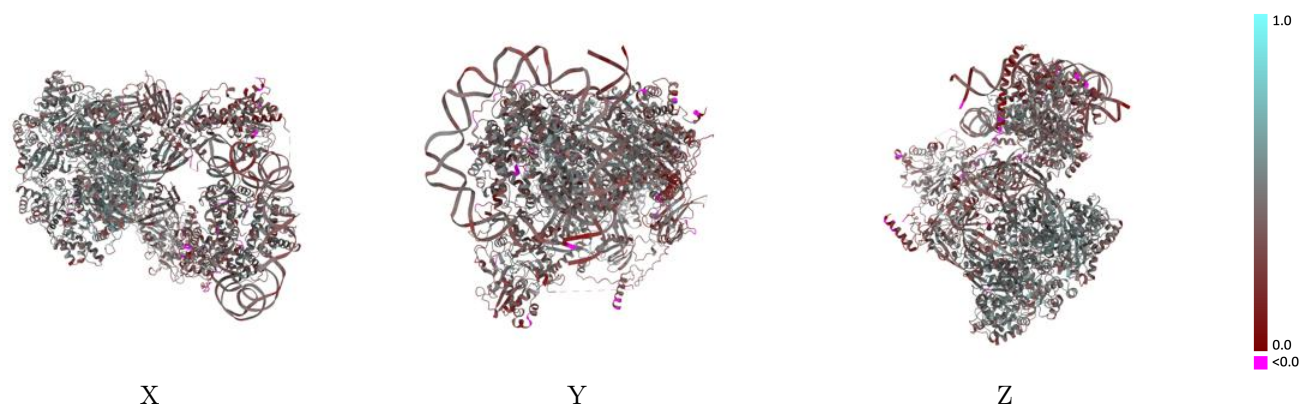
Y



Z

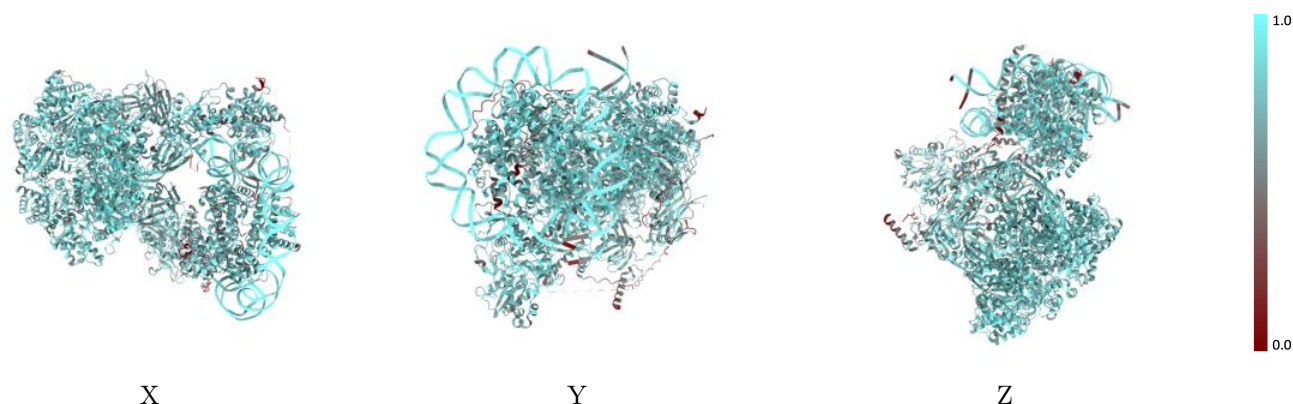
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



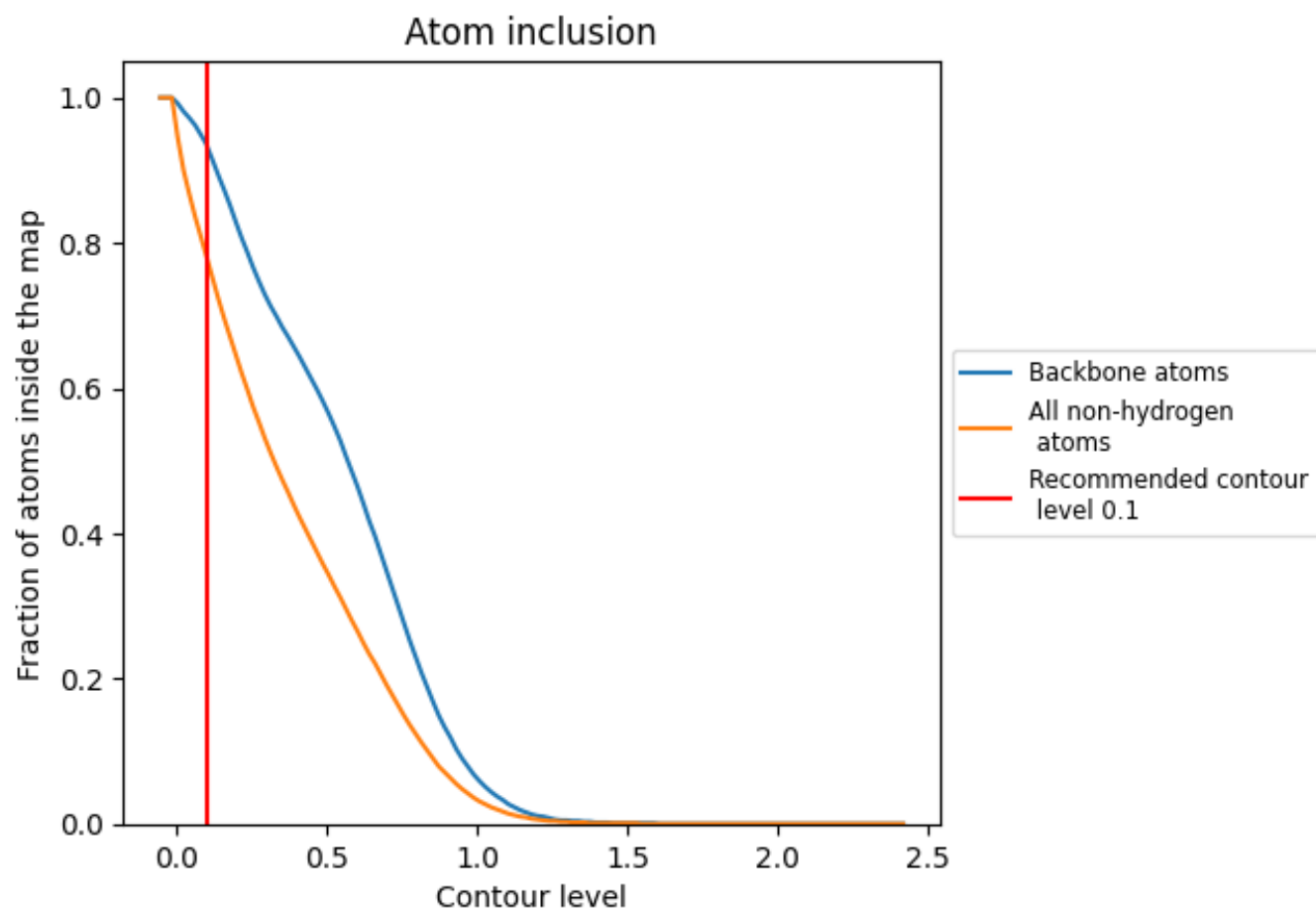
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 78% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7820	 0.4060
A	 0.7670	 0.3830
B	 0.4280	 0.1830
C	 0.7760	 0.3820
D	 0.7350	 0.3590
E	 0.8010	 0.4510
F	 0.7880	 0.4380
G	 0.7710	 0.4230
H	 0.7980	 0.4410
I	 0.7930	 0.4440
J	 0.8130	 0.4530
Q	 0.6710	 0.3420
R	 0.7580	 0.3760
S	 0.8400	 0.4430
T	 0.8090	 0.4240
U	 0.7160	 0.3880
V	 0.8040	 0.4350
W	 0.8210	 0.4270
X	 0.8460	 0.4420
Y	 0.8670	 0.3640
Z	 0.8820	 0.3780

