



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 01:05 am GMT

PDB ID : 3N2O  
Title : X-ray crystal structure of arginine decarboxylase complexed with Arginine from *Vibrio vulnificus*  
Authors : Deng, X.; Lee, J.; Michael, A.J.; Tomchick, D.R.; Goldsmith, E.J.; Phillips, M.A.  
Deposited on : 2010-05-18  
Resolution : 2.30 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	1.13
EDS	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

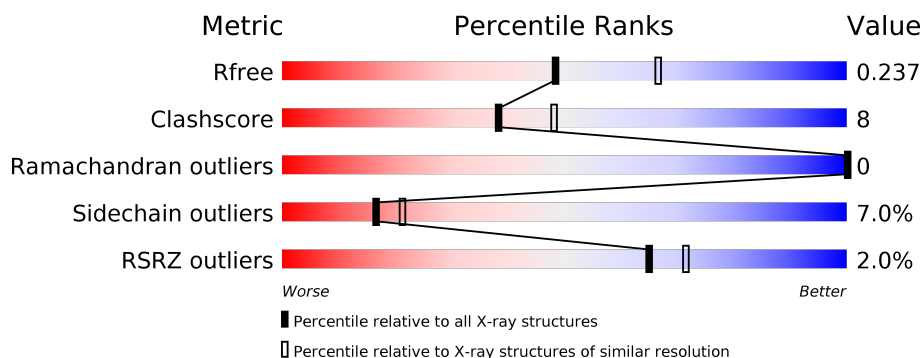
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	648	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>19%</div> <div>• •</div> </div> </div>
1	B	648	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>• •</div> </div> </div>
1	C	648	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>20%</div> <div>• •</div> </div> </div>
1	D	648	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>18%</div> <div>• •</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	AG2	A	1002	-	-	-	X
3	AG2	C	1002	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20592 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 Biosynthetic arginine decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	630	Total	C	N	O	S	0	0	0
			5022	3165	871	968	18			
1	B	629	Total	C	N	O	S	0	0	0
			5013	3159	869	967	18			
1	C	628	Total	C	N	O	S	0	0	0
			5005	3153	868	966	18			
1	D	629	Total	C	N	O	S	0	0	0
			5013	3159	869	967	18			

There are 32 discrepancies between the modelled and reference sequences:

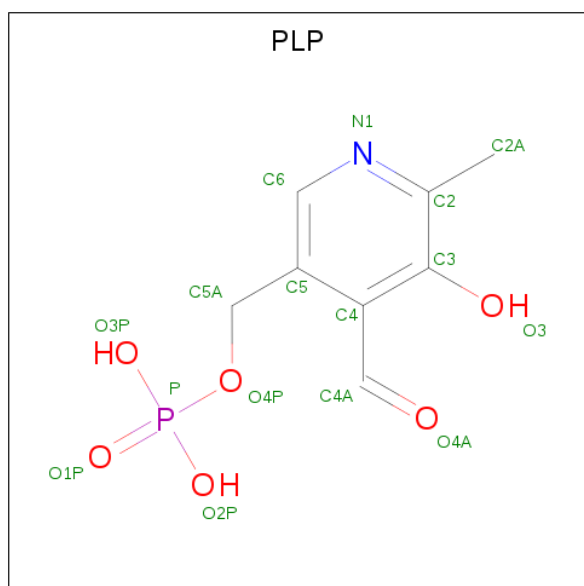
Chain	Residue	Modelled	Actual	Comment	Reference
A	641	LEU	-	EXPRESSION TAG	UNP Q7MK24
A	642	GLU	-	EXPRESSION TAG	UNP Q7MK24
A	643	HIS	-	EXPRESSION TAG	UNP Q7MK24
A	644	HIS	-	EXPRESSION TAG	UNP Q7MK24
A	645	HIS	-	EXPRESSION TAG	UNP Q7MK24
A	646	HIS	-	EXPRESSION TAG	UNP Q7MK24
A	647	HIS	-	EXPRESSION TAG	UNP Q7MK24
A	648	HIS	-	EXPRESSION TAG	UNP Q7MK24
B	641	LEU	-	EXPRESSION TAG	UNP Q7MK24
B	642	GLU	-	EXPRESSION TAG	UNP Q7MK24
B	643	HIS	-	EXPRESSION TAG	UNP Q7MK24
B	644	HIS	-	EXPRESSION TAG	UNP Q7MK24
B	645	HIS	-	EXPRESSION TAG	UNP Q7MK24
B	646	HIS	-	EXPRESSION TAG	UNP Q7MK24
B	647	HIS	-	EXPRESSION TAG	UNP Q7MK24
B	648	HIS	-	EXPRESSION TAG	UNP Q7MK24
C	641	LEU	-	EXPRESSION TAG	UNP Q7MK24
C	642	GLU	-	EXPRESSION TAG	UNP Q7MK24
C	643	HIS	-	EXPRESSION TAG	UNP Q7MK24
C	644	HIS	-	EXPRESSION TAG	UNP Q7MK24
C	645	HIS	-	EXPRESSION TAG	UNP Q7MK24

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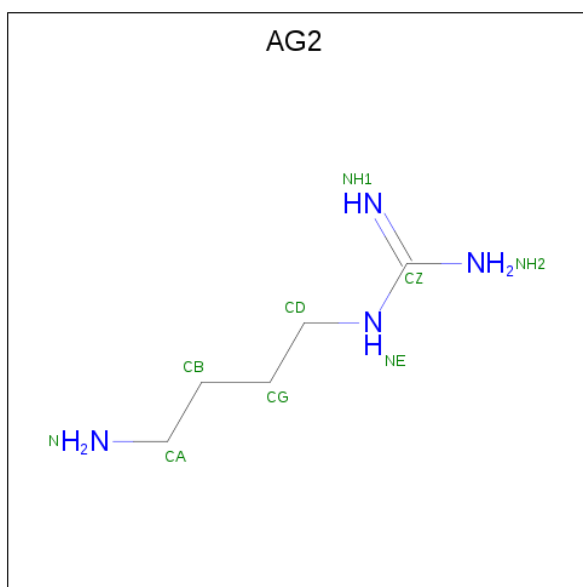
Chain	Residue	Modelled	Actual	Comment	Reference
C	646	HIS	-	EXPRESSION TAG	UNP Q7MK24
C	647	HIS	-	EXPRESSION TAG	UNP Q7MK24
C	648	HIS	-	EXPRESSION TAG	UNP Q7MK24
D	641	LEU	-	EXPRESSION TAG	UNP Q7MK24
D	642	GLU	-	EXPRESSION TAG	UNP Q7MK24
D	643	HIS	-	EXPRESSION TAG	UNP Q7MK24
D	644	HIS	-	EXPRESSION TAG	UNP Q7MK24
D	645	HIS	-	EXPRESSION TAG	UNP Q7MK24
D	646	HIS	-	EXPRESSION TAG	UNP Q7MK24
D	647	HIS	-	EXPRESSION TAG	UNP Q7MK24
D	648	HIS	-	EXPRESSION TAG	UNP Q7MK24

- 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		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is AGMATINE (three-letter code: AG2) (formula:  $C_5H_{14}N_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			9	5	4		
3	B	1	Total	C	N	0	0
			9	5	4		
3	C	1	Total	C	N	0	0
			9	5	4		
3	D	1	Total	C	N	0	0
			9	5	4		

- Molecule 4 is water.

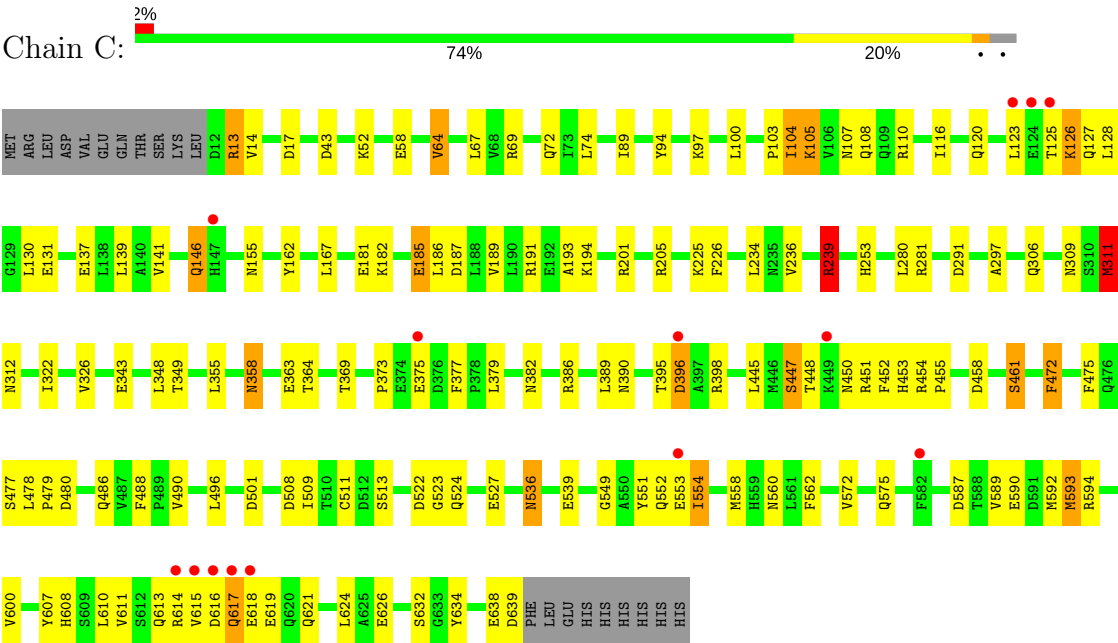
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	140	Total	O	0	0
			140	140		
4	C	103	Total	O	0	0
			103	103		
4	D	99	Total	O	0	0
			99	99		

These plots are drawn for all protein, RNA and DNA 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.

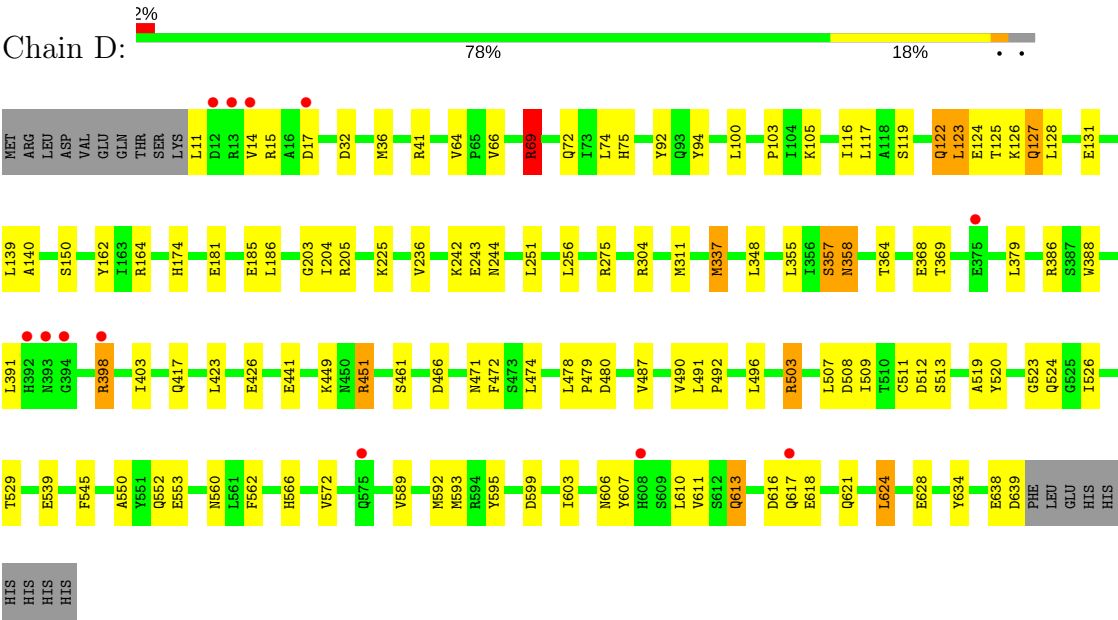
- Chain A:
- 
- Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 2.00). The x-axis lists amino acids from MET to Y634. A color scale at the top indicates conservation levels: red (high) to grey (low), with markers at 76% and 19%. Red dots above specific residues indicate high conservation.

- Chain B:
- 
- 2%
- 79%
- 15%
- •
- MET ARG LEU ASP VAL GLU GLN THR SER LYS L11 D11 R13 V14 D17 Y18 N19 W23 D32 M36 Y37 V38 S39 P40 R41 S42 L50 I53 Q61 V64 R69 F70 P71 Q72 R77 Y94 K97 V101 K105 E115 I116 L117 Q120 A121

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● Molecule 1: Biosynthetic arginine decarboxylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.65Å 119.36Å 121.84Å 90.00° 96.30° 90.00°	Depositor
Resolution (Å)	121.10 – 2.30 49.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.8 (121.10-2.30) 98.8 (49.69-2.30)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.66 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.179 , 0.239 0.179 , 0.237	Depositor DCC
$R_{free}$ test set	6366 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.6	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 50.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20592	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: AG2, PLP

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	0.99	3/5119 (0.1%)	0.90	7/6939 (0.1%)
1	B	1.05	3/5110 (0.1%)	0.96	9/6928 (0.1%)
1	C	1.05	6/5102 (0.1%)	0.93	7/6917 (0.1%)
1	D	1.01	2/5110 (0.0%)	0.91	8/6928 (0.1%)
All	All	1.03	14/20441 (0.1%)	0.93	31/27712 (0.1%)

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	185	GLU	CG-CD	6.70	1.61	1.51
1	B	185	GLU	CG-CD	6.58	1.61	1.51
1	C	311	MET	CG-SD	-6.52	1.64	1.81
1	A	185	GLU	CG-CD	6.20	1.61	1.51
1	C	551	TYR	CD1-CE1	-5.77	1.30	1.39

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	69	ARG	NE-CZ-NH2	-9.01	115.80	120.30
1	B	517	ILE	CG1-CB-CG2	-8.84	91.94	111.40
1	B	201	ARG	NE-CZ-NH2	-8.17	116.22	120.30
1	D	123	LEU	CA-CB-CG	7.72	133.05	115.30
1	A	502	ARG	NE-CZ-NH2	-7.50	116.55	120.30

There are no chirality outliers.

There are no planarity outliers.

## 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	5022	0	4918	90	0
1	B	5013	0	4905	83	0
1	C	5005	0	4893	102	0
1	D	5013	0	4905	82	0
2	A	15	0	6	1	0
2	B	15	0	7	0	0
2	C	15	0	6	1	0
2	D	15	0	6	0	0
3	A	9	0	14	3	0
3	B	9	0	14	1	0
3	C	9	0	14	0	0
3	D	9	0	14	0	0
4	A	101	0	0	0	0
4	B	140	0	0	1	0
4	C	103	0	0	1	0
4	D	99	0	0	0	0
All	All	20592	0	19702	326	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 8.

The worst 5 of 326 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:554:ILE:HG23	1:A:555:LEU:CD1	1.79	1.12
1:A:554:ILE:HG23	1:A:555:LEU:HD12	1.31	1.08
1:B:590:GLU:HG3	1:B:600:VAL:HG11	1.35	1.06
1:C:396:ASP:OD1	1:C:398:ARG:HD3	1.61	1.00
1:B:191:ARG:HH11	1:B:191:ARG:HG3	1.27	0.98

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	628/648 (97%)	606 (96%)	22 (4%)	0	100	100
1	B	627/648 (97%)	610 (97%)	17 (3%)	0	100	100
1	C	626/648 (97%)	605 (97%)	21 (3%)	0	100	100
1	D	627/648 (97%)	606 (97%)	21 (3%)	0	100	100
All	All	2508/2592 (97%)	2427 (97%)	81 (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	549/567 (97%)	516 (94%)	33 (6%)	21	28
1	B	548/567 (97%)	509 (93%)	39 (7%)	16	21
1	C	547/567 (96%)	502 (92%)	45 (8%)	12	15
1	D	548/567 (97%)	511 (93%)	37 (7%)	17	22
All	All	2192/2268 (97%)	2038 (93%)	154 (7%)	16	21

5 of 154 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	560	ASN
1	C	281	ARG
1	D	524	GLN

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Mol	Chain	Res	Type
1	B	624	LEU
1	C	110	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	524	GLN
1	C	146	GLN
1	D	524	GLN
1	B	536	ASN
1	B	571	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

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	$\# Z  > 2$
2	PLP	A	1001	1	15,15,16	2.16	4 (26%)	20,22,23	1.40	4 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	AG2	A	1002	-	8,8,8	2.86	3 (37%)	7,8,8	3.15	3 (42%)
2	PLP	B	1001	1	15,15,16	1.77	3 (20%)	20,22,23	1.53	3 (15%)
3	AG2	B	1002	-	8,8,8	3.00	3 (37%)	7,8,8	2.54	3 (42%)
2	PLP	C	1001	1	15,15,16	2.47	5 (33%)	20,22,23	1.93	6 (30%)
3	AG2	C	1002	-	8,8,8	2.98	3 (37%)	7,8,8	2.88	3 (42%)
2	PLP	D	1001	1	15,15,16	2.29	5 (33%)	20,22,23	1.50	5 (25%)
3	AG2	D	1002	-	8,8,8	3.05	3 (37%)	7,8,8	2.83	3 (42%)

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
2	PLP	A	1001	1	-	0/6/6/8	0/1/1/1
3	AG2	A	1002	-	-	0/6/6/6	0/0/0/0
2	PLP	B	1001	1	-	0/6/6/8	0/1/1/1
3	AG2	B	1002	-	-	0/6/6/6	0/0/0/0
2	PLP	C	1001	1	-	0/6/6/8	0/1/1/1
3	AG2	C	1002	-	-	0/6/6/6	0/0/0/0
2	PLP	D	1001	1	-	0/6/6/8	0/1/1/1
3	AG2	D	1002	-	-	0/6/6/6	0/0/0/0

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1001	PLP	C3-C2	-5.80	1.36	1.40
2	A	1001	PLP	C3-C2	-4.57	1.37	1.40
2	D	1001	PLP	C3-C2	-4.38	1.37	1.40
2	D	1001	PLP	C4A-C4	-4.21	1.43	1.51
2	A	1001	PLP	P-O2P	-3.89	1.39	1.54

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1002	AG2	NH2-CZ-NE	-5.28	106.84	119.30
3	B	1002	AG2	NE-CZ-NH1	-5.06	111.48	120.58
3	C	1002	AG2	NE-CZ-NH1	-4.92	111.74	120.58
3	A	1002	AG2	NH2-CZ-NE	-4.80	107.98	119.30
3	A	1002	AG2	NE-CZ-NH1	-4.72	112.10	120.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	PLP	1	0
3	A	1002	AG2	3	0
3	B	1002	AG2	1	0
2	C	1001	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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	630/648 (97%)	-0.10	12 (1%) 66 73	16, 26, 46, 68	0
1	B	629/648 (97%)	0.02	12 (1%) 66 73	13, 25, 45, 69	0
1	C	628/648 (96%)	-0.04	14 (2%) 62 69	14, 26, 50, 68	0
1	D	629/648 (97%)	-0.03	12 (1%) 66 73	15, 26, 51, 68	0
All	All	2516/2592 (97%)	-0.04	50 (1%) 65 71	13, 26, 48, 69	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	LEU	6.9
1	D	393	ASN	5.6
1	D	398	ARG	4.7
1	B	124	GLU	4.7
1	D	617	GLN	4.1

### 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 carbohydrates 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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	AG2	C	1002	9/9	0.61	0.42	49,54,63,64	0
3	AG2	D	1002	9/9	0.67	0.31	41,46,52,52	0
3	AG2	B	1002	9/9	0.70	0.35	45,49,53,54	0
3	AG2	A	1002	9/9	0.79	0.53	49,52,58,58	0
2	PLP	D	1001	15/16	0.92	0.14	19,27,34,36	0
2	PLP	C	1001	15/16	0.95	0.14	20,30,36,40	0
2	PLP	A	1001	15/16	0.97	0.10	25,28,34,35	0
2	PLP	B	1001	15/16	0.97	0.16	21,29,32,35	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.