



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:50 PM GMT

PDB ID : 4AM8  
Title : Crystal structure of the R54G mutant of putrescine transcarbamylase from *Enterococcus faecalis* bound to a curing guanidinium ion  
Authors : Polo, L.M.; Rubio, V.  
Deposited on : 2012-03-08  
Resolution : 1.99 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

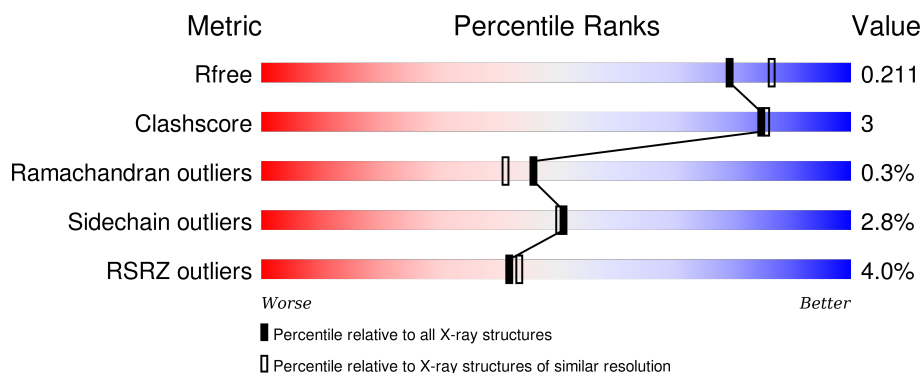
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.99 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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	355	<div> <div>3%</div> <div>89% 6% 5%</div> </div>
1	B	355	<div> <div>3%</div> <div>89% 5% 5%</div> </div>
1	C	355	<div> <div>4%</div> <div>86% 7% 6%</div> </div>
1	D	355	<div> <div>5%</div> <div>90% 7% ..</div> </div>
1	E	355	<div> <div>5%</div> <div>85% 8% 7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	355	

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
5	GAI	F	1338	-	-	-	X
6	TRS	A	1340	-	-	-	X
6	TRS	B	1342	-	-	-	X
6	TRS	F	1340	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 16546 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 PUTRESCINE CARBAMOYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2603	1641	433	507	22			
1	B	336	Total	C	N	O	S	0	0	0
			2603	1643	431	508	21			
1	C	332	Total	C	N	O	S	0	0	0
			2560	1617	427	495	21			
1	D	349	Total	C	N	O	S	0	0	0
			2670	1686	448	514	22			
1	E	331	Total	C	N	O	S	0	0	0
			2543	1607	426	488	22			
1	F	331	Total	C	N	O	S	0	0	0
			2564	1620	424	498	22			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	340	SER	-	EXPRESSION TAG	UNP Q837U7
A	341	ALA	-	EXPRESSION TAG	UNP Q837U7
A	342	ALA	-	EXPRESSION TAG	UNP Q837U7
A	343	LYS	-	EXPRESSION TAG	UNP Q837U7
A	344	LEU	-	EXPRESSION TAG	UNP Q837U7
A	345	ALA	-	EXPRESSION TAG	UNP Q837U7
A	346	ALA	-	EXPRESSION TAG	UNP Q837U7
A	347	ALA	-	EXPRESSION TAG	UNP Q837U7
A	348	LEU	-	EXPRESSION TAG	UNP Q837U7
A	349	GLU	-	EXPRESSION TAG	UNP Q837U7
A	350	HIS	-	EXPRESSION TAG	UNP Q837U7
A	351	HIS	-	EXPRESSION TAG	UNP Q837U7
A	352	HIS	-	EXPRESSION TAG	UNP Q837U7
A	353	HIS	-	EXPRESSION TAG	UNP Q837U7
A	354	HIS	-	EXPRESSION TAG	UNP Q837U7
A	355	HIS	-	EXPRESSION TAG	UNP Q837U7
A	54	GLY	ARG	ENGINEERED MUTATION	UNP Q837U7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	340	SER	-	EXPRESSION TAG	UNP Q837U7
B	341	ALA	-	EXPRESSION TAG	UNP Q837U7
B	342	ALA	-	EXPRESSION TAG	UNP Q837U7
B	343	LYS	-	EXPRESSION TAG	UNP Q837U7
B	344	LEU	-	EXPRESSION TAG	UNP Q837U7
B	345	ALA	-	EXPRESSION TAG	UNP Q837U7
B	346	ALA	-	EXPRESSION TAG	UNP Q837U7
B	347	ALA	-	EXPRESSION TAG	UNP Q837U7
B	348	LEU	-	EXPRESSION TAG	UNP Q837U7
B	349	GLU	-	EXPRESSION TAG	UNP Q837U7
B	350	HIS	-	EXPRESSION TAG	UNP Q837U7
B	351	HIS	-	EXPRESSION TAG	UNP Q837U7
B	352	HIS	-	EXPRESSION TAG	UNP Q837U7
B	353	HIS	-	EXPRESSION TAG	UNP Q837U7
B	354	HIS	-	EXPRESSION TAG	UNP Q837U7
B	355	HIS	-	EXPRESSION TAG	UNP Q837U7
B	54	GLY	ARG	ENGINEERED MUTATION	UNP Q837U7
C	340	SER	-	EXPRESSION TAG	UNP Q837U7
C	341	ALA	-	EXPRESSION TAG	UNP Q837U7
C	342	ALA	-	EXPRESSION TAG	UNP Q837U7
C	343	LYS	-	EXPRESSION TAG	UNP Q837U7
C	344	LEU	-	EXPRESSION TAG	UNP Q837U7
C	345	ALA	-	EXPRESSION TAG	UNP Q837U7
C	346	ALA	-	EXPRESSION TAG	UNP Q837U7
C	347	ALA	-	EXPRESSION TAG	UNP Q837U7
C	348	LEU	-	EXPRESSION TAG	UNP Q837U7
C	349	GLU	-	EXPRESSION TAG	UNP Q837U7
C	350	HIS	-	EXPRESSION TAG	UNP Q837U7
C	351	HIS	-	EXPRESSION TAG	UNP Q837U7
C	352	HIS	-	EXPRESSION TAG	UNP Q837U7
C	353	HIS	-	EXPRESSION TAG	UNP Q837U7
C	354	HIS	-	EXPRESSION TAG	UNP Q837U7
C	355	HIS	-	EXPRESSION TAG	UNP Q837U7
C	54	GLY	ARG	ENGINEERED MUTATION	UNP Q837U7
D	340	SER	-	EXPRESSION TAG	UNP Q837U7
D	341	ALA	-	EXPRESSION TAG	UNP Q837U7
D	342	ALA	-	EXPRESSION TAG	UNP Q837U7
D	343	LYS	-	EXPRESSION TAG	UNP Q837U7
D	344	LEU	-	EXPRESSION TAG	UNP Q837U7
D	345	ALA	-	EXPRESSION TAG	UNP Q837U7
D	346	ALA	-	EXPRESSION TAG	UNP Q837U7
D	347	ALA	-	EXPRESSION TAG	UNP Q837U7

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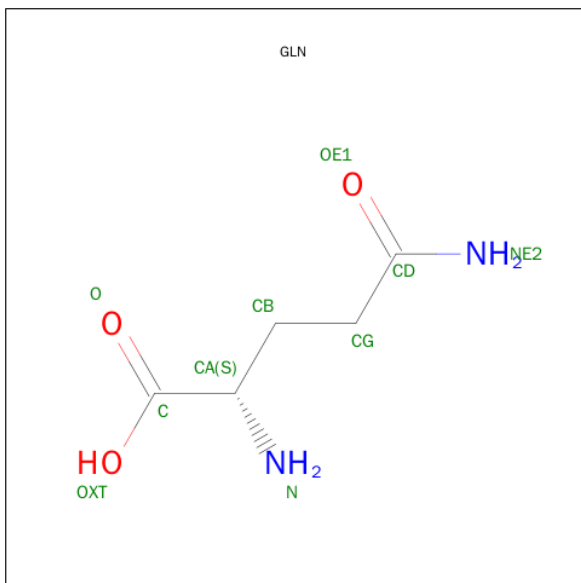
Chain	Residue	Modelled	Actual	Comment	Reference
D	348	LEU	-	EXPRESSION TAG	UNP Q837U7
D	349	GLU	-	EXPRESSION TAG	UNP Q837U7
D	350	HIS	-	EXPRESSION TAG	UNP Q837U7
D	351	HIS	-	EXPRESSION TAG	UNP Q837U7
D	352	HIS	-	EXPRESSION TAG	UNP Q837U7
D	353	HIS	-	EXPRESSION TAG	UNP Q837U7
D	354	HIS	-	EXPRESSION TAG	UNP Q837U7
D	355	HIS	-	EXPRESSION TAG	UNP Q837U7
D	54	GLY	ARG	ENGINEERED MUTATION	UNP Q837U7
E	340	SER	-	EXPRESSION TAG	UNP Q837U7
E	341	ALA	-	EXPRESSION TAG	UNP Q837U7
E	342	ALA	-	EXPRESSION TAG	UNP Q837U7
E	343	LYS	-	EXPRESSION TAG	UNP Q837U7
E	344	LEU	-	EXPRESSION TAG	UNP Q837U7
E	345	ALA	-	EXPRESSION TAG	UNP Q837U7
E	346	ALA	-	EXPRESSION TAG	UNP Q837U7
E	347	ALA	-	EXPRESSION TAG	UNP Q837U7
E	348	LEU	-	EXPRESSION TAG	UNP Q837U7
E	349	GLU	-	EXPRESSION TAG	UNP Q837U7
E	350	HIS	-	EXPRESSION TAG	UNP Q837U7
E	351	HIS	-	EXPRESSION TAG	UNP Q837U7
E	352	HIS	-	EXPRESSION TAG	UNP Q837U7
E	353	HIS	-	EXPRESSION TAG	UNP Q837U7
E	354	HIS	-	EXPRESSION TAG	UNP Q837U7
E	355	HIS	-	EXPRESSION TAG	UNP Q837U7
E	54	GLY	ARG	ENGINEERED MUTATION	UNP Q837U7
F	340	SER	-	EXPRESSION TAG	UNP Q837U7
F	341	ALA	-	EXPRESSION TAG	UNP Q837U7
F	342	ALA	-	EXPRESSION TAG	UNP Q837U7
F	343	LYS	-	EXPRESSION TAG	UNP Q837U7
F	344	LEU	-	EXPRESSION TAG	UNP Q837U7
F	345	ALA	-	EXPRESSION TAG	UNP Q837U7
F	346	ALA	-	EXPRESSION TAG	UNP Q837U7
F	347	ALA	-	EXPRESSION TAG	UNP Q837U7
F	348	LEU	-	EXPRESSION TAG	UNP Q837U7
F	349	GLU	-	EXPRESSION TAG	UNP Q837U7
F	350	HIS	-	EXPRESSION TAG	UNP Q837U7
F	351	HIS	-	EXPRESSION TAG	UNP Q837U7
F	352	HIS	-	EXPRESSION TAG	UNP Q837U7
F	353	HIS	-	EXPRESSION TAG	UNP Q837U7
F	354	HIS	-	EXPRESSION TAG	UNP Q837U7
F	355	HIS	-	EXPRESSION TAG	UNP Q837U7

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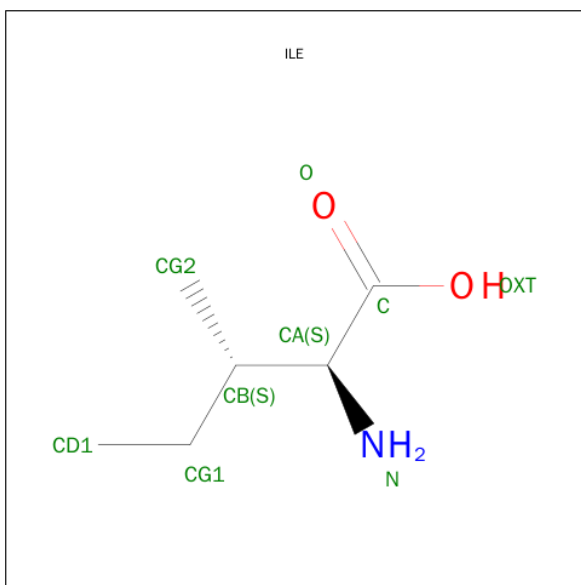
Chain	Residue	Modelled	Actual	Comment	Reference
F	54	GLY	ARG	ENGINEERED MUTATION	UNP Q837U7

- Molecule 2 is GLUTAMINE (three-letter code: GLN) (formula:  $C_5H_{10}N_2O_3$ ).



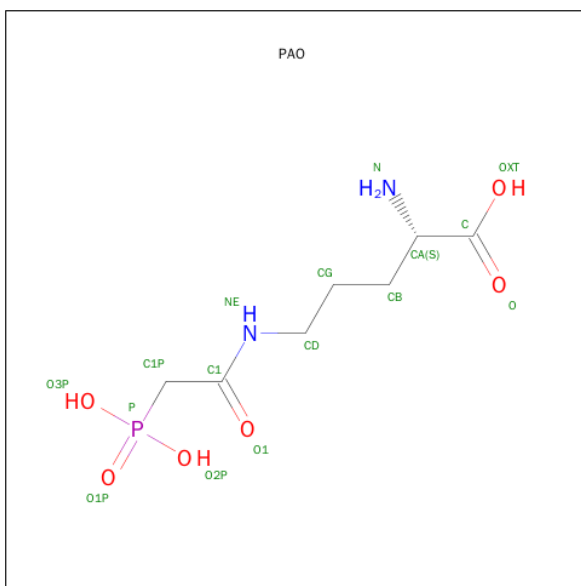
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			5	3	1	1		
2	C	1	Total	C	N	O	0	0
			5	3	1	1		
2	E	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 3 is ISOLEUCINE (three-letter code: ILE) (formula:  $C_6H_{13}NO_2$ ).



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

- Molecule 4 is N-(PHOSPHONOACETYL)-L-ORNITHINE (three-letter code: PAO) (formula:  $C_7H_{15}N_2O_6P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			16	7	2	6	1		
4	B	1	Total	C	N	O	P	0	0
			16	7	2	6	1		

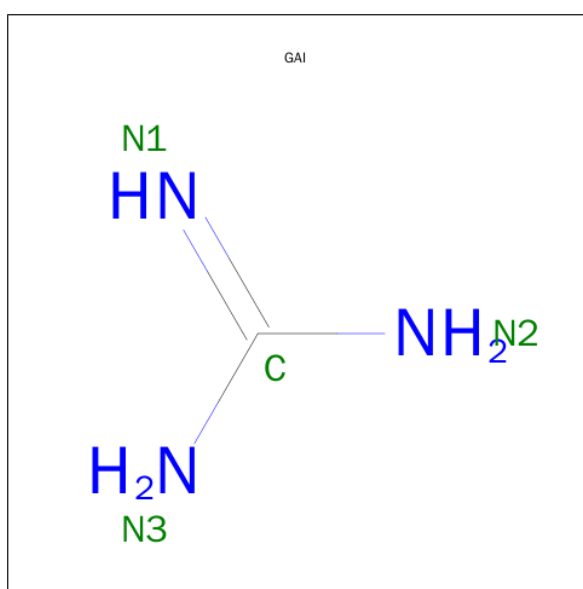
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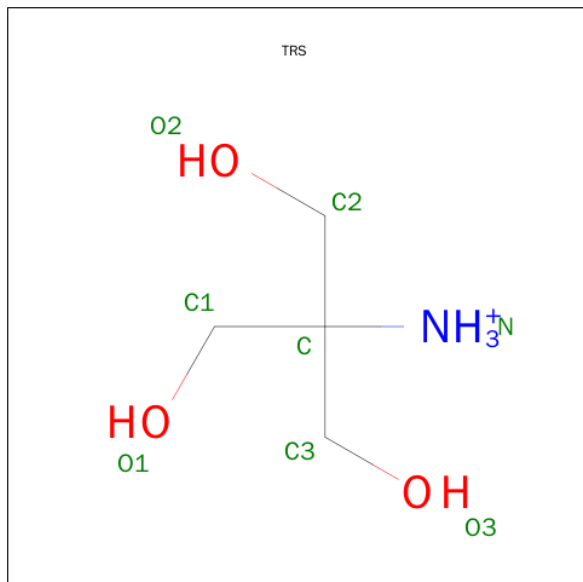
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			16	7	2	6	1		
4	D	1	Total	C	N	O	P	0	0
			16	7	2	6	1		
4	E	1	Total	C	N	O	P	0	0
			16	7	2	6	1		
4	F	1	Total	C	N	O	P	0	0
			16	7	2	6	1		

- Molecule 5 is GUANIDINE (three-letter code: GAI) (formula:  $\text{CH}_5\text{N}_3$ ).



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

- Molecule 6 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula:  $C_4H_{12}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			8	4	1	3		
6	B	1	Total	C	N	O	0	0
			8	4	1	3		
6	C	1	Total	C	N	O	0	0
			8	4	1	3		
6	F	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 7 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ni	0	0
			1	1		
7	D	1	Total	Ni	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	197	Total	O	0	0
			197	197		
8	B	156	Total	O	0	0
			156	156		

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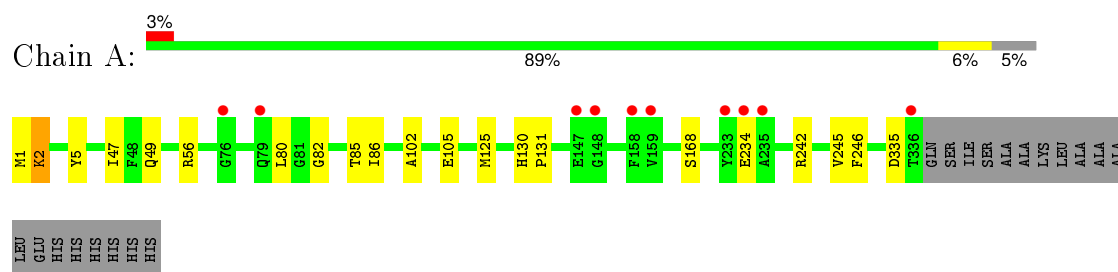
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	122	Total 122	O 122	0	0
8	D	178	Total 178	O 178	0	0
8	E	87	Total 87	O 87	0	0
8	F	85	Total 85	O 85	0	0

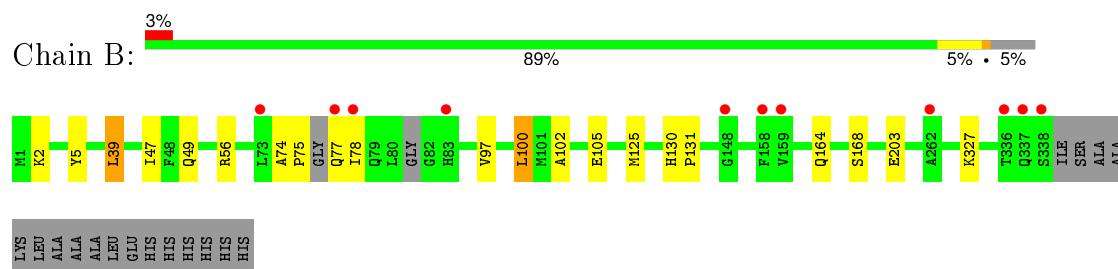
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

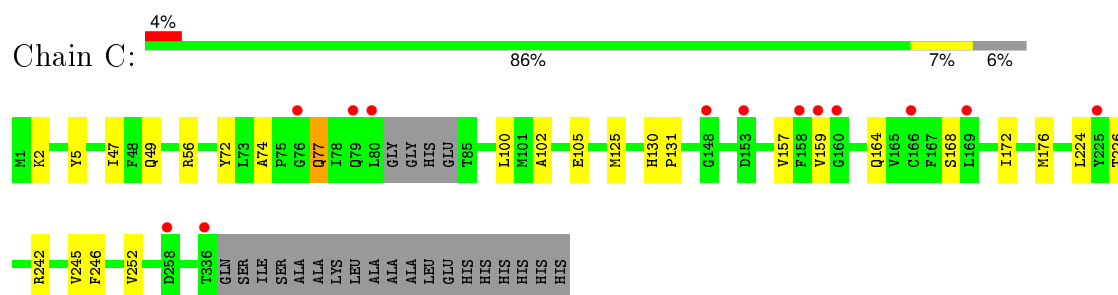
#### • Molecule 1: PUTRESCINE CARBAMOYLTRANSFERASE



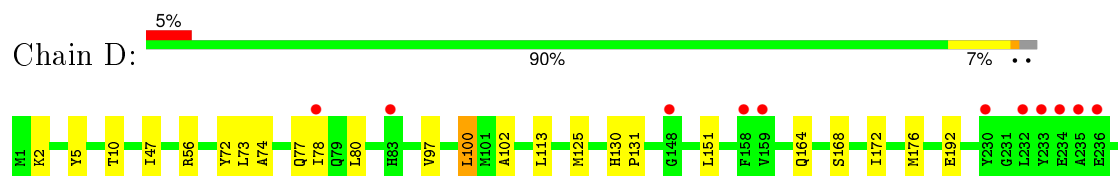
#### • Molecule 1: PUTRESCINE CARBAMOYLTRANSFERASE

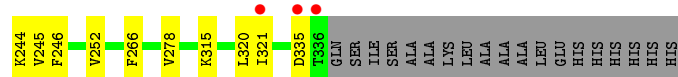


#### • Molecule 1: PUTRESCINE CARBAMOYLTRANSFERASE



#### • Molecule 1: PUTRESCINE CARBAMOYLTRANSFERASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	103.69 Å   130.60 Å   164.16 Å 90.00°   104.25°   90.00°	Depositor
Resolution (Å)	25.00 – 1.99 24.97 – 1.99	Depositor EDS
% Data completeness (in resolution range)	89.8 (25.00-1.99) 89.8 (24.97-1.99)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.55 (at 1.99 Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.182 , 0.206 0.186 , 0.211	Depositor DCC
$R_{free}$ test set	6552 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	23.8	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.9	EDS
Estimated twinning fraction	0.018 for -1/2*h+1/2*k-1/2*l, 1/2*h-1/2*k-1/2*l, -h-k 0.010 for -1/2*h-1/2*k-1/2*l, -1/2*h-1/2*k+1/2*l, -h+k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 130140 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16546	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NI, TRS, GAI, PAO

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	0.45	0/2651	0.58	0/3585
1	B	0.43	0/2648	0.59	1/3578 (0.0%)
1	C	0.41	0/2606	0.56	0/3525
1	D	0.42	0/2718	0.56	0/3678
1	E	0.41	0/2589	0.57	0/3503
1	F	0.42	0/2610	0.56	0/3528
All	All	0.42	0/15822	0.57	1/21397 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	39	LEU	CA-CB-CG	5.09	127.00	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	2603	0	2508	13	0
1	B	2603	0	2505	9	1
1	C	2560	0	2464	13	0
1	D	2670	0	2580	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2543	0	2451	21	0
1	F	2564	0	2474	20	1
2	A	5	0	1	0	0
2	C	5	0	1	0	0
2	E	5	0	1	1	0
3	B	5	0	1	0	0
4	A	16	0	12	1	0
4	B	16	0	12	0	0
4	C	16	0	12	0	0
4	D	16	0	12	0	0
4	E	16	0	12	0	0
4	F	16	0	12	0	0
5	A	4	0	4	1	0
5	B	4	0	4	0	0
5	C	4	0	4	0	0
5	D	4	0	4	0	0
5	E	4	0	4	0	0
5	F	8	0	8	0	0
6	A	8	0	12	0	0
6	B	8	0	12	0	0
6	C	8	0	12	0	0
6	F	8	0	12	0	0
7	A	1	0	0	0	0
7	D	1	0	0	0	0
8	A	197	0	0	0	0
8	B	156	0	0	1	0
8	C	122	0	0	0	0
8	D	178	0	0	1	0
8	E	87	0	0	0	0
8	F	85	0	0	0	0
All	All	16546	0	15134	90	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 (90) 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:F:266:PHE:CZ	1:F:278:VAL:HG11	2.07	0.89
1:A:245:VAL:HG23	1:A:246:PHE:CD2	2.07	0.88
1:C:245:VAL:HG13	1:C:246:PHE:CD2	2.12	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:LEU:O	1:A:86:ILE:HD11	1.76	0.84
1:F:245:VAL:HG13	1:F:246:PHE:CD2	2.18	0.79
1:D:73:LEU:HB3	1:D:78:ILE:HD13	1.65	0.79
1:E:245:VAL:HG13	1:E:246:PHE:CD2	2.17	0.79
1:A:1:MET:HE2	1:A:2:LYS:H	1.50	0.76
1:D:77:GLN:C	1:D:78:ILE:HD12	2.11	0.71
1:C:159:VAL:HG11	1:C:252:VAL:CG2	2.21	0.70
1:B:203:GLU:HG3	1:D:10:THR:HG21	1.73	0.68
1:F:266:PHE:HZ	1:F:278:VAL:HG11	1.58	0.67
1:D:319:ASP:OD1	1:D:321:ILE:HG22	1.95	0.67
1:F:252:VAL:HB	1:F:278:VAL:HG12	1.78	0.65
1:E:156:VAL:HG11	1:E:169:LEU:HD21	1.79	0.64
1:A:242:ARG:HA	1:A:245:VAL:HG22	1.81	0.61
1:E:242:ARG:HA	1:E:245:VAL:HG12	1.83	0.60
1:F:242:ARG:HA	1:F:245:VAL:HG12	1.84	0.59
1:B:49:GLN:HE21	1:B:105:GLU:H	1.50	0.59
1:E:336:THR:O	2:E:337:GLN:CB	2.52	0.57
1:F:49:GLN:HE21	1:F:105:GLU:H	1.53	0.56
1:E:141:MET:O	1:E:145:LEU:HD13	2.06	0.56
1:C:242:ARG:HA	1:C:245:VAL:HG12	1.89	0.55
1:F:1:MET:HG2	1:F:315:LYS:HD3	1.89	0.53
1:A:1:MET:HE2	1:A:2:LYS:N	2.21	0.52
1:C:49:GLN:HE21	1:C:105:GLU:H	1.56	0.52
1:A:49:GLN:HE21	1:A:105:GLU:H	1.56	0.52
1:A:245:VAL:CG2	1:A:246:PHE:CD2	2.86	0.52
1:D:321:ILE:HD12	1:D:321:ILE:O	2.10	0.52
8:B:2046:HOH:O	1:C:77:GLN:NE2	2.42	0.52
1:F:224:LEU:HD23	1:F:224:LEU:C	2.30	0.52
1:E:49:GLN:HE21	1:E:105:GLU:H	1.56	0.51
1:A:1:MET:HE3	1:A:1:MET:HA	1.93	0.51
1:F:49:GLN:NE2	1:F:105:GLU:H	2.09	0.51
1:C:159:VAL:CG1	1:C:226:THR:HB	2.41	0.50
1:D:192:GLU:H	1:D:192:GLU:CD	2.14	0.50
1:E:169:LEU:HD23	1:E:173:THR:HG23	1.93	0.50
1:E:169:LEU:HD22	1:E:180:PHE:CE1	2.46	0.50
1:B:74:ALA:HB1	1:B:75:PRO:HD2	1.93	0.50
1:E:333:PHE:O	1:E:336:THR:O	2.30	0.49
1:B:49:GLN:NE2	1:B:105:GLU:H	2.10	0.48
1:D:346:ALA:HB2	1:F:320:LEU:HD13	1.95	0.48
1:D:349:GLU:C	1:F:321:ILE:HD11	2.35	0.48
1:E:321:ILE:H	1:E:321:ILE:HD12	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:332:VAL:O	1:E:336:THR:HG22	2.14	0.47
1:D:78:ILE:HD12	1:D:78:ILE:N	2.29	0.46
1:C:49:GLN:NE2	1:C:105:GLU:H	2.13	0.46
1:E:141:MET:O	1:E:145:LEU:CD1	2.64	0.45
1:B:75:PRO:O	1:B:77:GLN:N	2.49	0.45
1:E:142:VAL:HA	1:E:145:LEU:HD13	1.99	0.45
1:B:97:VAL:HG21	1:B:100:LEU:HD13	1.99	0.45
1:E:5:TYR:CE2	1:E:131:PRO:HB2	2.52	0.44
1:C:72:TYR:CE2	1:C:74:ALA:HB2	2.51	0.44
1:F:102:ALA:HB3	1:F:110:ILE:HD13	1.98	0.44
1:D:5:TYR:CE2	1:D:131:PRO:HB2	2.53	0.44
1:D:72:TYR:CE2	1:D:74:ALA:HB2	2.52	0.44
1:B:47:ILE:O	1:B:102:ALA:HA	2.18	0.44
1:E:49:GLN:NE2	1:E:105:GLU:H	2.16	0.44
1:A:5:TYR:CE2	1:A:131:PRO:HB2	2.53	0.43
1:A:47:ILE:O	1:A:102:ALA:HA	2.18	0.43
1:E:169:LEU:O	1:E:169:LEU:HD23	2.18	0.43
1:F:5:TYR:CE2	1:F:131:PRO:HB2	2.54	0.43
1:E:47:ILE:O	1:E:102:ALA:HA	2.18	0.43
1:C:5:TYR:CE2	1:C:131:PRO:HB2	2.53	0.43
1:B:74:ALA:HB1	1:B:75:PRO:CD	2.49	0.43
1:E:5:TYR:CD2	1:E:304:LEU:HD21	2.54	0.43
1:D:47:ILE:O	1:D:102:ALA:HA	2.18	0.43
1:B:5:TYR:CE2	1:B:131:PRO:HB2	2.54	0.42
1:E:242:ARG:HA	1:E:245:VAL:CG1	2.50	0.42
1:C:47:ILE:O	1:C:102:ALA:HA	2.19	0.42
1:F:47:ILE:O	1:F:102:ALA:HA	2.19	0.42
1:D:151:LEU:HB2	8:D:2107:HOH:O	2.20	0.42
1:E:107:HIS:O	1:E:110:ILE:HG22	2.19	0.42
1:F:226:THR:HG21	1:F:278:VAL:HG13	2.01	0.41
1:A:1:MET:CE	1:A:2:LYS:H	2.27	0.41
1:F:97:VAL:HG21	1:F:100:LEU:HD13	2.01	0.41
1:C:245:VAL:CG1	1:C:246:PHE:CD2	2.95	0.41
1:D:319:ASP:OD1	1:D:321:ILE:CG2	2.68	0.41
1:F:172:ILE:O	1:F:176:MET:HG2	2.21	0.41
1:A:82:GLY:O	1:A:85:THR:HG22	2.21	0.41
1:F:188:PHE:CE1	1:F:245:VAL:HG21	2.56	0.41
1:A:49:GLN:NE2	1:A:105:GLU:H	2.18	0.41
1:D:346:ALA:CB	1:F:320:LEU:HD13	2.50	0.41
1:D:97:VAL:HG21	1:D:100:LEU:HD13	2.03	0.41
4:A:1338:PAO:O	5:A:1339:GAI:N1	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:169:LEU:HD23	1:E:173:THR:CG2	2.51	0.40
1:F:242:ARG:HA	1:F:245:VAL:CG1	2.50	0.40
1:D:172:ILE:O	1:D:176:MET:HG2	2.21	0.40
1:C:157:VAL:HB	1:C:224:LEU:HD12	2.02	0.40
1:C:172:ILE:O	1:C:176:MET:HG2	2.22	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:B:327:LYS:NZ	1:F:244:LYS:O[2_555]	2.15	0.05

## 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	334/355 (94%)	327 (98%)	6 (2%)	1 (0%)	46	41
1	B	330/355 (93%)	323 (98%)	6 (2%)	1 (0%)	46	41
1	C	328/355 (92%)	321 (98%)	6 (2%)	1 (0%)	46	41
1	D	347/355 (98%)	339 (98%)	7 (2%)	1 (0%)	46	41
1	E	327/355 (92%)	320 (98%)	6 (2%)	1 (0%)	46	41
1	F	327/355 (92%)	320 (98%)	6 (2%)	1 (0%)	46	41
All	All	1993/2130 (94%)	1950 (98%)	37 (2%)	6 (0%)	46	41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	125	MET
1	B	125	MET
1	C	125	MET

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Mol	Chain	Res	Type
1	D	125	MET
1	E	125	MET
1	F	125	MET

### 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	279/306 (91%)	273 (98%)	6 (2%)	60	62
1	B	278/306 (91%)	270 (97%)	8 (3%)	50	49
1	C	272/306 (89%)	265 (97%)	7 (3%)	54	54
1	D	281/306 (92%)	272 (97%)	9 (3%)	46	44
1	E	270/306 (88%)	262 (97%)	8 (3%)	48	47
1	F	274/306 (90%)	265 (97%)	9 (3%)	45	43
All	All	1654/1836 (90%)	1607 (97%)	47 (3%)	51	50

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	56	ARG
1	A	130	HIS
1	A	168	SER
1	A	234	GLU
1	A	335	ASP
1	B	2	LYS
1	B	39	LEU
1	B	56	ARG
1	B	78	ILE
1	B	100	LEU
1	B	130	HIS
1	B	164	GLN
1	B	168	SER
1	C	2	LYS

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Mol	Chain	Res	Type
1	C	56	ARG
1	C	77	GLN
1	C	100	LEU
1	C	130	HIS
1	C	164	GLN
1	C	168	SER
1	D	2	LYS
1	D	56	ARG
1	D	80	LEU
1	D	100	LEU
1	D	113	LEU
1	D	130	HIS
1	D	164	GLN
1	D	168	SER
1	D	321	ILE
1	E	2	LYS
1	E	56	ARG
1	E	86	ILE
1	E	130	HIS
1	E	145	LEU
1	E	164	GLN
1	E	168	SER
1	E	169	LEU
1	F	2	LYS
1	F	56	ARG
1	F	77	GLN
1	F	100	LEU
1	F	130	HIS
1	F	164	GLN
1	F	168	SER
1	F	234	GLU
1	F	335	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	41	ASN
1	A	49	GLN
1	A	201	ASN
1	A	310	ASN
1	A	323	GLN

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Mol	Chain	Res	Type
1	B	37	GLN
1	B	41	ASN
1	B	49	GLN
1	B	189	GLN
1	B	201	ASN
1	B	310	ASN
1	B	323	GLN
1	C	41	ASN
1	C	49	GLN
1	C	77	GLN
1	C	201	ASN
1	C	310	ASN
1	D	41	ASN
1	D	77	GLN
1	D	79	GLN
1	D	201	ASN
1	D	310	ASN
1	E	37	GLN
1	E	41	ASN
1	E	49	GLN
1	E	189	GLN
1	E	201	ASN
1	E	254	GLN
1	E	310	ASN
1	E	323	GLN
1	F	41	ASN
1	F	49	GLN
1	F	189	GLN
1	F	201	ASN
1	F	310	ASN
1	F	323	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](#)

Of 23 ligands modelled in this entry, 2 are monoatomic - leaving 21 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	$\# Z  > 2$
4	PAO	A	1338	-	12,15,15	1.30	2 (16%)	14,20,20	0.74	0
5	GAI	A	1339	-	0,3,3	0.00	-	0,3,3	0.00	-
6	TRS	A	1340	-	7,7,7	0.68	0	9,9,9	1.75	2 (22%)
2	GLN	A	337	-	3,4,9	0.60	0	0,4,11	0.00	-
4	PAO	B	1340	-	12,15,15	1.42	1 (8%)	14,20,20	0.78	1 (7%)
5	GAI	B	1341	-	0,3,3	0.00	-	0,3,3	0.00	-
6	TRS	B	1342	-	7,7,7	0.72	0	9,9,9	1.52	2 (22%)
3	ILE	B	339	-	3,4,8	0.46	0	0,4,10	0.00	-
4	PAO	C	1338	-	12,15,15	1.00	1 (8%)	14,20,20	1.12	2 (14%)
5	GAI	C	1339	-	0,3,3	0.00	-	0,3,3	0.00	-
6	TRS	C	1340	-	7,7,7	0.64	0	9,9,9	1.81	2 (22%)
2	GLN	C	337	-	3,4,9	0.44	0	0,4,11	0.00	-
4	PAO	D	1350	-	12,15,15	1.23	1 (8%)	14,20,20	1.16	1 (7%)
5	GAI	D	1351	-	0,3,3	0.00	-	0,3,3	0.00	-
4	PAO	E	1338	-	12,15,15	1.25	2 (16%)	14,20,20	0.85	0
5	GAI	E	1339	-	0,3,3	0.00	-	0,3,3	0.00	-
2	GLN	E	337	-	3,4,9	0.48	0	0,4,11	0.00	-
4	PAO	F	1337	-	12,15,15	1.19	2 (16%)	14,20,20	1.06	1 (7%)
5	GAI	F	1338	-	0,3,3	0.00	-	0,3,3	0.00	-
5	GAI	F	1339	-	0,3,3	0.00	-	0,3,3	0.00	-
6	TRS	F	1340	-	7,7,7	0.94	0	9,9,9	1.46	2 (22%)

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
4	PAO	A	1338	-	-	0/12/16/16	0/0/0/0
5	GAI	A	1339	-	-	0/0/0/0	0/0/0/0
6	TRS	A	1340	-	-	0/9/9/9	0/0/0/0
2	GLN	A	337	-	-	0/0/2/9	0/0/0/0
4	PAO	B	1340	-	-	0/12/16/16	0/0/0/0
5	GAI	B	1341	-	-	0/0/0/0	0/0/0/0
6	TRS	B	1342	-	-	0/9/9/9	0/0/0/0
3	ILE	B	339	-	-	0/0/2/10	0/0/0/0
4	PAO	C	1338	-	-	0/12/16/16	0/0/0/0
5	GAI	C	1339	-	-	0/0/0/0	0/0/0/0
6	TRS	C	1340	-	-	0/9/9/9	0/0/0/0
2	GLN	C	337	-	-	0/0/2/9	0/0/0/0
4	PAO	D	1350	-	-	0/12/16/16	0/0/0/0
5	GAI	D	1351	-	-	0/0/0/0	0/0/0/0
4	PAO	E	1338	-	-	0/12/16/16	0/0/0/0
5	GAI	E	1339	-	-	0/0/0/0	0/0/0/0
2	GLN	E	337	-	-	0/0/2/9	0/0/0/0
4	PAO	F	1337	-	-	0/12/16/16	0/0/0/0
5	GAI	F	1338	-	-	0/0/0/0	0/0/0/0
5	GAI	F	1339	-	-	0/0/0/0	0/0/0/0
6	TRS	F	1340	-	-	0/9/9/9	0/0/0/0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1338	PAO	P-O2P	2.04	1.59	1.54
4	C	1338	PAO	P-O2P	2.18	1.60	1.54
4	F	1337	PAO	P-O2P	2.24	1.60	1.54
4	F	1337	PAO	P-C1P	2.45	1.83	1.79
4	E	1338	PAO	P-C1P	2.53	1.83	1.79
4	A	1338	PAO	P-O3P	2.65	1.61	1.54
4	E	1338	PAO	P-O2P	2.73	1.61	1.54
4	D	1350	PAO	P-O2P	3.35	1.63	1.54
4	B	1340	PAO	P-C1P	4.03	1.85	1.79

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1340	TRS	O2-C2-C	-3.76	103.58	111.18
6	F	1340	TRS	O2-C2-C	-3.06	104.99	111.18
6	A	1340	TRS	C3-C-C2	-2.94	104.41	110.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1337	PAO	P-C1P-C1	-2.76	107.68	114.41
6	B	1342	TRS	C3-C-C2	-2.58	105.19	110.78
6	C	1340	TRS	O3-C3-C	-2.45	106.23	111.18
4	B	1340	PAO	P-C1P-C1	-2.45	108.43	114.41
4	D	1350	PAO	P-C1P-C1	-2.41	108.53	114.41
4	C	1338	PAO	P-C1P-C1	-2.11	109.26	114.41
4	C	1338	PAO	O3P-P-C1P	2.11	111.65	107.01
6	F	1340	TRS	C3-C-C1	2.16	115.46	110.78
6	B	1342	TRS	C3-C-N	2.39	112.44	108.09
6	A	1340	TRS	C3-C-N	3.55	114.54	108.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1338	PAO	1	0
5	A	1339	GAI	1	0
2	E	337	GLN	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 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	336/355 (94%)	-0.12	10 (2%) 54 55	12, 19, 34, 50	1 (0%)
1	B	336/355 (94%)	-0.03	11 (3%) 50 51	13, 22, 40, 67	4 (1%)
1	C	332/355 (93%)	-0.02	13 (3%) 43 45	12, 24, 39, 53	0
1	D	349/355 (98%)	0.06	19 (5%) 29 31	14, 22, 42, 61	4 (1%)
1	E	331/355 (93%)	0.21	17 (5%) 32 33	16, 31, 49, 57	1 (0%)
1	F	331/355 (93%)	0.14	11 (3%) 50 51	15, 29, 48, 63	1 (0%)
All	All	2015/2130 (94%)	0.04	81 (4%) 42 44	12, 24, 44, 67	11 (0%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	336	THR	6.6
1	E	233	TYR	6.0
1	B	73	LEU	5.1
1	D	233	TYR	4.8
1	A	336	THR	4.6
1	C	336	THR	4.3
1	A	233	TYR	4.0
1	D	148	GLY	4.0
1	B	336	THR	3.9
1	D	234	GLU	3.8
1	C	158	PHE	3.6
1	D	336	THR	3.6
1	A	234	GLU	3.5
1	F	335	ASP	3.4
1	D	345	ALA	3.3
1	B	83	HIS	3.2
1	F	76	GLY	3.2
1	E	148	GLY	3.2
1	A	148	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	337	GLN	3.1
1	E	1	MET	3.1
1	C	80	LEU	3.0
1	E	237	LEU	3.0
1	F	77	GLN	3.0
1	D	346	ALA	3.0
1	D	158	PHE	3.0
1	D	235	ALA	2.9
1	B	77	GLN	2.9
1	E	159	VAL	2.9
1	D	338	SER	2.8
1	D	321	ILE	2.8
1	E	169	LEU	2.8
1	D	347	ALA	2.8
1	E	335	ASP	2.8
1	E	234	GLU	2.7
1	D	339	ILE	2.7
1	F	169	LEU	2.7
1	B	148	GLY	2.7
1	C	225	TYR	2.7
1	E	77	GLN	2.6
1	D	83	HIS	2.6
1	E	235	ALA	2.6
1	E	75	PRO	2.6
1	B	338	SER	2.6
1	C	159	VAL	2.6
1	F	234	GLU	2.5
1	D	232	LEU	2.5
1	F	321	ILE	2.5
1	F	235	ALA	2.5
1	D	337	GLN	2.5
1	C	169	LEU	2.5
1	C	166	CYS	2.5
1	D	236	GLU	2.4
1	B	78	ILE	2.4
1	A	79	GLN	2.4
1	D	78	ILE	2.4
1	E	76	GLY	2.4
1	A	159	VAL	2.4
1	F	78	ILE	2.4
1	C	79	GLN	2.3
1	B	159	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	158	PHE	2.3
1	A	235	ALA	2.3
1	C	148	GLY	2.3
1	D	230	TYR	2.3
1	A	158	PHE	2.2
1	F	158	PHE	2.2
1	E	187	GLY	2.2
1	F	336	THR	2.2
1	B	262	ALA	2.1
1	C	160	GLY	2.1
1	E	321	ILE	2.1
1	F	72	TYR	2.1
1	A	76	GLY	2.1
1	A	147	GLU	2.1
1	E	158	PHE	2.1
1	C	76	GLY	2.1
1	C	258	ASP	2.1
1	D	159	VAL	2.0
1	E	236	GLU	2.0
1	C	153	ASP	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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	GAI	F	1338	4/4	0.87	0.17	4.14	28,30,30,31	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
6	TRS	F	1340	8/8	0.86	0.18	3.61	39,42,42,44	0
6	TRS	A	1340	8/8	0.72	0.22	3.40	28,34,35,36	0
6	TRS	B	1342	8/8	0.87	0.12	2.58	23,25,25,25	0
6	TRS	C	1340	8/8	0.85	0.15	1.46	27,30,31,33	0
5	GAI	E	1339	4/4	0.91	0.28	1.37	41,41,42,42	0
2	GLN	A	337	5/10	0.62	0.28	1.27	44,46,47,47	0
5	GAI	A	1339	4/4	0.84	0.17	0.58	33,33,34,35	0
5	GAI	F	1339	4/4	0.95	0.11	0.19	28,28,28,28	0
2	GLN	C	337	5/10	0.79	0.18	0.12	44,44,45,46	0
5	GAI	D	1351	4/4	0.97	0.14	0.03	41,41,41,42	0
4	PAO	C	1338	16/16	0.97	0.09	-0.36	14,16,20,22	0
4	PAO	B	1340	16/16	0.98	0.10	-0.37	13,15,18,19	0
4	PAO	F	1337	16/16	0.98	0.09	-0.68	18,19,22,23	0
4	PAO	E	1338	16/16	0.97	0.08	-0.79	23,27,30,31	0
4	PAO	A	1338	16/16	0.97	0.08	-1.02	13,15,18,18	0
4	PAO	D	1350	16/16	0.97	0.07	-1.13	15,17,21,21	0
7	NI	A	1341	1/1	1.00	0.04	-2.85	15,15,15,15	0
7	NI	D	1352	1/1	1.00	0.03	-3.94	19,19,19,19	0
3	ILE	B	339	5/9	0.62	0.21	-	48,49,51,52	5
5	GAI	B	1341	4/4	0.97	0.07	-	22,24,24,24	0
2	GLN	E	337	5/10	0.71	0.32	-	40,42,43,44	0
5	GAI	C	1339	4/4	0.95	0.11	-	26,26,27,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.