



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2QZV / pdb_00002qzv
Title : Draft Crystal Structure of the Vault Shell at 9 Angstroms Resolution
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Deposited on : 2007-08-17
Resolution : 9.00 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

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

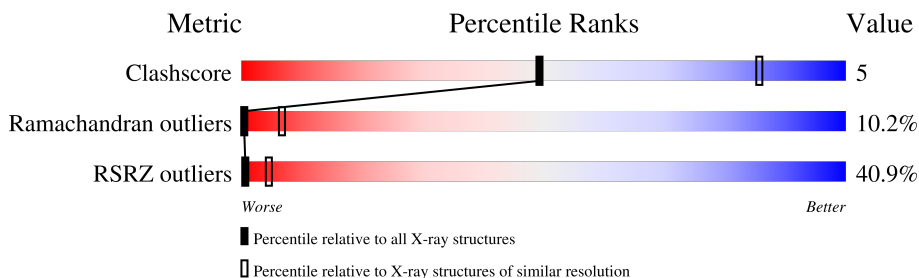
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 9.00 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)

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	873	34% 69% 14% • 14%
1	B	873	36% 70% 14% • 14%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7404 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 Major vault protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	749	Total	C	N	O	0	0	0
			3702	2204	749	749			
1	B	749	Total	C	N	O	0	0	0
			3702	2204	749	749			

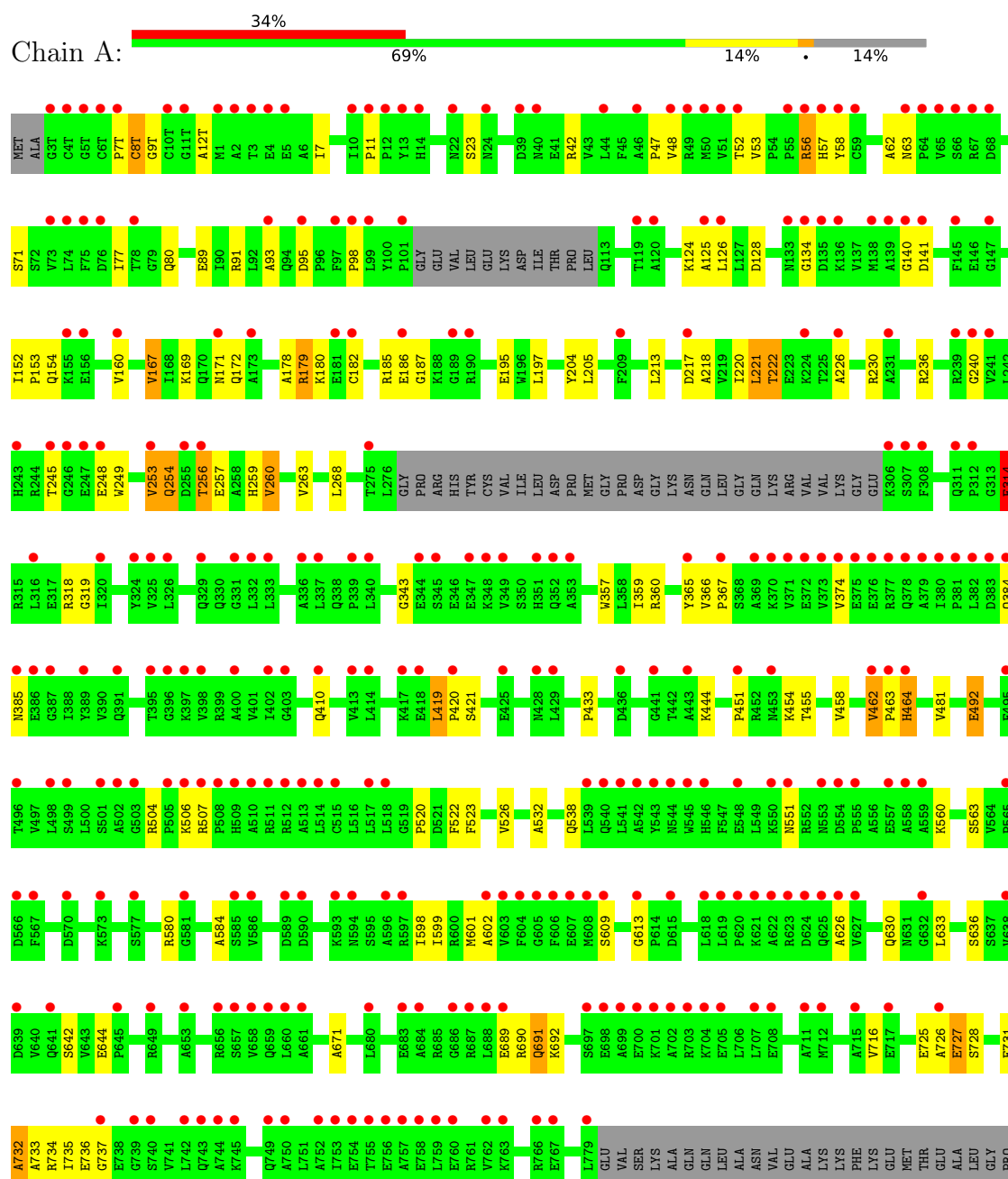
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1T	MET	-	expression tag	UNP Q62667
A	2T	ALA	-	expression tag	UNP Q62667
A	3T	GLY	-	expression tag	UNP Q62667
A	4T	CYS	-	expression tag	UNP Q62667
A	5T	GLY	-	expression tag	UNP Q62667
A	6T	CYS	-	expression tag	UNP Q62667
A	7T	PRO	-	expression tag	UNP Q62667
A	8T	CYS	-	expression tag	UNP Q62667
A	9T	GLY	-	expression tag	UNP Q62667
A	10T	CYS	-	expression tag	UNP Q62667
A	11T	GLY	-	expression tag	UNP Q62667
A	12T	ALA	-	expression tag	UNP Q62667
B	1T	MET	-	expression tag	UNP Q62667
B	2T	ALA	-	expression tag	UNP Q62667
B	3T	GLY	-	expression tag	UNP Q62667
B	4T	CYS	-	expression tag	UNP Q62667
B	5T	GLY	-	expression tag	UNP Q62667
B	6T	CYS	-	expression tag	UNP Q62667
B	7T	PRO	-	expression tag	UNP Q62667
B	8T	CYS	-	expression tag	UNP Q62667
B	9T	GLY	-	expression tag	UNP Q62667
B	10T	CYS	-	expression tag	UNP Q62667
B	11T	GLY	-	expression tag	UNP Q62667
B	12T	ALA	-	expression tag	UNP Q62667

3 Residue-property plots

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



Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	631.45Å 464.72Å 584.57Å 90.00° 123.84° 90.00°	Depositor
Resolution (Å)	200.00 – 9.00 200.00 – 9.00	Depositor EDS
% Data completeness (in resolution range)	98.0 (200.00-9.00) 91.2 (200.00-9.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.22	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 8.44Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.615 , (Not available) 0.545 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	-1.2	Xtriage
Anisotropy	4.910	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.38	EDS
Total number of atoms	7404	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.46% 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	0.53	0/3699	1.18	30/5148 (0.6%)
1	B	0.52	0/3699	1.18	29/5148 (0.6%)
All	All	0.53	0/7398	1.18	59/10296 (0.6%)

There are no bond length outliers.

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	THR	N-CA-C	10.63	125.87	108.96
1	B	222	THR	N-CA-C	10.63	125.86	108.96
1	B	366	VAL	N-CA-C	9.29	116.74	107.55
1	A	366	VAL	N-CA-C	9.28	116.74	107.55
1	A	259	HIS	N-CA-C	7.62	119.59	111.28

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	3702	0	1718	33	0
1	B	3702	0	1718	32	0
All	All	7404	0	3436	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 5.

The worst 5 of 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:98:PRO:CB	1:B:156:GLU:CB	2.42	0.98
1:A:692:LYS:CB	1:B:688:LEU:HA	2.32	0.58
1:A:56:ARG:O	1:A:58:TYR:N	2.36	0.58
1:B:56:ARG:O	1:B:58:TYR:N	2.36	0.58
1:A:172:GLN:HA	1:A:217:ASP:HA	1.86	0.57

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	743/873 (85%)	524 (70%)	141 (19%)	78 (10%)	0	6
1	B	743/873 (85%)	528 (71%)	142 (19%)	73 (10%)	0	7
All	All	1486/1746 (85%)	1052 (71%)	283 (19%)	151 (10%)	0	7

5 of 151 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8(T)	CYS
1	A	57	HIS
1	A	71	SER
1	A	160	VAL
1	A	179	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 [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, 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	749/873 (85%)	1.98	295 (39%) 1 5	50, 50, 50, 50	0
1	B	749/873 (85%)	2.18	317 (42%) 0 4	50, 50, 50, 50	0
All	All	1498/1746 (85%)	2.08	612 (40%) 0 4	50, 50, 50, 50	0

The worst 5 of 612 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	713	SER	15.8
1	A	756	GLU	14.7
1	B	351	HIS	14.6
1	B	416	GLU	14.0
1	A	544	ASN	13.4

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.