



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 06:33 pm GMT

PDB ID : 5T5M  
Title : TUNGSTEN-CONTAINING FORMYLMETHANOFURAN DEHYDROGENASE FROM METHANOTHERMOBACTER WOLFEII, TRIGONAL FORM AT 2.5 Å.  
Authors : Wagner, T.; Ermler, U.; Shima, S.  
Deposited on : 2016-08-31  
Resolution : 2.50 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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

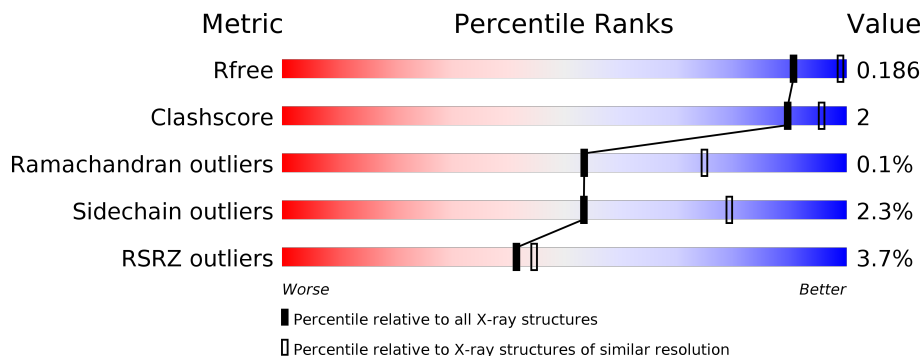
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	111664	4155 (2.50-2.50)
Clashscore	122126	4827 (2.50-2.50)
Ramachandran outliers	120053	4735 (2.50-2.50)
Sidechain outliers	120020	4737 (2.50-2.50)
RSRZ outliers	108989	4058 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	569	<div> <div>2%</div> <div>92%</div> <div>7%</div> <div>.</div> </div>
2	B	432	<div> <div>9%</div> <div>93%</div> <div>6%</div> <div>.</div> </div>
3	C	270	<div> <div>%</div> <div>97%</div> <div>.</div> </div>
4	D	130	<div> <div>4%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>
5	F	349	<div> <div>2%</div> <div>91%</div> <div>7%</div> <div>.</div> </div>
6	G	82	<div> <div>2%</div> <div>89%</div> <div>7%</div> <div>..</div> </div>

## 2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 14415 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 Tungsten formylmethanofuran dehydrogenase subunit fwdA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	569	Total	C	N	O	S	0	0	0
			4419	2812	735	849	23			

- Molecule 2 is a protein called Tungsten formylmethanofuran dehydrogenase subunit fwdB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	429	Total	C	N	O	S	0	2	0
			3375	2122	593	629	31			

- Molecule 3 is a protein called Tungsten-containing formylmethanofuran dehydrogenase 2 subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	269	Total	C	N	O	S	0	0	0
			1994	1254	336	391	13			

- Molecule 4 is a protein called Tungsten formylmethanofuran dehydrogenase subunit fwdD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	126	Total	C	N	O	S	0	0	0
			977	625	158	185	9			

- Molecule 5 is a protein called Tungsten formylmethanofuran dehydrogenase subunit fwdF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	342	Total	C	N	O	S	0	0	0
			2610	1611	435	523	41			

- Molecule 6 is a protein called Tungsten formylmethanofuran dehydrogenase subunit fwdG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	80	Total	C	N	O	S	0	0	0
			572	354	96	113	9			

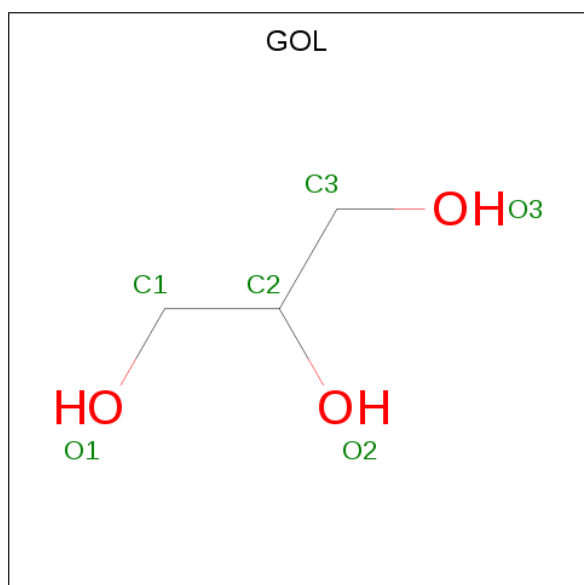
- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 8 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	2	Total	Zn	0	0
			2	2		

- Molecule 9 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

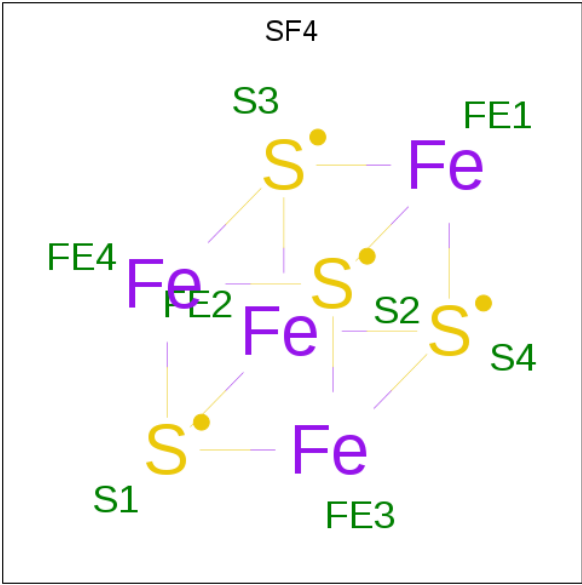


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			6	3	3		
9	A	1	Total	C	O	0	0
			6	3	3		
9	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 10 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total K 1 1	0	0

- Molecule 11 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe<sub>4</sub>S<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	B	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	F	1	Total Fe S 8 4 4	0	0
11	G	1	Total Fe S 8 4 4	0	0

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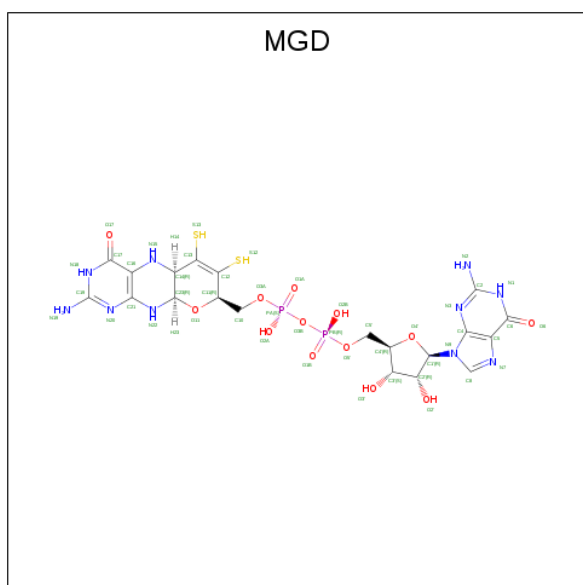
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	G	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 12 is TUNGSTEN ION (three-letter code: W) (formula: W).

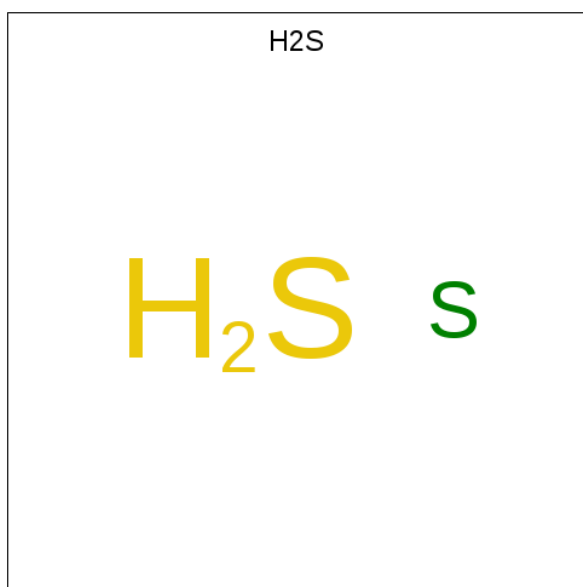
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	B	1	Total	W	0	0
			1	1		

- Molecule 13 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (three-letter code: MGD) (formula: C<sub>20</sub>H<sub>26</sub>N<sub>10</sub>O<sub>13</sub>P<sub>2</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
13	B	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		
13	B	1	Total	C	N	O	P	S	0	0
			47	20	10	13	2	2		

- Molecule 14 is HYDROSULFURIC ACID (three-letter code: H2S) (formula: H<sub>2</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	B	1	Total S 1 1	0	0

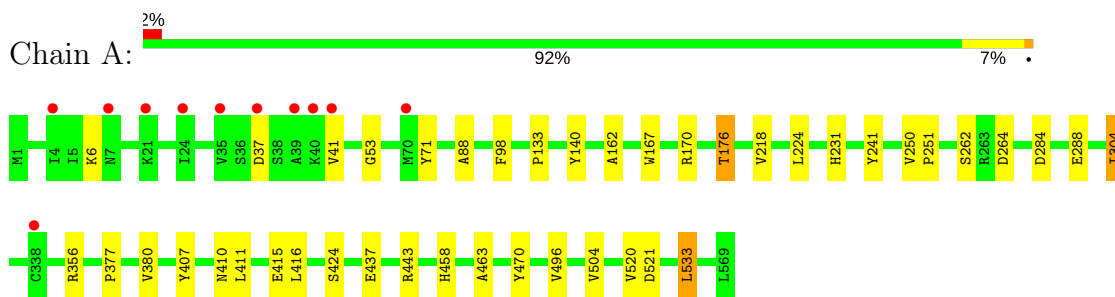
- Molecule 15 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
15	A	97	Total O 97 97	0	0
15	B	69	Total O 69 69	0	0
15	C	38	Total O 38 38	0	0
15	D	10	Total O 10 10	0	0
15	F	39	Total O 39 39	0	0
15	G	7	Total O 7 7	0	0

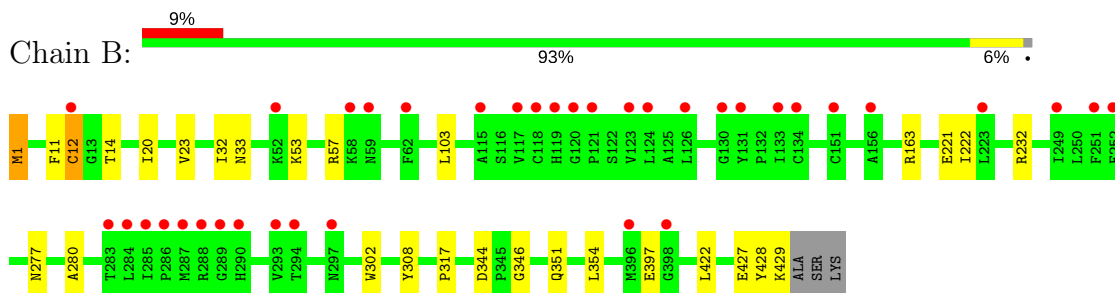
### 3 Residue-property plots [i](#)

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

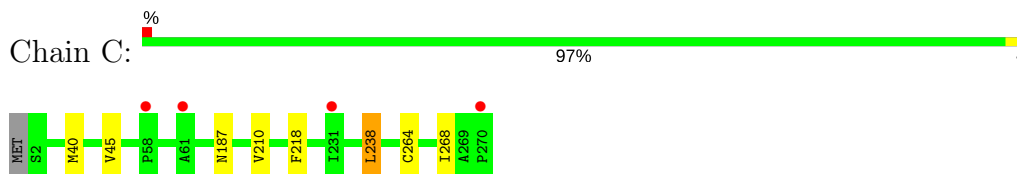
- Molecule 1: Tungsten formylmethanofuran dehydrogenase subunit fwdA



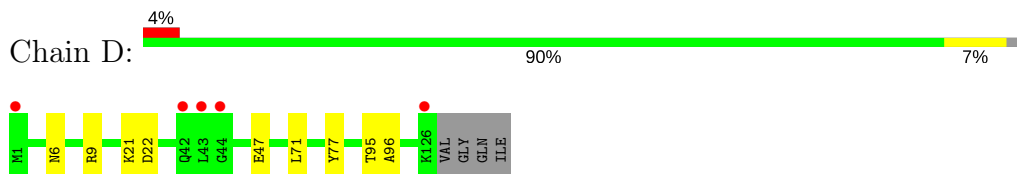
- Molecule 2: Tungsten formylmethanofuran dehydrogenase subunit fwdB



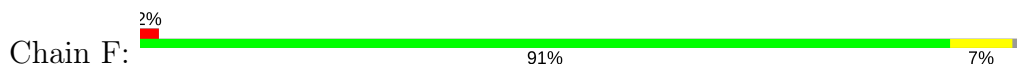
- Molecule 3: Tungsten-containing formylmethanofuran dehydrogenase 2 subunit C



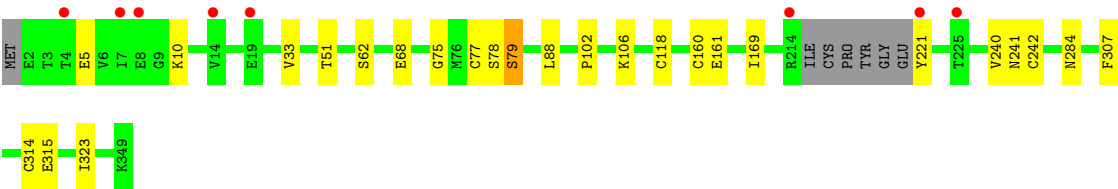
- Molecule 4: Tungsten formylmethanofuran dehydrogenase subunit fwdD



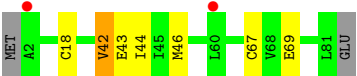
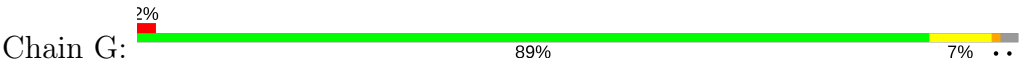
- Molecule 5: Tungsten formylmethanofuran dehydrogenase subunit fwdF







● Molecule 6: Tungsten formylmethanofuran dehydrogenase subunit fwdG



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.54Å 105.54Å 340.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.22 – 2.50 48.22 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.22-2.50) 99.9 (48.22-2.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.158 , 0.182 0.162 , 0.186	Depositor DCC
$R_{free}$ test set	3638 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.0	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 46.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	14415	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, MGD, SF4, ZN, H2S, KCX, W, K

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	0/4523	0.50	0/6161
2	B	0.37	0/3451	0.52	0/4669
3	C	0.33	0/2027	0.54	0/2729
4	D	0.32	0/996	0.52	0/1352
5	F	0.34	0/2646	0.52	0/3586
6	G	0.35	0/579	0.48	0/787
All	All	0.34	0/14222	0.51	0/19284

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4419	0	4272	21	0
2	B	3375	0	3325	13	0
3	C	1994	0	1962	3	0
4	D	977	0	1002	5	0
5	F	2610	0	2567	13	0
6	G	572	0	567	2	0
7	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	1	0	0	0	0
8	A	2	0	0	0	0
9	A	12	0	16	0	0
9	D	6	0	8	0	0
10	B	1	0	0	0	0
11	B	8	0	0	0	0
11	F	64	0	0	0	0
11	G	16	0	0	0	0
12	B	1	0	0	0	0
13	B	94	0	44	0	0
14	B	1	0	0	0	0
15	A	97	0	0	2	0
15	B	69	0	0	0	0
15	C	38	0	0	0	0
15	D	10	0	0	0	0
15	F	39	0	0	0	0
15	G	7	0	0	0	0
All	All	14415	0	13763	55	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 55 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:284:ASP:O	15:A:701:HOH:O	2.11	0.68
1:A:264:ASP:O	15:A:702:HOH:O	2.12	0.66
1:A:224:LEU:HD22	1:A:520:VAL:HG11	1.81	0.61
1:A:411:LEU:HG	1:A:416:LEU:HG	1.86	0.58
3:C:210:VAL:HG11	3:C:238:LEU:HD13	1.88	0.55

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	566/569 (100%)	543 (96%)	23 (4%)	0	100	100
2	B	429/432 (99%)	412 (96%)	16 (4%)	1 (0%)	49	71
3	C	267/270 (99%)	258 (97%)	9 (3%)	0	100	100
4	D	124/130 (95%)	118 (95%)	6 (5%)	0	100	100
5	F	338/349 (97%)	333 (98%)	5 (2%)	0	100	100
6	G	78/82 (95%)	78 (100%)	0	0	100	100
All	All	1802/1832 (98%)	1742 (97%)	59 (3%)	1 (0%)	53	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	428	TYR

### 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	470/470 (100%)	460 (98%)	10 (2%)	56	81
2	B	361/361 (100%)	352 (98%)	9 (2%)	50	77
3	C	203/204 (100%)	200 (98%)	3 (2%)	67	87
4	D	108/111 (97%)	106 (98%)	2 (2%)	60	83
5	F	306/312 (98%)	300 (98%)	6 (2%)	58	82
6	G	65/67 (97%)	61 (94%)	4 (6%)	20	38
All	All	1513/1525 (99%)	1479 (98%)	34 (2%)	53	80

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	302	TRP
3	C	187	ASN

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Mol	Chain	Res	Type
6	G	43	GLU
2	B	351	GLN
1	A	407	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	KCX	A	178	1,8	8,11,12	0.73	0	6,12,14	1.77	1 (16%)

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	KCX	A	178	1,8	-	0/6/10/12	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	KCX	CE-NZ-CX	-3.45	118.74	123.28

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 7 are monoatomic and 1 is modelled with single atom - leaving 16 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	$\# Z  > 2$
9	GOL	A	605	-	5,5,5	0.33	0	5,5,5	0.22	0
9	GOL	A	606	-	5,5,5	0.31	0	5,5,5	0.37	0
11	SF4	B	502	2	0,12,12	0.00	-	0,24,24	0.00	-
13	MGD	B	504	12	41,52,52	1.39	5 (12%)	39,81,81	2.01	11 (28%)
13	MGD	B	505	12	41,52,52	1.41	5 (12%)	39,81,81	2.44	13 (33%)
9	GOL	D	201	-	5,5,5	0.36	0	5,5,5	0.52	0
11	SF4	F	501	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	502	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	503	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	504	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	505	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	506	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	507	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	F	508	5	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	G	200	6	0,12,12	0.00	-	0,24,24	0.00	-
11	SF4	G	201	6	0,12,12	0.00	-	0,24,24	0.00	-

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
9	GOL	A	605	-	-	0/4/4/4	0/0/0/0
9	GOL	A	606	-	-	0/4/4/4	0/0/0/0
11	SF4	B	502	2	-	0/0/48/48	0/6/5/5
13	MGD	B	504	12	-	0/18/66/66	0/6/6/6
13	MGD	B	505	12	-	0/18/66/66	0/6/6/6
9	GOL	D	201	-	-	0/4/4/4	0/0/0/0
11	SF4	F	501	5	-	0/0/48/48	0/6/5/5
11	SF4	F	502	5	-	0/0/48/48	0/6/5/5
11	SF4	F	503	5	-	0/0/48/48	0/6/5/5
11	SF4	F	504	5	-	0/0/48/48	0/6/5/5
11	SF4	F	505	5	-	0/0/48/48	0/6/5/5
11	SF4	F	506	5	-	0/0/48/48	0/6/5/5
11	SF4	F	507	5	-	0/0/48/48	0/6/5/5
11	SF4	F	508	5	-	0/0/48/48	0/6/5/5
11	SF4	G	200	6	-	0/0/48/48	0/6/5/5
11	SF4	G	201	6	-	0/0/48/48	0/6/5/5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	B	504	MGD	C16-N15	-2.21	1.33	1.38
13	B	505	MGD	C8-N9	-2.01	1.34	1.36
13	B	505	MGD	C5-C4	2.45	1.46	1.40
13	B	504	MGD	C5-C4	3.00	1.47	1.40
13	B	505	MGD	C16-C21	3.04	1.47	1.41

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	505	MGD	C4'-O4'-C1'	-6.47	103.09	109.83
13	B	505	MGD	C6-C5-C4	-4.94	116.00	120.85
13	B	504	MGD	C5-C6-N1	-4.40	117.21	123.47
13	B	505	MGD	C5-C6-N1	-4.32	117.32	123.47
13	B	505	MGD	N3-C2-N1	-3.58	122.15	127.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.



No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	568/569 (99%)	-0.03	11 (1%) 66 69	41, 64, 94, 128	0
2	B	429/432 (99%)	0.49	37 (8%) 10 10	40, 62, 101, 143	0
3	C	269/270 (99%)	-0.17	4 (1%) 73 75	43, 60, 90, 122	0
4	D	126/130 (96%)	0.10	5 (3%) 38 41	52, 71, 96, 106	0
5	F	342/349 (97%)	0.15	8 (2%) 60 63	51, 68, 103, 131	0
6	G	80/82 (97%)	0.19	2 (2%) 57 60	59, 72, 97, 111	0
All	All	1814/1832 (99%)	0.13	67 (3%) 41 44	40, 65, 98, 143	0

The worst 5 of 67 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	F	221	TYR	5.3
6	G	2	ALA	5.2
3	C	270	PRO	4.7
5	F	14	VAL	4.0
2	B	12	CYS	3.9

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

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	KCX	A	178	12/13	0.99	0.18	48,50,56,57	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
10	K	B	501	1/1	0.73	0.29	133,133,133,133	0
9	GOL	A	606	6/6	0.82	0.38	57,59,61,66	0
9	GOL	D	201	6/6	0.86	0.17	53,54,57,59	0
9	GOL	A	605	6/6	0.90	0.15	52,53,56,64	0
7	MG	C	301	1/1	0.95	0.11	62,62,62,62	0
7	MG	A	604	1/1	0.96	0.16	42,42,42,42	0
13	MGD	B	505	47/47	0.97	0.20	50,54,58,61	0
7	MG	A	601	1/1	0.97	0.20	65,65,65,65	0
11	SF4	B	502	8/8	0.98	0.17	50,59,63,67	0
13	MGD	B	504	47/47	0.98	0.20	49,62,71,83	0
11	SF4	F	505	8/8	0.98	0.08	64,70,80,85	0
11	SF4	G	200	8/8	0.99	0.14	53,61,68,68	0
11	SF4	F	501	8/8	0.99	0.08	41,51,53,56	0
11	SF4	F	507	8/8	0.99	0.08	43,57,59,60	0
11	SF4	F	504	8/8	0.99	0.10	45,51,58,61	0
8	ZN	A	603	1/1	0.99	0.16	60,60,60,60	0
11	SF4	F	508	8/8	0.99	0.08	50,54,60,64	0
11	SF4	F	506	8/8	0.99	0.10	57,62,67,68	0
11	SF4	G	201	8/8	0.99	0.10	51,66,72,73	0
11	SF4	F	502	8/8	0.99	0.08	46,52,53,53	0
11	SF4	F	503	8/8	0.99	0.10	46,52,58,60	0
12	W	B	503	1/1	1.00	0.19	58,58,58,58	0
14	H2S	B	506	1/1	1.00	0.23	60,60,60,60	0
8	ZN	A	602	1/1	1.00	0.14	58,58,58,58	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.