



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:08 am GMT

PDB ID : 4ZM3
Title : Crystal structure of PLP-Dependent 3-Aminobenzoate Synthase PctV wild-type
Authors : Hirayama, A.; Miyanaga, A.; Kudo, F.; Eguchi, T.
Deposited on : 2015-05-02
Resolution : 2.27 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

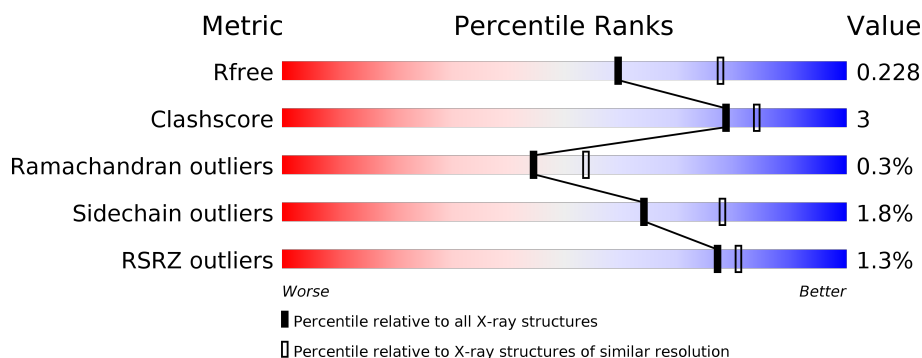
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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}	100719	5609 (2.30-2.26)
Clashscore	112137	6364 (2.30-2.26)
Ramachandran outliers	110173	6281 (2.30-2.26)
Sidechain outliers	110143	6281 (2.30-2.26)
RSRZ outliers	101464	5639 (2.30-2.26)

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 ≥ 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	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 76%, green 16%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 76% 7% • 16% </div> </div>
1	B	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 2%, yellow 76%, green 18%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 2% 76% 5% • 18% </div> </div>
1	C	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 75%, green 17%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 75% 7% 17% </div> </div>
1	D	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 77%, green 17%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 77% 5% • 17% </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
4	PEG	D	504	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12181 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 Aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			2960	1870	543	536	11			
1	B	381	Total	C	N	O	S	0	0	0
			2906	1836	534	526	10			
1	C	384	Total	C	N	O	S	0	0	0
			2925	1847	538	529	11			
1	D	387	Total	C	N	O	S	0	0	0
			2947	1859	540	536	12			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP A8R0K5
A	-18	GLY	-	expression tag	UNP A8R0K5
A	-17	SER	-	expression tag	UNP A8R0K5
A	-16	SER	-	expression tag	UNP A8R0K5
A	-15	HIS	-	expression tag	UNP A8R0K5
A	-14	HIS	-	expression tag	UNP A8R0K5
A	-13	HIS	-	expression tag	UNP A8R0K5
A	-12	HIS	-	expression tag	UNP A8R0K5
A	-11	HIS	-	expression tag	UNP A8R0K5
A	-10	HIS	-	expression tag	UNP A8R0K5
A	-9	SER	-	expression tag	UNP A8R0K5
A	-8	SER	-	expression tag	UNP A8R0K5
A	-7	GLY	-	expression tag	UNP A8R0K5
A	-6	LEU	-	expression tag	UNP A8R0K5
A	-5	VAL	-	expression tag	UNP A8R0K5
A	-4	PRO	-	expression tag	UNP A8R0K5
A	-3	ARG	-	expression tag	UNP A8R0K5
A	-2	GLY	-	expression tag	UNP A8R0K5
A	-1	SER	-	expression tag	UNP A8R0K5
A	0	HIS	-	expression tag	UNP A8R0K5
B	-19	MET	-	expression tag	UNP A8R0K5

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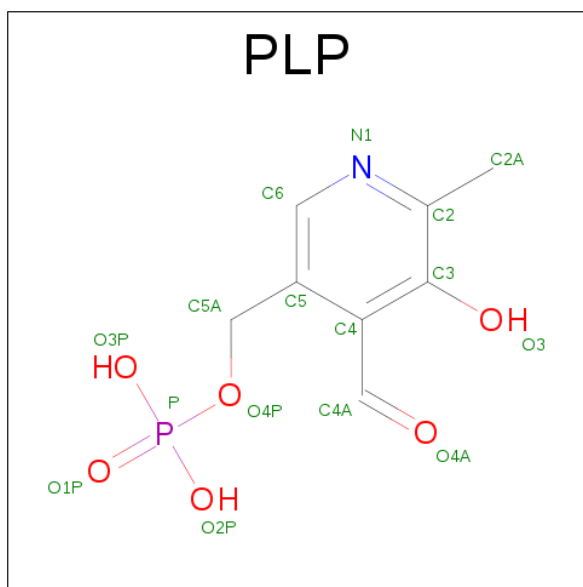
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP A8R0K5
B	-17	SER	-	expression tag	UNP A8R0K5
B	-16	SER	-	expression tag	UNP A8R0K5
B	-15	HIS	-	expression tag	UNP A8R0K5
B	-14	HIS	-	expression tag	UNP A8R0K5
B	-13	HIS	-	expression tag	UNP A8R0K5
B	-12	HIS	-	expression tag	UNP A8R0K5
B	-11	HIS	-	expression tag	UNP A8R0K5
B	-10	HIS	-	expression tag	UNP A8R0K5
B	-9	SER	-	expression tag	UNP A8R0K5
B	-8	SER	-	expression tag	UNP A8R0K5
B	-7	GLY	-	expression tag	UNP A8R0K5
B	-6	LEU	-	expression tag	UNP A8R0K5
B	-5	VAL	-	expression tag	UNP A8R0K5
B	-4	PRO	-	expression tag	UNP A8R0K5
B	-3	ARG	-	expression tag	UNP A8R0K5
B	-2	GLY	-	expression tag	UNP A8R0K5
B	-1	SER	-	expression tag	UNP A8R0K5
B	0	HIS	-	expression tag	UNP A8R0K5
C	-19	MET	-	expression tag	UNP A8R0K5
C	-18	GLY	-	expression tag	UNP A8R0K5
C	-17	SER	-	expression tag	UNP A8R0K5
C	-16	SER	-	expression tag	UNP A8R0K5
C	-15	HIS	-	expression tag	UNP A8R0K5
C	-14	HIS	-	expression tag	UNP A8R0K5
C	-13	HIS	-	expression tag	UNP A8R0K5
C	-12	HIS	-	expression tag	UNP A8R0K5
C	-11	HIS	-	expression tag	UNP A8R0K5
C	-10	HIS	-	expression tag	UNP A8R0K5
C	-9	SER	-	expression tag	UNP A8R0K5
C	-8	SER	-	expression tag	UNP A8R0K5
C	-7	GLY	-	expression tag	UNP A8R0K5
C	-6	LEU	-	expression tag	UNP A8R0K5
C	-5	VAL	-	expression tag	UNP A8R0K5
C	-4	PRO	-	expression tag	UNP A8R0K5
C	-3	ARG	-	expression tag	UNP A8R0K5
C	-2	GLY	-	expression tag	UNP A8R0K5
C	-1	SER	-	expression tag	UNP A8R0K5
C	0	HIS	-	expression tag	UNP A8R0K5
D	-19	MET	-	expression tag	UNP A8R0K5
D	-18	GLY	-	expression tag	UNP A8R0K5
D	-17	SER	-	expression tag	UNP A8R0K5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP A8R0K5
D	-15	HIS	-	expression tag	UNP A8R0K5
D	-14	HIS	-	expression tag	UNP A8R0K5
D	-13	HIS	-	expression tag	UNP A8R0K5
D	-12	HIS	-	expression tag	UNP A8R0K5
D	-11	HIS	-	expression tag	UNP A8R0K5
D	-10	HIS	-	expression tag	UNP A8R0K5
D	-9	SER	-	expression tag	UNP A8R0K5
D	-8	SER	-	expression tag	UNP A8R0K5
D	-7	GLY	-	expression tag	UNP A8R0K5
D	-6	LEU	-	expression tag	UNP A8R0K5
D	-5	VAL	-	expression tag	UNP A8R0K5
D	-4	PRO	-	expression tag	UNP A8R0K5
D	-3	ARG	-	expression tag	UNP A8R0K5
D	-2	GLY	-	expression tag	UNP A8R0K5
D	-1	SER	-	expression tag	UNP A8R0K5
D	0	HIS	-	expression tag	UNP A8R0K5

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



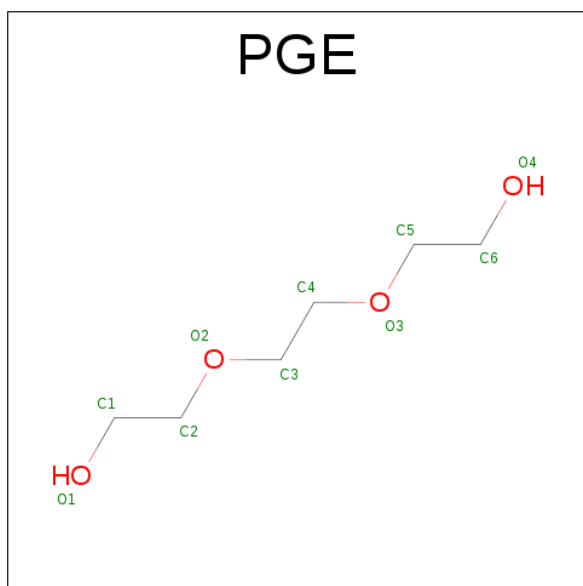
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			16	8	1	6	1		
2	B	1	Total	C	N	O	P	0	0
			16	8	1	6	1		
2	C	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

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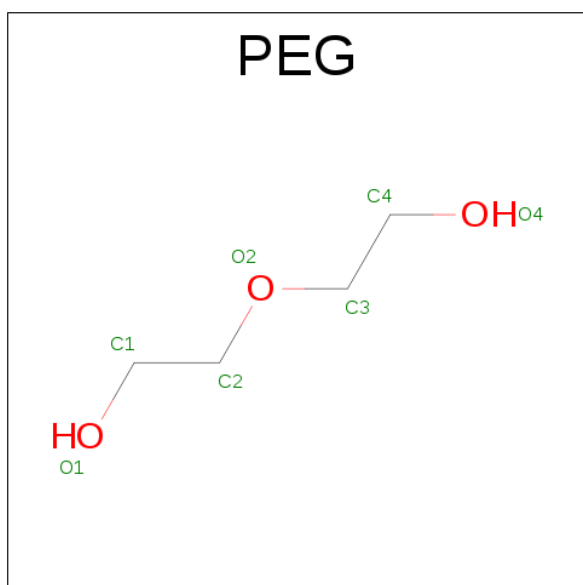
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0
4	D	1	Total C O 7 4 3	0	0

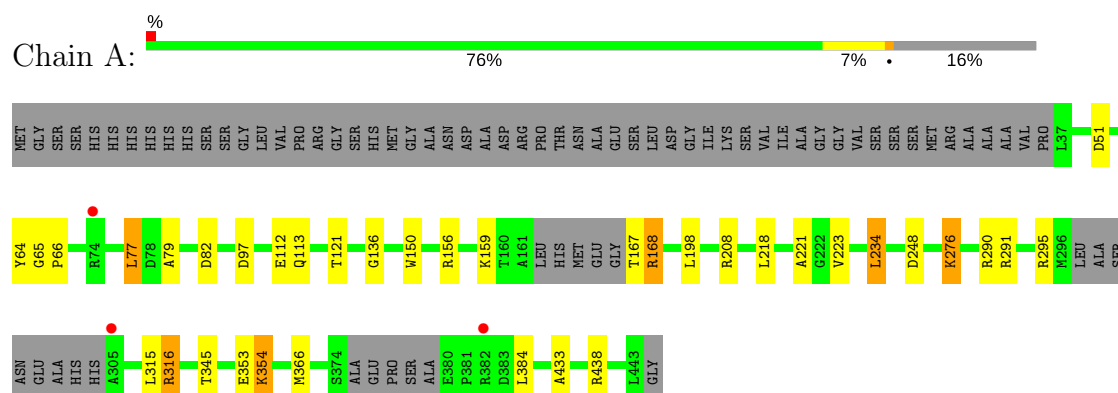
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	80	Total O 80 80	0	0
5	B	77	Total O 77 77	0	0
5	C	99	Total O 99 99	0	0
5	D	92	Total O 92 92	0	0

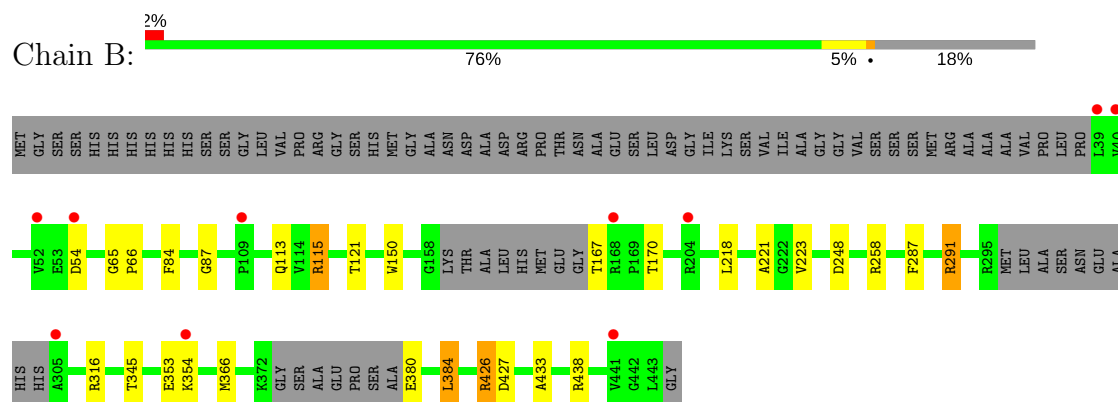
3 Residue-property plots

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.

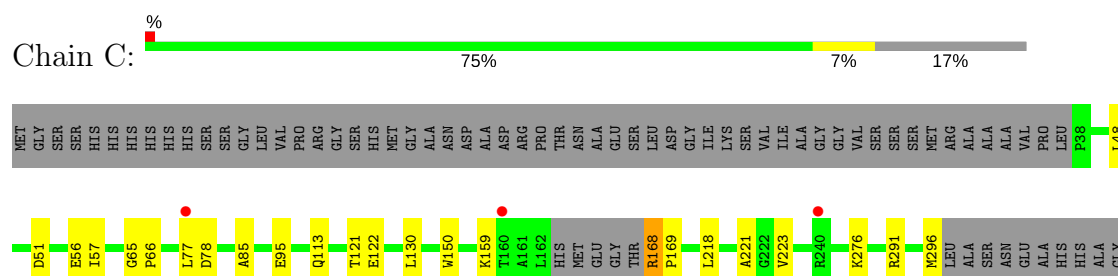
• Molecule 1: Aminotransferase

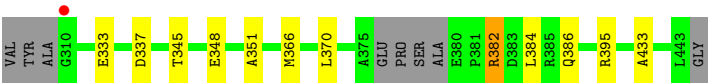


• Molecule 1: Aminotransferase

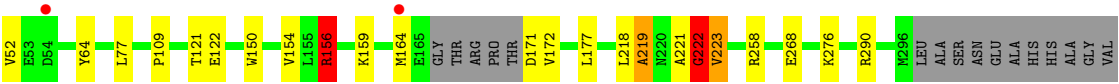
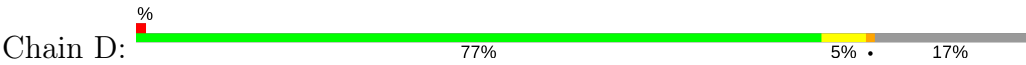


• Molecule 1: Aminotransferase





● Molecule 1: Aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.99Å 170.83Å 74.57Å 90.00° 98.33° 90.00°	Depositor
Resolution (Å)	42.85 – 2.27 42.85 – 2.27	Depositor EDS
% Data completeness (in resolution range)	94.8 (42.85-2.27) 94.8 (42.85-2.27)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.27Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.180 , 0.222 0.187 , 0.228	Depositor DCC
R_{free} test set	3225 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 55.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12181	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, PGE, 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	0.69	0/3016	0.85	7/4089 (0.2%)
1	B	0.66	0/2961	0.84	3/4015 (0.1%)
1	C	0.70	0/2980	0.83	3/4038 (0.1%)
1	D	0.73	0/3003	0.91	8/4070 (0.2%)
All	All	0.70	0/11960	0.86	21/16212 (0.1%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	156	ARG	NE-CZ-NH2	-10.01	115.29	120.30
1	D	156	ARG	NE-CZ-NH1	8.90	124.75	120.30
1	A	295	ARG	NE-CZ-NH1	7.61	124.10	120.30
1	D	334	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	D	258	ARG	NE-CZ-NH2	-6.67	116.96	120.30
1	A	77	LEU	CB-CA-C	6.52	122.58	110.20
1	C	366	MET	CG-SD-CE	-6.24	90.22	100.20
1	C	337	ASP	CB-CG-OD2	6.17	123.86	118.30
1	A	366	MET	CG-SD-CE	-6.11	90.43	100.20
1	D	222	GLY	N-CA-C	6.10	128.34	113.10
1	B	426	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	A	156	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	D	219	ALA	CB-CA-C	-5.83	101.35	110.10
1	D	290	ARG	CB-CG-CD	5.81	126.71	111.60
1	C	382	ARG	NE-CZ-NH1	5.77	123.19	120.30
1	B	366	MET	CG-SD-CE	-5.70	91.09	100.20
1	D	172	VAL	CB-CA-C	-5.53	100.90	111.40
1	A	234	LEU	CA-CB-CG	5.46	127.86	115.30
1	A	438	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	B	316	ARG	NE-CZ-NH2	-5.39	117.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	316	ARG	NE-CZ-NH2	-5.32	117.64	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	2960	0	2982	24	1
1	B	2906	0	2922	19	1
1	C	2925	0	2950	26	0
1	D	2947	0	2961	23	0
2	A	16	0	7	1	0
2	B	16	0	8	1	0
2	C	16	0	8	0	0
2	D	16	0	7	0	0
3	C	10	0	14	2	0
4	D	21	0	30	0	0
5	A	80	0	0	0	0
5	B	77	0	0	1	0
5	C	99	0	0	0	0
5	D	92	0	0	1	0
All	All	12181	0	11889	79	1

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 3.

All (79) 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:115:ARG:HD2	1:B:287:PHE:CE1	2.01	0.96
1:B:115:ARG:HD2	1:B:287:PHE:HE1	1.35	0.86
1:A:290:ARG:NH1	1:D:397:ARG:HD3	2.10	0.67
1:A:77:LEU:HB3	1:B:84:PHE:HB3	1.79	0.63
1:A:221:ALA:HB1	1:A:384:LEU:HD13	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:121:THR:HG21	1:D:150:TRP:CE2	2.33	0.63
1:A:113:GLN:HE21	1:A:291:ARG:HG2	1.65	0.62
1:C:85:ALA:HA	1:D:77:LEU:CD1	2.29	0.62
1:C:221:ALA:HB1	1:C:384:LEU:HD13	1.82	0.61
1:C:121:THR:HG21	1:C:150:TRP:CE2	2.35	0.61
1:A:290:ARG:HH11	1:D:397:ARG:HD3	1.65	0.61
1:C:85:ALA:HA	1:D:77:LEU:HD12	1.83	0.60
1:C:113:GLN:HE21	1:C:291:ARG:HG2	1.66	0.59
1:B:353:GLU:O	1:B:354:LYS:CG	2.51	0.59
1:A:290:ARG:NH1	1:D:397:ARG:CD	2.66	0.59
1:A:121:THR:HG21	1:A:150:TRP:CE2	2.38	0.58
1:B:121:THR:HG21	1:B:150:TRP:CE2	2.39	0.58
1:A:353:GLU:C	1:A:354:LYS:HD3	2.26	0.56
1:D:121:THR:HG21	1:D:150:TRP:CD2	2.41	0.56
1:B:353:GLU:O	1:B:354:LYS:HG3	2.06	0.55
1:D:334:ARG:NH2	5:D:602:HOH:O	2.33	0.55
1:C:348:GLU:HA	3:C:502:PGE:H42	1.89	0.55
1:C:130:LEU:CD1	1:C:296:MET:HB3	2.37	0.54
1:C:168:ARG:HG3	1:C:169:PRO:HD2	1.90	0.53
1:A:82:ASP:OD2	1:A:316:ARG:NH2	2.42	0.53
1:B:221:ALA:HB1	1:B:384:LEU:HG	1.92	0.52
1:C:56:GLU:C	1:C:57:ILE:HG13	2.30	0.52
1:D:64:TYR:O	1:D:276:LYS:HE3	2.10	0.52
1:A:79:ALA:HB1	1:A:316:ARG:NH1	2.26	0.51
1:B:221:ALA:HB1	1:B:384:LEU:CG	2.41	0.50
1:B:121:THR:HG21	1:B:150:TRP:CD2	2.47	0.50
1:C:121:THR:HG21	1:C:150:TRP:CD2	2.47	0.50
1:A:112:GLU:OE2	1:D:397:ARG:HD3	2.11	0.49
1:C:150:TRP:CZ2	1:D:122:GLU:HG3	2.46	0.49
1:D:218:LEU:O	1:D:223:VAL:HA	2.12	0.49
1:A:97:ASP:HA	1:A:315:LEU:HD23	1.94	0.49
1:A:113:GLN:HE21	1:A:291:ARG:CG	2.24	0.49
1:B:345:THR:CG2	1:B:433:ALA:HB2	2.43	0.48
1:C:351:ALA:HB3	3:C:502:PGE:H4	1.94	0.48
1:D:109:PRO:HB2	1:D:268:GLU:OE2	2.14	0.48
1:B:113:GLN:HE21	1:B:291:ARG:HG2	1.79	0.48
1:B:354:LYS:O	1:B:354:LYS:HG3	2.12	0.47
1:C:345:THR:CG2	1:C:433:ALA:HB2	2.44	0.47
1:C:48:LEU:HD13	1:C:56:GLU:OE2	2.13	0.47
1:C:95:GLU:HG2	1:D:52:VAL:HG12	1.95	0.47
1:C:113:GLN:HE21	1:C:291:ARG:CG	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:345:THR:CG2	1:D:433:ALA:HB2	2.45	0.46
1:A:345:THR:CG2	1:A:433:ALA:HB2	2.45	0.46
1:A:113:GLN:NE2	1:A:291:ARG:HG2	2.30	0.46
1:A:218:LEU:O	1:A:223:VAL:HA	2.16	0.45
1:D:219:ALA:C	1:D:221:ALA:N	2.66	0.45
1:A:121:THR:HG21	1:A:150:TRP:CD2	2.51	0.45
1:B:218:LEU:O	1:B:223:VAL:HA	2.17	0.45
1:C:113:GLN:NE2	1:C:291:ARG:HG2	2.31	0.44
1:C:122:GLU:HG3	1:D:150:TRP:CZ2	2.52	0.44
1:C:218:LEU:O	1:C:223:VAL:HA	2.18	0.44
1:B:248:ASP:OD2	2:B:501:PLP:N1	2.51	0.43
1:A:136:GLY:HA3	1:D:177:LEU:HD22	1.99	0.43
1:A:65:GLY:N	1:A:66:PRO:CD	2.81	0.43
1:D:154:VAL:O	1:D:156:ARG:HD3	2.19	0.43
1:A:248:ASP:OD2	2:A:501:PLP:N1	2.52	0.42
1:A:51:ASP:OD1	1:A:51:ASP:C	2.57	0.42
1:C:150:TRP:CZ2	1:D:122:GLU:HB2	2.54	0.42
1:B:113:GLN:HE21	1:B:291:ARG:CG	2.32	0.42
1:B:113:GLN:NE2	1:B:291:ARG:HG2	2.35	0.42
1:B:65:GLY:N	1:B:66:PRO:CD	2.83	0.42
1:C:65:GLY:N	1:C:66:PRO:CD	2.82	0.42
1:B:353:GLU:O	1:B:354:LYS:HG2	2.20	0.42
1:C:51:ASP:OD1	1:C:51:ASP:C	2.57	0.42
1:A:168:ARG:HE	1:A:168:ARG:HB3	1.59	0.41
1:D:222:GLY:C	1:D:367:SER:HG	2.23	0.41
1:C:370:LEU:HD23	1:C:395:ARG:HB3	2.01	0.41
1:C:382:ARG:HG2	1:C:386:GLN:OE1	2.20	0.41
1:A:64:TYR:O	1:A:276:LYS:HE3	2.21	0.41
1:D:370:LEU:HD23	1:D:395:ARG:HB3	2.02	0.41
1:C:95:GLU:HG2	1:D:52:VAL:CG1	2.50	0.41
1:A:198:LEU:CD2	1:A:234:LEU:HD12	2.51	0.40
1:B:87:GLY:HA2	5:B:638:HOH:O	2.21	0.40
1:C:77:LEU:HD23	1:C:78:ASP:N	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:ARG:NH1	1:B:54:ASP:OD2[1_655]	2.14	0.06

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	381/464 (82%)	370 (97%)	10 (3%)	1 (0%)	44	54
1	B	373/464 (80%)	364 (98%)	9 (2%)	0	100	100
1	C	376/464 (81%)	366 (97%)	9 (2%)	1 (0%)	44	54
1	D	381/464 (82%)	370 (97%)	9 (2%)	2 (0%)	32	38
All	All	1511/1856 (81%)	1470 (97%)	37 (2%)	4 (0%)	44	54

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	222	GLY
1	D	223	VAL
1	A	276	LYS
1	C	276	LYS

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	300/355 (84%)	296 (99%)	4 (1%)	73	85
1	B	294/355 (83%)	284 (97%)	10 (3%)	42	55
1	C	297/355 (84%)	294 (99%)	3 (1%)	80	89
1	D	299/355 (84%)	295 (99%)	4 (1%)	73	85
All	All	1190/1420 (84%)	1169 (98%)	21 (2%)	64	78

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	LYS
1	A	167	THR
1	A	168	ARG
1	A	354	LYS
1	B	115	ARG
1	B	167	THR
1	B	170	THR
1	B	258	ARG
1	B	291	ARG
1	B	380	GLU
1	B	384	LEU
1	B	426	ARG
1	B	427	ASP
1	B	438	ARG
1	C	159	LYS
1	C	168	ARG
1	C	333	GLU
1	D	156	ARG
1	D	159	LYS
1	D	164	MET
1	D	171	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	GLN
1	A	262	GLN
1	B	113	GLN
1	B	262	GLN
1	C	113	GLN
1	D	113	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	501	-	16,16,16	4.27	4 (25%)	22,23,23	1.54	4 (18%)
2	PLP	B	501	-	16,16,16	4.24	4 (25%)	22,23,23	1.86	7 (31%)
2	PLP	C	501	-	16,16,16	4.07	4 (25%)	22,23,23	1.90	7 (31%)
3	PGE	C	502	-	9,9,9	0.64	0	8,8,8	0.79	0
2	PLP	D	501	-	16,16,16	3.03	3 (18%)	22,23,23	1.69	4 (18%)
4	PEG	D	502	-	6,6,6	0.59	0	5,5,5	0.85	0
4	PEG	D	503	-	6,6,6	0.61	0	5,5,5	0.43	0
4	PEG	D	504	-	6,6,6	0.77	0	5,5,5	0.58	0

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	501	-	-	0/8/8/8	0/1/1/1
2	PLP	B	501	-	-	0/8/8/8	0/1/1/1
2	PLP	C	501	-	-	0/8/8/8	0/1/1/1
3	PGE	C	502	-	-	0/7/7/7	0/0/0/0
2	PLP	D	501	-	-	0/8/8/8	0/1/1/1
4	PEG	D	502	-	-	0/4/4/4	0/0/0/0
4	PEG	D	503	-	-	0/4/4/4	0/0/0/0
4	PEG	D	504	-	-	0/4/4/4	0/0/0/0

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	PLP	C6-C5	2.08	1.42	1.37
2	A	501	PLP	C6-C5	2.52	1.43	1.37
2	C	501	PLP	C6-C5	2.78	1.43	1.37
2	D	501	PLP	C4-C3	3.14	1.46	1.40
2	A	501	PLP	C4-C3	4.04	1.47	1.40
2	B	501	PLP	C4-C5	4.07	1.47	1.42
2	B	501	PLP	C4-C3	4.39	1.48	1.40
2	C	501	PLP	C4-C5	4.45	1.47	1.42
2	C	501	PLP	C4-C3	4.84	1.48	1.40
2	A	501	PLP	C4-C5	5.87	1.49	1.42
2	D	501	PLP	C4-C5	5.96	1.49	1.42
2	D	501	PLP	C3-C2	9.68	1.47	1.40
2	C	501	PLP	C3-C2	14.42	1.50	1.40
2	A	501	PLP	C3-C2	15.05	1.51	1.40
2	B	501	PLP	C3-C2	15.24	1.51	1.40

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	PLP	C3-C4-C5	-3.76	115.38	118.24
2	C	501	PLP	C4-C3-C2	-3.73	117.86	120.15
2	D	501	PLP	C3-C4-C5	-3.62	115.49	118.24
2	D	501	PLP	O4A-C4A-C4	-3.40	117.26	125.08
2	B	501	PLP	O4A-C4A-C4	-3.18	117.77	125.08
2	D	501	PLP	O3P-P-O4P	-3.17	98.29	106.73
2	B	501	PLP	C4-C3-C2	-2.97	118.33	120.15
2	C	501	PLP	O4A-C4A-C4	-2.80	118.64	125.08
2	C	501	PLP	C3-C4-C5	-2.62	116.25	118.24
2	C	501	PLP	O2P-P-O4P	-2.57	99.89	106.73
2	A	501	PLP	O3P-P-O4P	-2.39	100.37	106.73
2	B	501	PLP	O4P-P-O1P	-2.29	100.04	106.47
2	C	501	PLP	O3P-P-O4P	-2.03	101.33	106.73
2	D	501	PLP	C6-N1-C2	2.02	123.15	119.26
2	B	501	PLP	O2P-P-O1P	2.07	118.62	110.50
2	A	501	PLP	C3-C4-C4A	2.08	122.96	119.91
2	A	501	PLP	O3P-P-O2P	2.39	117.27	107.61
2	C	501	PLP	O3P-P-O2P	2.78	118.82	107.61
2	B	501	PLP	O4P-C5A-C5	2.93	115.20	109.32
2	B	501	PLP	C2A-C2-C3	3.10	124.66	120.96
2	C	501	PLP	C3-C4-C4A	3.36	124.83	119.91
2	B	501	PLP	O3-C3-C2	3.71	125.56	117.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	PLP	1	0
2	B	501	PLP	1	0
3	C	502	PGE	2	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

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	389/464 (83%)	-0.15	3 (0%) 86 89	19, 30, 55, 76	0
1	B	381/464 (82%)	-0.03	10 (2%) 56 63	20, 34, 57, 87	0
1	C	384/464 (82%)	-0.24	4 (1%) 82 85	17, 29, 50, 70	0
1	D	387/464 (83%)	-0.11	3 (0%) 86 89	19, 29, 50, 66	0
All	All	1541/1856 (83%)	-0.13	20 (1%) 77 81	17, 31, 54, 87	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	305	ALA	3.5
1	B	52	VAL	3.0
1	B	109	PRO	2.8
1	D	441	VAL	2.7
1	B	40	VAL	2.7
1	B	39	LEU	2.6
1	B	441	VAL	2.6
1	C	240	ARG	2.6
1	C	160	THR	2.6
1	B	354	LYS	2.6
1	D	164	MET	2.6
1	B	54	ASP	2.5
1	A	74	ARG	2.2
1	B	168	ARG	2.2
1	C	77	LEU	2.1
1	B	305	ALA	2.1
1	A	382	ARG	2.0
1	C	310	GLY	2.0
1	D	54	ASP	2.0
1	B	204	ARG	2.0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th 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	LLDF	B-factors(Å ²)	Q<0.9
4	PEG	D	504	7/7	0.86	0.23	4.69	42,45,47,47	0
3	PGE	C	502	10/10	0.92	0.15	1.00	38,43,46,49	0
4	PEG	D	503	7/7	0.84	0.17	0.64	44,48,57,57	0
2	PLP	D	501	16/16	0.93	0.14	0.11	29,36,45,55	0
2	PLP	B	501	16/16	0.96	0.12	-0.38	25,31,40,48	0
2	PLP	C	501	16/16	0.97	0.10	-0.45	20,26,30,32	0
4	PEG	D	502	7/7	0.92	0.13	-0.63	34,38,40,41	0
2	PLP	A	501	16/16	0.97	0.10	-1.11	19,28,38,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.