



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 01:00 AM GMT

PDB ID : 2O1S  
Title : 1-deoxy-D-xylulose 5-phosphate synthase (DXS) from Escherichia coli  
Authors : Xiang, S.; Usunow, G.; Lange, G.; Busch, M.; Tong, L.  
Deposited on : 2006-11-29  
Resolution : 2.40 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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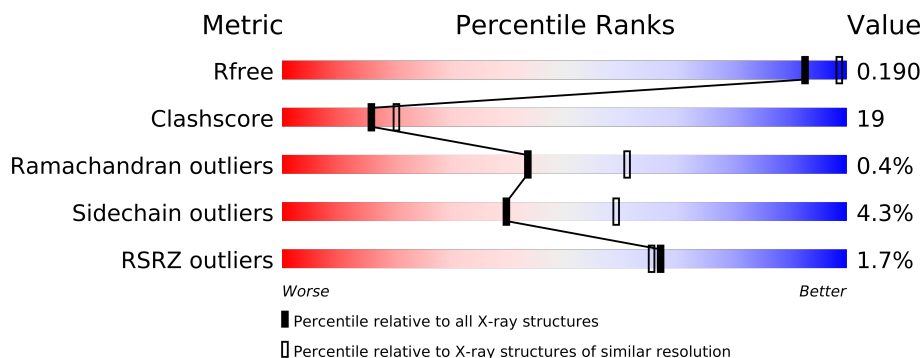
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	621	
1	B	621	
1	C	621	
1	D	621	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 16515 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 1-deoxy-D-xylulose-5-phosphatesynthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	536	Total	C	N	O	S	Se	0	0	0
			4122	2627	708	764	5	18			
1	B	493	Total	C	N	O	S	Se	0	0	0
			3800	2432	643	702	5	18			
1	C	536	Total	C	N	O	S	Se	0	0	0
			4123	2628	708	764	5	18			
1	D	487	Total	C	N	O	S	Se	0	0	0
			3734	2384	631	696	5	18			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	159	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	164	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	174	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	183	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	236	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	269	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	281	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	340	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	346	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	352	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	446	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	449	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	460	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	515	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	532	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	546	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	562	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	574	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	600	MSE	MET	MODIFIED RESIDUE	UNP P77488
A	611	MSE	MET	MODIFIED RESIDUE	UNP P77488

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Chain	Residue	Modelled	Actual	Comment	Reference
A	621	LEU	-	CLONING ARTIFACT	UNP P77488
B	1	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	159	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	164	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	174	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	183	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	236	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	269	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	281	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	340	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	346	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	352	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	446	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	449	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	460	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	515	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	532	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	546	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	562	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	574	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	600	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	611	MSE	MET	MODIFIED RESIDUE	UNP P77488
B	621	LEU	-	CLONING ARTIFACT	UNP P77488
C	1	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	159	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	164	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	174	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	183	MSE	MET	MODIFIED RESIDUE	UNP P77488
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C	546	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	562	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	574	MSE	MET	MODIFIED RESIDUE	UNP P77488

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Chain	Residue	Modelled	Actual	Comment	Reference
C	600	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	611	MSE	MET	MODIFIED RESIDUE	UNP P77488
C	621	LEU	-	CLONING ARTIFACT	UNP P77488
D	1	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	159	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	164	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	174	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	183	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	236	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	269	MSE	MET	MODIFIED RESIDUE	UNP P77488
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D	460	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	515	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	532	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	546	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	562	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	574	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	600	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	611	MSE	MET	MODIFIED RESIDUE	UNP P77488
D	621	LEU	-	CLONING ARTIFACT	UNP P77488

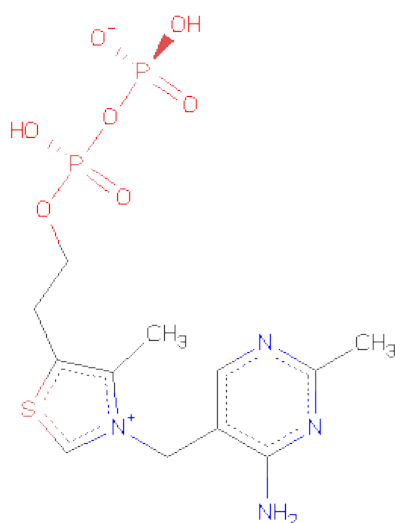
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

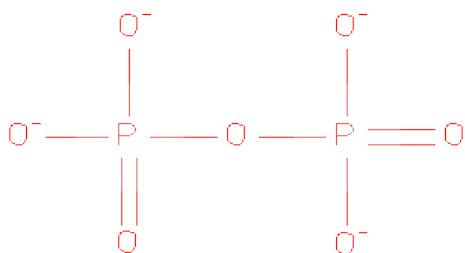
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total K 1 1	0	0
3	A	1	Total K 1 1	0	0
3	D	1	Total K 1 1	0	0
3	C	1	Total K 1 1	0	0

- Molecule 4 is THIAMIN DIPHOSPHATE (three-letter code: TDP) (formula:  $C_{12}H_{18}N_4O_7P_2S$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
4	C	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0

- Molecule 5 is DIPHOSPHATE (three-letter code: DPO) (formula:  $O_7P_2$ ).



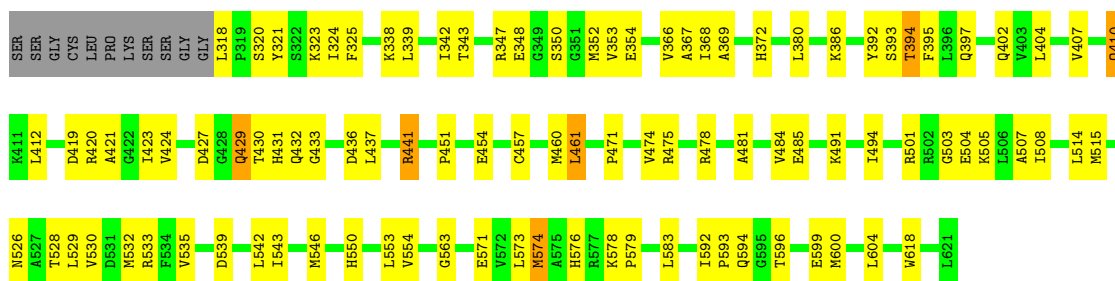
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			9	7	2		
5	D	1	Total	O	P	0	0
			9	7	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	210	Total	O	0	0
			210	210		
6	B	134	Total	O	0	0
			134	134		
6	C	186	Total	O	0	0
			186	186		
6	D	128	Total	O	0	0
			128	128		

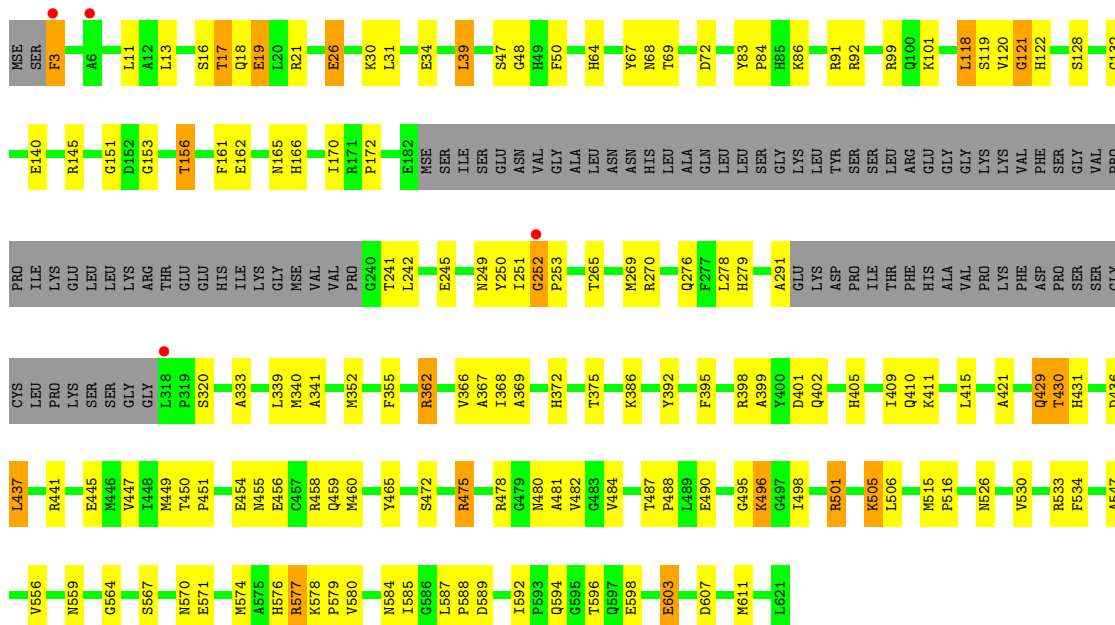






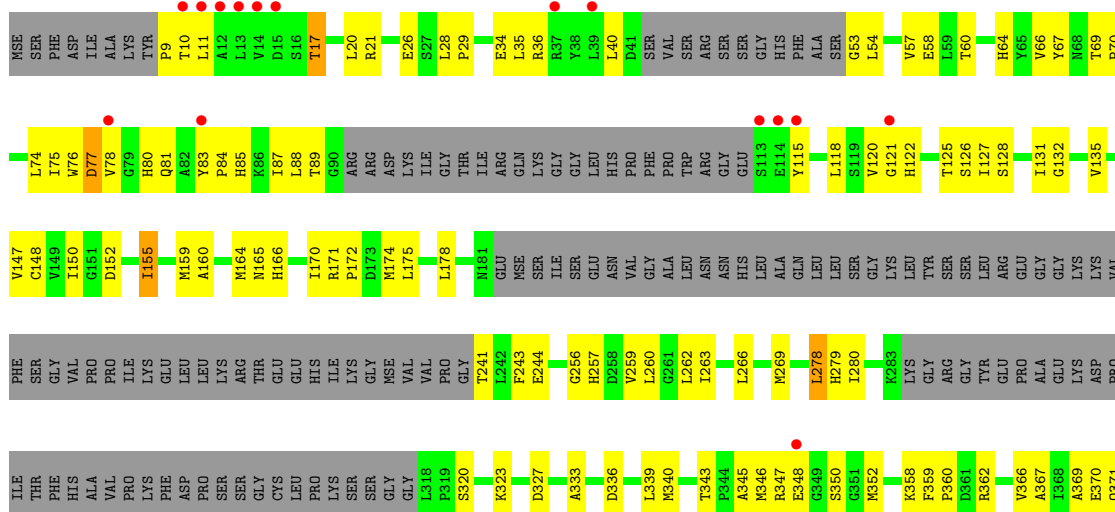
• Molecule 1: 1-deoxy-D-xylulose-5-phosphatesynthase

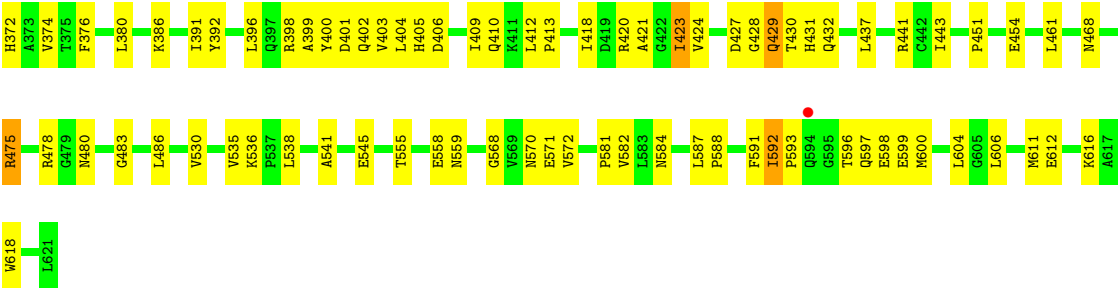
Chain C: 



• Molecule 1: 1-deoxy-D-xylulose-5-phosphatesynthase

Chain D: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.79Å 171.15Å 94.80Å 90.00° 107.25° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 29.77 – 2.41	Depositor EDS
% Data completeness (in resolution range)	89.0 (30.00-2.40) 89.7 (29.77-2.41)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.30 (at 2.42Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.191 , 0.234 0.192 , 0.190	Depositor DCC
$R_{free}$ test set	4603 reflections (5.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.5	Xtriage
Anisotropy	0.312	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 17.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 91600 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	16515	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DPO, K, TDP, MG

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	0.33	0/4191	0.61	1/5644 (0.0%)
1	B	0.33	0/3861	0.60	0/5203
1	C	0.33	0/4191	0.61	0/5644
1	D	0.31	0/3788	0.58	0/5101
All	All	0.32	0/16031	0.60	1/21592 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	339	LEU	CA-CB-CG	5.12	127.08	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4122	0	4133	132	0
1	B	3800	0	3813	171	0
1	C	4123	0	4136	145	0
1	D	3734	0	3757	175	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	26	0	16	2	0
4	C	26	0	16	3	0
5	B	9	0	0	0	0
5	D	9	0	0	0	0
6	A	210	0	0	7	0
6	B	134	0	0	6	0
6	C	186	0	0	4	0
6	D	128	0	0	4	0
All	All	16515	0	15871	588	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

The worst 5 of 588 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:A:3001:TDP:C2	4:A:3001:TDP:H2	0.97	1.50
4:C:3002:TDP:C2	4:C:3002:TDP:H2	0.97	1.47
1:B:350:SER:HB2	1:B:352:MSE:HE2	1.34	1.10
1:B:503:GLY:H	1:B:528:THR:HG22	1.19	1.08
1:D:423:ILE:HD11	1:D:597:GLN:HA	1.39	1.04

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	530/621 (85%)	501 (94%)	26 (5%)	3 (1%)	33	47
1	B	483/621 (78%)	463 (96%)	19 (4%)	1 (0%)	56	74
1	C	530/621 (85%)	507 (96%)	19 (4%)	4 (1%)	27	39
1	D	477/621 (77%)	458 (96%)	18 (4%)	1 (0%)	56	74
All	All	2020/2484 (81%)	1929 (96%)	82 (4%)	9 (0%)	43	61

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	252	GLY
1	A	48	GLY
1	C	505	LYS
1	D	77	ASP
1	C	48	GLY

### 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	433/485 (89%)	413 (95%)	20 (5%)	37	55
1	B	401/485 (83%)	385 (96%)	16 (4%)	42	63
1	C	433/485 (89%)	409 (94%)	24 (6%)	30	46
1	D	395/485 (81%)	383 (97%)	12 (3%)	53	75
All	All	1662/1940 (86%)	1590 (96%)	72 (4%)	40	59

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	441	ARG
1	C	26	GLU
1	D	429	GLN
1	B	461	LEU
1	C	3	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	432	GLN
1	C	276	GLN
1	D	431	HIS
1	B	480	ASN
1	B	576	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	TDP	A	3001	2	27,27,27	1.76	6 (22%)	40,40,40	1.96	13 (32%)
5	DPO	B	4001	2	8,8,8	3.92	5 (62%)	13,13,13	1.53	4 (30%)
4	TDP	C	3002	2	27,27,27	1.76	6 (22%)	40,40,40	1.96	13 (32%)
5	DPO	D	4002	2	8,8,8	3.93	6 (75%)	13,13,13	1.54	5 (38%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	TDP	A	3001	2	-	0/17/17/17	0/2/2/2
5	DPO	B	4001	2	-	0/6/6/6	0/0/0/0
4	TDP	C	3002	2	-	0/17/17/17	0/2/2/2
5	DPO	D	4002	2	-	0/6/6/6	0/0/0/0

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	4002	DPO	P2-O6	5.72	1.61	1.51
5	B	4001	DPO	P1-O2	5.70	1.61	1.51
5	B	4001	DPO	P2-O6	5.68	1.61	1.51
5	D	4002	DPO	P1-O2	5.66	1.61	1.51
5	D	4002	DPO	P1-O1	5.03	1.61	1.51

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	3002	TDP	C4-C5-S1	-4.56	106.20	109.93
4	A	3001	TDP	C4-C5-S1	-4.27	106.44	109.93
4	A	3001	TDP	C5A-C5-C4	4.00	130.35	127.44
4	C	3002	TDP	C5-C4-N3	3.75	115.14	107.53
4	A	3001	TDP	C5-C4-N3	3.71	115.06	107.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	536/621 (86%)	-0.55	2 (0%) 90 90	3, 14, 31, 43	0
1	B	493/621 (79%)	-0.30	14 (2%) 50 48	3, 17, 53, 62	0
1	C	536/621 (86%)	-0.52	4 (0%) 84 84	4, 13, 30, 42	0
1	D	487/621 (78%)	-0.26	16 (3%) 44 42	5, 19, 44, 58	0
All	All	2052/2484 (82%)	-0.41	36 (1%) 67 63	3, 16, 40, 62	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	15	ASP	3.8
1	B	111	GLY	3.5
1	B	109	TRP	3.5
1	B	8	TYR	3.2
1	B	106	PRO	3.1

### 6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	DPO	D	4002	9/9	0.16	-0.18	50,51,54,54	0
2	MG	C	1003	1/1	0.15	-0.20	26,26,26,26	0
4	TDP	A	3001	26/26	0.09	-0.32	5,13,16,16	0
2	MG	B	1002	1/1	0.12	-0.41	48,48,48,48	0
5	DPO	B	4001	9/9	0.15	-0.42	50,51,55,56	0
4	TDP	C	3002	26/26	0.09	-0.70	4,13,16,18	0
3	K	D	2004	1/1	0.07	-0.80	34,34,34,34	0
2	MG	A	1001	1/1	0.07	-0.86	9,9,9,9	0
2	MG	D	1004	1/1	0.10	-0.87	61,61,61,61	0
3	K	B	2002	1/1	0.06	-1.55	14,14,14,14	0
3	K	C	2003	1/1	0.07	-1.99	24,24,24,24	0
3	K	A	2001	1/1	0.05	-2.62	23,23,23,23	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.