



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:14 PM UTC

PDB ID : 2C61 / pdb_00002c61
Title : Crystal structure of the non-catalytic B subunit of A-type ATPase from *M. mazei* Go1
Authors : Schaefer, I.; Bailer, S.M.; Dueser, M.; Boersch, M.; Bernal, R.A.; Grueber, G.; Stock, D.
Deposited on : 2005-11-06
Resolution : 1.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/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>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

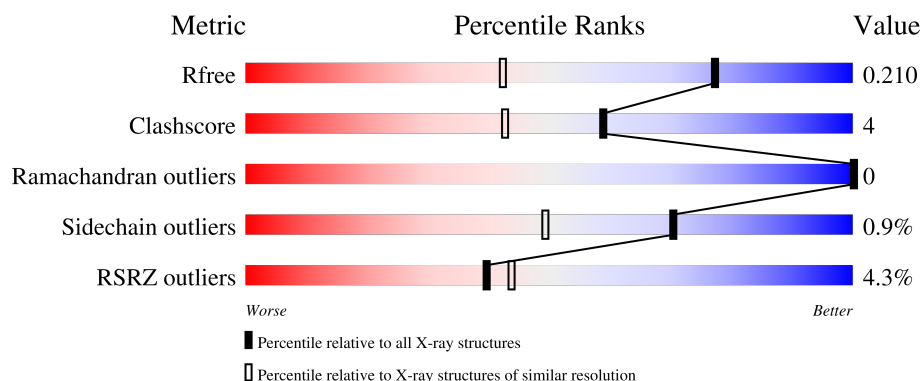
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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 ≥ 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	469	4% 84% 8% 8%
1	B	469	4% 80% 10% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7354 atoms, of which 0 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 A-TYPE ATP SYNTHASE NON-CATALYTIC SUBUNIT B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	432	Total	C	N	O	S	0	0	1
			3323	2101	580	631	11			
1	B	425	Total	C	N	O	S	0	0	0
			3283	2081	568	623	11			

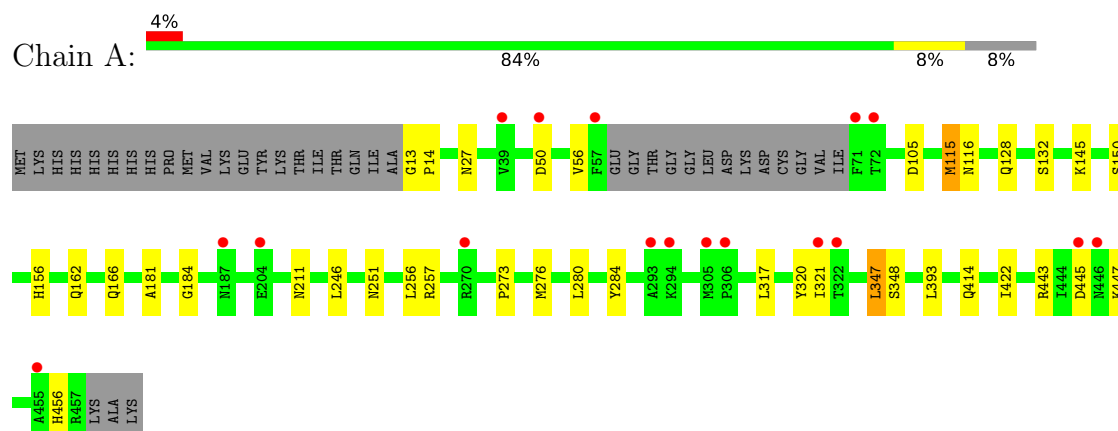
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	380	Total	O	0	0
			380	380		
2	B	368	Total	O	0	0
			368	368		

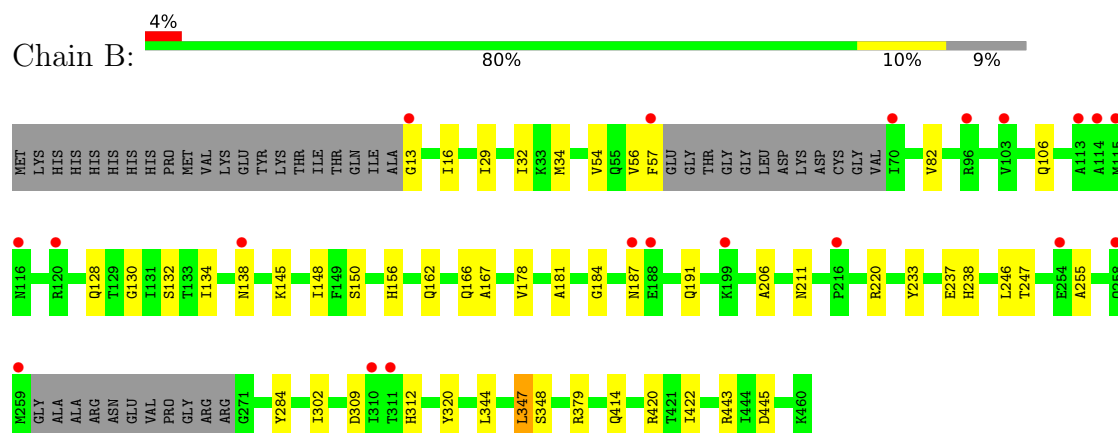
3 Residue-property plots [i](#)

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: A-TYPE ATP SYNTHASE NON-CATALYTIC SUBUNIT B



• Molecule 1: A-TYPE ATP SYNTHASE NON-CATALYTIC SUBUNIT B



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.62Å 96.42Å 130.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.32 – 1.50 34.32 – 1.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.32-1.50) 99.1 (34.32-1.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.186 , 0.211 0.184 , 0.210	Depositor DCC
R_{free} test set	7403 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7354	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

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	0.64	1/3387 (0.0%)	0.85	3/4594 (0.1%)
1	B	0.63	0/3345	0.81	5/4532 (0.1%)
All	All	0.63	1/6732 (0.0%)	0.83	8/9126 (0.1%)

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	A	0	2
1	B	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	456	HIS	C-N	-7.03	1.23	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	ARG	N-CA-C	-14.13	96.05	113.28
1	A	348	SER	N-CA-C	9.54	124.27	108.73
1	B	348	SER	N-CA-C	7.30	120.42	108.52
1	B	247	THR	CA-C-N	5.98	132.46	121.70
1	B	247	THR	C-N-CA	5.98	132.46	121.70
1	B	13	GLY	CA-C-N	5.51	125.48	120.03
1	B	13	GLY	C-N-CA	5.51	125.48	120.03
1	A	115	MET	N-CA-C	5.09	121.64	110.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	256	LEU	Peptide
1	A	347	LEU	Peptide
1	B	347	LEU	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	3323	0	3324	27	0
1	B	3283	0	3295	32	0
2	A	380	0	0	6	0
2	B	368	0	0	1	0
All	All	7354	0	6619	58	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 4.

All (58) 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)
1:A:251:ASN:HB3	2:A:2168:HOH:O	1.40	1.17
1:A:50:ASP:OD1	2:A:2049:HOH:O	1.94	0.84
1:B:184:GLY:H	1:B:211:ASN:HD22	1.30	0.77
1:B:148:ILE:HB	1:B:302:ILE:HD13	1.70	0.74
1:A:184:GLY:H	1:A:211:ASN:HD22	1.34	0.74
1:B:134:ILE:HA	1:B:138:ASN:OD1	1.89	0.72
1:A:321:ILE:HG22	1:A:321:ILE:O	1.88	0.71
1:B:156:HIS:HB2	1:B:302:ILE:HD12	1.72	0.70
1:A:280:LEU:HG	2:A:2244:HOH:O	1.91	0.69
1:A:132:SER:H	1:A:414:GLN:HE22	1.43	0.66
1:B:132:SER:H	1:B:414:GLN:HE22	1.46	0.63
1:A:443:ARG:NH2	2:A:2370:HOH:O	2.34	0.61
1:A:162:GLN:HE21	1:A:166:GLN:HE22	1.48	0.60
1:B:162:GLN:HE21	1:B:166:GLN:HE22	1.48	0.59
1:A:184:GLY:H	1:A:211:ASN:ND2	2.03	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ILE:O	1:A:321:ILE:CG2	2.54	0.54
1:B:150:SER:OG	1:B:156:HIS:HD2	1.90	0.54
1:A:280:LEU:HD11	1:A:317:LEU:HD23	1.90	0.53
1:B:344:LEU:CD1	1:B:379:ARG:HD3	2.38	0.53
1:A:156:HIS:HE1	2:A:2215:HOH:O	1.91	0.52
1:B:220:ARG:HD2	1:B:255:ALA:HB2	1.92	0.52
1:B:106:GLN:NE2	1:B:237:GLU:OE1	2.45	0.49
1:B:184:GLY:H	1:B:211:ASN:ND2	2.02	0.49
1:B:233:TYR:OH	1:B:238:HIS:HE1	1.96	0.48
1:A:13:GLY:N	1:A:56:VAL:O	2.47	0.47
1:A:145:LYS:HD3	1:A:284:TYR:O	2.15	0.47
1:B:187:ASN:O	1:B:191:GLN:HG2	2.14	0.47
1:B:344:LEU:HD12	1:B:379:ARG:HD3	1.97	0.47
1:A:184:GLY:HA3	2:A:2168:HOH:O	2.16	0.46
1:B:150:SER:OG	1:B:156:HIS:CD2	2.69	0.46
1:B:156:HIS:HE1	2:B:2187:HOH:O	1.99	0.45
1:A:128:GLN:NE2	1:A:422:ILE:H	2.15	0.45
1:A:445:ASP:OD2	1:A:447:LYS:HG2	2.17	0.45
1:B:128:GLN:NE2	1:B:422:ILE:H	2.15	0.45
1:B:145:LYS:HD3	1:B:284:TYR:O	2.17	0.45
1:B:181:ALA:HB3	1:B:246:LEU:HD23	1.99	0.44
1:A:150:SER:OG	1:A:156:HIS:HD2	2.01	0.43
1:B:162:GLN:HE21	1:B:166:GLN:NE2	2.15	0.43
1:A:162:GLN:HE21	1:A:166:GLN:NE2	2.14	0.43
1:A:181:ALA:HB3	1:A:246:LEU:HD23	1.99	0.43
1:B:29:ILE:HD12	1:B:57:PHE:HZ	1.84	0.43
1:B:128:GLN:O	1:B:167:ALA:HA	2.19	0.43
1:B:309:ASP:HA	1:B:312:HIS:O	2.20	0.42
1:B:16:ILE:HG13	1:B:56:VAL:HG21	2.02	0.42
1:B:132:SER:H	1:B:414:GLN:NE2	2.14	0.42
1:A:115:MET:O	1:A:116:ASN:C	2.62	0.41
1:A:347:LEU:HD22	1:B:347:LEU:HD22	2.01	0.41
1:A:27:ASN:HD22	1:A:27:ASN:HA	1.69	0.41
1:B:34:MET:HA	1:B:34:MET:HE2	2.02	0.41
1:A:273:PRO:HG2	1:A:276:MET:HG2	2.02	0.41
1:A:13:GLY:HA3	1:A:14:PRO:HD3	1.93	0.41
1:B:148:ILE:CB	1:B:302:ILE:HD13	2.46	0.41
1:B:32:ILE:HD11	1:B:54:VAL:HG11	2.03	0.41
1:B:130:GLY:HA2	1:B:420:ARG:O	2.20	0.40
1:A:150:SER:OG	1:A:156:HIS:CD2	2.74	0.40
1:A:184:GLY:N	1:A:211:ASN:HD22	2.11	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:VAL:HG13	1:B:238:HIS:CE1	2.56	0.40
1:B:178:VAL:O	1:B:206:ALA:HA	2.22	0.40

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	428/469 (91%)	418 (98%)	10 (2%)	0	100	100
1	B	419/469 (89%)	410 (98%)	9 (2%)	0	100	100
All	All	847/938 (90%)	828 (98%)	19 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	352/384 (92%)	349 (99%)	3 (1%)	70	49
1	B	349/384 (91%)	346 (99%)	3 (1%)	70	49
All	All	701/768 (91%)	695 (99%)	6 (1%)	70	49

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	105	ASP
1	A	320	TYR
1	A	393	LEU
1	B	320	TYR
1	B	443	ARG
1	B	445	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	128	GLN
1	A	138	ASN
1	A	156	HIS
1	A	166	GLN
1	A	211	ASN
1	A	238	HIS
1	A	312	HIS
1	A	414	GLN
1	A	431	GLN
1	B	128	GLN
1	B	156	HIS
1	B	166	GLN
1	B	187	ASN
1	B	191	GLN
1	B	211	ASN
1	B	238	HIS
1	B	414	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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, 95th 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 ²)	Q<0.9
1	A	432/469 (92%)	0.14	17 (3%) 43 47	8, 15, 26, 36	0
1	B	425/469 (90%)	0.10	20 (4%) 36 40	8, 14, 27, 34	0
All	All	857/938 (91%)	0.12	37 (4%) 40 44	8, 14, 26, 36	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	258	GLN	4.3
1	B	115	MET	4.1
1	B	70	ILE	4.0
1	A	455	ALA	3.7
1	B	113	ALA	3.5
1	A	72	THR	3.5
1	A	293	ALA	3.4
1	A	187	ASN	3.3
1	A	270	ARG	3.3
1	A	445	ASP	3.2
1	B	114	ALA	3.2
1	B	120	ARG	3.1
1	A	71	PHE	3.1
1	A	50	ASP	3.0
1	B	96	ARG	3.0
1	A	306	PRO	2.9
1	A	321	ILE	2.9
1	B	254	GLU	2.8
1	B	259	MET	2.8
1	B	57	PHE	2.8
1	B	216	PRO	2.8
1	B	311	THR	2.7
1	B	310	ILE	2.7
1	B	187	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	322	THR	2.6
1	B	199	LYS	2.5
1	B	138	ASN	2.5
1	A	305	MET	2.4
1	B	116	ASN	2.4
1	A	57	PHE	2.3
1	A	39	VAL	2.3
1	A	204	GLU	2.3
1	B	13	GLY	2.2
1	A	294	LYS	2.2
1	A	446	ASN	2.1
1	B	188	GLU	2.1
1	B	103	VAL	2.0

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.