wwPDB EM Validation Summary Report (i)

May 11, 2024 – 05:33 pm BST

PDB ID	:	6RE4
EMDB ID	:	EMD-4841
Title	:	Cryo-EM structure of Polytomella F-ATP synthase, Rotary substate 2B, focussed refinement of F1 head and rotor
Authors	:	Murphy, B.J.; Klusch, N.; Yildiz, O.; Kuhlbrandt, W.
Deposited on	:	2019-04-12
Resolution	:	3.00 Å(reported)

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

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

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

The following versions of software and data (see references (1)) were used in the production of this report:

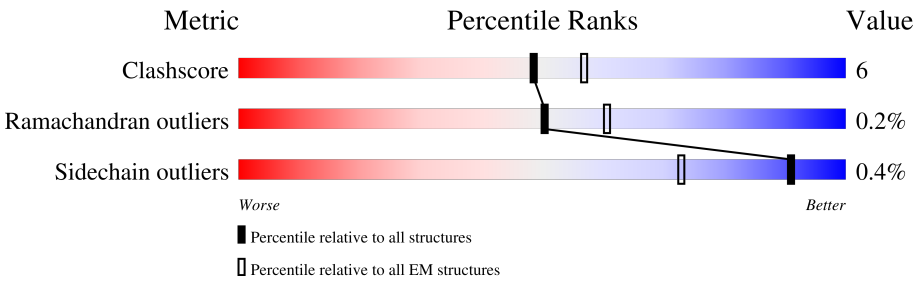
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.00 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 <=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	127	36% 49% 9% 42%
1	B	127	26% 43% 15% 42%
1	C	127	31% 46% 13% 42%
1	D	127	31% 50% 8% 42%
1	E	127	35% 48% 10% 42%
1	F	127	29% 46% 13% 42%
1	G	127	22% 45% 13% 42%
1	H	127	28% 46% 12% 42%

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Mol	Chain	Length	Quality of chain
1	I	127	31% 43% 14% 42%
1	J	127	31% 46% 13% 42%
2	P	229	7% 42% 7% 50%
3	Q	74	34% 86% 11%
4	R	199	35% 81% 8% 11%
5	S	317	15% 70% 17% 13%
6	T	562	6% 74% 10% 15%
6	U	562	7% 78% 14% 7%
6	V	562	12% 79% 13% 7%
7	X	574	14% 82% 11% 6%
7	Y	574	9% 78% 12% 9%
7	Z	574	16% 78% 16% 6%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 33863 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 Mitochondrial ATP synthase subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	74	514	340	83	88	3	0	0
1	B	74	514	340	83	88	3	0	0
1	C	74	514	340	83	88	3	0	0
1	D	74	514	340	83	88	3	0	0
1	E	74	514	340	83	88	3	0	0
1	F	74	514	340	83	88	3	0	0
1	G	74	514	340	83	88	3	0	0
1	H	74	514	340	83	88	3	0	0
1	I	74	514	340	83	88	3	0	0
1	J	74	514	340	83	88	3	0	0

- Molecule 2 is a protein called Mitochondrial ATP synthase subunit OSCP.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	P	114	895	576	147	171	1	0	0

- Molecule 3 is a protein called epsilon: Polytomella F-ATP synthase epsilon subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	Q	72	561	358	102	99	2	0	0

- Molecule 4 is a protein called Mitochondrial ATP synthase subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	R	177	1303	833	213	256	1	0	0

- Molecule 5 is a protein called ATP synthase gamma chain, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	S	277	2130	1327	377	416	10	0	0

- Molecule 6 is a protein called ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	T	478	3609	2294	640	664	11	0	0
6	U	523	3978	2537	702	728	11	0	0
6	V	520	3961	2527	700	723	11	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	266	ARG	LYS	conflict	UNP A0ZW40
U	266	ARG	LYS	conflict	UNP A0ZW40
V	266	ARG	LYS	conflict	UNP A0ZW40

- Molecule 7 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	X	538	4087	2568	692	814	13	0	0
7	Y	520	3952	2484	669	786	13	0	0
7	Z	539	4095	2572	693	817	13	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	350	ALA	GLY	conflict	UNP A0ZW41
X	387	LEU	ARG	conflict	UNP A0ZW41
Y	350	ALA	GLY	conflict	UNP A0ZW41

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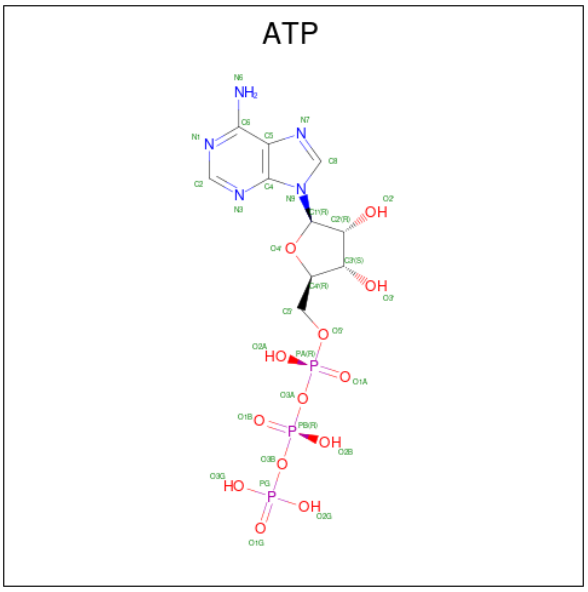
Chain	Residue	Modelled	Actual	Comment	Reference
Y	387	LEU	ARG	conflict	UNP A0ZW41
Z	350	ALA	GLY	conflict	UNP A0ZW41
Z	387	LEU	ARG	conflict	UNP A0ZW41

- Molecule 8 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
8	T	1	Total	C	N	O	P	0
			31	10	5	13	3	
8	U	1	Total	C	N	O	P	0
			31	10	5	13	3	
8	V	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
9	T	1	Total	Mg	0
			1	1	
9	U	1	Total	Mg	0
			1	1	
9	V	1	Total	Mg	0
			1	1	
9	Y	1	Total	Mg	0
			1	1	

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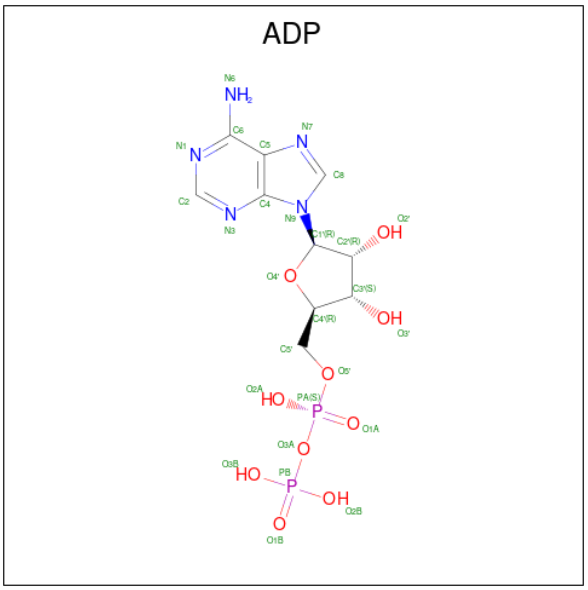
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
9	Z	1	1	1	0

- Molecule 10 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



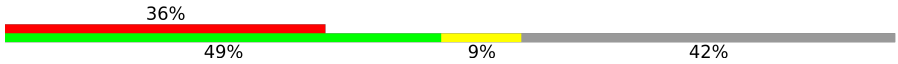
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
10	Y	1	27	10	5	10	2	0
			Total	C	N	O	P	
10	Z	1	27	10	5	10	2	0

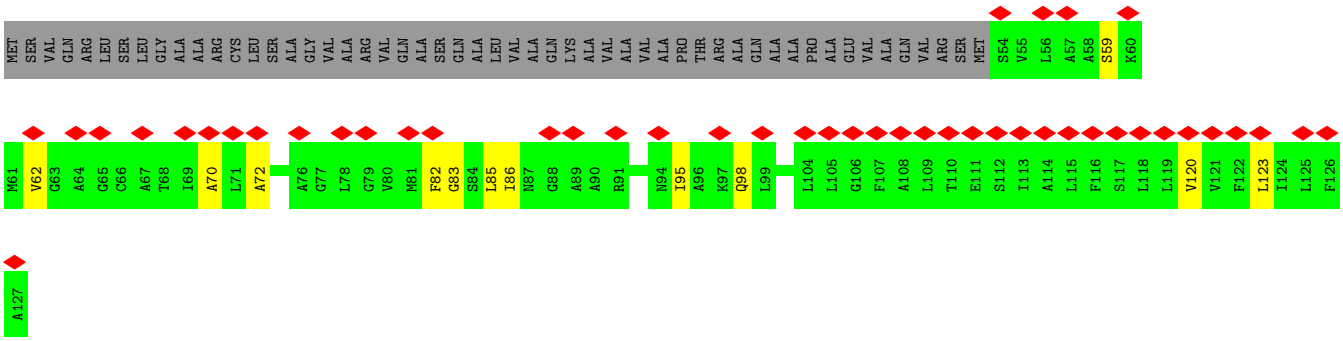
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Mitochondrial ATP synthase subunit c

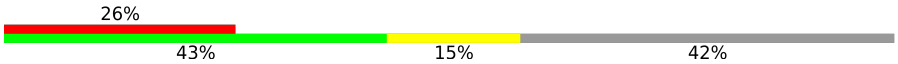
Chain A:

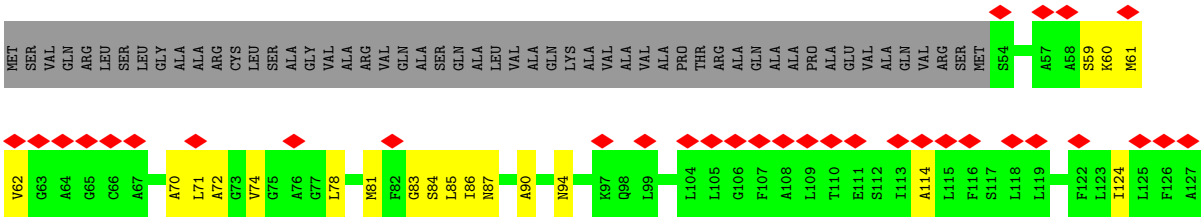




• Molecule 1: Mitochondrial ATP synthase subunit c

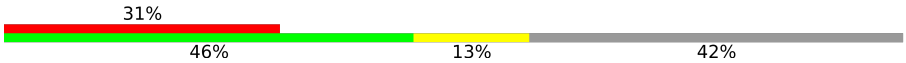
Chain B:

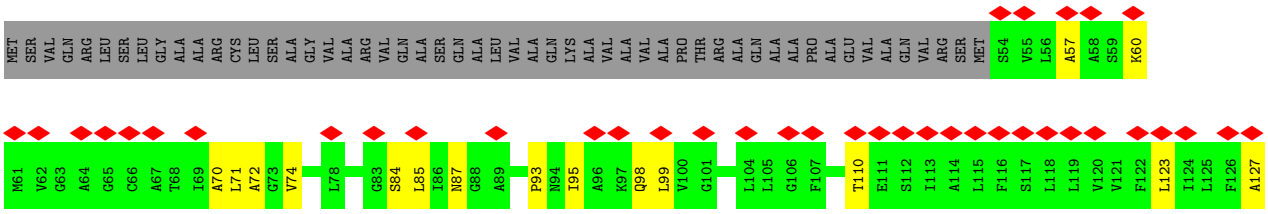




• Molecule 1: Mitochondrial ATP synthase subunit c

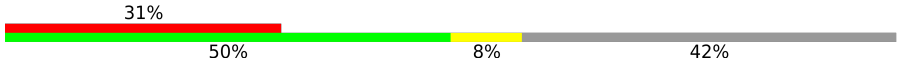
Chain C:

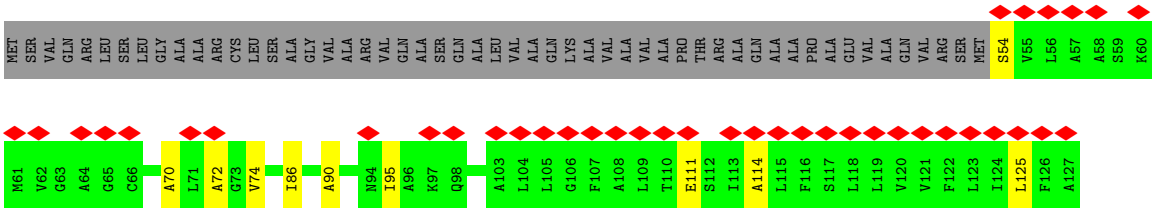




• Molecule 1: Mitochondrial ATP synthase subunit c

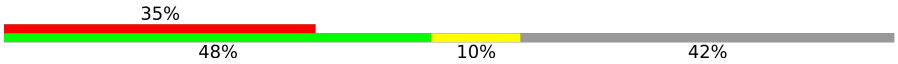
Chain D:

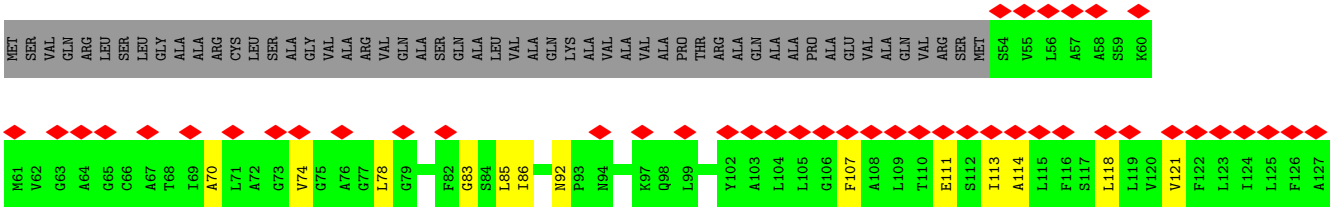




- Molecule 1: Mitochondrial ATP synthase subunit c

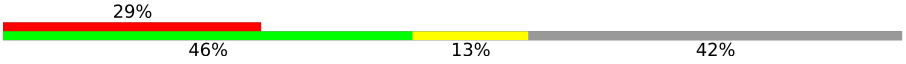
Chain E:

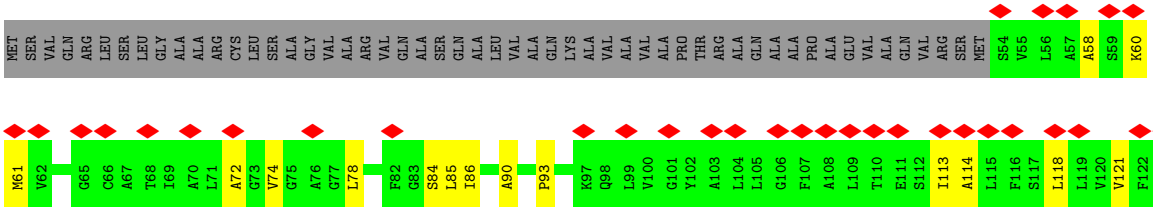




- Molecule 1: Mitochondrial ATP synthase subunit c

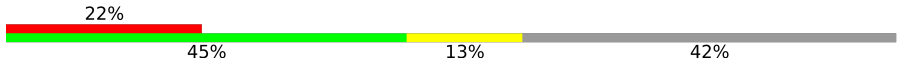
Chain F:

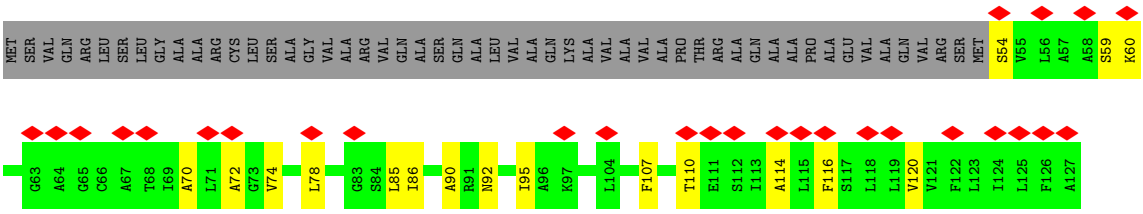




- Molecule 1: Mitochondrial ATP synthase subunit c

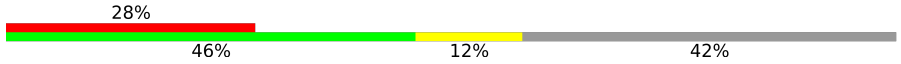
Chain G:

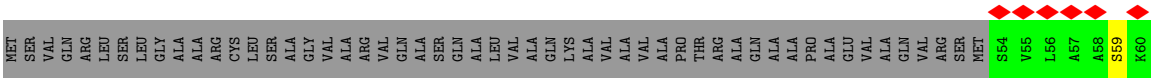


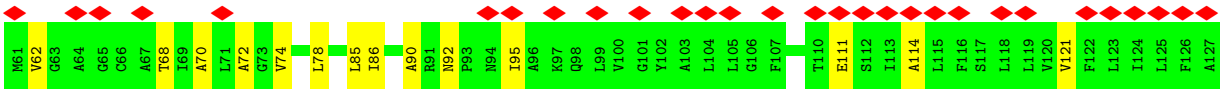


- Molecule 1: Mitochondrial ATP synthase subunit c

Chain H:

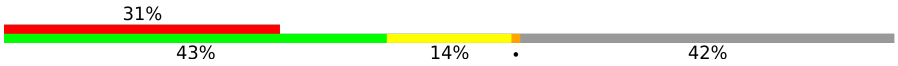


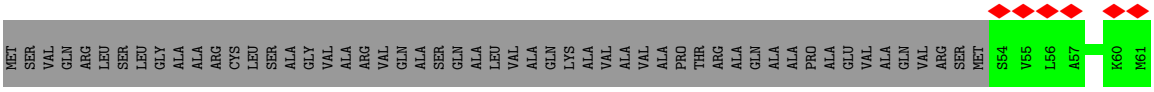


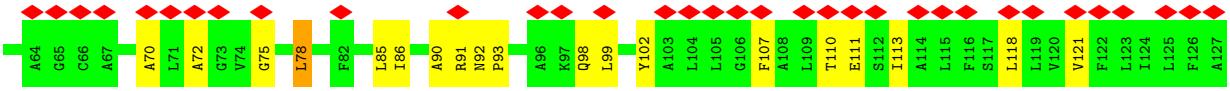


• Molecule 1: Mitochondrial ATP synthase subunit c

Chain I:

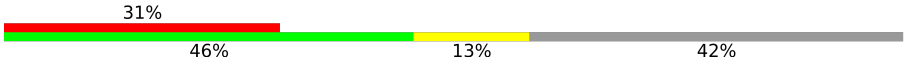


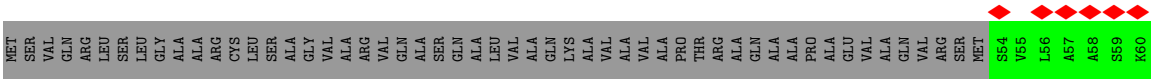




• Molecule 1: Mitochondrial ATP synthase subunit c

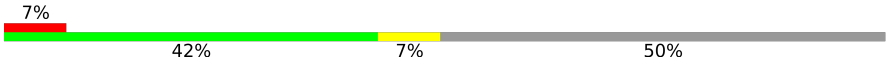
Chain J:

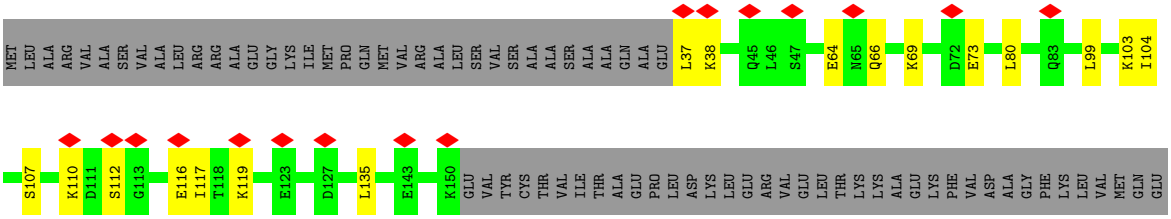




• Molecule 2: Mitochondrial ATP synthase subunit OSCP

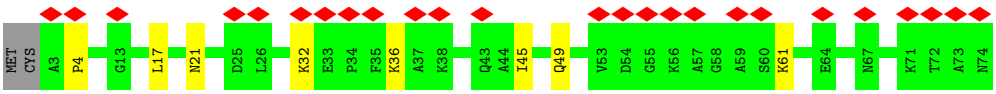
Chain P:





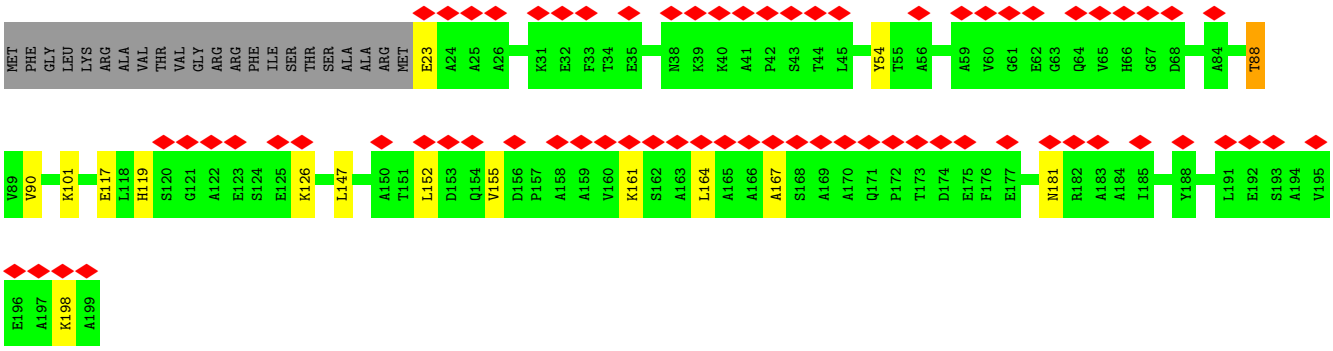
• Molecule 3: epsilon: Polytomella F-ATP synthase epsilon subunit

Chain Q:



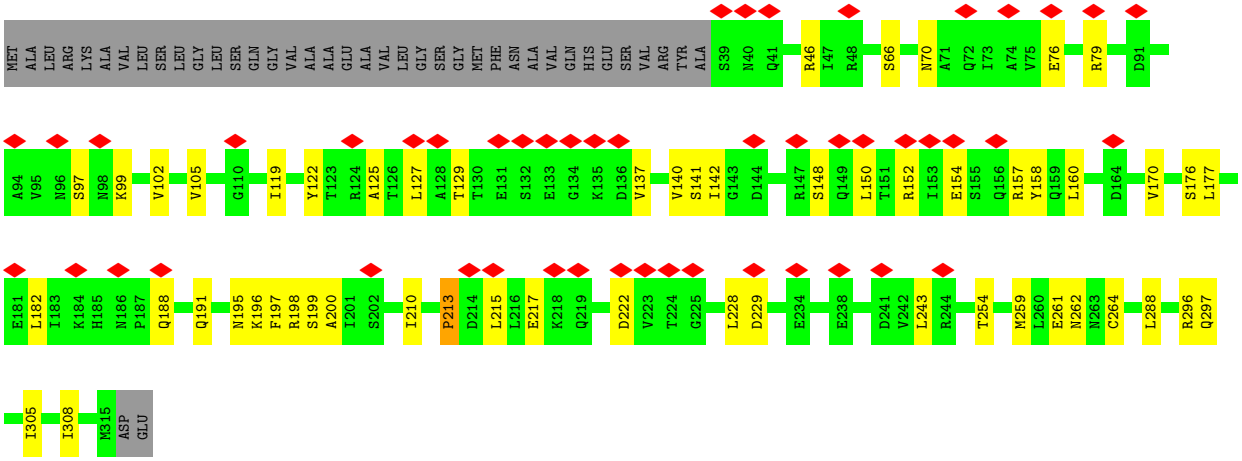
• Molecule 4: Mitochondrial ATP synthase subunit delta

Chain R:



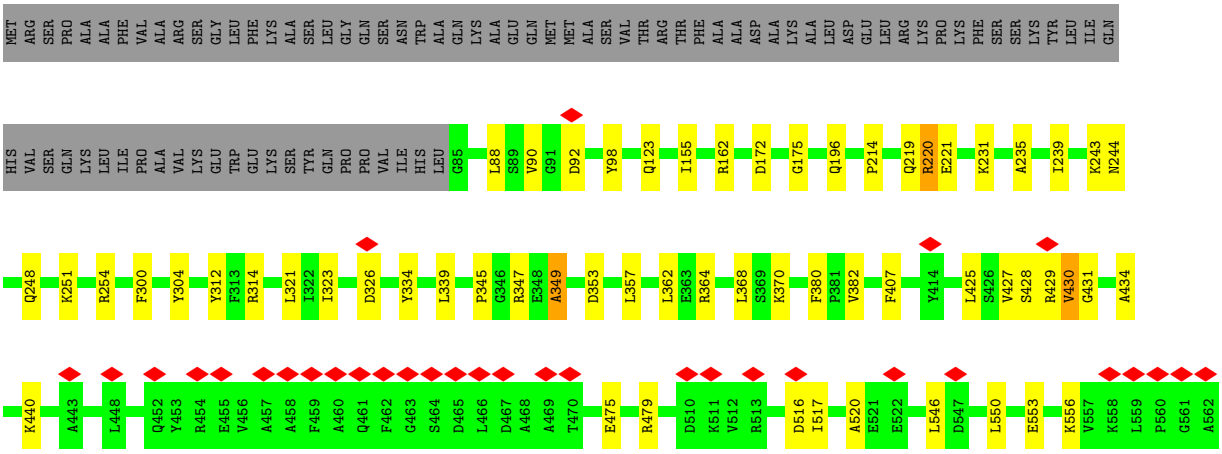
• Molecule 5: ATP synthase gamma chain, mitochondrial

Chain S:



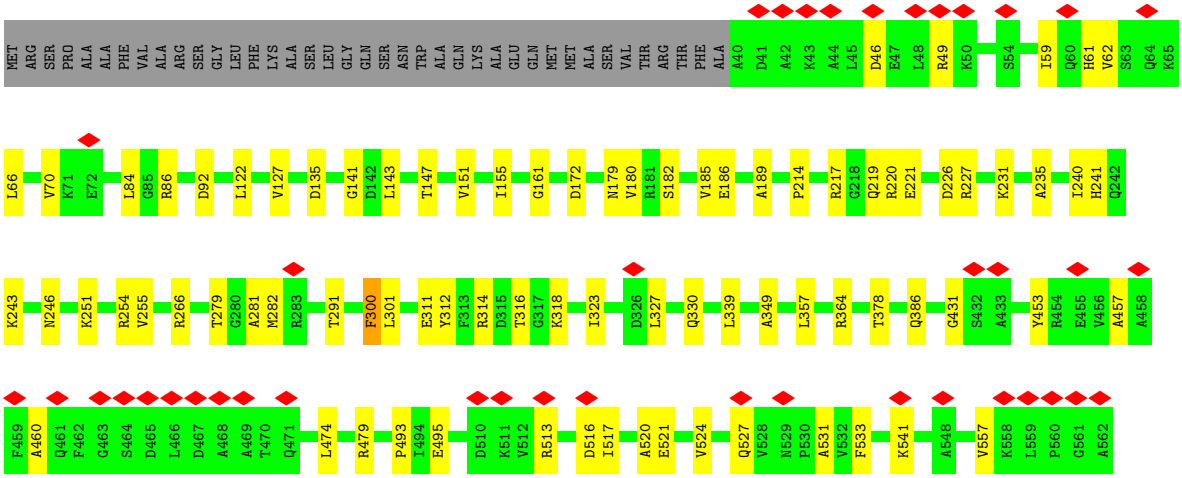
• Molecule 6: ATP synthase subunit alpha

Chain T:



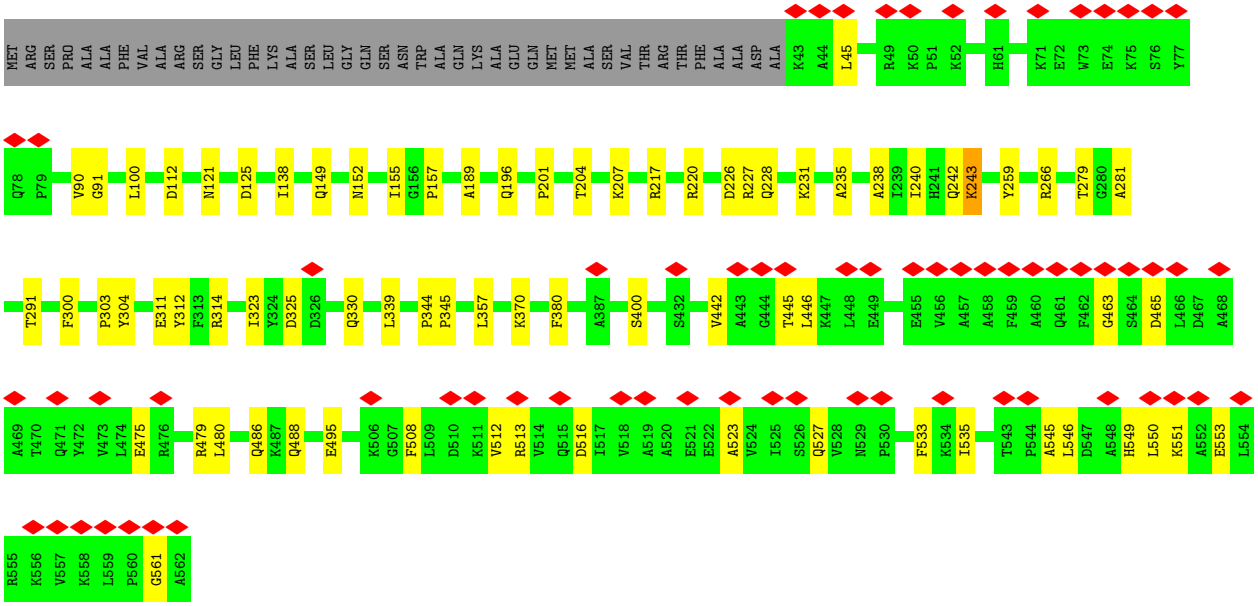
• Molecule 6: ATP synthase subunit alpha

Chain U:



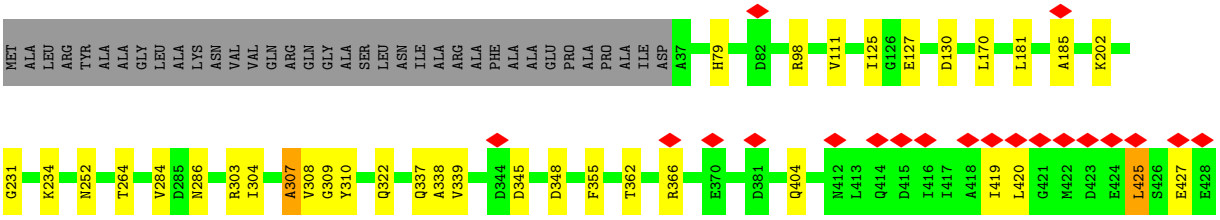
- Molecule 6: ATP synthase subunit alpha

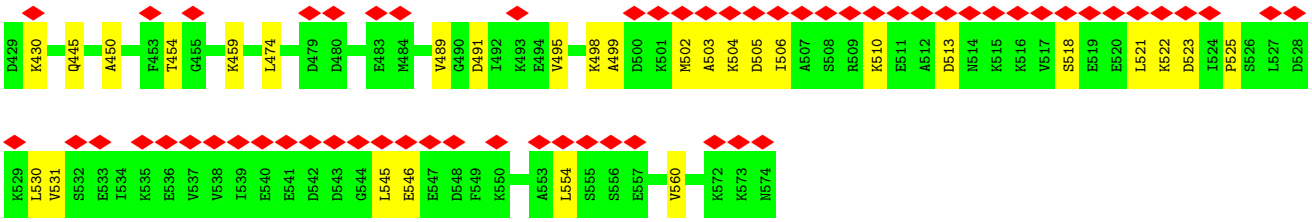
Chain V:



- Molecule 7: ATP synthase subunit beta

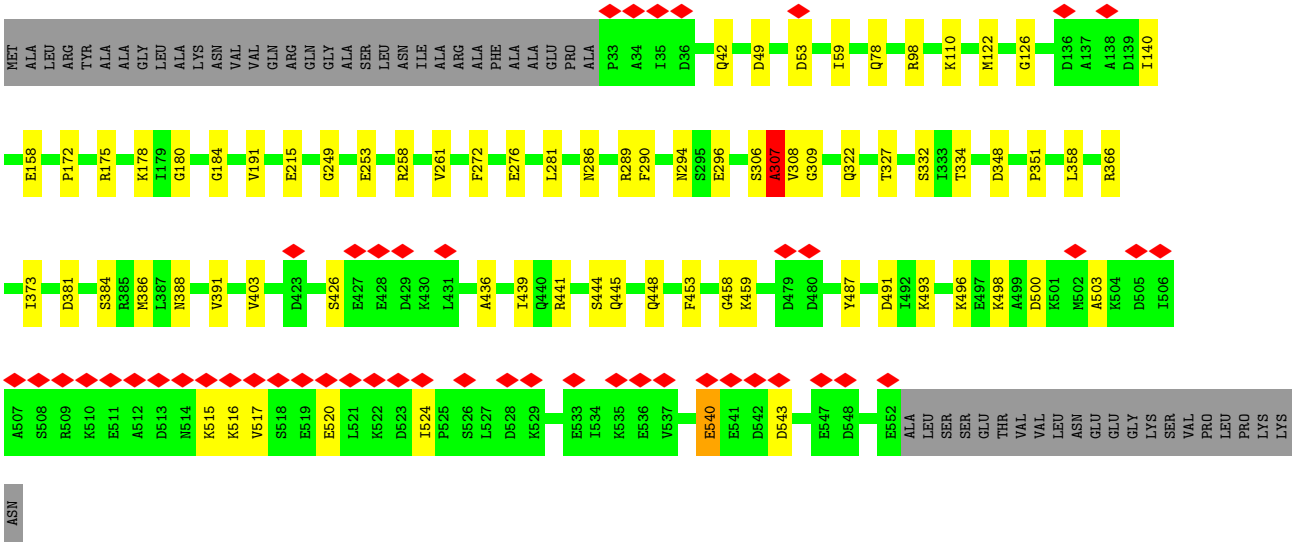
Chain X:





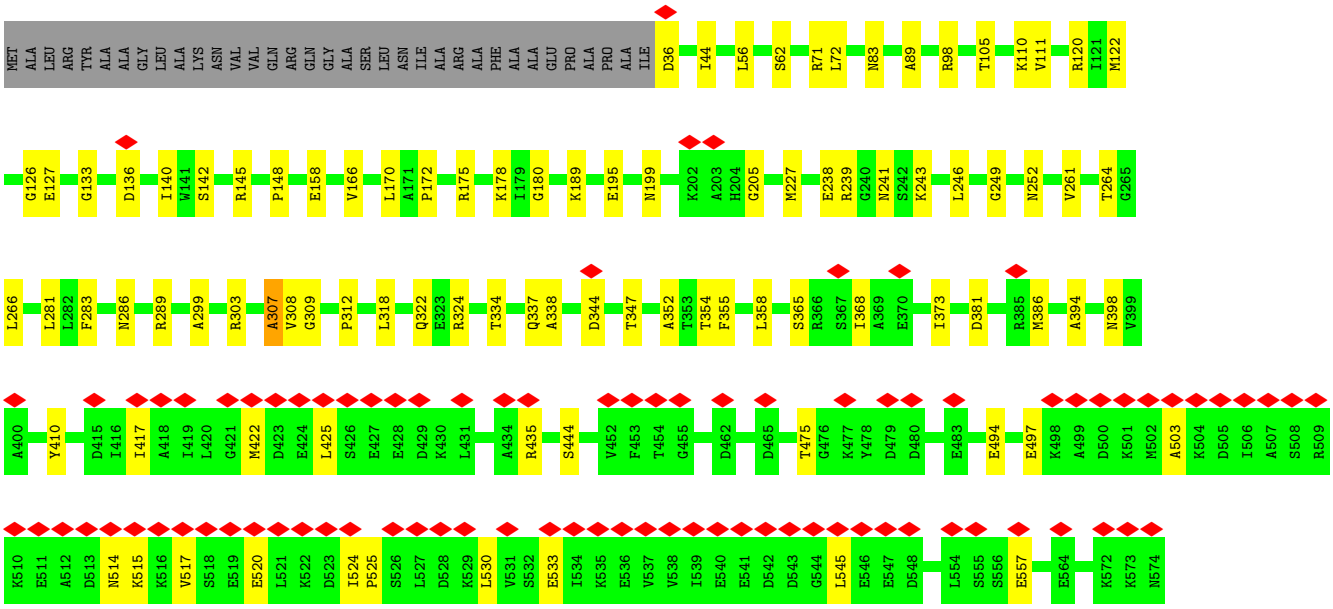
• Molecule 7: ATP synthase subunit beta

Chain Y:



• Molecule 7: ATP synthase subunit beta

Chain Z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72402	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 ($e^-/Å^2$)	35	Depositor
Minimum defocus (nm)	-400	Depositor
Maximum defocus (nm)	-5000	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.200	Depositor
Minimum map value	-0.109	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	505.44, 505.44, 505.44	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.053, 1.053, 1.053	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: MG, ADP, ATP

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	0.35	0/520	0.56	0/704
1	B	0.38	0/520	0.58	0/704
1	C	0.37	0/519	0.54	0/701
1	D	0.36	0/520	0.56	0/704
1	E	0.33	0/520	0.58	0/704
1	F	0.40	0/520	0.54	0/704
1	G	0.47	0/520	0.59	0/704
1	H	0.45	0/520	0.54	0/704
1	I	0.42	0/520	0.58	0/704
1	J	0.37	0/520	0.59	1/704 (0.1%)
2	P	0.46	0/908	0.57	0/1229
3	Q	0.40	0/574	0.55	0/774
4	R	0.48	1/1336 (0.1%)	0.58	1/1827 (0.1%)
5	S	0.48	1/2153 (0.0%)	0.57	0/2901
6	T	0.64	1/3667 (0.0%)	0.61	0/4965
6	U	0.58	1/4047 (0.0%)	0.61	0/5479
6	V	0.57	0/4030	0.59	0/5456
7	X	0.57	0/4147	0.60	0/5619
7	Y	0.61	0/4011	0.62	1/5435 (0.0%)
7	Z	0.51	0/4155	0.59	1/5630 (0.0%)
All	All	0.54	4/34227 (0.0%)	0.59	4/46352 (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
7	X	0	1
7	Y	0	3
7	Z	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	T	349	ALA	C-N	-6.50	1.19	1.34
6	U	349	ALA	C-N	-5.62	1.21	1.34
5	S	264	CYS	CB-SG	-5.45	1.73	1.81
4	R	155	VAL	C-N	5.26	1.46	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	Y	500	ASP	CB-CG-OD2	6.34	124.01	118.30
7	Z	344	ASP	CB-CG-OD1	5.97	123.67	118.30
4	R	155	VAL	C-N-CA	-5.80	107.19	121.70
1	J	119	LEU	CA-CB-CG	5.04	126.89	115.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	X	307	ALA	Peptide
7	Y	307	ALA	Peptide
7	Y	503	ALA	Mainchain
7	Y	540	GLU	Peptide
7	Z	307	ALA	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	514	0	554	9	0
1	B	514	0	554	17	0
1	C	514	0	553	14	0
1	D	514	0	554	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	514	0	554	13	0
1	F	514	0	554	19	0
1	G	514	0	554	14	0
1	H	514	0	554	12	0
1	I	514	0	554	18	0
1	J	514	0	554	16	0
2	P	895	0	934	14	0
3	Q	561	0	565	7	0
4	R	1303	0	1266	11	0
5	S	2130	0	2180	36	0
6	T	3609	0	3731	50	0
6	U	3978	0	4116	53	0
6	V	3961	0	4106	51	0
7	X	4087	0	4110	50	0
7	Y	3952	0	3965	48	0
7	Z	4095	0	4114	59	0
8	T	31	0	12	0	0
8	U	31	0	12	0	0
8	V	31	0	12	2	0
9	T	1	0	0	0	0
9	U	1	0	0	0	0
9	V	1	0	0	0	0
9	Y	1	0	0	0	0
9	Z	1	0	0	0	0
10	Y	27	0	12	3	0
10	Z	27	0	12	1	0
All	All	33863	0	34686	422	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 6.

The worst 5 of 422 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:78:LEU:HD11	1:E:111:GLU:OE2	1.26	1.31
7:Z:514:ASN:O	7:Z:517:VAL:HG22	1.32	1.22
7:X:498:LYS:O	7:X:502:MET:HG2	1.50	1.08
7:Z:514:ASN:O	7:Z:517:VAL:CG2	2.03	1.06
1:F:118:LEU:HA	1:F:121:VAL:HG12	1.42	1.00

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	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
1	B	72/127 (57%)	72 (100%)	0	0	100	100
1	C	71/127 (56%)	70 (99%)	1 (1%)	0	100	100
1	D	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
1	E	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
1	F	72/127 (57%)	72 (100%)	0	0	100	100
1	G	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
1	H	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
1	I	72/127 (57%)	69 (96%)	3 (4%)	0	100	100
1	J	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
2	P	112/229 (49%)	105 (94%)	7 (6%)	0	100	100
3	Q	70/74 (95%)	65 (93%)	5 (7%)	0	100	100
4	R	175/199 (88%)	160 (91%)	15 (9%)	0	100	100
5	S	275/317 (87%)	261 (95%)	13 (5%)	1 (0%)	34	72
6	T	476/562 (85%)	460 (97%)	15 (3%)	1 (0%)	47	82
6	U	521/562 (93%)	496 (95%)	24 (5%)	1 (0%)	47	82
6	V	518/562 (92%)	500 (96%)	18 (4%)	0	100	100
7	X	536/574 (93%)	507 (95%)	27 (5%)	2 (0%)	34	72
7	Y	518/574 (90%)	481 (93%)	34 (7%)	3 (1%)	25	64
7	Z	537/574 (94%)	496 (92%)	39 (7%)	2 (0%)	34	72
All	All	4457/5497 (81%)	4238 (95%)	209 (5%)	10 (0%)	50	82

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	T	430	VAL

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Mol	Chain	Res	Type
7	X	308	VAL
7	Y	308	VAL
7	Z	308	VAL
7	X	505	ASP

5.3.2 Protein sidechains (i)

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	50/86 (58%)	50 (100%)	0	100	100
1	B	50/86 (58%)	50 (100%)	0	100	100
1	C	50/86 (58%)	50 (100%)	0	100	100
1	D	50/86 (58%)	50 (100%)	0	100	100
1	E	50/86 (58%)	50 (100%)	0	100	100
1	F	50/86 (58%)	50 (100%)	0	100	100
1	G	50/86 (58%)	49 (98%)	1 (2%)	55	83
1	H	50/86 (58%)	50 (100%)	0	100	100
1	I	50/86 (58%)	49 (98%)	1 (2%)	55	83
1	J	50/86 (58%)	50 (100%)	0	100	100
2	P	99/196 (50%)	99 (100%)	0	100	100
3	Q	56/58 (97%)	56 (100%)	0	100	100
4	R	134/151 (89%)	133 (99%)	1 (1%)	84	94
5	S	235/265 (89%)	235 (100%)	0	100	100
6	T	378/448 (84%)	375 (99%)	3 (1%)	81	93
6	U	419/448 (94%)	414 (99%)	5 (1%)	71	90
6	V	418/448 (93%)	415 (99%)	3 (1%)	84	94
7	X	446/469 (95%)	445 (100%)	1 (0%)	93	98
7	Y	429/469 (92%)	429 (100%)	0	100	100
7	Z	447/469 (95%)	447 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3561/4281 (83%)	3546 (100%)	15 (0%)	91 97

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	U	220	ARG
6	V	300	PHE
6	U	300	PHE
7	X	425	LEU
6	V	220	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
6	V	241	HIS
7	X	199	ASN
6	V	244	ASN
6	V	488	GLN
7	X	294	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)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 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	$\#\|Z\| > 2$
8	ATP	V	1001	9	26,33,33	1.02	0	31,52,52	1.46	4 (12%)
8	ATP	U	1001	9	26,33,33	0.97	1 (3%)	31,52,52	1.50	5 (16%)
8	ATP	T	1001	9	26,33,33	0.99	0	31,52,52	1.63	6 (19%)
10	ADP	Y	601	9	24,29,29	0.65	0	29,45,45	0.70	1 (3%)
10	ADP	Z	601	9	24,29,29	0.95	1 (4%)	29,45,45	1.40	4 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	ATP	V	1001	9	-	4/18/38/38	0/3/3/3
8	ATP	U	1001	9	-	0/18/38/38	0/3/3/3
8	ATP	T	1001	9	-	2/18/38/38	0/3/3/3
10	ADP	Y	601	9	-	6/12/32/32	0/3/3/3
10	ADP	Z	601	9	-	5/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	Z	601	ADP	C5-C4	2.05	1.46	1.40
8	U	1001	ATP	C5-C4	2.02	1.46	1.40

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	V	1001	ATP	PA-O3A-PB	-3.64	120.35	132.83
8	U	1001	ATP	PB-O3B-PG	-3.61	120.44	132.83
8	T	1001	ATP	PA-O3A-PB	-3.58	120.55	132.83
10	Z	601	ADP	PA-O3A-PB	-3.53	120.72	132.83
8	U	1001	ATP	N3-C2-N1	-3.42	123.34	128.68

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	V	1001	ATP	C5'-O5'-PA-O3A
10	Y	601	ADP	PA-O3A-PB-O3B
10	Y	601	ADP	C5'-O5'-PA-O3A
10	Z	601	ADP	C5'-O5'-PA-O1A
10	Z	601	ADP	C5'-O5'-PA-O3A

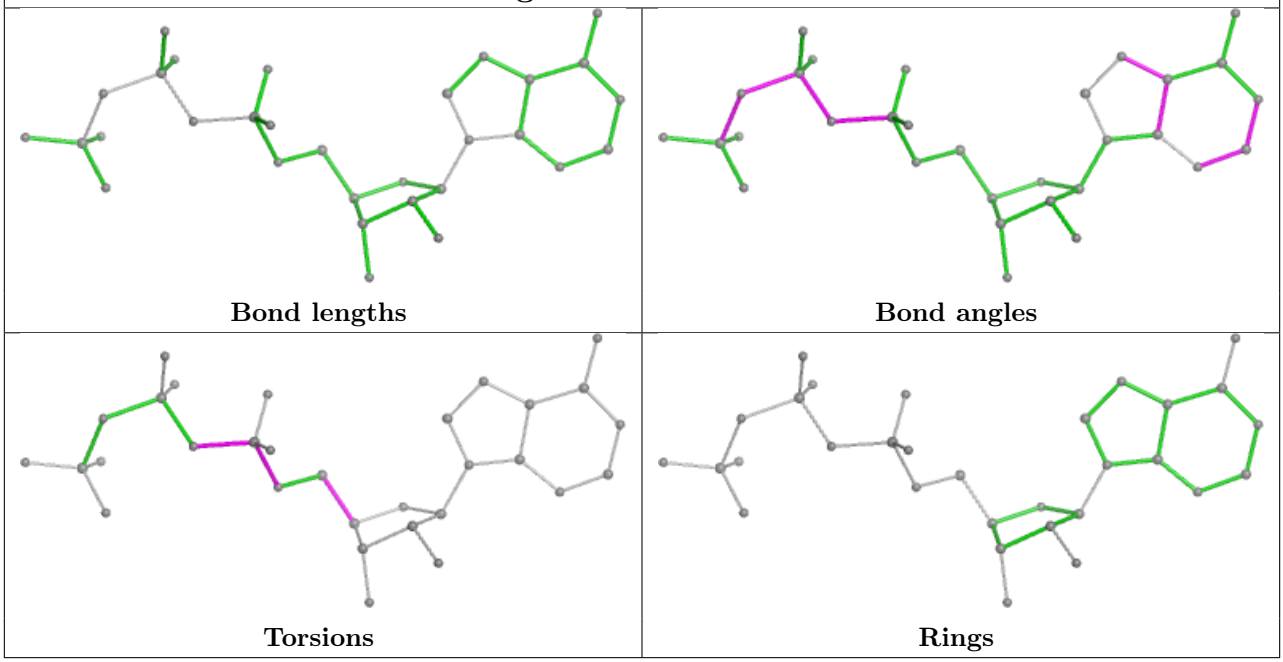
There are no ring outliers.

3 monomers are involved in 6 short contacts:

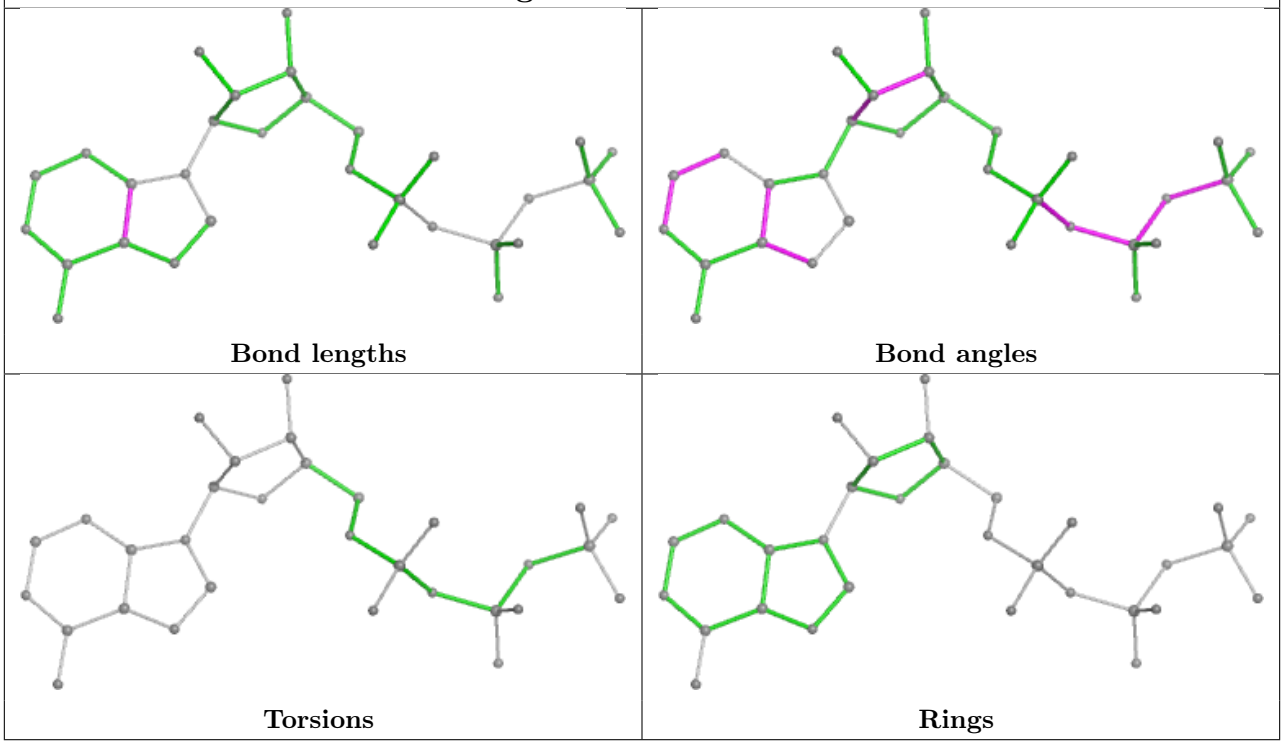
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	V	1001	ATP	2	0
10	Y	601	ADP	3	0
10	Z	601	ADP	1	0

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

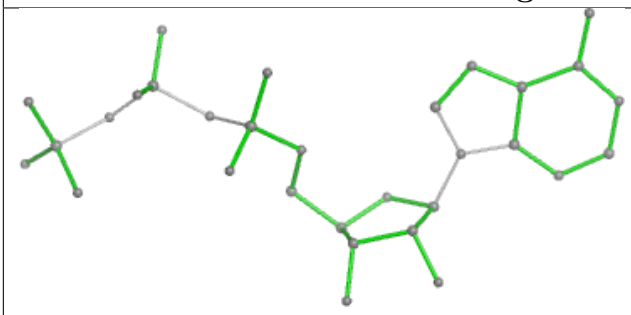
Ligand ATP V 1001



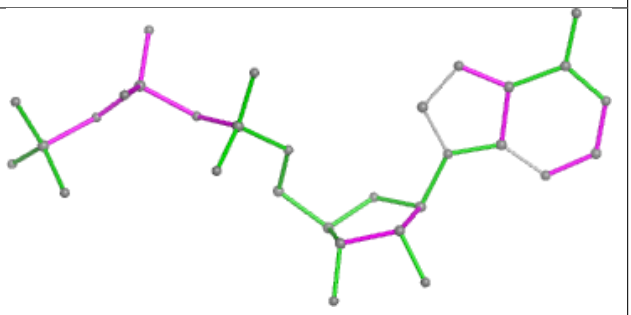
Ligand ATP U 1001



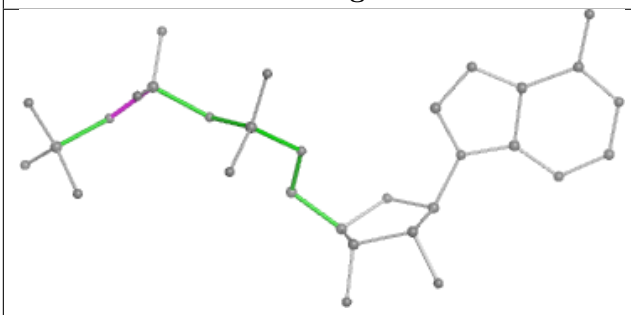
Ligand ATP T 1001



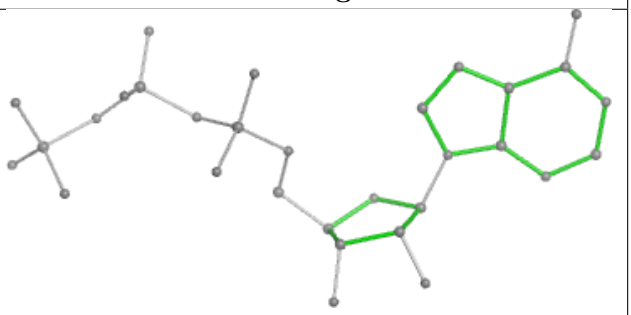
Bond lengths



Bond angles

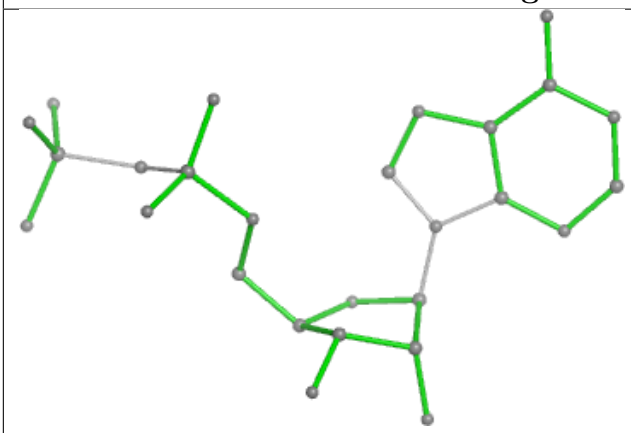


Torsions

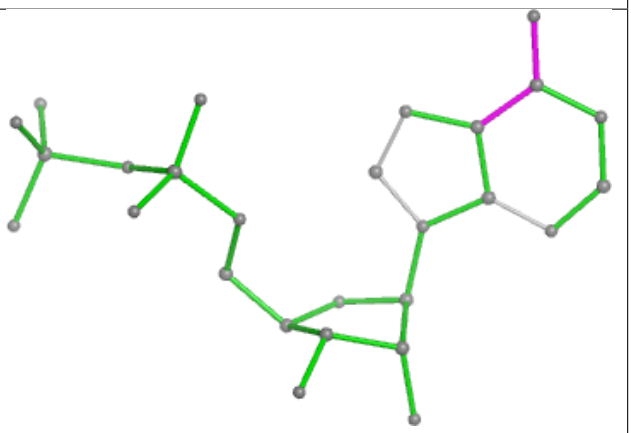


Rings

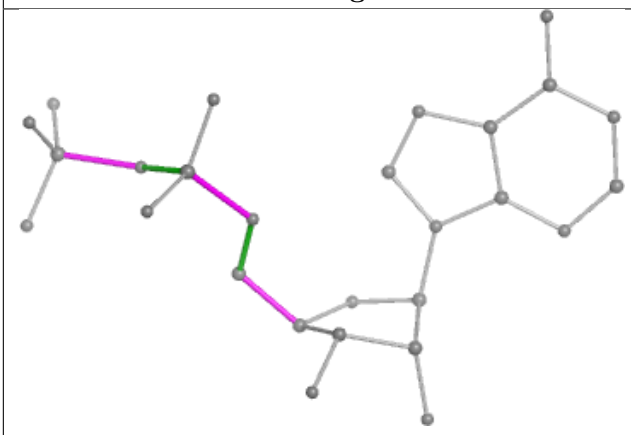
Ligand ADP Y 601



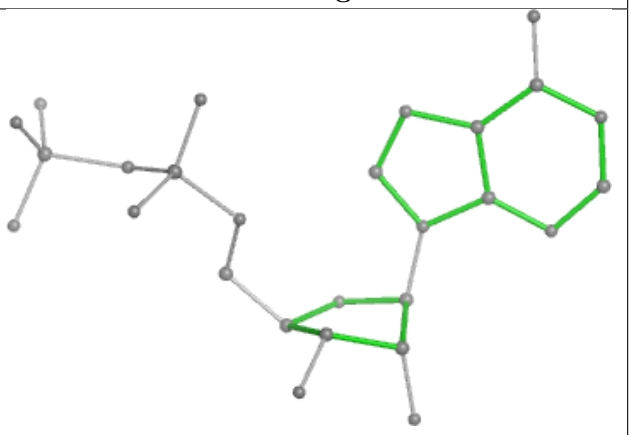
Bond lengths



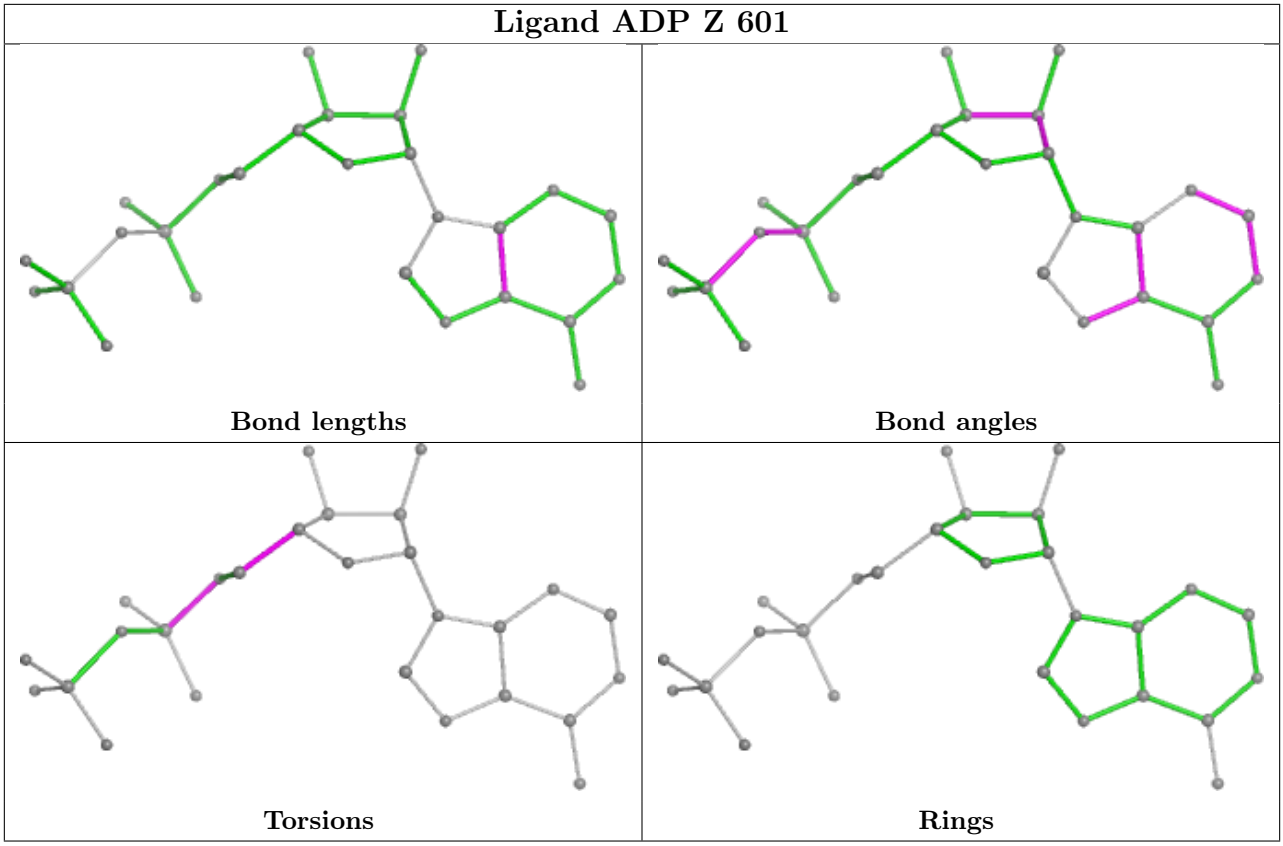
Bond angles



Torsions



Rings



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1
6	T	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	126:PHE	C	127:ALA	N	3.83
1	T	349:ALA	C	350:PHE	N	1.19

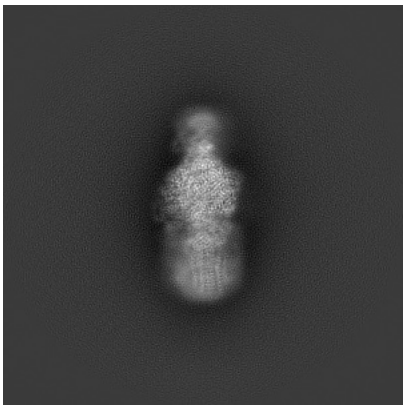
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-4841. These allow visual inspection of the internal detail of the map and identification of artifacts.

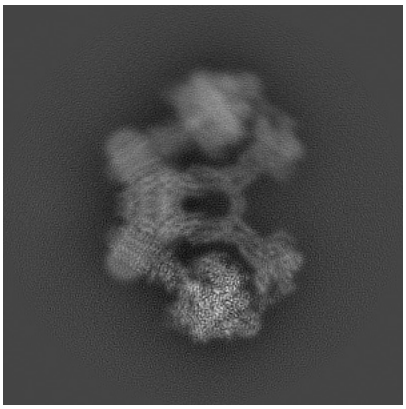
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

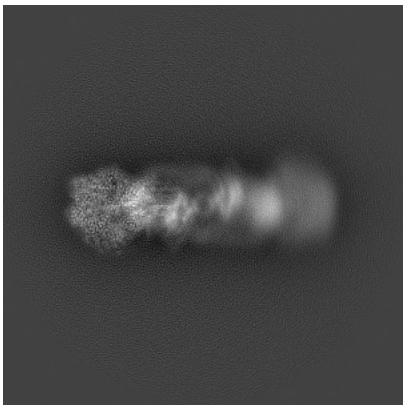
6.1.1 Primary map



X

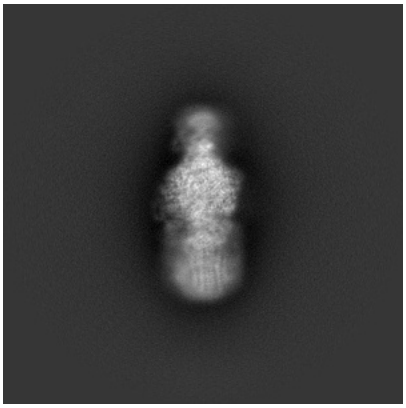


Y

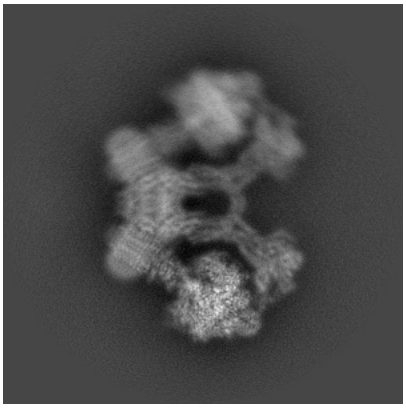


Z

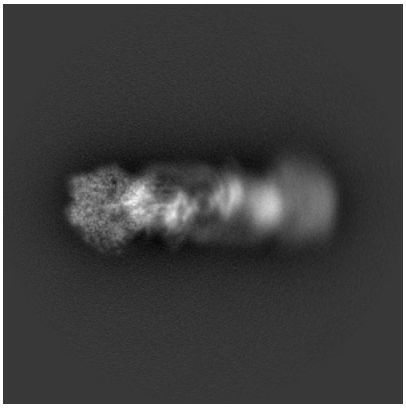
6.1.2 Raw map



X



Y

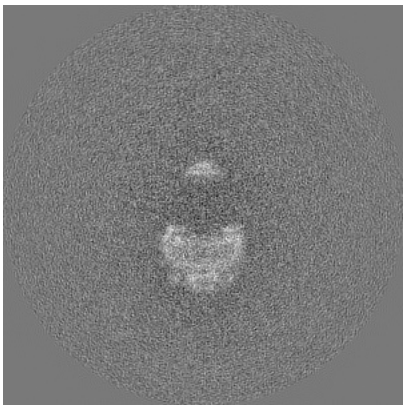


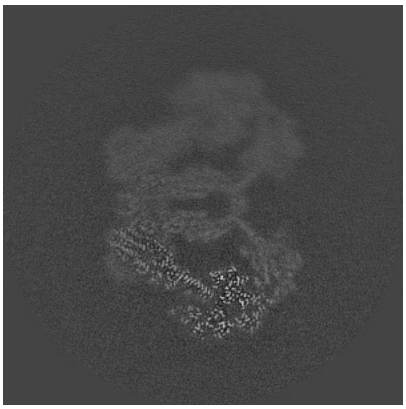
Z

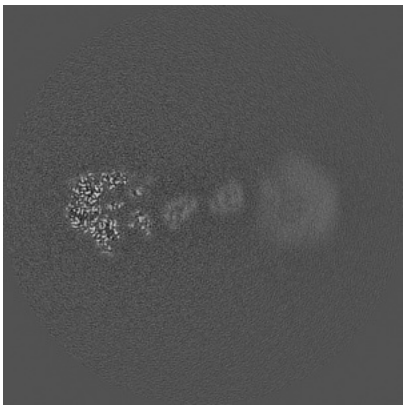
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

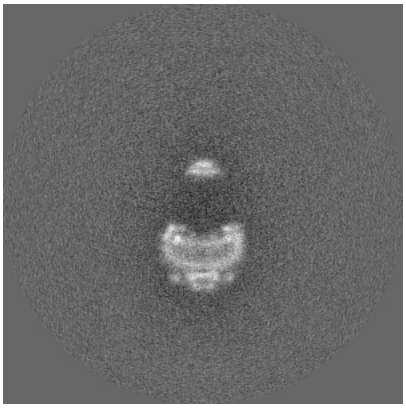
6.2.1 Primary map

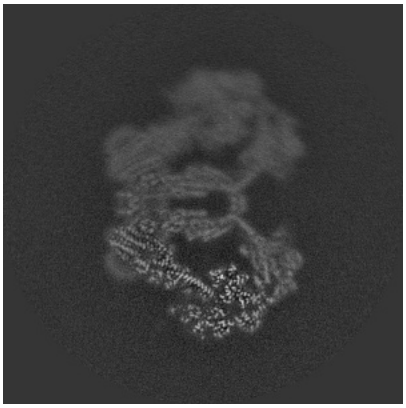

X Index: 240

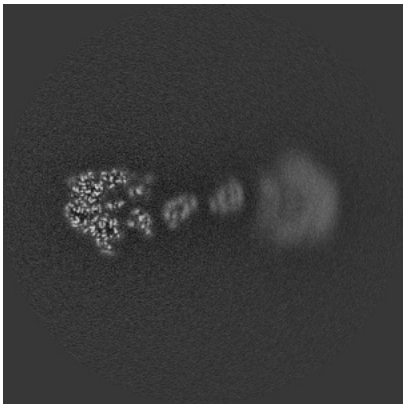

Y Index: 240


Z Index: 240

6.2.2 Raw map


X Index: 240

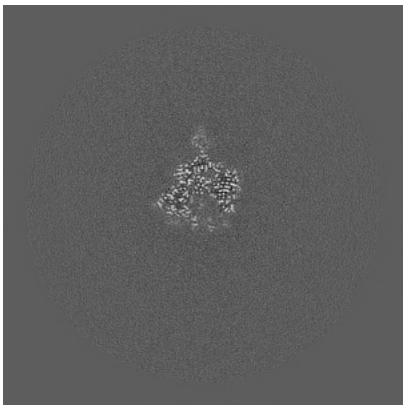

Y Index: 240


Z Index: 240

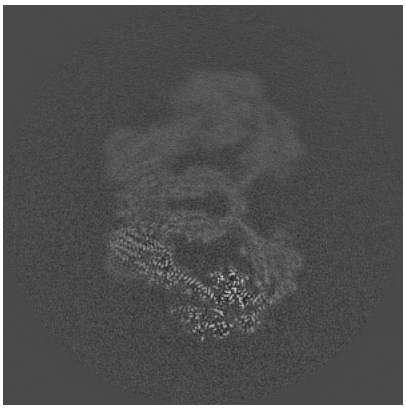
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

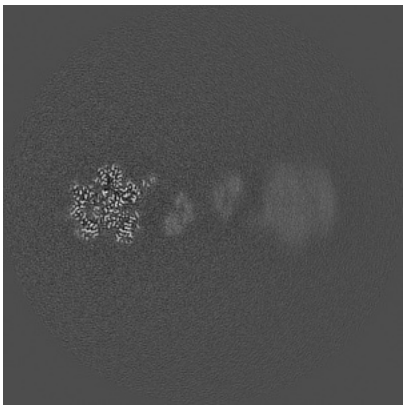
6.3.1 Primary map



X Index: 127

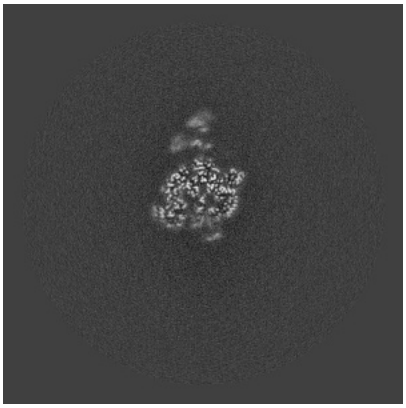


Y Index: 239

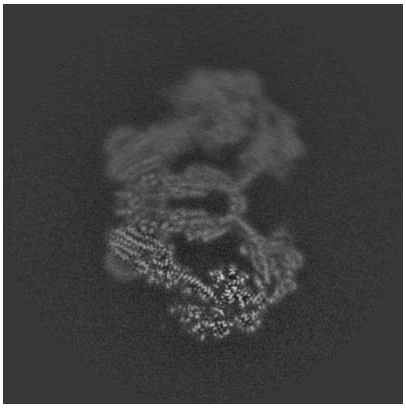


Z Index: 268

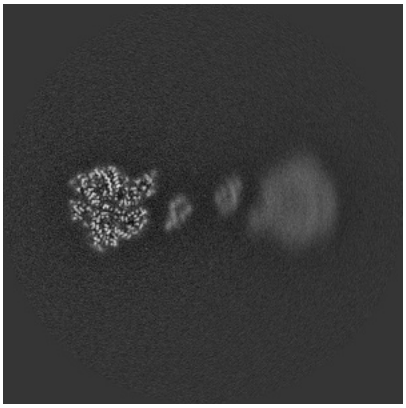
6.3.2 Raw map



X Index: 136



Y Index: 239

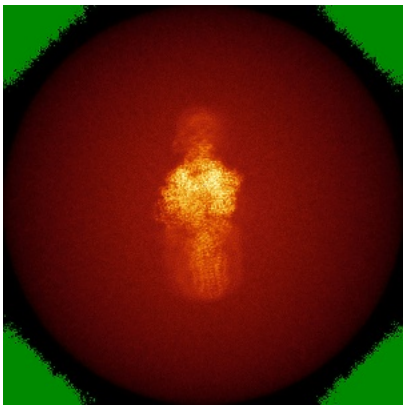


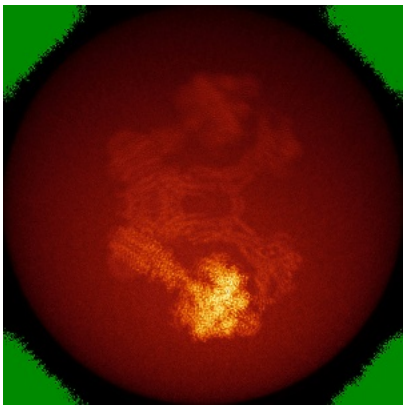
Z Index: 257

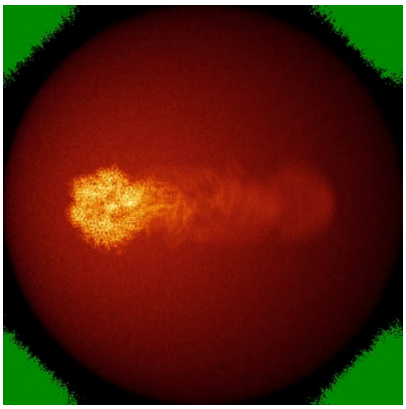
The images above show the largest variance slices of the map in three orthogonal directions.

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

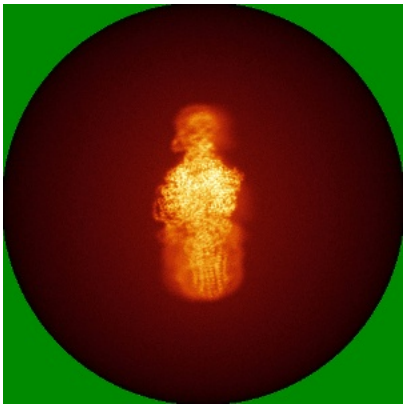
6.4.1 Primary map

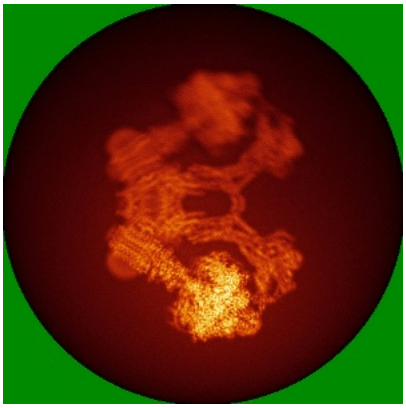

X

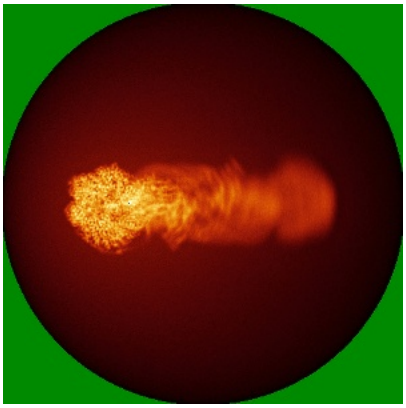

Y


Z

6.4.2 Raw map


X


Y


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

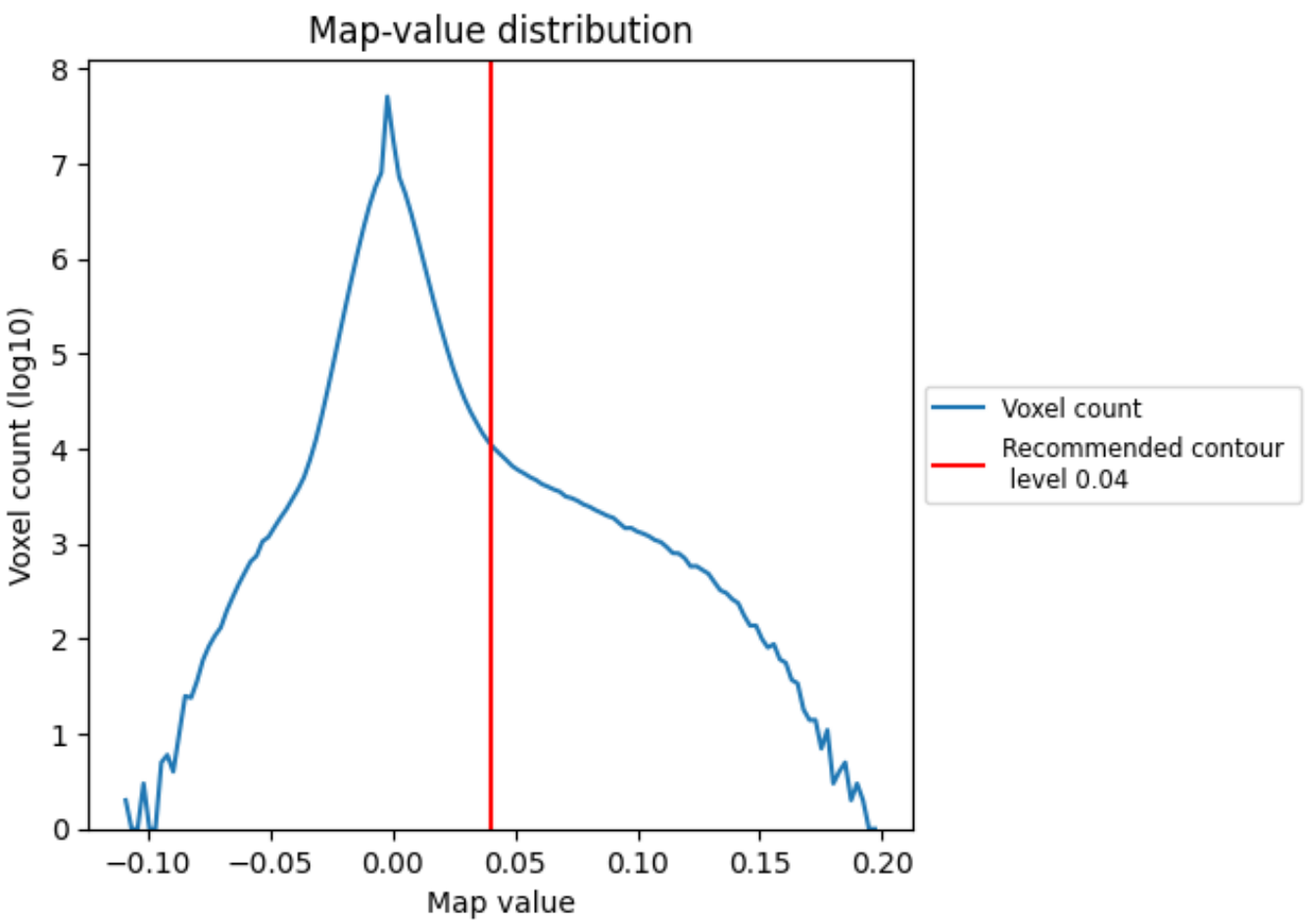
6.6 Mask visualisation (i)

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

7 Map analysis (i)

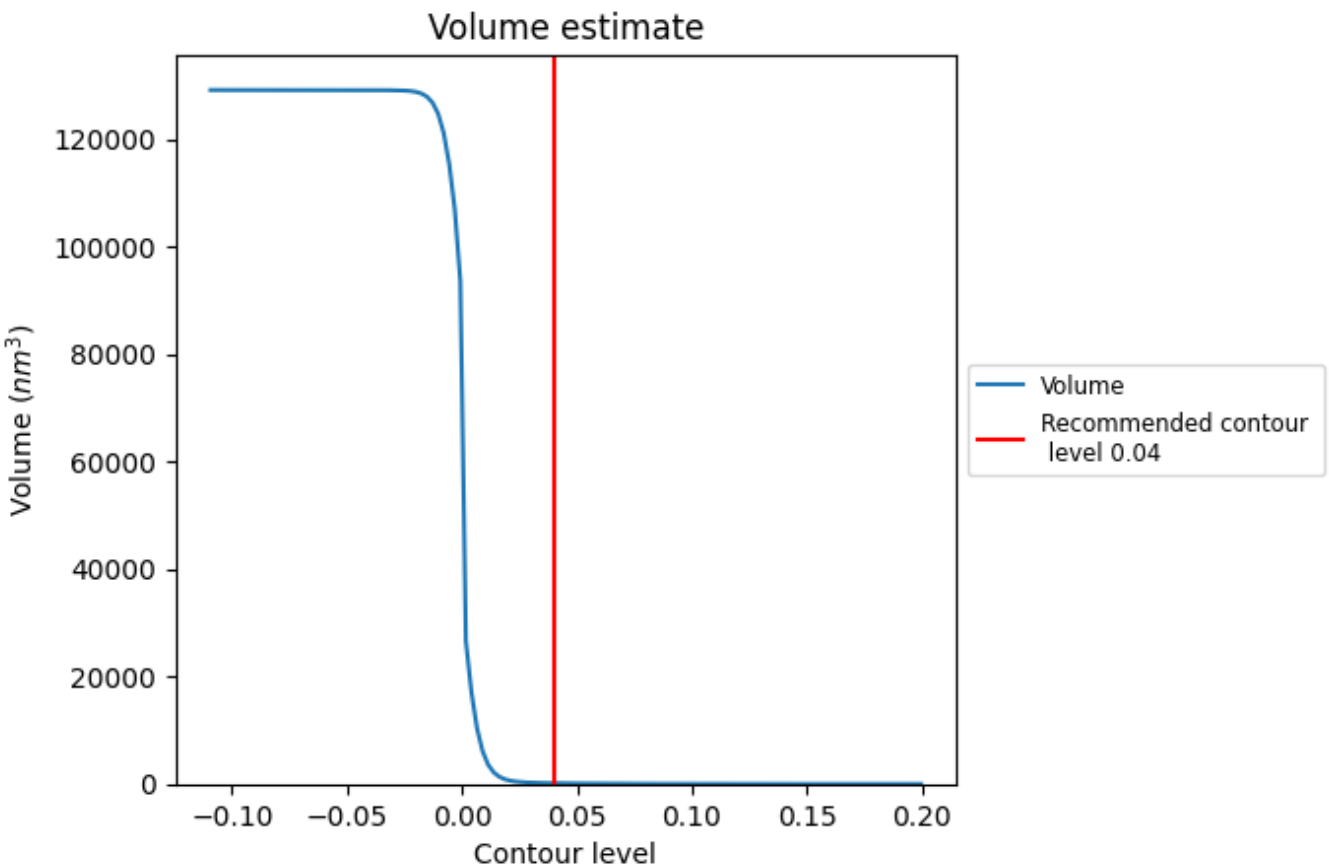
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

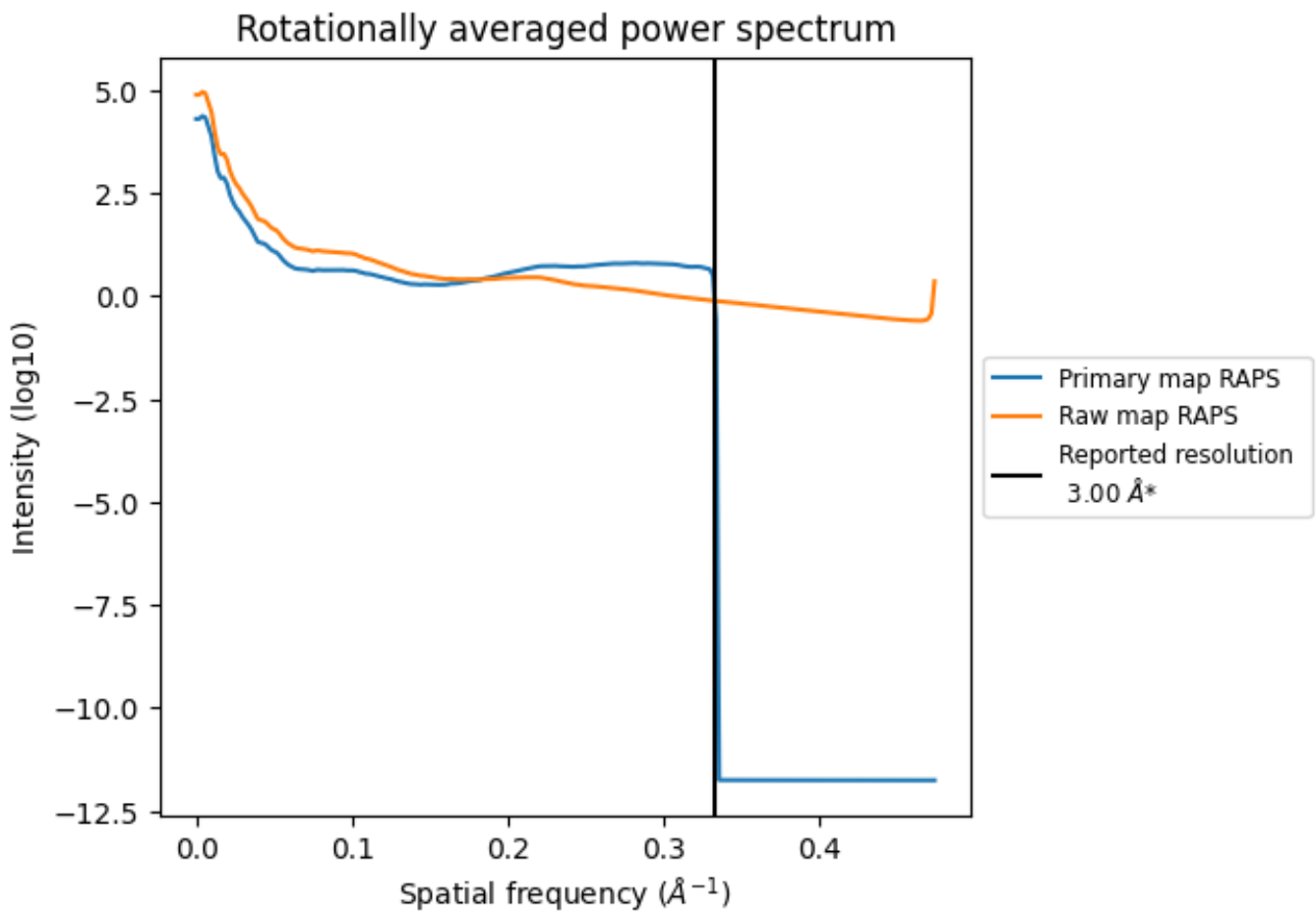
7.2 Volume estimate (i)



The volume at the recommended contour level is 138 nm^3; this corresponds to an approximate mass of 124 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

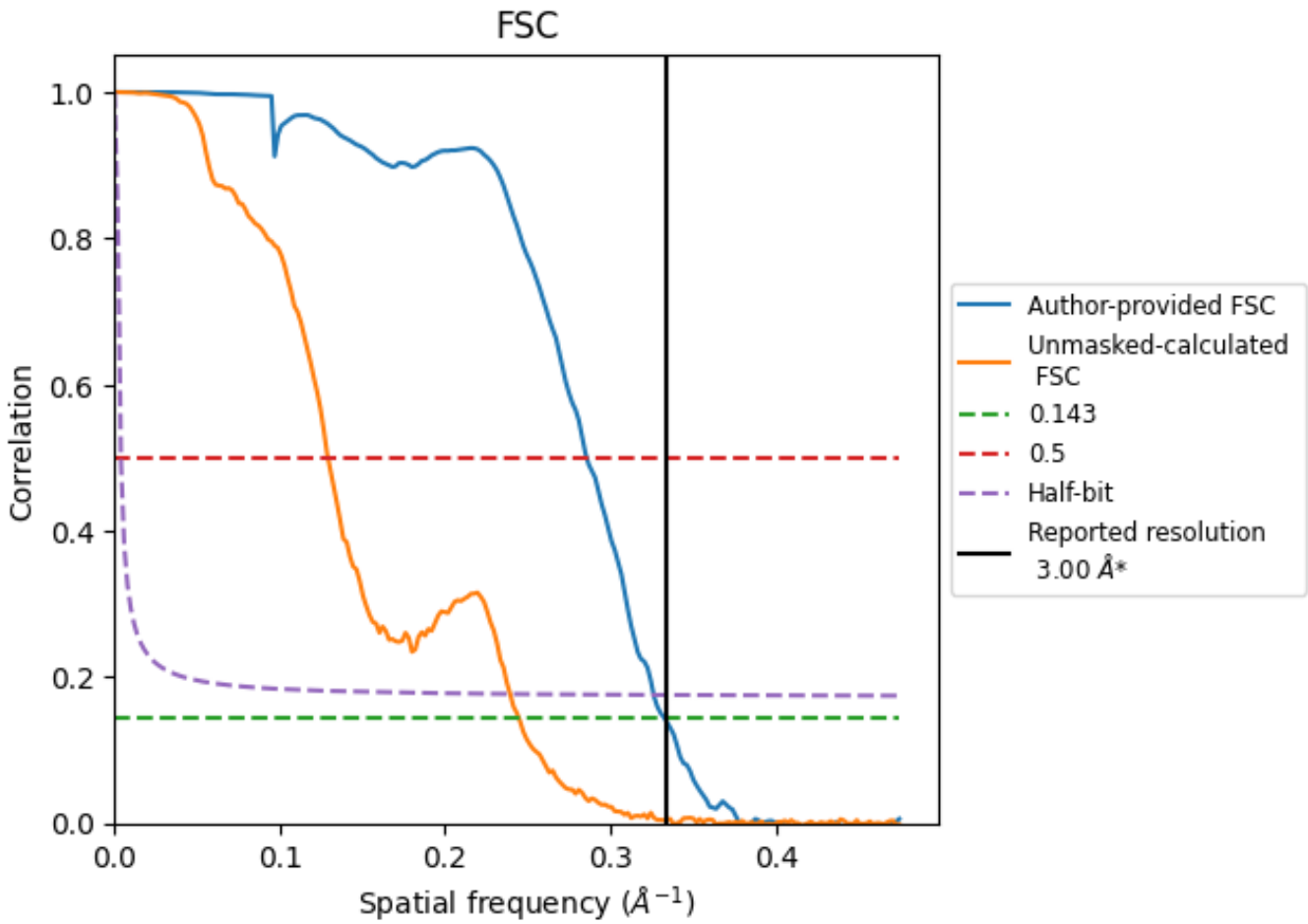


*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

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 0.333 Å^{-1}

8.2 Resolution estimates (i)

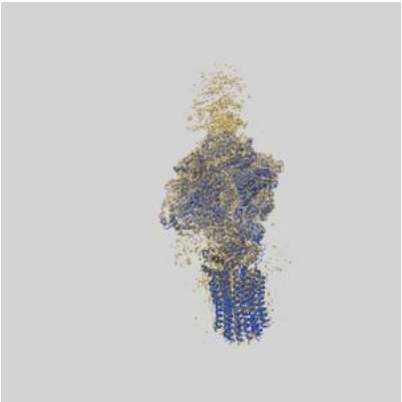
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.00	3.50	3.06
Unmasked-calculated*	4.09	7.75	4.18

*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 4.09 differs from the reported value 3.0 by more than 10 %

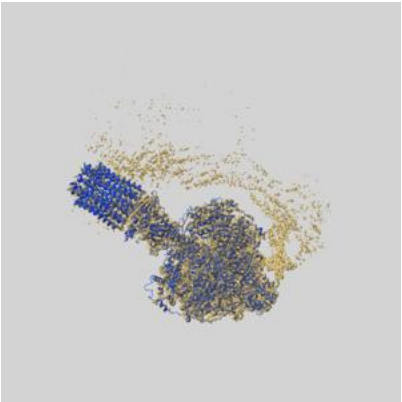
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-4841 and PDB model 6RE4. Per-residue inclusion information can be found in section 3 on page 8.

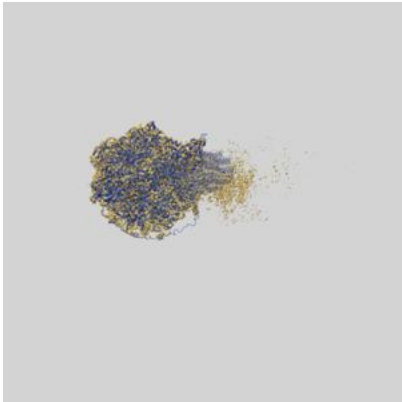
9.1 Map-model overlay (i)



X



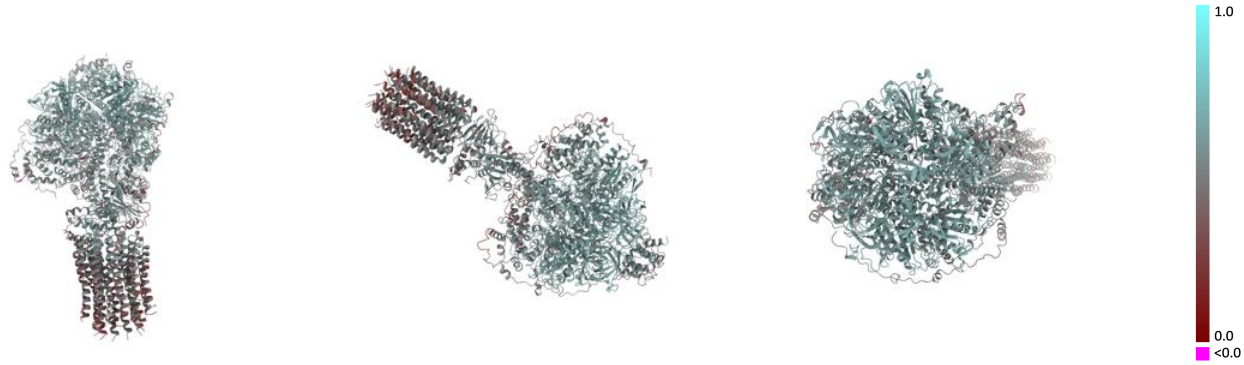
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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.

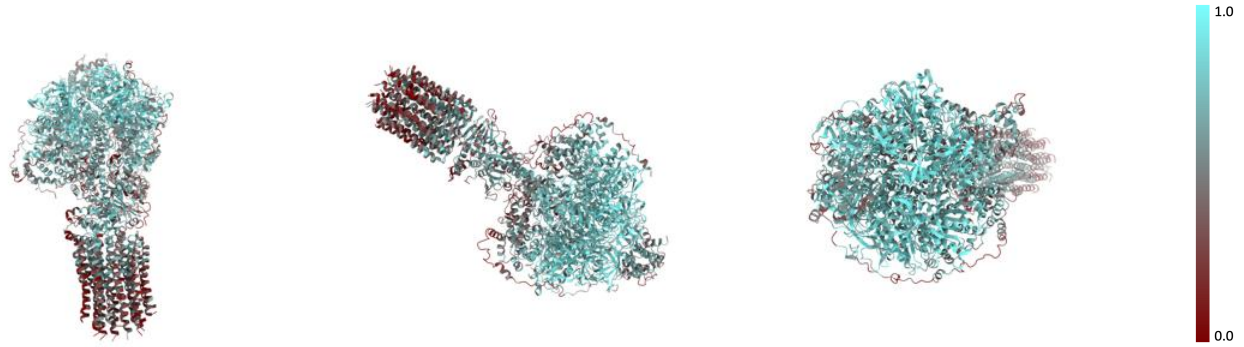
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

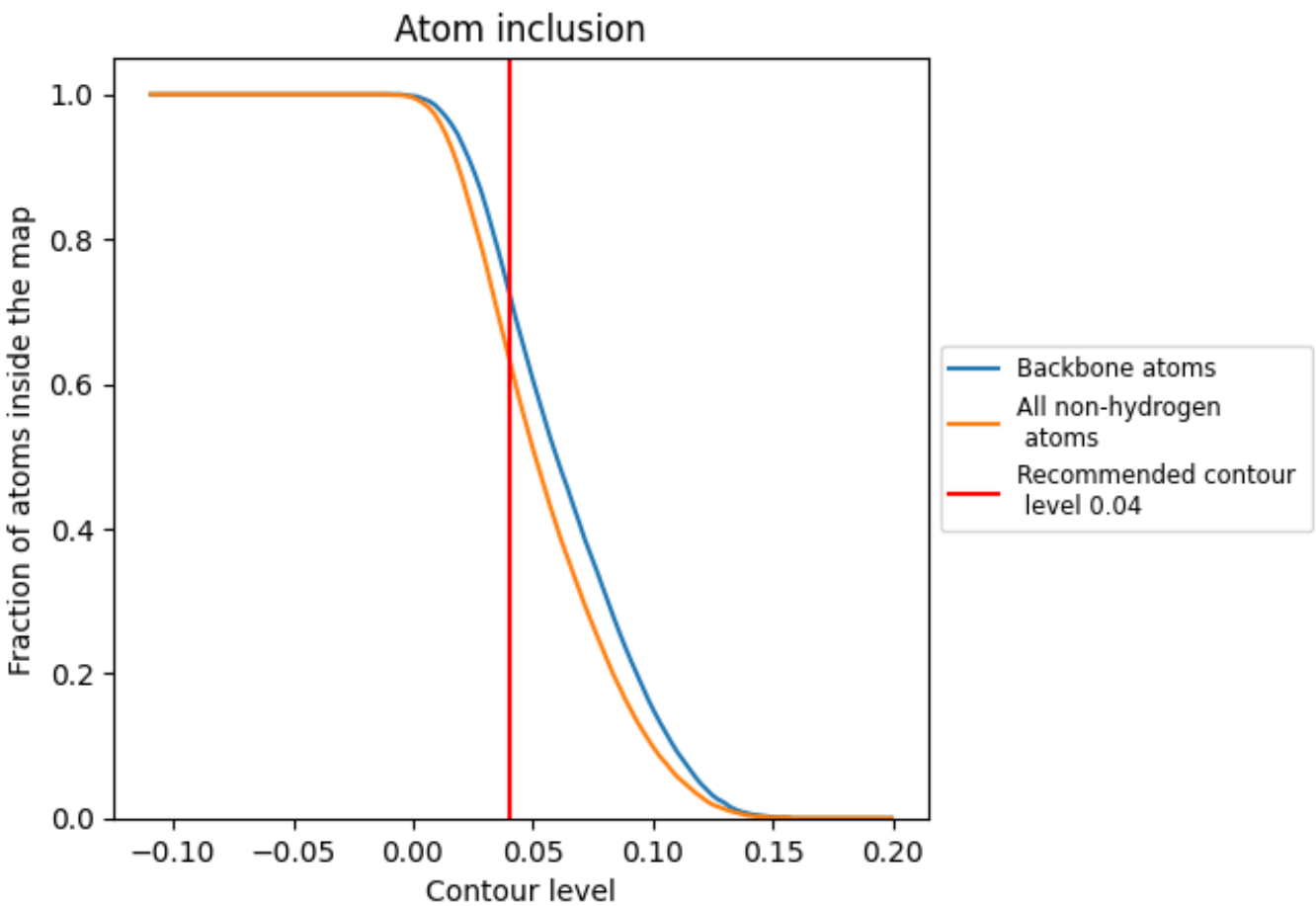
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.04).

9.4 Atom inclusion (i)



At the recommended contour level, 73% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6360	0.5370
A	0.3560	0.4460
B	0.4300	0.4410
C	0.3950	0.4270
D	0.3660	0.4120
E	0.3620	0.4200
F	0.4110	0.4460
G	0.4640	0.4680
H	0.4250	0.4410
I	0.3660	0.4260
J	0.3840	0.4180
P	0.5930	0.5230
Q	0.5150	0.5130
R	0.4720	0.4900
S	0.6090	0.5330
T	0.7570	0.5810
U	0.7200	0.5650
V	0.6920	0.5550
X	0.6930	0.5630
Y	0.7320	0.5750
Z	0.6420	0.5460