



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 04:21 PM UTC

PDB ID : 4B2Q / pdb_00004b2q
EMDB ID : EMD-2161
Title : Model of the yeast F1Fo-ATP synthase dimer based on subtomogram average
Authors : Davies, K.M.; Kuehlbrandt, W.
Deposited on : 2012-07-17
Resolution : 37.00 Å(reported)
Based on initial model : 2WPD

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

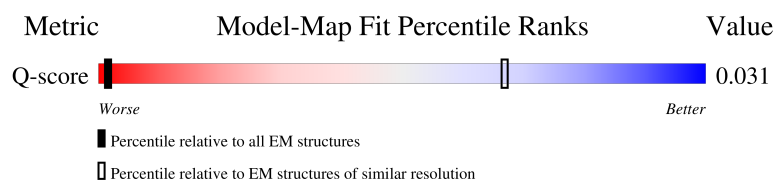
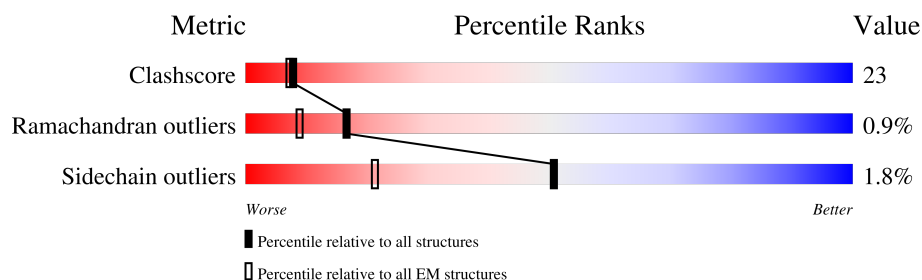
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 37.00 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3 (37.00 - 37.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	485	
1	C	485	
1	a	485	
1	c	485	

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Mol	Chain	Length	Quality of chain
2	B	486	
2	b	486	
3	D	470	
3	d	470	
4	E	473	
4	F	473	
4	e	473	
4	f	473	
5	G	278	
5	g	278	
6	H	132	
6	h	132	
7	I	59	
7	i	59	
8	J	76	
8	K	76	
8	L	76	
8	M	76	
8	N	76	
8	O	76	
8	P	76	
8	Q	76	
8	R	76	
8	S	76	
8	j	76	

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Mol	Chain	Length	Quality of chain
8	k	76	41% 68% 32%
8	l	76	68% 32%
8	m	76	61% 39%
8	n	76	24% 63% 37%
8	o	76	62% 61% 39%
8	p	76	58% 62% 38%
8	q	76	39% 66% 34%
8	r	76	36% 74% 26%
8	s	76	49% 71% 29%
9	T	129	35% 50% 14%
9	t	129	38% 47% 13%
10	U	120	8% 48% 40% 12%
10	u	120	7% 50% 38% 12%
11	V	66	47% 39% 11%
11	v	66	48% 39% 9%
12	W	120	25% 30% 43% 18% 8%
12	w	120	27% 31% 42% 18% 8%

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 70306 atoms, of which 1786 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 ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	485	Total	C	N	O	S	0	0
			3692	2334	651	704	3		
1	C	485	Total	C	N	O	S	0	0
			3692	2334	651	704	3		
1	a	485	Total	C	N	O	S	0	0
			3692	2334	651	704	3		
1	c	485	Total	C	N	O	S	0	0
			3692	2334	651	704	3		

- Molecule 2 is a protein called ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	485	Total	C	N	O	S	0	0
			3685	2328	651	703	3		
2	b	485	Total	C	N	O	S	0	0
			3685	2328	651	703	3		

- Molecule 3 is a protein called ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	470	Total	C	N	O	S	0	0
			3549	2250	604	689	6		
3	d	470	Total	C	N	O	S	0	0
			3549	2250	604	689	6		

- Molecule 4 is a protein called ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	473	Total	C	N	O	S	0	0
			3572	2262	608	696	6		
4	F	472	Total	C	N	O	S	0	0
			3566	2259	607	694	6		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	473	Total	C	N	O	S	0	0
			3572	2262	608	696	6		
4	f	472	Total	C	N	O	S	0	0
			3566	2259	607	694	6		

- Molecule 5 is a protein called ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	269	Total	C	N	O	S	0	0
			2086	1309	362	405	10		
5	g	269	Total	C	N	O	S	0	0
			2086	1309	362	405	10		

- Molecule 6 is a protein called ATP SYNTHASE SUBUNIT DELTA, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	132	Total	C	N	O	S	0	0
			990	624	165	199	2		
6	h	132	Total	C	N	O	S	0	0
			990	624	165	199	2		

- Molecule 7 is a protein called ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	59	Total	C	N	O	S	0	0
			392	243	71	78			
7	i	59	Total	C	N	O	S	0	0
			392	243	71	78			

- Molecule 8 is a protein called ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	76	Total	C	N	O	S	0	0
			545	364	84	93	4		
8	K	76	Total	C	N	O	S	0	0
			545	364	84	93	4		
8	L	76	Total	C	N	O	S	0	0
			545	364	84	93	4		
8	M	76	Total	C	N	O	S	0	0
			545	364	84	93	4		
8	N	76	Total	C	N	O	S	0	0
			545	364	84	93	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	P	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	Q	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	R	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	S	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	j	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	k	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	l	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	m	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	n	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	o	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	p	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	q	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	r	76	Total 545	C 364	N 84	O 93	S 4	0	0
8	s	76	Total 545	C 364	N 84	O 93	S 4	0	0

- Molecule 9 is a protein called ATP SYNTHASE SUBUNIT B, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	T	129	Total 1077	C 671	N 200	O 200	S 6	0	0
9	t	129	Total 1077	C 671	N 200	O 200	S 6	0	0

- Molecule 10 is a protein called ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	120	Total	C	N	O	S	0	0
			969	620	161	186	2		
10	u	120	Total	C	N	O	S	0	0
			969	620	161	186	2		

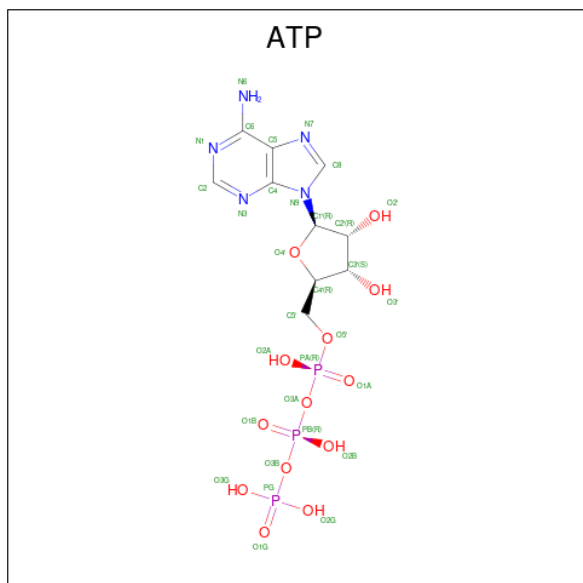
- Molecule 11 is a protein called ATP SYNTHASE-COUPPLING FACTOR 6, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	V	65	Total	C	N	O	S	0	0
			542	346	90	104	2		
11	v	65	Total	C	N	O	S	0	0
			542	346	90	104	2		

- Molecule 12 is a protein called ATP SYNTHASE SUBUNIT O, MITOCHONDRIAL.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	W	110	Total	C	H	N	O	S	0	0
			1739	535	893	146	160	5		
12	w	110	Total	C	H	N	O	S	0	0
			1739	535	893	146	160	5		

- Molecule 13 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
13	A	1	Total	C	N	O	P	0
			31	10	5	13	3	

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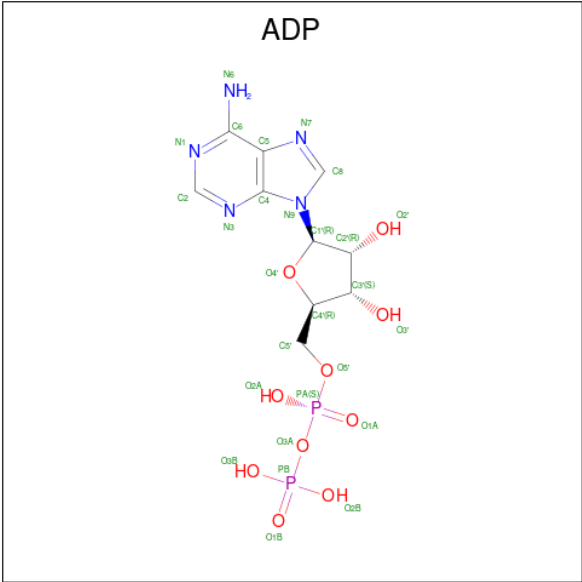
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Mol	Chain	Residues	Atoms					AltConf
13	B	1	Total	C	N	O	P	0
			31	10	5	13	3	
13	C	1	Total	C	N	O	P	0
			31	10	5	13	3	
13	a	1	Total	C	N	O	P	0
			31	10	5	13	3	
13	b	1	Total	C	N	O	P	0
			31	10	5	13	3	
13	c	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
14	A	1	Total	Mg	0
			1	1	
14	B	1	Total	Mg	0
			1	1	
14	C	1	Total	Mg	0
			1	1	
14	D	1	Total	Mg	0
			1	1	
14	F	1	Total	Mg	0
			1	1	
14	a	1	Total	Mg	0
			1	1	
14	b	1	Total	Mg	0
			1	1	
14	c	1	Total	Mg	0
			1	1	
14	d	1	Total	Mg	0
			1	1	
14	f	1	Total	Mg	0
			1	1	

- Molecule 15 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).

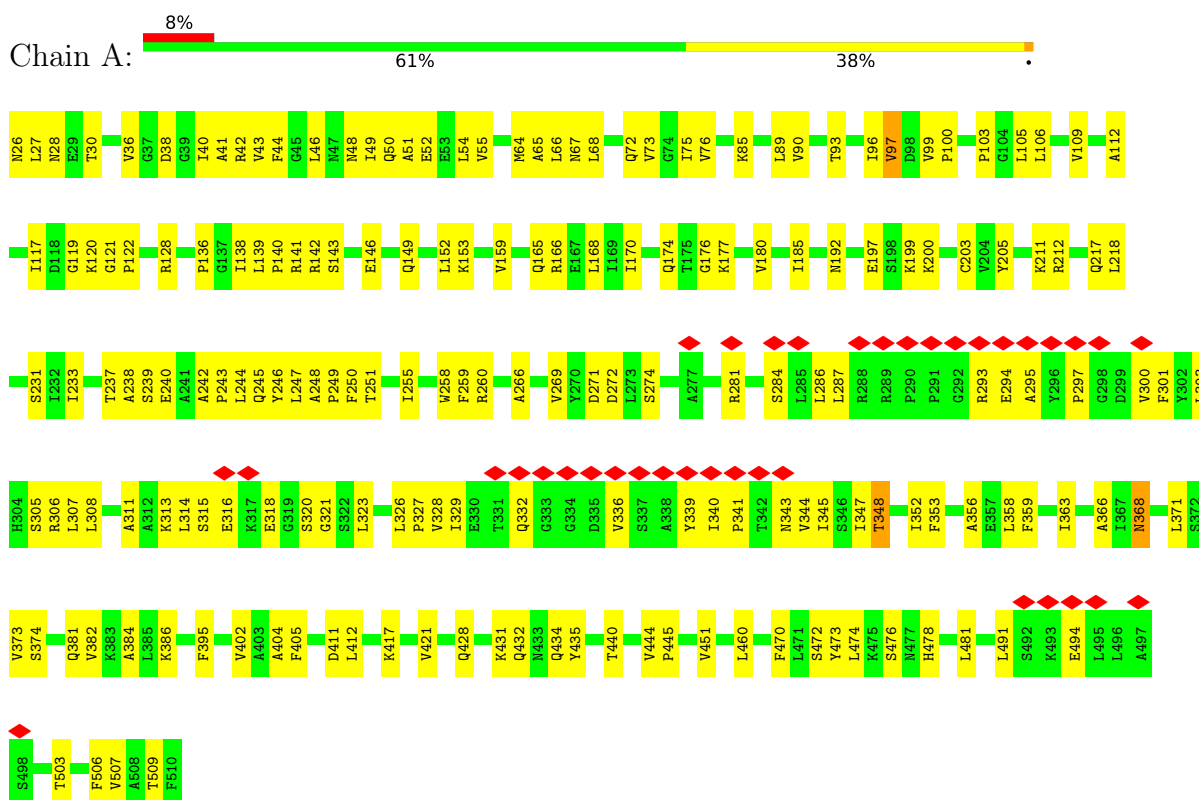


Mol	Chain	Residues	Atoms					AltConf
15	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
15	F	1	Total	C	N	O	P	0
			27	10	5	10	2	
15	d	1	Total	C	N	O	P	0
			27	10	5	10	2	
15	f	1	Total	C	N	O	P	0
			27	10	5	10	2	

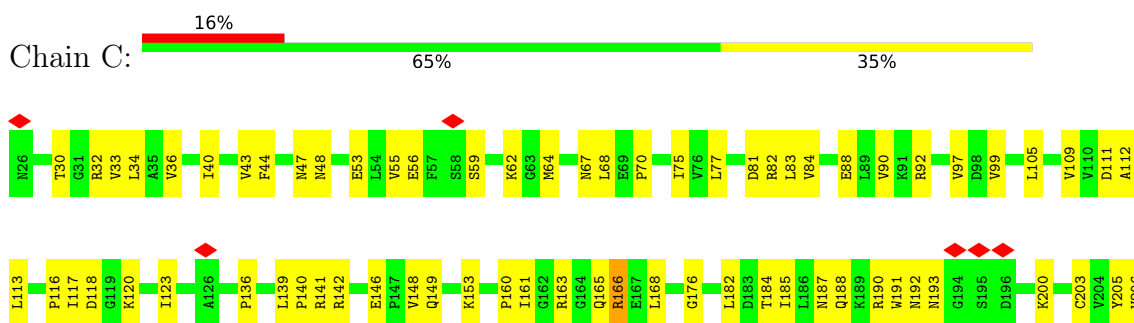
3 Residue-property plots

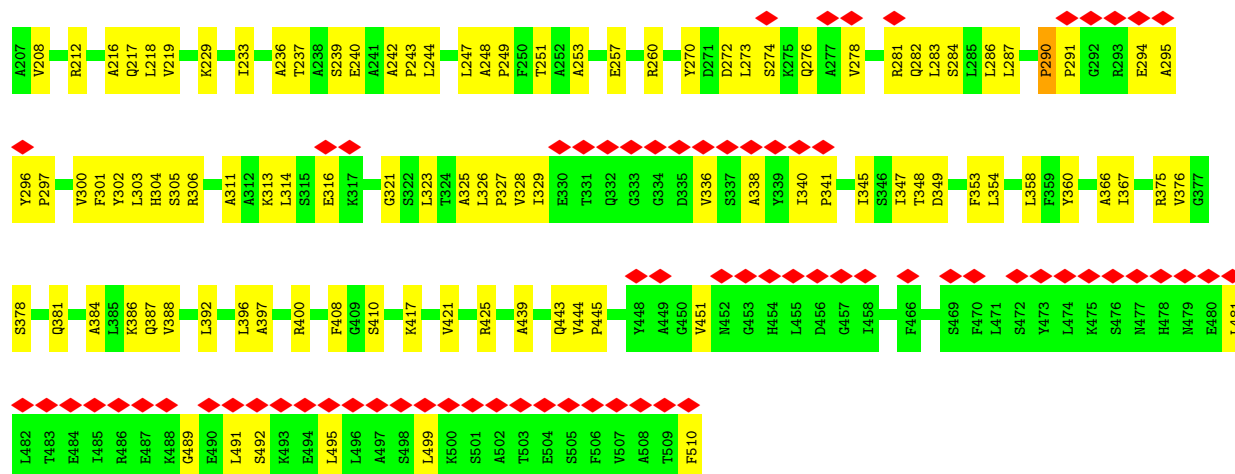
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

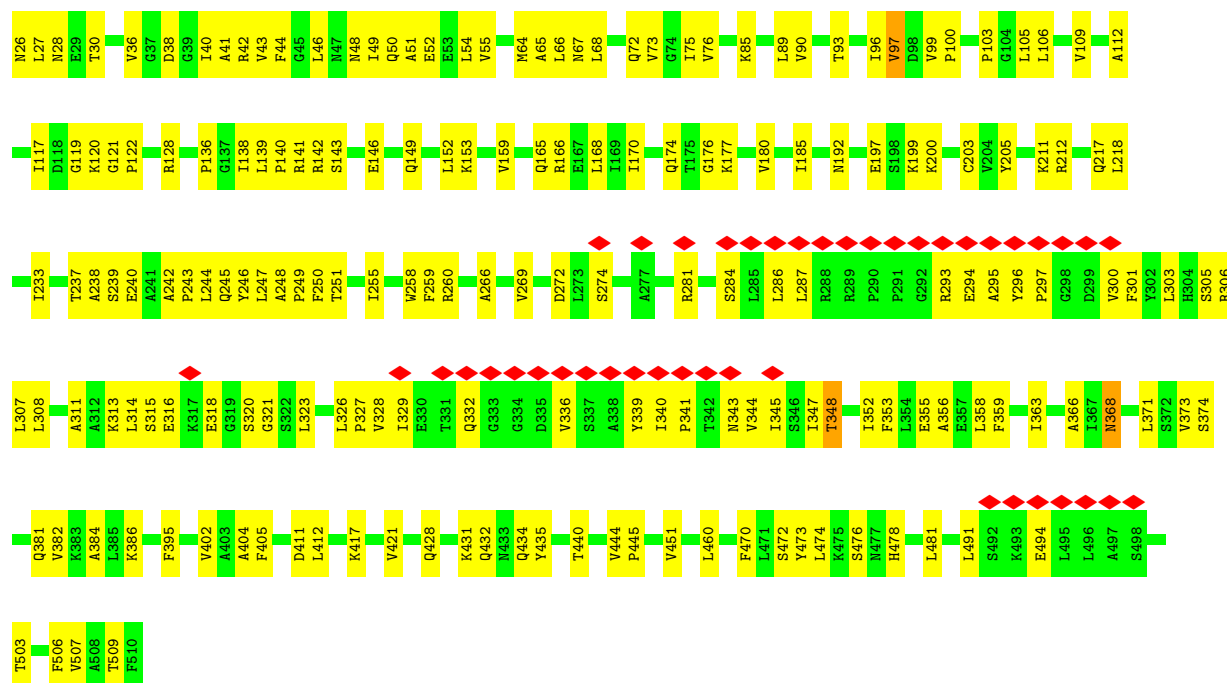


• Molecule 1: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

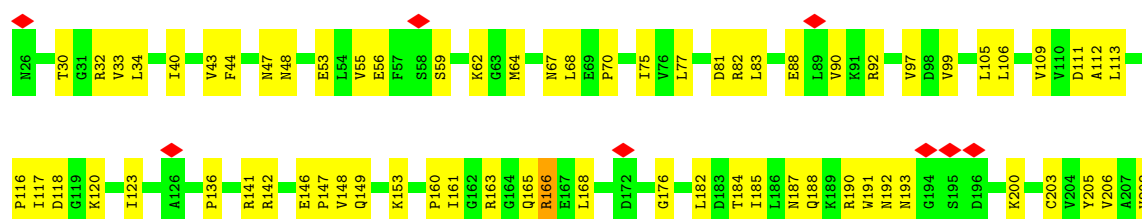


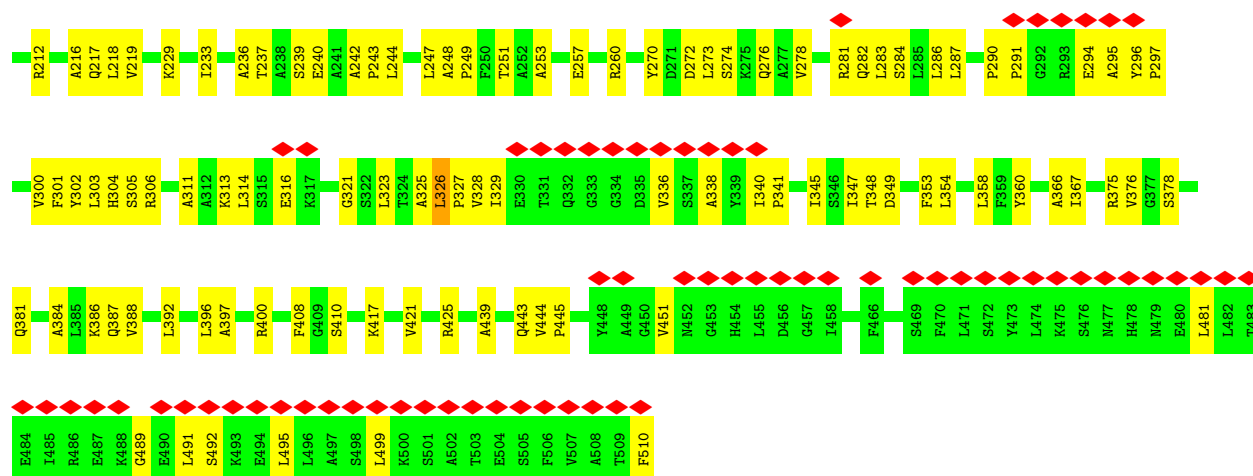


• Molecule 1: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

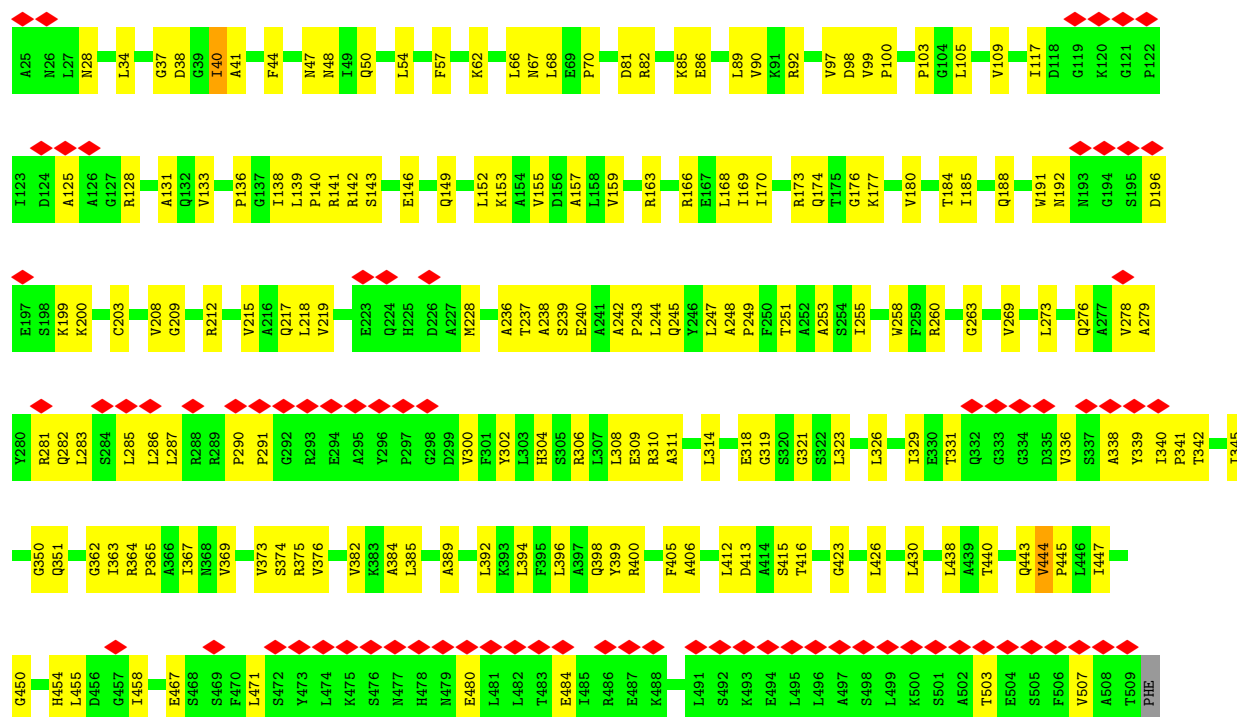


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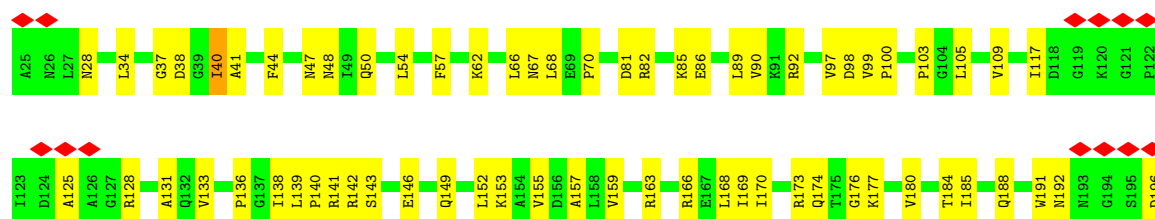


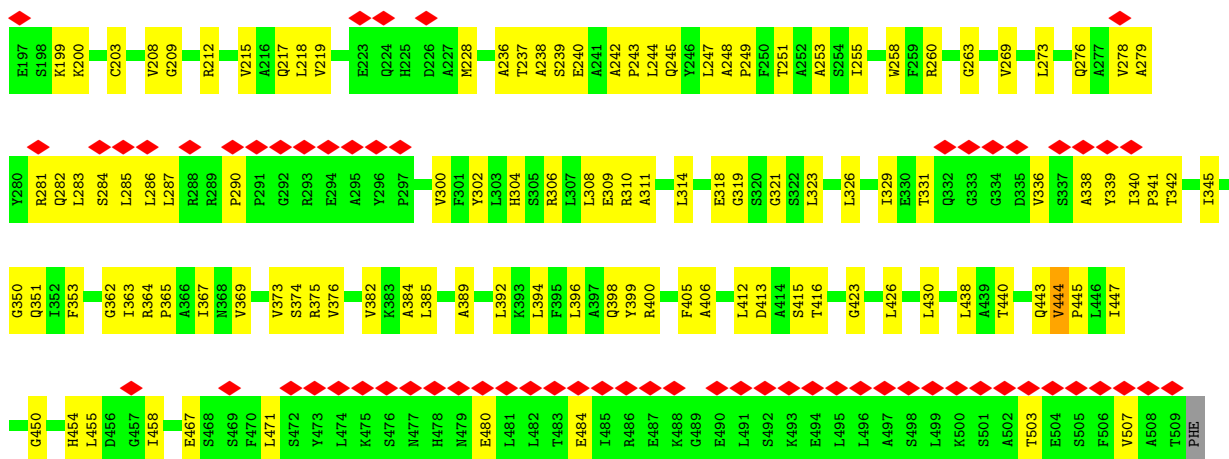


• Molecule 2: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

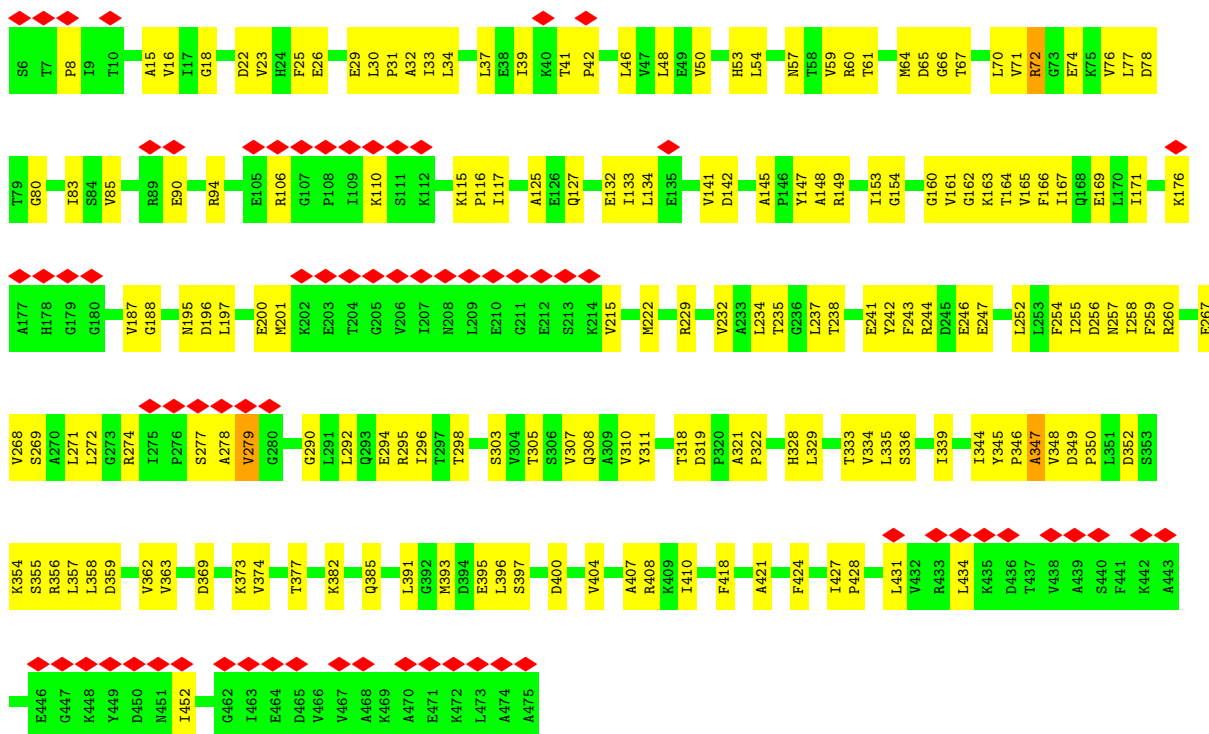


• Molecule 2: ATP SYNTHASE SUBUNIT ALPHA, MITOCHONDRIAL

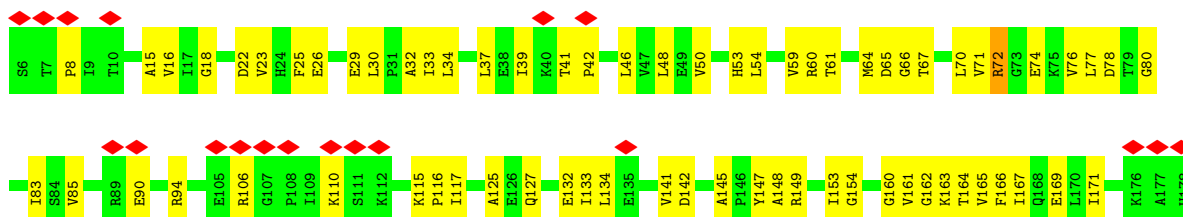


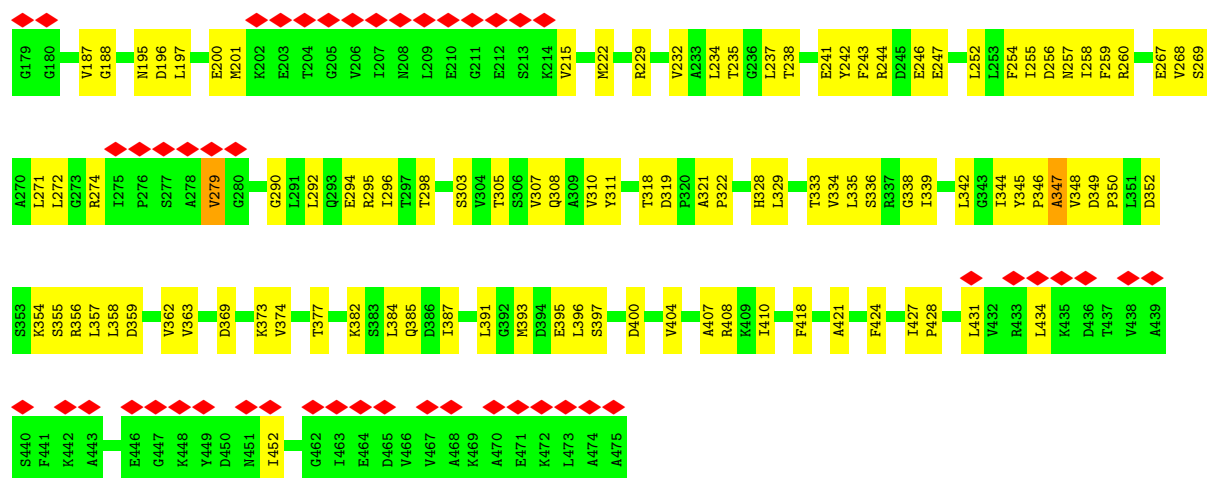


• Molecule 3: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

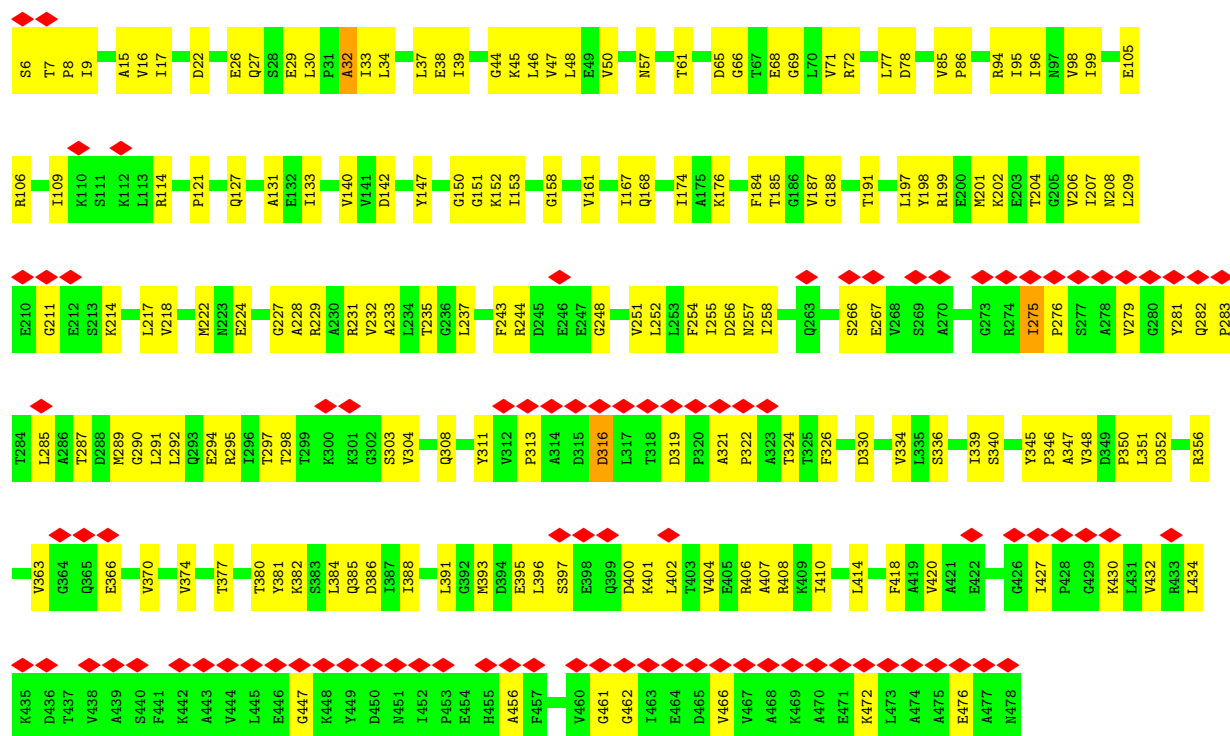


• Molecule 3: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

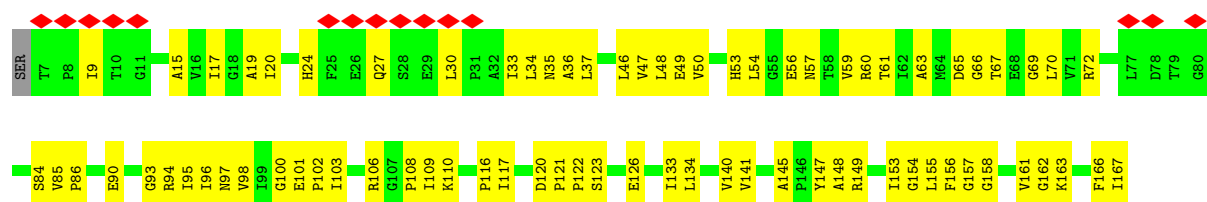


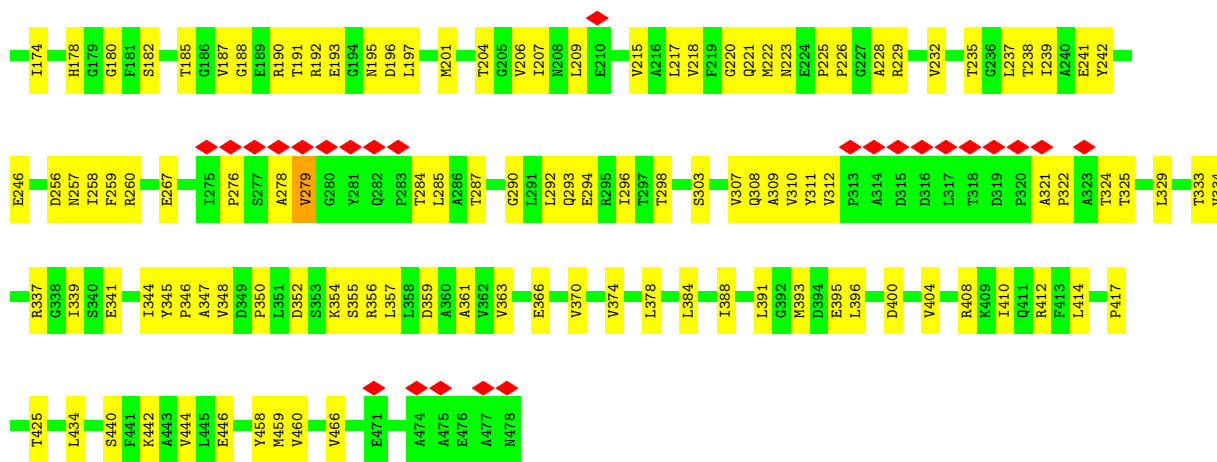


• Molecule 4: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

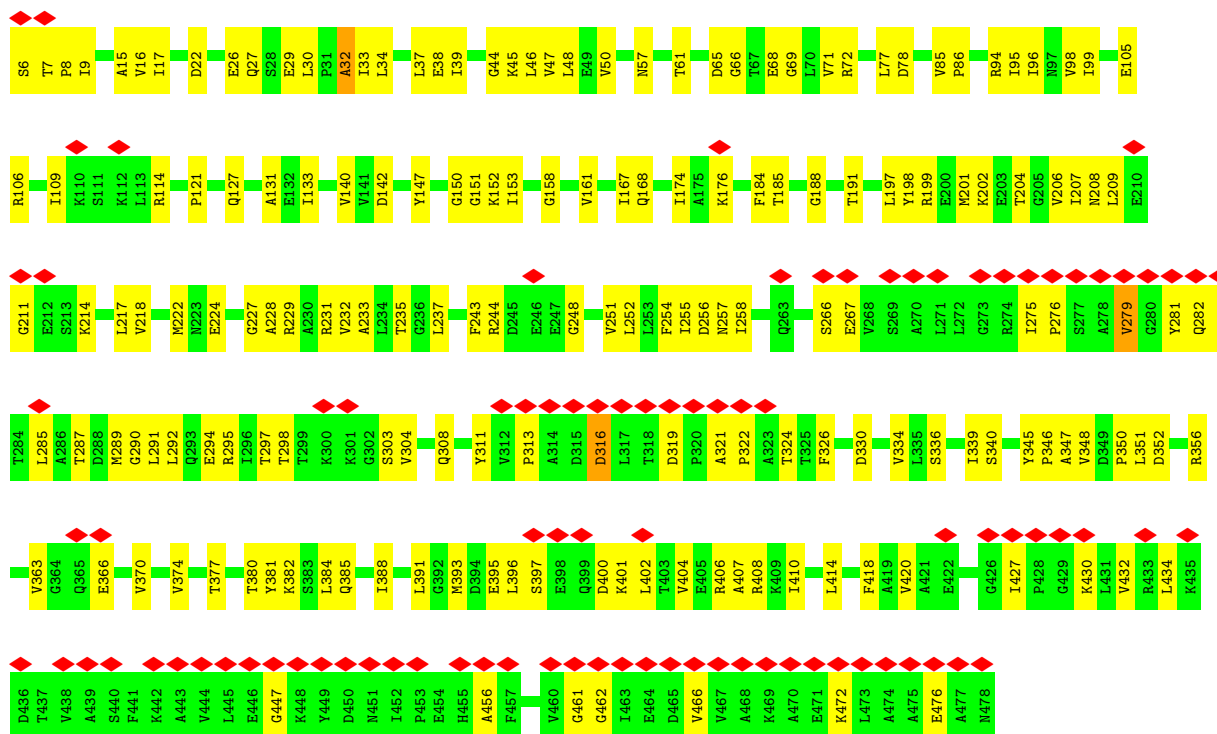


• Molecule 4: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

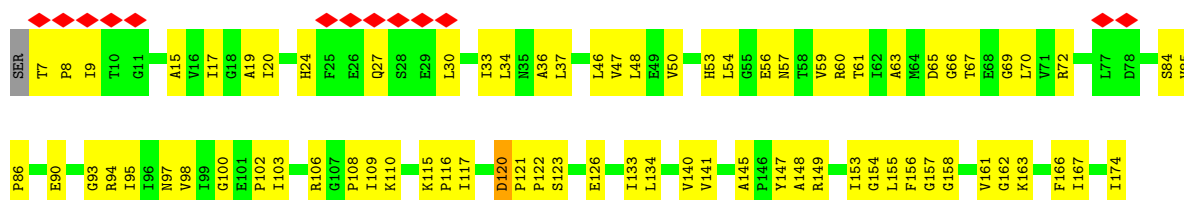


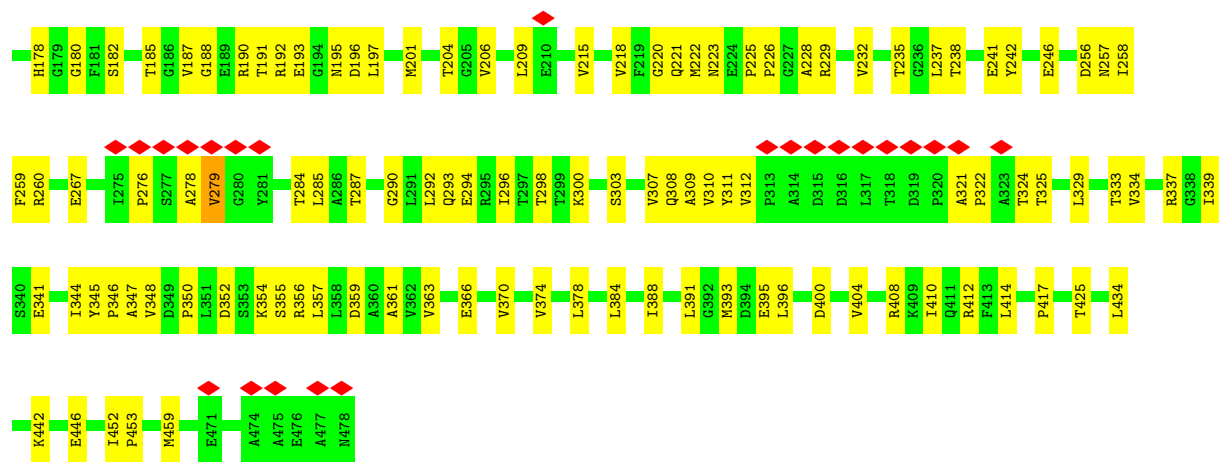


• Molecule 4: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

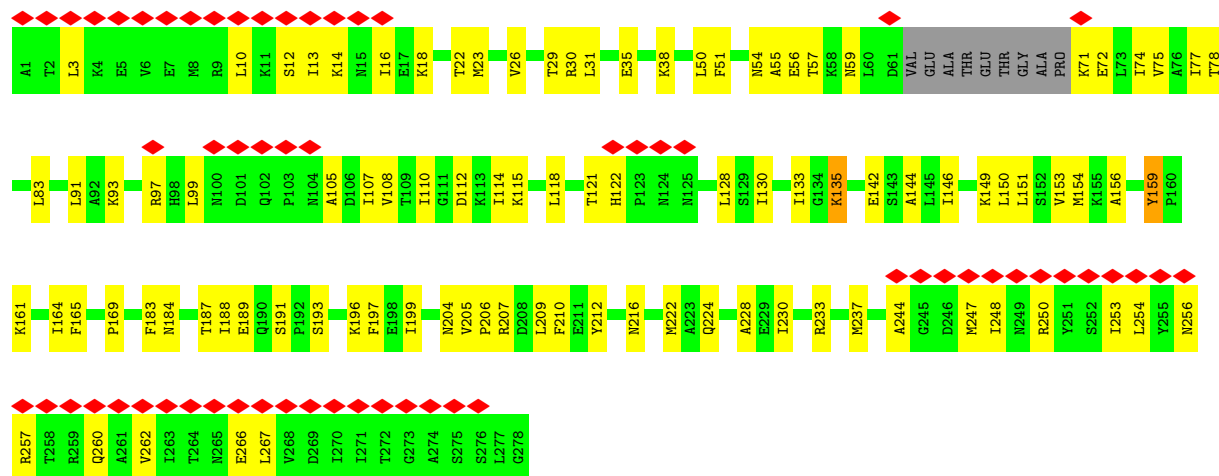


• Molecule 4: ATP SYNTHASE SUBUNIT BETA, MITOCHONDRIAL

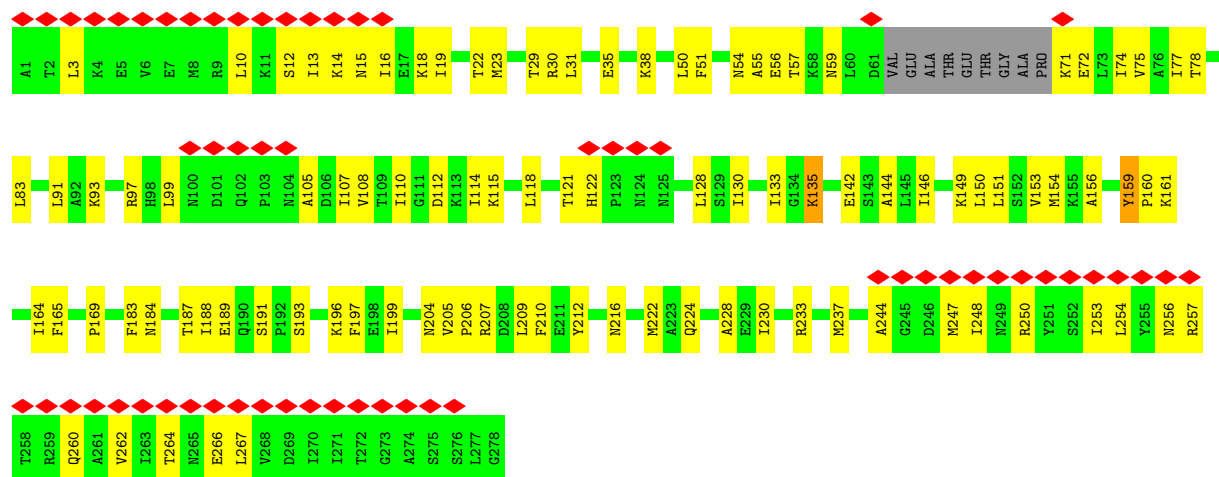




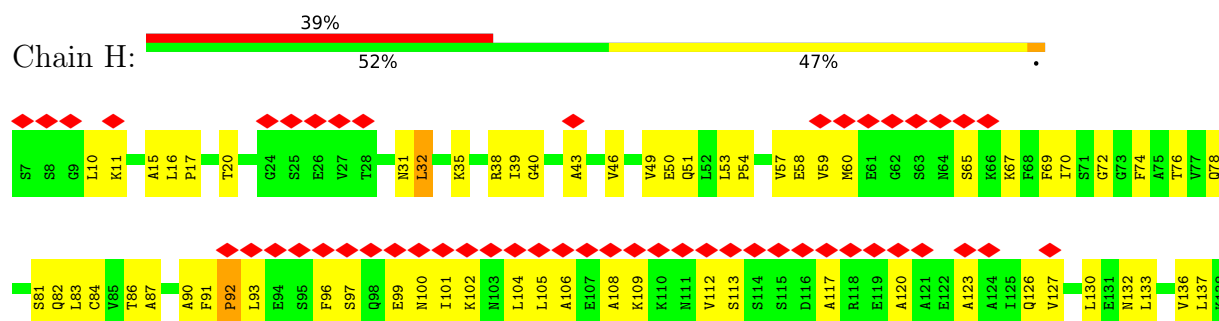
• Molecule 5: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL



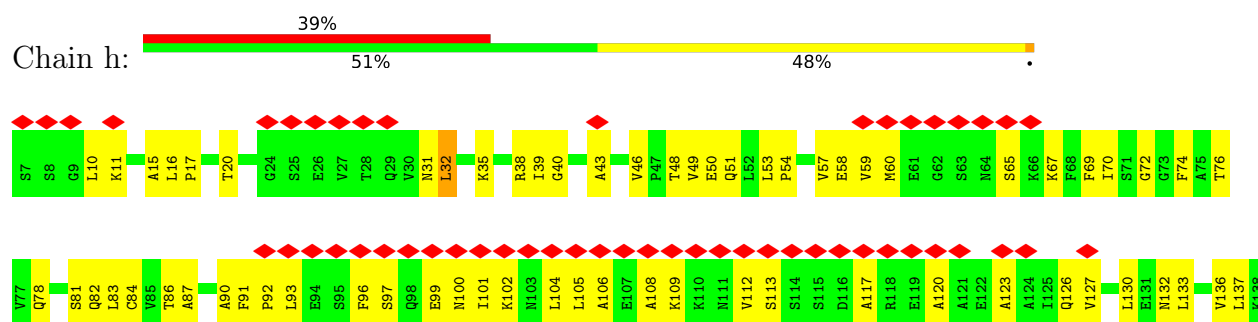
• Molecule 5: ATP SYNTHASE SUBUNIT GAMMA, MITOCHONDRIAL



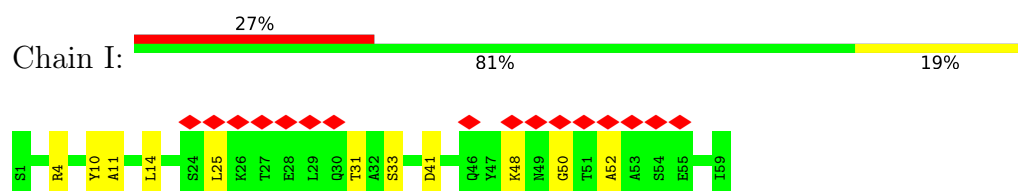
- Molecule 6: ATP SYNTHASE SUBUNIT DELTA, MITOCHONDRIAL



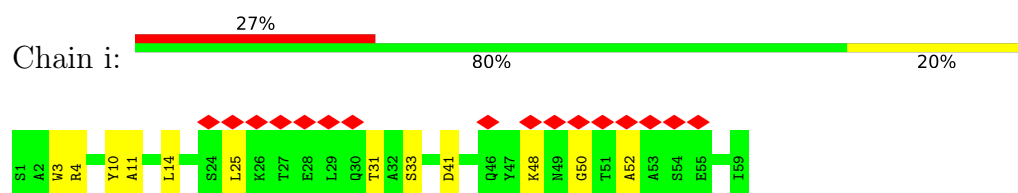
- Molecule 6: ATP SYNTHASE SUBUNIT DELTA, MITOCHONDRIAL



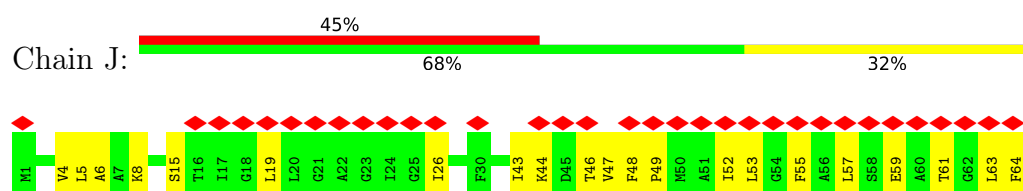
- Molecule 7: ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL



- Molecule 7: ATP SYNTHASE SUBUNIT EPSILON, MITOCHONDRIAL



- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL





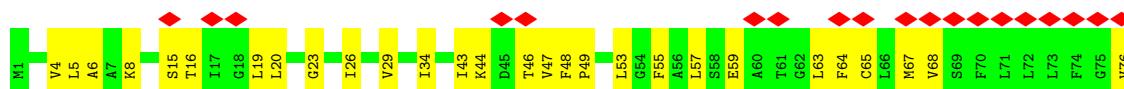
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



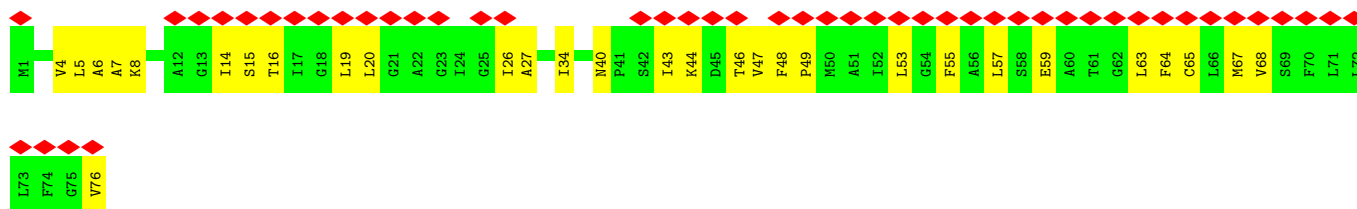
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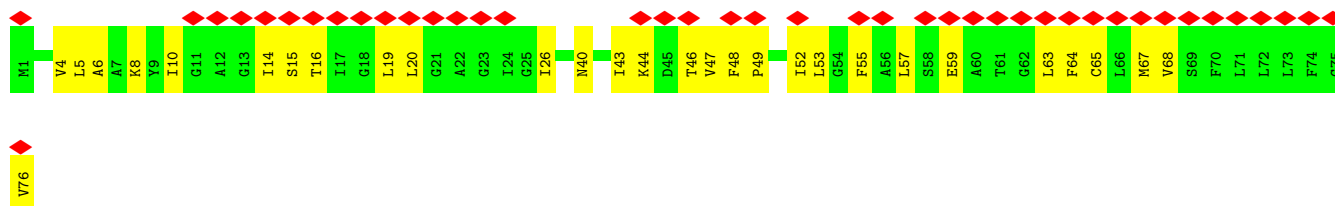
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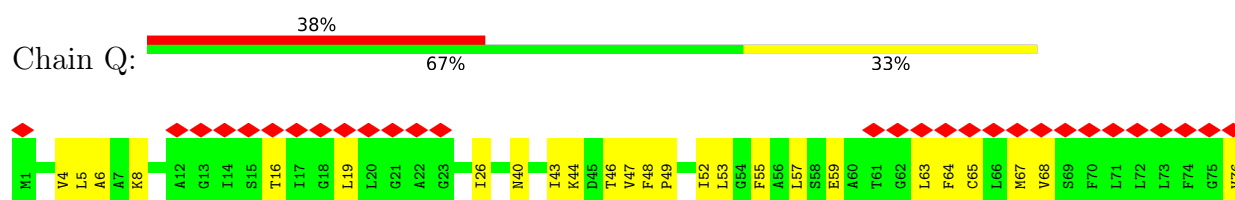
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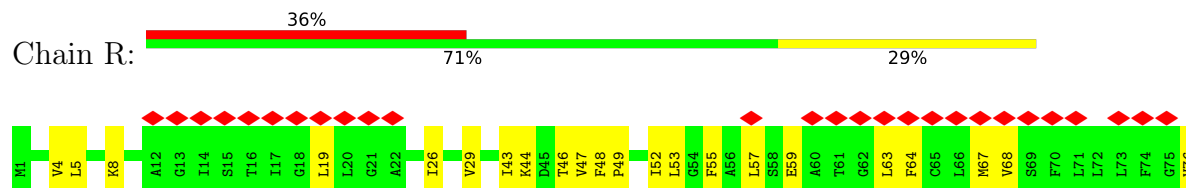
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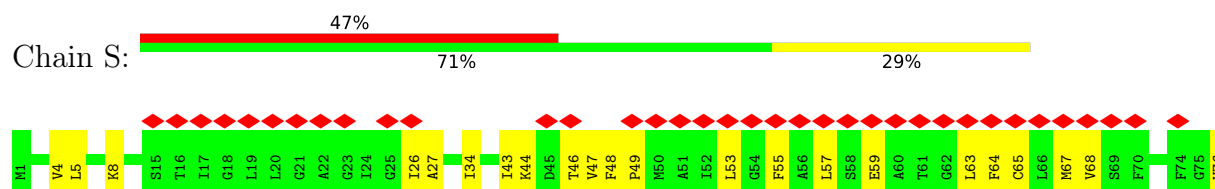
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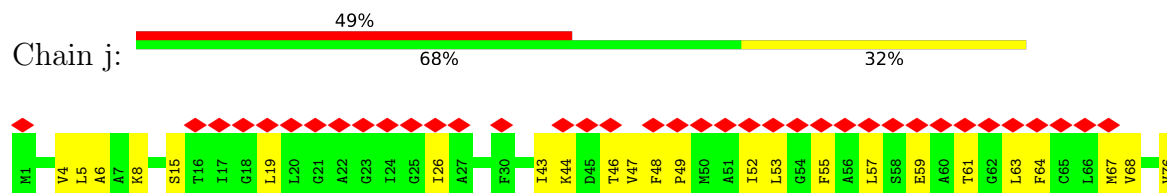
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



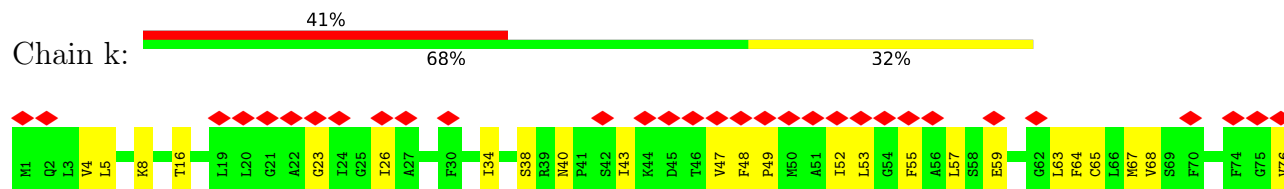
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



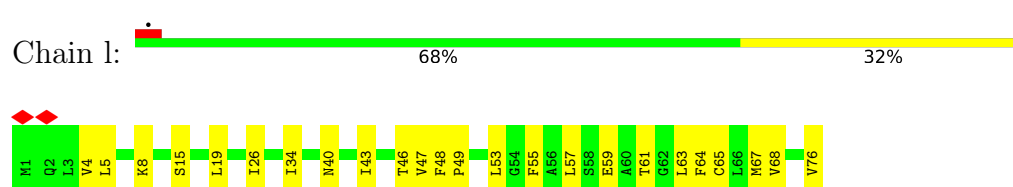
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



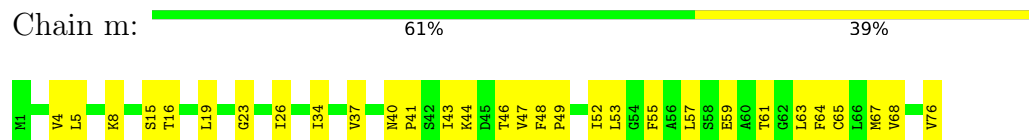
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



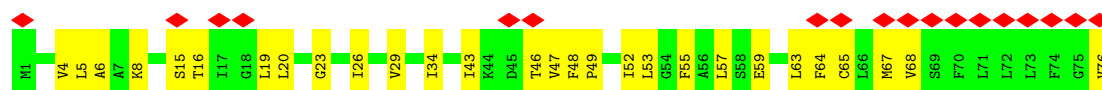
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



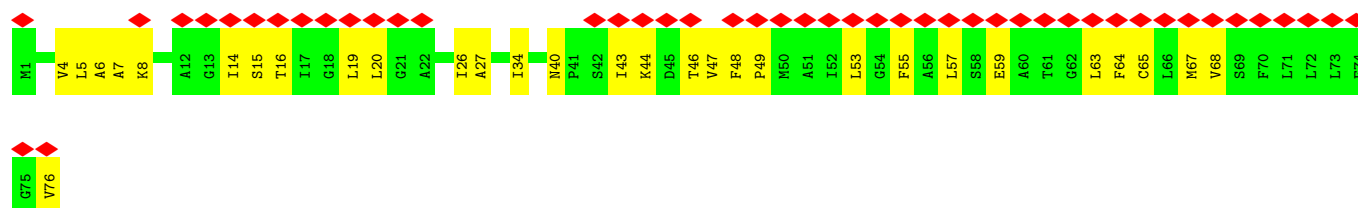
- Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



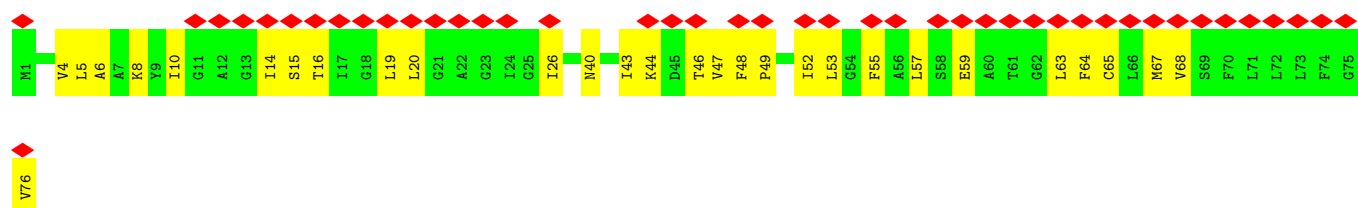
● Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



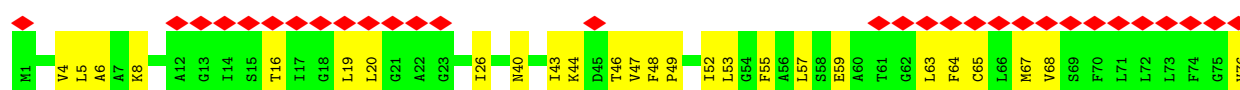
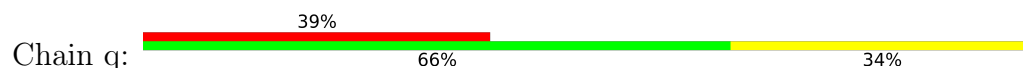
● Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



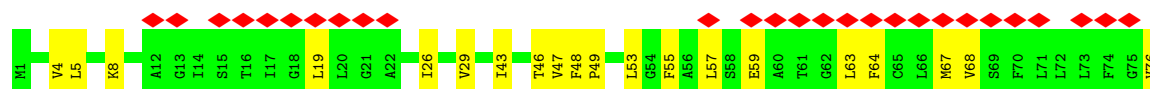
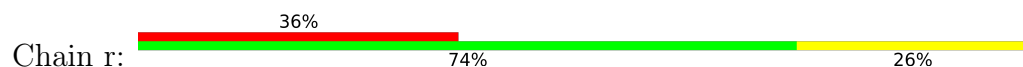
● Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



● Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL



● Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL

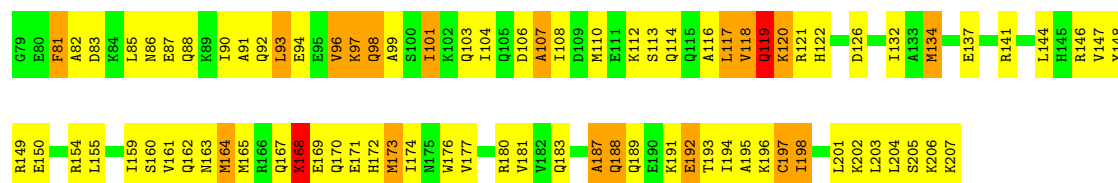
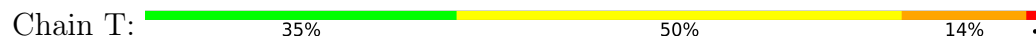


● Molecule 8: ATP SYNTHASE SUBUNIT 9, MITOCHONDRIAL

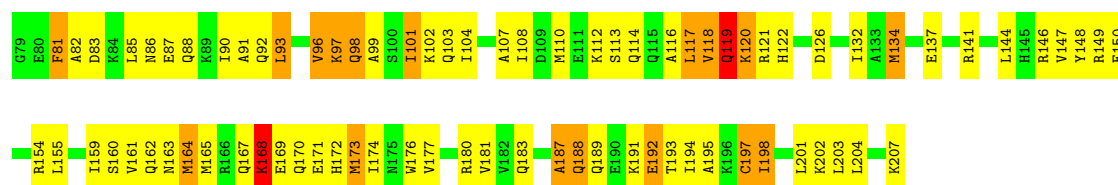




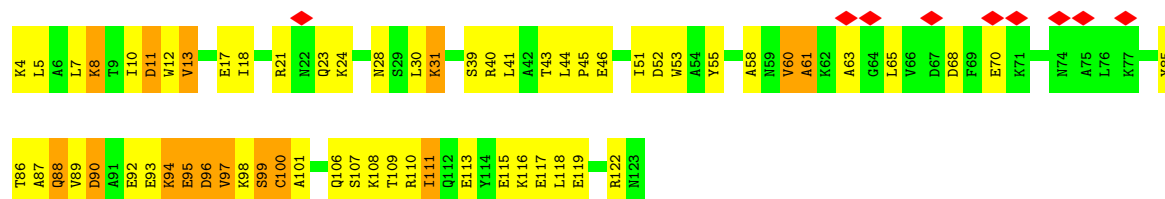
• Molecule 9: ATP SYNTHASE SUBUNIT B, MITOCHONDRIAL



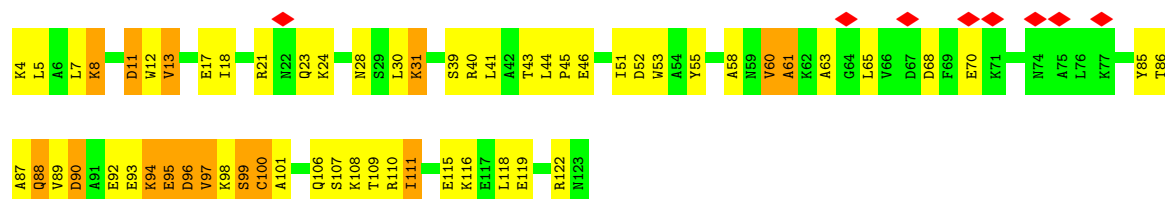
• Molecule 9: ATP SYNTHASE SUBUNIT B, MITOCHONDRIAL



• Molecule 10: ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL



• Molecule 10: ATP SYNTHASE SUBUNIT D, MITOCHONDRIAL



• Molecule 11: ATP SYNTHASE-COUPLING FACTOR 6, MITOCHONDRIAL

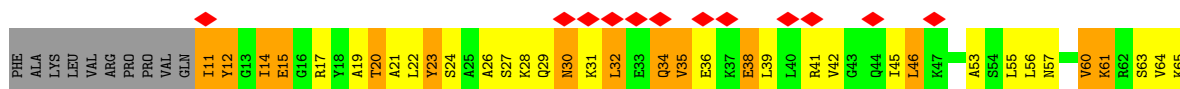




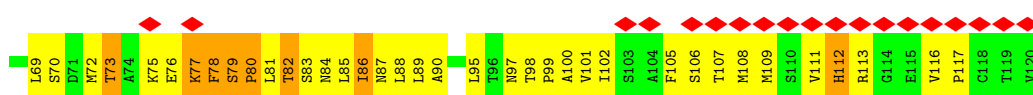
• Molecule 11: ATP SYNTHASE-COUPLING FACTOR 6, MITOCHONDRIAL



• Molecule 12: ATP SYNTHASE SUBUNIT O, MITOCHONDRIAL



• Molecule 12: ATP SYNTHASE SUBUNIT O, MITOCHONDRIAL



4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of tilted images used	121	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	160	Depositor
Minimum defocus (nm)	6500	Depositor
Maximum defocus (nm)	7500	Depositor
Magnification	24500	Depositor
Image detector	GATAN ULTRASCAN 1000 (2k x 2k)	Depositor
Maximum voxel value	11.211	Depositor
Minimum voxel value	0.610	Depositor
Average voxel value	5.106	Depositor
Voxel value standard deviation	1.447	Depositor
Recommended contour level	7.7	Depositor
Tomogram size ($\text{\AA}$)	518.4, 172.8, 345.6	wwPDB
Tomogram dimensions	90, 30, 60	wwPDB
Tomogram angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Grid spacing ($\text{\AA}$)	5.76, 5.76, 5.76	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, 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	0/3749	0.75	0/5073
1	C	0.36	0/3749	0.78	4/5073 (0.1%)
1	a	0.35	0/3749	0.75	2/5073 (0.0%)
1	c	0.36	0/3749	0.78	4/5073 (0.1%)
2	B	0.32	0/3741	0.70	1/5064 (0.0%)
2	b	0.32	0/3741	0.70	1/5064 (0.0%)
3	D	0.36	0/3605	0.76	4/4889 (0.1%)
3	d	0.36	0/3605	0.76	4/4889 (0.1%)
4	E	0.32	0/3628	0.76	4/4919 (0.1%)
4	F	0.35	0/3622	0.78	2/4911 (0.0%)
4	e	0.32	0/3628	0.76	4/4919 (0.1%)
4	f	0.35	0/3622	0.78	4/4911 (0.1%)
5	G	0.32	0/2111	0.70	2/2838 (0.1%)
5	g	0.32	0/2111	0.70	2/2838 (0.1%)
6	H	0.33	0/1004	0.75	0/1359
6	h	0.33	0/1004	0.75	0/1359
7	I	0.32	0/398	0.69	0/547
7	i	0.32	0/398	0.69	0/547
8	J	0.29	0/553	0.67	0/747
8	K	0.30	0/553	0.70	0/747
8	L	0.28	0/553	0.68	0/747
8	M	0.29	0/553	0.70	0/747
8	N	0.29	0/553	0.70	0/747
8	O	0.28	0/553	0.68	0/747
8	P	0.29	0/553	0.67	0/747
8	Q	0.29	0/553	0.68	0/747
8	R	0.28	0/553	0.67	0/747
8	S	0.29	0/553	0.66	0/747
8	j	0.29	0/553	0.68	0/747
8	k	0.30	0/553	0.70	0/747
8	l	0.28	0/553	0.68	0/747
8	m	0.29	0/553	0.70	0/747

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
8	n	0.29	0/553	0.70	0/747
8	o	0.28	0/553	0.68	0/747
8	p	0.29	0/553	0.67	0/747
8	q	0.28	0/553	0.68	0/747
8	r	0.28	0/553	0.68	0/747
8	s	0.28	0/553	0.65	0/747
9	T	1.10	3/1088 (0.3%)	0.98	4/1453 (0.3%)
9	t	1.10	3/1088 (0.3%)	0.98	4/1453 (0.3%)
10	U	0.74	0/988	1.09	1/1335 (0.1%)
10	u	0.74	1/988 (0.1%)	1.09	1/1335 (0.1%)
11	V	20.78	1/553 (0.2%)	1.13	3/738 (0.4%)
11	v	0.63	0/554	1.05	2/741 (0.3%)
12	W	0.34	0/857	0.71	0/1154
12	w	0.34	0/857	0.71	0/1154
All	All	1.90	8/69247 (0.0%)	0.76	53/93649 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	V	10	LYS	N-CA	488.34	10.74	1.46
9	T	168	LYS	C-N	-26.76	0.99	1.33
9	t	168	LYS	C-N	-26.74	0.99	1.33
9	T	173	MET	SD-CE	6.51	1.95	1.79
9	t	173	MET	SD-CE	6.49	1.95	1.79

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	V	10	LYS	N-CA-CB	-11.75	90.52	110.50
10	u	97	VAL	N-CA-C	-10.48	99.36	110.36
10	U	97	VAL	N-CA-C	-10.46	99.38	110.36
9	T	107	ALA	N-CA-C	-6.92	102.96	111.33
4	f	120	ASP	CA-C-N	6.91	124.63	119.66

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3692	0	3769	241	0
1	C	3692	0	3772	132	0
1	a	3692	0	3769	235	0
1	c	3692	0	3772	132	0
2	B	3685	0	3768	141	0
2	b	3685	0	3768	142	0
3	D	3549	0	3621	139	0
3	d	3549	0	3621	137	0
4	E	3572	0	3638	161	0
4	F	3566	0	3633	171	0
4	e	3572	0	3638	155	0
4	f	3566	0	3633	167	0
5	G	2086	0	2156	87	0
5	g	2086	0	2156	87	0
6	H	990	0	999	64	0
6	h	990	0	999	64	0
7	I	392	0	306	10	0
7	i	392	0	306	12	0
8	J	545	0	591	19	0
8	K	545	0	591	25	0
8	L	545	0	591	30	0
8	M	545	0	591	34	0
8	N	545	0	591	30	0
8	O	545	0	591	31	0
8	P	545	0	591	29	0
8	Q	545	0	591	26	0
8	R	545	0	591	22	0
8	S	545	0	591	20	0
8	j	545	0	591	19	0
8	k	545	0	591	25	0
8	l	545	0	591	29	0
8	m	545	0	591	35	0
8	n	545	0	591	30	0
8	o	545	0	591	30	0
8	p	545	0	591	29	0
8	q	545	0	591	27	0
8	r	545	0	591	20	0
8	s	545	0	591	20	0
9	T	1077	0	1104	173	0
9	t	1077	0	1104	167	0
10	U	969	0	980	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	u	969	0	980	80	0
11	V	542	0	520	91	0
11	v	542	0	521	92	0
12	W	846	893	889	143	0
12	w	846	893	889	141	0
13	A	31	0	12	5	0
13	B	31	0	12	1	0
13	C	31	0	12	1	0
13	a	31	0	12	5	0
13	b	31	0	12	1	0
13	c	31	0	12	1	0
14	A	1	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	D	1	0	0	0	0
14	F	1	0	0	0	0
14	a	1	0	0	0	0
14	b	1	0	0	0	0
14	c	1	0	0	0	0
14	d	1	0	0	0	0
14	f	1	0	0	0	0
15	D	27	0	12	2	0
15	F	27	0	12	2	0
15	d	27	0	12	2	0
15	f	27	0	12	2	0
All	All	68520	1786	70251	3128	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 23.

The worst 5 of 3128 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)
4:F:56:GLU:CD	12:W:53:ALA:HB2	1.25	1.60
1:a:122:PRO:CD	9:t:159:ILE:CG2	1.78	1.59
1:A:122:PRO:CD	9:T:159:ILE:CG2	1.78	1.57
1:A:27:LEU:CD2	9:T:202:LYS:HE2	1.35	1.56
4:f:56:GLU:CD	12:w:53:ALA:HB2	1.25	1.50

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	483/485 (100%)	444 (92%)	35 (7%)	4 (1%)	16	54
1	C	483/485 (100%)	450 (93%)	33 (7%)	0	100	100
1	a	483/485 (100%)	444 (92%)	35 (7%)	4 (1%)	16	54
1	c	483/485 (100%)	450 (93%)	33 (7%)	0	100	100
2	B	483/486 (99%)	447 (92%)	35 (7%)	1 (0%)	43	78
2	b	483/486 (99%)	447 (92%)	35 (7%)	1 (0%)	43	78
3	D	468/470 (100%)	443 (95%)	22 (5%)	3 (1%)	21	59
3	d	468/470 (100%)	443 (95%)	22 (5%)	3 (1%)	21	59
4	E	471/473 (100%)	436 (93%)	32 (7%)	3 (1%)	21	59
4	F	470/473 (99%)	438 (93%)	30 (6%)	2 (0%)	30	67
4	e	471/473 (100%)	436 (93%)	32 (7%)	3 (1%)	21	59
4	f	470/473 (99%)	438 (93%)	30 (6%)	2 (0%)	30	67
5	G	265/278 (95%)	247 (93%)	17 (6%)	1 (0%)	30	67
5	g	265/278 (95%)	247 (93%)	17 (6%)	1 (0%)	30	67
6	H	130/132 (98%)	115 (88%)	11 (8%)	4 (3%)	3	22
6	h	130/132 (98%)	115 (88%)	11 (8%)	4 (3%)	3	22
7	I	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
7	i	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
8	J	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
8	K	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
8	L	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	M	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
8	N	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
8	O	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	P	74/76 (97%)	68 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	Q	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	R	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	S	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
8	j	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
8	k	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
8	l	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	m	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
8	n	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
8	o	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	p	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
8	q	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	r	74/76 (97%)	70 (95%)	4 (5%)	0	100	100
8	s	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
9	T	127/129 (98%)	100 (79%)	19 (15%)	8 (6%)	1	13
9	t	127/129 (98%)	100 (79%)	19 (15%)	8 (6%)	1	13
10	U	118/120 (98%)	88 (75%)	24 (20%)	6 (5%)	1	15
10	u	118/120 (98%)	88 (75%)	24 (20%)	6 (5%)	1	15
11	V	60/66 (91%)	52 (87%)	6 (10%)	2 (3%)	3	21
11	v	61/66 (92%)	52 (85%)	7 (12%)	2 (3%)	3	21
12	W	108/120 (90%)	92 (85%)	8 (7%)	8 (7%)	1	10
12	w	108/120 (90%)	92 (85%)	8 (7%)	8 (7%)	1	10
All	All	8927/9072 (98%)	8182 (92%)	661 (7%)	84 (1%)	16	51

5 of 84 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	72	ARG
3	D	279	VAL
4	E	32	ALA
4	E	279	VAL
4	F	279	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	A	391/391 (100%)	391 (100%)	0	100	100
1	C	391/391 (100%)	390 (100%)	1 (0%)	86	86
1	a	391/391 (100%)	391 (100%)	0	100	100
1	c	391/391 (100%)	390 (100%)	1 (0%)	86	86
2	B	390/391 (100%)	389 (100%)	1 (0%)	86	86
2	b	390/391 (100%)	389 (100%)	1 (0%)	86	86
3	D	380/380 (100%)	379 (100%)	1 (0%)	86	86
3	d	380/380 (100%)	379 (100%)	1 (0%)	86	86
4	E	382/382 (100%)	381 (100%)	1 (0%)	86	86
4	F	381/382 (100%)	381 (100%)	0	100	100
4	e	382/382 (100%)	381 (100%)	1 (0%)	86	86
4	f	381/382 (100%)	381 (100%)	0	100	100
5	G	230/236 (98%)	230 (100%)	0	100	100
5	g	230/236 (98%)	230 (100%)	0	100	100
6	H	111/111 (100%)	110 (99%)	1 (1%)	70	79
6	h	111/111 (100%)	110 (99%)	1 (1%)	70	79
7	I	25/46 (54%)	25 (100%)	0	100	100
7	i	25/46 (54%)	25 (100%)	0	100	100
8	J	56/56 (100%)	56 (100%)	0	100	100
8	K	56/56 (100%)	56 (100%)	0	100	100
8	L	56/56 (100%)	56 (100%)	0	100	100
8	M	56/56 (100%)	56 (100%)	0	100	100
8	N	56/56 (100%)	56 (100%)	0	100	100
8	O	56/56 (100%)	56 (100%)	0	100	100
8	P	56/56 (100%)	56 (100%)	0	100	100
8	Q	56/56 (100%)	56 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	R	56/56 (100%)	56 (100%)	0	100	100
8	S	56/56 (100%)	56 (100%)	0	100	100
8	j	56/56 (100%)	56 (100%)	0	100	100
8	k	56/56 (100%)	56 (100%)	0	100	100
8	l	56/56 (100%)	56 (100%)	0	100	100
8	m	56/56 (100%)	56 (100%)	0	100	100
8	n	56/56 (100%)	56 (100%)	0	100	100
8	o	56/56 (100%)	56 (100%)	0	100	100
8	p	56/56 (100%)	56 (100%)	0	100	100
8	q	56/56 (100%)	56 (100%)	0	100	100
8	r	56/56 (100%)	56 (100%)	0	100	100
8	s	56/56 (100%)	56 (100%)	0	100	100
9	T	118/118 (100%)	103 (87%)	15 (13%)	4	16
9	t	118/118 (100%)	103 (87%)	15 (13%)	4	16
10	U	104/104 (100%)	88 (85%)	16 (15%)	2	12
10	u	104/104 (100%)	89 (86%)	15 (14%)	3	13
11	V	58/60 (97%)	49 (84%)	9 (16%)	2	12
11	v	58/60 (97%)	49 (84%)	9 (16%)	2	12
12	W	95/104 (91%)	73 (77%)	22 (23%)	1	5
12	w	95/104 (91%)	73 (77%)	22 (23%)	1	5
All	All	7232/7312 (99%)	7099 (98%)	133 (2%)	51	68

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	w	20	THR
12	w	34	GLN
12	w	86	ILE
12	W	15	GLU
12	W	14	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 180 such sidechains are listed below:

Mol	Chain	Res	Type
1	c	193	ASN
4	f	35	ASN
1	c	276	GLN
3	d	249	GLN
5	g	54	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 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$
13	ATP	b	1510	14	32,33,33	1.46	7 (21%)	48,52,52	1.78	11 (22%)
15	ADP	d	1476	14	28,29,29	1.45	4 (14%)	43,45,45	1.91	11 (25%)
15	ADP	F	1479	14	28,29,29	1.41	6 (21%)	43,45,45	1.90	11 (25%)
13	ATP	a	1511	14	32,33,33	1.39	4 (12%)	48,52,52	1.78	8 (16%)
13	ATP	c	1511	14	32,33,33	1.42	6 (18%)	48,52,52	1.79	8 (16%)
15	ADP	D	1476	14	28,29,29	1.45	4 (14%)	43,45,45	1.90	11 (25%)
13	ATP	A	1511	14	32,33,33	1.40	5 (15%)	48,52,52	1.78	8 (16%)
15	ADP	f	1479	14	28,29,29	1.42	6 (21%)	43,45,45	1.89	11 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	ATP	C	1511	14	32,33,33	1.43	6 (18%)	48,52,52	1.80	8 (16%)
13	ATP	B	1510	14	32,33,33	1.46	7 (21%)	48,52,52	1.78	11 (22%)

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
13	ATP	b	1510	14	-	5/22/38/38	0/3/3/3
15	ADP	d	1476	14	-	0/16/32/32	0/3/3/3
15	ADP	F	1479	14	-	1/16/32/32	0/3/3/3
13	ATP	a	1511	14	-	7/22/38/38	0/3/3/3
13	ATP	c	1511	14	-	5/22/38/38	0/3/3/3
15	ADP	D	1476	14	-	0/16/32/32	0/3/3/3
13	ATP	A	1511	14	-	7/22/38/38	0/3/3/3
15	ADP	f	1479	14	-	1/16/32/32	0/3/3/3
13	ATP	C	1511	14	-	5/22/38/38	0/3/3/3
13	ATP	B	1510	14	-	5/22/38/38	0/3/3/3

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	D	1476	ADP	C5-C4	4.90	1.47	1.39
15	d	1476	ADP	C5-C4	4.89	1.47	1.39
13	c	1511	ATP	C5-C4	4.72	1.47	1.39
13	C	1511	ATP	C5-C4	4.71	1.47	1.39
13	B	1510	ATP	C5-C4	4.69	1.47	1.39

The worst 5 of 98 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	a	1511	ATP	C5-C4-N3	-6.06	118.37	126.72
13	A	1511	ATP	C5-C4-N3	-6.06	118.38	126.72
15	d	1476	ADP	C5-C4-N3	-5.99	118.47	126.72
15	D	1476	ADP	C5-C4-N3	-5.97	118.49	126.72
13	C	1511	ATP	C5-C4-N3	-5.89	118.61	126.72

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

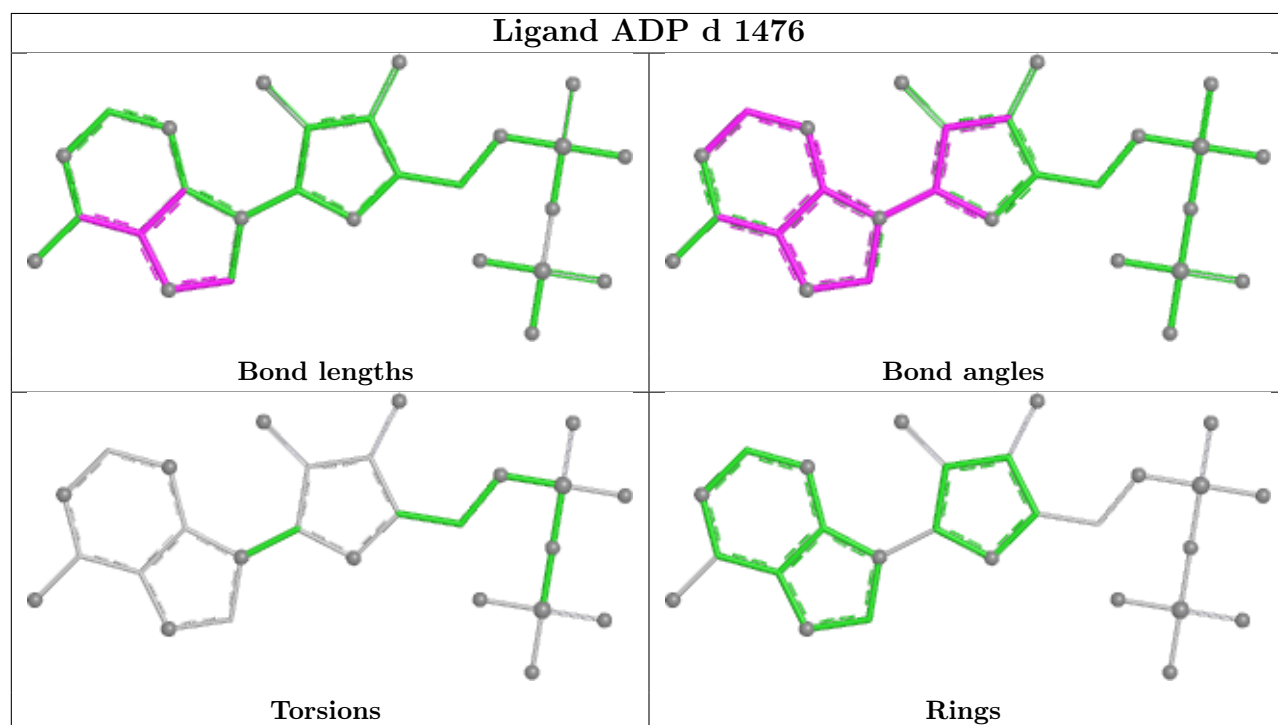
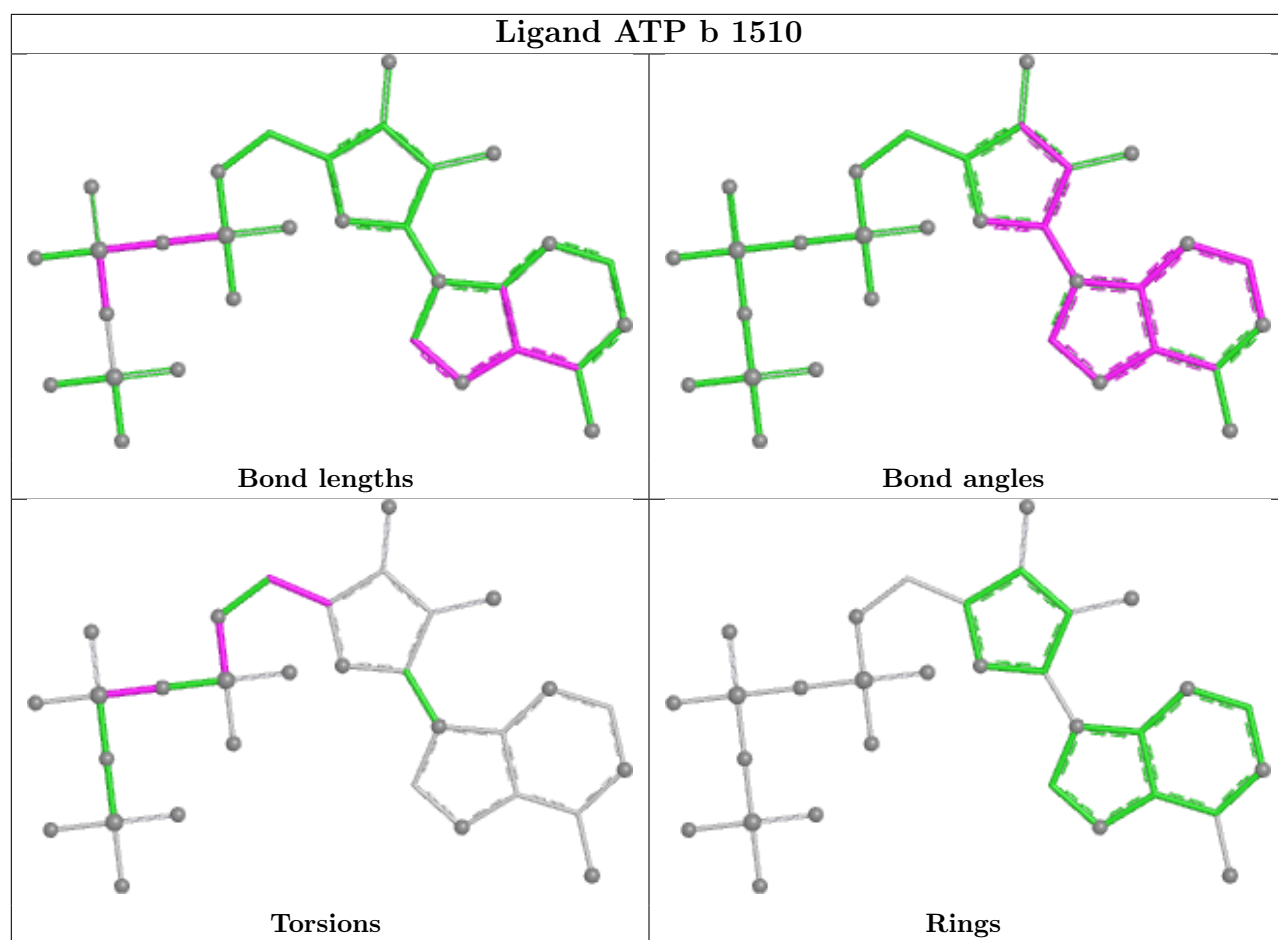
Mol	Chain	Res	Type	Atoms
13	A	1511	ATP	C5'-O5'-PA-O1A
13	A	1511	ATP	C5'-O5'-PA-O2A
13	A	1511	ATP	C5'-O5'-PA-O3A
13	A	1511	ATP	O4'-C4'-C5'-O5'
13	B	1510	ATP	C5'-O5'-PA-O1A

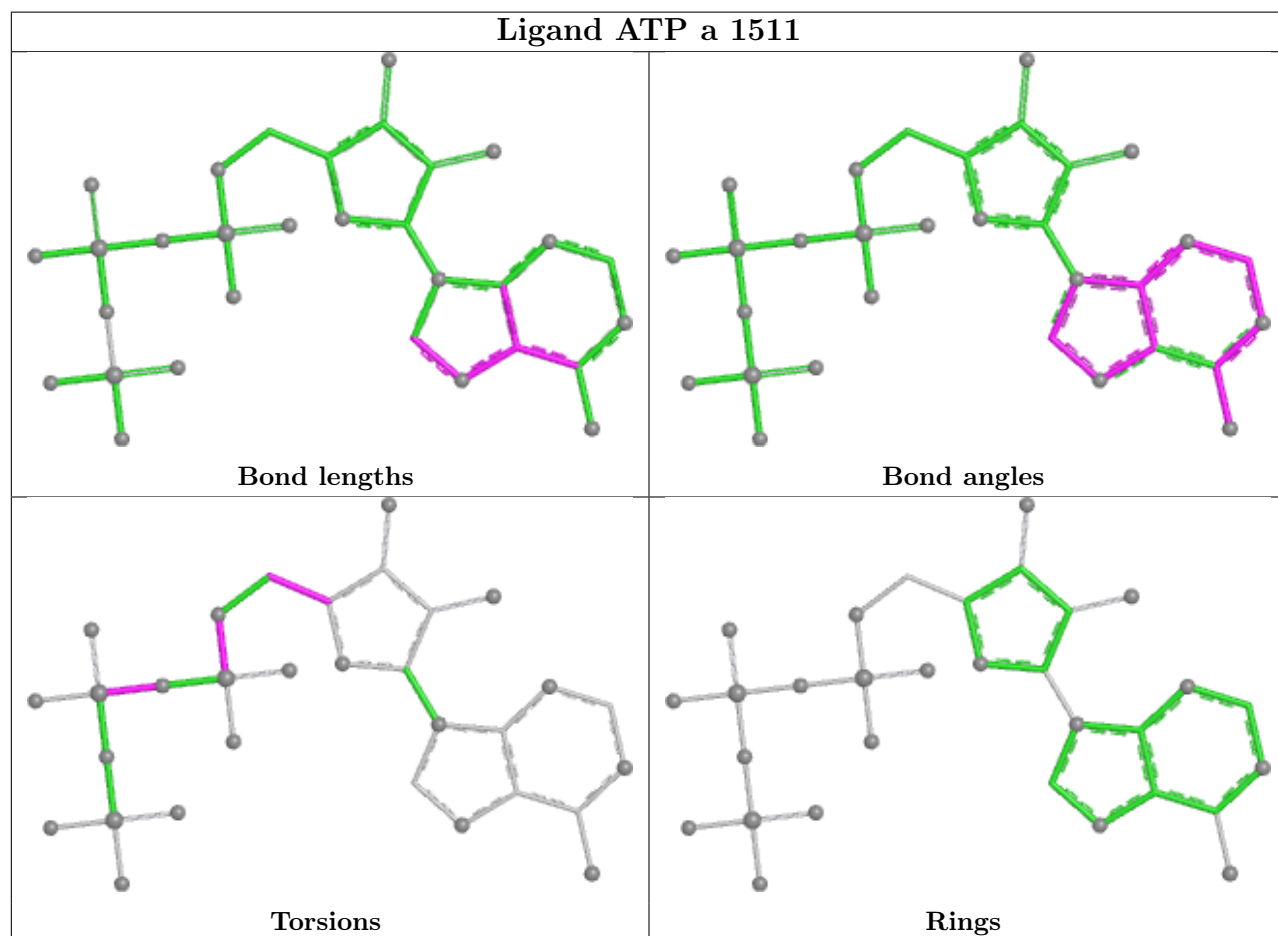
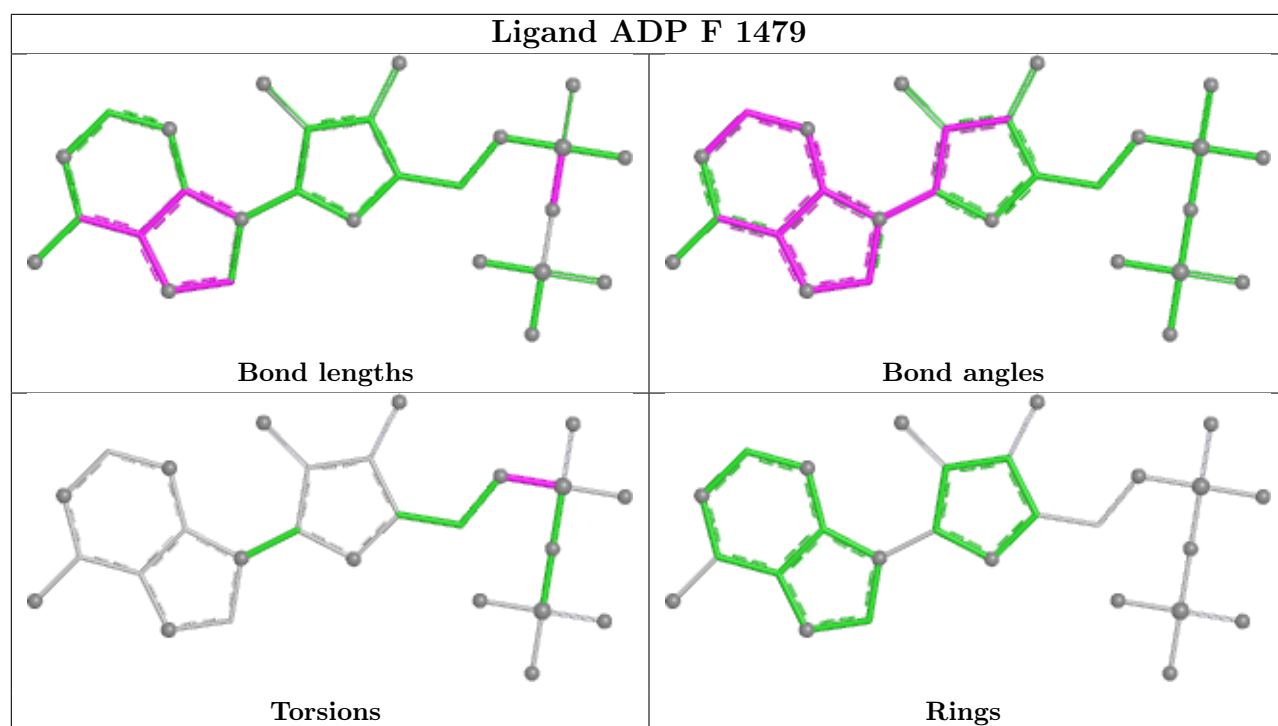
There are no ring outliers.

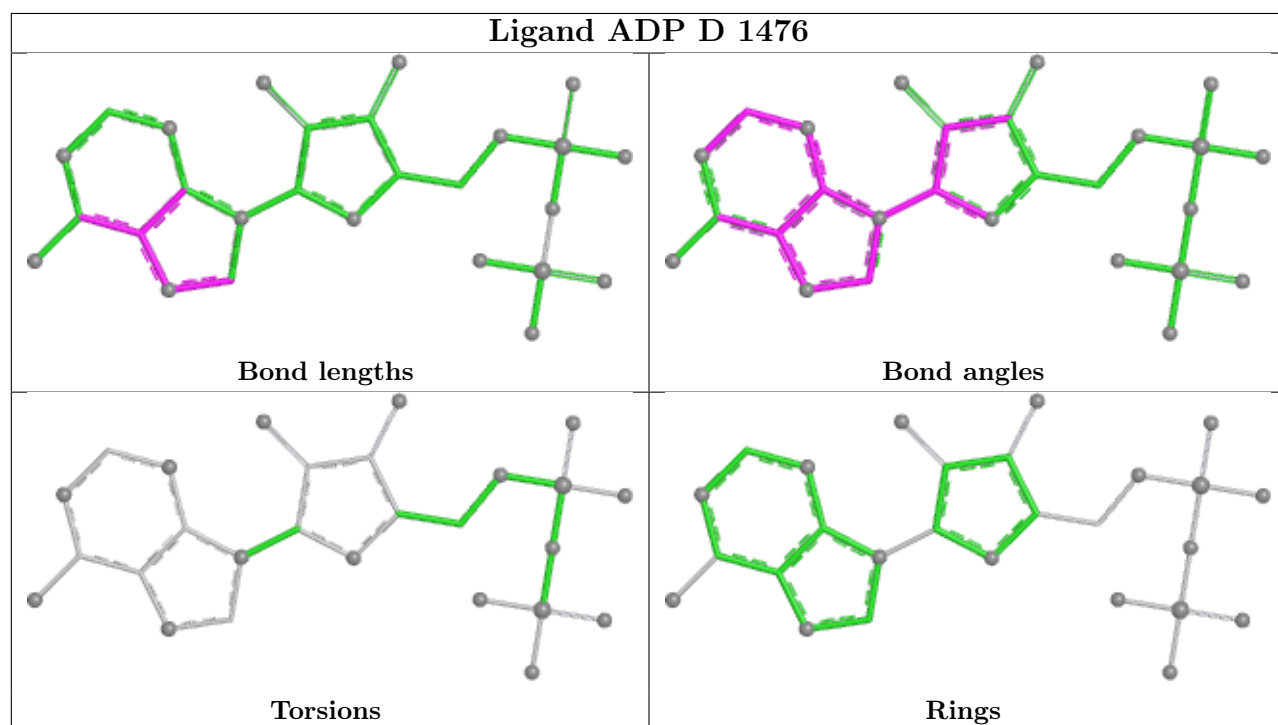
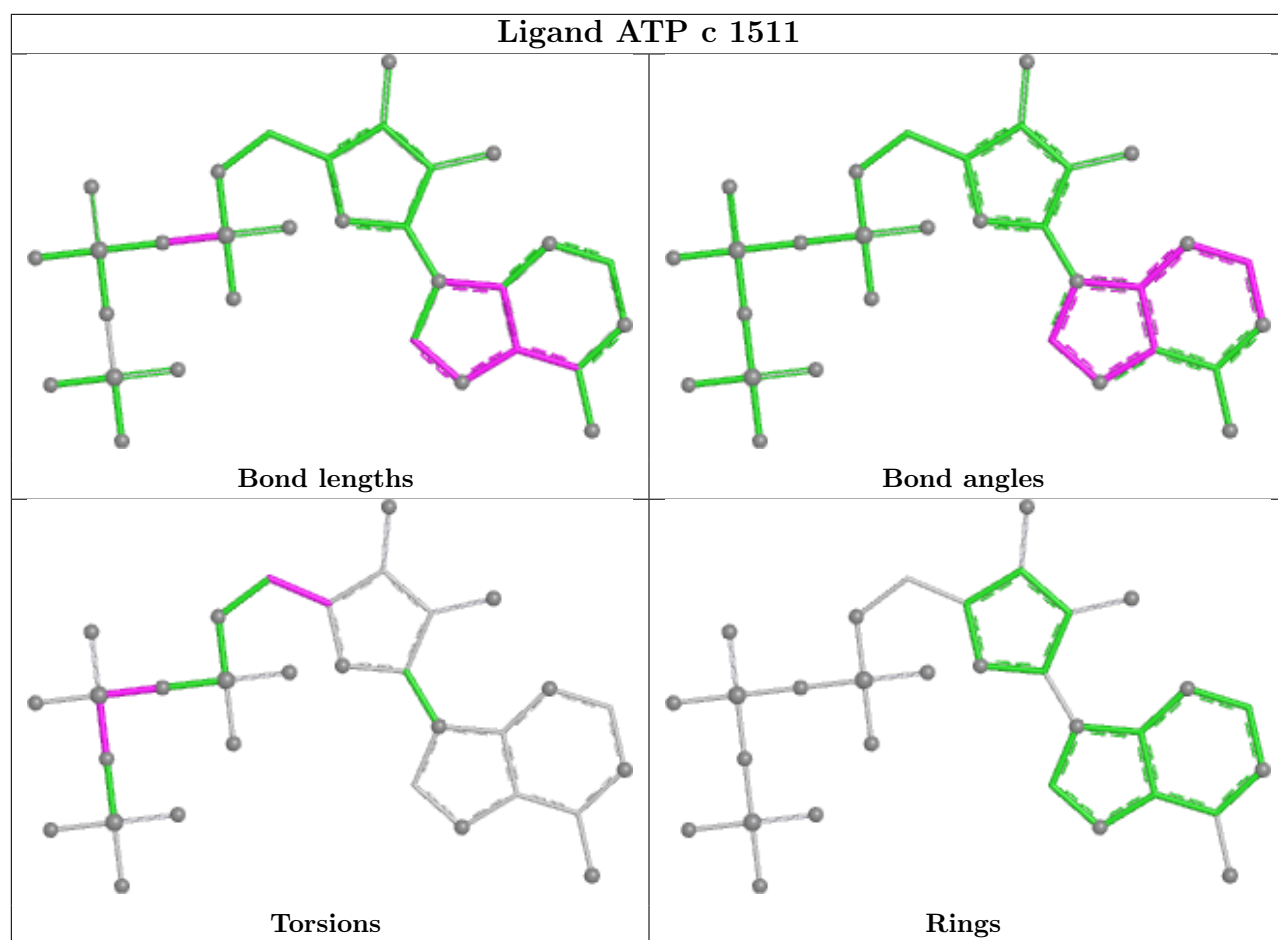
10 monomers are involved in 22 short contacts:

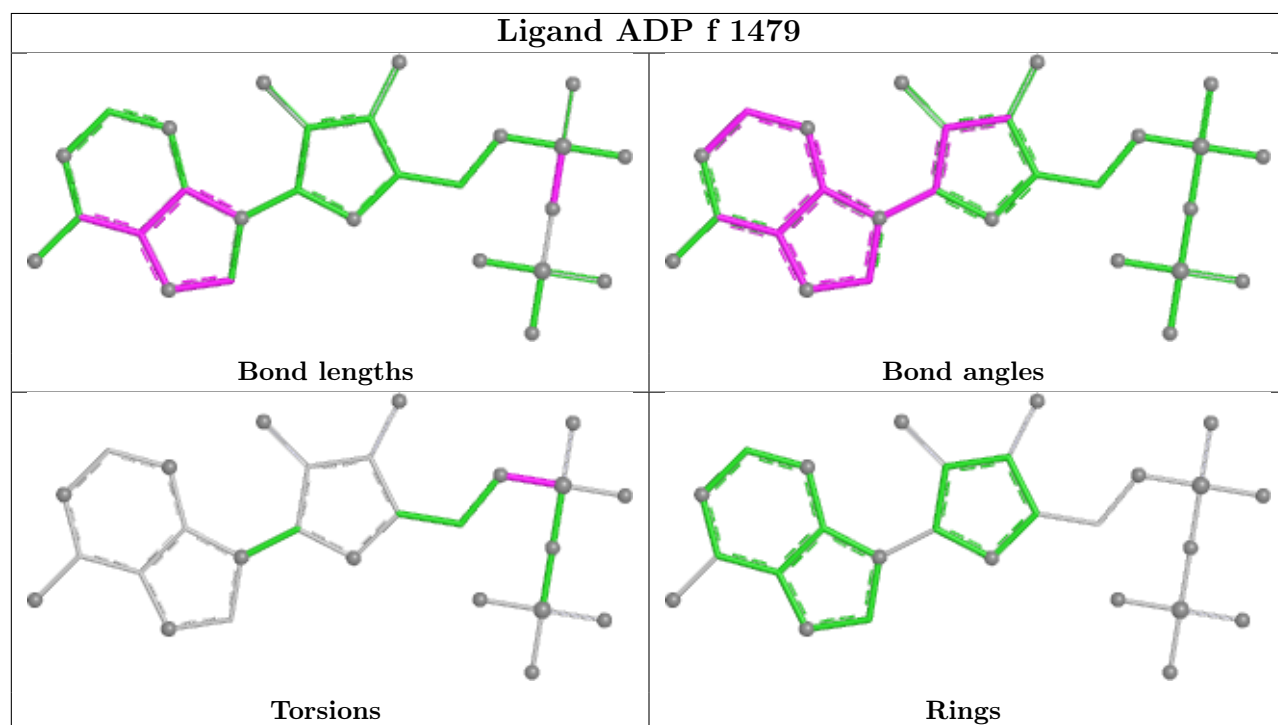
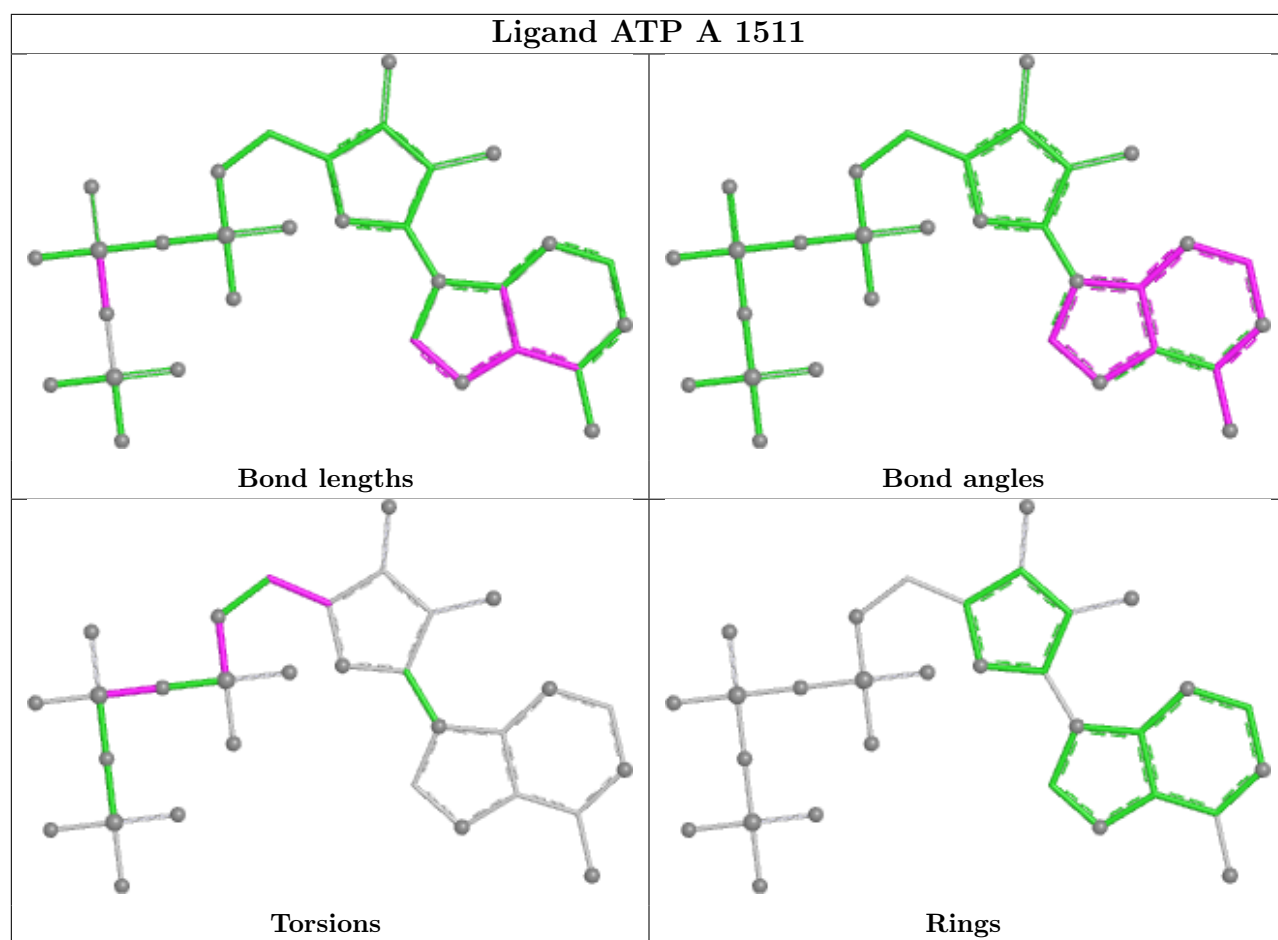
Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	b	1510	ATP	1	0
15	d	1476	ADP	2	0
15	F	1479	ADP	2	0
13	a	1511	ATP	5	0
13	c	1511	ATP	1	0
15	D	1476	ADP	2	0
13	A	1511	ATP	5	0
15	f	1479	ADP	2	0
13	C	1511	ATP	1	0
13	B	1510	ATP	1	0

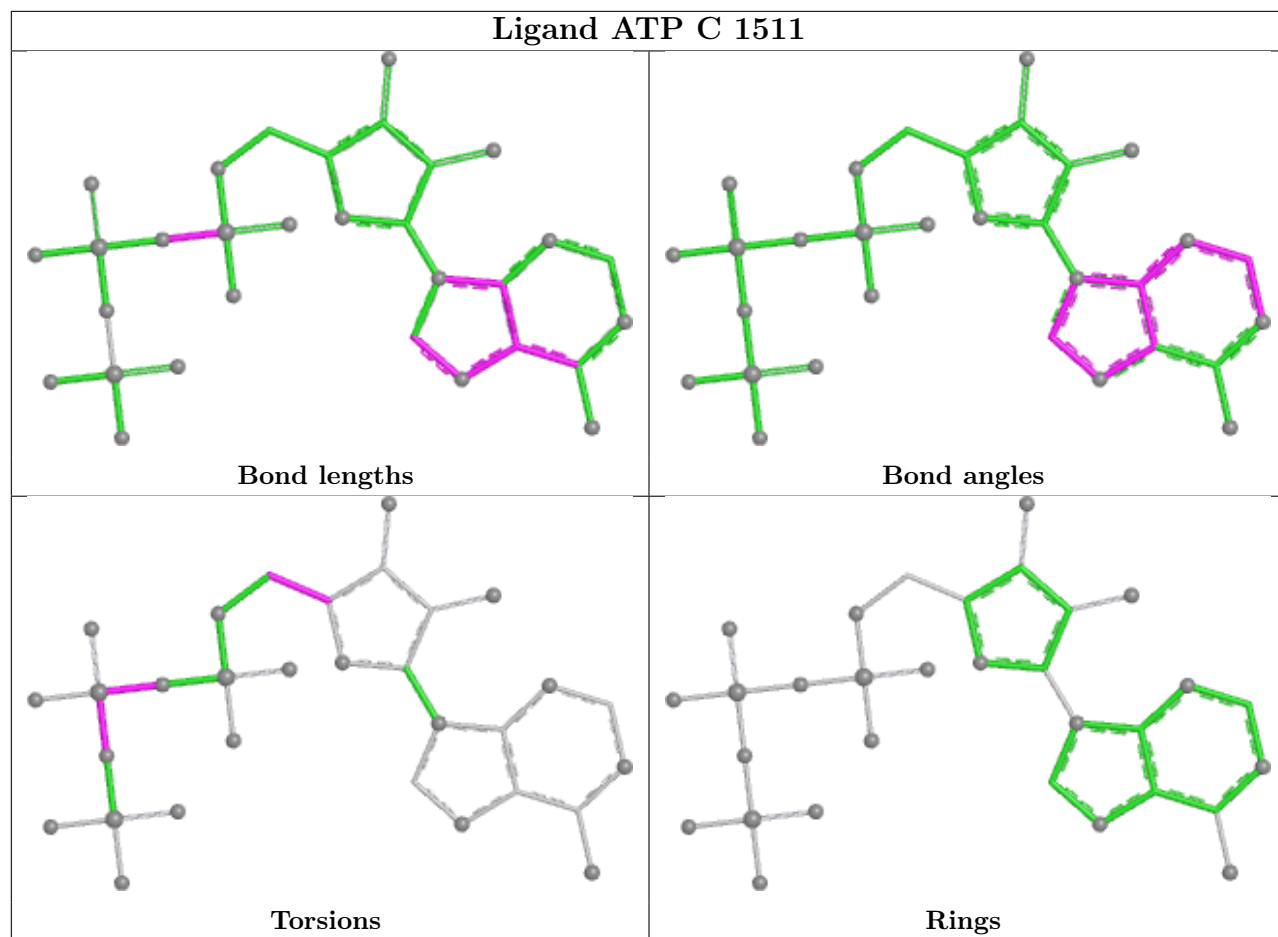
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

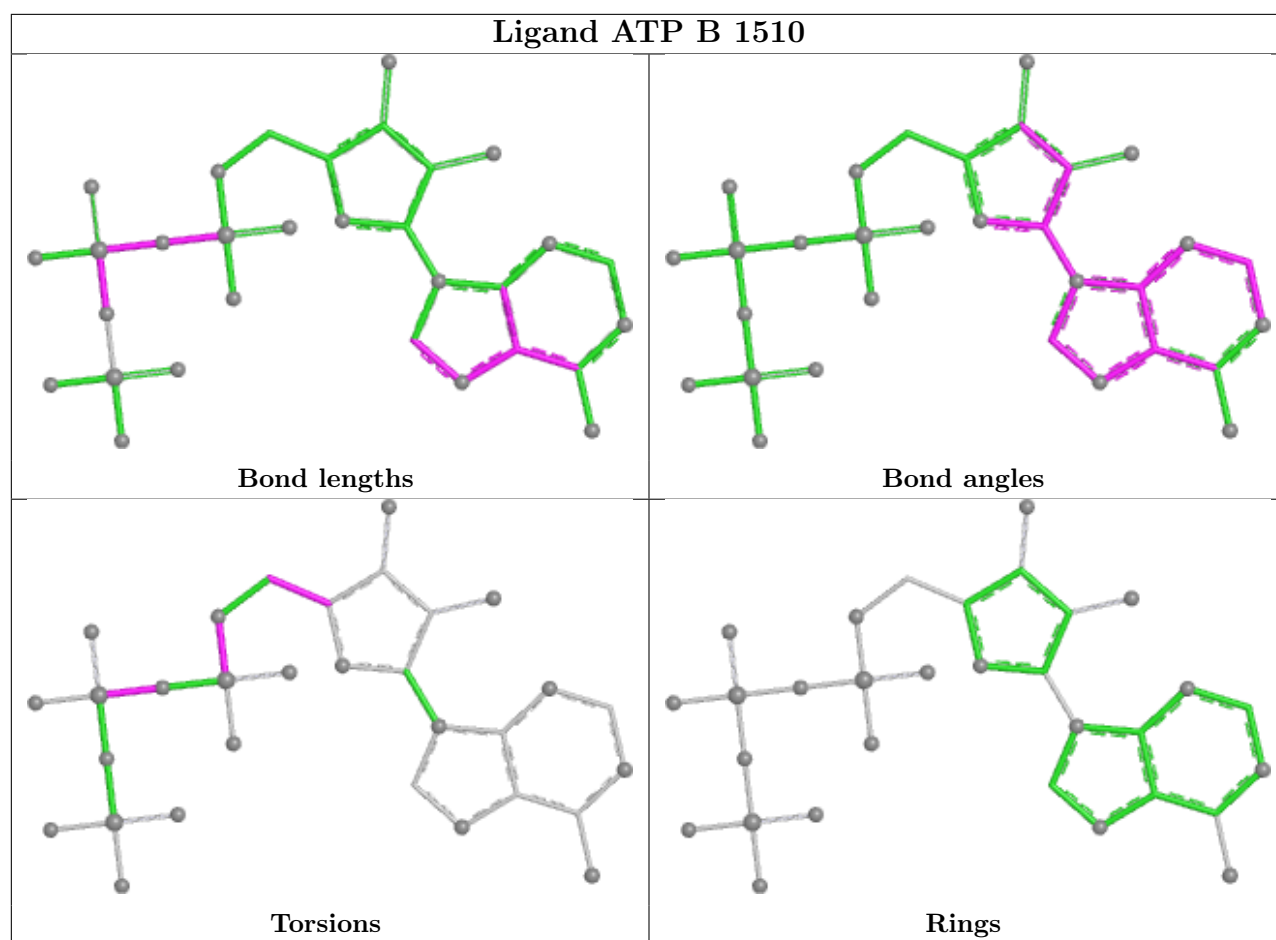












5.7 Other polymers [i](#)

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
11	V	1
9	T	1
9	t	1

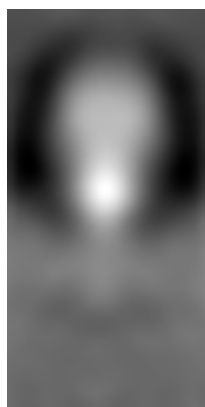
All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	9:GLN	C	10:LYS	N	9.37
1	T	168:LYS	C	169:GLU	N	0.99
1	t	168:LYS	C	169:GLU	N	0.99

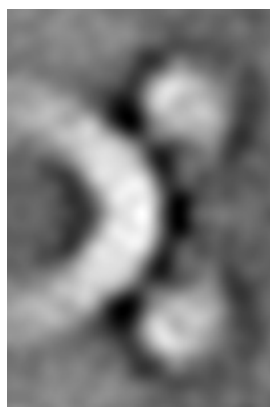
6 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2161. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

6.1 Orthogonal projections [i](#)



X



Y



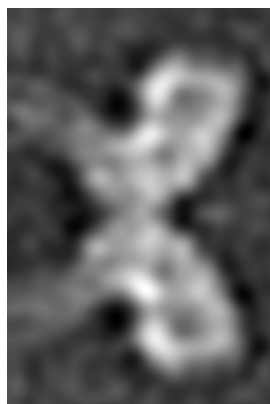
Z

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

6.2 Central slices [i](#)



X Index: 45



Y Index: 15



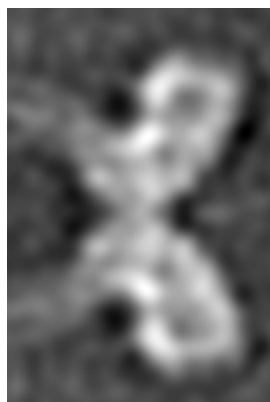
Z Index: 30

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

6.3 Largest variance slices [i](#)



X Index: 62



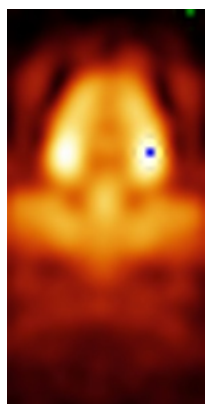
Y Index: 14



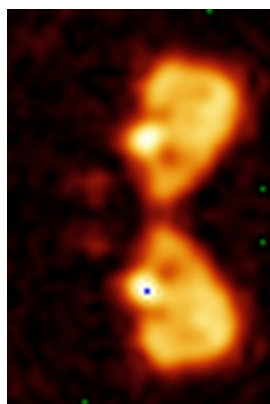
Z Index: 36

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

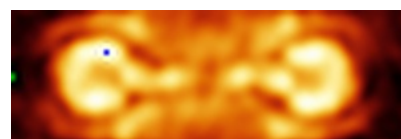
6.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

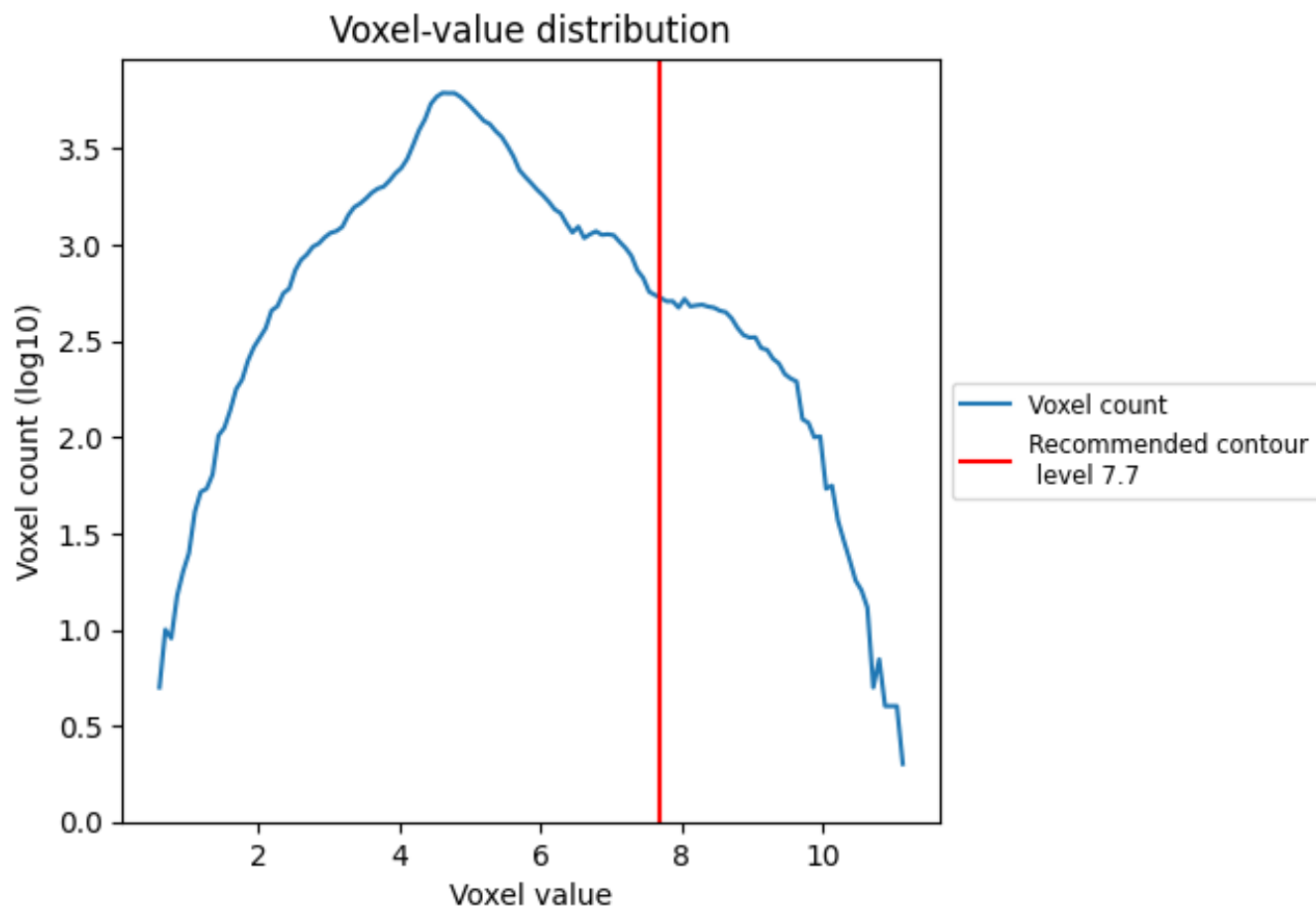
6.5 Mask visualisation [i](#)

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

7 Tomogram analysis [i](#)

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

7.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

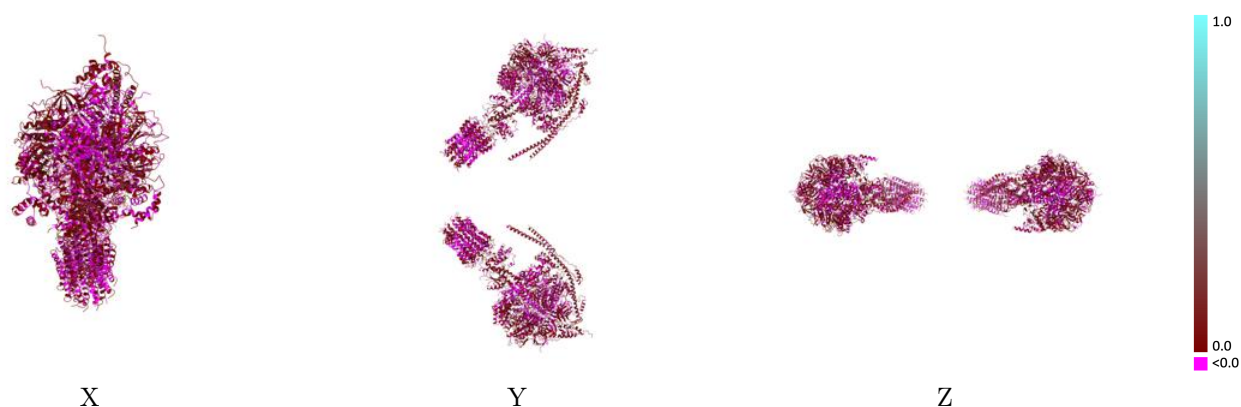
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2161 and PDB model 4B2Q. Per-residue inclusion information can be found in section 3 on page 11.

8.1 Map-model overlay [i](#)

This section was not generated.

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

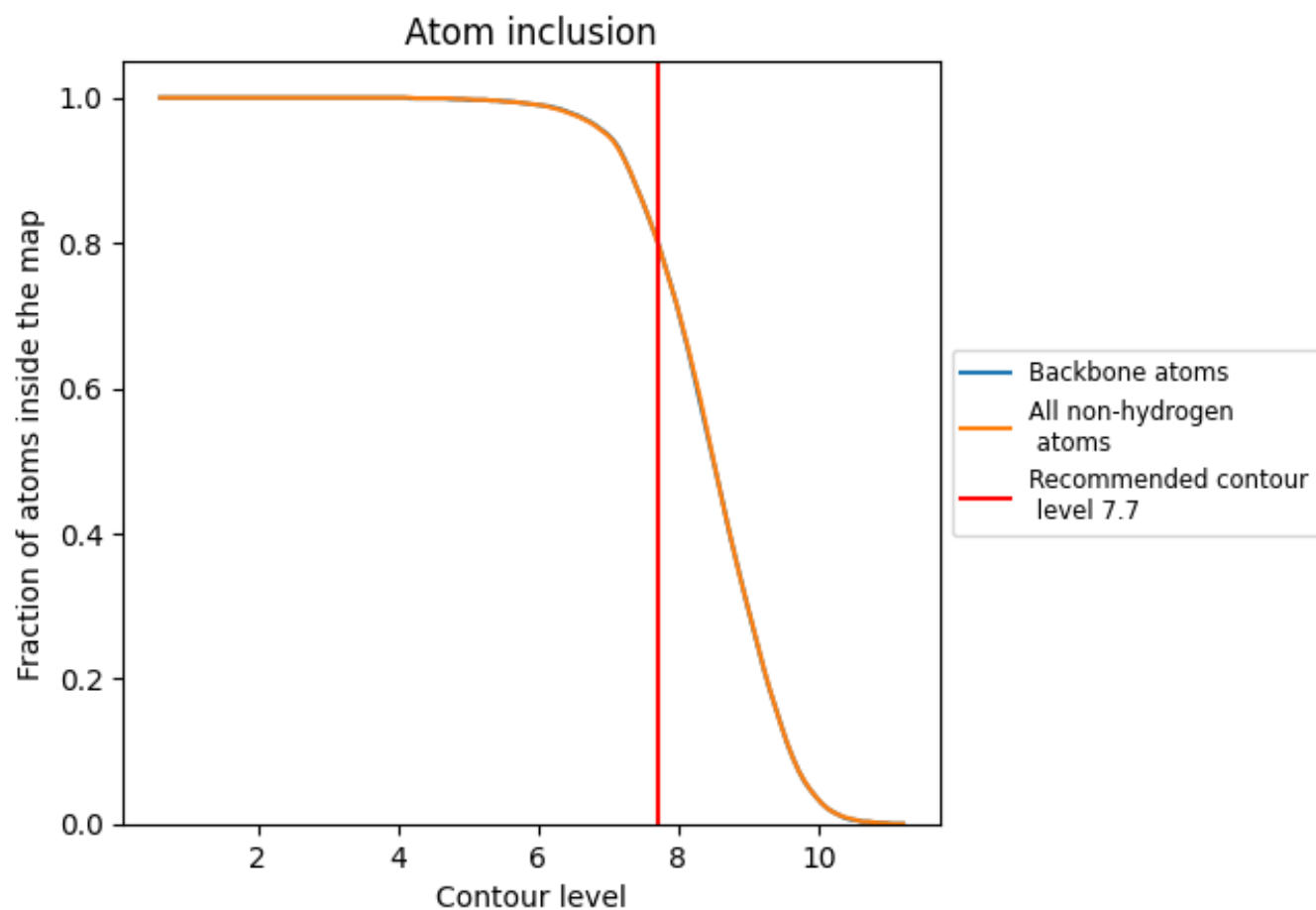


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

8.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (7.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.0310
A	 0.9100	 0.0020
B	 0.8240	 0.0350
C	 0.8190	 0.0260
D	 0.8450	 0.0330
E	 0.7930	 0.0410
F	 0.9100	 0.0440
G	 0.7630	 0.0290
H	 0.5930	 0.0220
I	 0.7420	 0.0330
J	 0.5350	 0.0230
K	 0.6750	 0.0070
L	 0.9410	 -0.0020
M	 0.9830	 0.0260
N	 0.6750	 0.0080
O	 0.3400	 -0.0010
P	 0.4350	 0.0070
Q	 0.5830	 0.0260
R	 0.6330	 0.0290
S	 0.5170	 -0.0040
T	 0.9940	 0.1120
U	 0.9040	 0.0650
V	 0.9620	 0.0560
W	 0.7100	 0.0510
a	 0.9020	 0.0010
b	 0.8240	 0.0320
c	 0.8200	 0.0270
d	 0.8480	 0.0330
e	 0.7900	 0.0440
f	 0.9150	 0.0400
g	 0.7690	 0.0230
h	 0.5760	 0.0290
i	 0.7340	 0.0280
j	 0.5040	 0.0230
k	 0.5500	 0.0090



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Chain	Atom inclusion	Q-score
l	 0.9430	 0.0110
m	 0.9890	 0.0270
n	 0.7160	 0.0010
o	 0.3430	 -0.0060
p	 0.3970	 -0.0040
q	 0.5720	 0.0130
r	 0.6350	 0.0240
s	 0.5310	 0.0040
t	 0.9950	 0.1110
u	 0.9120	 0.0700
v	 0.9700	 0.0610
w	 0.6890	 0.0370