



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 6RUD / pdb_00006rud
Title : WOLINELLA SUCCINOGENES L-ASPARAGINASE P1
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Deposited on : 2019-05-28
Resolution : 1.70 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

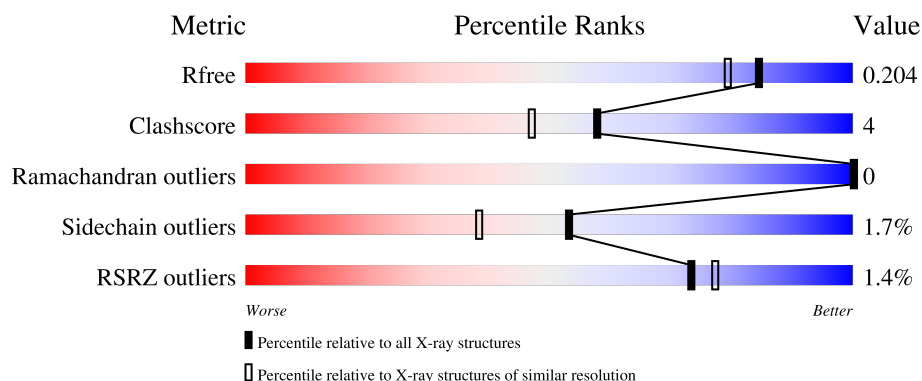
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 ≥ 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	328	2% 89% 7% ..
1	B	328	% 90% 7% ..
1	C	328	% 89% 7% .
1	D	328	2% 89% 7% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10438 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 L-asparaginase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2363	1484	407	464	8			
1	B	321	Total	C	N	O	S	0	0	0
			2382	1494	410	470	8			
1	C	317	Total	C	N	O	S	0	0	0
			2357	1481	406	462	8			
1	D	319	Total	C	N	O	S	0	0	0
			2367	1486	408	465	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	121	PRO	SER	conflict	UNP P50286
B	121	PRO	SER	conflict	UNP P50286
C	121	PRO	SER	conflict	UNP P50286
D	121	PRO	SER	conflict	UNP P50286

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	222	Total	O	0	0
			222	222		
2	B	250	Total	O	0	0
			250	250		
2	C	258	Total	O	0	0
			258	258		
2	D	239	Total	O	0	0
			239	239		

- Molecule 1: L-asparaginase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.82Å 109.17Å 87.70Å 90.00° 95.50° 90.00°	Depositor
Resolution (Å)	30.00 – 1.70 30.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.1 (30.00-1.70) 97.1 (30.00-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.160 , 0.194 0.171 , 0.204	Depositor DCC
R_{free} test set	6262 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	10.6	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10438	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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

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	1.06	0/2394	1.24	2/3245 (0.1%)
1	B	1.05	0/2413	1.22	0/3270
1	C	1.07	0/2388	1.25	4/3237 (0.1%)
1	D	1.05	0/2398	1.24	3/3250 (0.1%)
All	All	1.06	0/9593	1.24	9/13002 (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	C	0	1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	14	THR	CB-CA-C	9.13	124.73	109.84
1	C	14	THR	N-CA-CB	-7.88	97.73	109.95
1	D	321	GLU	CB-CG-CD	6.71	124.01	112.60
1	D	33	THR	CA-CB-OG1	6.20	118.89	109.60
1	A	321	GLU	CB-CG-CD	6.18	123.10	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	30	GLY	Peptide

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	2363	0	2424	20	0
1	B	2382	0	2438	23	0
1	C	2357	0	2419	21	0
1	D	2367	0	2427	24	0
2	A	222	0	0	10	0
2	B	250	0	0	8	0
2	C	258	0	0	6	0
2	D	239	0	0	10	0
All	All	10438	0	9708	86	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.

The worst 5 of 86 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:D:180:THR:C	2:D:401:HOH:O	1.78	1.26
1:D:29:ALA:HB1	2:D:590:HOH:O	1.47	1.13
1:D:57:SER:HB2	2:D:402:HOH:O	0.94	1.12
1:D:29:ALA:CB	2:D:590:HOH:O	2.03	0.94
1:D:34:VAL:O	1:D:38:LEU:HD13	1.69	0.92

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	314/328 (96%)	304 (97%)	10 (3%)	0	100	100
1	B	317/328 (97%)	305 (96%)	12 (4%)	0	100	100
1	C	313/328 (95%)	302 (96%)	11 (4%)	0	100	100
1	D	315/328 (96%)	306 (97%)	9 (3%)	0	100	100
All	All	1259/1312 (96%)	1217 (97%)	42 (3%)	0	100	100

There are no Ramachandran outliers to report.

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 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	255/264 (97%)	251 (98%)	4 (2%)	55	41
1	B	257/264 (97%)	252 (98%)	5 (2%)	50	34
1	C	254/264 (96%)	251 (99%)	3 (1%)	63	51
1	D	255/264 (97%)	250 (98%)	5 (2%)	48	32
All	All	1021/1056 (97%)	1004 (98%)	17 (2%)	53	38

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	125	MET
1	D	316	LYS
1	B	33	THR
1	B	55	ILE
1	C	14	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	252	ASN
1	D	201	HIS
1	D	259	ASN

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Mol	Chain	Res	Type
1	D	252	ASN
1	B	81	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 [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	318/328 (96%)	-0.41	6 (1%) 66 71	6, 9, 21, 41	0
1	B	321/328 (97%)	-0.37	4 (1%) 76 80	6, 10, 24, 34	0
1	C	317/328 (96%)	-0.37	3 (0%) 81 83	6, 9, 21, 32	0
1	D	319/328 (97%)	-0.37	5 (1%) 70 75	6, 10, 23, 30	0
All	All	1275/1312 (97%)	-0.38	18 (1%) 73 77	6, 10, 23, 41	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	29	ALA	4.5
1	D	143	LYS	3.3
1	D	29	ALA	2.7
1	A	143	LYS	2.7
1	A	263	LYS	2.7

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.