



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 07:41 PM UTC

PDB ID : 5GAS / pdb_00005gas
EMDB ID : EMD-8017
Title : Thermus thermophilus V/A-ATPase, conformation 2
Authors : Schep, D.G.; Zhao, J.; Rubinstein, J.L.
Deposited on : 2016-02-05
Resolution : 9.50 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
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

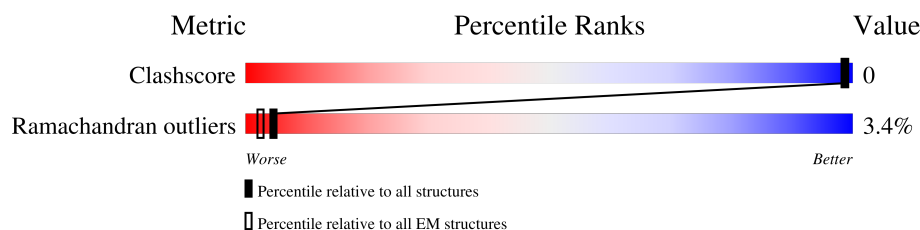
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



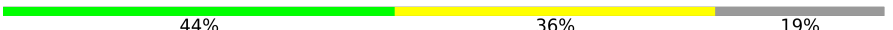
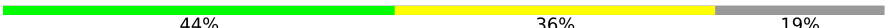
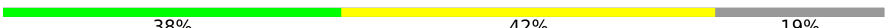
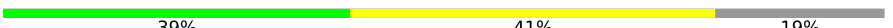
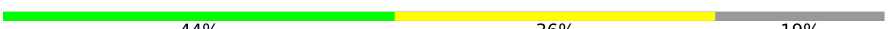
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	577	 57% 41% .
1	B	577	 58% 41% .
1	C	577	 55% 43% .
2	D	457	 53% 46% .
2	E	457	 58% 40% .
2	F	457	 59% 40% .
3	G	186	 55% 43% ...
3	H	186	 54% 44% ..
4	I	105	 57% 38% 5%
4	J	105	 62% 32% . 5%

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Mol	Chain	Length	Quality of chain
5	K	210	 55% 43% .
6	L	100	 58% 40% .
7	M	323	 57% 42% .
8	N	652	 52% 42% . 5%
9	O	99	 44% 36% 19%
9	P	99	 44% 36% 19%
9	Q	99	 37% 43% 19%
9	R	99	 46% 34% 19%
9	S	99	 38% 42% 19%
9	T	99	 36% 44% 19%
9	U	99	 39% 41% 19%
9	V	99	 34% 46% 19%
9	W	99	 46% 34% 19%
9	X	99	 42% 38% 19%
9	Y	99	 44% 36% 19%
9	Z	99	 43% 37% 19%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 23487 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 V-type ATP synthase alpha chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	577	Total	C	N	O	0	0
			2307	1154	577	576		
1	B	577	Total	C	N	O	0	0
			2307	1154	577	576		
1	C	577	Total	C	N	O	0	0
			2307	1154	577	576		

- Molecule 2 is a protein called V-type ATP synthase beta chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	D	457	Total	C	N	O	0	0
			1827	914	457	456		
2	E	457	Total	C	N	O	0	0
			1827	914	457	456		
2	F	457	Total	C	N	O	0	0
			1827	914	457	456		

- Molecule 3 is a protein called V-type ATP synthase subunit E.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	G	184	Total	C	N	O	0	0
			734	368	184	182		
3	H	184	Total	C	N	O	0	0
			734	368	184	182		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	134	MET	LEU	conflict	UNP P74901
G	171	MET	LEU	conflict	UNP P74901
G	178	MET	LEU	conflict	UNP P74901
H	134	MET	LEU	conflict	UNP P74901
H	171	MET	LEU	conflict	UNP P74901

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Chain	Residue	Modelled	Actual	Comment	Reference
H	178	MET	LEU	conflict	UNP P74901

- Molecule 4 is a protein called V-type ATPase subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	I	100	Total	C	N	O	0	0
			399	200	100	99		
4	J	100	Total	C	N	O	0	0
			399	200	100	99		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	16	GLY	-	insertion	UNP Q72J66
J	16	GLY	-	insertion	UNP Q72J66

- Molecule 5 is a protein called V-type ATP synthase subunit D.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	K	210	Total	C	N	O	0	0
			839	420	210	209		

- Molecule 6 is a protein called V-type ATP synthase subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	L	100	Total	C	N	O	0	0
			399	200	100	99		

- Molecule 7 is a protein called V-type ATP synthase subunit C.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	M	320	Total	C	N	O	0	0
			1279	640	320	319		

- Molecule 8 is a protein called Archaeal/vacuolar-type H⁺-ATPase subunit I.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	N	619	Total	C	N	O	0	0
			2474	1238	619	617		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	154	ARG	LYS	conflict	UNP H9ZQR4
N	164	ALA	VAL	conflict	UNP H9ZQR4
N	173	PRO	ALA	conflict	UNP H9ZQR4

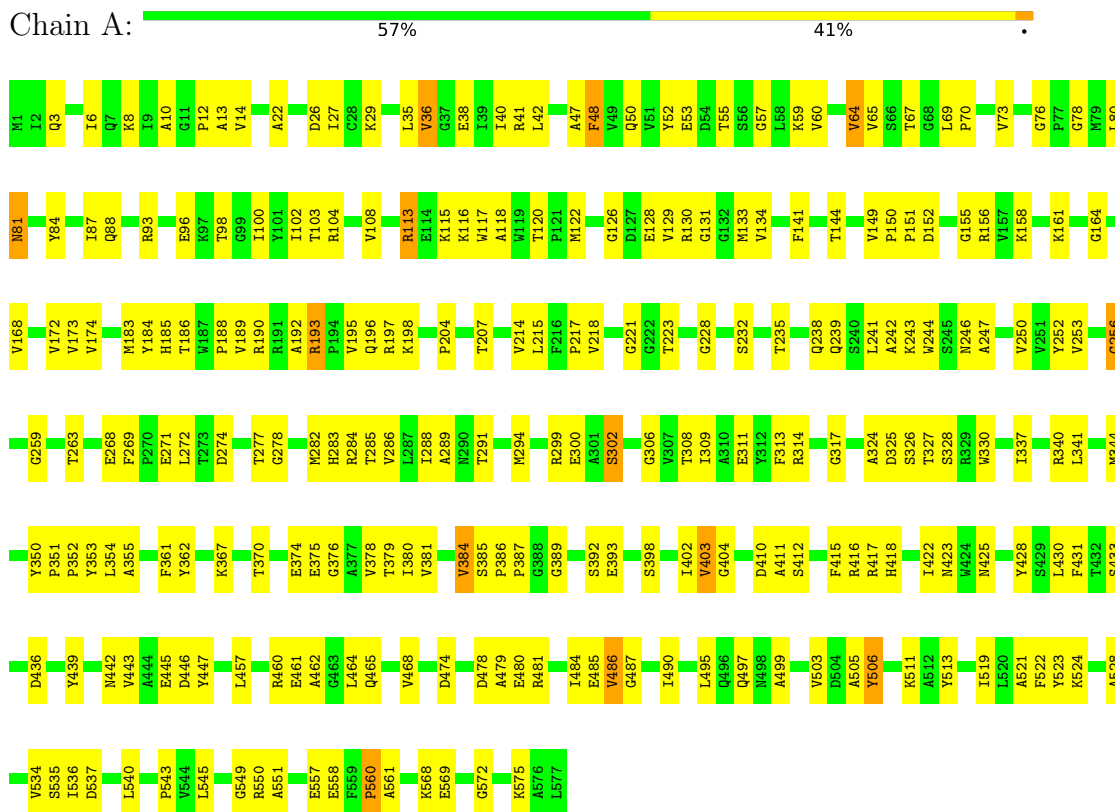
- Molecule 9 is a protein called Vacuolar type ATP synthase subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	O	80	Total 319	C 160	N 80	O 79	0	0
9	P	80	Total 319	C 160	N 80	O 79	0	0
9	Q	80	Total 319	C 160	N 80	O 79	0	0
9	R	80	Total 319	C 160	N 80	O 79	0	0
9	S	80	Total 319	C 160	N 80	O 79	0	0
9	T	80	Total 319	C 160	N 80	O 79	0	0
9	U	80	Total 319	C 160	N 80	O 79	0	0
9	V	80	Total 319	C 160	N 80	O 79	0	0
9	W	80	Total 319	C 160	N 80	O 79	0	0
9	X	80	Total 319	C 160	N 80	O 79	0	0
9	Y	80	Total 319	C 160	N 80	O 79	0	0
9	Z	80	Total 319	C 160	N 80	O 79	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: V-type ATP synthase alpha chain



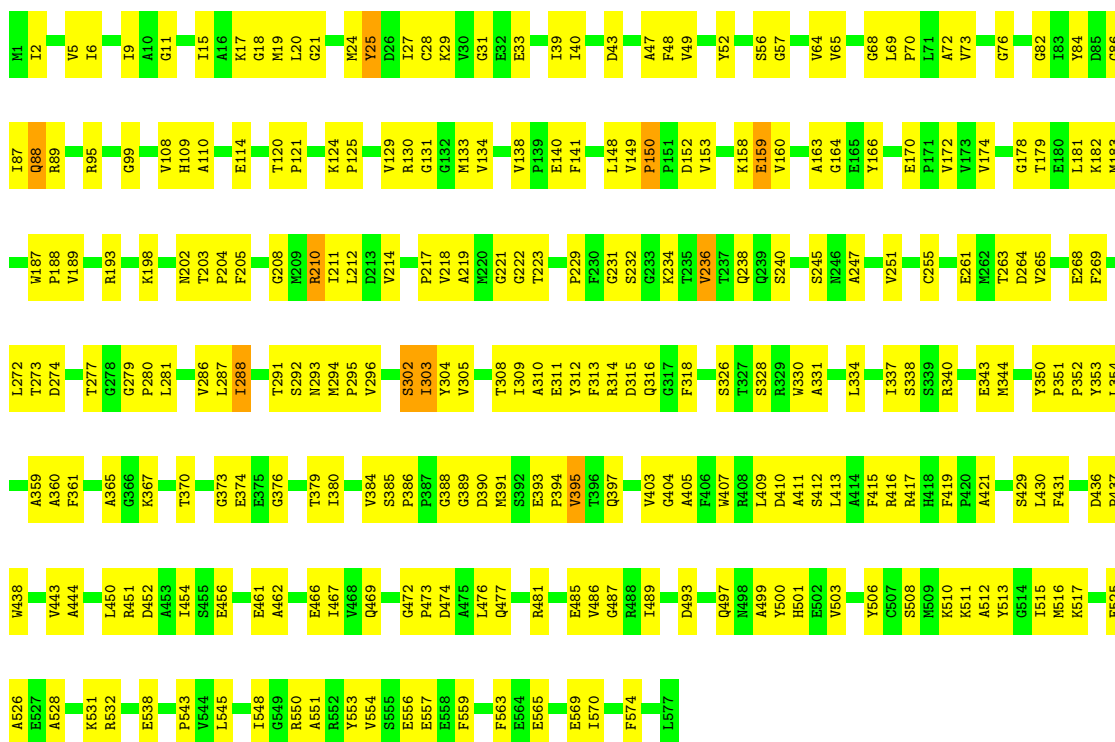
- Molecule 1: V-type ATP synthase alpha chain





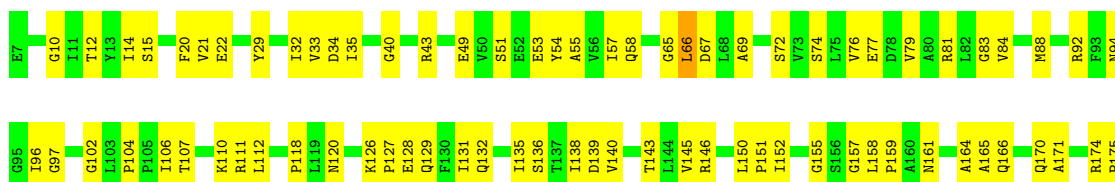
• Molecule 1: V-type ATP synthase alpha chain

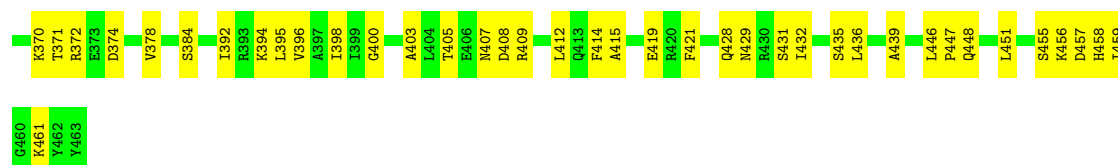
Chain C: 55% 43% .



• Molecule 2: V-type ATP synthase beta chain

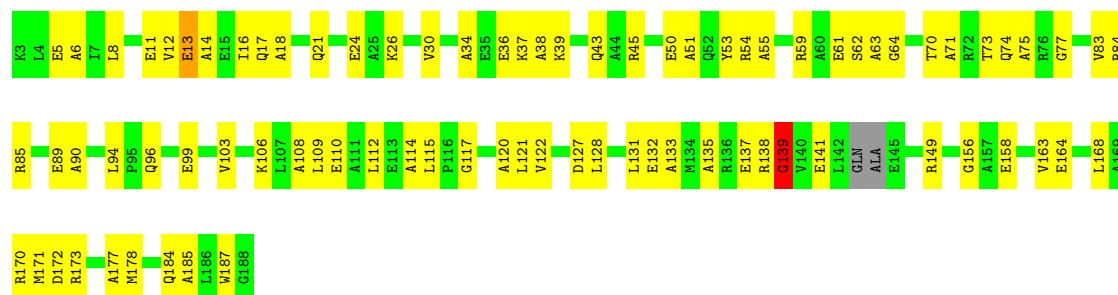
Chain D: 53% 46% .





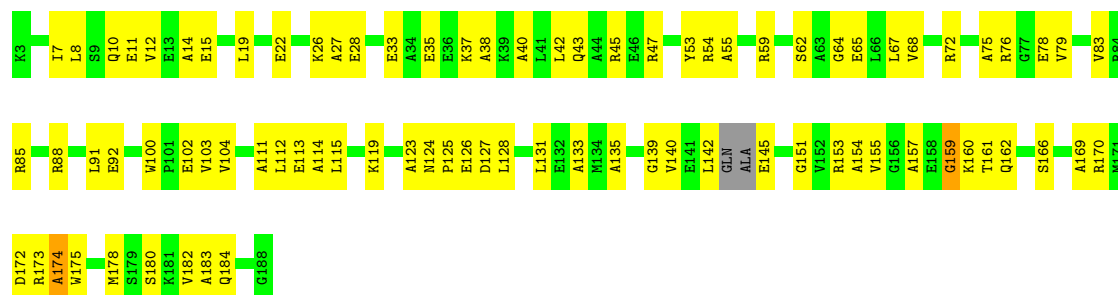
• Molecule 3: V-type ATP synthase subunit E

Chain G: 55% 43%



• Molecule 3: V-type ATP synthase subunit E

Chain H: 54% 44%



• Molecule 4: V-type ATPase subunit G

Chain I: 57% 38% 5%



• Molecule 4: V-type ATPase subunit G

Chain J: 62% 32% 5%



E117
V118
L119
P120

• Molecule 5: V-type ATP synthase subunit D

Chain K:  55% 43%

S2 S5 S6 P6 M9 Q13 Q17 Q18 L18 L19 L20 A21 Q22 V25 K30 K31 K32 D33 A34 L35 V36 F39 F40 G41 E45 A46 P47 E48 K51 K58 E59 A60 A63 A64 L64 L65 L66 A67 F70 F71 G72 F73 E74 V75 V76 A77 P84 P85 L86 E90 N95 V96 W97 P102 R103 T107 F108 P116 V117 G118 T119 P120 A121 E125 A126 S127 R128 E176 R177 F178 I179 Q180 L183 R188 R193 L194 K195 K198 E205 A206 E207 G210 G211

• Molecule 6: V-type ATP synthase subunit F

Chain L:  58% 40%

M1 A2 V3 I4 A5 D6 P7 A10 F13 R14 L15 L18 E19 A23 S24 S25 A34 A35 E27 E28 A29 L32 L33 E34 T35 L36 V37 E38 R39 A43 L44 V45 A46 A50 L51 L52 P55 E56 R57 E60 M63 R66 P69 N95 V70 L71 L72 A75 K78 E79 A80 F81 Q82 G83 M90 K96 T97 I98 G99 F100

• Molecule 7: V-type ATP synthase subunit C

Chain M:  57% 42%

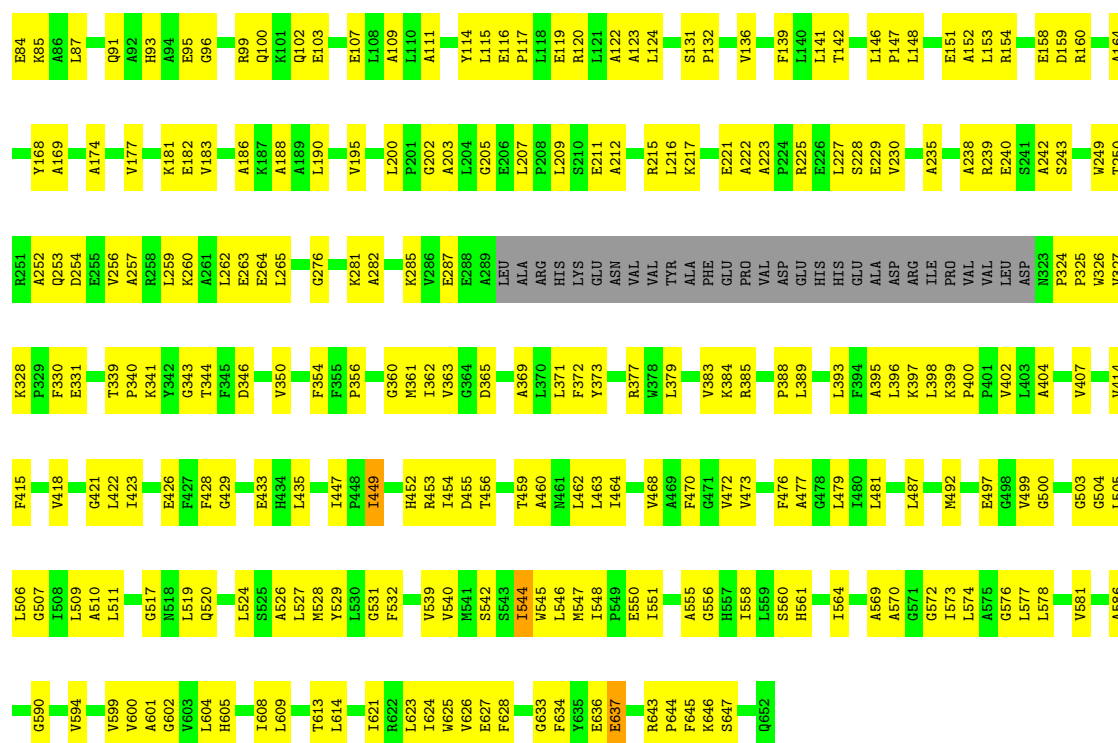
MET ALA D3 D4 F5 A6 Y7 L8 R11 V12 R13 V14 F24 F25 Q26 E27 F33 A34 D35 F36 E38 L39 Y45 G46 G47 A50 G53 P55 D56 R59 T64 Q65 L72 G78 A83 V84 L88 H94 N95 L96 Q97 A98 L99 R100 R101 A102 K103 P108 F109 E110 E111 V112 L113 P116 E121 E122 V123 W124 R125 Q131 D132 P133 A134 G135 G136 A137 A141 V142 P143 G144 H145 A148 V154 E157 L161 A162 R163 V164 E165 L168 A169 K170 R171 F172 F173 E174 D175 V176 A177 K178 L183 A187 L188 R189 D190 Y191 L192 A193 L194 E195 V196 D197 A198 E199 R202 A213 A216 F217 F218 L219 K220 G221 F224 V225 D226 R227 V228 R229 F230 A231 W234 Y238 A239 D242 E243 L244 S245 G246 T247 P248 F249 S250 G254 L258 K259 A260 L261 E262 R263 G264 C267 L270

K271 Q278 D279 L281 G282 V283 G284 L285 V286 K287 A288 Y289 W295 E296 A297 R301 A304 R305 R306 A307 Y308 L311 Q315 V316 E317 E318 V320 V321 C322 PRO

• Molecule 8: Archaeal/vacuolar-type H⁺-ATPase subunit I

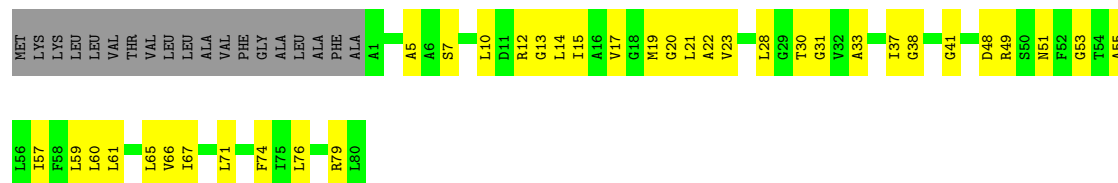
Chain N:  52% 42% 5%

MET ILE ALA PRO M1 V5 L6 A13 K14 E15 Q18 Q21 V25 T30 L31 R32 P33 E34 A35 L36 S37 A38 Y39 S42 A47 E48 R51 A54 A57 G58 A59 T62 L63 S64 L65 L66 L67 A70 E71 P72 P75 F76 P77 A82 A83



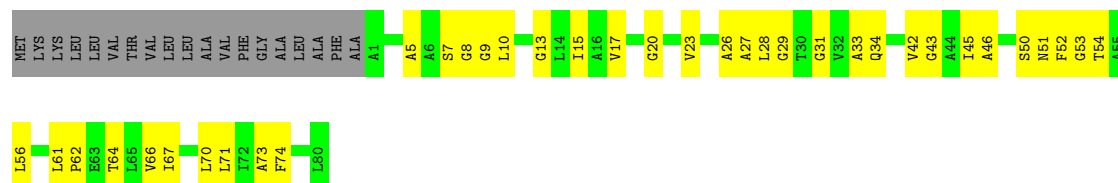
• Molecule 9: Vacuolar type ATP synthase subunit

Chain O: 44% 36% 19%



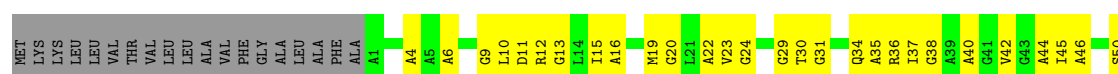
• Molecule 9: Vacuolar type ATP synthase subunit

Chain P: 44% 36% 19%



• Molecule 9: Vacuolar type ATP synthase subunit

Chain Q: 37% 43% 19%





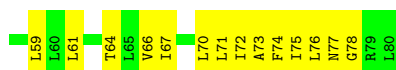
- Molecule 9: Vacuolar type ATP synthase subunit

Chain R: 46% 34% 19%



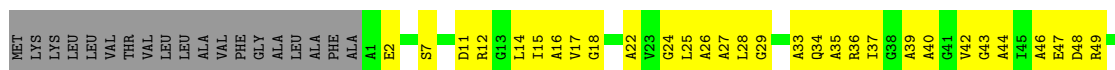
- Molecule 9: Vacuolar type ATP synthase subunit

Chain S: 38% 42% 19%



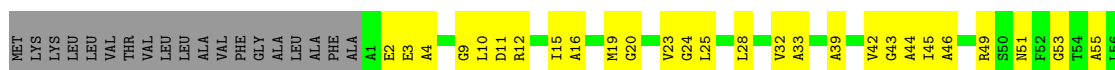
- Molecule 9: Vacuolar type ATP synthase subunit

Chain T: 36% 44% 19%



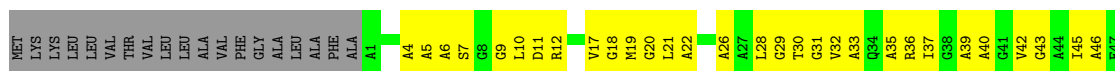
- Molecule 9: Vacuolar type ATP synthase subunit

Chain U: 39% 41% 19%



- Molecule 9: Vacuolar type ATP synthase subunit

Chain V: 34% 46% 19%





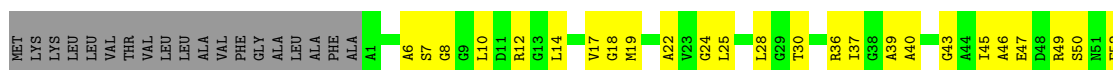
- Molecule 9: Vacuolar type ATP synthase subunit

Chain W: 46% 34% 19%



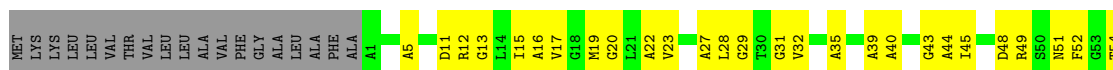
- Molecule 9: Vacuolar type ATP synthase subunit

Chain X: 42% 38% 19%



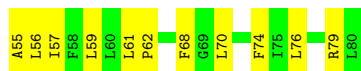
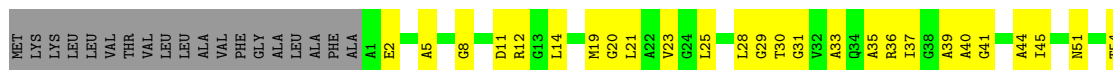
- Molecule 9: Vacuolar type ATP synthase subunit

Chain Y: 44% 36% 19%



- Molecule 9: Vacuolar type ATP synthase subunit

Chain Z: 43% 37% 19%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9721	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35.7	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	6000	Depositor
Magnification	34483	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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	2.50	117/2306 (5.1%)	2.86	222/2881 (7.7%)
1	B	2.54	112/2306 (4.9%)	2.85	225/2881 (7.8%)
1	C	2.60	139/2306 (6.0%)	2.86	227/2881 (7.9%)
2	D	2.54	100/1826 (5.5%)	2.89	193/2281 (8.5%)
2	E	2.52	88/1826 (4.8%)	2.79	174/2281 (7.6%)
2	F	2.50	83/1826 (4.5%)	2.88	185/2281 (8.1%)
3	G	2.57	33/732 (4.5%)	2.86	73/912 (8.0%)
3	H	2.58	42/732 (5.7%)	2.95	70/912 (7.7%)
4	I	2.43	18/398 (4.5%)	2.78	43/496 (8.7%)
4	J	2.33	12/398 (3.0%)	2.91	40/496 (8.1%)
5	K	2.53	45/838 (5.4%)	3.00	100/1046 (9.6%)
6	L	2.69	26/398 (6.5%)	2.79	29/496 (5.8%)
7	M	2.49	65/1278 (5.1%)	3.09	160/1596 (10.0%)
8	N	2.51	114/2472 (4.6%)	3.08	342/3087 (11.1%)
9	O	2.59	22/318 (6.9%)	3.09	41/396 (10.4%)
9	P	2.28	12/318 (3.8%)	3.25	45/396 (11.4%)
9	Q	2.70	20/318 (6.3%)	3.21	50/396 (12.6%)
9	R	2.45	11/318 (3.5%)	3.05	37/396 (9.3%)
9	S	2.61	19/318 (6.0%)	3.19	44/396 (11.1%)
9	T	2.49	14/318 (4.4%)	3.52	62/396 (15.7%)
9	U	2.61	15/318 (4.7%)	3.15	46/396 (11.6%)
9	V	2.69	20/318 (6.3%)	3.41	62/396 (15.7%)
9	W	2.43	12/318 (3.8%)	3.12	43/396 (10.9%)
9	X	2.53	19/318 (6.0%)	3.01	40/396 (10.1%)
9	Y	2.69	21/318 (6.6%)	3.09	43/396 (10.9%)
9	Z	2.52	17/318 (5.3%)	3.09	46/396 (11.6%)
All	All	2.53	1196/23458 (5.1%)	2.95	2642/29279 (9.0%)

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
1	B	0	1
3	G	0	1
7	M	0	1
All	All	0	3

The worst 5 of 1196 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	375	GLU	C-N	17.10	1.42	1.33
8	N	520	GLN	C-N	10.10	1.41	1.33
3	H	55	ALA	CA-C	-9.92	1.40	1.52
9	Y	15	ILE	CA-C	-9.74	1.40	1.52
2	E	454	ILE	CA-C	-9.73	1.40	1.52

The worst 5 of 2642 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	218	VAL	N-CA-C	-13.59	100.80	113.71
9	T	52	PHE	CA-C-N	13.45	135.09	120.03
9	T	52	PHE	C-N-CA	13.45	135.09	120.03
2	D	194	MET	N-CA-C	-13.25	97.22	114.31
7	M	45	TYR	CA-C-N	12.47	135.73	120.14

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	485	GLU	Mainchain
3	G	139	GLY	Peptide
7	M	3	ASP	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	A	2307	0	654	0	0
1	B	2307	0	654	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2307	0	654	0	0
2	D	1827	0	510	0	0
2	E	1827	0	510	1	0
2	F	1827	0	510	0	0
3	G	734	0	191	1	0
3	H	734	0	191	0	0
4	I	399	0	100	1	0
4	J	399	0	100	0	0
5	K	839	0	230	0	0
6	L	399	0	119	0	0
7	M	1279	0	357	0	0
8	N	2474	0	691	1	0
9	O	319	0	109	0	0
9	P	319	0	109	0	0
9	Q	319	0	109	0	0
9	R	319	0	109	0	0
9	S	319	0	109	0	0
9	T	319	0	109	0	0
9	U	319	0	109	0	0
9	V	319	0	109	0	0
9	W	319	0	109	0	0
9	X	319	0	109	0	0
9	Y	319	0	109	0	0
9	Z	319	0	109	0	0
All	All	23487	0	6779	3	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 0.

All (3) 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:I:21:GLY:HA3	8:N:30:THR:H	1.75	0.52
3:G:121:LEU:H	3:G:139:GLY:HA3	1.85	0.41
2:E:318:ASP:C	2:E:320:ASP:H	2.29	0.40

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	575/577 (100%)	477 (83%)	69 (12%)	29 (5%)	1	16
1	B	575/577 (100%)	491 (85%)	64 (11%)	20 (4%)	3	20
1	C	575/577 (100%)	473 (82%)	70 (12%)	32 (6%)	1	14
2	D	455/457 (100%)	375 (82%)	63 (14%)	17 (4%)	2	20
2	E	455/457 (100%)	365 (80%)	72 (16%)	18 (4%)	2	18
2	F	455/457 (100%)	361 (79%)	71 (16%)	23 (5%)	1	15
3	G	180/186 (97%)	159 (88%)	14 (8%)	7 (4%)	2	19
3	H	180/186 (97%)	161 (89%)	12 (7%)	7 (4%)	2	19
4	I	98/105 (93%)	96 (98%)	0	2 (2%)	6	31
4	J	98/105 (93%)	95 (97%)	2 (2%)	1 (1%)	12	49
5	K	208/210 (99%)	163 (78%)	34 (16%)	11 (5%)	1	15
6	L	98/100 (98%)	72 (74%)	19 (19%)	7 (7%)	1	11
7	M	318/323 (98%)	306 (96%)	11 (4%)	1 (0%)	36	72
8	N	615/652 (94%)	570 (93%)	34 (6%)	11 (2%)	6	34
9	O	78/99 (79%)	75 (96%)	3 (4%)	0	100	100
9	P	78/99 (79%)	73 (94%)	2 (3%)	3 (4%)	2	19
9	Q	78/99 (79%)	72 (92%)	6 (8%)	0	100	100
9	R	78/99 (79%)	75 (96%)	1 (1%)	2 (3%)	4	25
9	S	78/99 (79%)	74 (95%)	3 (4%)	1 (1%)	9	42
9	T	78/99 (79%)	76 (97%)	2 (3%)	0	100	100
9	U	78/99 (79%)	73 (94%)	4 (5%)	1 (1%)	9	42
9	V	78/99 (79%)	73 (94%)	3 (4%)	2 (3%)	4	25
9	W	78/99 (79%)	74 (95%)	4 (5%)	0	100	100
9	X	78/99 (79%)	74 (95%)	3 (4%)	1 (1%)	9	42
9	Y	78/99 (79%)	72 (92%)	6 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	Z	78/99 (79%)	72 (92%)	5 (6%)	1 (1%)	9	42
All	All	5821/6157 (94%)	5047 (87%)	577 (10%)	197 (3%)	4	21

5 of 197 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	417	ARG
1	B	85	ASP
1	B	326	SER
1	C	109	HIS
1	C	210	ARG

5.3.2 Protein sidechains [i](#)

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

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8017. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.