



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 09:19 PM BST

PDB ID : 2Q3U  
Title : Ensemble refinement of the protein crystal structure of gene product from Arabidopsis thaliana At5g08170, agmatine iminohydrolase  
Authors : Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)  
Deposited on : 2007-05-30  
Resolution : 1.53 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

<https://www.wwpdb.org/validation/2017/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:

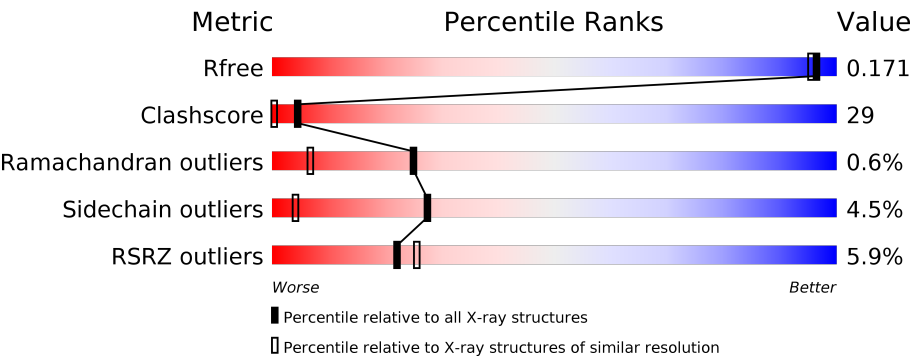
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.53 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1-A	383	<div><div>4%</div><div><div></div><div>52%</div><div>36%</div><div>7%</div><div>5%</div></div></div>
1	1-B	383	<div><div>8%</div><div><div></div><div>56%</div><div>34%</div><div>•</div><div>5%</div></div></div>
1	2-A	383	<div><div>4%</div><div><div></div><div>53%</div><div>34%</div><div>7%</div><div>5%</div></div></div>
1	2-B	383	<div><div>8%</div><div><div></div><div>55%</div><div>34%</div><div>5%</div><div>5%</div></div></div>
1	3-A	383	<div><div>4%</div><div><div></div><div>54%</div><div>34%</div><div>6%</div><div>5%</div></div></div>
1	3-B	383	<div><div>8%</div><div><div></div><div>57%</div><div>30%</div><div>7%</div><div>5%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	4-A	383	
1	4-B	383	
1	5-A	383	
1	5-B	383	
1	6-A	383	
1	6-B	383	
1	7-A	383	
1	7-B	383	
1	8-A	383	
1	8-B	383	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	2-A	908	-	-	X	-
3	EDO	2-B	911	-	-	X	-
3	EDO	3-A	908	-	-	X	-
3	EDO	3-B	911	-	-	X	-
3	EDO	4-B	911	-	-	X	-
3	EDO	5-A	908	-	-	X	-
3	EDO	5-B	911	-	-	X	-
3	EDO	6-A	908	-	-	X	-
3	EDO	6-B	911	-	-	X	-
3	EDO	7-A	908	-	-	X	-
3	EDO	7-B	911	-	-	X	-
3	EDO	8-A	903	-	-	X	-
3	EDO	8-A	908	-	-	X	-
3	EDO	8-B	911	-	-	X	-
4	MPO	1-A	9000	-	-	-	X
4	MPO	2-A	9000	-	-	-	X
4	MPO	3-A	9000	-	-	-	X
4	MPO	4-A	9000	-	-	-	X
4	MPO	5-A	9000	-	-	-	X
4	MPO	6-A	9000	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MPO	7-A	9000	-	-	-	X
4	MPO	8-A	9000	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 53040 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 Agmatine deiminase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	2-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	3-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	4-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	5-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	6-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	7-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	8-A	365	Total	C	N	O	S	Se	0	0	0
			2902	1822	517	549	7	7			
1	1-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	2-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	3-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	4-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	5-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	6-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	7-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			
1	8-B	363	Total	C	N	O	S	Se	0	0	0
			2882	1811	512	545	7	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	15	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	49	GLY	ASP	VARIANT	UNP Q8GWW7
A	85	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	87	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	159	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	190	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	228	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
A	284	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	15	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	49	GLY	ASP	VARIANT	UNP Q8GWW7
B	85	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	87	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	159	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	190	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	228	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7
B	284	MSE	MET	MODIFIED RESIDUE	UNP Q8GWW7

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

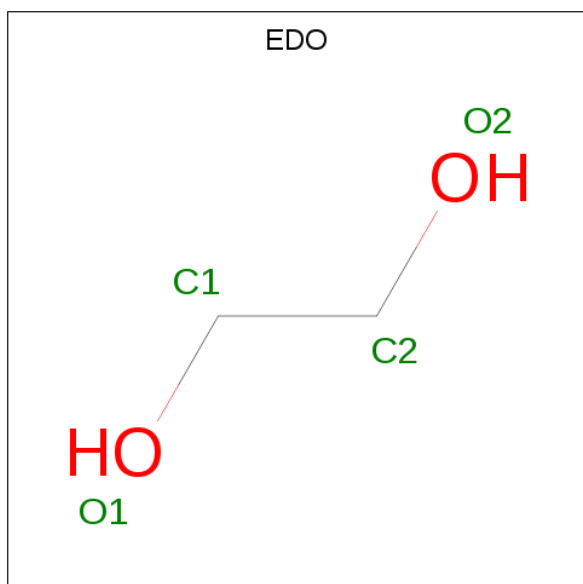
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	7-B	1	Total Mg 1 1	0	0
2	3-A	1	Total Mg 1 1	0	0
2	8-B	1	Total Mg 1 1	0	0
2	3-B	1	Total Mg 1 1	0	0
2	5-B	1	Total Mg 1 1	0	0
2	4-A	1	Total Mg 1 1	0	0
2	1-B	1	Total Mg 1 1	0	0
2	5-A	1	Total Mg 1 1	0	0
2	6-B	1	Total Mg 1 1	0	0
2	8-A	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	1-A	1	Total 1	Mg 1	0	0
2	6-A	1	Total 1	Mg 1	0	0
2	2-B	1	Total 1	Mg 1	0	0
2	2-A	1	Total 1	Mg 1	0	0
2	4-B	1	Total 1	Mg 1	0	0
2	7-A	1	Total 1	Mg 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-A	1	Total 4	C 2	O 2	0	0
3	2-A	1	Total 4	C 2	O 2	0	0
3	3-A	1	Total 4	C 2	O 2	0	0
3	4-A	1	Total 4	C 2	O 2	0	0
3	5-A	1	Total 4	C 2	O 2	0	0
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-A	1	Total 4	C 2	O 2	0	0
3	2-A	1	Total 4	C 2	O 2	0	0
3	3-A	1	Total 4	C 2	O 2	0	0
3	4-A	1	Total 4	C 2	O 2	0	0
3	5-A	1	Total 4	C 2	O 2	0	0
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-A	1	Total 4	C 2	O 2	0	0
3	2-A	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	3-A	1	Total 4	C 2	O 2	0	0
3	4-A	1	Total 4	C 2	O 2	0	0
3	5-A	1	Total 4	C 2	O 2	0	0
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-A	1	Total 4	C 2	O 2	0	0
3	2-A	1	Total 4	C 2	O 2	0	0
3	3-A	1	Total 4	C 2	O 2	0	0
3	4-A	1	Total 4	C 2	O 2	0	0
3	5-A	1	Total 4	C 2	O 2	0	0
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-A	1	Total 4	C 2	O 2	0	0
3	2-A	1	Total 4	C 2	O 2	0	0
3	3-A	1	Total 4	C 2	O 2	0	0
3	4-A	1	Total 4	C 2	O 2	0	0
3	5-A	1	Total 4	C 2	O 2	0	0
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-A	1	Total 4	C 2	O 2	0	0
3	2-A	1	Total 4	C 2	O 2	0	0
3	3-A	1	Total 4	C 2	O 2	0	0
3	4-A	1	Total 4	C 2	O 2	0	0
3	5-A	1	Total 4	C 2	O 2	0	0
3	6-A	1	Total 4	C 2	O 2	0	0
3	7-A	1	Total 4	C 2	O 2	0	0
3	8-A	1	Total 4	C 2	O 2	0	0
3	1-B	1	Total 4	C 2	O 2	0	0
3	2-B	1	Total 4	C 2	O 2	0	0
3	3-B	1	Total 4	C 2	O 2	0	0
3	4-B	1	Total 4	C 2	O 2	0	0
3	5-B	1	Total 4	C 2	O 2	0	0
3	6-B	1	Total 4	C 2	O 2	0	0
3	7-B	1	Total 4	C 2	O 2	0	0
3	8-B	1	Total 4	C 2	O 2	0	0
3	1-B	1	Total 4	C 2	O 2	0	0
3	2-B	1	Total 4	C 2	O 2	0	0
3	3-B	1	Total 4	C 2	O 2	0	0
3	4-B	1	Total 4	C 2	O 2	0	0

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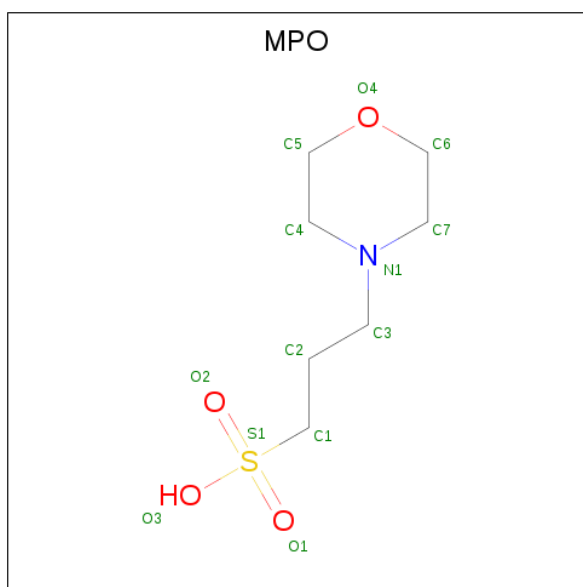
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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3	6-B	1	Total 4	C 2	O 2	0	0
3	7-B	1	Total 4	C 2	O 2	0	0
3	8-B	1	Total 4	C 2	O 2	0	0
3	1-B	1	Total 4	C 2	O 2	0	0
3	2-B	1	Total 4	C 2	O 2	0	0
3	3-B	1	Total 4	C 2	O 2	0	0
3	4-B	1	Total 4	C 2	O 2	0	0
3	5-B	1	Total 4	C 2	O 2	0	0
3	6-B	1	Total 4	C 2	O 2	0	0
3	7-B	1	Total 4	C 2	O 2	0	0
3	8-B	1	Total 4	C 2	O 2	0	0
3	1-B	1	Total 4	C 2	O 2	0	0
3	2-B	1	Total 4	C 2	O 2	0	0
3	3-B	1	Total 4	C 2	O 2	0	0
3	4-B	1	Total 4	C 2	O 2	0	0
3	5-B	1	Total 4	C 2	O 2	0	0
3	6-B	1	Total 4	C 2	O 2	0	0
3	7-B	1	Total 4	C 2	O 2	0	0
3	8-B	1	Total 4	C 2	O 2	0	0
3	1-B	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	2-B	1	Total 4	C 2	O 2	0	0
3	3-B	1	Total 4	C 2	O 2	0	0
3	4-B	1	Total 4	C 2	O 2	0	0
3	5-B	1	Total 4	C 2	O 2	0	0
3	6-B	1	Total 4	C 2	O 2	0	0
3	7-B	1	Total 4	C 2	O 2	0	0
3	8-B	1	Total 4	C 2	O 2	0	0
3	1-B	1	Total 4	C 2	O 2	0	0
3	2-B	1	Total 4	C 2	O 2	0	0
3	3-B	1	Total 4	C 2	O 2	0	0
3	4-B	1	Total 4	C 2	O 2	0	0
3	5-B	1	Total 4	C 2	O 2	0	0
3	6-B	1	Total 4	C 2	O 2	0	0
3	7-B	1	Total 4	C 2	O 2	0	0
3	8-B	1	Total 4	C 2	O 2	0	0

- Molecule 4 is 3[N-MORPHOLINO]PROPANE SULFONIC ACID (three-letter code: MPO) (formula: C<sub>7</sub>H<sub>15</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	1-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	2-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	3-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	4-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	5-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	6-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	7-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	8-A	1	Total	C	N	O	S	0	0
			13	7	1	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1-A	404	Total	O	0	0
			404	404		
5	2-A	409	Total	O	0	0
			409	409		
5	3-A	404	Total	O	0	0
			404	404		
5	4-A	410	Total	O	0	0
			410	410		

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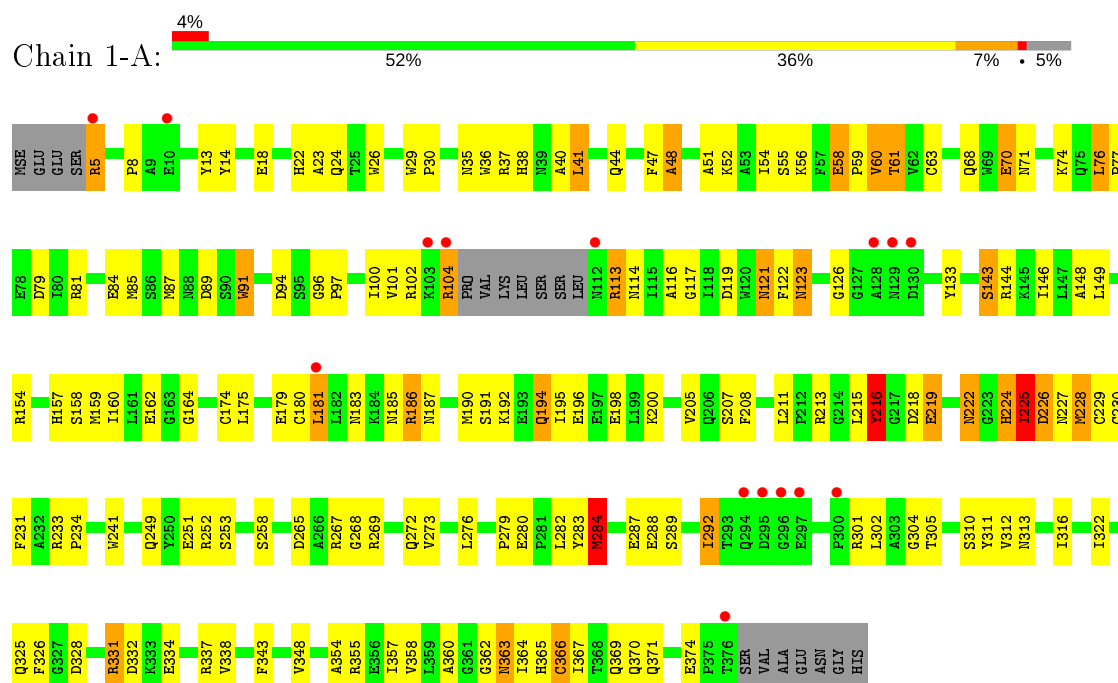
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	5-A	407	Total 407	O 407	0	0
5	6-A	403	Total 403	O 403	0	0
5	7-A	405	Total 405	O 405	0	0
5	8-A	409	Total 409	O 409	0	0
5	1-B	375	Total 375	O 375	0	0
5	2-B	370	Total 370	O 370	0	0
5	3-B	375	Total 375	O 375	0	0
5	4-B	369	Total 369	O 369	0	0
5	5-B	372	Total 372	O 372	0	0
5	6-B	376	Total 376	O 376	0	0
5	7-B	374	Total 374	O 374	0	0
5	8-B	370	Total 370	O 370	0	0

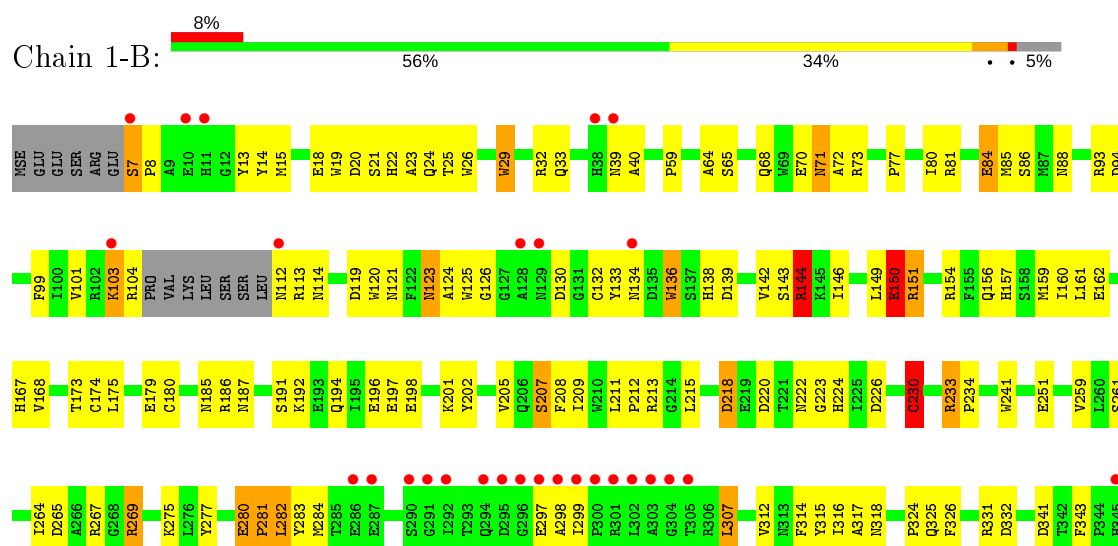
### 3 Residue-property plots

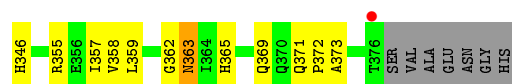
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Agmatine deiminase

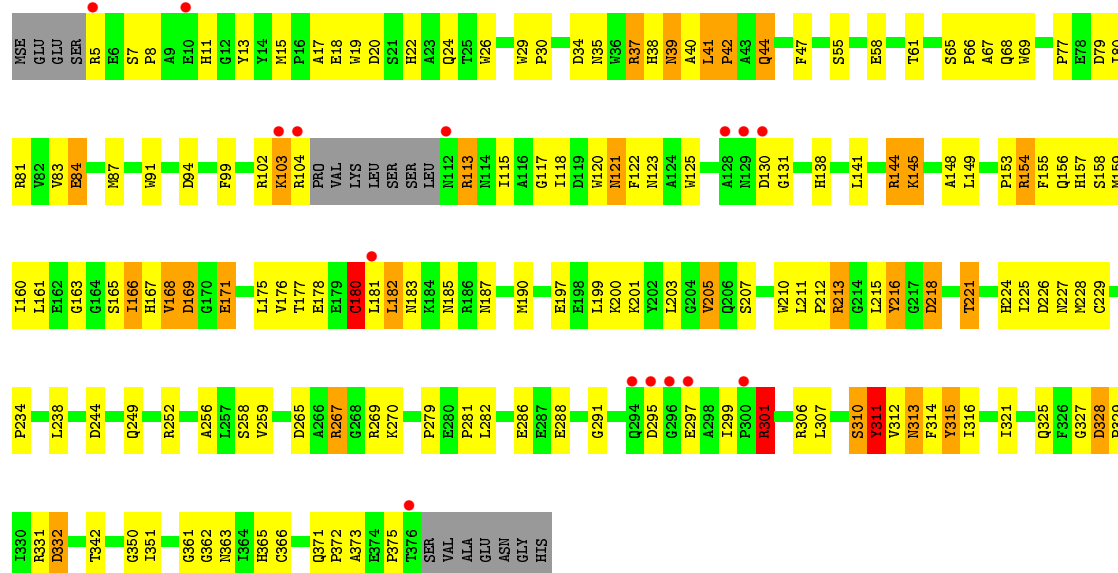


#### • Molecule 1: Agmatine deiminase

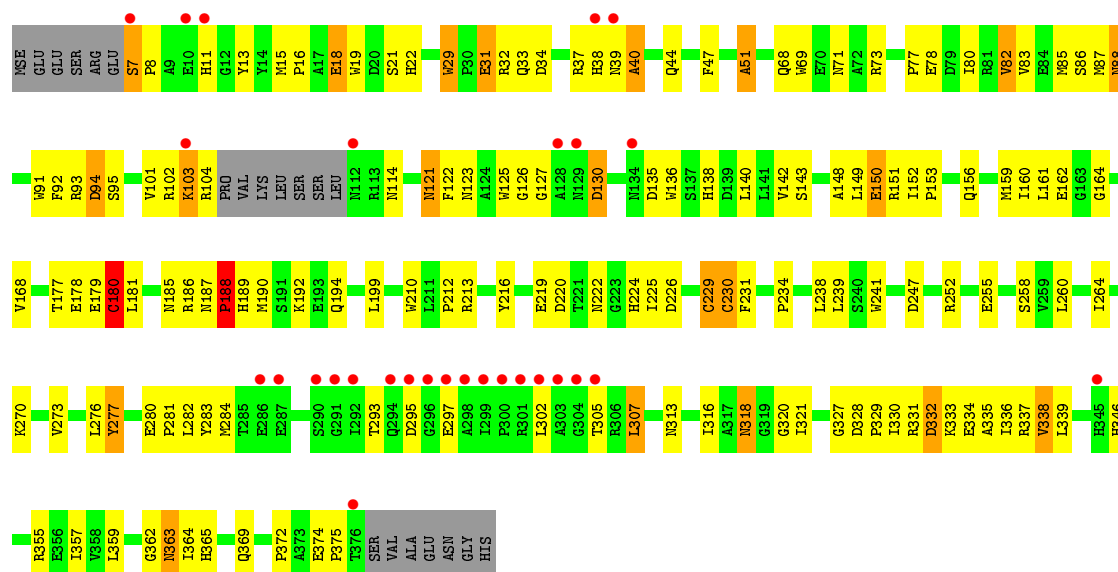




- Molecule 1: Agmatine deiminase

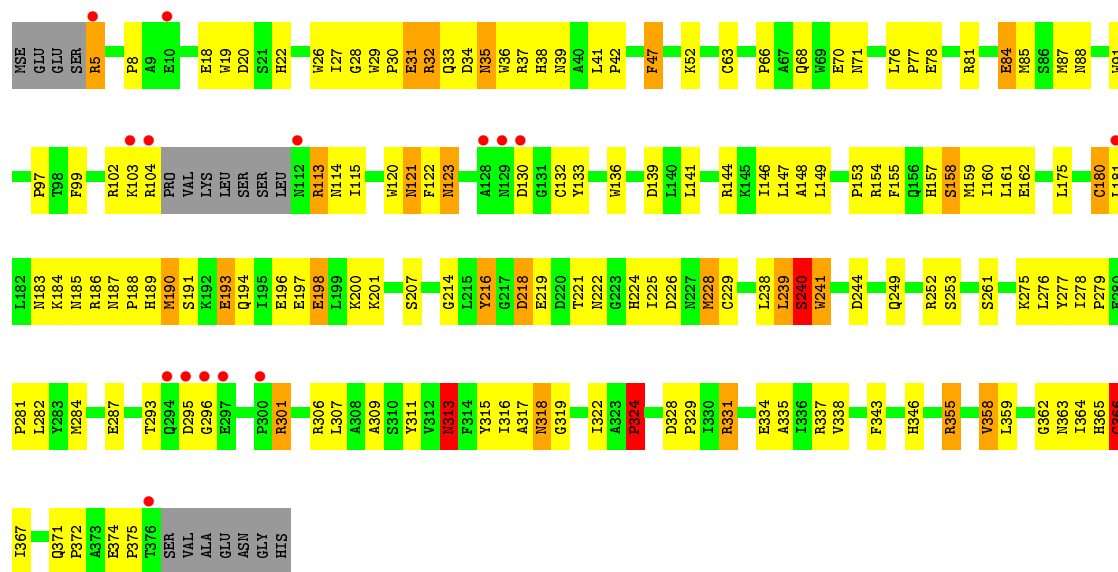


- Molecule 1: Agmatine deiminase

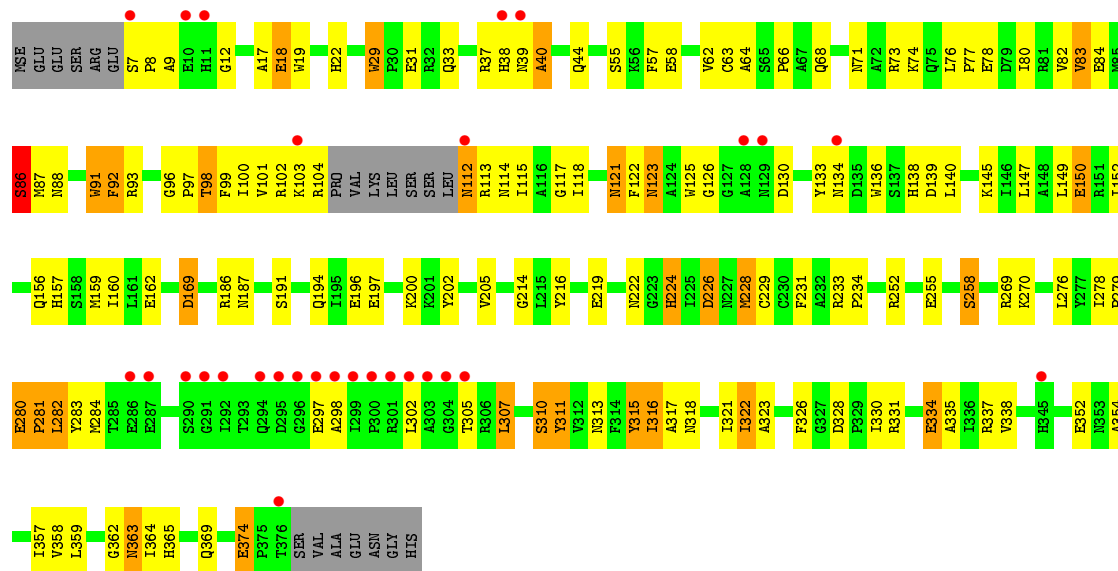


- Molecule 1: Agmatine deiminase

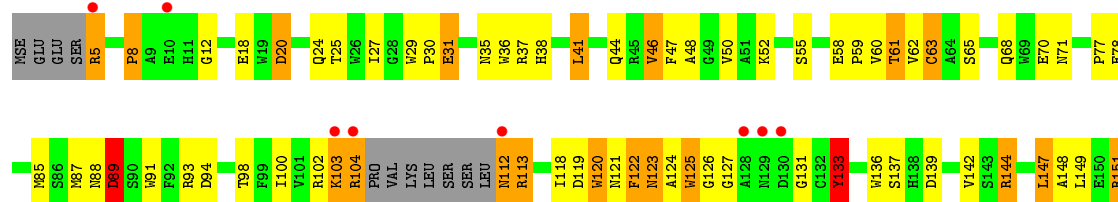


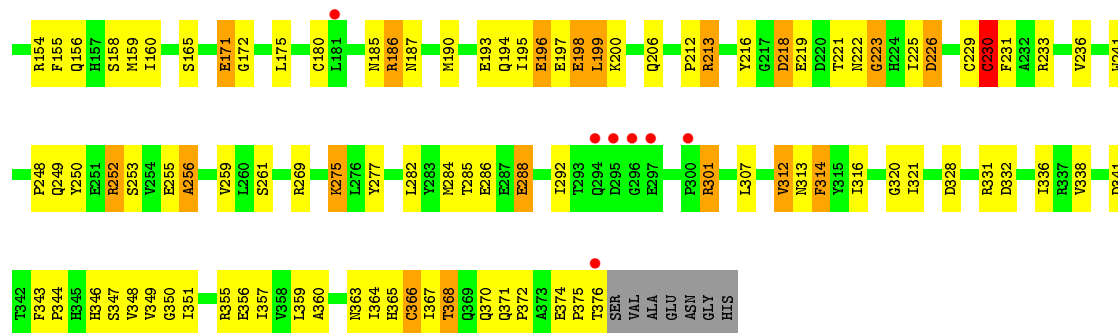


• Molecule 1: Agmatine deiminase

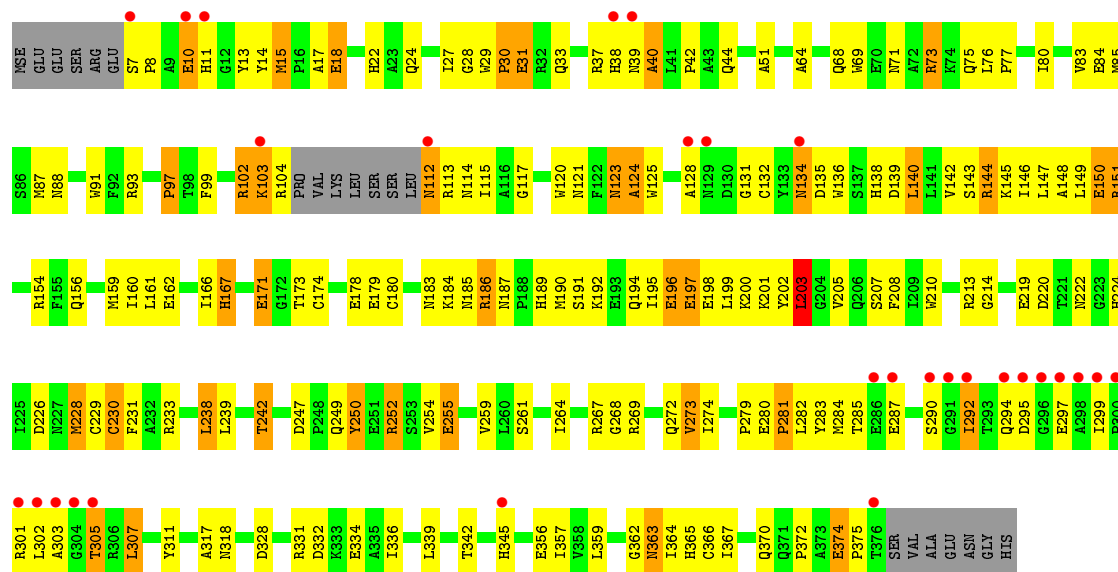


• Molecule 1: Agmatine deiminase

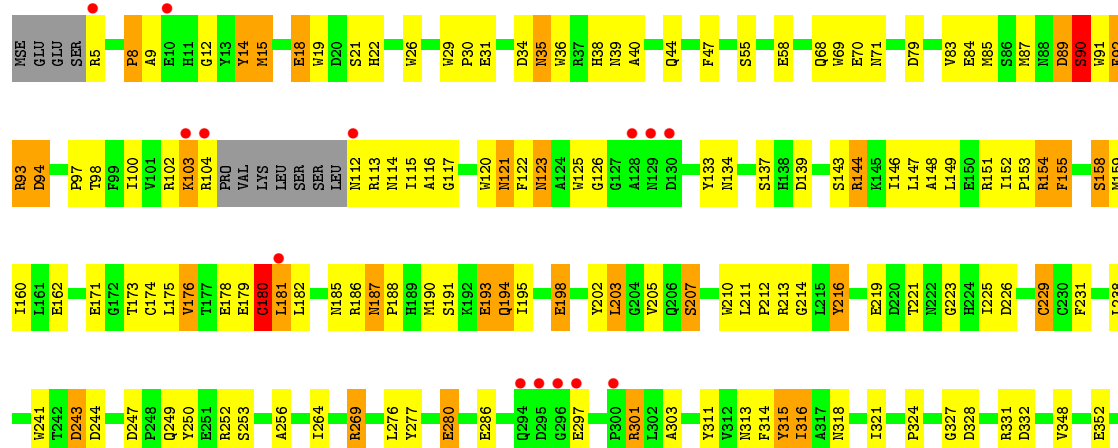


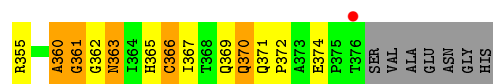


• Molecule 1: Agmatine deiminase

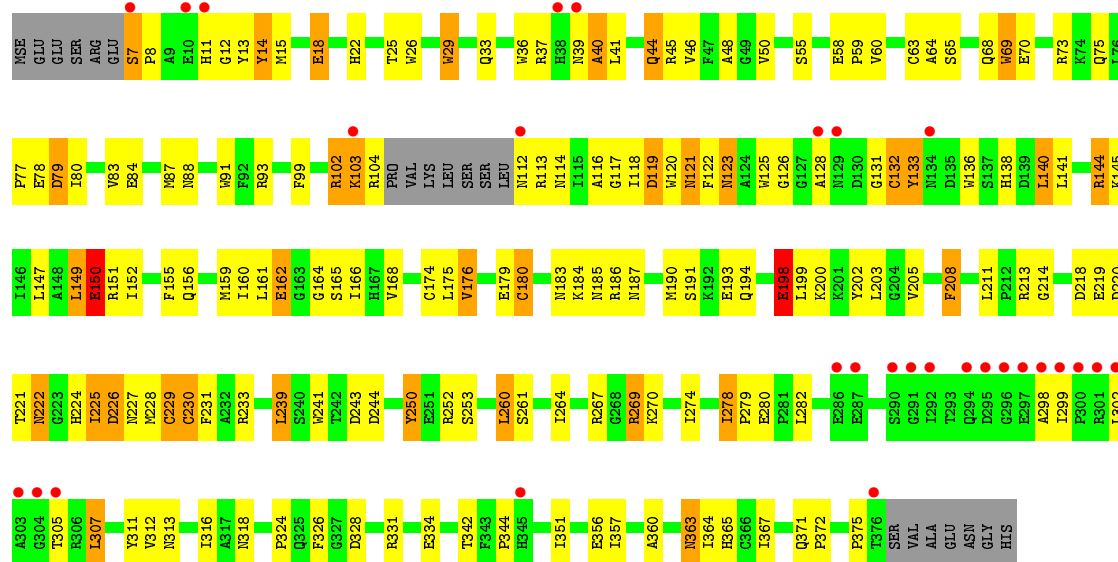


• Molecule 1: Agmatine deiminase

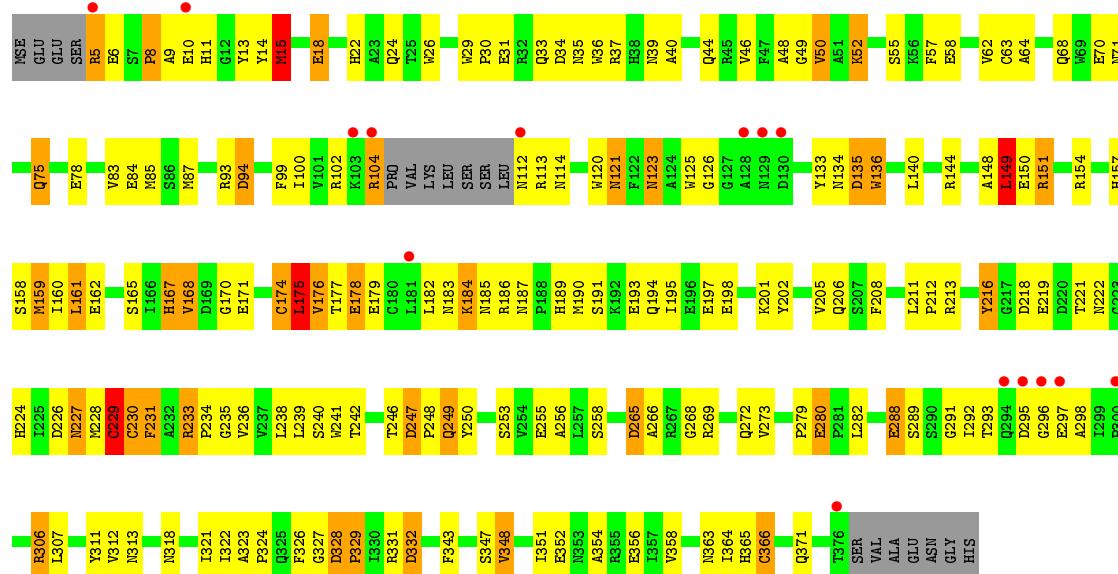




• Molecule 1: Agmatine deiminase

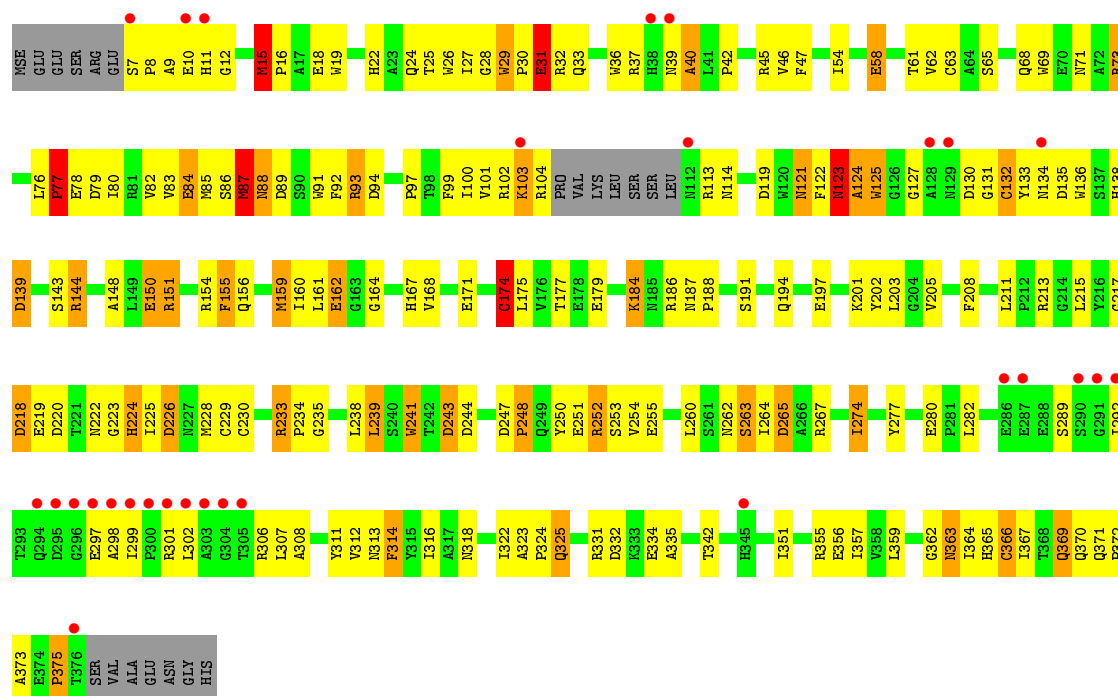


• Molecule 1: Agmatine deiminase

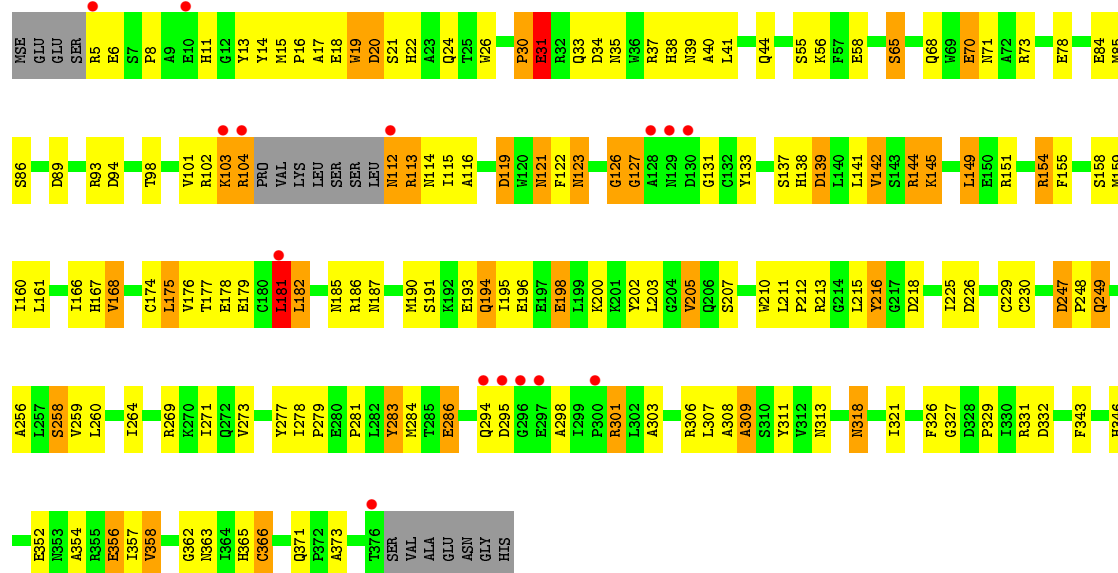


• Molecule 1: Agmatine deiminase



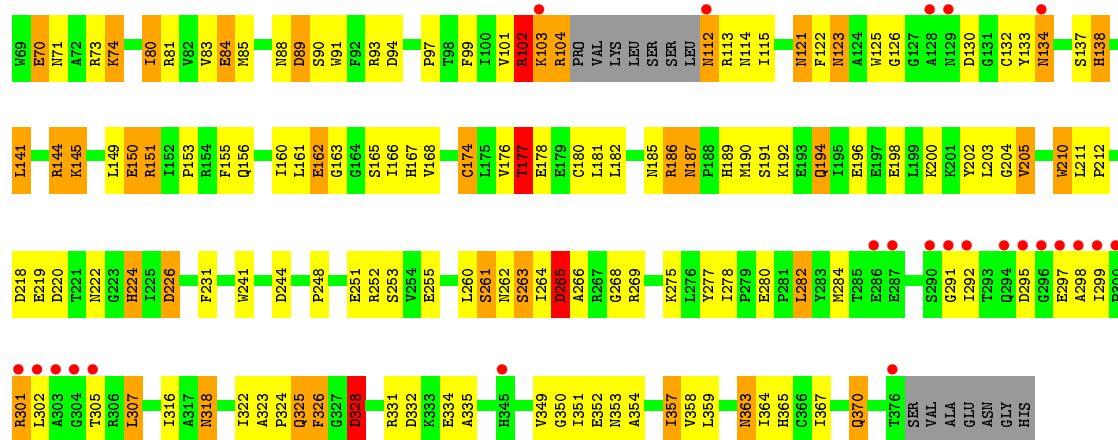


• Molecule 1: Agmatine deiminase

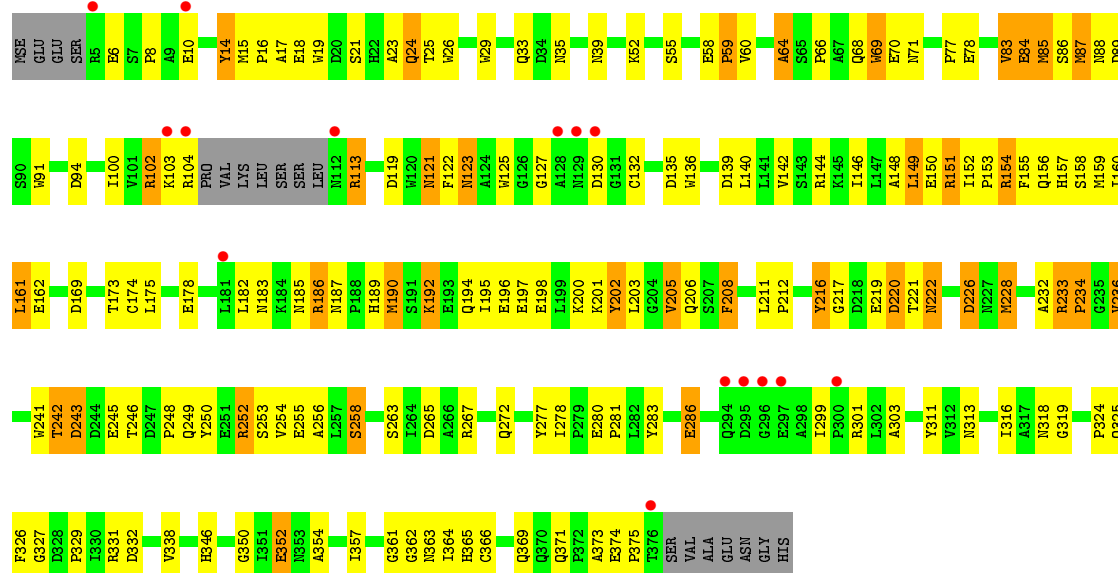


• Molecule 1: Agmatine deiminase

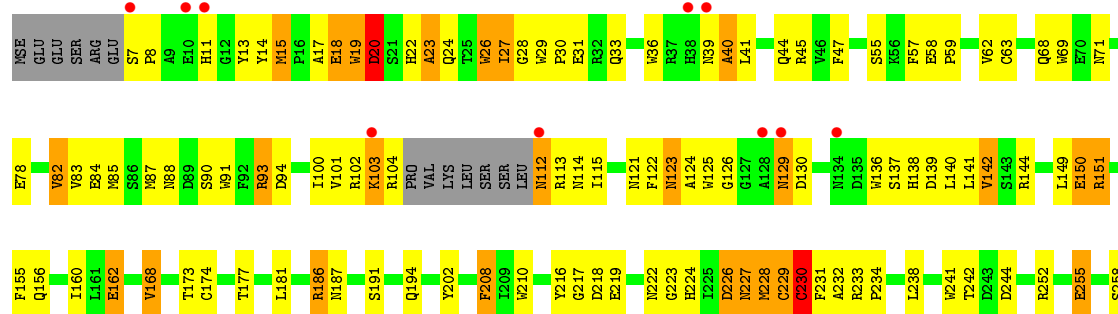


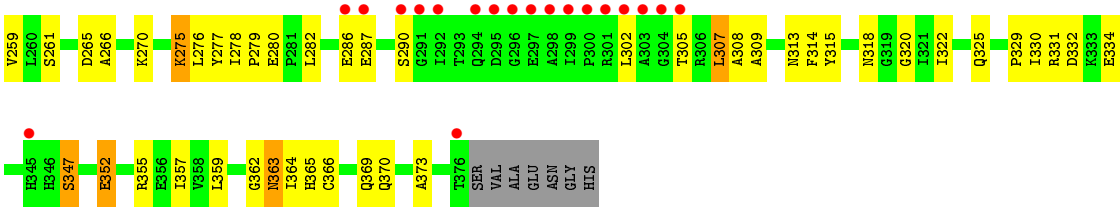


- Molecule 1: Agmatine deiminase



- Molecule 1: Agmatine deiminase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.02Å 115.81Å 66.63Å 90.00° 97.10° 90.00°	Depositor
Resolution (Å)	19.87 – 1.53 19.87 – 1.53	Depositor EDS
% Data completeness (in resolution range)	91.8 (19.87-1.53) 91.9 (19.87-1.53)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.11 (at 1.53Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.135 , 0.171 0.139 , 0.171	Depositor DCC
$R_{free}$ test set	6038 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.6	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 46.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	53040	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.66% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MPO, MG, 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	1-A	1.58	20/2968 (0.7%)	1.40	28/4021 (0.7%)
1	1-B	1.52	15/2948 (0.5%)	1.32	19/3995 (0.5%)
1	2-A	1.59	28/2968 (0.9%)	1.36	21/4021 (0.5%)
1	2-B	1.57	19/2948 (0.6%)	1.31	13/3995 (0.3%)
1	3-A	1.52	18/2968 (0.6%)	1.39	28/4021 (0.7%)
1	3-B	1.49	20/2948 (0.7%)	1.27	12/3995 (0.3%)
1	4-A	1.61	28/2968 (0.9%)	1.43	27/4021 (0.7%)
1	4-B	1.59	37/2948 (1.3%)	1.36	20/3995 (0.5%)
1	5-A	1.71	39/2968 (1.3%)	1.48	28/4021 (0.7%)
1	5-B	1.69	22/2948 (0.7%)	1.45	28/3995 (0.7%)
1	6-A	1.78	47/2968 (1.6%)	1.56	28/4021 (0.7%)
1	6-B	1.71	40/2948 (1.4%)	1.48	29/3995 (0.7%)
1	7-A	1.71	35/2968 (1.2%)	1.50	34/4021 (0.8%)
1	7-B	1.71	43/2948 (1.5%)	1.45	20/3995 (0.5%)
1	8-A	1.74	45/2968 (1.5%)	1.51	31/4021 (0.8%)
1	8-B	1.69	39/2948 (1.3%)	1.35	9/3995 (0.2%)
All	All	1.64	495/47328 (1.0%)	1.42	375/64128 (0.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1-A	0	1
1	1-B	0	2
1	2-A	0	1
1	3-B	0	1
1	4-A	0	2
1	5-A	0	2
1	5-B	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	6-B	0	1
1	7-A	0	2
1	7-B	0	2
1	8-A	0	2
1	8-B	0	1
All	All	0	19

The worst 5 of 495 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1-A	230	CYS	CB-SG	-18.60	1.50	1.82
1	8-B	230	CYS	CB-SG	18.04	2.12	1.82
1	5-B	174	CYS	CB-SG	-17.96	1.51	1.82
1	4-B	230	CYS	CB-SG	-17.44	1.52	1.82
1	2-B	230	CYS	CB-SG	15.05	2.07	1.82

The worst 5 of 375 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	6-A	306	ARG	NE-CZ-NH1	15.13	127.87	120.30
1	5-B	174	CYS	CA-CB-SG	-13.16	90.31	114.00
1	4-B	151	ARG	NE-CZ-NH2	-13.04	113.78	120.30
1	2-A	265	ASP	CB-CG-OD1	12.68	129.71	118.30
1	5-A	331	ARG	NE-CZ-NH2	-12.39	114.10	120.30

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1-A	216	TYR	Sidechain
1	1-B	13	TYR	Sidechain
1	1-B	202	TYR	Sidechain
1	2-A	311	TYR	Sidechain
1	3-B	315	TYR	Sidechain

## 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	1-A	2902	0	2786	172	0
1	1-B	2882	0	2767	130	0
1	2-A	2902	0	2786	168	0
1	2-B	2882	0	2767	166	0
1	3-A	2902	0	2786	153	0
1	3-B	2882	0	2767	141	0
1	4-A	2902	0	2786	166	0
1	4-B	2882	0	2767	193	0
1	5-A	2902	0	2786	141	0
1	5-B	2882	0	2767	184	0
1	6-A	2902	0	2786	185	0
1	6-B	2882	0	2767	211	0
1	7-A	2902	0	2786	131	0
1	7-B	2882	0	2767	193	0
1	8-A	2902	0	2786	167	0
1	8-B	2882	0	2767	151	0
2	1-A	1	0	0	0	0
2	1-B	1	0	0	0	0
2	2-A	1	0	0	0	0
2	2-B	1	0	0	0	0
2	3-A	1	0	0	0	0
2	3-B	1	0	0	0	0
2	4-A	1	0	0	0	0
2	4-B	1	0	0	0	0
2	5-A	1	0	0	0	0
2	5-B	1	0	0	0	0
2	6-A	1	0	0	1	0
2	6-B	1	0	0	0	0
2	7-A	1	0	0	0	0
2	7-B	1	0	0	0	0
2	8-A	1	0	0	0	0
2	8-B	1	0	0	0	0
3	1-A	28	0	42	4	0
3	1-B	24	0	36	7	0
3	2-A	28	0	42	8	0
3	2-B	24	0	36	10	0
3	3-A	28	0	42	11	0
3	3-B	24	0	36	10	0
3	4-A	28	0	42	2	0
3	4-B	24	0	36	7	0
3	5-A	28	0	42	8	0
3	5-B	24	0	36	10	0
3	6-A	28	0	42	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	6-B	24	0	36	13	0
3	7-A	28	0	42	9	0
3	7-B	24	0	36	12	0
3	8-A	28	0	42	18	0
3	8-B	24	0	36	13	0
4	1-A	13	0	15	0	0
4	2-A	13	0	15	0	0
4	3-A	13	0	15	0	0
4	4-A	13	0	15	0	0
4	5-A	13	0	15	1	0
4	6-A	13	0	15	1	0
4	7-A	13	0	15	0	0
4	8-A	13	0	15	1	0
5	1-A	404	0	0	17	0
5	1-B	375	0	0	23	0
5	2-A	409	0	0	25	0
5	2-B	370	0	0	18	0
5	3-A	404	0	0	27	0
5	3-B	375	0	0	24	0
5	4-A	410	0	0	30	0
5	4-B	369	0	0	22	0
5	5-A	407	0	0	20	0
5	5-B	372	0	0	27	0
5	6-A	403	0	0	31	0
5	6-B	376	0	0	25	0
5	7-A	405	0	0	23	0
5	7-B	374	0	0	28	0
5	8-A	409	0	0	19	0
5	8-B	370	0	0	22	0
All	All	53040	0	45168	2624	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 29.

The worst 5 of 2624 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:B:166:ILE:CD1	1:B:166:ILE:CG1	1.77	1.55
1:B:100:ILE:CD1	1:B:100:ILE:CG1	1.79	1.55
1:B:195:ILE:CG1	1:B:195:ILE:CD1	1.81	1.55
1:B:188:PRO:CD	1:B:188:PRO:CG	1.74	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:ILE:CG1	1:B:225:ILE:CD1	1.82	1.53

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	1-A	361/383 (94%)	342 (95%)	17 (5%)	2 (1%)	25	7
1	1-B	359/383 (94%)	336 (94%)	22 (6%)	1 (0%)	41	19
1	2-A	361/383 (94%)	346 (96%)	15 (4%)	0	100	100
1	2-B	359/383 (94%)	336 (94%)	21 (6%)	2 (1%)	25	7
1	3-A	361/383 (94%)	342 (95%)	16 (4%)	3 (1%)	19	4
1	3-B	359/383 (94%)	337 (94%)	20 (6%)	2 (1%)	25	7
1	4-A	361/383 (94%)	342 (95%)	18 (5%)	1 (0%)	41	19
1	4-B	359/383 (94%)	335 (93%)	18 (5%)	6 (2%)	9	1
1	5-A	361/383 (94%)	349 (97%)	11 (3%)	1 (0%)	41	19
1	5-B	359/383 (94%)	337 (94%)	20 (6%)	2 (1%)	25	7
1	6-A	361/383 (94%)	329 (91%)	30 (8%)	2 (1%)	25	7
1	6-B	359/383 (94%)	330 (92%)	26 (7%)	3 (1%)	19	4
1	7-A	361/383 (94%)	340 (94%)	17 (5%)	4 (1%)	14	2
1	7-B	359/383 (94%)	332 (92%)	24 (7%)	3 (1%)	19	4
1	8-A	361/383 (94%)	339 (94%)	20 (6%)	2 (1%)	25	7
1	8-B	359/383 (94%)	336 (94%)	22 (6%)	1 (0%)	41	19
All	All	5760/6128 (94%)	5408 (94%)	317 (6%)	35 (1%)	25	7

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	3-A	318	ASN
1	8-A	318	ASN
1	2-B	318	ASN
1	3-B	322	ILE
1	4-B	292	ILE

### 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	1-A	310/318 (98%)	297 (96%)	13 (4%)	30	5
1	1-B	308/318 (97%)	294 (96%)	14 (4%)	27	4
1	2-A	310/318 (98%)	298 (96%)	12 (4%)	32	6
1	2-B	308/318 (97%)	299 (97%)	9 (3%)	42	13
1	3-A	310/318 (98%)	295 (95%)	15 (5%)	25	3
1	3-B	308/318 (97%)	296 (96%)	12 (4%)	32	6
1	4-A	310/318 (98%)	297 (96%)	13 (4%)	30	5
1	4-B	308/318 (97%)	294 (96%)	14 (4%)	27	4
1	5-A	310/318 (98%)	297 (96%)	13 (4%)	30	5
1	5-B	308/318 (97%)	297 (96%)	11 (4%)	35	8
1	6-A	310/318 (98%)	290 (94%)	20 (6%)	17	2
1	6-B	308/318 (97%)	290 (94%)	18 (6%)	20	2
1	7-A	310/318 (98%)	297 (96%)	13 (4%)	30	5
1	7-B	308/318 (97%)	286 (93%)	22 (7%)	14	1
1	8-A	310/318 (98%)	300 (97%)	10 (3%)	39	10
1	8-B	308/318 (97%)	295 (96%)	13 (4%)	30	5
All	All	4944/5088 (97%)	4722 (96%)	222 (4%)	27	4

5 of 222 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	4-B	307	LEU

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Mol	Chain	Res	Type
1	5-B	307	LEU
1	8-A	192	LYS
1	5-A	15	MSE
1	5-A	180	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 292 such sidechains are listed below:

Mol	Chain	Res	Type
1	4-B	39	ASN
1	5-A	313	ASN
1	8-A	365	HIS
1	4-B	88	ASN
1	4-B	294	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 128 ligands modelled in this entry, 16 are monoatomic - leaving 112 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
3	EDO	1-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	8-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	7-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	2-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	6-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	6-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	3-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	5-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	7-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	3-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	7-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
3	EDO	1-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	8-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	1-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	4-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	8-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	6-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	6-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	4-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	3-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
3	EDO	6-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
3	EDO	2-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	1-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	7-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	8-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
3	EDO	5-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	2-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
3	EDO	2-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	8-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	4-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
3	EDO	3-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	1-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	2-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	8-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	8-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	4-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	1-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	3-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	7-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	1-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	7-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	5-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
4	MPO	1-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	4-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
4	MPO	5-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)
3	EDO	4-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	2-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	3-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	5-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	3-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	3-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	8-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	7-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	3-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	5-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	8-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	1-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	5-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	6-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	2-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	7-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	7-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
4	MPO	8-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)
3	EDO	6-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
3	EDO	6-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	5-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
3	EDO	6-A	903	-	3,3,3	0.62	0	2,2,2	0.82	0
3	EDO	7-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	2-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	5-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
4	MPO	4-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)
3	EDO	5-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	4-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	4-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
3	EDO	2-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	3-B	913	-	3,3,3	0.74	0	2,2,2	0.50	0
3	EDO	2-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	1-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	2-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
3	EDO	8-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	6-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	6-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	5-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
4	MPO	3-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)
3	EDO	3-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	8-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
4	MPO	6-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)
3	EDO	3-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	3-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	4-B	911	-	3,3,3	0.88	0	2,2,2	0.43	0
3	EDO	8-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	5-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	1-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	1-A	902	-	3,3,3	0.91	0	2,2,2	0.29	0
3	EDO	2-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	6-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	4-B	905	-	3,3,3	0.22	0	2,2,2	0.58	0
3	EDO	8-A	910	-	3,3,3	0.60	0	2,2,2	0.47	0
3	EDO	7-A	901	-	3,3,3	0.62	0	2,2,2	0.31	0
3	EDO	6-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	4-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	7-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	1-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	4-B	909	-	3,3,3	0.42	0	2,2,2	0.66	0
3	EDO	2-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
3	EDO	7-A	908	-	3,3,3	0.92	0	2,2,2	0.42	0
3	EDO	5-B	904	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	4-A	906	-	3,3,3	0.65	0	2,2,2	0.25	0
4	MPO	2-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)
3	EDO	5-B	912	-	3,3,3	0.98	0	2,2,2	0.55	0
3	EDO	1-A	907	-	3,3,3	0.97	0	2,2,2	0.58	0
4	MPO	7-A	9000	-	13,13,13	3.76	6 (46%)	17,17,17	5.54	5 (29%)

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
3	EDO	1-B	909	-	-	1/1/1/1	-
3	EDO	8-B	904	-	-	1/1/1/1	-
3	EDO	7-A	903	-	-	1/1/1/1	-
3	EDO	2-A	903	-	-	1/1/1/1	-
3	EDO	6-B	913	-	-	1/1/1/1	-
3	EDO	6-A	901	-	-	1/1/1/1	-
3	EDO	3-B	904	-	-	1/1/1/1	-
3	EDO	5-A	906	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	7-B	911	-	-	1/1/1/1	-
3	EDO	3-B	905	-	-	0/1/1/1	-
3	EDO	7-A	907	-	-	0/1/1/1	-
3	EDO	1-B	913	-	-	1/1/1/1	-
3	EDO	8-A	903	-	-	1/1/1/1	-
3	EDO	1-B	911	-	-	1/1/1/1	-
3	EDO	4-A	901	-	-	1/1/1/1	-
3	EDO	8-A	901	-	-	1/1/1/1	-
3	EDO	6-A	908	-	-	1/1/1/1	-
3	EDO	6-B	909	-	-	1/1/1/1	-
3	EDO	4-B	912	-	-	1/1/1/1	-
3	EDO	3-A	902	-	-	0/1/1/1	-
3	EDO	6-A	907	-	-	0/1/1/1	-
3	EDO	2-B	912	-	-	1/1/1/1	-
3	EDO	1-B	905	-	-	0/1/1/1	-
3	EDO	7-B	909	-	-	1/1/1/1	-
3	EDO	8-A	907	-	-	0/1/1/1	-
3	EDO	5-A	903	-	-	1/1/1/1	-
3	EDO	2-A	907	-	-	0/1/1/1	-
3	EDO	2-A	901	-	-	1/1/1/1	-
3	EDO	8-B	911	-	-	1/1/1/1	-
3	EDO	4-A	902	-	-	0/1/1/1	-
3	EDO	3-A	906	-	-	1/1/1/1	-
3	EDO	1-A	901	-	-	1/1/1/1	-
3	EDO	2-A	910	-	-	1/1/1/1	-
3	EDO	8-B	909	-	-	1/1/1/1	-
3	EDO	8-B	905	-	-	0/1/1/1	-
3	EDO	4-B	913	-	-	1/1/1/1	-
3	EDO	1-A	903	-	-	1/1/1/1	-
3	EDO	3-A	903	-	-	1/1/1/1	-
3	EDO	7-B	913	-	-	1/1/1/1	-
3	EDO	1-A	906	-	-	1/1/1/1	-
3	EDO	7-B	905	-	-	0/1/1/1	-
3	EDO	5-B	911	-	-	1/1/1/1	-
4	MPO	1-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	4-A	910	-	-	1/1/1/1	-
4	MPO	5-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	4-A	903	-	-	1/1/1/1	-
3	EDO	2-B	905	-	-	0/1/1/1	-
3	EDO	3-A	910	-	-	1/1/1/1	-
3	EDO	5-A	901	-	-	1/1/1/1	-
3	EDO	3-B	909	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	3-A	901	-	-	1/1/1/1	-
3	EDO	8-B	912	-	-	1/1/1/1	-
3	EDO	7-A	906	-	-	1/1/1/1	-
3	EDO	3-B	912	-	-	1/1/1/1	-
3	EDO	5-B	905	-	-	0/1/1/1	-
3	EDO	8-B	913	-	-	1/1/1/1	-
3	EDO	1-B	904	-	-	1/1/1/1	-
3	EDO	5-B	913	-	-	1/1/1/1	-
3	EDO	6-B	905	-	-	0/1/1/1	-
3	EDO	2-B	904	-	-	1/1/1/1	-
3	EDO	7-B	904	-	-	1/1/1/1	-
3	EDO	7-A	902	-	-	0/1/1/1	-
4	MPO	8-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	6-A	902	-	-	0/1/1/1	-
3	EDO	6-B	911	-	-	1/1/1/1	-
3	EDO	5-A	907	-	-	0/1/1/1	-
3	EDO	6-A	903	-	-	1/1/1/1	-
3	EDO	7-A	910	-	-	1/1/1/1	-
3	EDO	2-B	911	-	-	1/1/1/1	-
3	EDO	5-A	902	-	-	0/1/1/1	-
4	MPO	4-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	5-B	909	-	-	1/1/1/1	-
3	EDO	4-B	904	-	-	1/1/1/1	-
3	EDO	4-A	907	-	-	0/1/1/1	-
3	EDO	2-B	913	-	-	1/1/1/1	-
3	EDO	3-B	913	-	-	1/1/1/1	-
3	EDO	2-B	909	-	-	1/1/1/1	-
3	EDO	1-B	912	-	-	1/1/1/1	-
3	EDO	2-A	902	-	-	0/1/1/1	-
3	EDO	8-A	908	-	-	1/1/1/1	-
3	EDO	6-B	912	-	-	1/1/1/1	-
3	EDO	6-A	910	-	-	1/1/1/1	-
3	EDO	5-A	908	-	-	1/1/1/1	-
4	MPO	3-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	3-A	907	-	-	0/1/1/1	-
3	EDO	8-A	902	-	-	0/1/1/1	-
4	MPO	6-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	3-B	911	-	-	1/1/1/1	-
3	EDO	3-A	908	-	-	1/1/1/1	-
3	EDO	4-B	911	-	-	1/1/1/1	-
3	EDO	8-A	906	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	5-A	910	-	-	1/1/1/1	-
3	EDO	1-A	910	-	-	1/1/1/1	-
3	EDO	1-A	902	-	-	0/1/1/1	-
3	EDO	2-A	908	-	-	1/1/1/1	-
3	EDO	6-A	906	-	-	1/1/1/1	-
3	EDO	4-B	905	-	-	0/1/1/1	-
3	EDO	8-A	910	-	-	1/1/1/1	-
3	EDO	7-A	901	-	-	1/1/1/1	-
3	EDO	6-B	904	-	-	1/1/1/1	-
3	EDO	4-A	908	-	-	1/1/1/1	-
3	EDO	7-B	912	-	-	1/1/1/1	-
3	EDO	1-A	908	-	-	1/1/1/1	-
3	EDO	4-B	909	-	-	1/1/1/1	-
3	EDO	2-A	906	-	-	1/1/1/1	-
3	EDO	7-A	908	-	-	1/1/1/1	-
3	EDO	5-B	904	-	-	1/1/1/1	-
3	EDO	4-A	906	-	-	1/1/1/1	-
4	MPO	2-A	9000	-	-	2/7/15/15	0/1/1/1
3	EDO	5-B	912	-	-	1/1/1/1	-
3	EDO	1-A	907	-	-	0/1/1/1	-
4	MPO	7-A	9000	-	-	2/7/15/15	0/1/1/1

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	6-A	9000	MPO	C1-S1	11.52	1.93	1.77
4	1-A	9000	MPO	C1-S1	11.52	1.93	1.77
4	5-A	9000	MPO	C1-S1	11.52	1.93	1.77
4	8-A	9000	MPO	C1-S1	11.52	1.93	1.77
4	4-A	9000	MPO	C1-S1	11.52	1.93	1.77

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6-A	9000	MPO	O3-S1-O1	-14.29	76.36	111.27
4	1-A	9000	MPO	O3-S1-O1	-14.29	76.36	111.27
4	5-A	9000	MPO	O3-S1-O1	-14.29	76.36	111.27
4	8-A	9000	MPO	O3-S1-O1	-14.29	76.36	111.27
4	4-A	9000	MPO	O3-S1-O1	-14.29	76.36	111.27

There are no chirality outliers.

5 of 96 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	7-B	911	EDO	O1-C1-C2-O2
3	1-B	911	EDO	O1-C1-C2-O2
3	8-B	911	EDO	O1-C1-C2-O2
3	6-B	911	EDO	O1-C1-C2-O2
3	2-B	911	EDO	O1-C1-C2-O2

There are no ring outliers.

58 monomers are involved in 152 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	7-A	903	EDO	2	0
3	2-A	903	EDO	3	0
3	6-B	913	EDO	3	0
3	5-A	906	EDO	2	0
3	7-B	911	EDO	8	0
3	1-B	913	EDO	2	0
3	8-A	903	EDO	6	0
3	1-B	911	EDO	2	0
3	6-A	908	EDO	4	0
3	4-B	912	EDO	2	0
3	2-B	912	EDO	2	0
3	1-B	905	EDO	2	0
3	7-B	909	EDO	1	0
3	8-A	907	EDO	2	0
3	5-A	903	EDO	2	0
3	8-B	911	EDO	8	0
3	3-A	906	EDO	2	0
3	8-B	905	EDO	1	0
3	1-A	903	EDO	1	0
3	3-A	903	EDO	2	0
3	7-B	913	EDO	1	0
3	1-A	906	EDO	1	0
3	5-B	911	EDO	6	0
4	5-A	9000	MPO	1	0
3	4-A	903	EDO	1	0
3	8-B	912	EDO	2	0
3	7-A	906	EDO	1	0
3	3-B	912	EDO	2	0
3	8-B	913	EDO	2	0
3	5-B	913	EDO	1	0
3	6-B	905	EDO	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	8-A	9000	MPO	1	0
3	6-B	911	EDO	6	0
3	6-A	903	EDO	1	0
3	2-B	911	EDO	7	0
3	2-B	913	EDO	1	0
3	3-B	913	EDO	1	0
3	1-B	912	EDO	1	0
3	8-A	908	EDO	7	0
3	6-B	912	EDO	2	0
3	6-A	910	EDO	1	0
3	5-A	908	EDO	4	0
4	6-A	9000	MPO	1	0
3	3-B	911	EDO	7	0
3	3-A	908	EDO	7	0
3	4-B	911	EDO	5	0
3	8-A	906	EDO	2	0
3	2-A	908	EDO	4	0
3	6-A	906	EDO	1	0
3	8-A	910	EDO	1	0
3	6-B	904	EDO	1	0
3	4-A	908	EDO	1	0
3	7-B	912	EDO	2	0
3	1-A	908	EDO	2	0
3	2-A	906	EDO	1	0
3	7-A	908	EDO	6	0
3	5-B	904	EDO	1	0
3	5-B	912	EDO	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	1-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	2-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	2-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	3-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	3-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	4-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	4-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	5-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	5-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	6-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	6-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	7-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	7-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
1	8-A	358/383 (93%)	-0.16	15 (4%)	36	41	7, 14, 32, 56	358 (100%)
1	8-B	356/383 (92%)	-0.07	29 (8%)	12	13	8, 15, 46, 72	356 (100%)
All	All	5712/6128 (93%)	-0.11	352 (6%)	22	23	7, 14, 39, 72	5712 (100%)

The worst 5 of 352 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-B	295	ASP	10.6
1	2-B	295	ASP	10.6
1	3-B	295	ASP	10.6
1	4-B	295	ASP	10.6
1	5-B	295	ASP	10.6

## 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 monosaccharides 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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MPO	6-A	9000	13/13	0.76	0.45	38,46,55,55	13
4	MPO	1-A	9000	13/13	0.76	0.45	38,46,55,55	13
4	MPO	5-A	9000	13/13	0.76	0.45	38,46,55,55	13
4	MPO	8-A	9000	13/13	0.76	0.45	37,46,55,55	13
4	MPO	4-A	9000	13/13	0.76	0.45	38,46,55,55	13
4	MPO	3-A	9000	13/13	0.76	0.45	38,46,55,55	13
4	MPO	2-A	9000	13/13	0.76	0.45	38,46,55,55	13
4	MPO	7-A	9000	13/13	0.76	0.45	38,46,55,55	13
3	EDO	8-A	903	4/4	0.80	0.20	43,44,48,50	4
3	EDO	4-A	903	4/4	0.80	0.20	43,43,48,50	4
3	EDO	7-A	903	4/4	0.80	0.20	43,43,48,50	4
3	EDO	6-A	903	4/4	0.80	0.20	43,44,48,50	4
3	EDO	5-A	903	4/4	0.80	0.20	43,43,48,50	4
3	EDO	1-A	903	4/4	0.80	0.20	43,43,48,50	4
3	EDO	3-A	903	4/4	0.80	0.20	43,43,48,50	4
3	EDO	2-A	903	4/4	0.80	0.20	43,44,48,50	4
3	EDO	4-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	1-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	2-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	3-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	7-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	5-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	8-B	913	4/4	0.82	0.16	29,31,34,37	4
3	EDO	6-B	913	4/4	0.82	0.16	28,31,34,37	4
3	EDO	3-A	908	4/4	0.83	0.23	27,30,31,43	4
3	EDO	2-A	908	4/4	0.83	0.23	27,31,31,43	4
3	EDO	4-A	908	4/4	0.83	0.23	27,30,31,43	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	1-A	908	4/4	0.83	0.23	27,31,31,43	4
3	EDO	8-A	908	4/4	0.83	0.23	27,30,31,43	4
3	EDO	7-A	908	4/4	0.83	0.23	27,30,31,43	4
3	EDO	5-A	908	4/4	0.83	0.23	27,30,31,43	4
3	EDO	6-A	908	4/4	0.83	0.23	27,30,31,43	4
3	EDO	6-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	2-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	7-B	911	4/4	0.85	0.21	22,28,30,36	4
3	EDO	5-B	911	4/4	0.85	0.21	20,28,31,36	4
3	EDO	3-B	911	4/4	0.85	0.21	22,28,31,36	4
3	EDO	6-B	911	4/4	0.85	0.21	21,28,30,36	4
3	EDO	4-B	911	4/4	0.85	0.21	21,28,31,36	4
3	EDO	8-B	911	4/4	0.85	0.21	21,28,31,36	4
3	EDO	2-B	911	4/4	0.85	0.21	21,28,30,36	4
3	EDO	7-B	912	4/4	0.85	0.22	31,34,36,39	4
3	EDO	4-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	1-B	911	4/4	0.85	0.21	21,28,31,36	4
3	EDO	8-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	1-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	5-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	3-B	912	4/4	0.85	0.22	31,34,36,38	4
3	EDO	6-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	5-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	2-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	8-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	4-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	7-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	1-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	3-A	906	4/4	0.86	0.21	41,42,43,44	4
3	EDO	6-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	3-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	2-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	1-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	8-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	7-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	4-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	5-B	909	4/4	0.88	0.23	41,42,45,47	4
3	EDO	4-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	3-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	5-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	1-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	7-A	910	4/4	0.91	0.07	42,47,47,48	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	8-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	2-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	6-A	910	4/4	0.91	0.07	42,47,47,48	4
3	EDO	6-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	7-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	1-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	2-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	4-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	5-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	8-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	3-B	905	4/4	0.93	0.07	35,36,39,39	4
3	EDO	2-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	6-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	4-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	1-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	5-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	7-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	8-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	3-A	901	4/4	0.94	0.11	32,33,33,35	4
3	EDO	2-A	902	4/4	0.95	0.12	27,27,29,33	4
3	EDO	3-A	902	4/4	0.95	0.12	27,27,29,33	4
3	EDO	4-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	8-A	902	4/4	0.95	0.12	27,28,29,33	4
3	EDO	6-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	6-A	902	4/4	0.95	0.12	27,28,29,33	4
3	EDO	7-A	902	4/4	0.95	0.12	27,27,30,33	4
3	EDO	1-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	3-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	8-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	4-A	902	4/4	0.95	0.12	27,27,29,33	4
3	EDO	5-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	2-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	5-A	902	4/4	0.95	0.12	27,28,29,33	4
3	EDO	1-A	902	4/4	0.95	0.12	27,27,29,33	4
3	EDO	7-B	904	4/4	0.95	0.08	35,37,38,41	4
3	EDO	5-A	907	4/4	0.97	0.11	27,31,32,32	4
3	EDO	2-A	907	4/4	0.97	0.11	27,31,32,32	4
3	EDO	7-A	907	4/4	0.97	0.11	27,31,32,32	4
3	EDO	3-A	907	4/4	0.97	0.11	27,30,32,32	4
3	EDO	4-A	907	4/4	0.97	0.11	27,31,32,32	4
3	EDO	8-A	907	4/4	0.97	0.11	27,30,32,32	4
3	EDO	1-A	907	4/4	0.97	0.11	27,31,32,32	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	6-A	907	4/4	0.97	0.11	27,31,32,32	4
2	MG	2-A	802	1/1	0.99	0.05	15,15,15,15	1
2	MG	6-A	802	1/1	0.99	0.05	20,20,20,20	1
2	MG	5-A	802	1/1	0.99	0.05	15,15,15,15	1
2	MG	3-A	802	1/1	0.99	0.05	12,12,12,12	1
2	MG	8-A	802	1/1	0.99	0.05	17,17,17,17	1
2	MG	5-B	801	1/1	0.99	0.04	20,20,20,20	1
2	MG	1-B	801	1/1	0.99	0.04	15,15,15,15	1
2	MG	1-A	802	1/1	0.99	0.05	12,12,12,12	1
2	MG	8-B	801	1/1	0.99	0.04	17,17,17,17	1
2	MG	2-B	801	1/1	0.99	0.04	15,15,15,15	1
2	MG	6-B	801	1/1	0.99	0.04	18,18,18,18	1
2	MG	4-A	802	1/1	0.99	0.05	12,12,12,12	1
2	MG	7-A	802	1/1	0.99	0.05	15,15,15,15	1
2	MG	3-B	801	1/1	0.99	0.04	15,15,15,15	1
2	MG	7-B	801	1/1	0.99	0.04	19,19,19,19	1
2	MG	4-B	801	1/1	0.99	0.04	15,15,15,15	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.