



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 08:36 AM GMT

PDB ID : 4D9B  
Title : Pyridoxamine 5' phosphate (PMP) bound form of Salmonella typhimurium  
D-Cysteine desulphydrase obtained after co-crystallization with D-cycloserine  
Authors : Bharath, S.R.; Shveta, B.; Rajesh, K.H.; Savithri, H.S.; Murthy, M.R.N.  
Deposited on : 2012-01-11  
Resolution : 1.67 Å(reported)

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

---

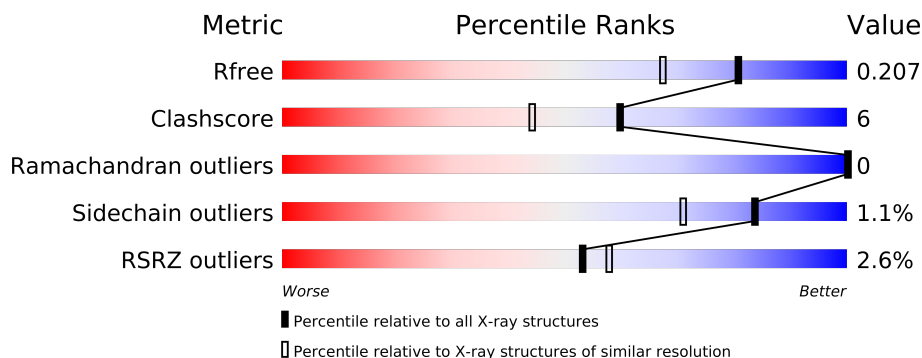
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.67 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	3587 (1.70-1.66)
Clashscore	79885	4225 (1.70-1.66)
Ramachandran outliers	78287	4144 (1.70-1.66)
Sidechain outliers	78261	4143 (1.70-1.66)
RSRZ outliers	66119	3587 (1.70-1.66)

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	342	
1	B	342	
1	C	342	
1	D	342	

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

Mol	Type	Chain	Res	Geometry	Electron density
4	EDO	A	404	-	X
4	EDO	B	403	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10773 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 D-cysteine desulfhydrase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	6	0
			2472	1578	417	468	9			
1	B	328	Total	C	N	O	S	0	1	0
			2427	1549	411	458	9			
1	C	322	Total	C	N	O	S	0	4	0
			2411	1538	407	456	10			
1	D	328	Total	C	N	O	S	3	4	0
			2461	1573	416	463	9			

There are 56 discrepancies between the modelled and reference sequences:

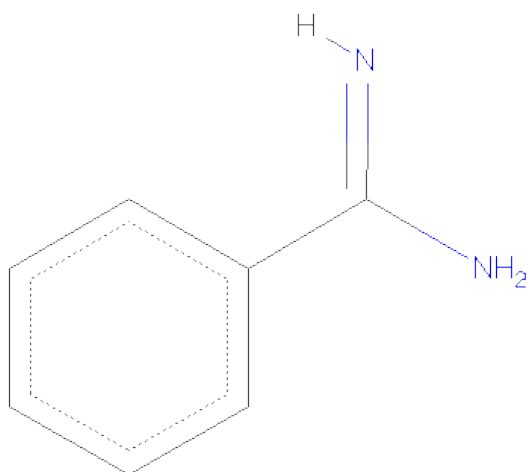
Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
A	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
A	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
A	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
A	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
A	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
A	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
A	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
A	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7
B	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
B	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
B	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
B	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
B	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7

*Continued on next page...*

*Continued from previous page...*

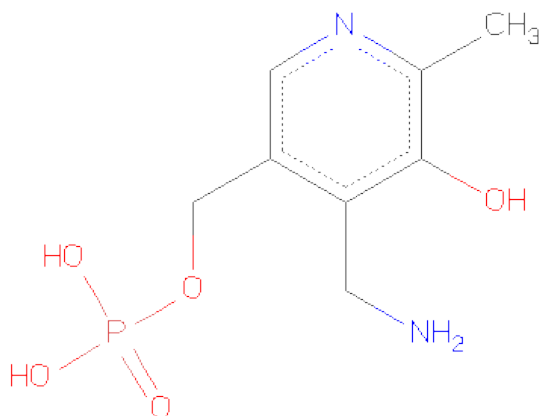
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
B	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
B	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
B	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
B	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7
C	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
C	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
C	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
C	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
C	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
C	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
C	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
C	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
C	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7
D	-13	MET	-	EXPRESSION TAG	UNP Q8ZNT7
D	-12	ARG	-	EXPRESSION TAG	UNP Q8ZNT7
D	-11	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
D	-10	SER	-	EXPRESSION TAG	UNP Q8ZNT7
D	-9	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-8	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-7	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-6	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-5	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-4	HIS	-	EXPRESSION TAG	UNP Q8ZNT7
D	-3	GLY	-	EXPRESSION TAG	UNP Q8ZNT7
D	-2	MET	-	EXPRESSION TAG	UNP Q8ZNT7
D	-1	ALA	-	EXPRESSION TAG	UNP Q8ZNT7
D	0	SER	-	EXPRESSION TAG	UNP Q8ZNT7

- Molecule 2 is BENZAMIDINE (three-letter code: BEN) (formula: C<sub>7</sub>H<sub>8</sub>N<sub>2</sub>).



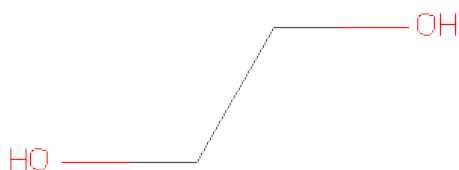
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			9	7	2		
2	C	1	Total	C	N	0	0
			9	7	2		
2	D	1	Total	C	N	0	0
			9	7	2		

- Molecule 3 is 4'-DEOXY-4'-AMINOPYRIDOXAL-5'-PHOSPHATE (three-letter code: PMP) (formula:  $C_8H_{13}N_2O_5P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			16	8	2	5	1		
3	B	1	Total	C	N	O	P	0	0
			16	8	2	5	1		
3	C	1	Total	C	N	O	P	0	0
			16	8	2	5	1		
3	D	1	Total	C	N	O	P	0	0
			16	8	2	5	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 5 is water.

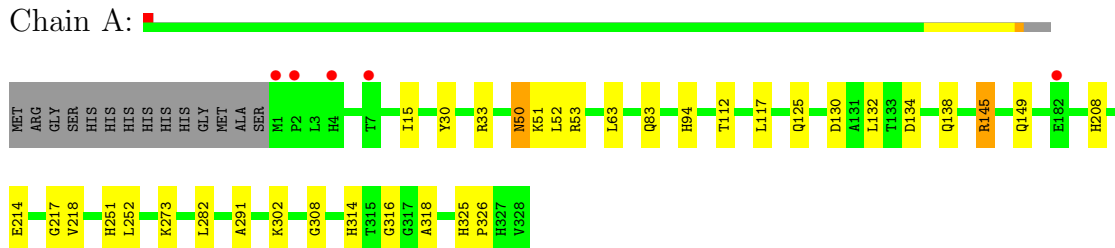
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	256	Total 256	O 256	0	0
5	B	191	Total 191	O 191	0	0
5	C	192	Total 192	O 192	0	0
5	D	248	Total 248	O 248	0	0

### 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.

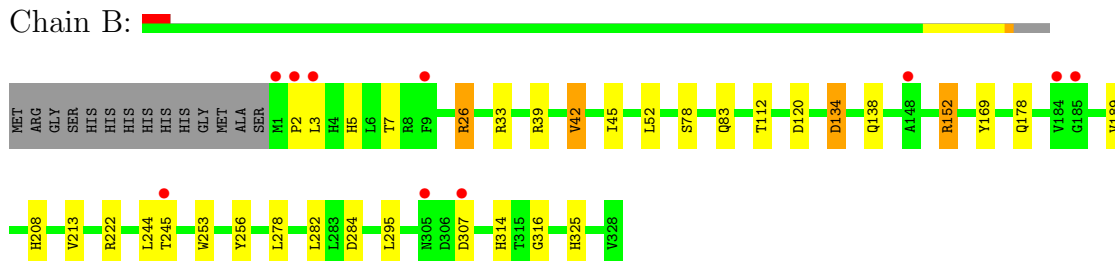
- Molecule 1: D-cysteine desulfhydrase

Chain A:



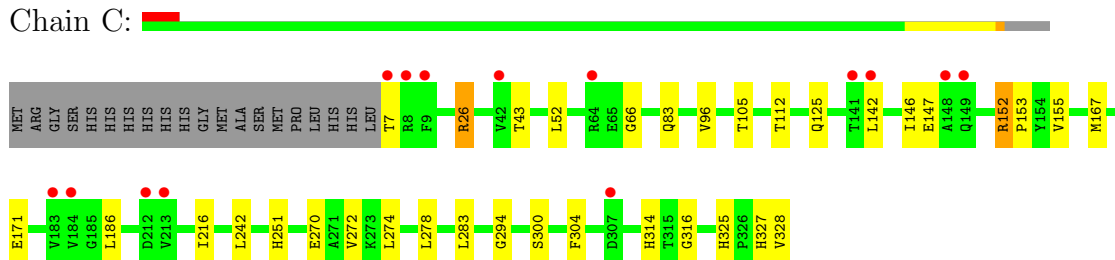
- Molecule 1: D-cysteine desulfhydrase

Chain B:



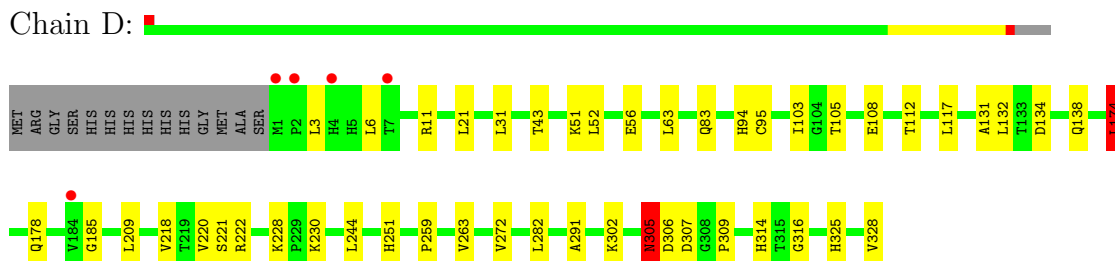
- Molecule 1: D-cysteine desulfhydrase

Chain C:



- Molecule 1: D-cysteine desulfhydrase

Chain D:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.32Å 164.93Å 68.31Å 90.00° 118.97° 90.00°	Depositor
Resolution (Å)	39.91 – 1.67 39.91 – 1.67	Depositor EDS
% Data completeness (in resolution range)	97.5 (39.91-1.67) 97.5 (39.91-1.67)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 1.67Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.171 , 0.206 0.173 , 0.207	Depositor DCC
$R_{free}$ test set	7191 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.0	Xtriage
Anisotropy	0.127	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 35.2	EDS
Estimated twinning fraction	0.000 for -h-l,k,h 0.000 for l,k,-h-l 0.019 for h,-k,-h-l 0.023 for -h-l,-k,l 0.020 for l,-k,h	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 143545 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10773	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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: BEN, PMP, EDO

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	1.27	2/2539 (0.1%)	1.09	4/3461 (0.1%)
1	B	1.26	5/2477 (0.2%)	1.10	8/3379 (0.2%)
1	C	1.24	2/2465 (0.1%)	1.08	4/3358 (0.1%)
1	D	1.31	8/2517 (0.3%)	1.11	6/3429 (0.2%)
All	All	1.27	17/9998 (0.2%)	1.10	22/13627 (0.2%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	214	GLU	CG-CD	5.83	1.60	1.51
1	C	270	GLU	CG-CD	5.78	1.60	1.51
1	D	131	ALA	CA-CB	5.65	1.64	1.52
1	C	294	GLY	N-CA	5.62	1.54	1.46
1	A	318	ALA	CA-CB	5.59	1.64	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	26	ARG	NE-CZ-NH2	-9.61	115.50	120.30
1	C	26	ARG	NE-CZ-NH2	-9.43	115.58	120.30
1	C	26	ARG	NE-CZ-NH1	7.88	124.24	120.30
1	B	222	ARG	NE-CZ-NH2	-7.83	116.39	120.30
1	B	26	ARG	NE-CZ-NH1	7.37	123.98	120.30

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	2472	0	2486	32	0
1	B	2427	0	2436	21	0
1	C	2411	0	2428	30	0
1	D	2461	0	2482	41	0
2	A	9	0	7	0	0
2	C	9	0	7	1	0
2	D	9	0	7	0	0
3	A	16	0	10	0	0
3	B	16	0	10	1	0
3	C	16	0	10	0	0
3	D	16	0	10	0	0
4	A	8	0	12	0	0
4	B	8	0	12	4	0
4	C	4	0	6	0	0
4	D	4	0	6	0	0
5	A	256	0	0	7	0
5	B	191	0	0	4	0
5	C	192	0	0	6	0
5	D	248	0	0	7	0
All	All	10773	0	9929	118	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 6.

The worst 5 of 118 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:3:LEU:HD23	1:B:244:LEU:HD11	1.31	1.12
1:D:105:THR:OG1	1:D:328[A]:VAL:HG12	1.54	1.06
1:C:105:THR:OG1	1:C:328[A]:VAL:HG12	1.64	0.96
1:B:152:ARG:HB3	1:B:152:ARG:HH11	1.34	0.93
1:D:178:GLN:HG3	5:D:748:HOH:O	1.73	0.89

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	332/342 (97%)	321 (97%)	11 (3%)	0	100	100
1	B	327/342 (96%)	314 (96%)	13 (4%)	0	100	100
1	C	323/342 (94%)	311 (96%)	12 (4%)	0	100	100
1	D	329/342 (96%)	320 (97%)	9 (3%)	0	100	100
All	All	1311/1368 (96%)	1266 (97%)	45 (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	257/267 (96%)	255 (99%)	2 (1%)	89	81
1	B	250/267 (94%)	245 (98%)	5 (2%)	68	45
1	C	250/267 (94%)	248 (99%)	2 (1%)	89	81
1	D	254/267 (95%)	252 (99%)	2 (1%)	89	81
All	All	1011/1068 (95%)	1000 (99%)	11 (1%)	84	71

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	152	ARG
1	B	178	GLN
1	C	171	GLU
1	B	33	ARG
1	C	152	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	301	GLN
1	C	83	GLN
1	D	251	HIS
1	B	325	HIS
1	C	138	GLN

### 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 ⓘ

13 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	BEN	A	401	-	9,9,9	2.70	5 (55%)	11,11,11	1.43	1 (9%)
3	PMP	A	402	-	16,16,16	0.94	1 (6%)	23,23,23	2.00	3 (13%)
4	EDO	A	403	-	3,3,3	0.69	0	2,2,2	0.13	0
4	EDO	A	404	-	3,3,3	0.88	0	2,2,2	1.17	0
3	PMP	B	401	-	16,16,16	2.32	5 (31%)	23,23,23	2.62	8 (34%)
4	EDO	B	402	-	3,3,3	0.58	0	2,2,2	1.03	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	B	403	-	3,3,3	0.31	0	2,2,2	0.28	0
2	BEN	C	401	-	9,9,9	2.19	1 (11%)	11,11,11	2.09	2 (18%)
3	PMP	C	402	-	16,16,16	1.88	4 (25%)	23,23,23	2.79	9 (39%)
4	EDO	C	403	-	3,3,3	0.82	0	2,2,2	0.96	0
2	BEN	D	401	-	9,9,9	2.68	4 (44%)	11,11,11	1.94	4 (36%)
3	PMP	D	402	-	16,16,16	1.08	1 (6%)	23,23,23	1.16	2 (8%)
4	EDO	D	403	-	3,3,3	1.24	0	2,2,2	1.02	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	BEN	A	401	-	-	0/4/4/4	0/1/1/1
3	PMP	A	402	-	-	0/8/8/8	0/1/1/1
4	EDO	A	403	-	-	0/1/1/1	0/0/0/0
4	EDO	A	404	-	-	0/1/1/1	0/0/0/0
3	PMP	B	401	-	-	0/8/8/8	0/1/1/1
4	EDO	B	402	-	-	0/1/1/1	0/0/0/0
4	EDO	B	403	-	-	0/1/1/1	0/0/0/0
2	BEN	C	401	-	-	0/4/4/4	0/1/1/1
3	PMP	C	402	-	-	0/8/8/8	0/1/1/1
4	EDO	C	403	-	-	0/1/1/1	0/0/0/0
2	BEN	D	401	-	-	0/4/4/4	0/1/1/1
3	PMP	D	402	-	-	0/8/8/8	0/1/1/1
4	EDO	D	403	-	-	0/1/1/1	0/0/0/0

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	PMP	C3-C2	-6.54	1.36	1.40
2	C	401	BEN	C1-C	-6.13	1.42	1.49
2	D	401	BEN	C1-C	-6.09	1.42	1.49
2	A	401	BEN	C1-C	-4.90	1.44	1.49
3	C	402	PMP	C3-C4	4.89	1.48	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	402	PMP	C6-C5-C4	8.86	124.82	118.10

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	PMP	C6-C5-C4	7.25	123.60	118.10
3	A	402	PMP	C6-C5-C4	6.92	123.35	118.10
3	B	401	PMP	O3-C3-C2	5.63	127.61	117.61
2	C	401	BEN	C1-C-N2	5.32	126.39	117.99

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	328/342 (95%)	-0.31	5 (1%) 70 75	11, 17, 33, 44	0
1	B	328/342 (95%)	-0.09	10 (3%) 48 53	13, 20, 42, 52	0
1	C	322/342 (94%)	0.13	14 (4%) 34 37	13, 23, 40, 52	0
1	D	328/342 (95%)	-0.27	5 (1%) 70 75	11, 17, 34, 42	1 (0%)
All	All	1306/1368 (95%)	-0.14	34 (2%) 53 58	11, 19, 38, 52	1 (0%)

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	184	VAL	5.5
1	B	1	MET	4.6
1	A	1	MET	4.4
1	C	183	VAL	4.4
1	C	8	ARG	4.2

### 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( $\text{\AA}^2$ )	Q<0.9
4	EDO	B	403	4/4	0.13	7.58	24,30,30,33	0
4	EDO	A	404	4/4	0.11	2.81	25,28,30,31	0
4	EDO	A	403	4/4	0.15	1.97	36,37,40,41	0
4	EDO	B	402	4/4	0.11	1.87	29,33,35,35	0
4	EDO	D	403	4/4	0.12	1.55	23,27,32,32	0
2	BEN	C	401	9/9	0.12	1.19	27,31,34,36	0
3	PMP	D	402	16/16	0.10	1.06	11,13,16,18	0
2	BEN	A	401	9/9	0.07	0.93	14,15,17,18	0
3	PMP	B	401	16/16	0.08	0.43	11,15,20,22	0
2	BEN	D	401	9/9	0.07	0.14	13,14,16,17	0
3	PMP	C	402	16/16	0.09	0.11	14,18,22,23	0
3	PMP	A	402	16/16	0.09	0.08	11,13,17,22	0
4	EDO	C	403	4/4	0.07	-0.47	28,28,30,30	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.