



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:05 am BST

PDB ID : 1VP4
Title : Crystal structure of a putative aminotransferase (tm1131) from thermotoga maritima msb8 at 1.82 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2004-10-08
Resolution : 1.82 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

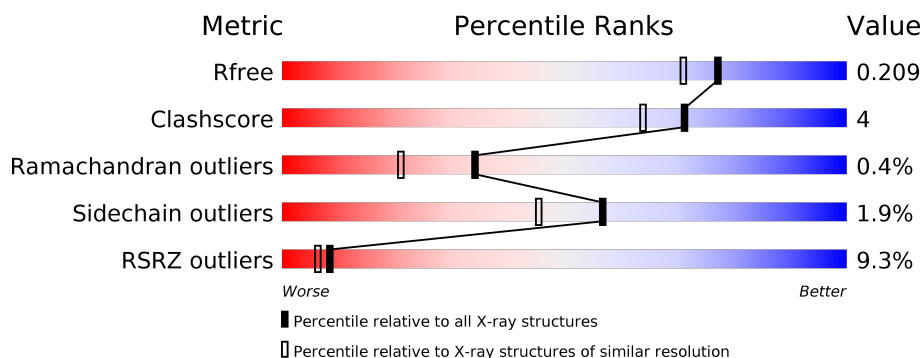
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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}	130704	7484 (1.84-1.80)
Clashscore	141614	8401 (1.84-1.80)
Ramachandran outliers	138981	8290 (1.84-1.80)
Sidechain outliers	138945	8290 (1.84-1.80)
RSRZ outliers	127900	7371 (1.84-1.80)

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 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	425	<div> <div>8%</div> <div>90%</div> <div>8%</div> <div>..</div> </div>
1	B	425	<div> <div>10%</div> <div>88%</div> <div>8%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	UNL	A	601	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7074 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, putative.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	420	Total	C	N	O	S	Se	0	6	0
			3292	2142	535	602	5	8			
1	B	416	Total	C	N	O	S	Se	0	5	0
			3277	2133	536	596	4	8			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MSE	-	LEADER SEQUENCE	UNP Q9X0L5
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9X0L5
A	-9	SER	-	LEADER SEQUENCE	UNP Q9X0L5
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9X0L5
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9X0L5
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9X0L5
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9X0L5
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9X0L5
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9X0L5
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9X0L5
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9X0L5
A	0	HIS	-	LEADER SEQUENCE	UNP Q9X0L5
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	16	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	89	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	155	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	258	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	315	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	353	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
A	380	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	-11	MSE	-	CLONING ARTIFACT	UNP Q9X0L5
B	-10	GLY	-	CLONING ARTIFACT	UNP Q9X0L5
B	-9	SER	-	CLONING ARTIFACT	UNP Q9X0L5
B	-8	ASP	-	CLONING ARTIFACT	UNP Q9X0L5
B	-7	LYS	-	CLONING ARTIFACT	UNP Q9X0L5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	ILE	-	CLONING ARTIFACT	UNP Q9X0L5
B	-5	HIS	-	CLONING ARTIFACT	UNP Q9X0L5
B	-4	HIS	-	CLONING ARTIFACT	UNP Q9X0L5
B	-3	HIS	-	CLONING ARTIFACT	UNP Q9X0L5
B	-2	HIS	-	CLONING ARTIFACT	UNP Q9X0L5
B	-1	HIS	-	CLONING ARTIFACT	UNP Q9X0L5
B	0	HIS	-	CLONING ARTIFACT	UNP Q9X0L5
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	16	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	89	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	155	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	258	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	315	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	353	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5
B	380	MSE	MET	MODIFIED RESIDUE	UNP Q9X0L5

- PLP
-
- The diagram shows the chemical structure of PLP (Pyridoxal Phosphate). It consists of a central pyridine ring. At the 2-position of the ring, there is a hydroxyl group (-OH) labeled O3. At the 3-position, there is a carboxylate group (-COO-) labeled C4A and O4A. At the 4-position, there is a phosphate group (-PO3^2-) labeled P, O1P, O2P, and O3P. At the 5-position, there is a hydroxymethyl group (-CH2OH) labeled C5A and O4P. The nitrogen atom of the pyridine ring is labeled N1. The carbon atoms of the ring are labeled C2, C3, C4, C5, and C6. The phosphate group is shown with a central phosphorus atom (P) bonded to four oxygen atoms (O1P, O2P, O3P, and O4P). The hydroxyl group is shown with an oxygen atom (O3) bonded to a hydrogen atom (H). The carboxylate group is shown with a carbon atom (C4A) double-bonded to an oxygen atom (O4A) and single-bonded to another oxygen atom (O4P).

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O 8 8	0	0
3	A	1	Total O 5 5	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	1
			5	2	3		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		
5	A	1	Total	C	O	0	0
			3	1	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 3 1 2	0	0
5	A	1	Total C O 3 1 2	0	0
5	A	1	Total C O 3 1 2	0	0
5	A	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 5 2 3	0	1
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0
5	B	1	Total C O 3 1 2	0	0

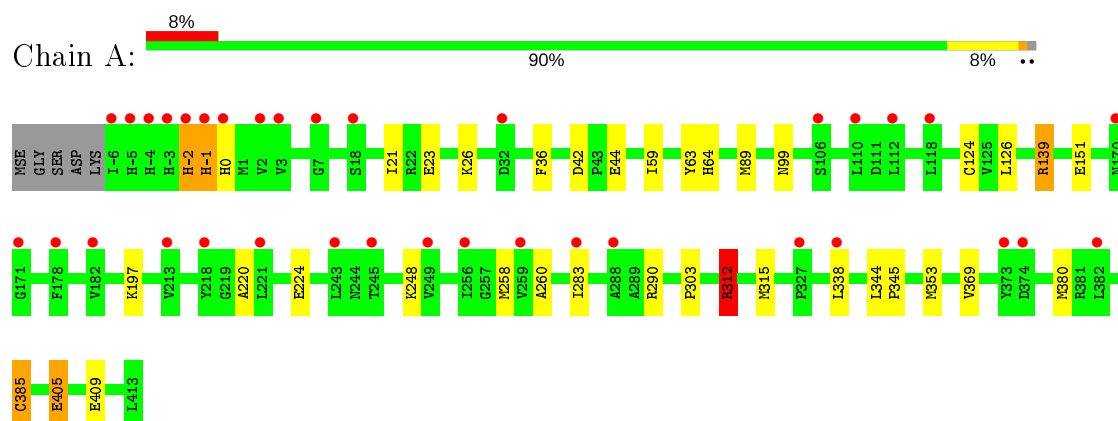
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	187	Total O 187 187	0	0
6	B	166	Total O 166 166	0	0

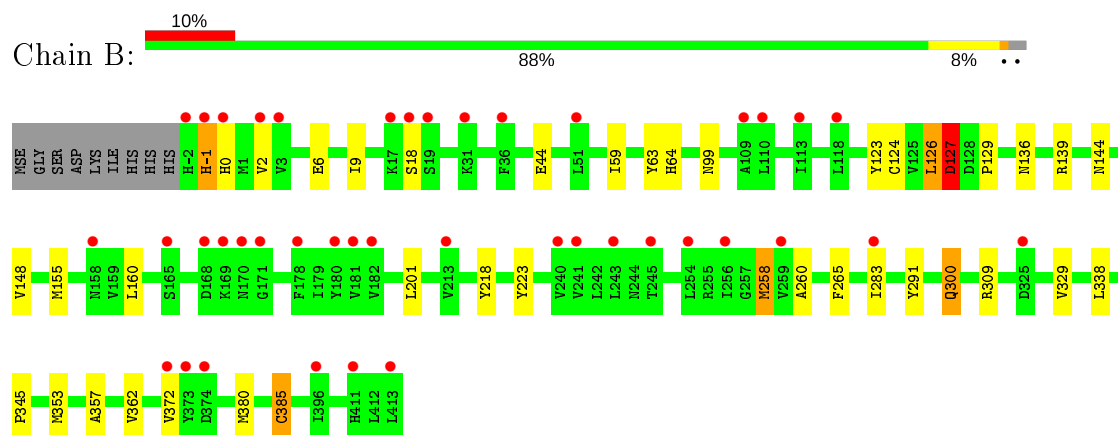
3 Residue-property plots [i](#)

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, putative



- Molecule 1: aminotransferase, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	165.12Å 165.12Å 68.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.41 – 1.82 28.41 – 1.82	Depositor EDS
% Data completeness (in resolution range)	98.1 (28.41-1.82) 98.1 (28.41-1.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.179 , 0.203 0.185 , 0.209	Depositor DCC
R_{free} test set	4716 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	26.8	Xtriage
Anisotropy	0.274	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7074	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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: FMT, UNL, EDO, 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	0.79	3/3378 (0.1%)	0.81	4/4566 (0.1%)
1	B	0.76	4/3362 (0.1%)	0.77	3/4544 (0.1%)
All	All	0.77	7/6740 (0.1%)	0.79	7/9110 (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	A	0	2
1	B	0	1
All	All	0	3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	385[A]	CYS	CB-SG	-8.82	1.67	1.82
1	A	385[B]	CYS	CB-SG	-8.82	1.67	1.82
1	B	385[A]	CYS	CB-SG	-7.96	1.68	1.82
1	B	385[B]	CYS	CB-SG	-7.96	1.68	1.82
1	B	124	CYS	CB-SG	-5.25	1.73	1.81
1	B	127	ASP	CB-CG	5.08	1.62	1.51
1	A	405	GLU	CG-CD	5.04	1.59	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	127	ASP	CB-CG-OD1	9.90	127.21	118.30
1	A	312	ARG	NE-CZ-NH2	-9.78	115.41	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	A	290	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	B	258	MSE	CG-SE-CE	5.24	110.43	98.90
1	A	42	ASP	CB-CG-OD1	5.17	122.95	118.30
1	B	127	ASP	CB-CG-OD2	-5.03	113.78	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	-1	HIS	Peptide
1	A	-2	HIS	Peptide
1	B	0	HIS	Peptide

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	3292	0	3249	21	0
1	B	3277	0	3256	24	0
2	A	15	0	6	2	0
2	B	15	0	7	2	0
3	A	5	0	0	2	0
3	B	8	0	0	1	0
4	A	12	0	18	0	0
4	B	12	0	18	0	0
5	A	56	0	19	0	0
5	B	29	0	10	1	0
6	A	187	0	0	1	0
6	B	166	0	0	0	0
All	All	7074	0	6583	46	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.

All (46) 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:315:MSE:CE	1:A:315:MSE:SE	2.15	1.44
3:A:601:UNL:O5	3:A:601:UNL:O1	1.69	1.08
1:A:248:LYS:HZ2	2:A:501:PLP:C4A	1.38	1.05
1:A:59:ILE:HD11	1:A:283[B]:ILE:HD11	1.59	0.83
1:A:338:LEU:HD22	1:A:385[B]:CYS:SG	2.18	0.82
1:A:224:GLU:OE1	1:A:312:ARG:NH2	2.15	0.78
1:B:338:LEU:HD22	1:B:385[B]:CYS:SG	2.31	0.70
1:B:59:ILE:HD11	1:B:283[B]:ILE:HD11	1.73	0.69
1:B:291:TYR:OH	1:B:300:GLN:NE2	2.26	0.68
1:A:405:GLU:O	1:A:409:GLU:HG2	2.00	0.61
3:A:601:UNL:O4	3:A:601:UNL:O2	2.18	0.60
1:B:218:TYR:HH	2:B:501:PLP:HO3	1.53	0.55
1:A:64:HIS:NE2	1:B:44:GLU:OE2	2.38	0.55
1:A:353:MSE:HE1	1:A:380:MSE:HE1	1.90	0.53
1:A:21:ILE:HD11	1:A:369:VAL:HG11	1.89	0.53
1:B:155:MSE:HE1	1:B:160:LEU:HD22	1.90	0.53
1:B:148:VAL:HG11	1:B:155:MSE:HE3	1.90	0.53
1:B:6:GLU:HA	1:B:9:ILE:HD12	1.91	0.52
1:A:139:ARG:HD3	6:A:808:HOH:O	2.09	0.52
1:B:218:TYR:OH	2:B:501:PLP:O3	2.29	0.49
1:A:89[B]:MSE:CE	1:A:220:ALA:HB2	2.44	0.48
3:B:601:UNL:O5	3:B:601:UNL:O7	2.32	0.48
1:B:265:PHE:CB	5:B:606[B]:FMT:H	2.44	0.47
1:B:136:ASN:HA	1:B:139:ARG:HG2	1.97	0.47
1:A:312:ARG:C	1:A:312:ARG:HD2	2.36	0.46
1:B:127:ASP:HB2	1:B:129:PRO:O	2.15	0.45
1:B:59:ILE:O	1:B:63:TYR:HB3	2.18	0.44
1:A:44:GLU:OE2	1:B:64:HIS:NE2	2.50	0.44
1:A:151:GLU:OE1	1:A:197:LYS:NZ	2.48	0.44
1:A:248:LYS:CE	2:A:501:PLP:C4A	2.83	0.44
1:B:357:ALA:HB1	1:B:362:VAL:O	2.17	0.43
1:B:223:TYR:HB3	1:B:309:ARG:HD3	1.99	0.43
1:B:329:VAL:HG22	1:B:345:PRO:HD3	2.00	0.43
1:B:123:TYR:HA	1:B:144:ASN:O	2.19	0.43
1:B:353:MSE:HE1	1:B:380:MSE:HE1	2.01	0.42
1:B:99:ASN:O	1:B:260:ALA:HA	2.19	0.42
1:A:59:ILE:O	1:A:63:TYR:HB3	2.19	0.42
1:B:353:MSE:CE	1:B:380:MSE:HE1	2.49	0.42
1:A:36:PHE:CD1	1:A:315:MSE:CE	3.03	0.42
1:B:126:LEU:HD11	1:B:372:VAL:HG21	2.02	0.42
1:B:-1:HIS:O	1:B:2:VAL:HG23	2.20	0.42
1:A:99:ASN:O	1:A:260:ALA:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:GLU:O	1:A:26:LYS:HB2	2.20	0.41
1:B:148:VAL:CB	1:B:155:MSE:HE3	2.51	0.41
1:A:312:ARG:C	1:A:312:ARG:CD	2.90	0.40
1:A:344:LEU:HB3	1:A:345:PRO:CD	2.50	0.40

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	424/425 (100%)	415 (98%)	7 (2%)	2 (0%)	29	15
1	B	419/425 (99%)	409 (98%)	9 (2%)	1 (0%)	47	33
All	All	843/850 (99%)	824 (98%)	16 (2%)	3 (0%)	34	21

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	-1	HIS
1	A	0	HIS
1	B	-1	HIS

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	342/364 (94%)	334 (98%)	8 (2%)	50	37
1	B	344/364 (94%)	338 (98%)	6 (2%)	60	50
All	All	686/728 (94%)	672 (98%)	14 (2%)	57	43

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-2	HIS
1	A	124[A]	CYS
1	A	124[B]	CYS
1	A	126	LEU
1	A	139	ARG
1	A	258	MSE
1	A	303	PRO
1	A	312	ARG
1	B	18	SER
1	B	126	LEU
1	B	127	ASP
1	B	201	LEU
1	B	258	MSE
1	B	300	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	ASN
1	B	80	GLN
1	B	175	GLN
1	B	300	GLN
1	B	317	ASN

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 39 ligands modelled in this entry, 2 are unknown - leaving 37 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	$\# Z > 2$
5	FMT	B	611	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	605	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	611[A]	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	611[B]	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	B	603	-	3,3,3	0.47	0	2,2,2	0.22	0
5	FMT	B	612	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	607	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	A	603	-	3,3,3	0.36	0	2,2,2	0.28	0
5	FMT	A	617	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	613	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	622	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	A	602	-	3,3,3	0.54	0	2,2,2	0.43	0
4	EDO	B	602	-	3,3,3	0.59	0	2,2,2	0.41	0
2	PLP	B	501	1	15,15,16	1.33	3 (20%)	20,22,23	1.32	2 (10%)
5	FMT	A	610	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	606	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	607	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	B	604	-	3,3,3	0.37	0	2,2,2	0.30	0
5	FMT	A	612	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	616	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	609	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	605	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	614	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	606[B]	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	613	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	606[A]	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	608	-	0,2,2	0.00	-	0,1,1	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FMT	B	608	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	B	610	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	615	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	621	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	620	-	0,2,2	0.00	-	0,1,1	0.00	-
5	FMT	A	619	-	0,2,2	0.00	-	0,1,1	0.00	-
2	PLP	A	501	1	15,15,16	1.49	3 (20%)	20,22,23	1.73	6 (30%)
5	FMT	A	618	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	A	604	-	3,3,3	0.34	0	2,2,2	0.42	0
5	FMT	A	609	-	0,2,2	0.00	-	0,1,1	0.00	-

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	B	501	1	-	0/6/6/8	0/1/1/1
4	EDO	B	603	-	-	1/1/1/1	-
2	PLP	A	501	1	-	0/6/6/8	0/1/1/1
4	EDO	B	604	-	-	0/1/1/1	-
4	EDO	A	604	-	-	0/1/1/1	-
4	EDO	A	603	-	-	0/1/1/1	-
4	EDO	A	602	-	-	0/1/1/1	-
4	EDO	B	602	-	-	1/1/1/1	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	PLP	C3-C2	-2.80	1.38	1.40
2	A	501	PLP	C5-C4	-2.78	1.37	1.40
2	A	501	PLP	C2-N1	2.38	1.38	1.33
2	A	501	PLP	C3-C2	-2.36	1.38	1.40
2	B	501	PLP	C2-N1	2.19	1.38	1.33
2	B	501	PLP	C6-N1	2.17	1.39	1.34

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	PLP	C5-C6-N1	-3.49	118.00	123.82
2	A	501	PLP	O3-C3-C2	2.63	123.22	117.49
2	B	501	PLP	C5-C6-N1	-2.62	119.45	123.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	PLP	C5A-C5-C6	2.50	123.48	119.37
2	A	501	PLP	O3P-P-O4P	2.17	112.50	106.73
2	B	501	PLP	C3-C4-C5	2.13	121.04	118.74
2	A	501	PLP	C3-C2-N1	-2.10	118.05	120.77
2	A	501	PLP	C3-C4-C5	2.07	120.98	118.74

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	602	EDO	O1-C1-C2-O2
4	B	603	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	PLP	2	0
5	B	606[B]	FMT	1	0
2	A	501	PLP	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	412/425 (96%)	0.54	35 (8%) 10 8	37, 43, 57, 97	0
1	B	408/425 (96%)	0.69	41 (10%) 7 5	37, 42, 56, 94	0
All	All	820/850 (96%)	0.61	76 (9%) 8 6	37, 43, 56, 97	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	-3	HIS	9.3
1	B	18	SER	8.9
1	B	0	HIS	8.8
1	A	-6	ILE	8.2
1	B	-1	HIS	8.0
1	B	411	HIS	5.9
1	B	19	SER	5.9
1	A	0	HIS	5.6
1	B	-2	HIS	5.2
1	B	213	VAL	5.1
1	B	373	TYR	4.7
1	B	17	LYS	4.6
1	B	325	ASP	4.4
1	B	3	VAL	4.4
1	B	413	LEU	4.3
1	B	181	VAL	4.3
1	A	-4	HIS	4.2
1	A	-1	HIS	4.2
1	A	2	VAL	4.1
1	B	2	VAL	4.1
1	B	374	ASP	4.0
1	B	243	LEU	4.0
1	A	-5	HIS	4.0
1	A	-2	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	243	LEU	3.9
1	A	171	GLY	3.9
1	A	32	ASP	3.6
1	B	31	LYS	3.5
1	A	213	VAL	3.5
1	B	171	GLY	3.4
1	B	241	VAL	3.3
1	B	170	ASN	3.2
1	B	158	ASN	3.2
1	A	249	VAL	3.1
1	B	169	LYS	3.0
1	A	3	VAL	3.0
1	B	259	VAL	3.0
1	B	283[A]	ILE	2.9
1	B	178	PHE	2.9
1	A	338	LEU	2.9
1	A	382	LEU	2.9
1	B	245	THR	2.8
1	A	18	SER	2.8
1	A	256	ILE	2.7
1	A	7	GLY	2.7
1	B	256	ILE	2.7
1	A	182	VAL	2.7
1	B	180	TYR	2.7
1	A	178	PHE	2.6
1	B	109	ALA	2.6
1	A	283[A]	ILE	2.6
1	A	373	TYR	2.5
1	B	168	ASP	2.4
1	B	165	SER	2.4
1	A	218	TYR	2.4
1	A	245	THR	2.4
1	B	51	LEU	2.4
1	A	327	PRO	2.3
1	B	110	LEU	2.3
1	B	182	VAL	2.3
1	B	240	VAL	2.3
1	A	221	LEU	2.3
1	B	254	LEU	2.2
1	B	396	ILE	2.2
1	A	110	LEU	2.2
1	B	118	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	118	LEU	2.1
1	A	374	ASP	2.1
1	A	288	ALA	2.1
1	B	113	ILE	2.1
1	A	106[A]	SER	2.1
1	A	259	VAL	2.0
1	B	372	VAL	2.0
1	B	36	PHE	2.0
1	A	112	LEU	2.0
1	A	170	ASN	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. 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	B-factors(Å ²)	Q<0.9
5	FMT	B	608	3/3	0.62	0.17	47,47,48,50	0
5	FMT	B	609	3/3	0.64	0.28	40,40,41,44	0
5	FMT	B	611	3/3	0.69	0.38	51,51,54,54	0
5	FMT	B	610	3/3	0.72	0.40	49,49,50,51	0
5	FMT	A	606	3/3	0.75	0.16	37,37,44,46	0
4	EDO	B	603	4/4	0.77	0.26	53,55,58,59	0
5	FMT	B	607	3/3	0.80	0.25	48,48,52,56	0
5	FMT	A	615	3/3	0.81	0.16	46,46,51,55	0
5	FMT	A	619	3/3	0.82	0.20	45,45,46,48	0
5	FMT	B	605	3/3	0.84	0.11	45,45,45,48	0
5	FMT	A	610	3/3	0.85	0.19	38,38,42,44	0
5	FMT	A	620	3/3	0.85	0.20	53,53,56,57	0
5	FMT	A	614	3/3	0.85	0.42	43,43,47,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	FMT	A	609	3/3	0.85	0.19	46,46,46,47	0
5	FMT	A	608	3/3	0.86	0.21	38,38,44,47	0
5	FMT	A	617	3/3	0.87	0.21	52,52,55,57	0
5	FMT	A	605	3/3	0.87	0.28	28,28,38,45	0
5	FMT	A	618	3/3	0.88	0.26	54,54,56,59	0
5	FMT	A	613	3/3	0.88	0.20	32,32,38,44	0
5	FMT	A	607	3/3	0.88	0.14	35,35,41,41	0
3	UNL	B	601	8/-	0.89	0.16	29,41,53,59	0
4	EDO	A	604	4/4	0.89	0.25	47,47,49,55	0
3	UNL	A	601	5/-	0.89	0.14	31,36,47,47	0
5	FMT	A	616	3/3	0.90	0.18	48,48,49,52	0
5	FMT	B	606[B]	3/3	0.90	0.20	25,25,29,32	3
5	FMT	A	611[A]	3/3	0.90	0.16	26,26,28,28	3
5	FMT	B	606[A]	3/3	0.90	0.20	25,25,31,33	3
5	FMT	A	611[B]	3/3	0.90	0.16	26,26,28,28	3
5	FMT	A	612	3/3	0.91	0.26	40,40,43,49	0
5	FMT	A	621	3/3	0.91	0.37	47,47,49,51	0
5	FMT	A	622	3/3	0.91	0.11	32,32,38,38	0
5	FMT	B	612	3/3	0.91	0.28	48,48,48,50	0
5	FMT	B	613	3/3	0.92	0.18	39,39,45,46	0
4	EDO	B	604	4/4	0.93	0.39	33,39,46,49	0
4	EDO	A	602	4/4	0.94	0.20	28,31,33,35	0
4	EDO	A	603	4/4	0.94	0.33	28,29,33,37	0
4	EDO	B	602	4/4	0.96	0.08	31,38,38,43	0
2	PLP	A	501	15/16	0.97	0.10	23,28,36,37	0
2	PLP	B	501	15/16	0.97	0.09	23,29,30,39	0

6.5 Other polymers ⓘ

There are no such residues in this entry.