

Full wwPDB X-ray Structure Validation Report (i)

Mar 10, 2024 - 01:07 AM EST

PDB ID	:	4DPQ
Title	:	The structure of dihydrodipicolinate synthase 2 from Arabidopsis thaliana in
		complex with (S)-lysine
Authors	:	Griffin, M.D.W.; Billakanti, J.M.; Gerrard, J.A.; Dobson, R.C.J.; Pearce, F.G.
Deposited on	:	2012-02-14
Resolution	:	2.20 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 (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 (1)) were used in the production of this report:

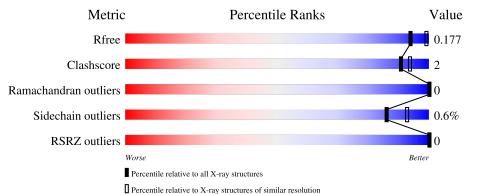
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA,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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 2.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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% 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	А	360	80%	5%•	15%
1	В	360	78%	7%	15%



4DPQ

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5065 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.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Δ	307	Total	С	Ν	0	\mathbf{S}	0	0	0
	1 A	307	2363	1502	411	440	10	0		
1	р	307	Total	С	Ν	0	S	0	0	0
I D	307	2356	1498	410	438	10	0	0	0	

• Molecule 1 is a protein called Dihydrodipicolinate synthase 2, chloroplastic.

Chain	Residue	Modelled	Actual	Comment	Reference
А	6	MET	-	expression tag	UNP Q9FVC8
А	7	HIS	-	expression tag	UNP Q9FVC8
А	8	HIS	-	expression tag	UNP Q9FVC8
А	9	HIS	-	expression tag	UNP Q9FVC8
А	10	HIS	-	expression tag	UNP Q9FVC8
A	11	HIS	-	expression tag	UNP Q9FVC8
А	12	HIS	-	expression tag	UNP Q9FVC8
А	13	GLY	-	expression tag	UNP Q9FVC8
А	14	LEU	-	expression tag	UNP Q9FVC8
A	15	PRO	-	expression tag	UNP Q9FVC8
А	16	ILE	-	expression tag	UNP Q9FVC8
A	17	PRO	-	expression tag	UNP Q9FVC8
A	18	ASN	-	expression tag	UNP Q9FVC8
A	19	PRO	-	expression tag	UNP Q9FVC8
А	20	LEU	-	expression tag	UNP Q9FVC8
А	21	LEU	-	expression tag	UNP Q9FVC8
А	22	GLY	-	expression tag	UNP Q9FVC8
А	23	LEU	-	expression tag	UNP Q9FVC8
А	24	ASP	-	expression tag	UNP Q9FVC8
А	25	SER	-	expression tag	UNP Q9FVC8
А	26	THR	-	expression tag	UNP Q9FVC8
А	27	GLU	-	expression tag	UNP Q9FVC8
А	28	ASN	-	expression tag	UNP Q9FVC8
А	29	LEU	-	expression tag	UNP Q9FVC8
А	30	TYR	-	expression tag	UNP Q9FVC8

There are 66 discrepancies between the modelled and reference sequences:

Continued on next page...



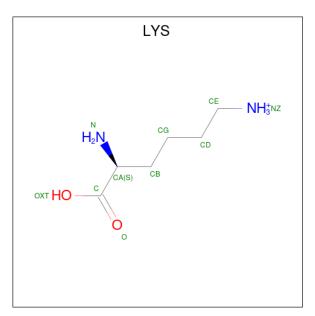
4I	\mathcal{D}	P	Q

		vious page			
Chain	Residue	Modelled	Actual	Comment	Reference
А	31	PHE	-	expression tag	UNP Q9FVC8
А	32	GLN	-	expression tag	UNP Q9FVC8
А	33	GLY	-	expression tag	UNP Q9FVC8
А	34	ILE	-	expression tag	UNP Q9FVC8
А	35	ASP	-	expression tag	UNP Q9FVC8
А	36	PRO	-	expression tag	UNP Q9FVC8
А	37	PHE	-	expression tag	UNP Q9FVC8
А	38	THR	-	expression tag	UNP Q9FVC8
В	6	MET	-	expression tag	UNP Q9FVC8
В	7	HIS	-	expression tag	UNP Q9FVC8
В	8	HIS	-	expression tag	UNP Q9FVC8
В	9	HIS	-	expression tag	UNP Q9FVC8
В	10	HIS	-	expression tag	UNP Q9FVC8
В	11	HIS	-	expression tag	UNP Q9FVC8
В	12	HIS	-	expression tag	UNP Q9FVC8
В	13	GLY	-	expression tag	UNP Q9FVC8
В	14	LEU	-	expression tag	UNP Q9FVC8
В	15	PRO	-	expression tag	UNP Q9FVC8
В	16	ILE	-	expression tag	UNP Q9FVC8
В	17	PRO	-	expression tag	UNP Q9FVC8
В	18	ASN	-	expression tag	UNP Q9FVC8
В	19	PRO	-	expression tag	UNP Q9FVC8
В	20	LEU	-	expression tag	UNP Q9FVC8
В	21	LEU	-	expression tag	UNP Q9FVC8
В	22	GLY	-	expression tag	UNP Q9FVC8
В	23	LEU	-	expression tag	UNP Q9FVC8
В	24	ASP	-	expression tag	UNP Q9FVC8
В	25	SER	-	expression tag	UNP Q9FVC8
В	26	THR	-	expression tag	UNP Q9FVC8
В	27	GLU	-	expression tag	UNP Q9FVC8
В	28	ASN	-	expression tag	UNP Q9FVC8
В	29	LEU	-	expression tag	UNP Q9FVC8
В	30	TYR	-	expression tag	UNP Q9FVC8
В	31	PHE	-	expression tag	UNP Q9FVC8
В	32	GLN	-	expression tag	UNP Q9FVC8
В	33	GLY	-	expression tag	UNP Q9FVC8
В	34	ILE		expression tag	UNP Q9FVC8
В	35	ASP	-	expression tag	UNP Q9FVC8
В	36	PRO	-	expression tag	UNP Q9FVC8
В	37	PHE	-	expression tag	UNP Q9FVC8
В	38	THR	-	expression tag	UNP Q9FVC8

• Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	3	Total Na 3 3	0	0
2	В	2	Total Na 2 2	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total C N O 10 6 2 2	0	0
3	В	1	Total C N O 10 6 2 2	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	161	Total O 161 161	0	0
4	В	160	Total O 160 160	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: Dihydrodipicolinate synthase 2, chloroplastic

Chain A:	80%	5%•	15%
MET HIS HIS HIS HIS HIS HIS HIS HIS CIY CIY CIY CIY CIY CIY CIY CIY CIY CIY	PHE GLN GLN GLY TLE ASP PRO PRO ALA ALA ALA ALA ALA ALA ALA FLA PRO PRO PRO PRO PRO ARG	SER LEU GLU VAL LYS	AJN THR N59 N59 N59 N59 N59 N59 N59 N59 N59 N59
V91 N167 N167 N167 N167 N167 N167 N167 N16	N300 P301 Y365 Y365		
• Molecule 1: Dihydrodipicolinate	synthase 2, chloroplastic		
Chain B:	78%	7%	15%
MET HIS HIS HIS HIS HIS HIS HIS HIS FIC FIC FIC FIC CIT FIC CIT CIT CIT CIT CIT CIT CIT CIT CIT C	PHE GLN GLN GLN ILE ALF PRO PRO ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	SER LEU GLU VAL LYS	ASN THR 118 159 160 160 164 V68



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	95.48Å 95.48Å 174.50Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.64 - 2.20	Depositor
Resolution (A)	36.64 - 2.20	EDS
% Data completeness	99.9 (36.64-2.20)	Depositor
(in resolution range)	99.9(36.64-2.20)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.12	Depositor
$< I/\sigma(I) > 1$	$2.52 (at 2.20 \text{\AA})$	Xtriage
Refinement program	REFMAC	Depositor
D D.	0.139 , 0.177	Depositor
R, R_{free}	0.140 , 0.177	DCC
R_{free} test set	2090 reflections $(5.02%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	23.9	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.42 , 44.1	EDS
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5065	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: 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		Bo	nd lengths	Bond angles		
	Unain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.94	3/2416~(0.1%)	1.02	7/3282~(0.2%)	
1	В	0.91	1/2409~(0.0%)	0.93	5/3274~(0.2%)	
All	All	0.93	4/4825~(0.1%)	0.98	12/6556~(0.2%)	

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
1	А	116	TRP	CD2-CE2	5.46	1.48	1.41
1	А	253	TRP	CD2-CE2	5.17	1.47	1.41
1	А	241	TRP	CD2-CE2	5.08	1.47	1.41
1	В	253	TRP	CD2-CE2	5.07	1.47	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	199	ARG	NE-CZ-NH2	-17.27	111.66	120.30
1	А	199	ARG	NE-CZ-NH1	12.48	126.54	120.30
1	А	199	ARG	CG-CD-NE	-6.66	97.81	111.80
1	А	146	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	В	178	LEU	CB-CG-CD2	-6.42	100.08	111.00
1	А	199	ARG	CD-NE-CZ	6.00	132.00	123.60
1	В	342	ARG	CG-CD-NE	5.98	124.36	111.80
1	В	199	ARG	NE-CZ-NH2	-5.71	117.45	120.30
1	В	364	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	А	250	ASP	CB-CG-OD1	5.16	122.95	118.30
1	А	88	ASP	CB-CG-OD1	5.05	122.85	118.30
1	В	273	ARG	NE-CZ-NH2	-5.00	117.80	120.30

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	А	2363	0	2332	8	0
1	В	2356	0	2319	11	0
2	А	3	0	0	0	0
2	В	2	0	0	0	0
3	А	10	0	12	0	0
3	В	10	0	12	0	0
4	А	161	0	0	0	0
4	В	160	0	0	0	0
All	All	5065	0	4675	16	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 2.

All (16) 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:364:ARG:NH2	1:B:153:GLU:OE2	2.19	0.64
1:B:60:THR:HG22	1:B:64:LYS:HE3	1.92	0.51
1:A:167:ASN:HB2	1:A:178:LEU:HD11	1.97	0.46
1:B:194:TYR:CD1	1:B:222:LYS:HD3	2.52	0.45
1:A:300:ASN:OD1	1:A:301:PRO:HA	2.16	0.44
1:A:68:VAL:HG21	1:A:273:ARG:HA	1.99	0.44
1:B:75:PRO:HB3	1:B:314:SER:HB2	2.00	0.44
1:B:143:ASN:HA	1:B:168:PRO:HA	2.00	0.44
1:A:213:SER:HA	1:A:218:LEU:HD23	1.99	0.44
1:B:294:TRP:CZ2	1:B:333:PHE:HB2	2.53	0.44
1:A:365:TYR:OXT	1:B:146:ARG:NH1	2.52	0.42
1:B:68:VAL:HG21	1:B:273:ARG:HA	2.01	0.42
1:A:72:ILE:HD13	1:A:91:VAL:HG22	2.01	0.42
1:A:199:ARG:HH21	1:B:171:GLY:HA2	1.85	0.41
1:B:205:PRO:HA	1:B:206:PRO:HD3	2.00	0.41
1:B:213:SER:HA	1:B:218:LEU:HD23	2.02	0.41

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	Perce	ntiles
1	А	305/360~(85%)	301 (99%)	4 (1%)	0	100	100
1	В	305/360~(85%)	302~(99%)	3~(1%)	0	100	100
All	All	610/720~(85%)	603~(99%)	7 (1%)	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	А	253/306~(83%)	251~(99%)	2(1%)	81 90		
1	В	251/306~(82%)	250~(100%)	1 (0%)	91 96		
All	All	504/612~(82%)	501 (99%)	3 (1%)	86 93		

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	214	GLN
1	А	273	ARG
1	В	251	SER

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such side chains are listed below:



Mol	Chain	Res	Type
1	В	352	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 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 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	Turne	Chain	Dec	Link	В	ond leng	gths	B	ond ang	gles
IVIOI	Type	Unam	Res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	LYS	А	404	-	8,9,9	1.36	2 (25%)	9,10,10	0.90	0
3	LYS	В	403	-	8,9,9	0.93	0	9,10,10	1.24	2 (22%)

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	LYS	A	404	-	-	0/9/9/9	-
3	LYS	В	403	-	-	0/9/9/9	-

All (2) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
3	А	404	LYS	O-C	2.77	1.30	1.22
3	А	404	LYS	CB-CA	2.03	1.57	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	В	403	LYS	OXT-C-CA	2.15	120.72	113.38
3	В	403	LYS	OXT-C-O	-2.05	119.44	124.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2		Z>2	$OWAB(Å^2)$	Q < 0.9
1	А	307/360~(85%)	-0.77	0	100	100	14, 22, 35, 47	0
1	В	307/360~(85%)	-0.90	0	100	100	15, 21, 34, 50	0
All	All	614/720~(85%)	-0.84	0	100	100	14, 22, 35, 50	0

There are no RSRZ outliers to report.

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^{th} 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	$B-factors(A^2)$	Q<0.9
2	NA	А	402	1/1	0.92	0.09	42,42,42,42	0
2	NA	В	402	1/1	0.96	0.21	40,40,40,40	0
2	NA	А	401	1/1	0.97	0.11	27,27,27,27	0
3	LYS	А	404	10/10	0.97	0.14	19,20,22,22	0
3	LYS	В	403	10/10	0.97	0.12	19,21,23,23	0
2	NA	В	401	1/1	0.98	0.07	27,27,27,27	0
2	NA	А	403	1/1	1.00	0.14	33,33,33,33	0



6.5 Other polymers (i)

There are no such residues in this entry.

