



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2014 – 01:44 AM GMT

PDB ID : 3Q10  
Title : Pantoate-beta-alanineligase from Yersinia pestis  
Authors : Osipiuk, J.; Maltseva, N.; Kwon, K.; Anderson, W.F.; Joachimiak, A.; Center  
for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2010-12-16  
Resolution : 1.83 Å(reported)

This is a full wwPDB validation 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 <http://wwpdb.org/ValidationPDFNotes.html>

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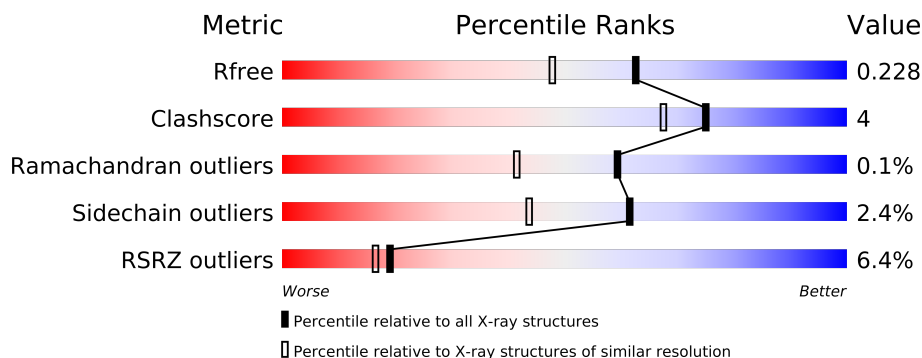
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.83 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))
$R_{free}$	66092	1857 (1.86-1.82)
Clashscore	79885	2149 (1.86-1.82)
Ramachandran outliers	78287	2124 (1.86-1.82)
Sidechain outliers	78261	2125 (1.86-1.82)
RSRZ outliers	66119	1857 (1.86-1.82)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	287	
1	B	287	
1	C	287	
1	D	287	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	GOL	B	603	-	X
3	GOL	B	605	-	X
3	GOL	D	604	-	X
5	CL	A	607	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9440 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Pantoate--beta-alanineligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	20	0
			2361	1504	410	437	10			
1	B	285	Total	C	N	O	S	0	15	0
			2320	1479	400	431	10			
1	C	284	Total	C	N	O	S	0	19	0
			2343	1498	405	429	11			
1	D	198	Total	C	N	O	S	0	5	0
			1590	1015	278	289	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP Q8ZBK7
A	-1	ASN	-	EXPRESSION TAG	UNP Q8ZBK7
A	0	ALA	-	EXPRESSION TAG	UNP Q8ZBK7
B	-2	SER	-	EXPRESSION TAG	UNP Q8ZBK7
B	-1	ASN	-	EXPRESSION TAG	UNP Q8ZBK7
B	0	ALA	-	EXPRESSION TAG	UNP Q8ZBK7
C	-2	SER	-	EXPRESSION TAG	UNP Q8ZBK7
C	-1	ASN	-	EXPRESSION TAG	UNP Q8ZBK7
C	0	ALA	-	EXPRESSION TAG	UNP Q8ZBK7
D	-2	SER	-	EXPRESSION TAG	UNP Q8ZBK7
D	-1	ASN	-	EXPRESSION TAG	UNP Q8ZBK7
D	0	ALA	-	EXPRESSION TAG	UNP Q8ZBK7

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P).

Image for chem-comp AMP is not available.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).

Image for chem-comp GOL is not available.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is IMIDAZOLE (three-letter code: IMD) (formula:  $C_3H_5N_2$ ).

Image for chem-comp IMD is not available.

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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula:  $Cl$ ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	292	Total	O	0	4
			292	292		

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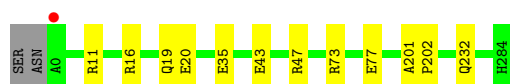
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	163	Total 163	O 163	0	0
6	C	196	Total 196	O 196	0	2
6	D	47	Total 47	O 47	0	0

### 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 errors 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.

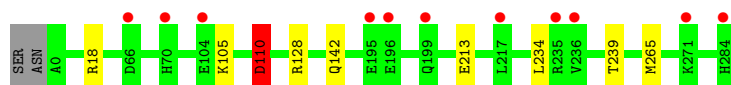
- Molecule 1: Pantoate--beta-alanineligase

Chain A: 



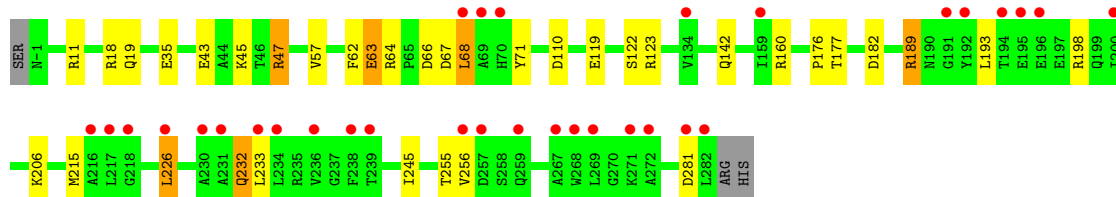
- Molecule 1: Pantoate--beta-alanineligase

Chain B: 



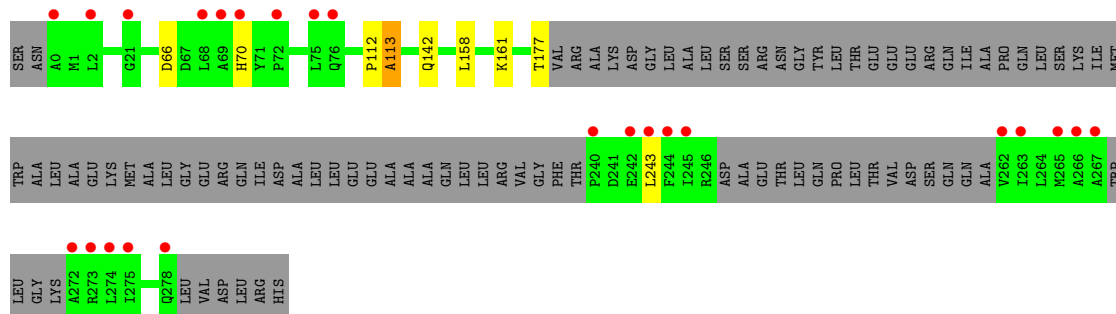
- Molecule 1: Pantoate--beta-alanineligase

Chain C: 



- Molecule 1: Pantoate--beta-alanineligase

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	44.81Å 77.24Å 98.46Å 101.33° 94.91° 94.37°	Depositor
Resolution (Å)	33.10 – 1.83 33.12 – 1.83	Depositor EDS
% Data completeness (in resolution range)	96.4 (33.10-1.83) 96.4 (33.12-1.83)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.22 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.174 , 0.211 0.188 , 0.228	Depositor DCC
$R_{free}$ test set	5527 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.5	Xtriage
Anisotropy	0.714	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 36.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 109539 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	9440	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CL, IMD, AMP

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	0.97	2/2461 (0.1%)	0.87	4/3331 (0.1%)
1	B	0.73	0/2404	0.76	4/3260 (0.1%)
1	C	0.84	0/2439	0.85	3/3306 (0.1%)
1	D	0.61	0/1633	0.69	0/2212
All	All	0.82	2/8937 (0.0%)	0.80	11/12109 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	35[A]	GLU	CD-OE1	5.25	1.31	1.25
1	A	35[B]	GLU	CD-OE1	5.25	1.31	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	233	LEU	CA-CB-CG	6.00	129.11	115.30
1	B	110[A]	ASP	CB-CG-OD2	5.96	123.66	118.30
1	B	110[B]	ASP	CB-CG-OD2	5.96	123.66	118.30
1	B	110[A]	ASP	CB-CG-OD1	-5.54	113.31	118.30
1	B	110[B]	ASP	CB-CG-OD1	-5.54	113.31	118.30
1	A	73[A]	ARG	NE-CZ-NH2	5.46	123.03	120.30
1	A	73[B]	ARG	NE-CZ-NH2	5.46	123.03	120.30
1	A	11[A]	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	A	11[B]	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	C	47	ARG	NE-CZ-NH2	-5.19	117.70	120.30
1	C	67	ASP	CB-CG-OD1	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.



## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2361	0	0	6	0
1	B	2320	0	0	5	0
1	C	2343	0	0	20	0
1	D	1590	0	0	4	0
2	A	23	0	0	0	0
2	B	23	0	0	0	0
2	C	23	0	0	1	0
2	D	23	0	0	0	0
3	A	6	0	0	0	0
3	B	12	0	0	0	0
3	C	6	0	0	0	0
3	D	6	0	0	0	0
4	A	5	0	0	0	0
5	A	1	0	0	0	0
6	A	292	0	0	2	0
6	B	163	0	0	3	0
6	C	196	0	0	9	0
6	D	47	0	0	1	0
All	All	9440	0	0	35	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (35) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:63[B]:GLU:OE1	1:C:64[B]:ARG:NH2	1.91	1.02
2:C:501:AMP:C2	6:C:603:HOH:O	2.29	0.85
1:C:11[B]:ARG:NH1	1:C:11[B]:ARG:CG	2.44	0.79
1:C:189:ARG:NH2	6:C:674:HOH:O	2.29	0.66
1:C:62[B]:PHE:CE2	1:C:68[B]:LEU:CB	2.79	0.65
1:B:142:GLN:NE2	6:B:560:HOH:O	2.27	0.65
1:C:43[A]:GLU:OE2	1:C:47:ARG:NE	2.29	0.64
1:C:182:ASP:OD2	1:C:198:ARG:NH1	2.33	0.61
1:C:45:LYS:NZ	6:C:472:HOH:O	2.33	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:213:GLU:OE1	6:B:697:HOH:O	2.15	0.59
1:B:105:LYS:O	1:D:161:LYS:NZ	2.37	0.57
1:C:177:THR:OG1	6:C:513:HOH:O	2.18	0.56
1:C:19:GLN:NE2	6:C:465:HOH:O	2.40	0.54
1:A:16[B]:ARG:NE	1:A:20:GLU:OE2	2.41	0.54
1:C:18[A]:ARG:CD	1:C:142:GLN:NE2	2.71	0.54
1:C:160:ARG:NE	6:C:479:HOH:O	2.44	0.51
1:A:232:GLN:NE2	6:A:510:HOH:O	2.45	0.49
1:B:110[A]:ASP:OD1	1:B:128:ARG:NE	2.45	0.49
1:C:71:TYR:OH	6:C:520:HOH:O	2.20	0.49
1:C:226:LEU:CD1	1:C:245:ILE:CD1	2.92	0.48
1:D:112:PRO:O	1:D:113:ALA:CB	2.62	0.47
1:C:62[B]:PHE:CE2	1:C:68[B]:LEU:CG	2.97	0.47
1:C:256:VAL:N	6:C:690:HOH:O	2.47	0.47
1:C:57:VAL:CG1	1:C:62[B]:PHE:CZ	2.99	0.46
1:D:142:GLN:NE2	6:D:305:HOH:O	2.49	0.46
1:C:35:GLU:OE2	6:C:639:HOH:O	2.20	0.46
1:B:18:ARG:NE	6:B:441:HOH:O	2.49	0.45
1:C:215[A]:MET:CE	1:C:245:ILE:CD1	2.96	0.44
1:A:19[A]:GLN:OE1	6:A:572:HOH:O	2.21	0.42
1:A:201:ALA:N	1:A:202:PRO:CD	2.82	0.42
1:C:119[B]:GLU:OE2	1:C:123:ARG:NH1	2.53	0.41
1:A:43:GLU:OE2	1:A:47:ARG:NE	2.55	0.40

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	302/287 (105%)	297 (98%)	5 (2%)	0	100	100
1	B	298/287 (104%)	293 (98%)	5 (2%)	0	100	100
1	C	301/287 (105%)	294 (98%)	7 (2%)	0	100	100
1	D	195/287 (68%)	190 (97%)	4 (2%)	1 (0%)	38	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1096/1148 (96%)	1074 (98%)	21 (2%)	1 (0%)	59 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	113	ALA

### 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	258/240 (108%)	258 (100%)	0	100 100
1	B	253/240 (105%)	248 (98%)	5 (2%)	68 53
1	C	256/240 (107%)	239 (93%)	17 (7%)	24 7
1	D	173/240 (72%)	168 (97%)	5 (3%)	55 35
All	All	940/960 (98%)	913 (97%)	27 (3%)	61 35

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	110[A]	ASP
1	B	110[B]	ASP
1	B	234	LEU
1	B	239	THR
1	B	265	MET
1	C	63[A]	GLU
1	C	63[B]	GLU
1	C	66	ASP
1	C	68[A]	LEU
1	C	68[B]	LEU
1	C	110[A]	ASP
1	C	110[B]	ASP
1	C	122	SER
1	C	176	PRO
1	C	189	ARG

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Mol	Chain	Res	Type
1	C	193	LEU
1	C	206	LYS
1	C	226	LEU
1	C	232[A]	GLN
1	C	232[B]	GLN
1	C	255	THR
1	C	281	ASP
1	D	66[A]	ASP
1	D	66[B]	ASP
1	D	158	LEU
1	D	177	THR
1	D	243	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA chains 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 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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
2	AMP	A	501	-	25,25,25	1.33	4 (16%)	38,38,38	1.99	8 (21%)
3	GOL	A	601	-	5,5,5	0.99	0	5,5,5	1.22	0
4	IMD	A	606	-	5,5,5	1.45	2 (40%)	5,5,5	0.16	0
2	AMP	B	501	-	25,25,25	1.17	2 (8%)	38,38,38	1.94	7 (18%)
3	GOL	B	603	-	5,5,5	0.53	0	5,5,5	0.91	0
3	GOL	B	605	-	5,5,5	0.41	0	5,5,5	0.64	0
2	AMP	C	501	-	25,25,25	1.06	2 (8%)	38,38,38	2.13	10 (26%)
3	GOL	C	602	-	5,5,5	0.37	0	5,5,5	0.81	0
2	AMP	D	501	-	25,25,25	1.15	2 (8%)	38,38,38	2.20	9 (23%)
3	GOL	D	604	-	5,5,5	0.29	0	5,5,5	0.66	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	AMP	A	501	-	-	0/10/26/26	0/1/3/3
3	GOL	A	601	-	-	0/4/4/4	0/0/0/0
4	IMD	A	606	-	-	0/0/0/0	0/1/1/1
2	AMP	B	501	-	-	0/10/26/26	0/1/3/3
3	GOL	B	603	-	-	0/4/4/4	0/0/0/0
3	GOL	B	605	-	-	0/4/4/4	0/0/0/0
2	AMP	C	501	-	-	0/10/26/26	0/1/3/3
3	GOL	C	602	-	-	0/4/4/4	0/0/0/0
2	AMP	D	501	-	-	0/10/26/26	0/1/3/3
3	GOL	D	604	-	-	0/4/4/4	0/0/0/0

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	AMP	C4-N9	-3.90	1.32	1.37
2	A	501	AMP	C4-N9	-3.54	1.32	1.37
2	D	501	AMP	C4-N9	-3.37	1.32	1.37
2	C	501	AMP	C5-C4	2.97	1.47	1.40
2	D	501	AMP	C5-C4	2.84	1.46	1.40
2	A	501	AMP	C5-C4	2.36	1.45	1.40
4	A	606	IMD	C2-N3	2.28	1.36	1.31
2	B	501	AMP	C5-C4	2.20	1.45	1.40
2	C	501	AMP	C2-N3	2.13	1.36	1.32
4	A	606	IMD	C2-N1	2.12	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	AMP	O4'-C1'	2.08	1.44	1.41
2	A	501	AMP	P-O3P	-2.02	1.47	1.54

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	AMP	N3-C2-N1	-8.09	121.94	128.71
2	A	501	AMP	N3-C2-N1	-6.87	122.97	128.71
2	B	501	AMP	N3-C2-N1	-6.69	123.12	128.71
2	C	501	AMP	N3-C2-N1	-6.49	123.28	128.71
2	C	501	AMP	N3-C4-N9	5.62	135.57	125.43
2	A	501	AMP	N3-C4-N9	5.22	134.85	125.43
2	D	501	AMP	N3-C4-N9	5.20	134.82	125.43
2	B	501	AMP	C8-N9-C4	4.73	110.51	106.90
2	B	501	AMP	N3-C4-N9	4.71	133.93	125.43
2	C	501	AMP	C4-C5-N7	-4.23	105.90	109.52
2	D	501	AMP	O4'-C1'-N9	4.00	112.16	108.44
2	A	501	AMP	O4'-C1'-N9	3.86	112.03	108.44
2	D	501	AMP	C8-N9-C4	3.83	109.82	106.90
2	C	501	AMP	C8-N9-C4	3.61	109.66	106.90
2	A	501	AMP	C8-N9-C4	3.46	109.54	106.90
2	C	501	AMP	C5-C4-N3	-3.25	118.63	125.70
2	C	501	AMP	O4'-C1'-N9	3.09	111.31	108.44
2	D	501	AMP	C4-C5-N7	-3.07	106.89	109.52
2	A	501	AMP	C1'-N9-C4	-2.91	121.60	126.64
2	D	501	AMP	C5-C4-N3	-2.75	119.72	125.70
2	D	501	AMP	C2-N3-C4	2.55	121.27	114.01
2	A	501	AMP	C5-C4-N3	-2.54	120.17	125.70
2	C	501	AMP	C2-N3-C4	2.33	120.64	114.01
2	B	501	AMP	C5-C4-N3	-2.30	120.69	125.70
2	D	501	AMP	C2-N1-C6	2.26	122.85	118.77
2	A	501	AMP	N6-C6-N1	2.26	123.79	119.36
2	C	501	AMP	O2'-C2'-C1'	2.20	117.88	111.23
2	D	501	AMP	O2P-P-O1P	2.13	117.39	110.44
2	A	501	AMP	C2-N3-C4	2.09	119.97	114.01
2	B	501	AMP	C1'-N9-C4	-2.06	123.08	126.64
2	B	501	AMP	N6-C6-N1	2.05	123.39	119.36
2	B	501	AMP	O4'-C1'-C2'	-2.03	103.66	106.77
2	C	501	AMP	C8-N7-C5	2.00	109.79	103.58
2	C	501	AMP	P-O5'-C5'	2.00	123.98	118.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 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	285/287 (99%)	-0.24	1 (0%) 90 91	14, 23, 38, 47	0
1	B	285/287 (99%)	-0.02	11 (3%) 37 33	22, 37, 59, 71	0
1	C	284/287 (98%)	0.47	32 (11%) 6 5	13, 33, 71, 83	0
1	D	198/287 (68%)	0.52	24 (12%) 5 4	24, 47, 95, 113	0
All	All	1052/1148 (91%)	0.15	68 (6%) 19 16	13, 33, 68, 113	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	245	ILE	7.4
1	D	263	ILE	6.7
1	D	274	LEU	6.2
1	C	192	TYR	5.7
1	C	271	LYS	5.0
1	D	272	ALA	5.0
1	C	256	VAL	4.0
1	D	267	ALA	3.9
1	C	234	LEU	3.9
1	D	243	LEU	3.7
1	D	273	ARG	3.6
1	C	239	THR	3.6
1	C	282	LEU	3.5
1	D	240	PRO	3.4
1	C	268	TRP	3.3
1	C	69	ALA	3.2
1	D	69	ALA	3.1
1	C	272	ALA	3.1
1	D	76	GLN	3.1
1	D	2	LEU	3.1
1	C	269	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	191	GLY	3.0
1	D	70[A]	HIS	3.0
1	C	194	THR	3.0
1	C	195	GLU	3.0
1	D	278	GLN	2.9
1	D	262	VAL	2.9
1	C	200	ILE	2.9
1	B	236	VAL	2.9
1	C	231	ALA	2.8
1	C	217	LEU	2.8
1	A	0	ALA	2.7
1	C	236	VAL	2.7
1	B	195[A]	GLU	2.7
1	C	230	ALA	2.7
1	D	265	MET	2.6
1	C	281	ASP	2.6
1	B	196	GLU	2.6
1	C	257	ASP	2.6
1	B	66	ASP	2.5
1	C	267	ALA	2.5
1	B	70	HIS	2.4
1	D	244	PHE	2.4
1	C	70	HIS	2.4
1	C	134	VAL	2.4
1	B	104[A]	GLU	2.4
1	C	233	LEU	2.4
1	B	235[A]	ARG	2.3
1	C	196	GLU	2.3
1	C	159	ILE	2.3
1	C	218	GLY	2.3
1	B	217	LEU	2.3
1	B	284	HIS	2.3
1	C	226	LEU	2.2
1	D	68	LEU	2.2
1	C	238	PHE	2.2
1	D	0	ALA	2.2
1	D	275	ILE	2.2
1	B	271	LYS	2.2
1	D	21	GLY	2.2
1	C	68[A]	LEU	2.2
1	C	216	ALA	2.1
1	C	259	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	75	LEU	2.1
1	D	72	PRO	2.1
1	D	242	GLU	2.0
1	D	266	ALA	2.0
1	B	199	GLN	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	GOL	B	603	6/6	0.26	9.07	52,53,55,58	0
3	GOL	D	604	6/6	0.25	3.00	50,65,69,70	0
3	GOL	B	605	6/6	0.17	2.83	72,74,74,74	0
5	CL	A	607	1/1	0.17	2.52	32,32,32,32	0
3	GOL	C	602	6/6	0.21	1.57	25,36,38,43	0
2	AMP	B	501	23/23	0.12	1.03	29,36,46,50	0
4	IMD	A	606	5/5	0.13	0.93	70,70,71,71	0
3	GOL	A	601	6/6	0.15	0.44	25,35,39,45	0
2	AMP	D	501	23/23	0.13	0.27	56,67,72,75	0
2	AMP	A	501	23/23	0.11	-0.11	14,21,27,28	0
2	AMP	C	501	23/23	0.14	-0.34	25,40,47,48	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.