



wwPDB EM Model Validation Summary Report ⓘ

Mar 9, 2020 – 10:13 AM EDT

PDB ID : 6VQ7
EMDB ID : EMD-21318
Title : Mammalian V-ATPase from rat brain - composite model of rotational state 2 bound to ADP and SidK (built from focused refinement models)
Authors : Abbas, Y.M.; Rubinstein, J.L.
Deposited on : 2020-02-04
Resolution : 4.00 Å(reported)

This is a wwPDB EM Model Validation Summary Report for a publicly released PDB/EMDB 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

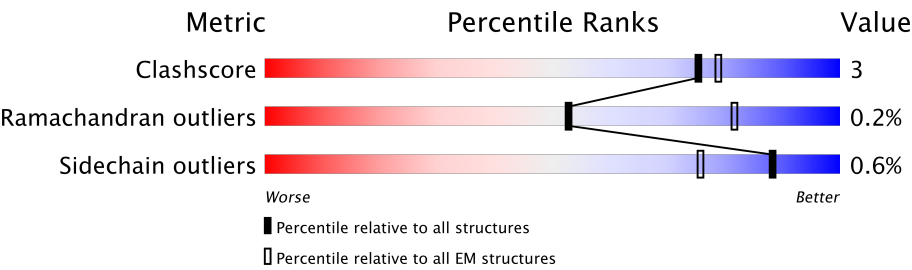
MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.8

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.00 Å.

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













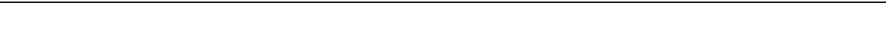

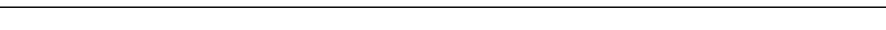
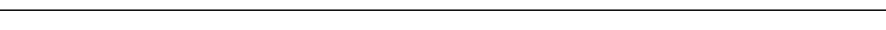
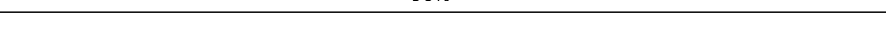

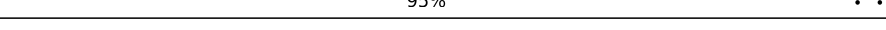
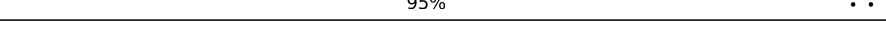
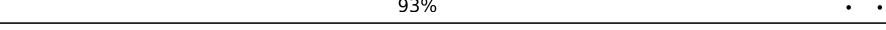
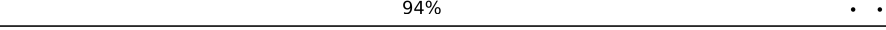
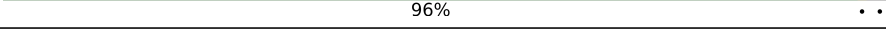
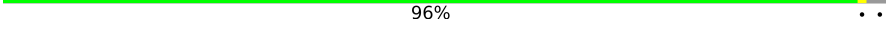
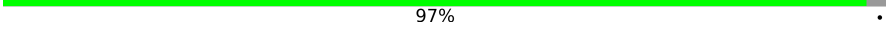
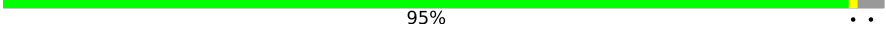
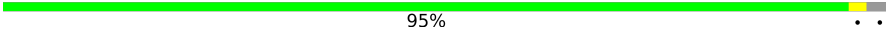
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

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 on 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	617	94% . .
1	B	617	93% . .
1	C	617	92% 5% .
2	D	511	86% . 10%
2	E	511	85% 5% 10%
2	F	511	86% . 10%
3	G	382	89% 5% 6%
4	H	247	75% 10% . 13%
5	I	226	91% 9%

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Mol	Chain	Length	Quality of chain
5	J	226	
5	K	226	
6	L	119	
7	M	118	
7	N	118	
7	O	118	
8	Q	301	
8	R	301	
8	S	301	
9	a	838	
10	b	205	
11	c	463	
12	d	351	
13	e	81	
14	f	98	
15	g	155	
15	h	155	
15	i	155	
15	j	155	
15	k	155	
15	l	155	
15	m	155	
15	n	155	
15	o	155	
16	p	350	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 62325 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 ATPase H⁺-transporting V1 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		
1	B	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		
1	C	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		

- Molecule 2 is a protein called V-type proton ATPase subunit B, brain isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	459	Total	C	N	O	S	0	0
			3595	2282	613	680	20		
2	E	459	Total	C	N	O	S	0	0
			3595	2282	613	680	20		
2	F	459	Total	C	N	O	S	0	0
			3595	2282	613	680	20		

- Molecule 3 is a protein called V-type proton ATPase subunit C 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	G	360	Total	C	N	O	0	0
			1790	1070	360	360		

- Molecule 4 is a protein called ATPase H⁺-transporting V1 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	214	Total	C	N	O	S	0	0
			1716	1086	310	315	5		

- Molecule 5 is a protein called V-type proton ATPase subunit E 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	225	Total	C	N	O	S	0	0
			1607	1005	296	299	7		
5	J	225	Total	C	N	O	S	0	0
			1607	1005	296	299	7		
5	K	225	Total	C	N	O	S	0	0
			1607	1005	296	299	7		

- Molecule 6 is a protein called V-type proton ATPase subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	110	Total	C	N	O	S	0	0
			866	548	154	163	1		

- Molecule 7 is a protein called V-type proton ATPase subunit G.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	114	Total	C	N	O	S	0	0
			714	426	147	138	3		
7	N	114	Total	C	N	O	S	0	0
			714	426	147	138	3		
7	O	114	Total	C	N	O	S	0	0
			714	426	147	138	3		

- Molecule 8 is a protein called Effector protein SidK.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	212	Total	C	N	O	S	0	0
			1722	1096	292	325	9		
8	R	232	Total	C	N	O	S	0	0
			1878	1197	316	354	11		
8	S	224	Total	C	N	O	S	0	0
			1824	1162	306	346	10		

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	0	GLY	-	expression tag	UNP Q5ZWW6
Q	279	ASP	-	expression tag	UNP Q5ZWW6
Q	280	TYR	-	expression tag	UNP Q5ZWW6
Q	281	LYS	-	expression tag	UNP Q5ZWW6
Q	282	ASP	-	expression tag	UNP Q5ZWW6
Q	283	HIS	-	expression tag	UNP Q5ZWW6
Q	284	ASP	-	expression tag	UNP Q5ZWW6

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	285	GLY	-	expression tag	UNP Q5ZWW6
Q	286	ASP	-	expression tag	UNP Q5ZWW6
Q	287	TYR	-	expression tag	UNP Q5ZWW6
Q	288	LYS	-	expression tag	UNP Q5ZWW6
Q	289	ASP	-	expression tag	UNP Q5ZWW6
Q	290	HIS	-	expression tag	UNP Q5ZWW6
Q	291	ASP	-	expression tag	UNP Q5ZWW6
Q	292	ILE	-	expression tag	UNP Q5ZWW6
Q	293	ASP	-	expression tag	UNP Q5ZWW6
Q	294	TYR	-	expression tag	UNP Q5ZWW6
Q	295	LYS	-	expression tag	UNP Q5ZWW6
Q	296	ASP	-	expression tag	UNP Q5ZWW6
Q	297	ASP	-	expression tag	UNP Q5ZWW6
Q	298	ASP	-	expression tag	UNP Q5ZWW6
Q	299	ASP	-	expression tag	UNP Q5ZWW6
Q	300	LYS	-	expression tag	UNP Q5ZWW6
R	0	GLY	-	expression tag	UNP Q5ZWW6
R	279	ASP	-	expression tag	UNP Q5ZWW6
R	280	TYR	-	expression tag	UNP Q5ZWW6
R	281	LYS	-	expression tag	UNP Q5ZWW6
R	282	ASP	-	expression tag	UNP Q5ZWW6
R	283	HIS	-	expression tag	UNP Q5ZWW6
R	284	ASP	-	expression tag	UNP Q5ZWW6
R	285	GLY	-	expression tag	UNP Q5ZWW6
R	286	ASP	-	expression tag	UNP Q5ZWW6
R	287	TYR	-	expression tag	UNP Q5ZWW6
R	288	LYS	-	expression tag	UNP Q5ZWW6
R	289	ASP	-	expression tag	UNP Q5ZWW6
R	290	HIS	-	expression tag	UNP Q5ZWW6
R	291	ASP	-	expression tag	UNP Q5ZWW6
R	292	ILE	-	expression tag	UNP Q5ZWW6
R	293	ASP	-	expression tag	UNP Q5ZWW6
R	294	TYR	-	expression tag	UNP Q5ZWW6
R	295	LYS	-	expression tag	UNP Q5ZWW6
R	296	ASP	-	expression tag	UNP Q5ZWW6
R	297	ASP	-	expression tag	UNP Q5ZWW6
R	298	ASP	-	expression tag	UNP Q5ZWW6
R	299	ASP	-	expression tag	UNP Q5ZWW6
R	300	LYS	-	expression tag	UNP Q5ZWW6
S	0	GLY	-	expression tag	UNP Q5ZWW6
S	279	ASP	-	expression tag	UNP Q5ZWW6
S	280	TYR	-	expression tag	UNP Q5ZWW6

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Chain	Residue	Modelled	Actual	Comment	Reference
S	281	LYS	-	expression tag	UNP Q5ZWW6
S	282	ASP	-	expression tag	UNP Q5ZWW6
S	283	HIS	-	expression tag	UNP Q5ZWW6
S	284	ASP	-	expression tag	UNP Q5ZWW6
S	285	GLY	-	expression tag	UNP Q5ZWW6
S	286	ASP	-	expression tag	UNP Q5ZWW6
S	287	TYR	-	expression tag	UNP Q5ZWW6
S	288	LYS	-	expression tag	UNP Q5ZWW6
S	289	ASP	-	expression tag	UNP Q5ZWW6
S	290	HIS	-	expression tag	UNP Q5ZWW6
S	291	ASP	-	expression tag	UNP Q5ZWW6
S	292	ILE	-	expression tag	UNP Q5ZWW6
S	293	ASP	-	expression tag	UNP Q5ZWW6
S	294	TYR	-	expression tag	UNP Q5ZWW6
S	295	LYS	-	expression tag	UNP Q5ZWW6
S	296	ASP	-	expression tag	UNP Q5ZWW6
S	297	ASP	-	expression tag	UNP Q5ZWW6
S	298	ASP	-	expression tag	UNP Q5ZWW6
S	299	ASP	-	expression tag	UNP Q5ZWW6
S	300	LYS	-	expression tag	UNP Q5ZWW6

- Molecule 9 is a protein called V-type proton ATPase 116 kDa subunit a isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	750	Total	C	N	O	S	0	0
			5009	3241	864	883	21		

- Molecule 10 is a protein called ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA_a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b	203	Total	C	N	O	S	0	0
			1503	996	237	259	11		

- Molecule 11 is a protein called V-type proton ATPase subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	c	41	Total	C	N	O	S	0	0
			337	228	51	54	4		

- Molecule 12 is a protein called V-type proton ATPase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	350	Total	C	N	O	S	0	0
			2833	1829	460	530	14		

- Molecule 13 is a protein called V-type proton ATPase subunit e 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	e	78	Total	C	N	O	S	0	0
			622	428	98	93	3		

- Molecule 14 is a protein called Ribonuclease K.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	f	84	Total	C	N	O	S	0	0
			452	282	85	85			

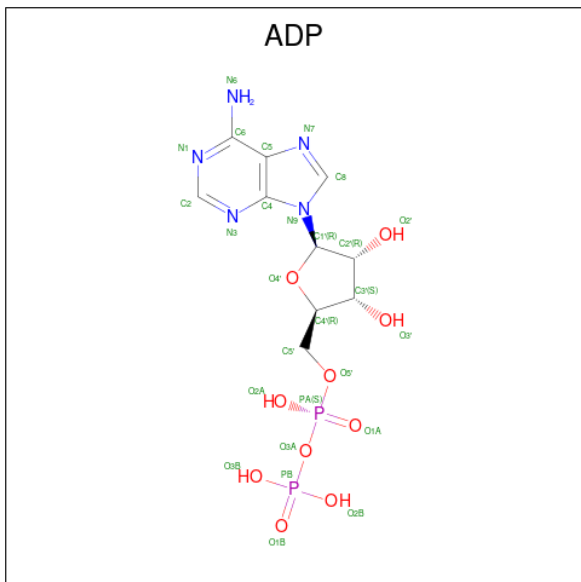
- Molecule 15 is a protein called V-type proton ATPase 16 kDa proteolipid subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	g	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	h	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	i	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	j	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	k	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	l	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	m	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	n	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		
15	o	150	Total	C	N	O	S	0	0
			1068	699	171	190	8		

- Molecule 16 is a protein called Renin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	52	Total	C	N	O	S	0	0
			432	290	63	76	3		

- Molecule 17 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

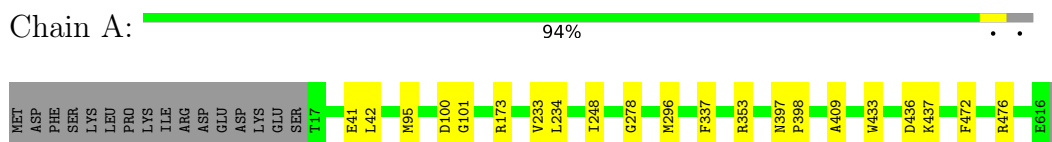
- Molecule 18 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
18	B	1	Total	Mg	0
			1	1	

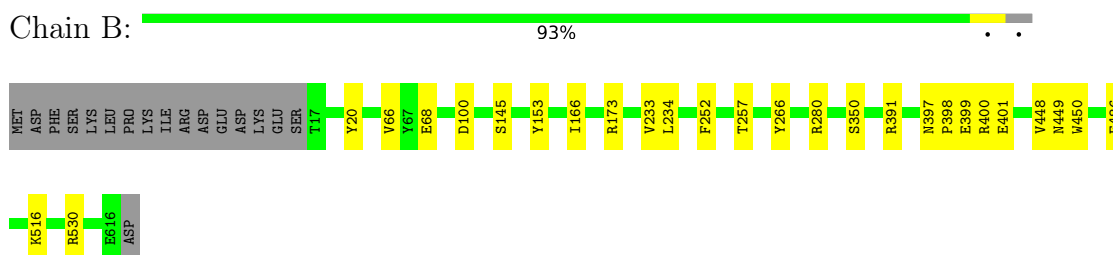
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

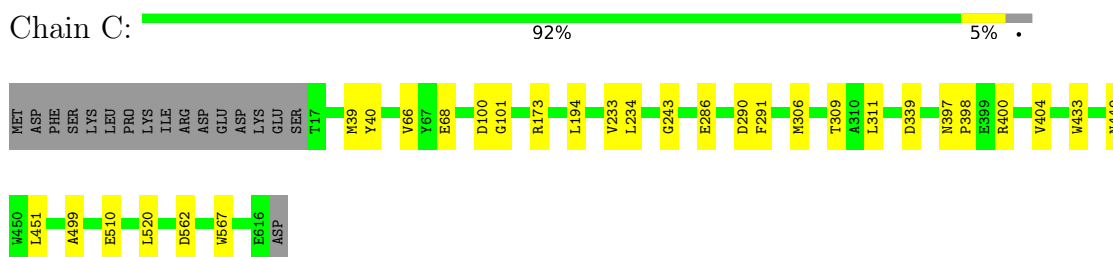
- Molecule 1: ATPase H⁺-transporting V1 subunit A



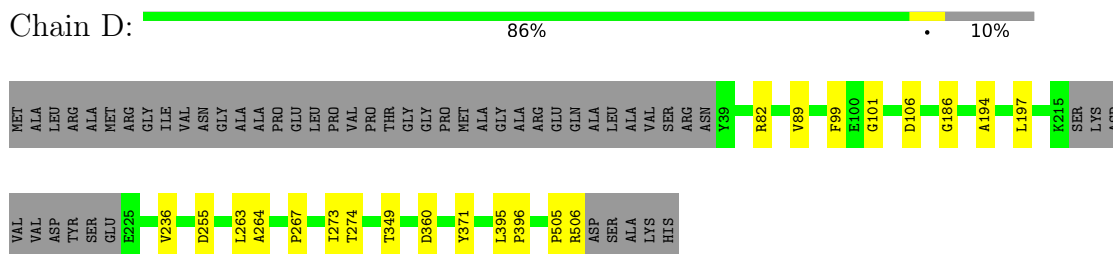
- Molecule 1: ATPase H⁺-transporting V1 subunit A




- Molecule 1: ATPase H⁺-transporting V1 subunit A

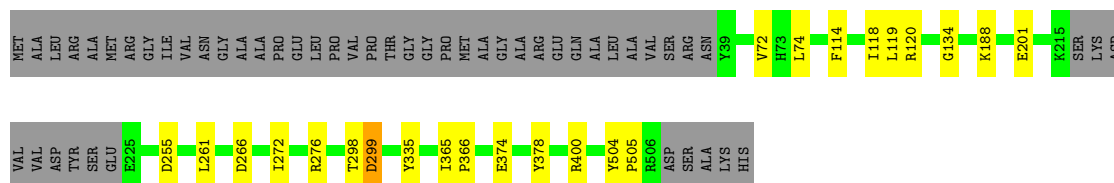


- Molecule 2: V-type proton ATPase subunit B, brain isoform



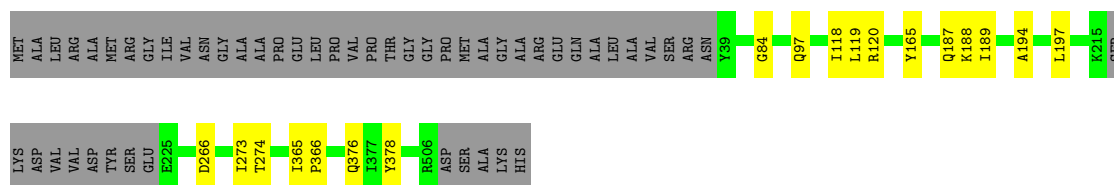
- Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain E:  85% 5% 10%




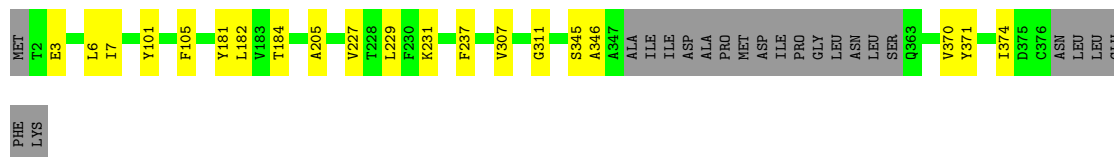
- Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain F:  86% 10%




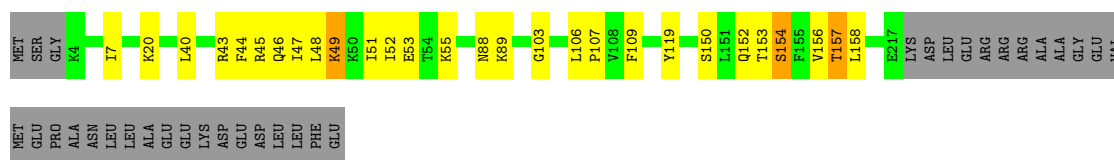
- Molecule 3: V-type proton ATPase subunit C 1

Chain G:  89% 5% 6%




- Molecule 4: ATPase H⁺-transporting V1 subunit D

Chain H:  75% 10% 13%



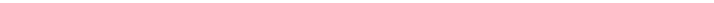
- Molecule 5: V-type proton ATPase subunit E 1

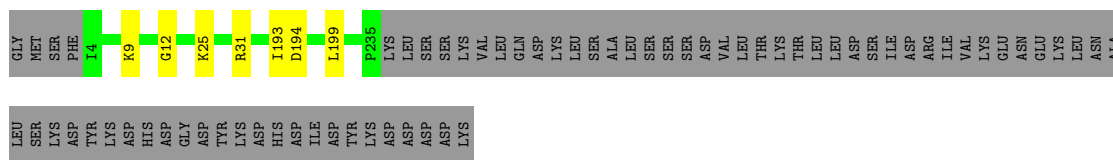
Chain I:  91% 9%



- Molecule 5: V-type proton ATPase subunit E 1

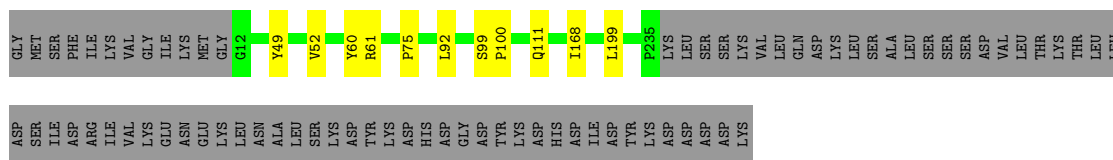
Chain J:  92% 7%

Chain R:  75% . 23%



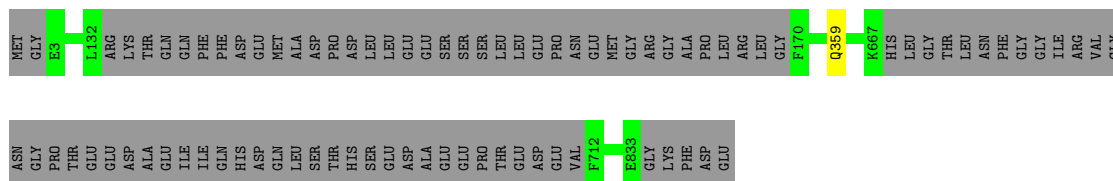
- Molecule 8: Effector protein SidK

Chain S: 71% . 26%



- Molecule 9: V-type proton ATPase 116 kDa subunit a isoform 1

Chain a: 89% 11%



- Molecule 10: ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA a

Chain b: 98%



- Molecule 11: V-type proton ATPase subunit S1

Chain c: 9% 91%



ALA MET LEU SER SER LEU THR TYR GLU PRO PHE LEU PHE GLY ALA THR VAL THR PHE LEU PHE THR ILE LEU ALA SER ARG PHE TYR PRO VAL MET SER ALA ARG TYR TRP PHE THR MET GLU ARG LEU LEU HIS THR ASN GLY SER VAL ALA HIS PHE ASN VAL SER GLN VAL THR GLY PRO SER ILE

TYR SER PHE HIS CYS GLU TYR VAL SER SER SER LYS LYS GLY SER LEU VAL THR ASN VAL PRO SER LEU TRP MET THR HIS ASN PHE GLN ILE THR MET ALA PHE ASN VAL THR GLY SER GLN PHE SER TYR VAL ALA HIS PHE ASP CYS R412 R448 R452 LYS GLY PRO SER THR

ILE THR LEU THR GLN ILE VAL

• Molecule 12: V-type proton ATPase subunit

Chain d:  99%


MET S2 K24 Q119 F353

• Molecule 13: V-type proton ATPase subunit e 2

Chain e:  96%

MET THR A3 W50 GLU

• Molecule 14: Ribonuclease K

Chain f:  86% 14%

MET ALA SER LEU L5 S37 ALA VAL L40 N50 LYS ARG GLU TYR MET VAL ARG

• Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain g:  95%


MET ALA ASP ILE LYS M6 T65 E139 L143 K155

• Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain h:  95%

MET ALA ASP ILE LYS M6 Y10 L143 K155

• Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain i:  93%

MET ALA ASP ILE LYS M6 M61 L135 E139 V140 L141 G142 L143 K155

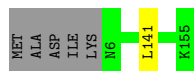
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:  94% ..



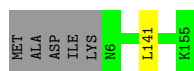
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain k:  96% ..



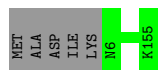
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain l:  96% ..



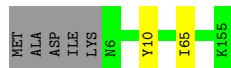
- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain m:  97% .



- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain n:  95% ..



- Molecule 15: V-type proton ATPase 16 kDa proteolipid subunit

Chain o:  95% ..



- Molecule 16: Renin receptor

Chain p:  15% 85%



ARG	LEU	ASP	THR	GLU	TRP
	VAL	LEU	PRO	THR	GLY
MET	ASP	LEU	PRO	PRO	LEU
ASP	ALA	PHE	VAL	VAL	ALA
	LEU	LEU	VAL	LEU	VAL
	GLN	SER	LEU	GLN	GLY
	LYS	GLU	GLU	ALA	LEU
	PHE	LEU	GLN	LEU	ASN
	ALA	GLN	ALA	ALA	LEU
	ASP	VAL	PRO	PRO	PHE
	ASP	LEU	SER	SER	HIS
	MET	HIS	GLU	GLU	ARG
	TYR	ASP	GLU	PRO	ARG
	SER	ILE	ARG	VAL	ALA
	LEU	SER	VAL	VAL	ALA
	TYR	SER	TYR	THR	THR
	GLY	LEU	MET	LEU	ILE
	GLY	LEU	VAL	VAL	MET
	ASN	SER	GLY	GLY	VAL
	ALA	ARG	THR	LYS	THR
	VAL	HIS	ALA	ALA	VAL
	VAL	HIS	LYS	ASN	LYS
	GLU	HIS	SER	GLY	GLY
	LEU	LEU	VAL	VAL	VAL
	VAL	ALA	PHE	PHE	ASP
	THR	LYS	GLU	GLU	LYS
	LYS	HIS	LEU	LEU	LEU
	SER	SER	SER	LEU	ALA
	PHE	PRO	VAL	VAL	LEU
	ASP	ASP	THR	THR	PRO
	THR	LEU	THR	GLY	GLY
	SER	TYR	ARG	ARG	SER
	LEU	SER	GLN	LEU	VAL
	VAL	LEU	LEU	LEU	ILE
	ARG	GLU	ARG	GLU	SER
	LYS	LEU	ASN	ASN	ASN
	SER	ALA	ASN	GLN	ALA
	ARG	GLY	VAL	VAL	VAL
	THR	LEU	VAL	SER	LEU
	ILE	ASP	PHE	ASN	ASP
	LEU	GLU	GLU	GLN	THR
	GLU	LEU	ASN	ASN	ASN
	GLU	LEU	ASN	ASN	ASN
	THR	GLY	SER	SER	THR
	ASN	TYR	ASN	LEU	LEU
	THR	GLU	LEU	LEU	THR
	GLN	ASP	PRO	LEU	VAL
	SER	SER	LEU	ALA	ALA
	ASN	GLN	ASN	ASN	ASN
	P292	GLN	SER	SER	THR
	H300	PHE	LEU	LEU	ILE
	T343	ARG	SER	ARG	HIS
	ASN	ALA	ASN	LEU	SER
	GLN	SER	ASN	ASN	PHE
	TYR	ARG	GLU	GLY	SER
	ILE	THR	VAL	VAL	GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	74789	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 ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.72	0/4746	0.53	0/6425
1	B	0.72	0/4746	0.53	0/6425
1	C	0.73	1/4746 (0.0%)	0.55	0/6425
2	D	0.70	0/3666	0.53	0/4967
2	E	0.70	0/3666	0.52	0/4967
2	F	0.68	0/3666	0.52	0/4967
3	G	0.38	0/1788	0.67	0/2494
4	H	0.81	0/1733	0.58	0/2319
5	I	0.58	0/1619	0.52	0/2192
5	J	0.58	0/1619	0.53	0/2192
5	K	0.57	0/1619	0.54	0/2192
6	L	0.80	0/880	0.75	0/1189
7	M	0.53	0/717	0.51	0/980
7	N	0.53	0/717	0.52	0/980
7	O	0.54	0/717	0.53	0/980
8	Q	0.69	0/1754	0.49	0/2362
8	R	0.69	0/1912	0.51	0/2575
8	S	0.70	0/1858	0.51	0/2505
9	a	0.50	0/5117	0.55	0/7008
10	b	0.51	0/1537	0.49	0/2088
11	c	0.53	0/347	0.56	0/466
12	d	0.73	0/2899	0.53	0/3927
13	e	0.46	0/646	0.46	0/889
14	f	0.40	0/459	0.49	0/635
15	g	0.50	0/1083	0.53	0/1466
15	h	0.48	0/1083	0.53	0/1466
15	i	0.49	0/1083	0.52	0/1466
15	j	0.48	0/1083	0.51	0/1466
15	k	0.49	0/1083	0.53	0/1466
15	l	0.48	0/1083	0.52	0/1466
15	m	0.53	0/1083	0.60	0/1466
15	n	0.47	0/1083	0.51	0/1466

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
15	o	0.49	0/1083	0.51	0/1466
16	p	0.50	0/445	0.60	0/609
All	All	0.63	1/63366 (0.0%)	0.54	0/85952

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	290	ASP	C-N	-5.22	1.22	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4651	0	4644	14	0
1	B	4651	0	4644	16	0
1	C	4651	0	4643	20	0
2	D	3595	0	3602	15	0
2	E	3595	0	3602	14	0
2	F	3595	0	3602	11	0
3	G	1790	0	794	12	0
4	H	1716	0	1817	41	0
5	I	1607	0	1516	16	0
5	J	1607	0	1516	14	0
5	K	1607	0	1516	24	0
6	L	866	0	865	12	0
7	M	714	0	551	6	0
7	N	714	0	551	3	0
7	O	714	0	551	13	0
8	Q	1722	0	1733	6	0
8	R	1878	0	1898	5	0
8	S	1824	0	1835	6	0
9	a	5009	0	4055	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	b	1503	0	1551	0	0
11	c	337	0	338	0	0
12	d	2833	0	2770	0	0
13	e	622	0	639	0	0
14	f	452	0	240	0	0
15	g	1068	0	1136	0	0
15	h	1068	0	1136	0	0
15	i	1068	0	1136	0	0
15	j	1068	0	1136	0	0
15	k	1068	0	1136	0	0
15	l	1068	0	1136	0	0
15	m	1068	0	1136	0	0
15	n	1068	0	1136	0	0
15	o	1068	0	1136	0	0
16	p	432	0	428	0	0
17	B	27	0	12	1	0
18	B	1	0	0	0	0
All	All	62325	0	60137	207	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 3.

The worst 5 of 207 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)
3:G:3:GLU:HA	3:G:374:ILE:O	1.47	1.13
4:H:45:ARG:HA	4:H:48:LEU:HD12	1.37	1.06
3:G:346:ALA:HB2	5:J:2:ALA:HB1	1.39	1.02
1:C:499:ALA:CB	4:H:103:GLY:HA2	1.94	0.96
3:G:345:SER:CB	5:J:4:SER:CB	2.47	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	598/617 (97%)	574 (96%)	23 (4%)	1 (0%)	49	84
1	B	598/617 (97%)	573 (96%)	24 (4%)	1 (0%)	49	84
1	C	598/617 (97%)	579 (97%)	19 (3%)	0	100	100
2	D	455/511 (89%)	443 (97%)	12 (3%)	0	100	100
2	E	455/511 (89%)	443 (97%)	9 (2%)	3 (1%)	24	65
2	F	455/511 (89%)	441 (97%)	12 (3%)	2 (0%)	36	76
3	G	356/382 (93%)	355 (100%)	1 (0%)	0	100	100
4	H	212/247 (86%)	207 (98%)	5 (2%)	0	100	100
5	I	223/226 (99%)	221 (99%)	2 (1%)	0	100	100
5	J	223/226 (99%)	221 (99%)	2 (1%)	0	100	100
5	K	223/226 (99%)	223 (100%)	0	0	100	100
6	L	108/119 (91%)	101 (94%)	5 (5%)	2 (2%)	9	46
7	M	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
7	N	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
7	O	112/118 (95%)	112 (100%)	0	0	100	100
8	Q	210/301 (70%)	204 (97%)	6 (3%)	0	100	100
8	R	230/301 (76%)	223 (97%)	6 (3%)	1 (0%)	36	76
8	S	222/301 (74%)	215 (97%)	6 (3%)	1 (0%)	31	72
9	a	744/838 (89%)	722 (97%)	21 (3%)	1 (0%)	53	87
10	b	201/205 (98%)	199 (99%)	2 (1%)	0	100	100
11	c	39/463 (8%)	39 (100%)	0	0	100	100
12	d	348/351 (99%)	330 (95%)	17 (5%)	1 (0%)	43	80
13	e	76/81 (94%)	74 (97%)	2 (3%)	0	100	100
14	f	80/98 (82%)	77 (96%)	3 (4%)	0	100	100
15	g	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	h	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	24	65
15	i	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	j	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	k	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
15	l	148/155 (96%)	146 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	m	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
15	n	148/155 (96%)	144 (97%)	3 (2%)	1 (1%)	24	65
15	o	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	24	65
16	p	50/350 (14%)	47 (94%)	2 (4%)	1 (2%)	8	45
All	All	8372/9848 (85%)	8149 (97%)	206 (2%)	17 (0%)	53	84

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	p	300	ASN
2	E	299	ASP
2	F	119	LEU
15	n	10	TYR
15	o	10	TYR

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	507/524 (97%)	505 (100%)	2 (0%)	92	96
1	B	507/524 (97%)	505 (100%)	2 (0%)	92	96
1	C	507/524 (97%)	506 (100%)	1 (0%)	94	97
2	D	393/431 (91%)	393 (100%)	0	100	100
2	E	393/431 (91%)	392 (100%)	1 (0%)	93	96
2	F	393/431 (91%)	392 (100%)	1 (0%)	93	96
4	H	183/212 (86%)	180 (98%)	3 (2%)	65	84
5	I	141/198 (71%)	141 (100%)	0	100	100
5	J	141/198 (71%)	141 (100%)	0	100	100
5	K	141/198 (71%)	141 (100%)	0	100	100
6	L	92/100 (92%)	92 (100%)	0	100	100
7	M	43/100 (43%)	43 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	N	43/100 (43%)	43 (100%)	0	100	100
7	O	43/100 (43%)	42 (98%)	1 (2%)	53	77
8	Q	191/274 (70%)	191 (100%)	0	100	100
8	R	208/274 (76%)	208 (100%)	0	100	100
8	S	203/274 (74%)	203 (100%)	0	100	100
9	a	354/743 (48%)	354 (100%)	0	100	100
10	b	156/158 (99%)	154 (99%)	2 (1%)	71	86
11	c	36/395 (9%)	35 (97%)	1 (3%)	47	72
12	d	305/306 (100%)	304 (100%)	1 (0%)	93	96
13	e	64/68 (94%)	64 (100%)	0	100	100
14	f	8/83 (10%)	8 (100%)	0	100	100
15	g	109/113 (96%)	106 (97%)	3 (3%)	47	72
15	h	109/113 (96%)	108 (99%)	1 (1%)	81	91
15	i	109/113 (96%)	103 (94%)	6 (6%)	24	57
15	j	109/113 (96%)	105 (96%)	4 (4%)	37	67
15	k	109/113 (96%)	108 (99%)	1 (1%)	81	91
15	l	109/113 (96%)	108 (99%)	1 (1%)	81	91
15	m	109/113 (96%)	109 (100%)	0	100	100
15	n	109/113 (96%)	108 (99%)	1 (1%)	81	91
15	o	109/113 (96%)	107 (98%)	2 (2%)	62	83
16	p	47/313 (15%)	47 (100%)	0	100	100
All	All	6080/7976 (76%)	6046 (99%)	34 (1%)	88	94

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

Mol	Chain	Res	Type
15	g	65	ILE
15	i	61	MET
15	n	65	ILE
15	g	143	LEU
2	F	376	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	181	ASN
4	H	137	ASN
9	a	762	HIS
1	C	268	ASN
9	a	548	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
17	ADP	B	701	18	24,29,29	0.67	0	25,45,45	0.73	1 (4%)

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
17	ADP	B	701	18	-	4/12/32/32	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
17	B	701	ADP	C5-C6-N6	2.16	123.78	120.38

There are no chirality outliers.

All (4) torsion outliers are listed below:

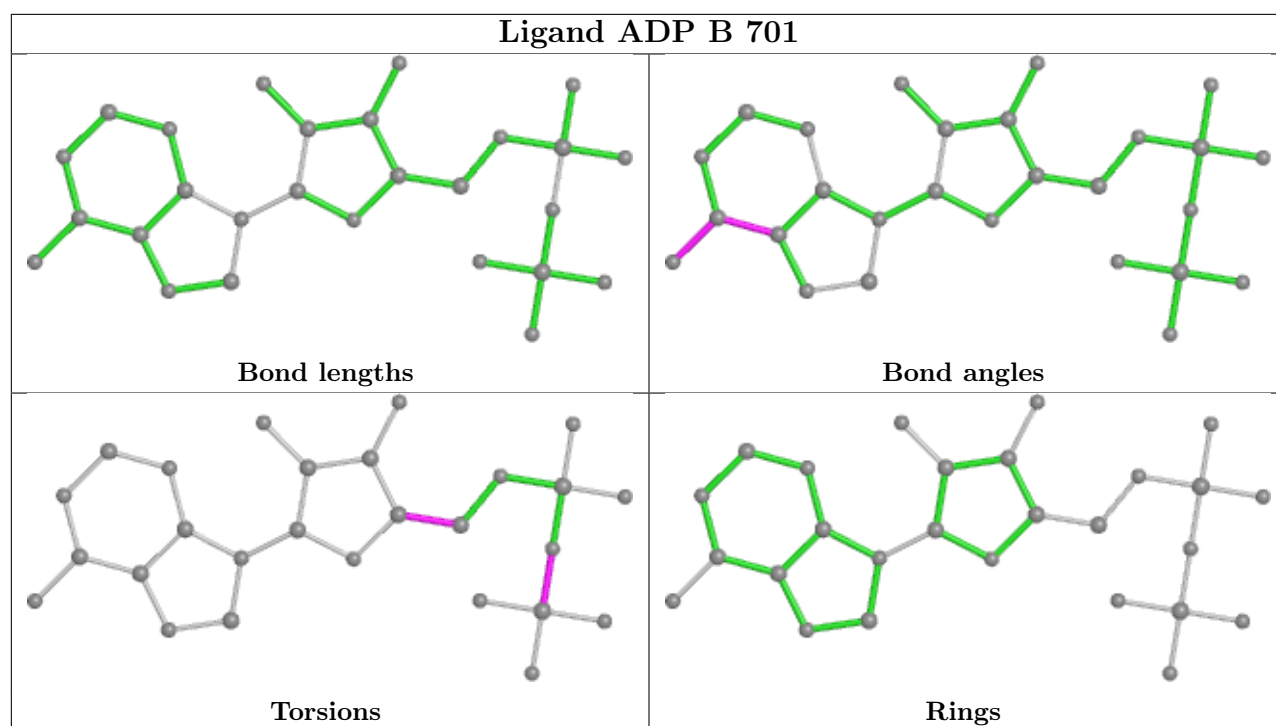
Mol	Chain	Res	Type	Atoms
17	B	701	ADP	O4'-C4'-C5'-O5'
17	B	701	ADP	C3'-C4'-C5'-O5'
17	B	701	ADP	PA-O3A-PB-O1B
17	B	701	ADP	PA-O3A-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	B	701	ADP	1	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.