



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 01:26 AM UTC

PDB ID : 6RDT / pdb_00006rdt
EMDB ID : EMD-4830
Title : Cryo-EM structure of Polytomella F-ATP synthase, Rotary substate 1E, composite map
Authors : Murphy, B.J.; Klusch, N.; Yildiz, O.; Kuhlbrandt, W.
Deposited on : 2019-04-12
Resolution : 3.40 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

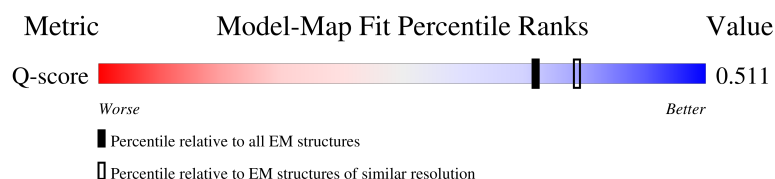
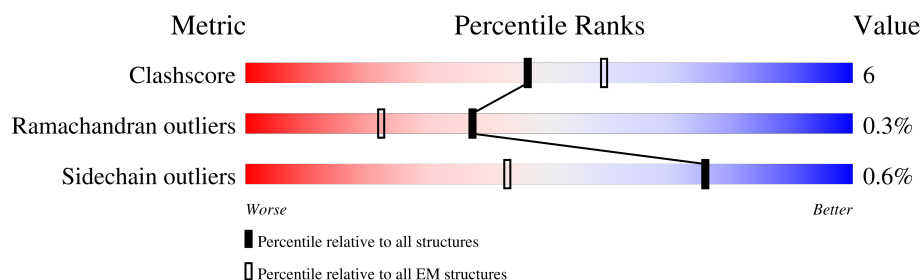
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 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.



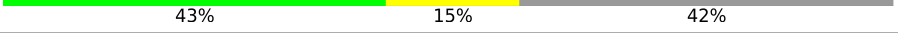
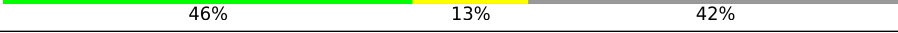
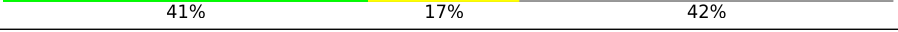
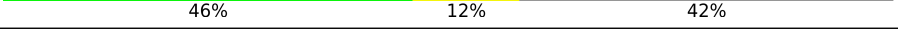
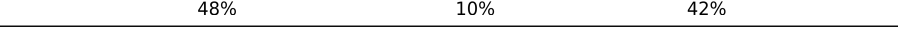
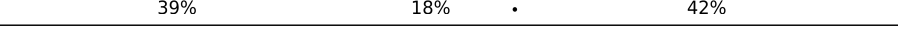
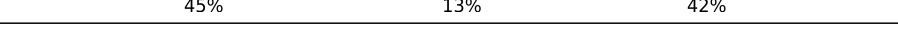
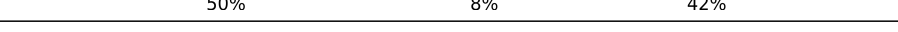
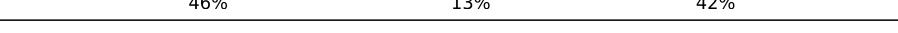
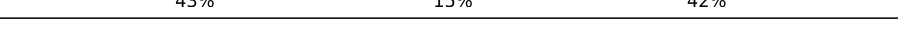
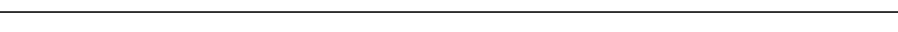
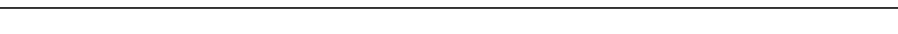
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	0	82	 90% 9% .
2	1	618	 82% 14% .
3	2	441	 89% 11%
4	3	325	 64% 11% 25%

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Mol	Chain	Length	Quality of chain
5	4	294	 88% 10%
6	5	123	 85% 15%
7	6	151	 74% 9% 18%
8	7	190	 77% 16% 7%
9	8	89	 92% 7%
10	9	97	 93% 7%
11	A	127	 43% 15% 42%
11	B	127	 46% 13% 42%
11	C	127	 41% 17% 42%
11	D	127	 46% 12% 42%
11	E	127	 48% 10% 42%
11	F	127	 39% 18% 42%
11	G	127	 45% 13% 42%
11	H	127	 50% 8% 42%
11	I	127	 46% 13% 42%
11	J	127	 43% 15% 42%
12	M	327	 58% 8% 34%
13	P	229	 65% 20% 16%
14	Q	74	 84% 14%
15	R	199	 76% 13% 11%
16	S	317	 71% 16% 13%
17	T	562	 76% 17% 7%
17	U	562	 78% 15% 7%
17	V	562	 73% 19% 7%
18	X	574	 80% 14% 6%

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Mol	Chain	Length	Quality of chain
18	Y	574	 74% 17% 9%
18	Z	574	 81% 13% 6%

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 53748 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 ASA-10: Polytomella F-ATP synthase associated subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	81	Total	C	N	O	S	0	0
			607	388	107	110	2		

- Molecule 2 is a protein called ATP synthase associated protein ASA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	595	Total	C	N	O	S	0	0
			4661	2958	798	900	5		

- Molecule 3 is a protein called ASA-2: Polytomella F-ATP synthase associated subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	2	441	Total	C	N	O	0	0
			3163	2020	532	611		

- Molecule 4 is a protein called Mitochondrial F1F0 ATP synthase associated 32 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	245	Total	C	N	O	S	0	0
			1874	1204	299	370	1		

- Molecule 5 is a protein called Mitochondrial ATP synthase associated protein ASA4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	290	Total	C	N	O	S	0	0
			2177	1385	356	434	2		

- Molecule 6 is a protein called Mitochondrial F1F0 ATP synthase associated 14 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	123	Total	C	N	O	S	0	0
			986	640	172	170	4		

- Molecule 7 is a protein called Mitochondrial ATP synthase subunit ASA6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	124	Total	C	N	O	S	0	0
			926	599	154	172	1		

- Molecule 8 is a protein called Mitochondrial ATP synthase associated protein ASA7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	176	Total	C	N	O	S	0	0
			1347	860	227	259	1		

- Molecule 9 is a protein called Mitochondrial ATP synthase subunit ASA8.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	8	88	Total	C	N	O	0	0
			692	456	115	121		

- Molecule 10 is a protein called ASA-9: Polytomella F-ATP synthase associated subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	97	Total	C	N	O	S	0	0
			776	514	124	132	6		

- Molecule 11 is a protein called Mitochondrial ATP synthase subunit c.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	74	Total	C	N	O	S	0	0
			514	340	83	88	3		
11	J	74	Total	C	N	O	S	0	0
			514	340	83	88	3		

- Molecule 12 is a protein called Mitochondrial ATP synthase subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	217	Total	C	N	O	S	0	0
			1640	1077	267	288	8		

- Molecule 13 is a protein called Mitochondrial ATP synthase subunit OSCP.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	193	Total	C	N	O	S	0	0
			1532	988	250	290	4		

- Molecule 14 is a protein called epsilon: Polytomella F-ATP synthase epsilon subunit.

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

- Molecule 15 is a protein called Mitochondrial ATP synthase subunit delta.

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

- Molecule 16 is a protein called ATP synthase gamma chain, mitochondrial.

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

- Molecule 17 is a protein called ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	523	Total	C	N	O	S	0	0
			3979	2537	703	728	11		

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Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	523	Total	C	N	O	S	0	0
			3980	2537	703	729	11		
17	V	520	Total	C	N	O	S	0	0
			3962	2527	700	724	11		

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 18 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	X	542	Total	C	N	O	S	0	0
			4115	2586	696	820	13		
18	Y	521	Total	C	N	O	S	0	0
			3957	2485	670	789	13		
18	Z	538	Total	C	N	O	S	0	0
			4087	2568	692	814	13		

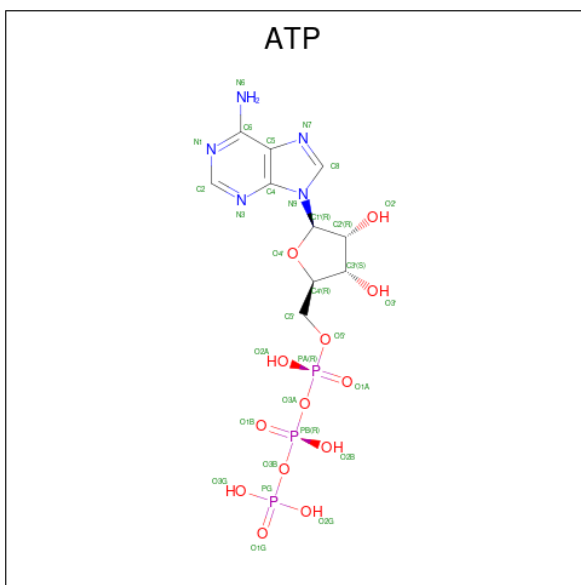
There are 6 discrepancies between the modelled and reference sequences:

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
Y	387	LEU	ARG	conflict	UNP A0ZW41
Z	350	ALA	GLY	conflict	UNP A0ZW41
Z	387	LEU	ARG	conflict	UNP A0ZW41

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
19	M	1	Total	Zn	0
			1	1	

- Molecule 20 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 21 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 22 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



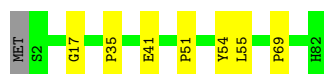
Mol	Chain	Residues	Atoms					AltConf
22	X	1	Total	C	N	O	P	0
			27	10	5	10	2	
22	Y	1	Total	C	N	O	P	0
			27	10	5	10	2	

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: ASA-10: *Polytomella* F-ATP synthase associated subunit 10

Chain 0: 



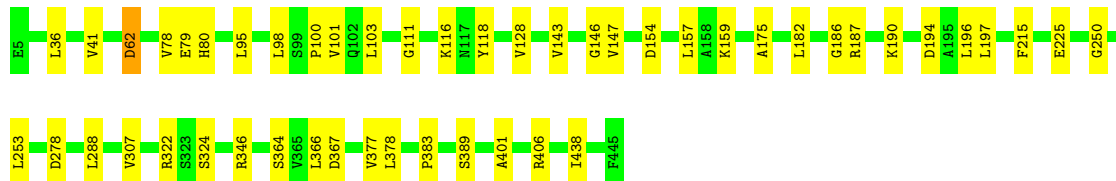
- Molecule 2: ATP synthase associated protein ASA1

Chain 1: 



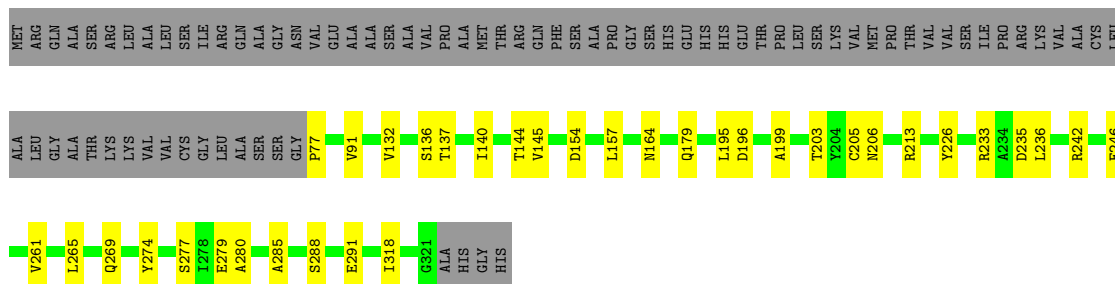
- Molecule 3: ASA-2: *Polytomella* F-ATP synthase associated subunit 2

Chain 2: 



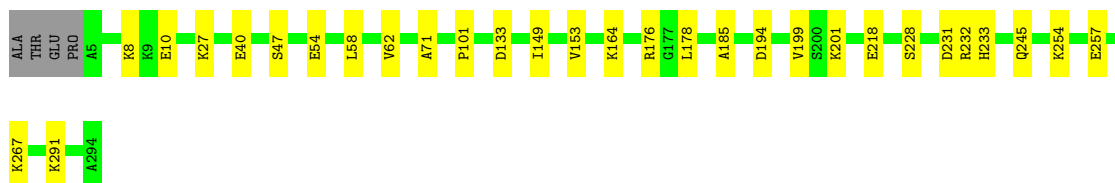
- Molecule 4: Mitochondrial F1F0 ATP synthase associated 32 kDa protein

Chain 3: 



- Molecule 5: Mitochondrial ATP synthase associated protein ASA4

Chain 4: 88% 10%



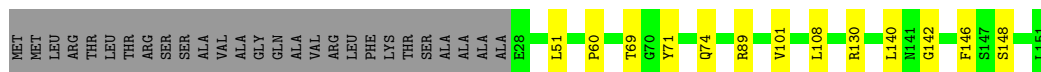
- Molecule 6: Mitochondrial F1F0 ATP synthase associated 14 kDa protein

Chain 5: 85% 15%



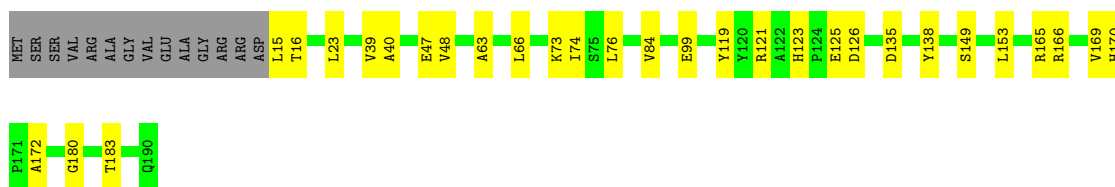
- Molecule 7: Mitochondrial ATP synthase subunit ASA6

Chain 6: 74% 9% 18%



- Molecule 8: Mitochondrial ATP synthase associated protein ASA7

Chain 7: 77% 16% 7%



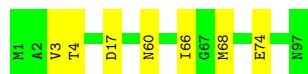
- Molecule 9: Mitochondrial ATP synthase subunit ASA8

Chain 8: 92% 7%

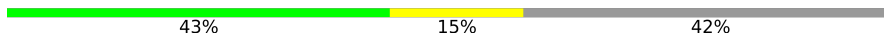


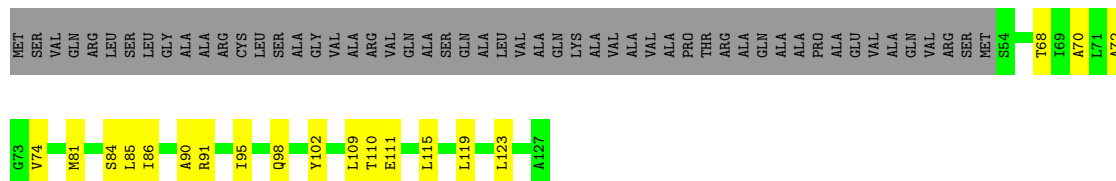
- Molecule 10: ASA-9: Polytomella F-ATP synthase associated subunit 9

Chain 9:  93% 7%

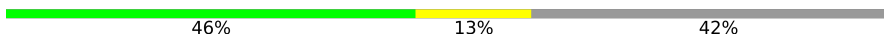


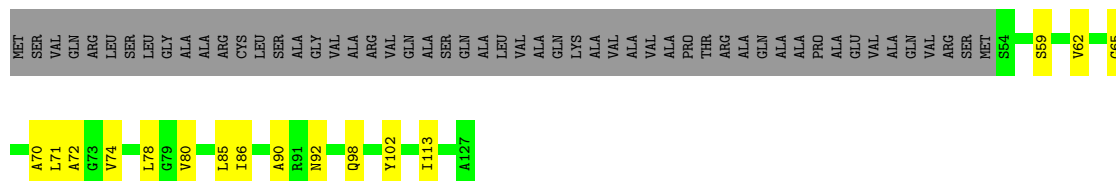
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain A:  43% 15% 42%

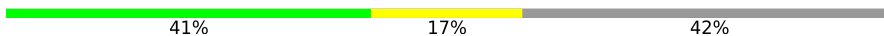


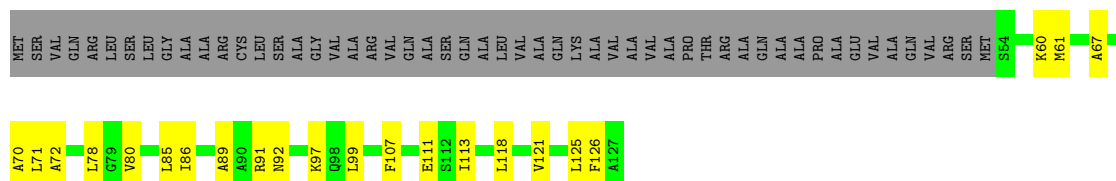
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain B:  46% 13% 42%

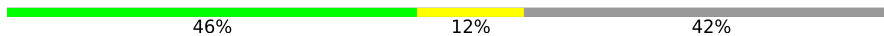


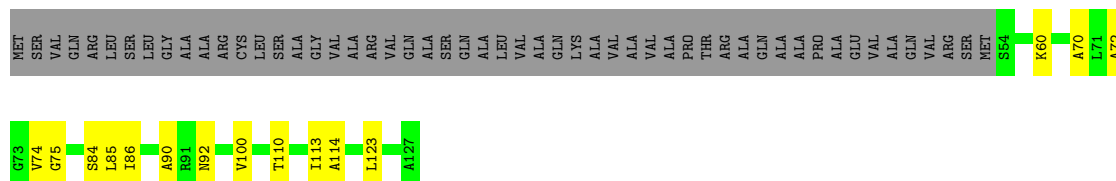
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain C:  41% 17% 42%

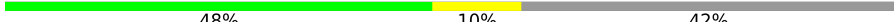


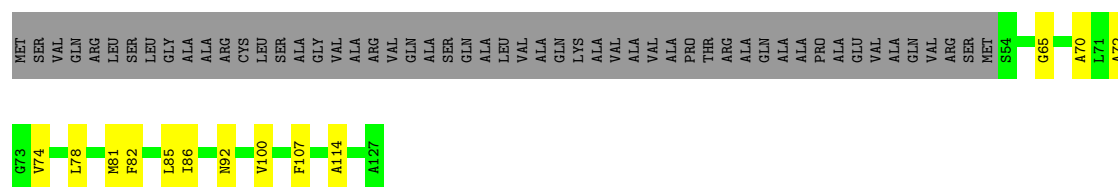
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain D:  46% 12% 42%

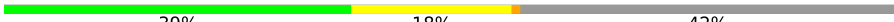


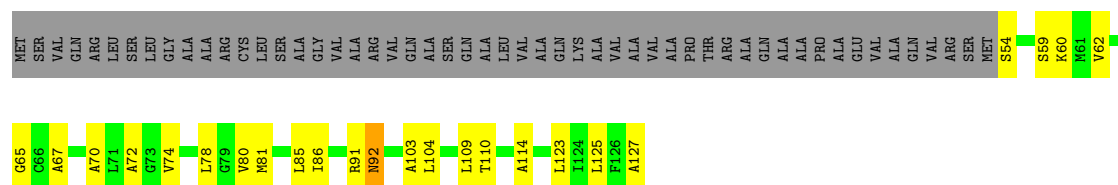
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain E:  48% 10% 42%

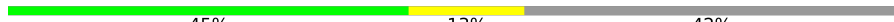


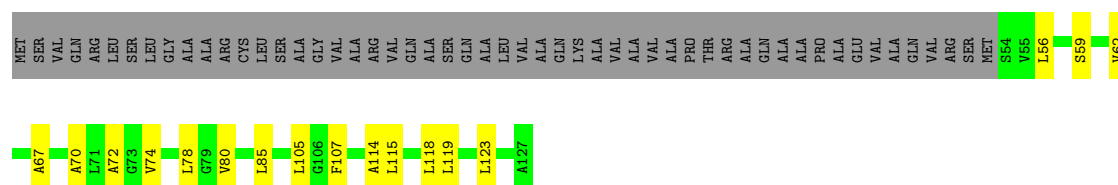
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain F:  39% 18% 42%



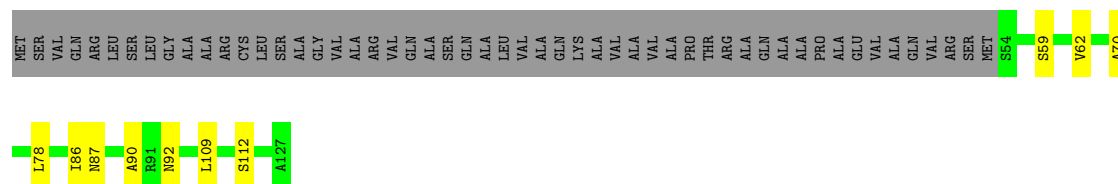
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain G:  45% 13% 42%

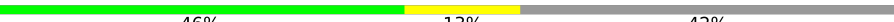


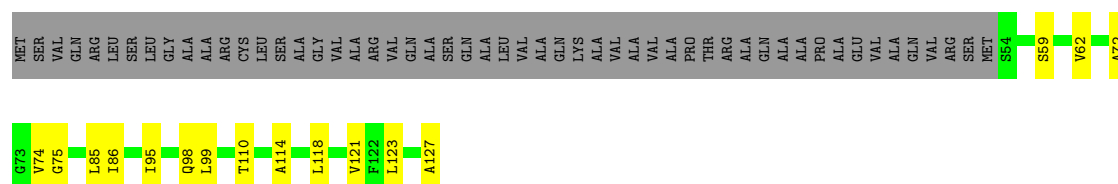
- Molecule 11: Mitochondrial ATP synthase subunit c

Chain H:  50% 8% 42%



- Molecule 11: Mitochondrial ATP synthase subunit c

Chain I:  46% 13% 42%



- Molecule 11: Mitochondrial ATP synthase subunit c

V74	G75	L78	F82	G83	S84	L85	I86	N92	P93	Q98	Y102	L109	T110	E111	A114	L115	L118	A127																																		
MET	VAL	GLN	ARG	LEU	SER	GLY	ALA	ALA	ARG	CYS	LEU	SER	GLY	VAL	ALA	ALA	SER	GLN	LEU	LEU	ALA	ALA	GLN	LYS	GLN	LYS	VAL	VAL	VAL	PRO	THR	ARG	ALA	GLN	ALA	ALA	PRO	ALA	GLU	VAL	ALA	GLN	VAL	ARG	SER	MET	S84	T69	A70	L71	A72	T73

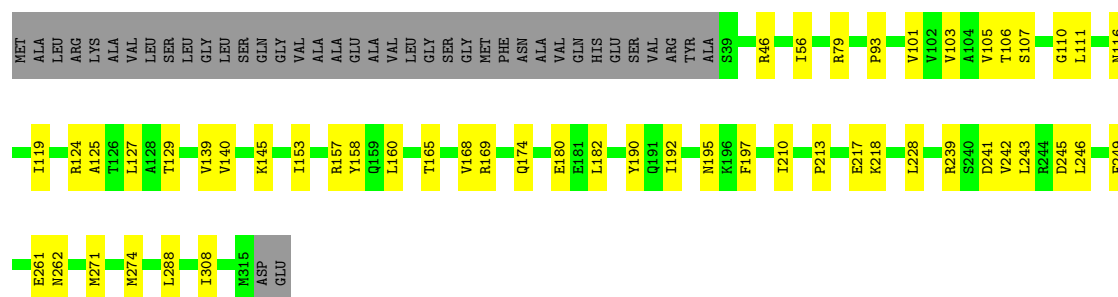
HIS	PHE	ILE	GLY	GLY	THR	TRP	PRO	PRO	MET	ALA	F219	R239	L250	L251	T255	V271	T274	V277	L281	V285	K321	I322	V323	K324	LYS	ILE	HIS	SER	PRO	ASN	VAL	LEU	SER	VAL	LEU	GLY	ARG	ILE	GLY	SER	LEU	LEU	GLY	ARG	SER	THR	GLN	CYS	GLY	PHE	THR	SER	THR	ARG	ASN	LEU	ASN	GLY	ILE	ASP	THR	SER	SER	SER	VAL	PHE	GLN	ALA	LEU	SER	SER	ASP	ASN	GLU	ASN	LYS	PRO	ALA	CYS
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K120	ME1
E123	LEU
	ARG
A126	VAL
	ALA
L134	SER
L135	VAL
E136	ALA
V137	LEU
T138	ARG
V139	ARG
M140	ALA
	GLY
K149	GLY
E150	LYS
E151	TLE
V152	TLE
V153	MET
C154	PRO
T155	GLN
V156	MET
	VAL
	ARG
E160	ALA
P161	LEU
	SER
K164	VAL
	SER
L170	ALA
T171	ALA
	SER
L184	ALA
V185	ALA
M186	GLN
Q187	ALA
E188	GLY
	L37
L194	P40
G197	L46
F198	S47
V199	G48
S203	A51
M209	Q52
S210	I53
K224	K63
L225	F77
I229	K82
	R101
	V108
	L109
	K110

Sequence logo for the 12th position. The y-axis represents information content in bits, ranging from 0 to 0.4. The x-axis lists amino acids: MET, CYS, A3, R10, L17, R18, N21, K32, K36, A41, Q49, K61, I69, and N74. MET and CYS are in grey boxes, A3 is in a green box, and the others are in yellow boxes. MET and CYS have very low information content (near 0). A3 has the highest information content, around 0.35 bits. R10, L17, R18, N21, K32, K36, A41, Q49, K61, I69, and N74 all have information content between 0.1 and 0.2 bits.

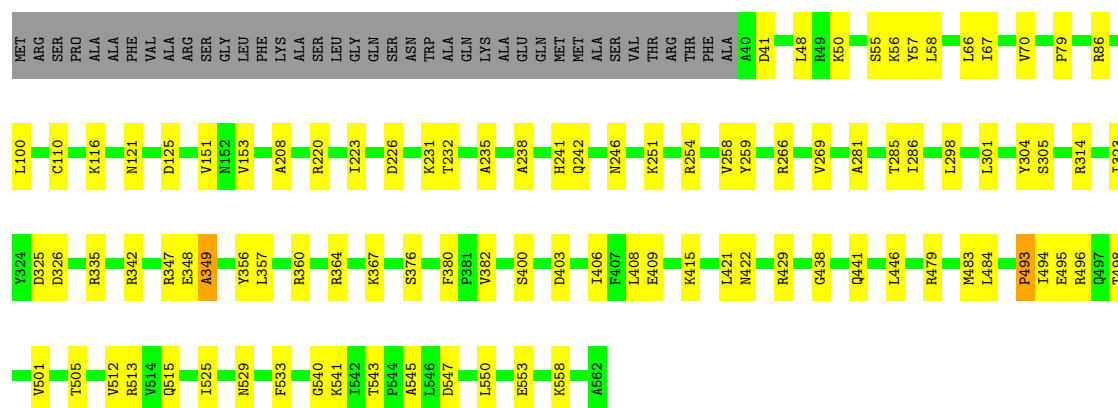
Q178	Q179	Q180	Q181	Q182	Q183	Q184	Q185	Q186	Q187	Q188	Q189	Q190	Q191	Q192	Q193	Q194	Q195	Q196	Q197	Q198	Q199	Q200	Q201	Q202	Q203	Q204	Q205	Q206	Q207	Q208	Q209	Q210	Q211	Q212	Q213	Q214	Q215	Q216	Q217	Q218	Q219	Q220	Q221	Q222	Q223	Q224	Q225	Q226	Q227	Q228	Q229	Q230	Q231	Q232	Q233	Q234	Q235	Q236	Q237	Q238	Q239	Q240	Q241	Q242	Q243	Q244	Q245	Q246	Q247	Q248	Q249	Q250	Q251	Q252	Q253	Q254	Q255	Q256	Q257	Q258	Q259	Q260	Q261	Q262	Q263	Q264	Q265	Q266	Q267	Q268	Q269	Q270	Q271	Q272	Q273	Q274	Q275	Q276	Q277	Q278	Q279	Q280	Q281	Q282	Q283	Q284	Q285	Q286	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299	Q300	Q301	Q302	Q303	Q304	Q305	Q306	Q307	Q308	Q309	Q310	Q311	Q312	Q313	Q314	Q315	Q316	Q317	Q318	Q319	Q320	Q321	Q322	Q323	Q324	Q325	Q326	Q327	Q328	Q329	Q330	Q331	Q332	Q333	Q334	Q335	Q336	Q337	Q338	Q339	Q340	Q341	Q342	Q343	Q344	Q345	Q346	Q347	Q348	Q349	Q350	Q351	Q352	Q353	Q354	Q355	Q356	Q357	Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416	Q417	Q418	Q419	Q420	Q421	Q422	Q423	Q424	Q425	Q426	Q427	Q428	Q429	Q430	Q431	Q432	Q433	Q434	Q435	Q436	Q437	Q438	Q439	Q440	Q441	Q442	Q443	Q444	Q445	Q446	Q447	Q448	Q449	Q450	Q451	Q452	Q453	Q454	Q455	Q456	Q457	Q458	Q459	Q460	Q461	Q462	Q463	Q464	Q465	Q466	Q467	Q468	Q469	Q470	Q471	Q472	Q473	Q474	Q475	Q476	Q477	Q478	Q479	Q480	Q481	Q482	Q483	Q484	Q485	Q486	Q487	Q488	Q489	Q490	Q491	Q492	Q493	Q494	Q495	Q496	Q497	Q498	Q499	Q500	Q501	Q502	Q503	Q504	Q505	Q506	Q507	Q508	Q509	Q510	Q511	Q512	Q513	Q514	Q515	Q516	Q517	Q518	Q519	Q520	Q521	Q522	Q523	Q524	Q525	Q526	Q527	Q528	Q529	Q530	Q531	Q532	Q533	Q534	Q535	Q536	Q537	Q538	Q539	Q540	Q541	Q542	Q543	Q544	Q545	Q546	Q547	Q548	Q549	Q550	Q551	Q552	Q553	Q554	Q555	Q556	Q557	Q558	Q559	Q560	Q561	Q562	Q563	Q564	Q565	Q566	Q567	Q568	Q569	Q570	Q571	Q572	Q573	Q574	Q575	Q576	Q577	Q578	Q579	Q580	Q581	Q582	Q583	Q584	Q585	Q586</
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Chain S:  71% 16% 13%



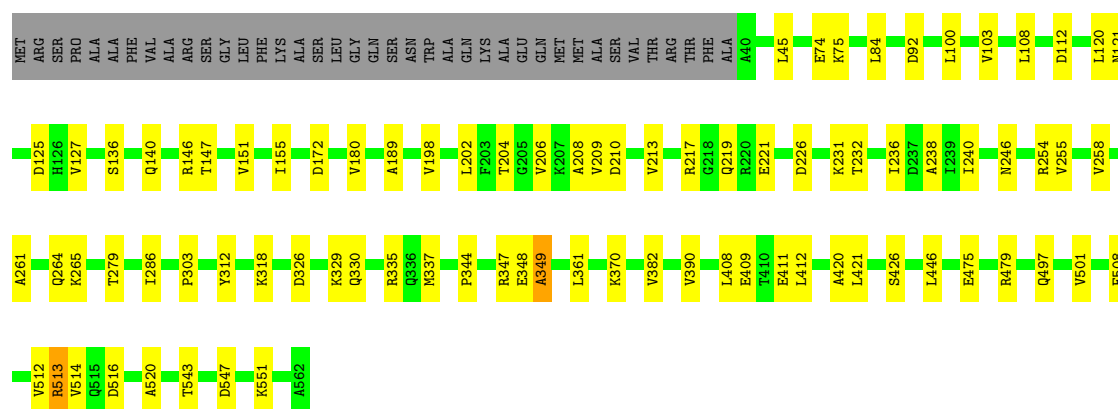
- Molecule 17: ATP synthase subunit alpha

Chain T:  76% 17% 7%



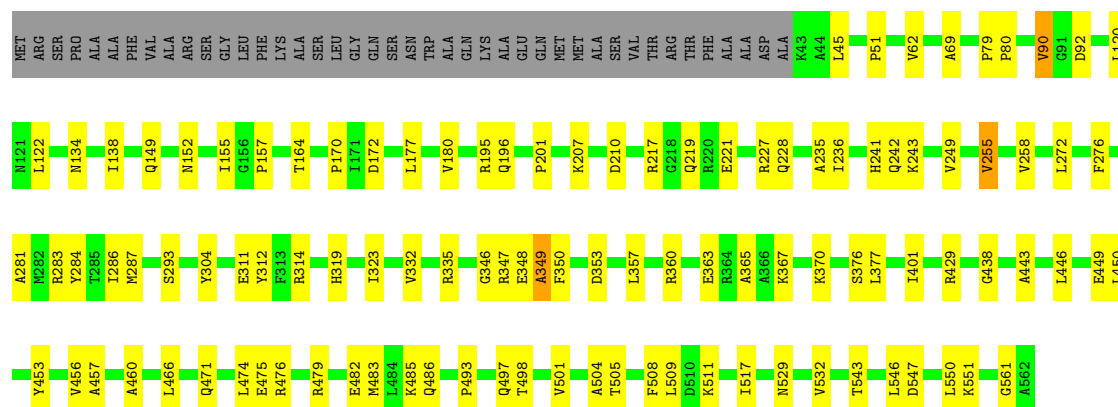
- Molecule 17: ATP synthase subunit alpha

Chain U:  78% 15% 7%



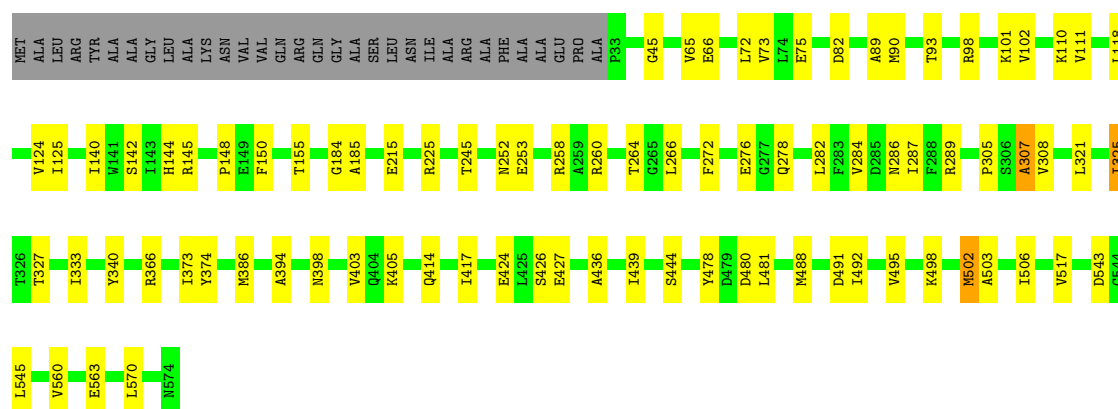
- Molecule 17: ATP synthase subunit alpha

Chain V:  73% 19% 7%



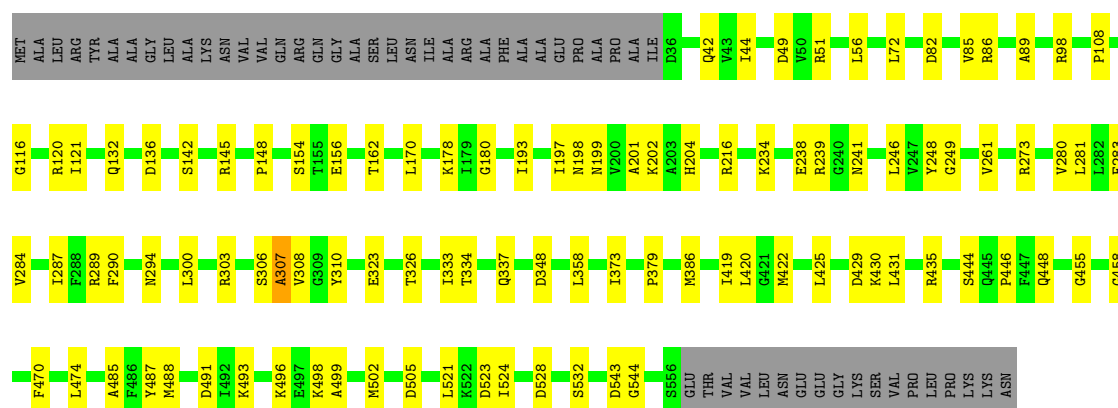
• Molecule 18: ATP synthase subunit beta

Chain X: 80% 14% 6%



• Molecule 18: ATP synthase subunit beta

Chain Y: 74% 17% 9%



• Molecule 18: ATP synthase subunit beta

Chain Z: 81% 13% 6%

D348	P349	A350	P351	A352	T353	K386	S426	D429	Q445	K459	F470	L474	Y487	M488	V489	G490	D491	K498	A503	K516	E519	L527	D528	L545	K550	N562	K566	L570	P571	K572	K573	N574												
E127	Q157	I159	I164	K165	V166	V167	R175	E219	R225	G231	K234	C244	M251	T264	F272	R273	E276	G277	Q278	D285	N286	R289	R303	I304	P305	S306	A307	V308	Q311	L314	T326	T327	I333	A338	V341	P342								
MET	ALA	LEU	ARG	TYR	ALA	ALA	GLY	LEU	ALA	LYS	ASN	VAL	VAL	GLN	ARG	GLN	GLY	ALA	SER	LEU	ASN	ILE	ALA	ALA	GLU	PRO	ALA	PRO	ALA	ILE	ASP	A37	R51	F52	D53	L56	I59	R71	Q78	D82	R86	R98	V111	G119

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	51482	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 ($e^-/\text{\AA}^2$)	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	32.611	Depositor
Minimum map value	-21.812	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.038	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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ATP, ADP, ZN

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	0	0.41	0/628	0.51	0/856
2	1	0.44	0/4750	0.52	1/6434 (0.0%)
3	2	0.33	0/3212	0.53	0/4371
4	3	0.39	0/1911	0.54	1/2601 (0.0%)
5	4	0.37	0/2216	0.52	1/3000 (0.0%)
6	5	0.54	0/1011	0.60	0/1376
7	6	0.48	0/946	0.61	0/1287
8	7	0.47	0/1374	0.52	0/1865
9	8	0.49	0/715	0.59	0/974
10	9	0.30	0/802	0.54	0/1084
11	A	0.32	0/520	0.56	0/704
11	B	0.27	0/520	0.58	0/704
11	C	0.28	0/519	0.55	0/701
11	D	0.26	0/520	0.54	0/704
11	E	0.29	0/520	0.54	0/704
11	F	0.28	0/520	0.54	0/704
11	G	0.25	0/520	0.55	0/704
11	H	0.24	0/520	0.57	0/704
11	I	0.25	0/520	0.53	0/704
11	J	0.34	0/520	0.58	0/704
12	M	0.46	0/1683	0.58	1/2295 (0.0%)
13	P	0.41	0/1553	0.64	2/2093 (0.1%)
14	Q	0.27	0/574	0.56	0/774
15	R	0.28	0/1336	0.54	0/1827
16	S	0.35	0/2153	0.54	0/2901
17	T	0.51	0/4047	0.61	2/5477 (0.0%)
17	U	0.53	0/4049	0.64	3/5481 (0.1%)
17	V	0.50	0/4031	0.61	3/5456 (0.1%)
18	X	0.51	0/4176	0.59	0/5659
18	Y	0.48	0/4015	0.61	0/5440
18	Z	0.46	0/4147	0.56	0/5619
All	All	0.44	0/54528	0.57	14/73907 (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
3	2	0	1
5	4	0	1
6	5	0	1
17	T	0	1
17	U	0	1
17	V	0	1
18	X	0	1
18	Y	0	1
18	Z	0	2
All	All	0	10

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	77	PRO	N-CA-CB	6.43	110.07	103.00
5	4	62	VAL	N-CA-C	-6.20	106.76	112.96
17	U	347	ARG	CA-C-N	6.00	132.99	121.54
17	U	347	ARG	C-N-CA	6.00	132.99	121.54
17	V	347	ARG	CA-C-N	5.91	132.83	121.54

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	324	SER	Peptide
5	4	47	SER	Peptide
6	5	119	LYS	Peptide
17	T	348	GLU	Peptide
17	U	348	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	607	0	584	4	0
2	1	4661	0	4695	60	0
3	2	3163	0	3262	30	0
4	3	1874	0	1826	23	0
5	4	2177	0	2169	20	0
6	5	986	0	1021	16	0
7	6	926	0	941	13	0
8	7	1347	0	1345	29	0
9	8	692	0	694	9	0
10	9	776	0	757	4	0
11	A	514	0	554	19	0
11	B	514	0	554	15	0
11	C	514	0	553	21	0
11	D	514	0	554	16	0
11	E	514	0	554	13	0
11	F	514	0	554	20	0
11	G	514	0	554	13	0
11	H	514	0	554	8	0
11	I	514	0	554	11	0
11	J	514	0	554	18	0
12	M	1640	0	1665	18	0
13	P	1532	0	1603	40	0
14	Q	561	0	565	7	0
15	R	1303	0	1266	16	0
16	S	2130	0	2180	33	0
17	T	3979	0	4119	66	0
17	U	3980	0	4119	53	0
17	V	3962	0	4105	64	0
18	X	4115	0	4138	53	0
18	Y	3957	0	3967	60	0
18	Z	4087	0	4110	44	0
19	M	1	0	0	0	0
20	T	31	0	12	1	0
20	U	31	0	12	0	0
20	V	31	0	12	0	0
21	T	1	0	0	0	0
21	U	1	0	0	0	0
21	V	1	0	0	0	0
21	X	1	0	0	0	0
21	Y	1	0	0	0	0
22	X	27	0	12	0	0
22	Y	27	0	12	0	0
All	All	53748	0	54730	665	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 665 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)
18:X:503:ALA:O	18:X:506:ILE:HG12	1.34	1.22
13:P:171:THR:HG22	13:P:186:MET:SD	2.03	0.98
13:P:184:LEU:HD12	13:P:184:LEU:O	1.66	0.95
18:X:503:ALA:O	18:X:506:ILE:CG1	2.21	0.88
13:P:171:THR:CG2	13:P:186:MET:SD	2.70	0.80

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	0	79/82 (96%)	73 (92%)	6 (8%)	0	100	100
2	1	593/618 (96%)	571 (96%)	22 (4%)	0	100	100
3	2	439/441 (100%)	413 (94%)	25 (6%)	1 (0%)	43	71
4	3	243/325 (75%)	233 (96%)	10 (4%)	0	100	100
5	4	288/294 (98%)	277 (96%)	11 (4%)	0	100	100
6	5	121/123 (98%)	115 (95%)	5 (4%)	1 (1%)	16	44
7	6	122/151 (81%)	107 (88%)	14 (12%)	1 (1%)	16	44
8	7	174/190 (92%)	165 (95%)	9 (5%)	0	100	100
9	8	86/89 (97%)	75 (87%)	11 (13%)	0	100	100
10	9	95/97 (98%)	84 (88%)	10 (10%)	1 (1%)	11	38
11	A	72/127 (57%)	69 (96%)	3 (4%)	0	100	100
11	B	72/127 (57%)	72 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	C	71/127 (56%)	70 (99%)	1 (1%)	0	100	100
11	D	72/127 (57%)	71 (99%)	1 (1%)	0	100	100
11	E	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
11	F	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
11	G	72/127 (57%)	68 (94%)	4 (6%)	0	100	100
11	H	72/127 (57%)	70 (97%)	2 (3%)	0	100	100
11	I	72/127 (57%)	69 (96%)	3 (4%)	0	100	100
11	J	72/127 (57%)	69 (96%)	3 (4%)	0	100	100
12	M	213/327 (65%)	205 (96%)	8 (4%)	0	100	100
13	P	191/229 (83%)	174 (91%)	17 (9%)	0	100	100
14	Q	70/74 (95%)	66 (94%)	4 (6%)	0	100	100
15	R	175/199 (88%)	164 (94%)	11 (6%)	0	100	100
16	S	275/317 (87%)	261 (95%)	14 (5%)	0	100	100
17	T	519/562 (92%)	481 (93%)	34 (7%)	4 (1%)	16	44
17	U	521/562 (93%)	489 (94%)	29 (6%)	3 (1%)	21	50
17	V	518/562 (92%)	493 (95%)	24 (5%)	1 (0%)	43	71
18	X	540/574 (94%)	494 (92%)	44 (8%)	2 (0%)	30	59
18	Y	519/574 (90%)	474 (91%)	42 (8%)	3 (1%)	21	50
18	Z	536/574 (93%)	503 (94%)	31 (6%)	2 (0%)	30	59
All	All	7036/8234 (86%)	6615 (94%)	402 (6%)	19 (0%)	37	65

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	383	PRO
17	T	56	LYS
17	T	493	PRO
17	U	349	ALA
18	X	308	VAL

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	0	63/64 (98%)	62 (98%)	1 (2%)	55	68
2	1	493/512 (96%)	490 (99%)	3 (1%)	78	80
3	2	312/312 (100%)	310 (99%)	2 (1%)	78	80
4	3	195/258 (76%)	193 (99%)	2 (1%)	68	75
5	4	220/223 (99%)	219 (100%)	1 (0%)	81	81
6	5	107/107 (100%)	107 (100%)	0	100	100
7	6	96/115 (84%)	96 (100%)	0	100	100
8	7	140/150 (93%)	140 (100%)	0	100	100
9	8	71/72 (99%)	71 (100%)	0	100	100
10	9	79/79 (100%)	79 (100%)	0	100	100
11	A	50/86 (58%)	50 (100%)	0	100	100
11	B	50/86 (58%)	50 (100%)	0	100	100
11	C	50/86 (58%)	50 (100%)	0	100	100
11	D	50/86 (58%)	49 (98%)	1 (2%)	48	65
11	E	50/86 (58%)	50 (100%)	0	100	100
11	F	50/86 (58%)	49 (98%)	1 (2%)	48	65
11	G	50/86 (58%)	50 (100%)	0	100	100
11	H	50/86 (58%)	50 (100%)	0	100	100
11	I	50/86 (58%)	50 (100%)	0	100	100
11	J	50/86 (58%)	50 (100%)	0	100	100
12	M	178/272 (65%)	177 (99%)	1 (1%)	78	80
13	P	171/196 (87%)	171 (100%)	0	100	100
14	Q	56/58 (97%)	56 (100%)	0	100	100
15	R	134/151 (89%)	134 (100%)	0	100	100
16	S	235/265 (89%)	233 (99%)	2 (1%)	70	76
17	T	419/448 (94%)	417 (100%)	2 (0%)	81	81
17	U	419/448 (94%)	414 (99%)	5 (1%)	63	72
17	V	418/448 (93%)	414 (99%)	4 (1%)	68	75
18	X	449/469 (96%)	445 (99%)	4 (1%)	70	76
18	Y	430/469 (92%)	426 (99%)	4 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	Z	446/469 (95%)	445 (100%)	1 (0%)	87	85
All	All	5631/6445 (87%)	5597 (99%)	34 (1%)	76	80

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	X	517	VAL
18	Y	204	HIS
18	Y	521	LEU
16	S	105	VAL
12	M	222	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 119 such sidechains are listed below:

Mol	Chain	Res	Type
15	R	137	HIS
18	Z	198	ASN
17	T	386	GLN
18	Z	78	GLN
18	Z	440	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 11 ligands modelled in this entry, 6 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
20	ATP	T	1001	21	32,33,33	1.31	5 (15%)	48,52,52	1.82	9 (18%)
22	ADP	Y	601	21	28,29,29	1.37	4 (14%)	43,45,45	1.82	8 (18%)
22	ADP	X	601	21	28,29,29	1.44	5 (17%)	43,45,45	1.87	7 (16%)
20	ATP	V	1001	21	32,33,33	1.38	6 (18%)	48,52,52	1.79	8 (16%)
20	ATP	U	1001	21	32,33,33	1.34	5 (15%)	48,52,52	1.85	8 (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
20	ATP	T	1001	21	-	2/22/38/38	0/3/3/3
22	ADP	Y	601	21	-	1/16/32/32	0/3/3/3
22	ADP	X	601	21	-	7/16/32/32	0/3/3/3
20	ATP	V	1001	21	-	1/22/38/38	0/3/3/3
20	ATP	U	1001	21	-	2/22/38/38	0/3/3/3

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	Y	601	ADP	C5-C4	4.24	1.46	1.39
20	U	1001	ATP	C5-C4	4.22	1.46	1.39
22	X	601	ADP	C5-C4	4.16	1.46	1.39
20	V	1001	ATP	C5-C4	4.13	1.46	1.39
20	T	1001	ATP	C5-C4	4.06	1.46	1.39

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	U	1001	ATP	C5-C4-N3	-6.37	117.95	126.72
22	Y	601	ADP	C5-C4-N3	-5.99	118.47	126.72
22	X	601	ADP	C5-C4-N3	-5.98	118.48	126.72
20	V	1001	ATP	C5-C4-N3	-5.78	118.76	126.72
20	T	1001	ATP	C5-C4-N3	-5.54	119.09	126.72

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

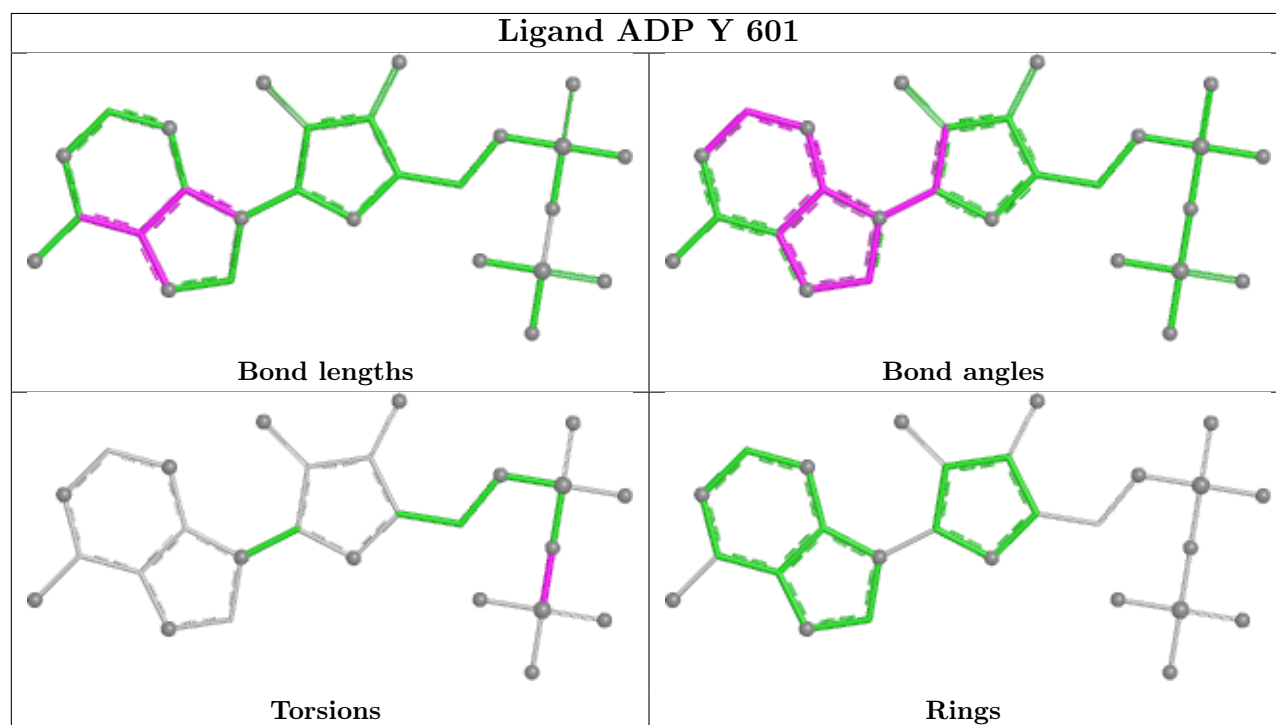
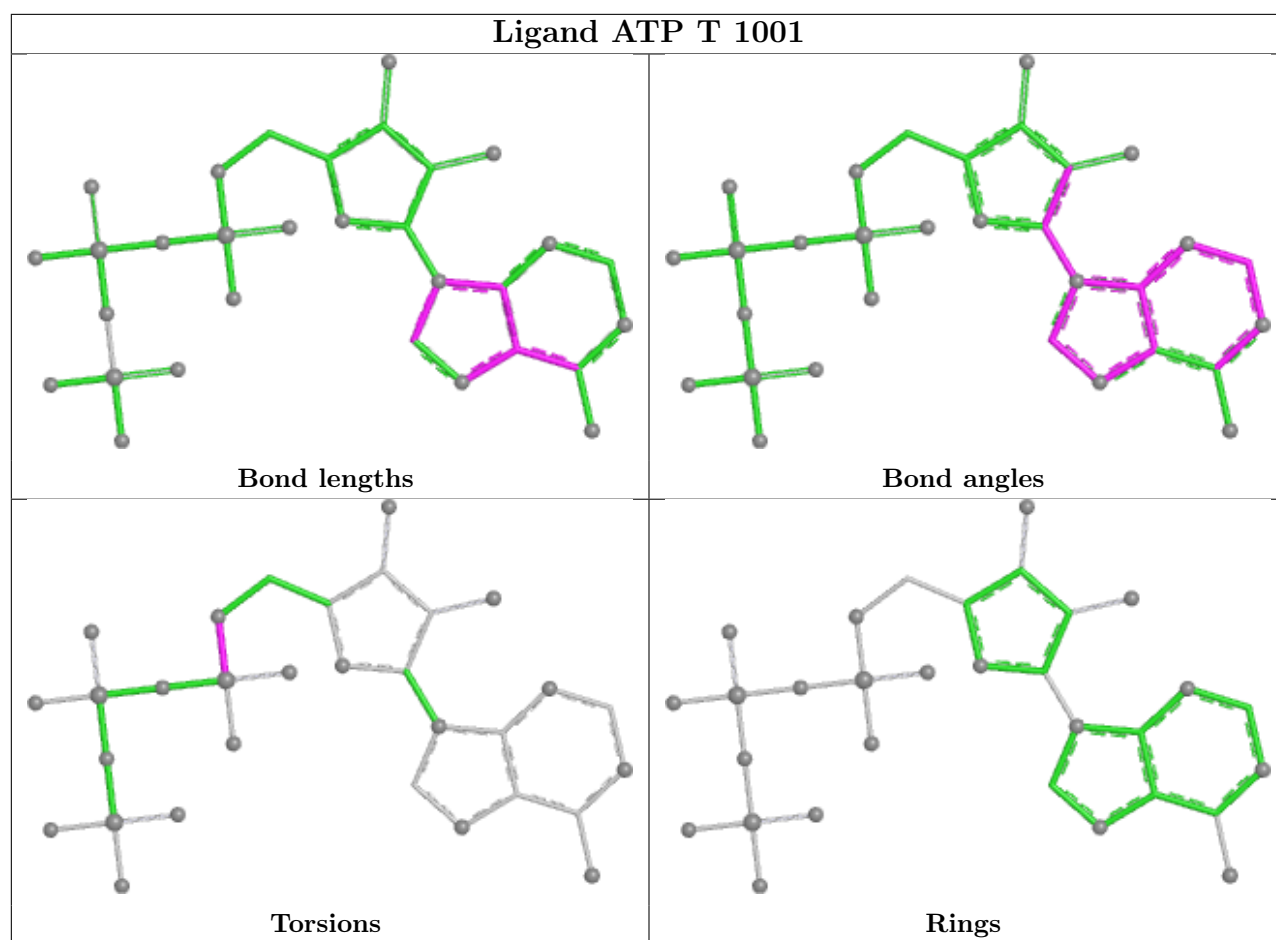
Mol	Chain	Res	Type	Atoms
20	T	1001	ATP	C5'-O5'-PA-O3A
22	X	601	ADP	PA-O3A-PB-O2B
20	U	1001	ATP	PA-O3A-PB-O1B
20	T	1001	ATP	C5'-O5'-PA-O1A
22	X	601	ADP	C5'-O5'-PA-O1A

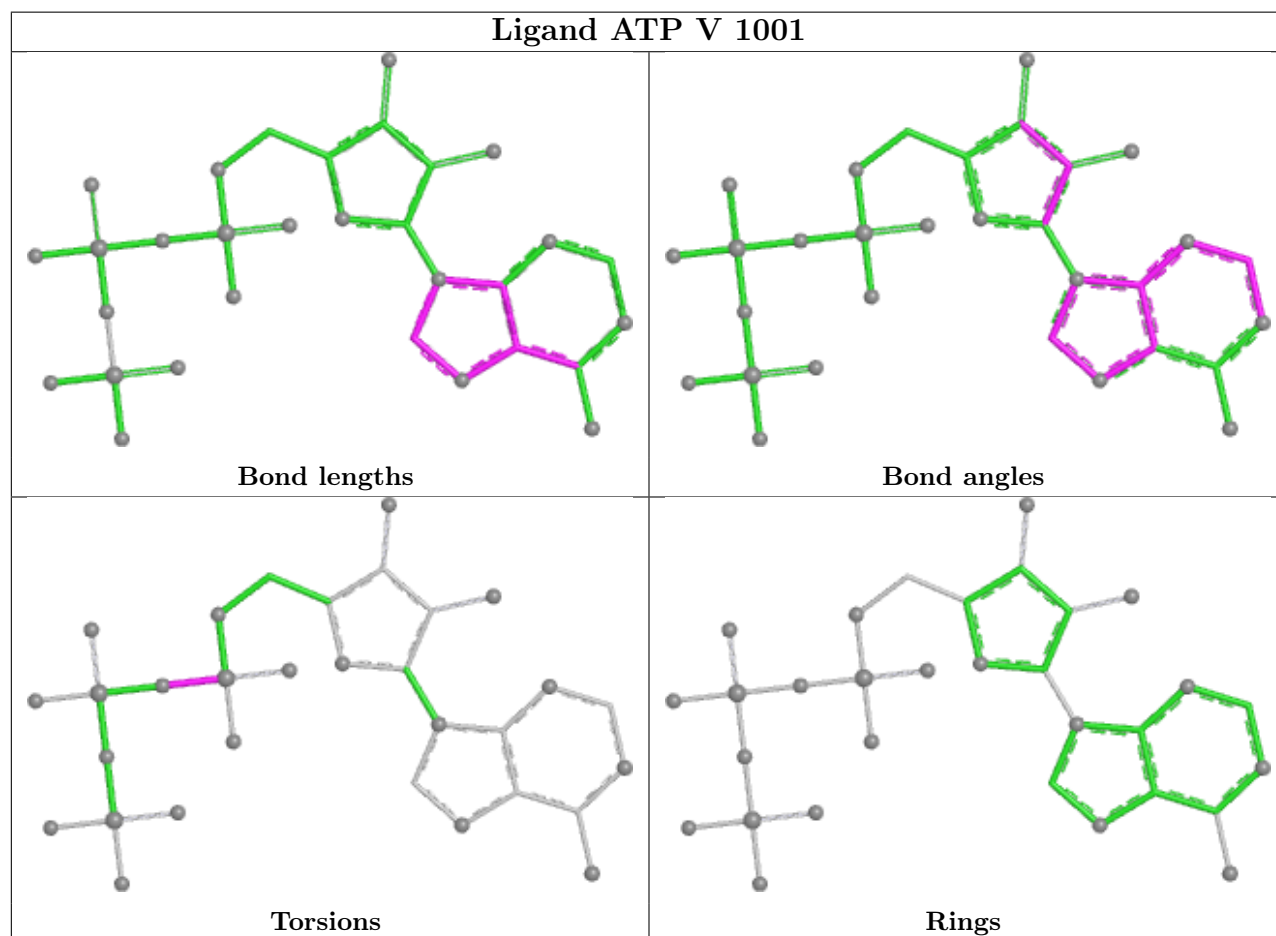
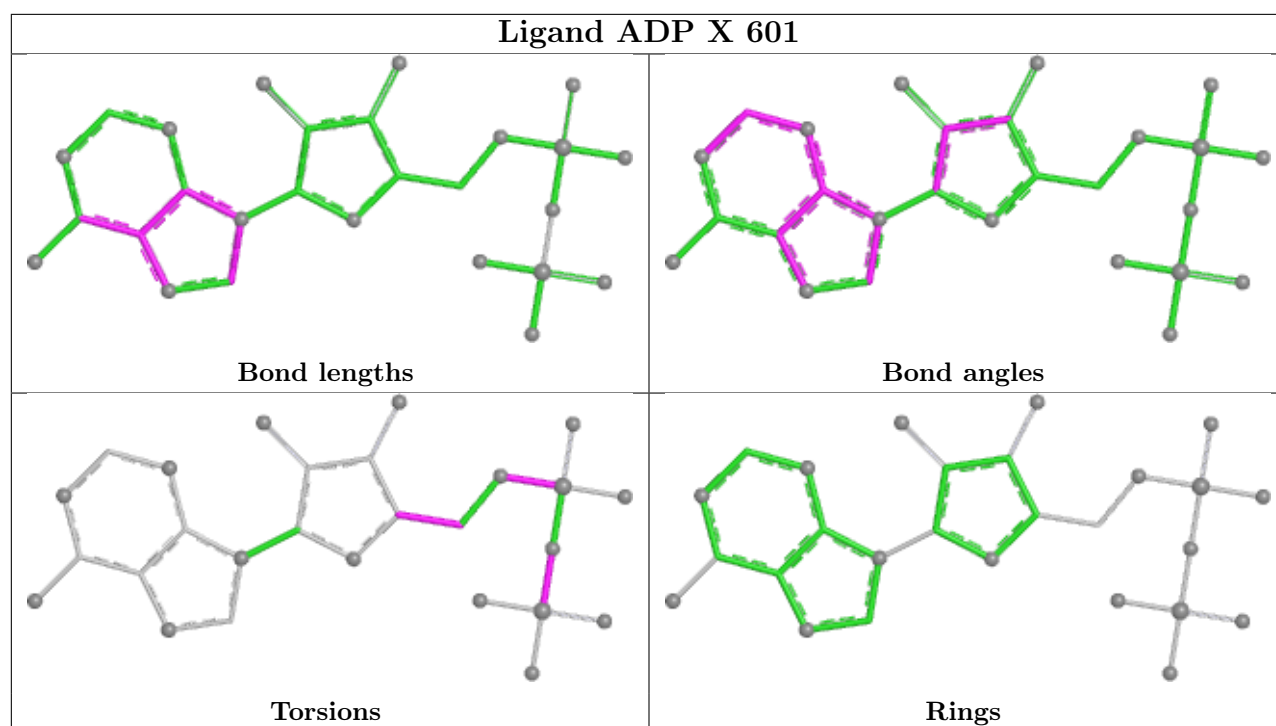
There are no ring outliers.

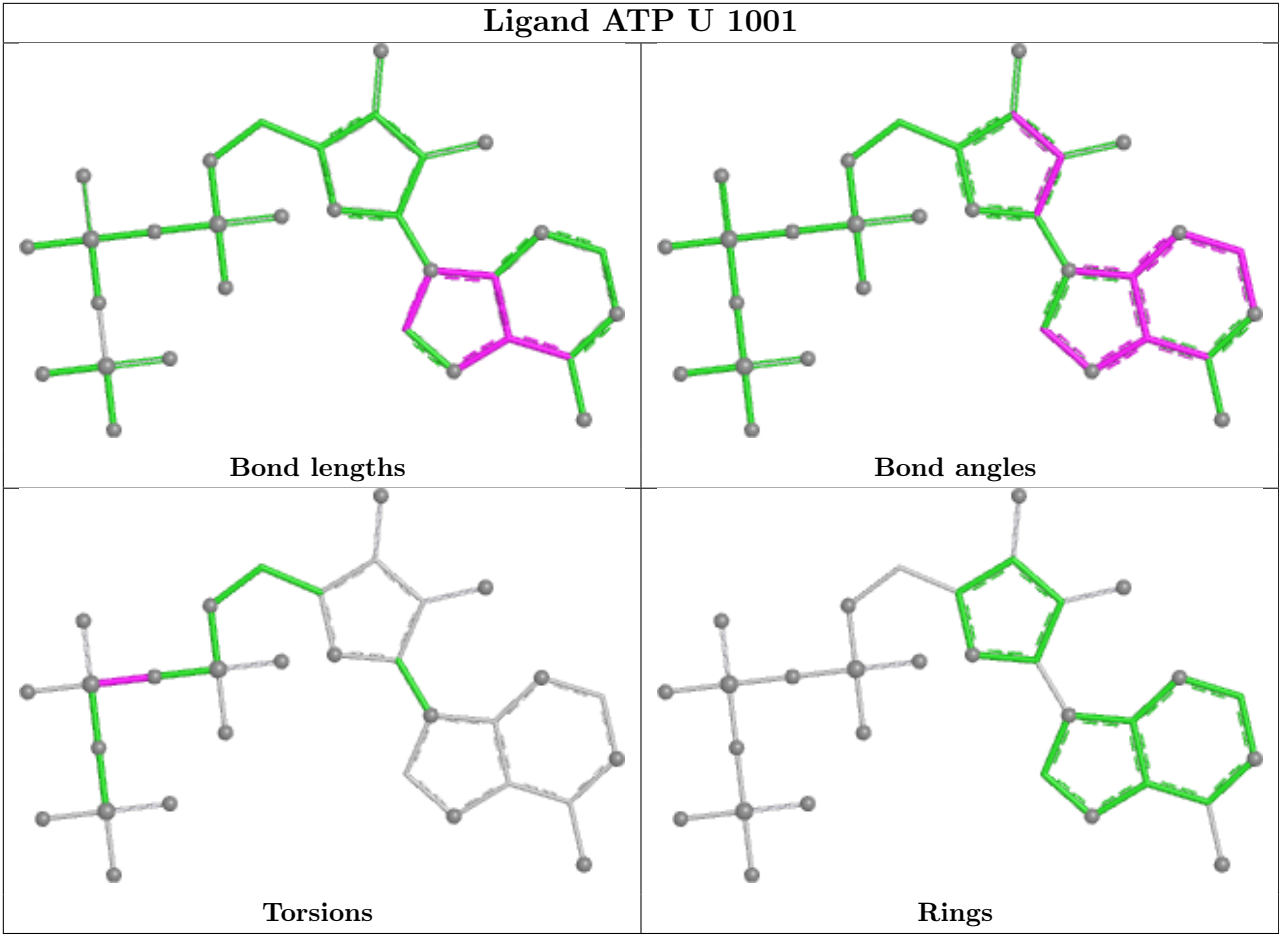
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
20	T	1001	ATP	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.







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
11	C	1
17	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	3.98
1	T	79:PRO	C	80:PRO	N	3.39

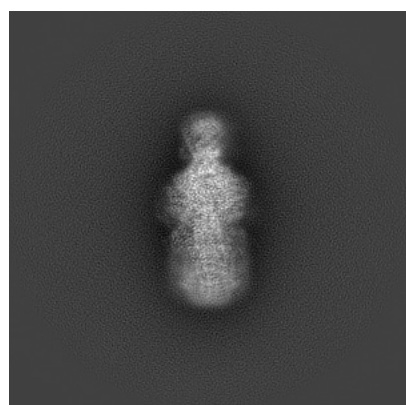
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4830. These allow visual inspection of the internal detail of the map and identification of artifacts.

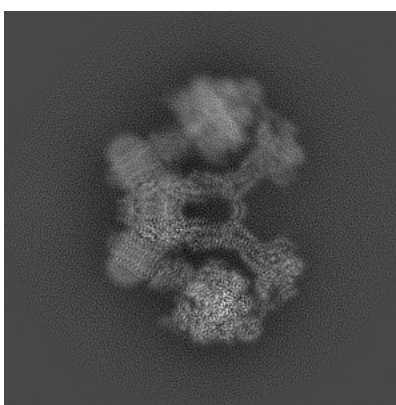
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

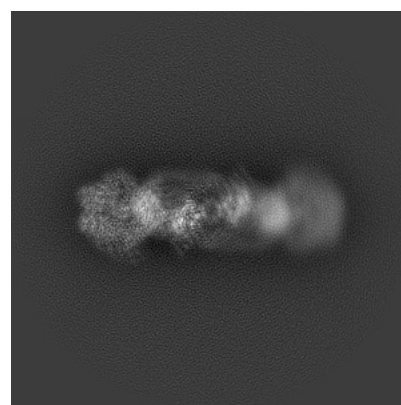
6.1.1 Primary map



X



Y

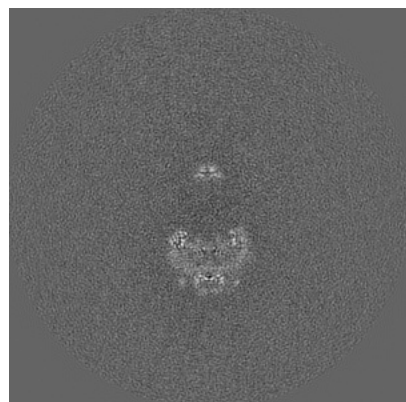


Z

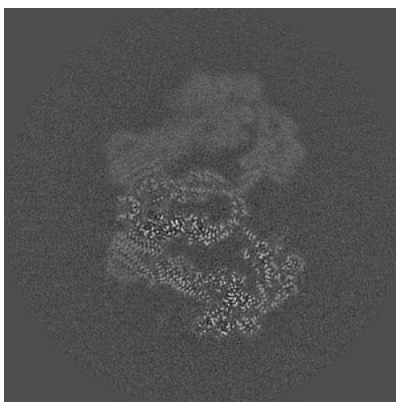
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

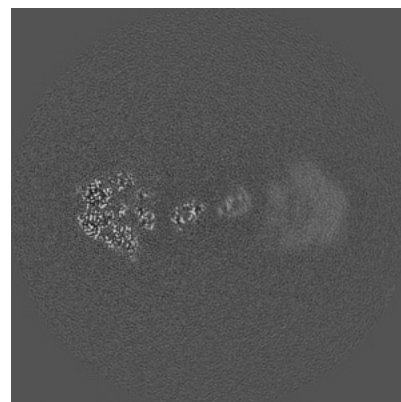
6.2.1 Primary map



X Index: 240



Y Index: 240

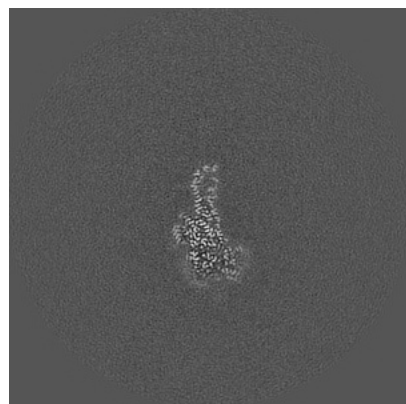


Z Index: 240

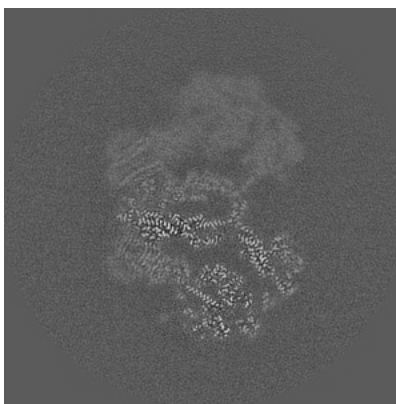
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

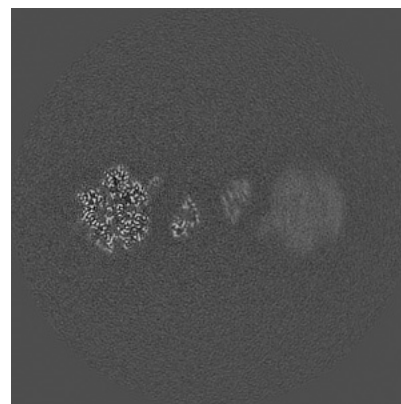
6.3.1 Primary map



X Index: 216



Y Index: 234

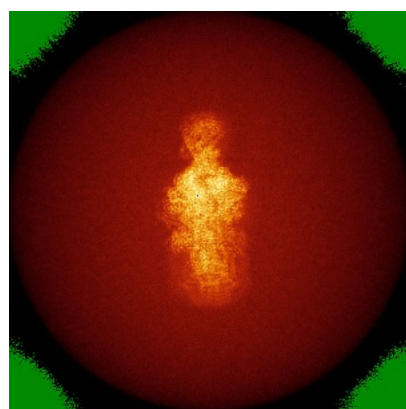


Z Index: 267

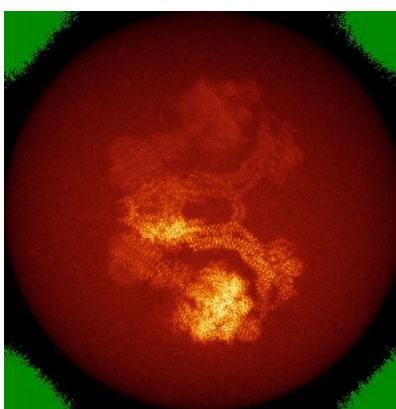
The images above show the largest variance slices of the map in three orthogonal directions.

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

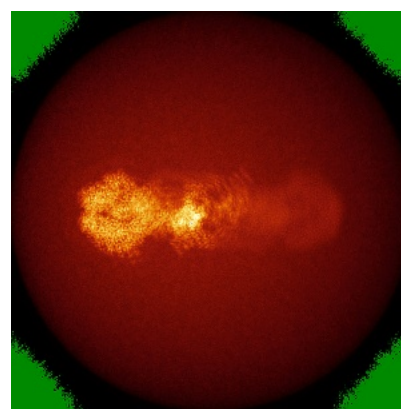
6.4.1 Primary map



X



Y

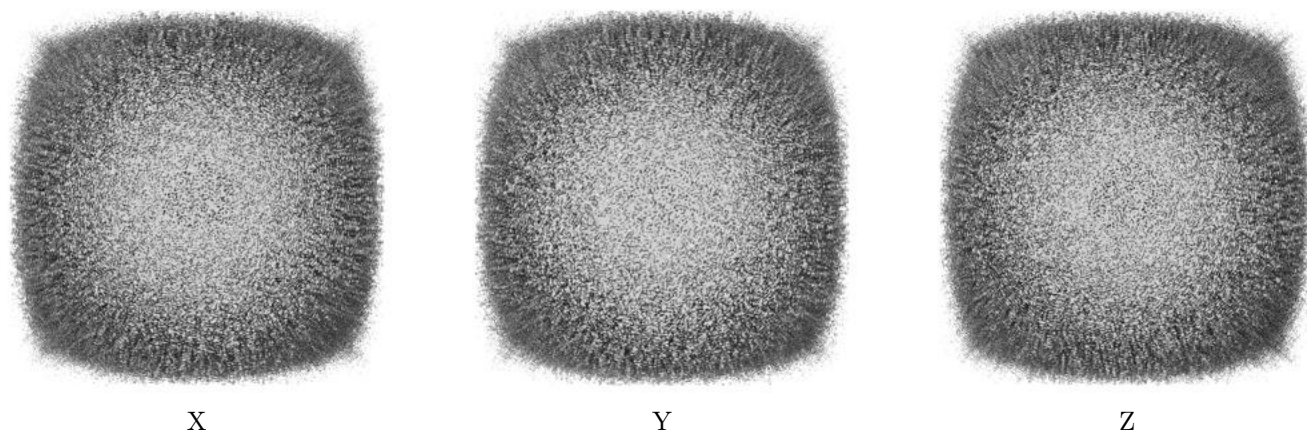


Z

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 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

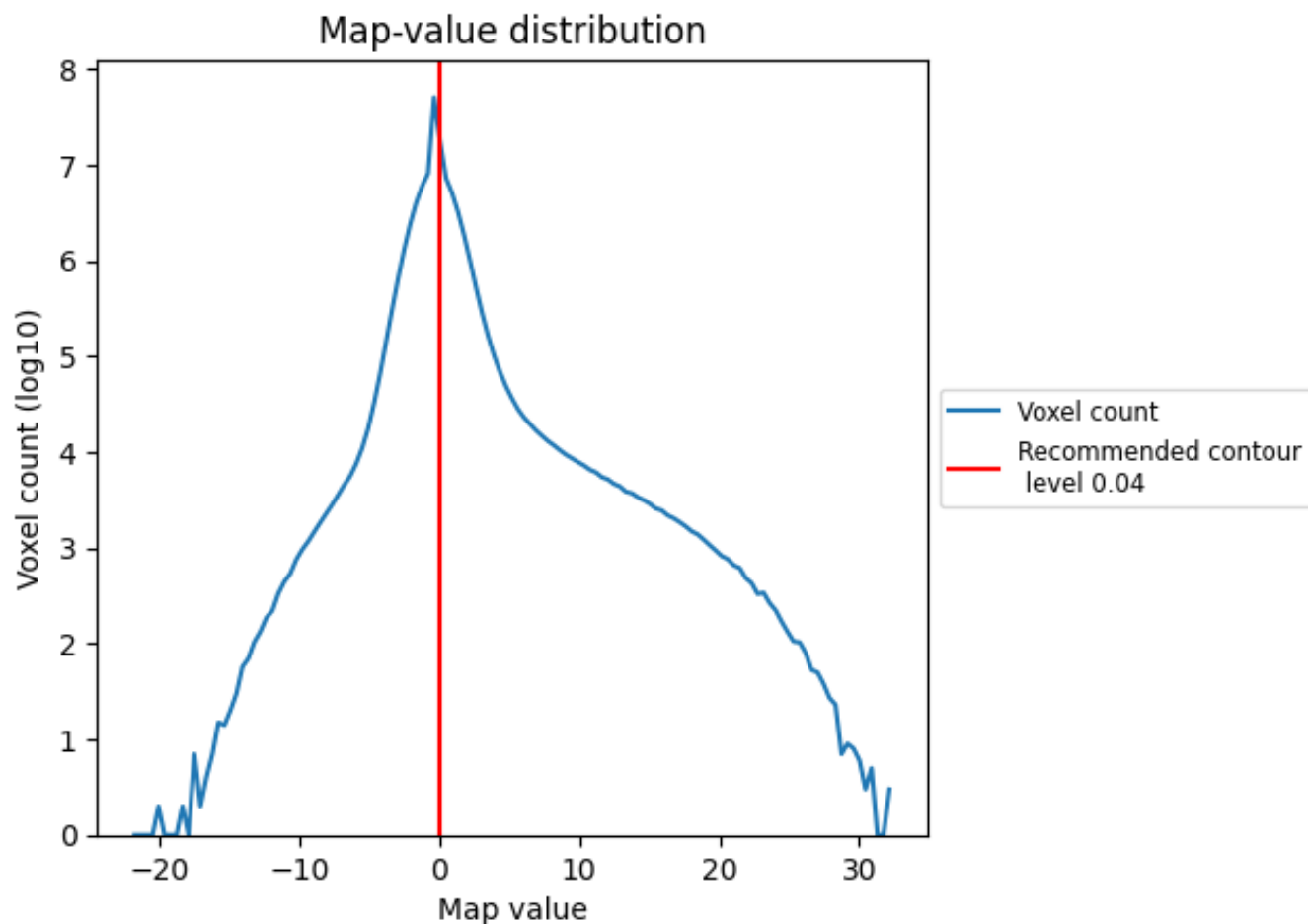
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

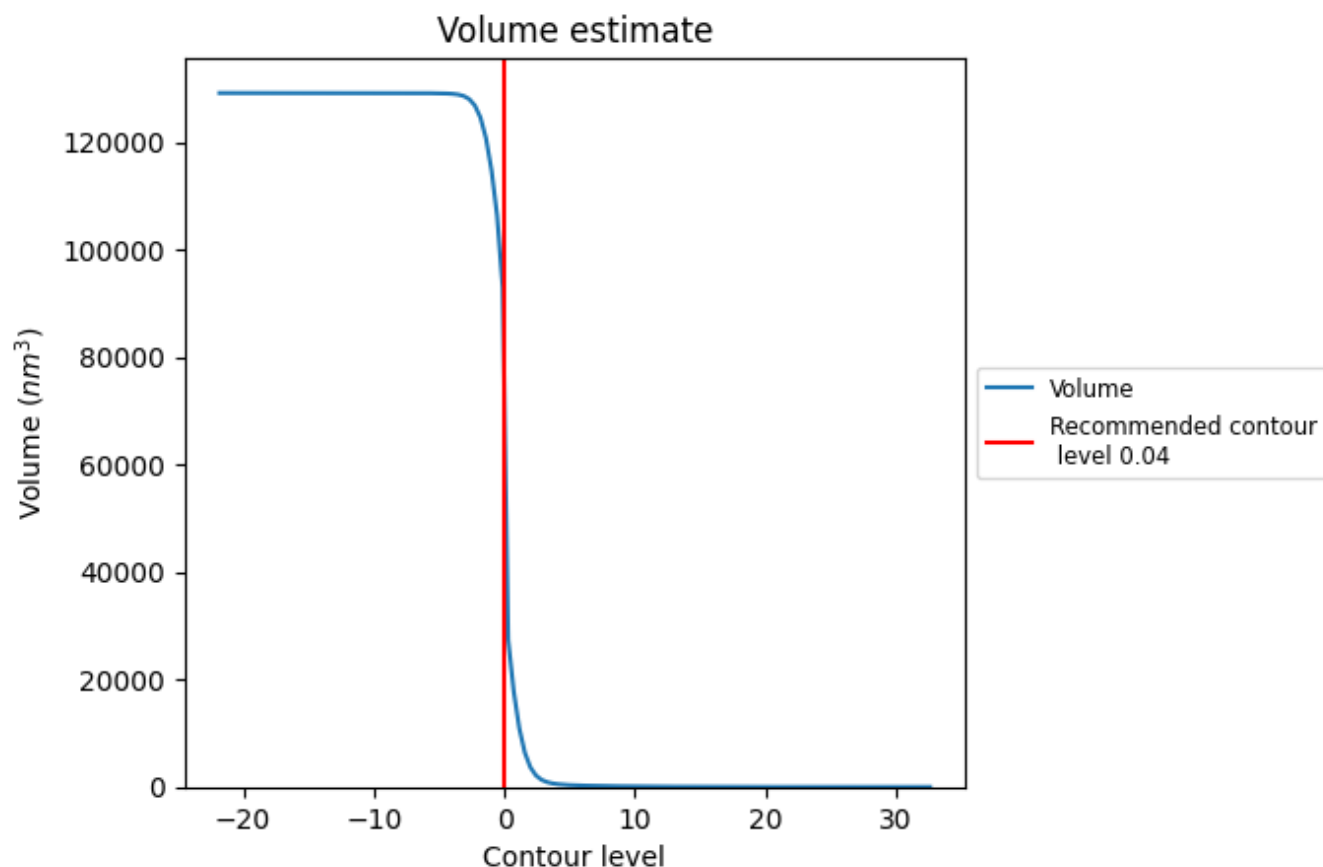
This section contains the results of statistical analysis of the map.

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.

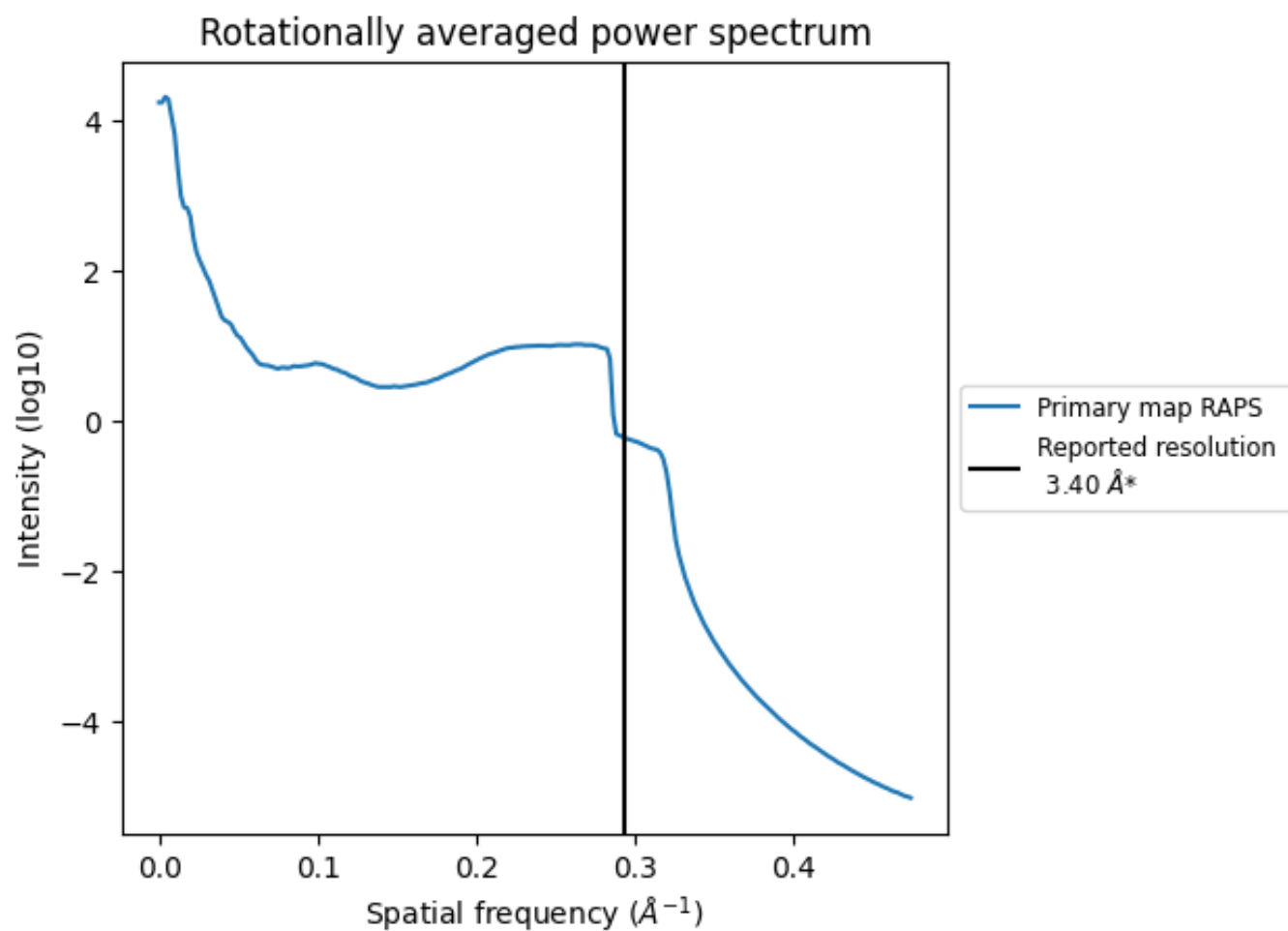
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 67007 nm^3 ; this corresponds to an approximate mass of 60529 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 0.294 Å⁻¹

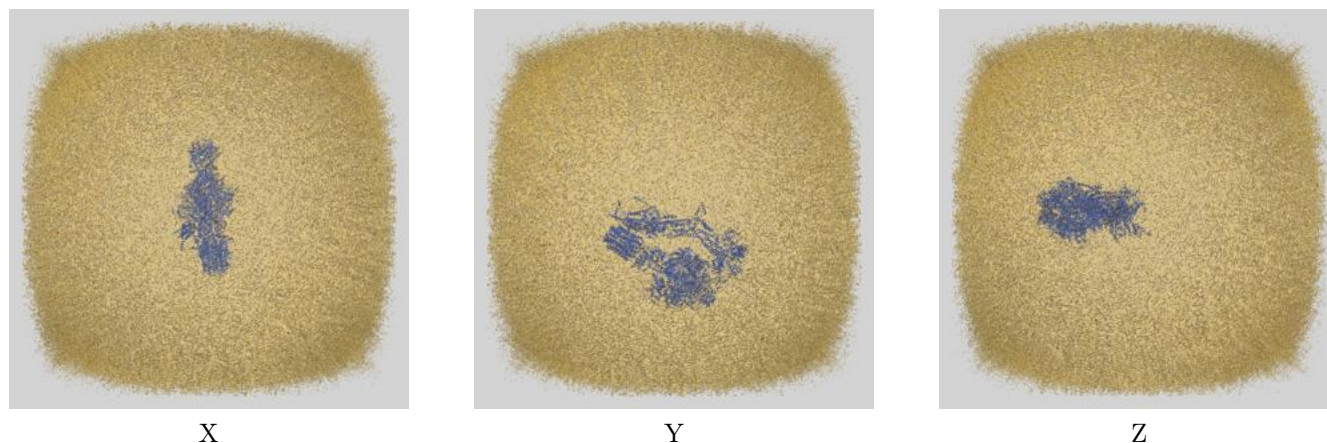
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

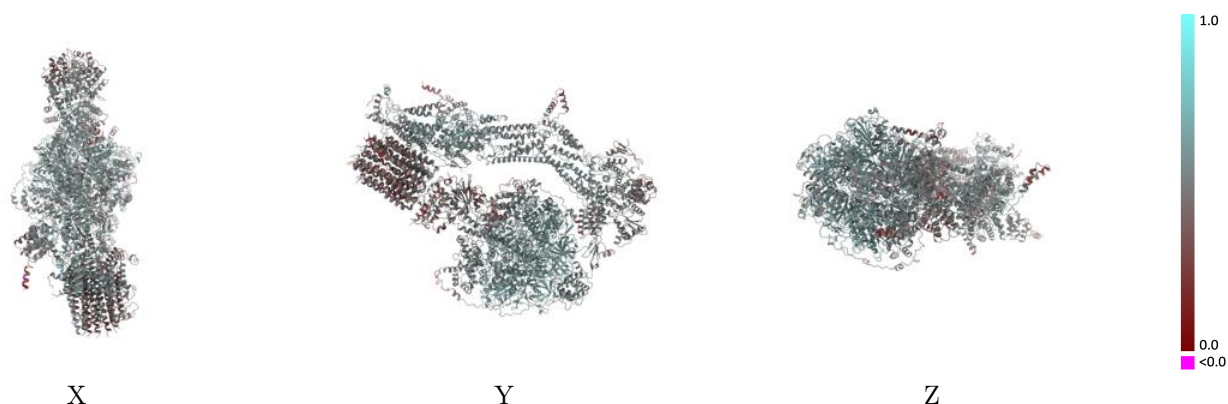
This section contains information regarding the fit between EMDB map EMD-4830 and PDB model 6RDT. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



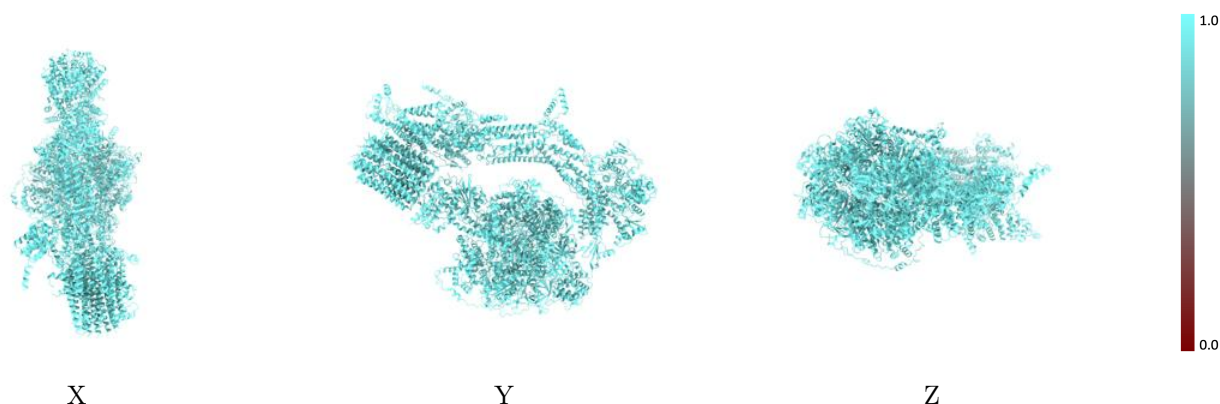
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



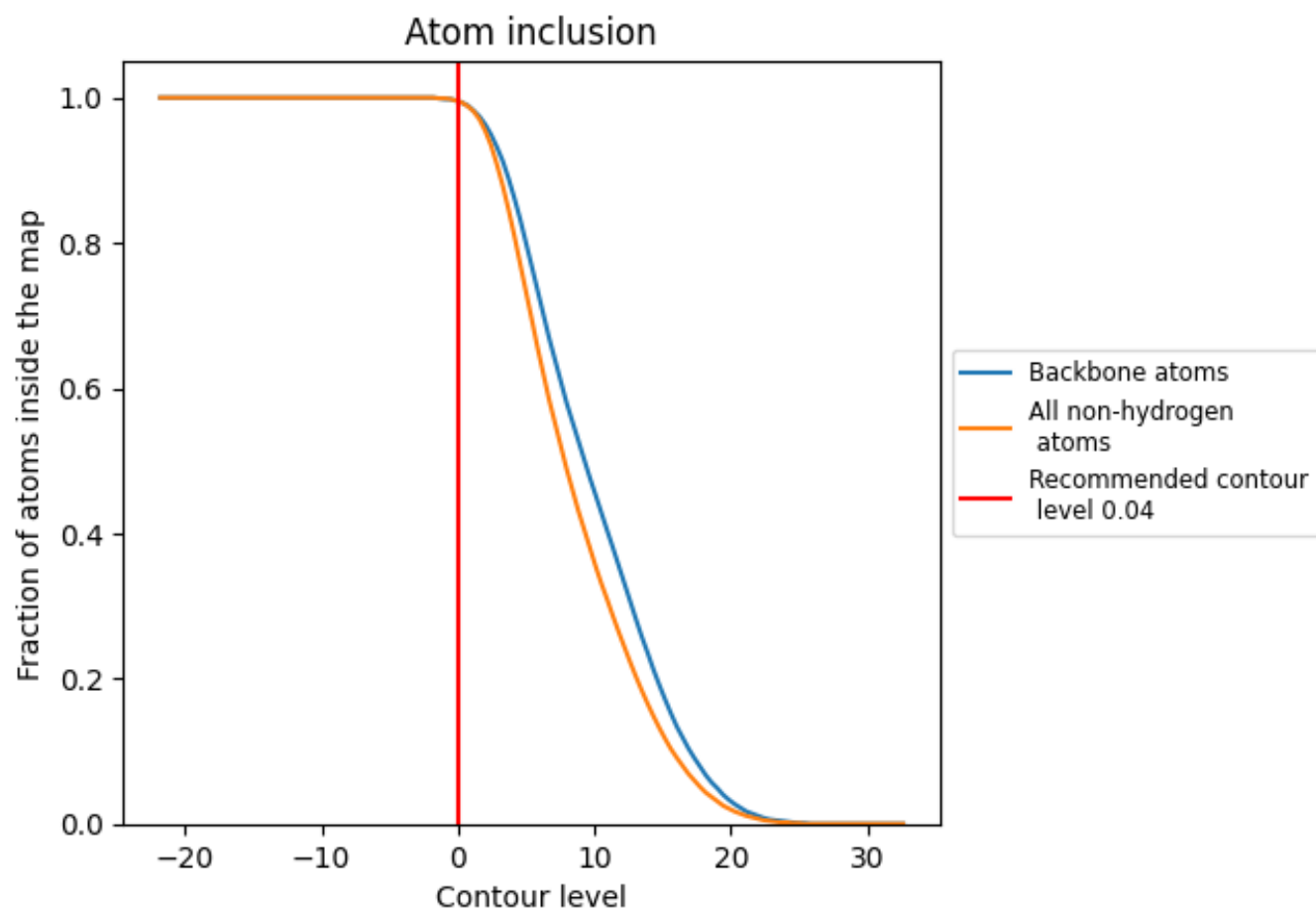
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9950	 0.5110
0	 0.9900	 0.5170
1	 0.9970	 0.5210
2	 0.9990	 0.4750
3	 0.9940	 0.4790
4	 0.9980	 0.4910
5	 0.9960	 0.5470
6	 0.9970	 0.5220
7	 0.9970	 0.5100
8	 0.9960	 0.5370
9	 0.9960	 0.4730
A	 0.9790	 0.4430
B	 0.9800	 0.4270
C	 0.9920	 0.3950
D	 0.9940	 0.3890
E	 0.9940	 0.3940
F	 0.9880	 0.4100
G	 0.9920	 0.3640
H	 0.9840	 0.3770
I	 0.9800	 0.3960
J	 0.9650	 0.4260
M	 0.9980	 0.5230
P	 0.9990	 0.5040
Q	 0.9950	 0.3990
R	 0.9930	 0.3980
S	 0.9940	 0.4750
T	 0.9980	 0.5550
U	 0.9980	 0.5580
V	 0.9960	 0.5560
X	 0.9960	 0.5590
Y	 0.9950	 0.5410
Z	 0.9960	 0.5430

