



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2021 – 01:42 PM EDT

PDB ID : 3DEN  
Title : Structure of E. coli DHDPS mutant Y107W  
Authors : Pearce, F.G.; Gerrard, J.A.; Perugini, M.A.; Jameson, G.B.  
Deposited on : 2008-06-10  
Resolution : 2.20 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

<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 : 2.23.2  
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) : 2.23.2

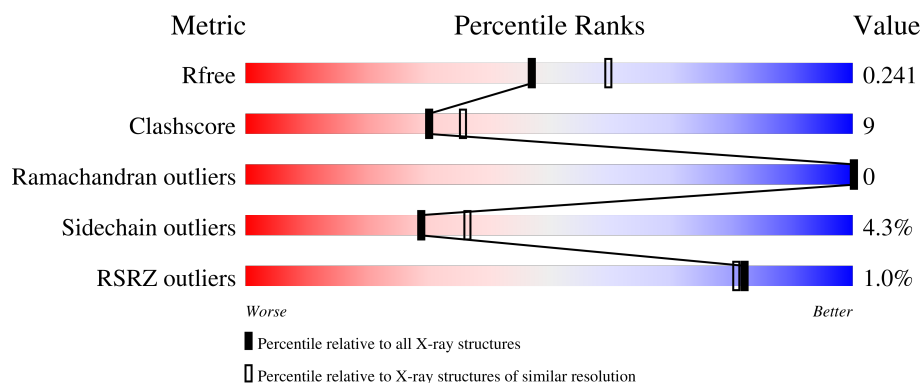
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 of 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	A	292	
1	B	292	

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	GOL	A	2647	-	-	X	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4934 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 Dihydrodipicolinate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	7	0
			2240	1410	389	427	14			
1	B	292	Total	C	N	O	S	0	3	0
			2211	1389	386	422	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	TRP	TYR	engineered mutation	UNP P0A6L2
B	107	TRP	TYR	engineered mutation	UNP P0A6L2

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

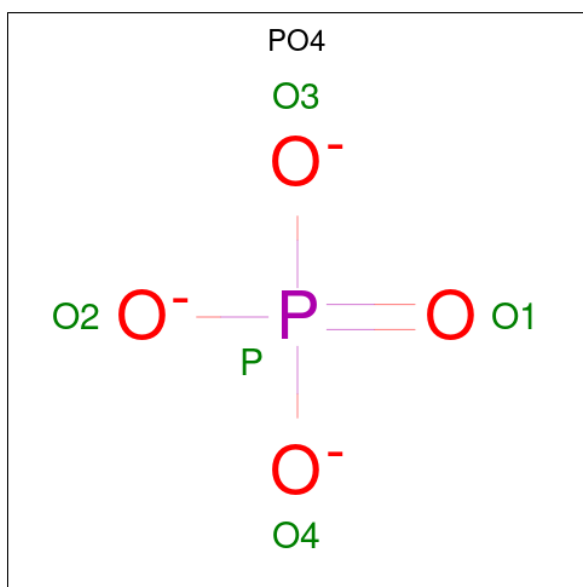
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		
2	B	1	Total	K	0	0
			1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		

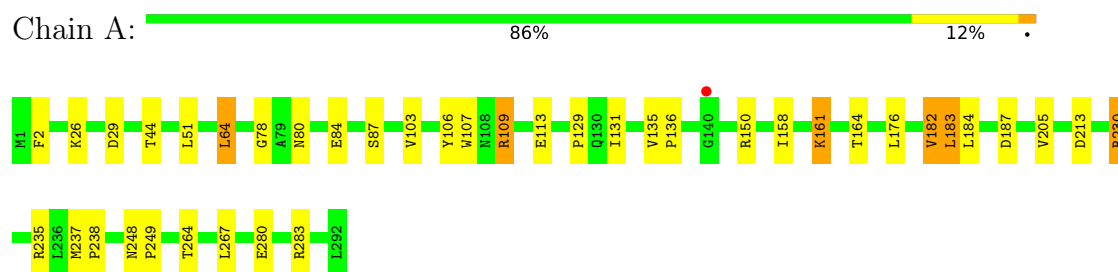
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	242	Total	O	0	0
			242	242		
5	B	206	Total	O	0	0
			206	206		

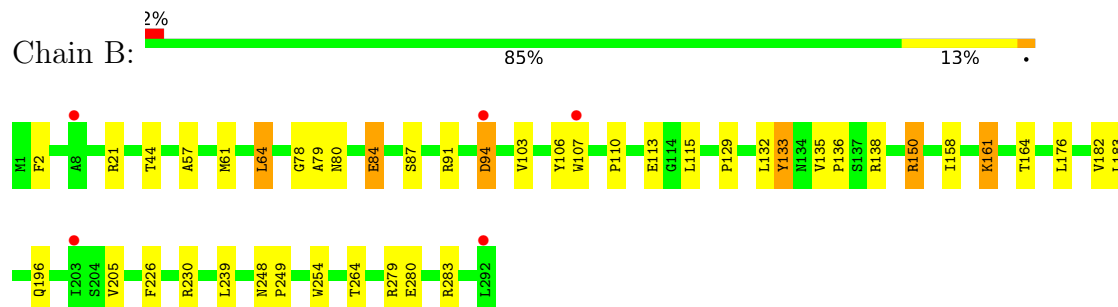
### 3 Residue-property plots

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: Dihydrodipicolinate synthase



#### • Molecule 1: Dihydrodipicolinate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	121.20Å 121.20Å 110.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.22 – 2.20 31.49 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (32.22-2.20) 99.1 (31.49-2.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.183 , 0.241 0.182 , 0.241	Depositor DCC
$R_{free}$ test set	2388 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	31.7	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 35.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.002 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4934	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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: K, KGC, GOL, PO4

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	0.92	1/2274 (0.0%)	0.87	7/3091 (0.2%)
1	B	0.89	1/2236 (0.0%)	0.87	3/3042 (0.1%)
All	All	0.91	2/4510 (0.0%)	0.87	10/6133 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	VAL	CB-CG1	-5.37	1.41	1.52
1	B	94	ASP	CG-OD2	5.05	1.36	1.25

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	21	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	B	21	ARG	NE-CZ-NH2	-7.28	116.66	120.30
1	A	64	LEU	CA-CB-CG	6.46	130.16	115.30
1	A	187	ASP	CB-CG-OD2	6.38	124.04	118.30
1	A	213	ASP	CB-CG-OD1	6.35	124.02	118.30
1	B	64	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	183	LEU	CA-CB-CG	5.62	128.24	115.30
1	A	187	ASP	CB-CG-OD1	-5.18	113.64	118.30
1	A	29	ASP	CB-CG-OD2	-5.11	113.70	118.30
1	A	29	ASP	CB-CG-OD1	5.00	122.80	118.30

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	2240	0	2252	49	0
1	B	2211	0	2208	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	18	0	24	19	0
4	A	5	0	0	0	0
4	B	10	0	0	0	0
5	A	242	0	0	11	0
5	B	206	0	0	3	0
All	All	4934	0	4484	83	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 9.

All (83) 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:A:84[B]:GLU:CG	3:A:2647:GOL:H11	1.38	1.50
1:A:84[B]:GLU:CG	3:A:2647:GOL:C1	2.24	1.16
1:A:84[B]:GLU:CD	3:A:2647:GOL:H11	1.67	1.14
1:A:26[B]:LYS:CE	5:A:343:HOH:O	1.92	1.13
1:A:84[B]:GLU:HG2	3:A:2647:GOL:H11	1.15	1.05
1:A:84[B]:GLU:HG2	3:A:2647:GOL:C1	1.87	0.97
1:A:26[B]:LYS:NZ	5:A:343:HOH:O	1.88	0.94
1:A:84[A]:GLU:OE1	3:A:2647:GOL:H31	1.68	0.93
1:A:84[A]:GLU:OE1	5:A:440:HOH:O	1.86	0.91
1:A:84[B]:GLU:OE2	3:A:2647:GOL:H11	1.74	0.86
1:A:26[B]:LYS:HE3	5:A:343:HOH:O	1.62	0.85
1:A:84[B]:GLU:OE2	3:A:2647:GOL:C1	2.31	0.78
1:B:106:TYR:O	1:B:107[A]:TRP:HB3	1.81	0.78
1:A:44:THR:OG1	1:B:107[A]:TRP:CZ2	2.36	0.78
1:A:44:THR:OG1	1:B:107[A]:TRP:HZ2	1.67	0.77
1:A:84[B]:GLU:HG3	3:A:2647:GOL:C1	2.14	0.76
3:A:2647:GOL:O3	5:A:439:HOH:O	2.04	0.75
1:A:280:GLU:OE2	1:A:283:ARG:NH1	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84[B]:GLU:HG3	3:A:2647:GOL:C3	2.20	0.72
1:A:84[B]:GLU:HG3	3:A:2647:GOL:H11	1.61	0.72
1:A:84[B]:GLU:CD	3:A:2647:GOL:C1	2.52	0.72
1:A:84[B]:GLU:HG3	3:A:2647:GOL:C2	2.21	0.71
1:A:106:TYR:O	1:A:107[A]:TRP:HB3	1.90	0.70
1:A:107[A]:TRP:HZ2	1:B:44:THR:HG1	1.40	0.70
1:B:91:ARG:NH1	5:B:312:HOH:O	2.20	0.68
1:A:84[B]:GLU:HG3	3:A:2647:GOL:H31	1.74	0.67
1:A:135:VAL:O	1:A:135:VAL:HG13	1.95	0.66
1:A:129:PRO:HB3	1:A:158:ILE:HG12	1.78	0.65
1:A:230[A]:ARG:NH1	5:A:321:HOH:O	2.20	0.65
1:B:230:ARG:NH1	5:B:369:HOH:O	2.30	0.64
1:B:136:PRO:HD2	1:B:164:THR:HG22	1.80	0.62
1:A:107[A]:TRP:HZ2	1:B:44:THR:OG1	1.82	0.62
1:B:79:ALA:CB	1:B:84:GLU:HG2	2.29	0.62
3:A:2647:GOL:C3	5:A:439:HOH:O	2.47	0.62
1:A:103:VAL:HG21	1:B:107[A]:TRP:CZ3	2.33	0.62
1:B:106:TYR:O	1:B:107[B]:TRP:HB3	2.00	0.61
1:A:80[B]:ASN:ND2	1:A:106:TYR:O	2.35	0.59
1:B:196:GLN:OE1	1:B:230:ARG:NH2	2.37	0.57
1:A:84[B]:GLU:OE2	3:A:2647:GOL:O1	2.22	0.56
1:B:161:KGC:H272	1:B:205:VAL:HG23	1.88	0.55
1:A:136:PRO:CD	1:A:164:THR:HG22	2.37	0.54
1:B:113:GLU:OE1	1:B:150:ARG:NH2	2.40	0.54
1:B:129:PRO:HB3	1:B:158:ILE:HG12	1.89	0.54
1:B:248:ASN:ND2	1:B:249:PRO:HA	2.22	0.54
1:A:107[A]:TRP:CZ3	1:B:103:VAL:HG21	2.42	0.54
1:B:79:ALA:HB1	1:B:84:GLU:HG2	1.90	0.54
1:B:80[B]:ASN:OD1	1:B:106:TYR:N	2.41	0.53
1:A:107[B]:TRP:CE3	5:A:444:HOH:O	2.62	0.52
3:A:2647:GOL:O3	5:A:312:HOH:O	2.19	0.52
1:A:136:PRO:HD2	1:A:164:THR:HG22	1.91	0.52
1:B:80[B]:ASN:OD1	1:B:106:TYR:O	2.27	0.51
1:B:136:PRO:CD	1:B:164:THR:HG22	2.40	0.51
1:A:84[A]:GLU:HB2	3:A:2647:GOL:H11	1.92	0.49
1:B:80[B]:ASN:ND2	1:B:106:TYR:CE1	2.80	0.49
1:B:254:TRP:CE2	1:B:279:ARG:HG3	2.47	0.49
1:B:110:PRO:HG2	1:B:115:LEU:CD2	2.41	0.49
1:A:107[B]:TRP:CZ3	5:A:444:HOH:O	2.56	0.48
1:B:280:GLU:OE2	1:B:283[A]:ARG:NH1	2.46	0.48
1:A:107[A]:TRP:CZ2	1:B:44:THR:OG1	2.59	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:PHE:O	1:A:182:VAL:HG11	2.15	0.46
1:A:113:GLU:OE1	1:A:150:ARG:NH2	2.47	0.46
1:B:2:PHE:O	1:B:182:VAL:HG11	2.14	0.46
1:B:106:TYR:O	1:B:107[B]:TRP:CB	2.60	0.46
1:B:254:TRP:CZ2	1:B:279:ARG:HG3	2.52	0.45
1:B:135:VAL:O	1:B:135:VAL:HG13	2.17	0.44
1:B:80[B]:ASN:ND2	1:B:106:TYR:CD1	2.86	0.44
1:A:237:MET:HB3	1:A:238:PRO:HD3	2.00	0.43
1:B:78:GLY:HA3	1:B:103:VAL:HG12	2.00	0.43
1:B:57:ALA:O	1:B:61:MET:HG2	2.18	0.43
1:A:107[B]:TRP:HZ3	5:A:444:HOH:O	1.99	0.43
1:A:109:ARG:HD3	1:B:138:ARG:HG2	2.00	0.43
1:A:248:ASN:ND2	1:A:249:PRO:HA	2.33	0.43
1:B:161:KGC:H272	1:B:205:VAL:CG2	2.49	0.43
1:B:132:LEU:O	1:B:161:KGC:N	2.51	0.42
1:A:78:GLY:HA3	1:A:103:VAL:HG12	2.01	0.42
1:A:2:PHE:CD1	1:A:131:ILE:HD11	2.53	0.42
1:A:106:TYR:O	1:A:107[A]:TRP:CB	2.60	0.42
1:A:2:PHE:O	1:A:184:LEU:HD21	2.19	0.41
1:A:135:VAL:O	1:A:135:VAL:CG1	2.67	0.41
1:A:161:KGC:H272	1:A:205:VAL:HG23	2.03	0.41
1:B:226:PHE:O	1:B:230:ARG:HB2	2.21	0.40
1:B:230:ARG:HD2	5:B:303:HOH:O	2.21	0.40
1:B:103:VAL:HA	1:B:133:TYR:HB3	2.02	0.40

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	296/292 (101%)	289 (98%)	7 (2%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	292/292 (100%)	287 (98%)	5 (2%)	0	100	100
All	All	588/584 (101%)	576 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	238/237 (100%)	227 (95%)	11 (5%)	27	34
1	B	233/237 (98%)	223 (96%)	10 (4%)	29	36
All	All	471/474 (99%)	450 (96%)	21 (4%)	29	34

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	64	LEU
1	A	87	SER
1	A	109	ARG
1	A	176	LEU
1	A	183	LEU
1	A	230[A]	ARG
1	A	230[B]	ARG
1	A	235	ARG
1	A	264	THR
1	A	267	LEU
1	B	64	LEU
1	B	84	GLU
1	B	87	SER
1	B	94	ASP
1	B	133	TYR
1	B	150	ARG
1	B	176	LEU

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Mol	Chain	Res	Type
1	B	183	LEU
1	B	239	LEU
1	B	264	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	GLN
1	A	233	ASN
1	A	241	ASN
1	A	248	ASN
1	B	53	HIS
1	B	90	GLN
1	B	172	GLN
1	B	233	ASN
1	B	248	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	KGC	B	161	1	12,18,19	1.85	2 (16%)	8,24,26	2.34	1 (12%)
1	KGC	A	161	1	12,18,19	1.90	1 (8%)	8,24,26	1.99	4 (50%)

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
1	KGC	B	161	1	-	0/8/28/30	0/1/1/1
1	KGC	A	161	1	-	0/8/28/30	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	161	KGC	O30-C28	5.89	1.45	1.35
1	B	161	KGC	O30-C28	5.63	1.44	1.35
1	B	161	KGC	O1-C	2.20	1.28	1.19

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	161	KGC	CE-NZ-C11	6.32	126.90	117.06
1	A	161	KGC	O30-C28-O29	3.31	123.75	120.80
1	A	161	KGC	CD-CG-CB	-2.81	103.69	113.62
1	A	161	KGC	CE-NZ-C11	2.77	121.37	117.06
1	A	161	KGC	C12-C27-C28	-2.17	101.21	104.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	161	KGC	3	0
1	A	161	KGC	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	PO4	A	296	-	4,4,4	0.82	0	6,6,6	0.49	0
4	PO4	B	295	-	4,4,4	0.85	0	6,6,6	0.77	0
3	GOL	A	2647	-	5,5,5	0.31	0	5,5,5	0.29	0
3	GOL	A	294	-	5,5,5	0.34	0	5,5,5	0.42	0
3	GOL	A	295	-	5,5,5	0.29	0	5,5,5	0.64	0
4	PO4	B	294	-	4,4,4	0.94	0	6,6,6	0.68	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
3	GOL	A	2647	-	-	2/4/4/4	-
3	GOL	A	294	-	-	2/4/4/4	-
3	GOL	A	295	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	294	GOL	O1-C1-C2-C3
3	A	295	GOL	C1-C2-C3-O3
3	A	295	GOL	O2-C2-C3-O3
3	A	294	GOL	O1-C1-C2-O2
3	A	295	GOL	O1-C1-C2-O2
3	A	2647	GOL	O2-C2-C3-O3
3	A	2647	GOL	C1-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 19 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2647	GOL	19	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	291/292 (99%)	-0.46	1 (0%) 94 93	19, 28, 42, 53	0
1	B	291/292 (99%)	-0.35	5 (1%) 70 68	24, 31, 43, 61	0
All	All	582/584 (99%)	-0.40	6 (1%) 82 81	19, 29, 43, 61	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	203	ILE	3.0
1	B	94	ASP	2.8
1	A	140	GLY	2.7
1	B	292	LEU	2.5
1	B	107[A]	TRP	2.2
1	B	8	ALA	2.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [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. 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(Å <sup>2</sup> )	Q<0.9
1	KGC	B	161	18/19	0.93	0.18	23,33,45,46	0
1	KGC	A	161	18/19	0.96	0.16	17,27,42,45	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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. 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
3	GOL	A	2647	6/6	0.79	0.50	30,30,31,33	6
4	PO4	A	296	5/5	0.81	0.29	44,45,46,48	5
3	GOL	A	295	6/6	0.82	0.43	25,26,26,28	6
3	GOL	A	294	6/6	0.90	0.28	22,23,24,24	6
4	PO4	B	294	5/5	0.96	0.12	33,36,37,37	5
4	PO4	B	295	5/5	0.96	0.08	39,40,41,41	5
2	K	A	293	1/1	0.99	0.03	30,30,30,30	0
2	K	B	293	1/1	0.99	0.05	36,36,36,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.