



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 14, 2016 – 09:53 PM EDT

PDB ID : 5H8J  
Title : Crystal structure of Medicago truncatula N-carbamoylputrescine amidohydrolase (MtCPA) in complex with cadaverine  
Authors : Sekula, B.; Ruszkowski, M.; Malinska, M.; Dauter, Z.  
Deposited on : 2015-12-23  
Resolution : 2.19 Å(reported)

This is a wwPDB X-ray Structure 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/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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027107  
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) : rb-20027107

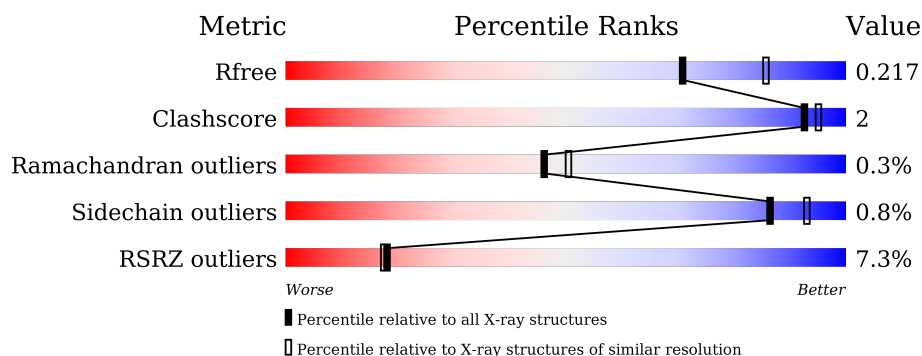
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.19 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	304	<div> <div>10%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>
1	B	304	<div> <div>4%</div> <div>95%</div> <div>.</div> <div>.</div> </div>
1	C	304	<div> <div>3%</div> <div>98%</div> <div>..</div> </div>
1	D	304	<div> <div>%</div> <div>94%</div> <div>.</div> <div>.</div> <div>.</div> </div>
1	E	304	<div> <div>%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
1	F	304	<div> <div>%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	304	
1	H	304	
1	I	304	
1	J	304	
1	K	304	
1	L	304	
1	M	304	
1	N	304	
1	O	304	
1	P	304	

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
2	GOL	A	402	-	-	-	X
2	GOL	B	402	-	-	-	X
2	GOL	C	403	-	-	-	X
2	GOL	C	404	-	-	-	X
2	GOL	E	402	-	-	-	X
2	GOL	E	403	-	-	-	X
2	GOL	F	403	-	-	-	X
2	GOL	I	402	-	-	-	X
2	GOL	M	404	-	-	-	X
2	GOL	N	402	-	-	-	X
2	GOL	O	403	-	-	-	X
3	PEG	L	402	-	-	-	X
4	EDO	A	405	-	-	-	X
4	EDO	C	405	-	-	-	X
4	EDO	F	404	-	-	-	X
4	EDO	I	404	-	-	-	X
4	EDO	K	404	-	-	-	X
4	EDO	L	403	-	-	-	X
4	EDO	N	403	-	-	-	X
5	N2P	B	401	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	N2P	C	401	-	-	-	X
5	N2P	D	401	-	-	-	X
5	N2P	E	401	-	-	-	X
5	N2P	F	402	-	-	-	X
5	N2P	G	401	-	-	-	X
5	N2P	J	401	-	-	-	X
5	N2P	K	401	-	-	-	X
5	N2P	L	401	-	-	-	X
5	N2P	M	401	-	-	-	X
5	N2P	N	401	-	-	-	X
5	N2P	O	401	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 41003 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 N-carbamoylputrescine amidohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	3	0
			2360	1508	407	435	10			
1	B	297	Total	C	N	O	S	0	0	0
			2357	1505	408	436	8			
1	C	301	Total	C	N	O	S	0	1	0
			2390	1524	412	444	10			
1	D	298	Total	C	N	O	S	0	3	0
			2382	1522	409	443	8			
1	E	297	Total	C	N	O	S	0	0	0
			2357	1505	408	436	8			
1	F	298	Total	C	N	O	S	0	0	0
			2365	1509	409	439	8			
1	G	295	Total	C	N	O	S	0	0	0
			2344	1497	405	434	8			
1	H	268	Total	C	N	O	S	0	0	0
			2131	1368	371	384	8			
1	I	292	Total	C	N	O	S	0	1	0
			2322	1484	400	429	9			
1	J	298	Total	C	N	O	S	0	1	0
			2369	1513	409	439	8			
1	K	301	Total	C	N	O	S	0	0	0
			2387	1522	412	444	9			
1	L	298	Total	C	N	O	S	0	2	0
			2374	1515	409	441	9			
1	M	298	Total	C	N	O	S	0	0	0
			2365	1509	409	439	8			
1	N	298	Total	C	N	O	S	0	1	0
			2369	1513	409	439	8			
1	O	298	Total	C	N	O	S	0	1	0
			2371	1513	409	441	8			
1	P	279	Total	C	N	O	S	0	1	0
			2217	1421	384	403	9			

There are 48 discrepancies between the modelled and reference sequences:

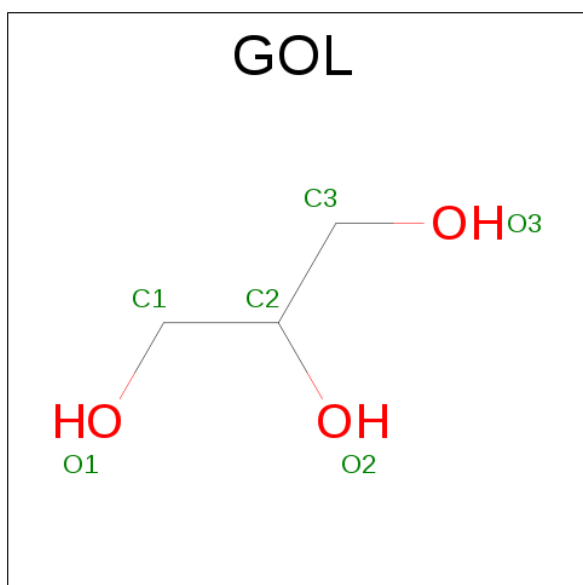
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP G7ITU5
A	-1	ASN	-	expression tag	UNP G7ITU5
A	0	ALA	-	expression tag	UNP G7ITU5
B	-2	SER	-	expression tag	UNP G7ITU5
B	-1	ASN	-	expression tag	UNP G7ITU5
B	0	ALA	-	expression tag	UNP G7ITU5
C	-2	SER	-	expression tag	UNP G7ITU5
C	-1	ASN	-	expression tag	UNP G7ITU5
C	0	ALA	-	expression tag	UNP G7ITU5
D	-2	SER	-	expression tag	UNP G7ITU5
D	-1	ASN	-	expression tag	UNP G7ITU5
D	0	ALA	-	expression tag	UNP G7ITU5
E	-2	SER	-	expression tag	UNP G7ITU5
E	-1	ASN	-	expression tag	UNP G7ITU5
E	0	ALA	-	expression tag	UNP G7ITU5
F	-2	SER	-	expression tag	UNP G7ITU5
F	-1	ASN	-	expression tag	UNP G7ITU5
F	0	ALA	-	expression tag	UNP G7ITU5
G	-2	SER	-	expression tag	UNP G7ITU5
G	-1	ASN	-	expression tag	UNP G7ITU5
G	0	ALA	-	expression tag	UNP G7ITU5
H	-2	SER	-	expression tag	UNP G7ITU5
H	-1	ASN	-	expression tag	UNP G7ITU5
H	0	ALA	-	expression tag	UNP G7ITU5
I	-2	SER	-	expression tag	UNP G7ITU5
I	-1	ASN	-	expression tag	UNP G7ITU5
I	0	ALA	-	expression tag	UNP G7ITU5
J	-2	SER	-	expression tag	UNP G7ITU5
J	-1	ASN	-	expression tag	UNP G7ITU5
J	0	ALA	-	expression tag	UNP G7ITU5
K	-2	SER	-	expression tag	UNP G7ITU5
K	-1	ASN	-	expression tag	UNP G7ITU5
K	0	ALA	-	expression tag	UNP G7ITU5
L	-2	SER	-	expression tag	UNP G7ITU5
L	-1	ASN	-	expression tag	UNP G7ITU5
L	0	ALA	-	expression tag	UNP G7ITU5
M	-2	SER	-	expression tag	UNP G7ITU5
M	-1	ASN	-	expression tag	UNP G7ITU5
M	0	ALA	-	expression tag	UNP G7ITU5
N	-2	SER	-	expression tag	UNP G7ITU5
N	-1	ASN	-	expression tag	UNP G7ITU5
N	0	ALA	-	expression tag	UNP G7ITU5

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	SER	-	expression tag	UNP G7ITU5
O	-1	ASN	-	expression tag	UNP G7ITU5
O	0	ALA	-	expression tag	UNP G7ITU5
P	-2	SER	-	expression tag	UNP G7ITU5
P	-1	ASN	-	expression tag	UNP G7ITU5
P	0	ALA	-	expression tag	UNP G7ITU5

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

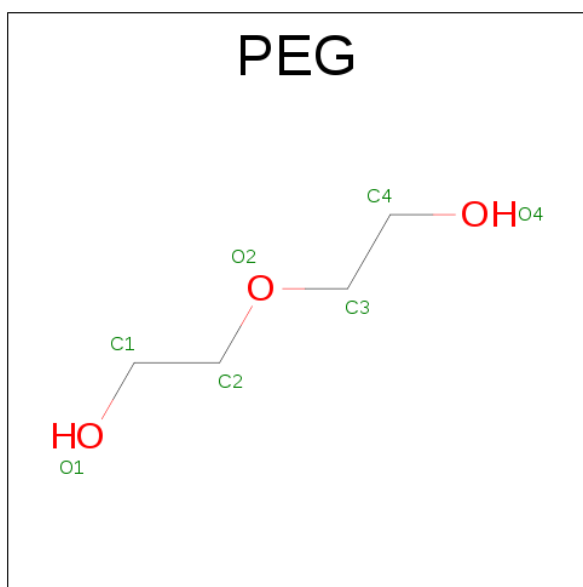
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	I	1	Total	C	O	0	0
			6	3	3		
2	I	1	Total	C	O	0	0
			6	3	3		
2	I	1	Total	C	O	0	0
			6	3	3		
2	K	1	Total	C	O	0	0
			6	3	3		
2	K	1	Total	C	O	0	0
			6	3	3		
2	M	1	Total	C	O	0	0
			6	3	3		
2	M	1	Total	C	O	0	0
			6	3	3		
2	M	1	Total	C	O	0	0
			6	3	3		
2	N	1	Total	C	O	0	0
			6	3	3		
2	O	1	Total	C	O	0	0
			6	3	3		
2	O	1	Total	C	O	0	0
			6	3	3		

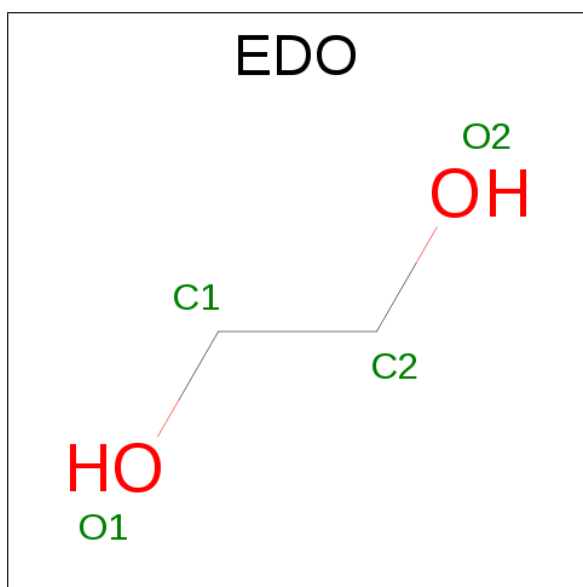
- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	G	1	Total	C	O	0	0
			7	4	3		
3	L	1	Total	C	O	0	0
			7	4	3		

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



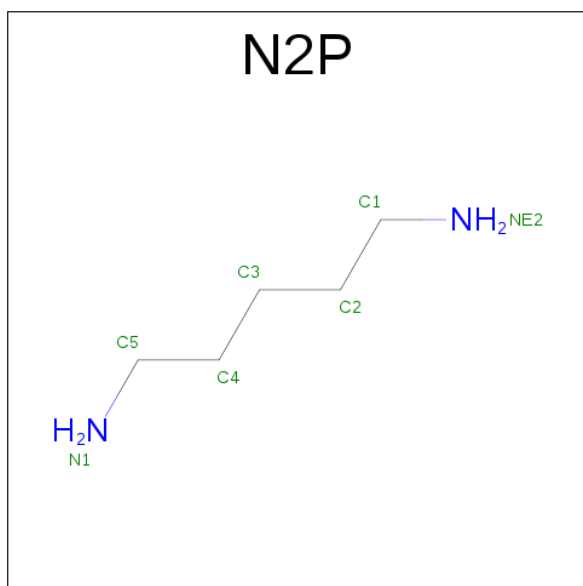
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	F	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	J	1	Total	C	O	0	0
			4	2	2		
4	K	1	Total	C	O	0	0
			4	2	2		
4	L	1	Total	C	O	0	0
			4	2	2		
4	N	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is PENTANE-1,5-DIAMINE (three-letter code: N2P) (formula: C<sub>5</sub>H<sub>14</sub>N<sub>2</sub>).



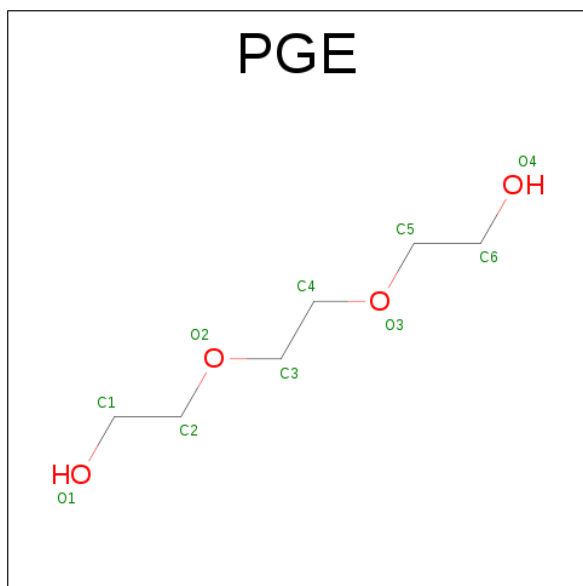
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	N	0	0
			7	5	2		
5	C	1	Total	C	N	0	0
			7	5	2		
5	D	1	Total	C	N	0	0
			7	5	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	E	1	Total	C	N	0	0
			7	5	2		
5	F	1	Total	C	N	0	0
			7	5	2		
5	G	1	Total	C	N	0	0
			7	5	2		
5	J	1	Total	C	N	0	0
			7	5	2		
5	K	1	Total	C	N	0	0
			7	5	2		
5	L	1	Total	C	N	0	0
			7	5	2		
5	M	1	Total	C	N	0	0
			7	5	2		
5	N	1	Total	C	N	0	0
			7	5	2		
5	O	1	Total	C	N	0	0
			7	5	2		

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



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

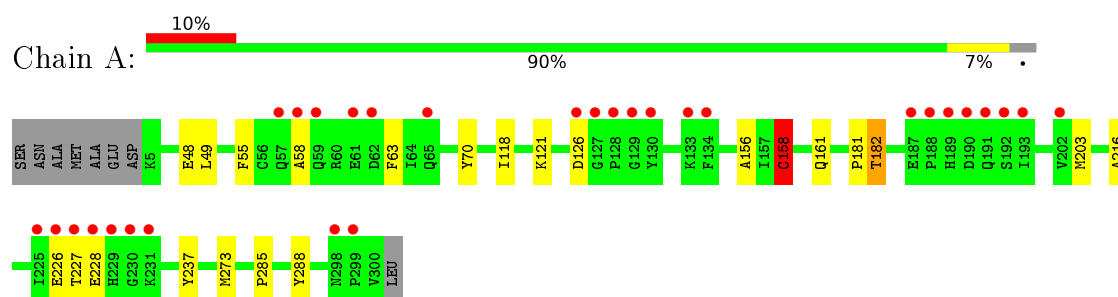
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	157	Total 157	O 157	0	0
7	B	233	Total 233	O 233	0	0
7	C	258	Total 258	O 258	0	0
7	D	288	Total 288	O 288	0	0
7	E	236	Total 236	O 236	0	0
7	F	177	Total 177	O 177	0	0
7	G	120	Total 120	O 120	0	0
7	H	38	Total 38	O 38	0	0
7	I	171	Total 171	O 171	0	0
7	J	232	Total 232	O 232	0	0
7	K	241	Total 241	O 241	0	0
7	L	277	Total 277	O 277	0	0
7	M	263	Total 263	O 263	0	0
7	N	253	Total 253	O 253	0	0
7	O	206	Total 206	O 206	0	0
7	P	92	Total 92	O 92	0	0

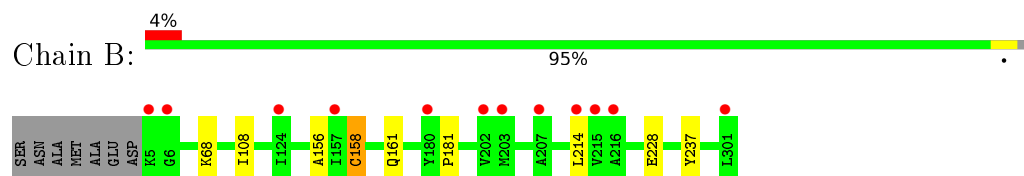
### 3 Residue-property plots [i](#)

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.

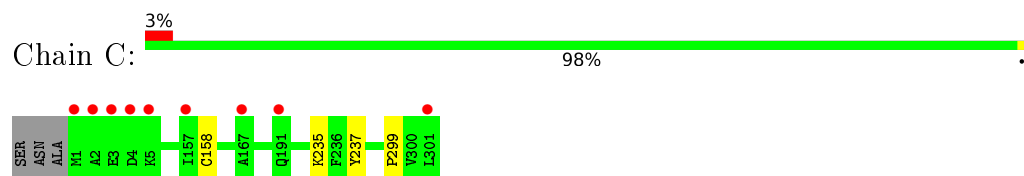
- Molecule 1: N-carbamoylputrescine amidohydrolase



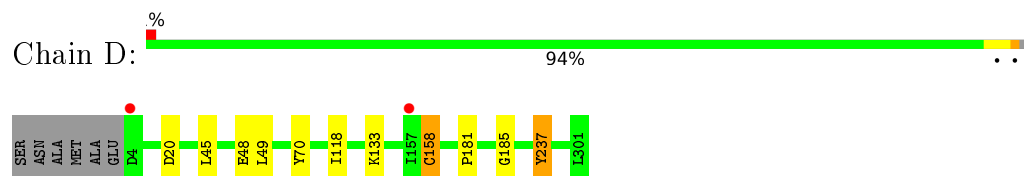
- Molecule 1: N-carbamoylputrescine amidohydrolase



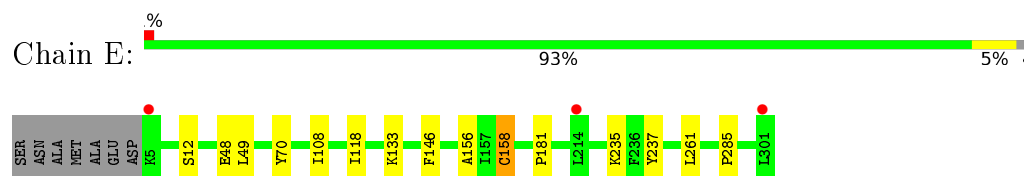
- Molecule 1: N-carbamoylputrescine amidohydrolase



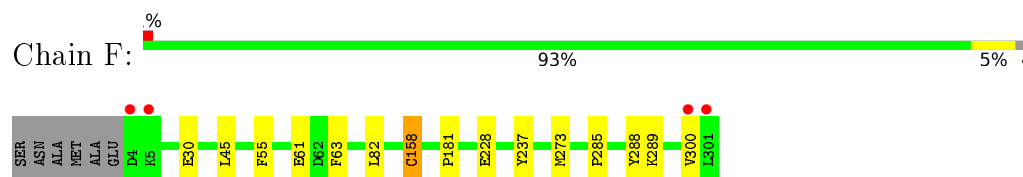
- Molecule 1: N-carbamoylputrescine amidohydrolase



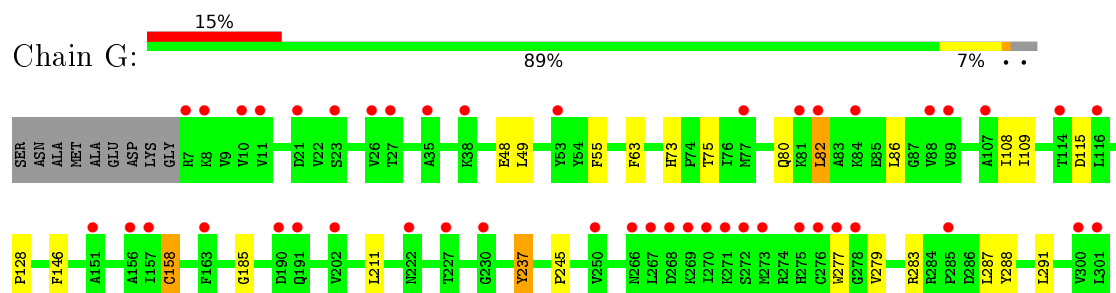
- Molecule 1: N-carbamoylputrescine amidohydrolase



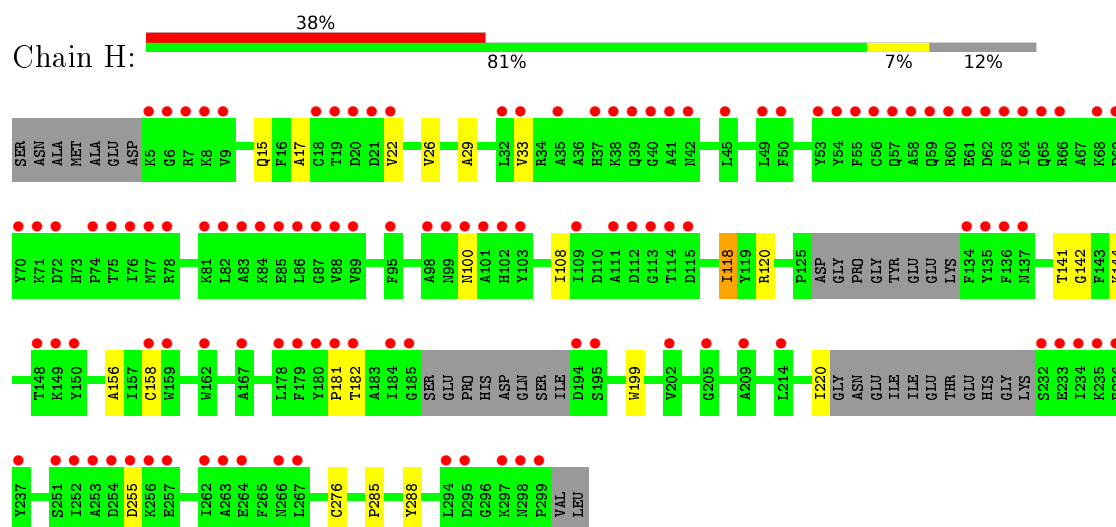
- Molecule 1: N-carbamoylputrescine amidohydrolase



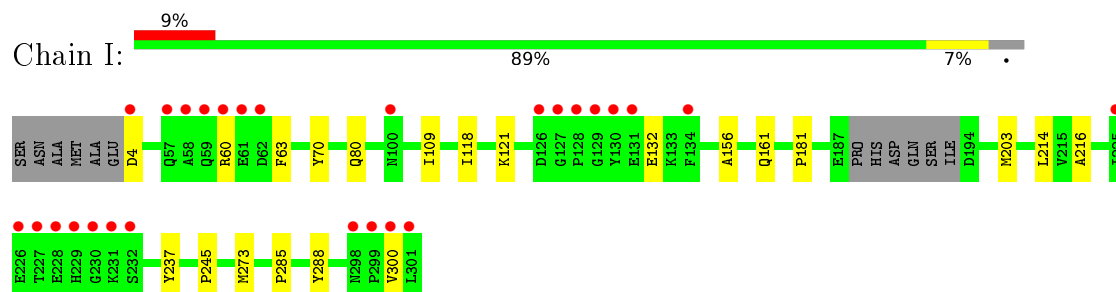
- Molecule 1: N-carbamoylputrescine amidohydrolase



- Molecule 1: N-carbamoylputrescine amidohydrolase

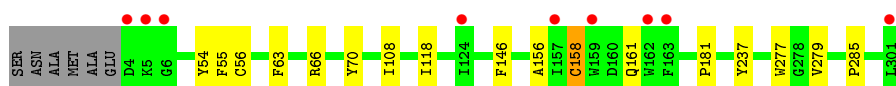


- Molecule 1: N-carbamoylputrescine amidohydrolase

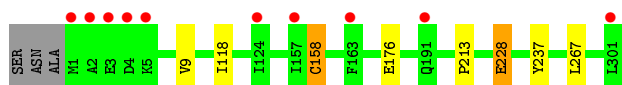


- Molecule 1: N-carbamoylputrescine amidohydrolase

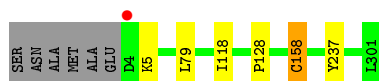




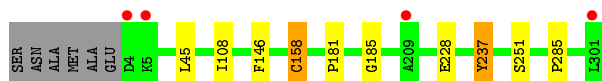
- Molecule 1: N-carbamoylputrescine amidohydrolase



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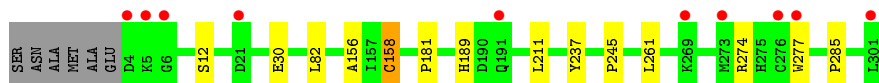
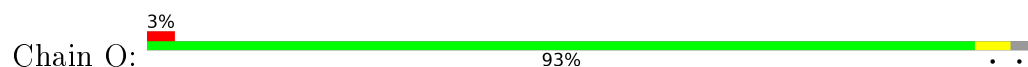
- Molecule 1: N-carbamoylputrescine amidohydrolase



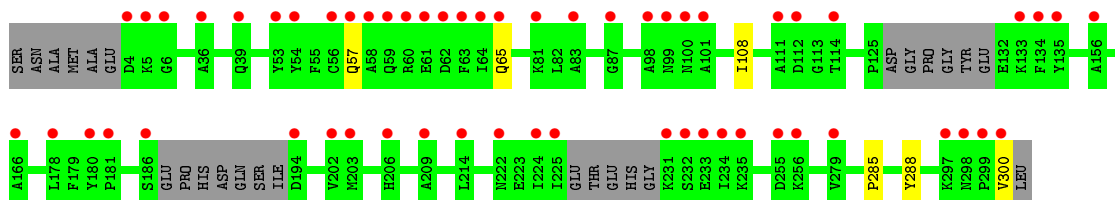
- Molecule 1: N-carbamoylputrescine amidohydrolase



- Molecule 1: N-carbamoylputrescine amidohydrolase



- Molecule 1: N-carbamoylputrescine amidohydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	152.27Å 211.04Å 208.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.56 – 2.19 39.56 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.1 (39.56-2.19) 99.1 (39.56-2.19)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.73 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.171 , 0.211 0.181 , 0.217	Depositor DCC
$R_{free}$ test set	3402 reflections (1.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.8	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.9	EDS
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	3 of 340107 reflections (0.001%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	41003	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.46 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.3540e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, GOL, N2P, PGE, 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	0.84	0/2425	0.76	1/3281 (0.0%)
1	B	0.87	0/2413	0.75	0/3264
1	C	0.90	0/2449	0.77	0/3312
1	D	0.95	1/2447 (0.0%)	0.79	0/3310
1	E	0.85	0/2413	0.76	0/3264
1	F	0.81	0/2421	0.73	0/3275
1	G	0.92	0/2400	0.74	0/3248
1	H	0.84	0/2179	0.71	0/2944
1	I	0.90	0/2378	0.76	0/3213
1	J	0.90	0/2428	0.76	0/3285
1	K	0.89	0/2443	0.75	0/3304
1	L	0.92	0/2436	0.77	0/3295
1	M	0.87	0/2421	0.76	0/3275
1	N	0.88	0/2428	0.76	0/3285
1	O	0.91	0/2430	0.74	0/3287
1	P	0.78	0/2268	0.69	0/3063
All	All	0.88	1/38379 (0.0%)	0.75	1/51905 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	20	ASP	CB-CG	5.65	1.63	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	CYS	CA-CB-SG	5.55	124.00	114.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2360	0	2329	14	0
1	B	2357	0	2319	7	0
1	C	2390	0	2351	5	0
1	D	2382	0	2346	8	0
1	E	2357	0	2319	11	0
1	F	2365	0	2323	12	0
1	G	2344	0	2303	17	0
1	H	2131	0	2113	15	0
1	I	2322	0	2289	12	0
1	J	2369	0	2332	13	0
1	K	2387	0	2346	7	0
1	L	2374	0	2334	6	0
1	M	2365	0	2323	8	0
1	N	2369	0	2332	6	0
1	O	2371	0	2329	12	0
1	P	2217	0	2198	4	0
2	A	18	0	24	0	0
2	B	6	0	8	1	0
2	C	18	0	24	0	0
2	D	6	0	8	0	0
2	E	12	0	16	0	0
2	F	12	0	16	1	0
2	G	6	0	8	0	0
2	H	6	0	8	0	0
2	I	18	0	24	0	0
2	K	12	0	16	0	0
2	M	18	0	24	0	0
2	N	6	0	8	0	0
2	O	12	0	16	0	0
3	A	7	0	10	0	0
3	G	7	0	10	0	0
3	L	7	0	10	0	0
4	A	4	0	6	0	0
4	C	4	0	6	0	0
4	D	4	0	6	0	0
4	F	4	0	6	0	0
4	I	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	J	4	0	6	0	0
4	K	4	0	6	0	0
4	L	4	0	6	0	0
4	N	4	0	6	0	0
5	B	7	0	14	3	0
5	C	7	0	14	3	0
5	D	7	0	14	3	0
5	E	7	0	14	3	0
5	F	7	0	14	3	0
5	G	7	0	14	2	0
5	J	7	0	14	4	0
5	K	7	0	14	3	0
5	L	7	0	14	3	0
5	M	7	0	14	2	0
5	N	7	0	14	3	0
5	O	7	0	14	3	0
6	B	10	0	14	0	0
7	A	157	0	0	1	0
7	B	233	0	0	2	0
7	C	258	0	0	2	0
7	D	288	0	0	0	0
7	E	236	0	0	1	0
7	F	177	0	0	3	0
7	G	120	0	0	0	0
7	H	38	0	0	0	0
7	I	171	0	0	0	0
7	J	232	0	0	0	0
7	K	241	0	0	0	0
7	L	277	0	0	0	0
7	M	263	0	0	0	0
7	N	253	0	0	2	0
7	O	206	0	0	0	0
7	P	92	0	0	0	0
All	All	41003	0	37352	150	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 2.

The worst 5 of 150 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:M:158:CYS:SG	5:M:401:N2P:H5C1	1.98	1.04
1:F:158:CYS:SG	5:F:402:N2P:H5C1	1.96	1.04
1:O:211:LEU:HD11	1:O:277:TRP:CE3	2.09	0.87
1:J:158:CYS:SG	5:J:401:N2P:H5C1	2.14	0.87
1:M:158:CYS:SG	5:M:401:N2P:C5	2.66	0.83

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	297/304 (98%)	280 (94%)	16 (5%)	1 (0%)	46	50
1	B	295/304 (97%)	286 (97%)	8 (3%)	1 (0%)	46	50
1	C	300/304 (99%)	289 (96%)	11 (4%)	0	100	100
1	D	299/304 (98%)	292 (98%)	6 (2%)	1 (0%)	46	50
1	E	295/304 (97%)	284 (96%)	10 (3%)	1 (0%)	46	50
1	F	296/304 (97%)	287 (97%)	8 (3%)	1 (0%)	46	50
1	G	293/304 (96%)	281 (96%)	11 (4%)	1 (0%)	46	50
1	H	260/304 (86%)	245 (94%)	14 (5%)	1 (0%)	39	42
1	I	289/304 (95%)	279 (96%)	10 (4%)	0	100	100
1	J	297/304 (98%)	289 (97%)	7 (2%)	1 (0%)	46	50
1	K	299/304 (98%)	290 (97%)	8 (3%)	1 (0%)	46	50
1	L	298/304 (98%)	290 (97%)	7 (2%)	1 (0%)	46	50
1	M	296/304 (97%)	285 (96%)	10 (3%)	1 (0%)	46	50
1	N	297/304 (98%)	284 (96%)	12 (4%)	1 (0%)	46	50
1	O	297/304 (98%)	282 (95%)	14 (5%)	1 (0%)	46	50
1	P	272/304 (90%)	264 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	4680/4864 (96%)	4507 (96%)	160 (3%)	13 (0%)	46 50

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	158	CYS
1	N	158	CYS
1	E	158	CYS
1	F	158	CYS
1	G	158	CYS

### 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	249/252 (99%)	244 (98%)	5 (2%)	63 76
1	B	247/252 (98%)	244 (99%)	3 (1%)	78 88
1	C	251/252 (100%)	250 (100%)	1 (0%)	93 97
1	D	251/252 (100%)	250 (100%)	1 (0%)	93 97
1	E	247/252 (98%)	246 (100%)	1 (0%)	93 97
1	F	248/252 (98%)	247 (100%)	1 (0%)	93 97
1	G	246/252 (98%)	244 (99%)	2 (1%)	86 93
1	H	222/252 (88%)	220 (99%)	2 (1%)	84 92
1	I	243/252 (96%)	241 (99%)	2 (1%)	86 93
1	J	249/252 (99%)	247 (99%)	2 (1%)	86 93
1	K	250/252 (99%)	248 (99%)	2 (1%)	86 93
1	L	250/252 (99%)	248 (99%)	2 (1%)	86 93
1	M	248/252 (98%)	246 (99%)	2 (1%)	86 93
1	N	249/252 (99%)	247 (99%)	2 (1%)	86 93
1	O	249/252 (99%)	248 (100%)	1 (0%)	93 97
1	P	232/252 (92%)	230 (99%)	2 (1%)	84 92

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	3931/4032 (98%)	3900 (99%)	31 (1%)	86	93

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	100	ASN
1	I	237	TYR
1	O	237	TYR
1	H	118	ILE
1	J	161	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	100	ASN
1	J	65	GLN
1	P	100	ASN
1	H	239	ASN
1	I	161	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

50 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	GOL	A	401	-	5,5,5	0.68	0	5,5,5	0.45	0
2	GOL	A	402	-	5,5,5	0.38	0	5,5,5	0.42	0
3	PEG	A	403	-	6,6,6	0.65	0	5,5,5	0.29	0
2	GOL	A	404	-	5,5,5	0.50	0	5,5,5	0.36	0
4	EDO	A	405	-	3,3,3	0.70	0	2,2,2	0.18	0
5	N2P	B	401	-	6,6,6	0.27	0	5,5,5	1.39	1 (20%)
2	GOL	B	402	-	5,5,5	0.45	0	5,5,5	0.44	0
6	PGE	B	403	-	9,9,9	0.60	0	8,8,8	0.30	0
5	N2P	C	401	-	6,6,6	0.24	0	5,5,5	1.20	1 (20%)
2	GOL	C	402	-	5,5,5	0.51	0	5,5,5	0.27	0
2	GOL	C	403	-	5,5,5	0.39	0	5,5,5	0.28	0
2	GOL	C	404	-	5,5,5	0.46	0	5,5,5	0.30	0
4	EDO	C	405	-	3,3,3	0.60	0	2,2,2	0.16	0
5	N2P	D	401	-	6,6,6	0.32	0	5,5,5	0.49	0
2	GOL	D	402	-	5,5,5	0.74	0	5,5,5	0.51	0
4	EDO	D	403	-	3,3,3	0.60	0	2,2,2	0.19	0
5	N2P	E	401	-	6,6,6	0.25	0	5,5,5	0.46	0
2	GOL	E	402	-	5,5,5	0.48	0	5,5,5	0.37	0
2	GOL	E	403	-	5,5,5	0.32	0	5,5,5	0.23	0
2	GOL	F	401	-	5,5,5	0.24	0	5,5,5	0.47	0
5	N2P	F	402	-	6,6,6	0.51	0	5,5,5	0.62	0
2	GOL	F	403	-	5,5,5	0.43	0	5,5,5	0.29	0
4	EDO	F	404	-	3,3,3	0.59	0	2,2,2	0.22	0
5	N2P	G	401	-	6,6,6	0.39	0	5,5,5	0.97	0
3	PEG	G	402	-	6,6,6	0.64	0	5,5,5	0.40	0
2	GOL	G	403	-	5,5,5	0.28	0	5,5,5	0.53	0
2	GOL	H	401	-	5,5,5	0.61	0	5,5,5	0.55	0
2	GOL	I	401	-	5,5,5	0.34	0	5,5,5	0.30	0
2	GOL	I	402	-	5,5,5	0.46	0	5,5,5	0.36	0
2	GOL	I	403	-	5,5,5	0.44	0	5,5,5	0.24	0
4	EDO	I	404	-	3,3,3	0.55	0	2,2,2	0.26	0
5	N2P	J	401	-	6,6,6	0.26	0	5,5,5	1.00	0
4	EDO	J	402	-	3,3,3	0.43	0	2,2,2	0.47	0
5	N2P	K	401	-	6,6,6	0.35	0	5,5,5	0.94	0
2	GOL	K	402	-	5,5,5	0.18	0	5,5,5	0.17	0
2	GOL	K	403	-	5,5,5	0.96	0	5,5,5	0.87	0
4	EDO	K	404	-	3,3,3	0.53	0	2,2,2	0.21	0
5	N2P	L	401	-	6,6,6	0.30	0	5,5,5	0.67	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	PEG	L	402	-	6,6,6	0.62	0	5,5,5	0.26	0
4	EDO	L	403	-	3,3,3	0.72	0	2,2,2	0.02	0
5	N2P	M	401	-	6,6,6	0.45	0	5,5,5	1.19	1 (20%)
2	GOL	M	402	-	5,5,5	0.31	0	5,5,5	0.33	0
2	GOL	M	403	-	5,5,5	1.24	0	5,5,5	0.75	0
2	GOL	M	404	-	5,5,5	0.36	0	5,5,5	0.16	0
5	N2P	N	401	-	6,6,6	0.50	0	5,5,5	0.40	0
2	GOL	N	402	-	5,5,5	0.43	0	5,5,5	0.27	0
4	EDO	N	403	-	3,3,3	0.55	0	2,2,2	0.16	0
5	N2P	O	401	-	6,6,6	0.55	0	5,5,5	0.87	0
2	GOL	O	402	-	5,5,5	0.16	0	5,5,5	0.63	0
2	GOL	O	403	-	5,5,5	0.41	0	5,5,5	0.17	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	GOL	A	401	-	-	0/4/4/4	0/0/0/0
2	GOL	A	402	-	-	0/4/4/4	0/0/0/0
3	PEG	A	403	-	-	0/4/4/4	0/0/0/0
2	GOL	A	404	-	-	0/4/4/4	0/0/0/0
4	EDO	A	405	-	-	0/1/1/1	0/0/0/0
5	N2P	B	401	-	-	0/4/4/4	0/0/0/0
2	GOL	B	402	-	-	0/4/4/4	0/0/0/0
6	PGE	B	403	-	-	0/7/7/7	0/0/0/0
5	N2P	C	401	-	-	0/4/4/4	0/0/0/0
2	GOL	C	402	-	-	0/4/4/4	0/0/0/0
2	GOL	C	403	-	-	0/4/4/4	0/0/0/0
2	GOL	C	404	-	-	0/4/4/4	0/0/0/0
4	EDO	C	405	-	-	0/1/1/1	0/0/0/0
5	N2P	D	401	-	-	0/4/4/4	0/0/0/0
2	GOL	D	402	-	-	0/4/4/4	0/0/0/0
4	EDO	D	403	-	-	0/1/1/1	0/0/0/0
5	N2P	E	401	-	-	0/4/4/4	0/0/0/0
2	GOL	E	402	-	-	0/4/4/4	0/0/0/0
2	GOL	E	403	-	-	0/4/4/4	0/0/0/0
2	GOL	F	401	-	-	0/4/4/4	0/0/0/0
5	N2P	F	402	-	-	0/4/4/4	0/0/0/0
2	GOL	F	403	-	-	0/4/4/4	0/0/0/0
4	EDO	F	404	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	N2P	G	401	-	-	0/4/4/4	0/0/0/0
3	PEG	G	402	-	-	0/4/4/4	0/0/0/0
2	GOL	G	403	-	-	0/4/4/4	0/0/0/0
2	GOL	H	401	-	-	0/4/4/4	0/0/0/0
2	GOL	I	401	-	-	0/4/4/4	0/0/0/0
2	GOL	I	402	-	-	0/4/4/4	0/0/0/0
2	GOL	I	403	-	-	0/4/4/4	0/0/0/0
4	EDO	I	404	-	-	0/1/1/1	0/0/0/0
5	N2P	J	401	-	-	0/4/4/4	0/0/0/0
4	EDO	J	402	-	-	0/1/1/1	0/0/0/0
5	N2P	K	401	-	-	0/4/4/4	0/0/0/0
2	GOL	K	402	-	-	0/4/4/4	0/0/0/0
2	GOL	K	403	-	-	0/4/4/4	0/0/0/0
4	EDO	K	404	-	-	0/1/1/1	0/0/0/0
5	N2P	L	401	-	-	0/4/4/4	0/0/0/0
3	PEG	L	402	-	-	0/4/4/4	0/0/0/0
4	EDO	L	403	-	-	0/1/1/1	0/0/0/0
5	N2P	M	401	-	-	0/4/4/4	0/0/0/0
2	GOL	M	402	-	-	0/4/4/4	0/0/0/0
2	GOL	M	403	-	-	0/4/4/4	0/0/0/0
2	GOL	M	404	-	-	0/4/4/4	0/0/0/0
5	N2P	N	401	-	-	0/4/4/4	0/0/0/0
2	GOL	N	402	-	-	0/4/4/4	0/0/0/0
4	EDO	N	403	-	-	0/1/1/1	0/0/0/0
5	N2P	O	401	-	-	0/4/4/4	0/0/0/0
2	GOL	O	402	-	-	0/4/4/4	0/0/0/0
2	GOL	O	403	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	401	N2P	C3-C4-C5	2.02	123.73	113.89
5	C	401	N2P	C3-C4-C5	2.42	125.66	113.89
5	B	401	N2P	C3-C4-C5	2.67	126.86	113.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	401	N2P	3	0
2	B	402	GOL	1	0
5	C	401	N2P	3	0
5	D	401	N2P	3	0
5	E	401	N2P	3	0
2	F	401	GOL	1	0
5	F	402	N2P	3	0
5	G	401	N2P	2	0
5	J	401	N2P	4	0
5	K	401	N2P	3	0
5	L	401	N2P	3	0
5	M	401	N2P	2	0
5	N	401	N2P	3	0
5	O	401	N2P	3	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	296/304 (97%)	0.30	30 (10%) 9 8	34, 55, 98, 126	0
1	B	297/304 (97%)	-0.06	12 (4%) 42 41	29, 41, 61, 93	0
1	C	301/304 (99%)	-0.17	9 (2%) 54 53	28, 40, 57, 109	0
1	D	298/304 (98%)	-0.29	2 (0%) 89 88	28, 37, 49, 85	0
1	E	297/304 (97%)	-0.20	3 (1%) 84 83	29, 41, 56, 83	0
1	F	298/304 (98%)	-0.24	4 (1%) 79 78	30, 51, 71, 92	0
1	G	295/304 (97%)	0.79	46 (15%) 3 2	52, 76, 101, 114	0
1	H	268/304 (88%)	2.02	115 (42%) 0 0	59, 97, 136, 155	0
1	I	292/304 (96%)	0.16	27 (9%) 11 10	33, 49, 101, 126	0
1	J	298/304 (98%)	-0.08	9 (3%) 54 53	29, 41, 59, 113	0
1	K	301/304 (99%)	-0.13	10 (3%) 50 49	28, 42, 60, 116	0
1	L	298/304 (98%)	-0.34	1 (0%) 94 94	28, 38, 52, 100	0
1	M	298/304 (98%)	-0.20	4 (1%) 79 78	28, 38, 54, 92	0
1	N	298/304 (98%)	-0.32	4 (1%) 79 78	29, 40, 55, 92	0
1	O	298/304 (98%)	-0.05	10 (3%) 49 47	36, 52, 73, 121	0
1	P	279/304 (91%)	0.98	57 (20%) 1 1	41, 69, 116, 140	0
All	All	4712/4864 (96%)	0.12	343 (7%) 18 17	28, 46, 98, 155	0

The worst 5 of 343 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	58	ALA	12.6
1	I	301	LEU	10.8
1	I	128	PRO	9.5
1	P	225	ILE	8.4
1	P	63	PHE	7.6

## 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
2	GOL	C	403	6/6	0.91	0.24	13.67	58,66,71,71	0
2	GOL	E	403	6/6	0.95	0.28	12.13	54,59,61,63	0
2	GOL	N	402	6/6	0.88	0.23	8.96	54,65,68,68	0
3	PEG	L	402	7/7	0.72	0.40	8.33	75,83,90,90	0
5	N2P	N	401	7/7	0.94	0.33	6.79	45,45,46,46	0
5	N2P	M	401	7/7	0.94	0.34	6.59	39,40,41,43	0
4	EDO	F	404	4/4	0.75	0.30	6.19	74,77,77,78	0
5	N2P	F	402	7/7	0.90	0.27	6.17	61,61,63,63	0
2	GOL	A	402	6/6	0.89	0.17	6.03	58,62,68,72	0
5	N2P	D	401	7/7	0.96	0.35	5.75	42,43,44,44	0
5	N2P	E	401	7/7	0.97	0.34	5.28	42,42,43,44	0
2	GOL	F	403	6/6	0.76	0.25	5.22	67,80,81,83	0
4	EDO	N	403	4/4	0.87	0.28	5.00	73,74,75,75	0
4	EDO	C	405	4/4	0.82	0.28	4.92	68,68,72,73	0
5	N2P	C	401	7/7	0.94	0.36	4.92	41,41,43,43	0
2	GOL	I	402	6/6	0.92	0.18	4.81	58,64,67,69	0
5	N2P	J	401	7/7	0.94	0.37	4.71	45,46,47,48	0
2	GOL	M	404	6/6	0.94	0.18	4.35	59,65,67,79	0
5	N2P	L	401	7/7	0.97	0.30	4.29	42,42,43,43	0
4	EDO	K	404	4/4	0.81	0.23	3.94	65,66,70,74	0
5	N2P	O	401	7/7	0.96	0.21	3.37	50,50,51,52	0
5	N2P	K	401	7/7	0.95	0.29	3.29	45,45,47,48	0
4	EDO	L	403	4/4	0.77	0.27	3.26	59,61,61,66	0
4	EDO	I	404	4/4	0.85	0.26	3.18	64,64,65,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	405	4/4	0.80	0.22	3.13	60,60,61,62	0
5	N2P	G	401	7/7	0.92	0.24	3.12	71,73,74,75	0
5	N2P	B	401	7/7	0.93	0.27	3.01	42,42,43,44	0
2	GOL	E	402	6/6	0.89	0.20	2.68	70,78,83,89	0
2	GOL	B	402	6/6	0.86	0.19	2.57	62,68,71,78	0
2	GOL	O	403	6/6	0.82	0.22	2.38	66,71,75,75	0
2	GOL	C	404	6/6	0.84	0.19	2.32	72,78,80,81	0
2	GOL	K	402	6/6	0.94	0.19	1.78	59,66,69,72	0
2	GOL	K	403	6/6	0.90	0.13	1.50	53,58,61,61	0
2	GOL	H	401	6/6	0.77	0.21	1.49	94,97,99,101	0
2	GOL	M	402	6/6	0.89	0.14	1.33	54,59,64,67	0
2	GOL	M	403	6/6	0.80	0.18	1.33	54,60,61,62	0
6	PGE	B	403	10/10	0.86	0.14	1.28	63,78,88,94	0
2	GOL	D	402	6/6	0.91	0.13	1.12	55,57,62,65	0
2	GOL	G	403	6/6	0.96	0.15	0.98	60,64,66,67	0
2	GOL	C	402	6/6	0.96	0.14	0.74	52,57,64,67	0
2	GOL	I	403	6/6	0.82	0.26	0.63	69,74,82,84	0
2	GOL	I	401	6/6	0.90	0.11	0.12	49,53,57,60	0
2	GOL	A	401	6/6	0.87	0.17	-0.08	80,83,85,86	0
2	GOL	F	401	6/6	0.93	0.09	-0.28	56,63,66,66	0
2	GOL	O	402	6/6	0.93	0.10	-0.52	62,63,63,64	0
4	EDO	D	403	4/4	0.79	0.27	-	74,75,78,79	0
3	PEG	G	402	7/7	0.83	0.13	-	72,76,84,86	0
4	EDO	J	402	4/4	0.90	0.14	-	68,68,69,70	0
2	GOL	A	404	6/6	0.80	0.20	-	69,74,76,77	0
3	PEG	A	403	7/7	0.69	0.32	-	81,85,92,92	0

## 6.5 Other polymers

There are no such residues in this entry.