wwPDB X-ray Structure Validation Summary Report (i)

Jun 13, 2024 – 10:55 AM EDT

PDB ID	:	1QJ3
Title	:	Crystal structure of 7,8-diaminopelargonic acid synthase in complex with 7-keto-8-aminopelargonic acid
Authors	:	Kaeck, H.; Sandmark, J.; Gibson, K.J.; Lindqvist, Y.; Schneider, G.
Deposited on	:	1999-06-21
Resolution	:	2.70 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 (i) 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 (i)) were used in the production of this report:

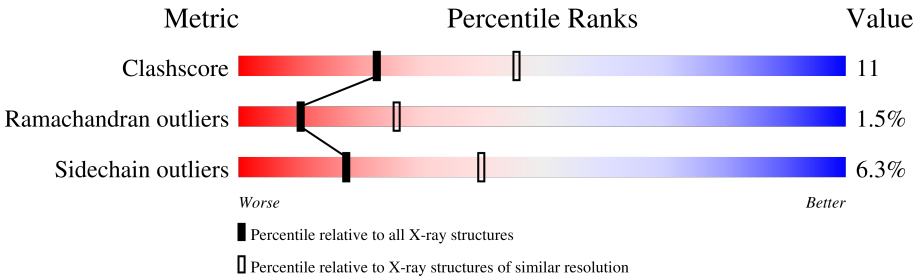
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (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 >=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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	429	70% 22%
1	B	429	69% 22%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6550 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.

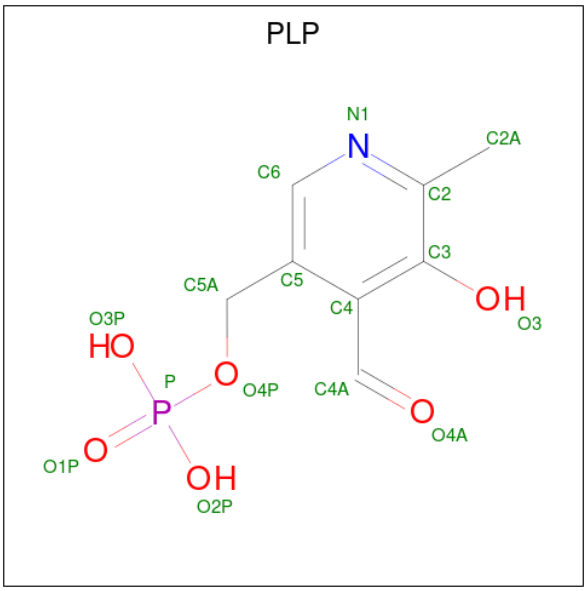
- Molecule 1 is a protein called 7,8-DIAMINOPELARGONIC ACID SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	416	Total	C	N	O	S	0	0	0
			3201	2030	558	582	31			
1	B	415	Total	C	N	O	S	4	0	0
			3197	2028	557	581	31			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	LEU	TRP	conflict	UNP P12995
B	14	LEU	TRP	conflict	UNP P12995

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

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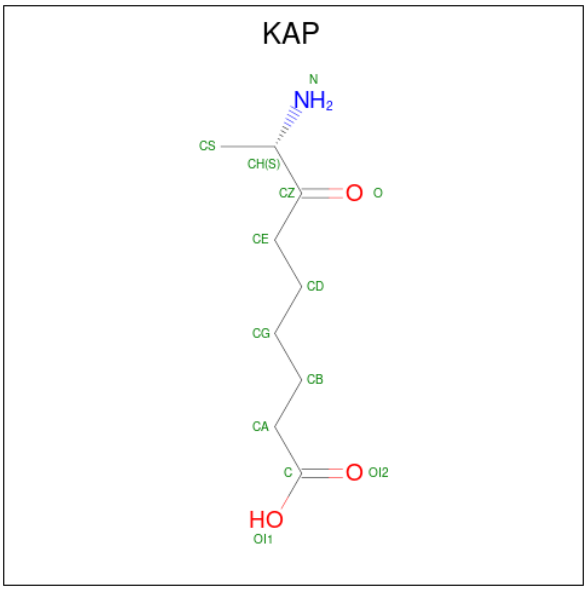
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C N O P 15 8 1 5 1	0	0

- Molecule 3 is 7-KETO-8-AMINOPELARGONIC ACID (three-letter code: KAP) (formula: $C_9H_{17}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 13 9 1 3	0	0
3	B	1	Total C N O 13 9 1 3	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	55	Total O 55 55	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	39	Total	O	0	0
			39	39		

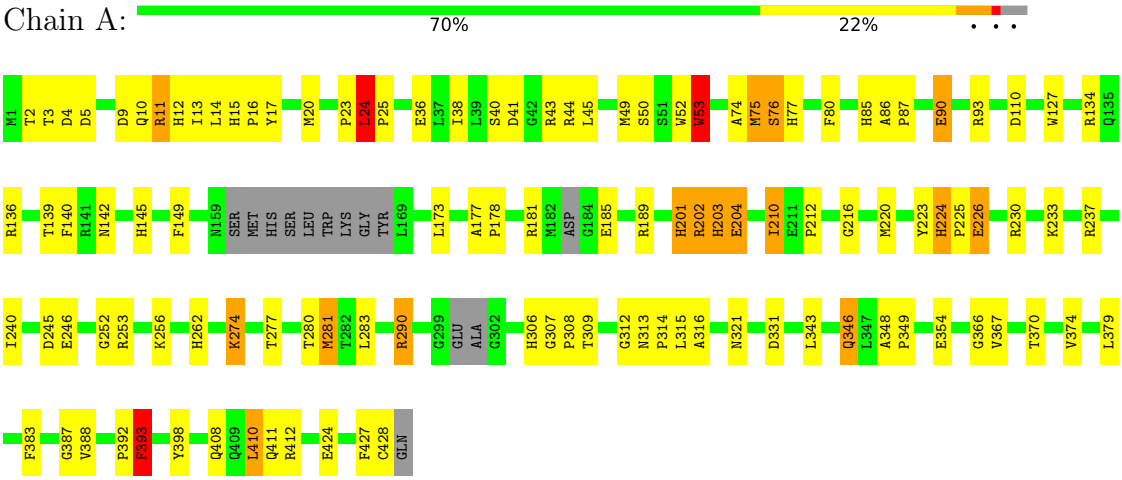
3 Residue-property plots (i)

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. 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.

Note EDS was not executed.

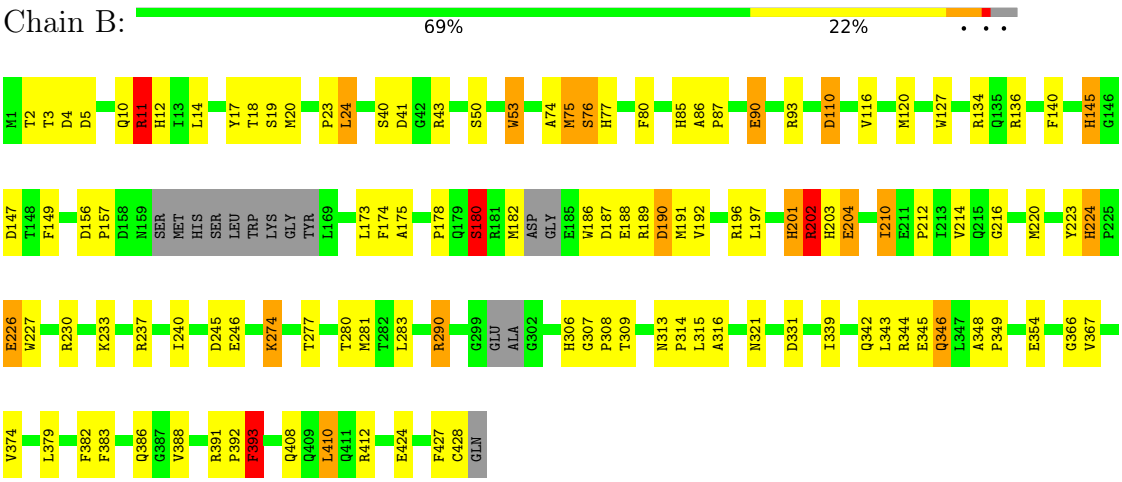
• Molecule 1: 7,8-DIAMINOPELARGONIC ACID SYNTHASE

Chain A:



• Molecule 1: 7,8-DIAMINOPELARGONIC ACID SYNTHASE

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.97Å 55.94Å 120.84Å 90.00° 95.69° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	99.9 (20.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.225 , 0.279	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6550	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PLP, KAP, NA

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	0.49	0/3272	1.42	32/4438 (0.7%)
1	B	0.49	0/3268	1.40	29/4433 (0.7%)
All	All	0.49	0/6540	1.41	61/8871 (0.7%)

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	1

There are no bond length outliers.

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	11	ARG	NE-CZ-NH2	30.34	135.47	120.30
1	B	11	ARG	NE-CZ-NH2	28.36	134.48	120.30
1	B	11	ARG	NE-CZ-NH1	-15.37	112.61	120.30
1	A	11	ARG	NE-CZ-NH1	-13.81	113.39	120.30
1	B	145	HIS	ND1-CG-CD2	-10.50	91.30	106.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	52	TRP	Mainchain

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	3201	0	3165	80	0
1	B	3197	0	3163	80	0
2	A	15	0	6	1	0
2	B	15	0	6	0	0
3	A	13	0	16	3	0
3	B	13	0	16	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	55	0	0	1	0
5	B	39	0	0	2	0
All	All	6550	0	6372	147	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 11.

The worst 5 of 147 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:B:140:PHE:HD2	1:B:178:PRO:HD3	1.45	0.81
1:B:140:PHE:CD2	1:B:178:PRO:HD3	2.20	0.77
1:B:77:HIS:HA	1:B:314:PRO:HD2	1.66	0.76
1:B:342:GLN:HG2	1:B:346:GLN:OE1	1.84	0.76
1:A:77:HIS:HA	1:A:314:PRO:HD2	1.66	0.75

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	408/429 (95%)	388 (95%)	15 (4%)	5 (1%)	13 32
1	B	407/429 (95%)	380 (93%)	20 (5%)	7 (2%)	9 23
All	All	815/858 (95%)	768 (94%)	35 (4%)	12 (2%)	10 26

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	274	LYS
1	B	274	LYS
1	A	216	GLY
1	B	216	GLY
1	A	75	MET

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	334/345 (97%)	315 (94%)	19 (6%)	20 44
1	B	334/345 (97%)	311 (93%)	23 (7%)	15 35
All	All	668/690 (97%)	626 (94%)	42 (6%)	18 40

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	110	ASP
1	B	210	ILE
1	B	180	SER
1	B	191	MET
1	B	344	ARG

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

Mol	Chain	Res	Type
1	B	142	ASN
1	B	145	HIS
1	B	386	GLN
1	B	335	GLN
1	B	342	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)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
3	KAP	B	1430	-	11,12,12	1.15	2 (18%)	11,14,14	2.60	3 (27%)
2	PLP	B	1429	1	15,15,16	1.41	2 (13%)	20,22,23	2.58	8 (40%)
3	KAP	A	1430	-	11,12,12	0.99	1 (9%)	11,14,14	3.35	3 (27%)
2	PLP	A	1429	1	15,15,16	1.42	3 (20%)	20,22,23	2.52	8 (40%)

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	KAP	B	1430	-	-	6/10/12/12	-
2	PLP	B	1429	1	-	2/6/6/8	0/1/1/1
3	KAP	A	1430	-	-	5/10/12/12	-
2	PLP	A	1429	1	-	2/6/6/8	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1429	PLP	O4P-C5A	-3.09	1.33	1.45
2	A	1429	PLP	O4P-C5A	-3.09	1.33	1.45
2	B	1429	PLP	O3-C3	-2.89	1.30	1.37
2	A	1429	PLP	O3-C3	-2.47	1.31	1.37
3	B	1430	KAP	CE-CZ	-2.28	1.48	1.51

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1430	KAP	CE-CZ-CH	8.75	133.79	116.94
3	B	1430	KAP	CE-CZ-CH	7.03	130.48	116.94
2	B	1429	PLP	O4P-C5A-C5	6.51	121.75	109.35
2	A	1429	PLP	O4P-C5A-C5	6.34	121.44	109.35
2	A	1429	PLP	C5A-C5-C6	-6.04	109.44	119.37

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1429	PLP	C4-C5-C5A-O4P
2	A	1429	PLP	C6-C5-C5A-O4P
2	B	1429	PLP	C4-C5-C5A-O4P
2	B	1429	PLP	C6-C5-C5A-O4P
3	B	1430	KAP	CD-CE-CZ-CH

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1430	KAP	3	0
3	A	1430	KAP	3	0
2	A	1429	PLP	1	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.