



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 20, 2023 – 09:21 PM JST

PDB ID : 7DQC  
Title : Crystal structure of nucleotide-free mutant A(S23C)3B(N64C)3 complex from *Enterococcus hirae* V-ATPase  
Authors : Maruyama, S.; Suzuki, K.; Mizutani, K.; Imai, F.L.; Ishizuka-Katsura, Y.; Shirouzu, M.; Murata, M.  
Deposited on : 2020-12-23  
Resolution : 2.71 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

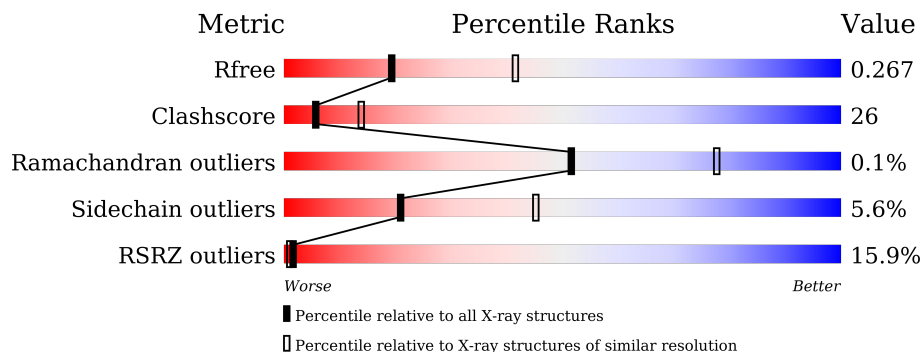
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.71 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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	600	
1	B	600	
1	C	600	
2	D	465	
2	E	465	
2	F	465	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 23860 atoms, of which 48 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 sodium ATPase catalytic subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	586	4529	2847	761	895	26	0	0	0
1	B	586	4501	2827	758	889	27	0	0	0
1	C	584	4456	2802	746	881	27	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP Q08636
A	-5	SER	-	expression tag	UNP Q08636
A	-4	SER	-	expression tag	UNP Q08636
A	-3	GLY	-	expression tag	UNP Q08636
A	-2	SER	-	expression tag	UNP Q08636
A	-1	SER	-	expression tag	UNP Q08636
A	0	GLY	-	expression tag	UNP Q08636
A	23	CYS	SER	engineered mutation	UNP Q08636
B	-6	GLY	-	expression tag	UNP Q08636
B	-5	SER	-	expression tag	UNP Q08636
B	-4	SER	-	expression tag	UNP Q08636
B	-3	GLY	-	expression tag	UNP Q08636
B	-2	SER	-	expression tag	UNP Q08636
B	-1	SER	-	expression tag	UNP Q08636
B	0	GLY	-	expression tag	UNP Q08636
B	23	CYS	SER	engineered mutation	UNP Q08636
C	-6	GLY	-	expression tag	UNP Q08636
C	-5	SER	-	expression tag	UNP Q08636
C	-4	SER	-	expression tag	UNP Q08636
C	-3	GLY	-	expression tag	UNP Q08636
C	-2	SER	-	expression tag	UNP Q08636
C	-1	SER	-	expression tag	UNP Q08636
C	0	GLY	-	expression tag	UNP Q08636

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Chain	Residue	Modelled	Actual	Comment	Reference
C	23	CYS	SER	engineered mutation	UNP Q08636

- Molecule 2 is a protein called V-type sodium ATPase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	448	Total	C	N	O	S	0	0	0
			3380	2137	590	638	15			
2	E	450	Total	C	N	O	S	0	0	0
			3347	2112	582	640	13			
2	F	450	Total	C	N	O	S	0	0	0
			3277	2068	568	627	14			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	GLY	-	expression tag	UNP Q08637
D	-5	SER	-	expression tag	UNP Q08637
D	-4	SER	-	expression tag	UNP Q08637
D	-3	GLY	-	expression tag	UNP Q08637
D	-2	SER	-	expression tag	UNP Q08637
D	-1	SER	-	expression tag	UNP Q08637
D	0	GLY	-	expression tag	UNP Q08637
D	64	CYS	ASN	engineered mutation	UNP Q08637
E	-6	GLY	-	expression tag	UNP Q08637
E	-5	SER	-	expression tag	UNP Q08637
E	-4	SER	-	expression tag	UNP Q08637
E	-3	GLY	-	expression tag	UNP Q08637
E	-2	SER	-	expression tag	UNP Q08637
E	-1	SER	-	expression tag	UNP Q08637
E	0	GLY	-	expression tag	UNP Q08637
E	64	CYS	ASN	engineered mutation	UNP Q08637
F	-6	GLY	-	expression tag	UNP Q08637
F	-5	SER	-	expression tag	UNP Q08637
F	-4	SER	-	expression tag	UNP Q08637
F	-3	GLY	-	expression tag	UNP Q08637
F	-2	SER	-	expression tag	UNP Q08637
F	-1	SER	-	expression tag	UNP Q08637
F	0	GLY	-	expression tag	UNP Q08637
F	64	CYS	ASN	engineered mutation	UNP Q08637

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	14	3	8	3	0	0
3	A	1	14	3	8	3	0	0
3	A	1	14	3	8	3	0	0
3	A	1	14	3	8	3	0	0
3	A	1	14	3	8	3	0	0
3	A	1	14	3	8	3	0	0

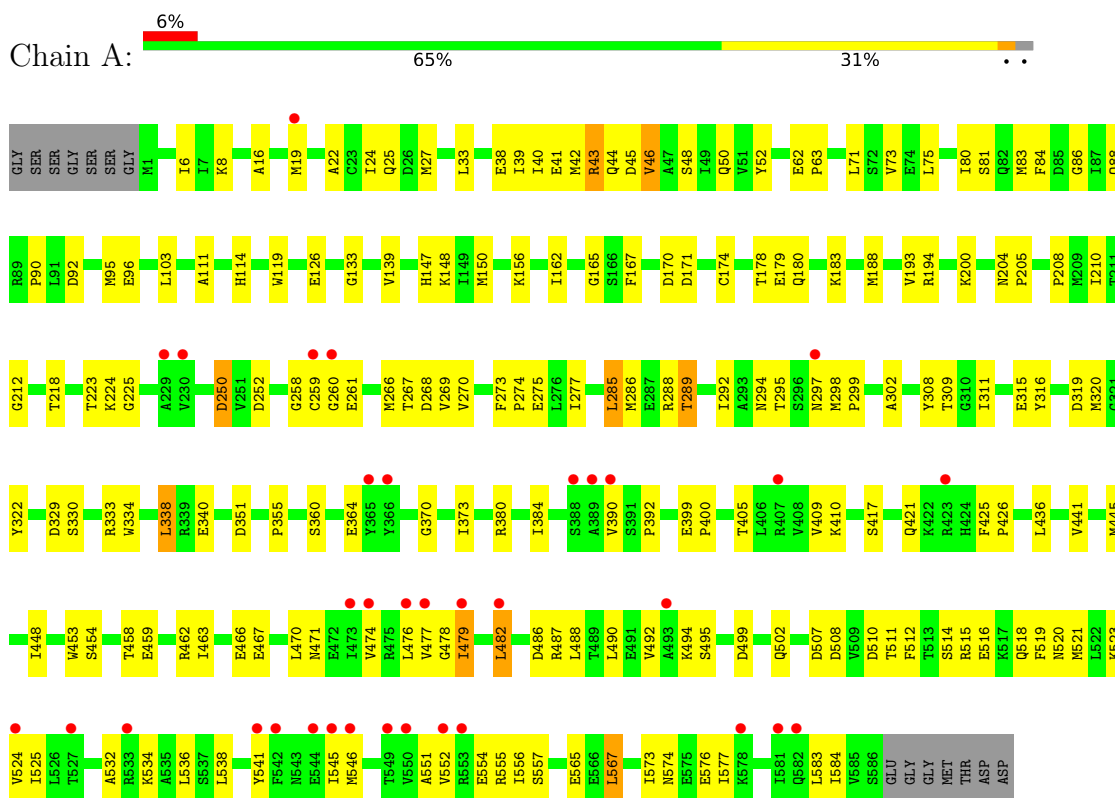
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	103	103	103	0	0
4	B	45	45	45	0	0
4	D	34	34	34	0	0
4	E	42	42	42	0	0
4	C	43	43	43	0	0
4	F	19	19	19	0	0

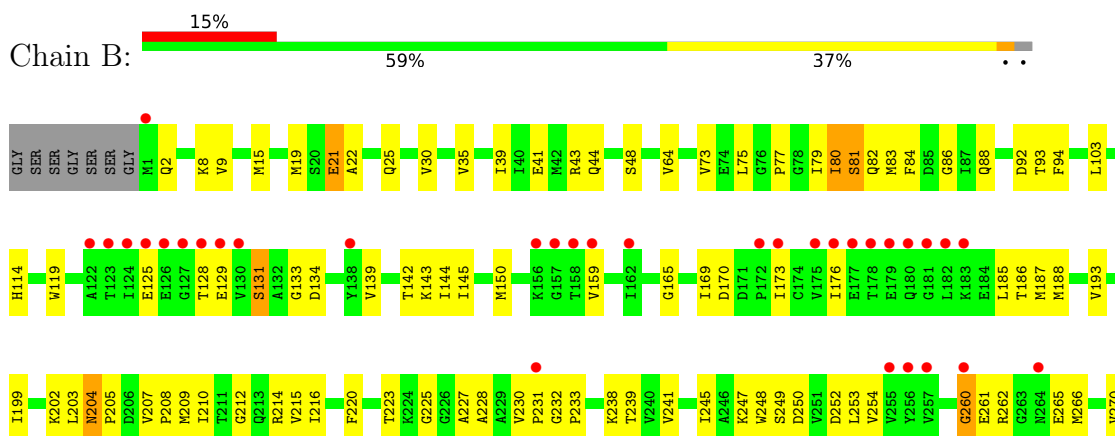
### 3 Residue-property plots i

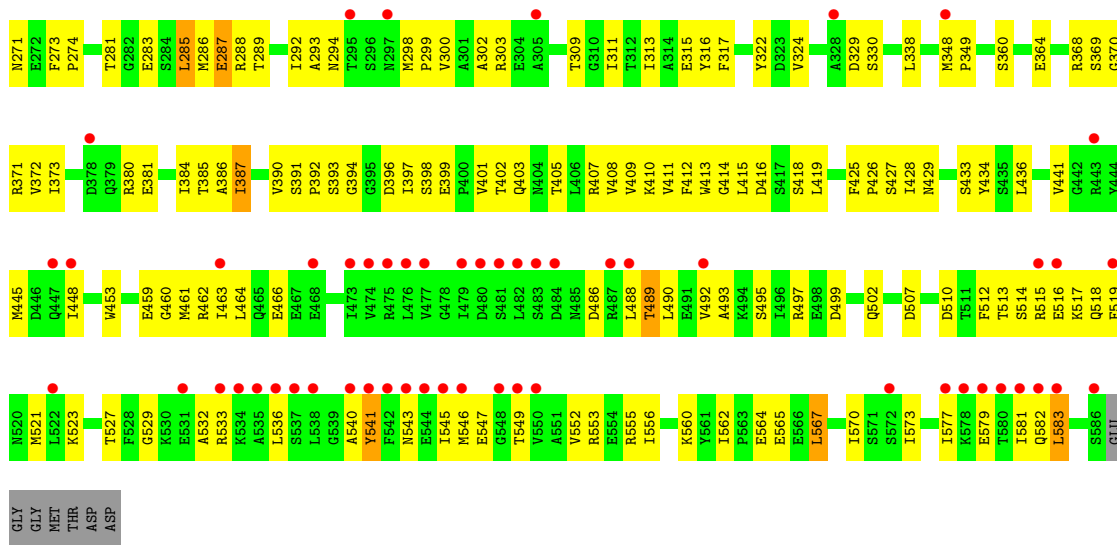
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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 sodium ATPase catalytic subunit A

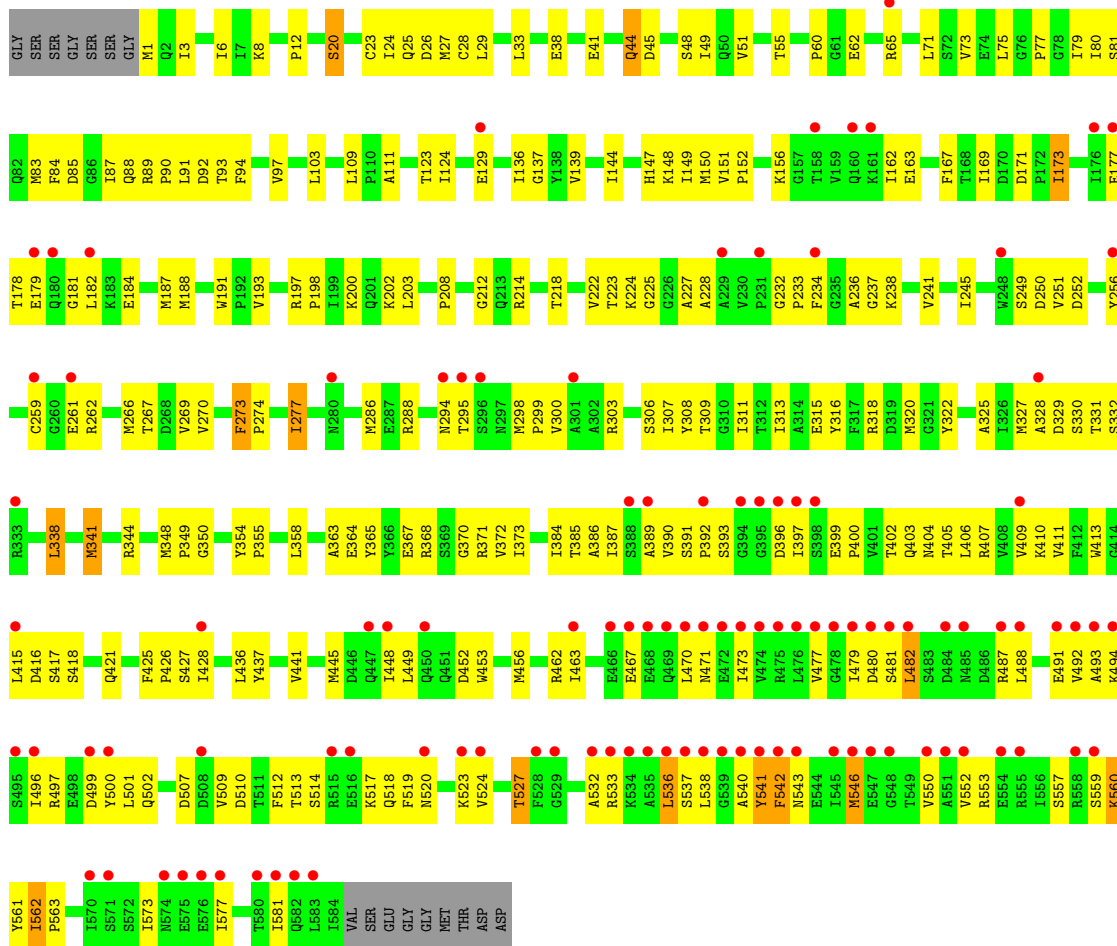


#### • Molecule 1: V-type sodium ATPase catalytic subunit A

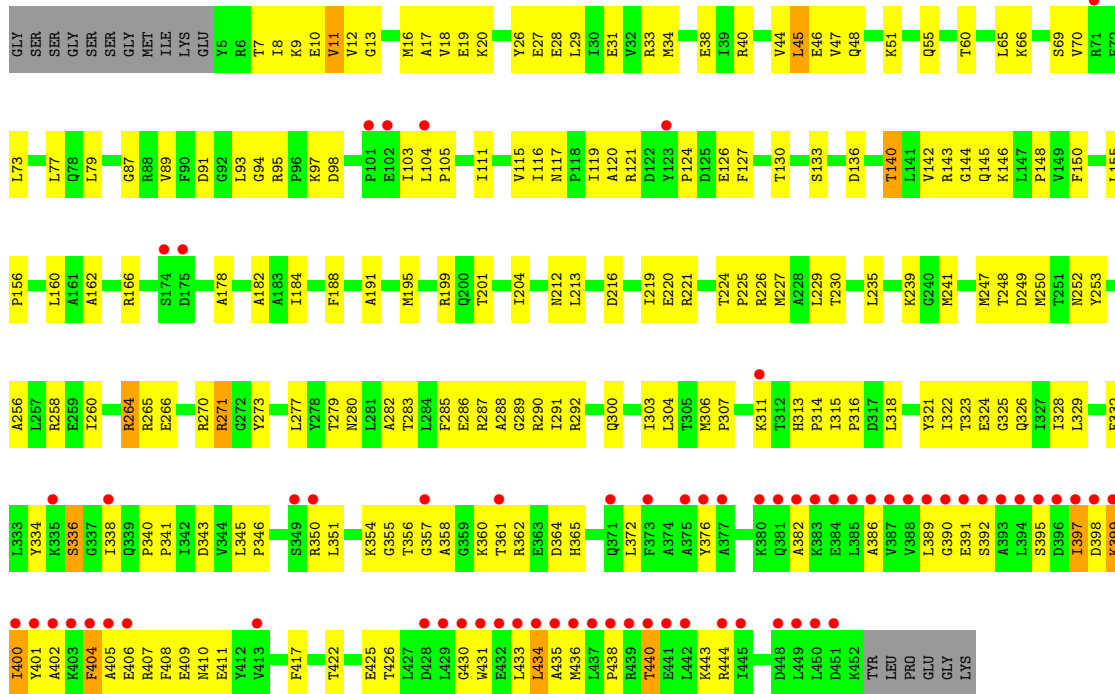




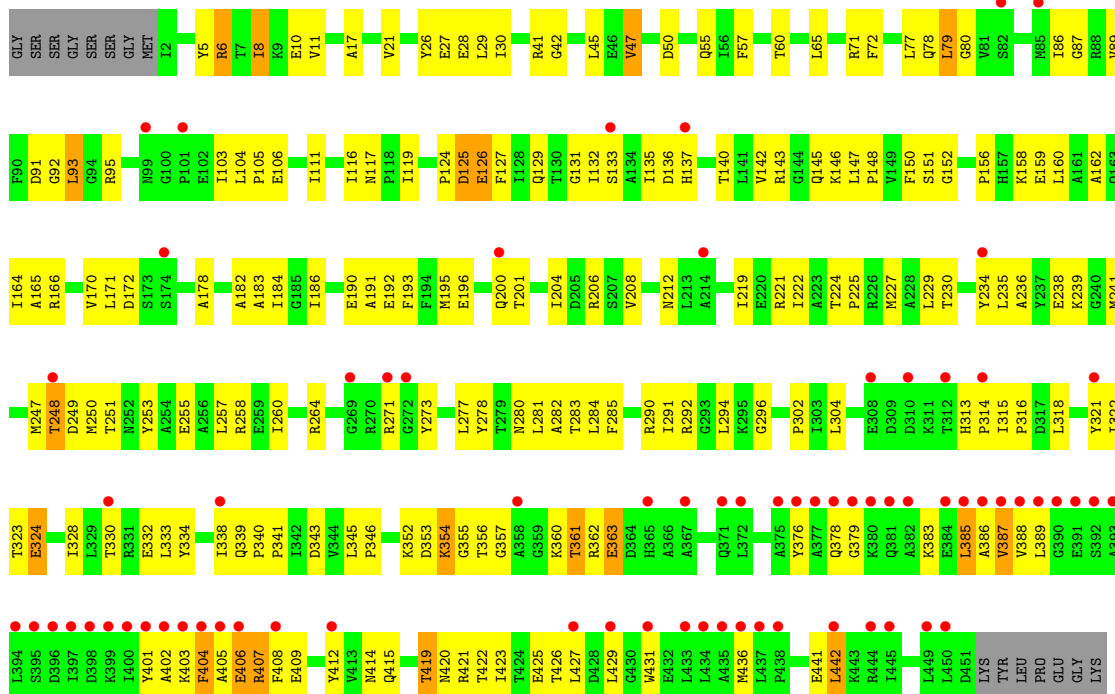
● Molecule 1: V-type sodium ATPase catalytic subunit A



● Molecule 2: V-type sodium ATPase subunit B

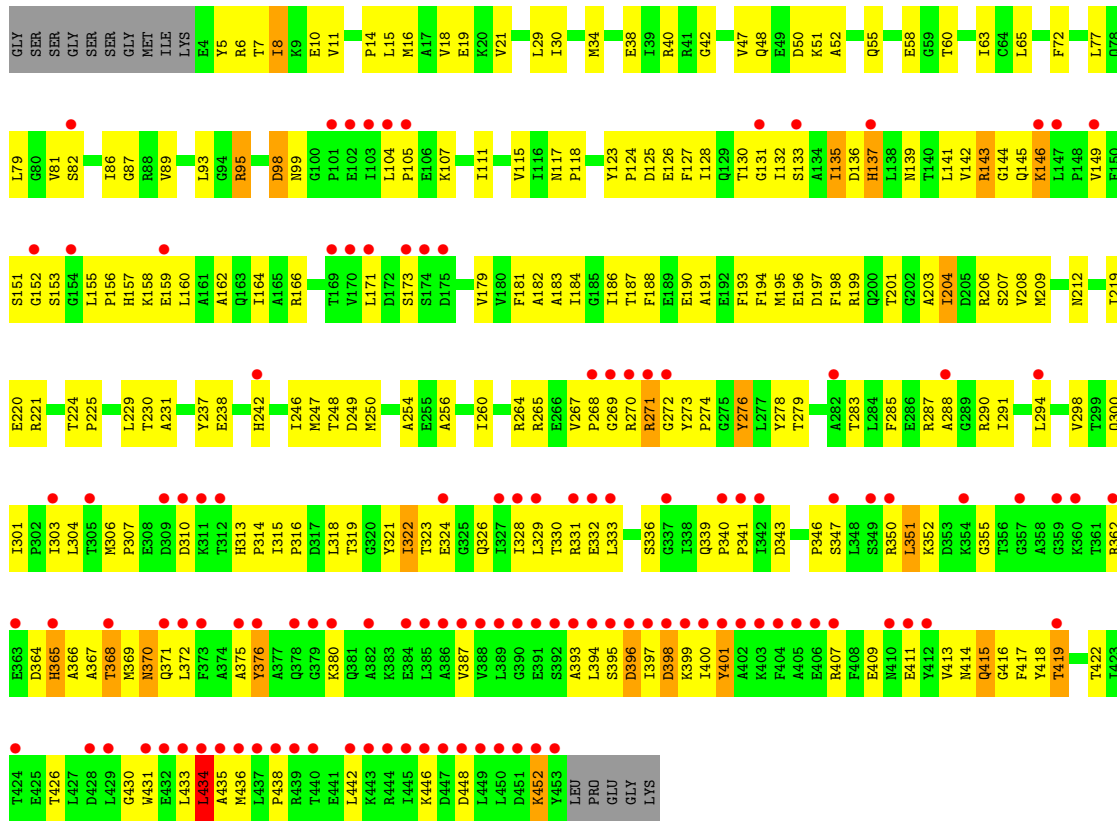


• Molecule 2: V-type sodium ATPase subunit B



• Molecule 2: V-type sodium ATPase subunit B





## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	122.08Å 121.83Å 129.11Å 90.00° 90.22° 90.00°	Depositor
Resolution (Å)	44.30 – 2.71 44.30 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.30-2.71) 99.8 (44.30-2.71)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.34 (at 2.69Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.234 , 0.266 0.238 , 0.267	Depositor DCC
$R_{free}$ test set	5266 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	61.6	Xtrriage
Anisotropy	0.155	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 72.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l 0.000 for -k,-h,-l 0.015 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	23860	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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: GOL

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	0.20	0/4605	0.38	0/6234
1	B	0.21	0/4577	0.40	1/6199 (0.0%)
1	C	0.21	0/4532	0.38	0/6148
2	D	0.21	0/3441	0.38	0/4658
2	E	0.22	0/3406	0.42	0/4616
2	F	0.23	0/3336	0.43	1/4536 (0.0%)
All	All	0.21	0/23897	0.40	2/32391 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	434	LEU	CB-CG-CD2	5.94	121.10	111.00
1	B	260	GLY	N-CA-C	-5.70	98.86	113.10

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	4529	0	4462	159	0
1	B	4501	0	4407	221	0
1	C	4456	0	4329	220	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	3380	0	3279	188	0
2	E	3347	0	3194	188	0
2	F	3277	0	3037	247	0
3	A	36	48	48	3	0
4	A	103	0	0	6	0
4	B	45	0	0	2	0
4	C	43	0	0	0	0
4	D	34	0	0	5	0
4	E	42	0	0	6	0
4	F	19	0	0	1	0
All	All	23812	48	22756	1180	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 26.

The worst 5 of 1180 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)
2:F:267:VAL:HG22	2:F:268:PRO:HD2	1.31	1.10
2:F:155:LEU:HD22	2:F:156:PRO:HD2	1.25	1.09
1:C:148:LYS:H	1:C:320:MET:HE3	1.22	1.01
2:D:89:VAL:HG21	2:D:195:MET:HE1	1.39	1.01
1:C:150:MET:HE1	1:C:320:MET:HA	1.41	1.00

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	584/600 (97%)	576 (99%)	8 (1%)	0	100   100
1	B	584/600 (97%)	573 (98%)	10 (2%)	1 (0%)	47   73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	582/600 (97%)	569 (98%)	13 (2%)	0	100	100
2	D	446/465 (96%)	431 (97%)	15 (3%)	0	100	100
2	E	448/465 (96%)	427 (95%)	20 (4%)	1 (0%)	47	73
2	F	448/465 (96%)	431 (96%)	16 (4%)	1 (0%)	47	73
All	All	3092/3195 (97%)	3007 (97%)	82 (3%)	3 (0%)	51	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	387	VAL
1	B	287	GLU
2	E	387	VAL

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	491/511 (96%)	476 (97%)	15 (3%)	40	69
1	B	484/511 (95%)	466 (96%)	18 (4%)	34	63
1	C	474/511 (93%)	451 (95%)	23 (5%)	25	52
2	D	335/387 (87%)	316 (94%)	19 (6%)	20	44
2	E	325/387 (84%)	300 (92%)	25 (8%)	13	30
2	F	304/387 (79%)	270 (89%)	34 (11%)	6	13
All	All	2413/2694 (90%)	2279 (94%)	134 (6%)	21	45

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	271	ARG
2	F	322	ILE
2	F	415	GLN
2	D	400	ILE

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Mol	Chain	Res	Type
2	D	399	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	GLN
1	B	82	GLN
1	B	403	GLN
2	F	137	HIS
2	F	167	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

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	$\# Z  > 2$
3	GOL	A	603	-	5,5,5	0.37	0	5,5,5	0.15	0
3	GOL	A	605	-	5,5,5	0.37	0	5,5,5	0.20	0
3	GOL	A	601	-	5,5,5	0.39	0	5,5,5	0.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	A	602	-	5,5,5	0.36	0	5,5,5	0.25	0
3	GOL	A	604	-	5,5,5	0.37	0	5,5,5	0.18	0
3	GOL	A	606	-	5,5,5	0.37	0	5,5,5	0.22	0

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
3	GOL	A	603	-	-	2/4/4/4	-
3	GOL	A	605	-	-	2/4/4/4	-
3	GOL	A	601	-	-	2/4/4/4	-
3	GOL	A	602	-	-	2/4/4/4	-
3	GOL	A	604	-	-	2/4/4/4	-
3	GOL	A	606	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	603	GOL	O1-C1-C2-C3
3	A	606	GOL	O1-C1-C2-C3
3	A	602	GOL	O1-C1-C2-C3
3	A	605	GOL	O1-C1-C2-C3
3	A	602	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	605	GOL	1	0
3	A	601	GOL	2	0

## 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.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	586/600 (97%)	0.61	35 (5%) 21 20	32, 52, 104, 139	0
1	B	586/600 (97%)	0.98	88 (15%) 2 1	42, 82, 137, 164	0
1	C	584/600 (97%)	1.21	109 (18%) 1 0	54, 87, 139, 158	0
2	D	448/465 (96%)	1.03	68 (15%) 2 1	48, 80, 152, 202	0
2	E	450/465 (96%)	1.08	73 (16%) 1 1	37, 72, 158, 209	0
2	F	450/465 (96%)	1.63	120 (26%) 0 0	51, 95, 172, 201	0
All	All	3104/3195 (97%)	1.07	493 (15%) 1 1	32, 77, 149, 209	0

The worst 5 of 493 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	435	ALA	11.0
2	F	449	LEU	9.5
2	F	385	LEU	9.2
2	E	394	LEU	9.1
1	C	476	LEU	9.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	A	603	6/6	0.29	0.39	101,121,125,125	0
3	GOL	A	601	6/6	0.34	0.35	114,136,139,139	0
3	GOL	A	605	6/6	0.50	0.32	113,136,138,138	0
3	GOL	A	602	6/6	0.81	0.27	88,106,108,108	0
3	GOL	A	604	6/6	0.86	0.33	77,93,95,95	0
3	GOL	A	606	6/6	0.88	0.26	91,109,112,112	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.