



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:21 PM GMT

PDB ID : 4EGB  
Title : 3.0 Angstrom resolution crystal structure of dTDP-glucose 4,6-dehydratase (rfbB) from Bacillus anthracis str. Ames in complex with NAD  
Authors : Halavaty, A.S.; Kuhn, M.; Shuvalova, L.; Minasov, G.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2012-03-30  
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

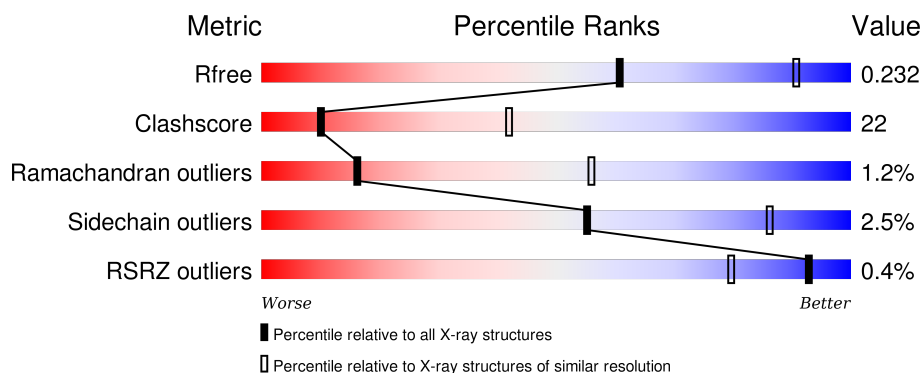
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	346	
1	B	346	
1	C	346	
1	D	346	
1	E	346	

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Mol	Chain	Length	Quality of chain
1	F	346	
1	G	346	
1	H	346	

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
5	SUC	B	406	-	-	-	X
5	SUC	E	406	-	-	-	X
5	SUC	H	405	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20705 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 dTDP-glucose 4,6-dehydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	311	Total	C	N	O	S	Se	0	0	0
			2507	1612	410	478	2	5			
1	B	308	Total	C	N	O	S	Se	0	0	0
			2487	1601	405	474	2	5			
1	C	310	Total	C	N	O	S	Se	0	0	0
			2503	1610	409	477	2	5			
1	D	309	Total	C	N	O	S	Se	0	0	0
			2493	1604	406	476	2	5			
1	E	311	Total	C	N	O	S	Se	0	0	0
			2507	1612	410	478	2	5			
1	F	309	Total	C	N	O	S	Se	0	0	0
			2493	1604	406	476	2	5			
1	G	309	Total	C	N	O	S	Se	0	0	0
			2493	1604	406	476	2	5			
1	H	310	Total	C	N	O	S	Se	0	1	0
			2512	1615	411	479	2	5			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
A	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
A	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
A	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
A	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
A	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
A	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
A	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
A	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
A	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
A	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
A	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
A	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
A	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
A	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
A	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
A	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
A	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
A	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
A	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
A	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
A	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
A	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
B	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
B	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
B	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
B	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
B	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
B	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
B	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
B	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
B	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
B	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
B	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
B	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
B	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0
B	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
B	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
B	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
B	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
B	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
B	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
B	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
B	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
B	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
B	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
B	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
C	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
C	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
C	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
C	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
C	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
C	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
C	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
C	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
C	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
C	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
C	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
C	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0
C	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
C	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
C	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
C	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
C	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
C	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
C	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
C	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
C	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
C	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
C	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
D	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
D	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
D	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
D	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
D	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
D	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
D	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
D	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
D	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
D	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
D	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
D	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
D	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0
D	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
D	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
D	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
D	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
D	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
D	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
D	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
D	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
D	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
D	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
D	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
E	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
E	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
E	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
E	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
E	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
E	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
E	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
E	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
E	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
E	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
E	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
E	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0
E	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
E	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
E	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
E	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
E	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
E	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
E	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
E	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
E	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
E	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
E	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
F	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
F	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
F	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
F	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
F	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
F	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
F	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
F	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
F	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
F	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
F	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
F	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
F	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0
F	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
F	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
F	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
F	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
F	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
F	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
F	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
F	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
F	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
F	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
G	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
G	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
G	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
G	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
G	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
G	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
G	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
G	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
G	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
G	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
G	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
G	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
G	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0
G	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
G	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
G	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
G	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
G	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
G	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
G	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
G	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
G	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
G	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
G	0	ALA	-	EXPRESSION TAG	UNP Q81TP0
H	-23	MSE	-	EXPRESSION TAG	UNP Q81TP0
H	-22	HIS	-	EXPRESSION TAG	UNP Q81TP0
H	-21	HIS	-	EXPRESSION TAG	UNP Q81TP0
H	-20	HIS	-	EXPRESSION TAG	UNP Q81TP0
H	-19	HIS	-	EXPRESSION TAG	UNP Q81TP0
H	-18	HIS	-	EXPRESSION TAG	UNP Q81TP0
H	-17	HIS	-	EXPRESSION TAG	UNP Q81TP0
H	-16	SER	-	EXPRESSION TAG	UNP Q81TP0
H	-15	SER	-	EXPRESSION TAG	UNP Q81TP0
H	-14	GLY	-	EXPRESSION TAG	UNP Q81TP0
H	-13	VAL	-	EXPRESSION TAG	UNP Q81TP0
H	-12	ASP	-	EXPRESSION TAG	UNP Q81TP0
H	-11	LEU	-	EXPRESSION TAG	UNP Q81TP0

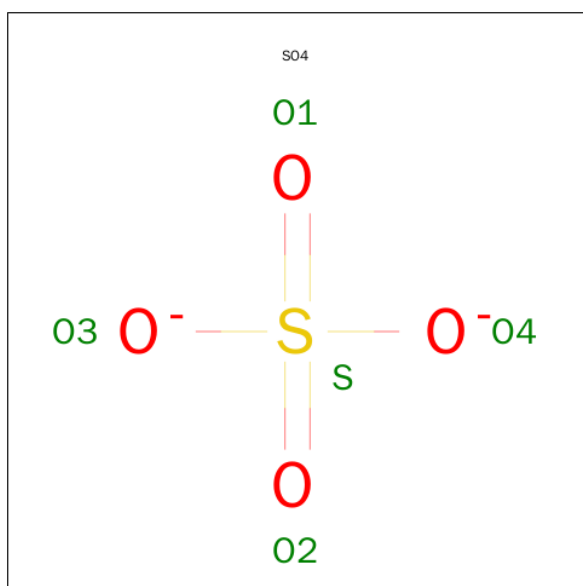
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Chain	Residue	Modelled	Actual	Comment	Reference
H	-10	GLY	-	EXPRESSION TAG	UNP Q81TP0
H	-9	THR	-	EXPRESSION TAG	UNP Q81TP0
H	-8	GLU	-	EXPRESSION TAG	UNP Q81TP0
H	-7	ASN	-	EXPRESSION TAG	UNP Q81TP0
H	-6	LEU	-	EXPRESSION TAG	UNP Q81TP0
H	-5	TYR	-	EXPRESSION TAG	UNP Q81TP0
H	-4	PHE	-	EXPRESSION TAG	UNP Q81TP0
H	-3	GLN	-	EXPRESSION TAG	UNP Q81TP0
H	-2	SER	-	EXPRESSION TAG	UNP Q81TP0
H	-1	ASN	-	EXPRESSION TAG	UNP Q81TP0
H	0	ALA	-	EXPRESSION TAG	UNP Q81TP0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	1
2	A	1	Total O S 5 4 1	0	1
2	A	1	Total O S 5 4 1	0	1
2	B	1	Total O S 5 4 1	0	1
2	B	1	Total O S 5 4 1	0	1
2	B	1	Total O S 5 4 1	0	0

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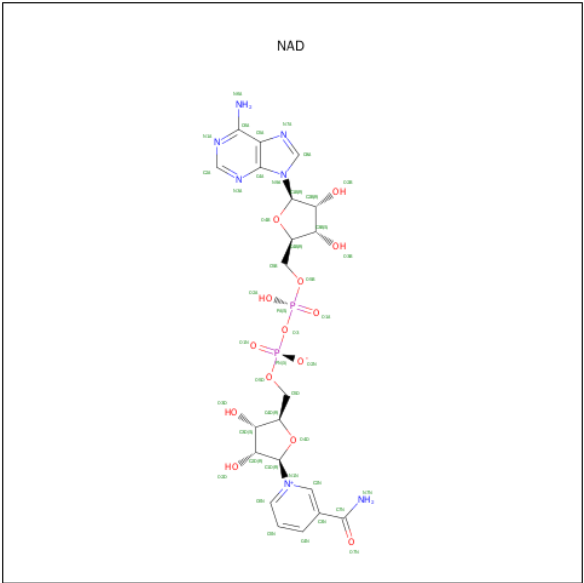
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total 5	O 4	S 1	0	1
2	C	1	Total 5	O 4	S 1	0	1
2	C	1	Total 5	O 4	S 1	0	0
2	C	1	Total 5	O 4	S 1	0	1
2	C	1	Total 5	O 4	S 1	0	0
2	C	1	Total 5	O 4	S 1	0	0
2	C	1	Total 5	O 4	S 1	0	0
2	D	1	Total 5	O 4	S 1	0	1
2	D	1	Total 5	O 4	S 1	0	1
2	D	1	Total 5	O 4	S 1	0	0
2	E	1	Total 5	O 4	S 1	0	1
2	E	1	Total 5	O 4	S 1	0	1
2	E	1	Total 5	O 4	S 1	0	0
2	E	1	Total 5	O 4	S 1	0	1
2	E	1	Total 5	O 4	S 1	0	0
2	F	1	Total 5	O 4	S 1	0	1
2	F	1	Total 5	O 4	S 1	0	1
2	F	1	Total 5	O 4	S 1	0	0
2	G	1	Total 5	O 4	S 1	0	1
2	G	1	Total 5	O 4	S 1	0	0
2	G	1	Total 5	O 4	S 1	0	1

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	1
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	1
			5	4	1		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

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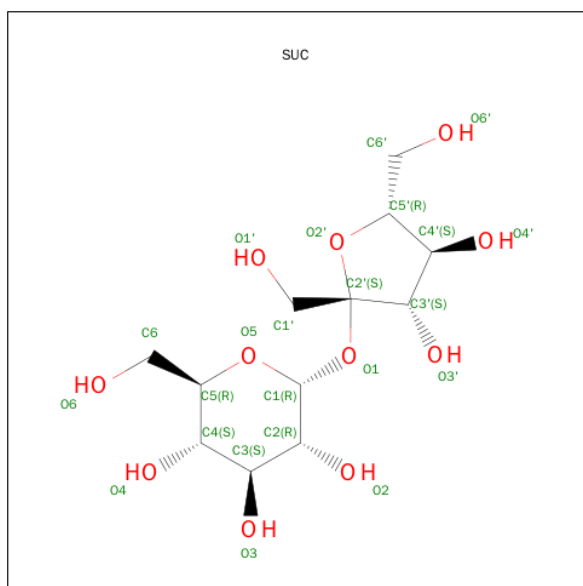
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total	Ni	0	0
			1	1		
4	B	1	Total	Ni	0	0
			1	1		
4	D	1	Total	Ni	0	0
			1	1		
4	C	1	Total	Ni	0	0
			1	1		

- Molecule 5 is SUGAR (SUCROSE) (three-letter code: SUC) (formula: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			23	12	11		
5	E	1	Total	C	O	0	0
			23	12	11		
5	F	1	Total	C	O	0	0
			23	12	11		
5	H	1	Total	C	O	0	0
			23	12	11		

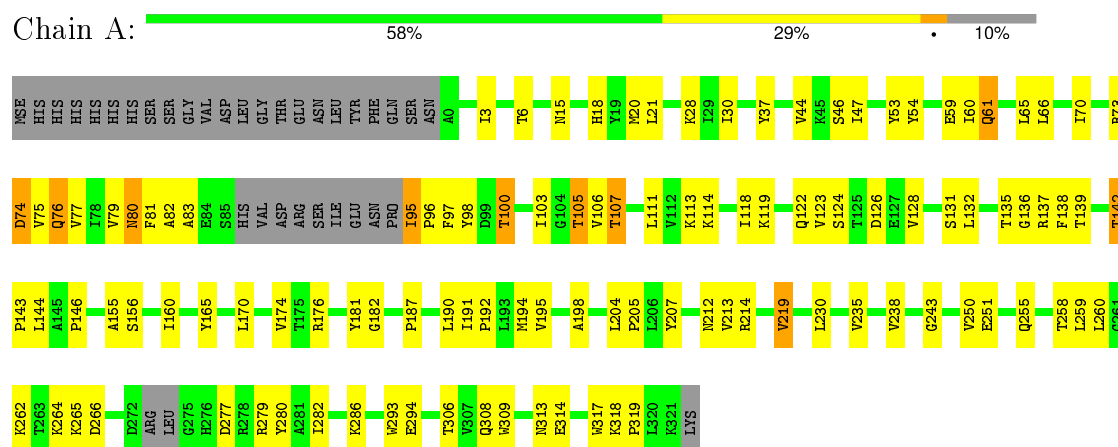
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	19	Total 19	O 19	0	0
6	B	13	Total 13	O 13	0	0
6	C	12	Total 12	O 12	0	0
6	D	9	Total 9	O 9	0	0
6	E	16	Total 16	O 16	0	0
6	F	16	Total 16	O 16	0	0
6	G	11	Total 11	O 11	0	0
6	H	11	Total 11	O 11	0	0

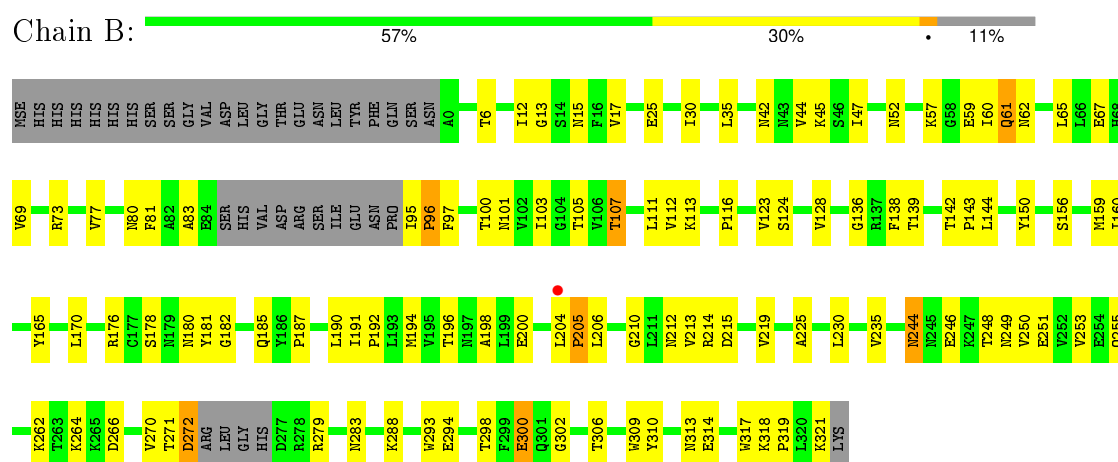
### 3 Residue-property plots

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

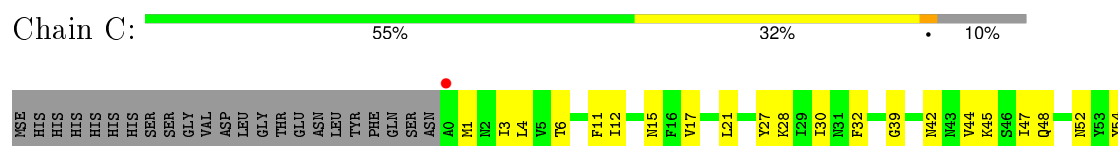
#### • Molecule 1: dTDP-glucose 4,6-dehydratase

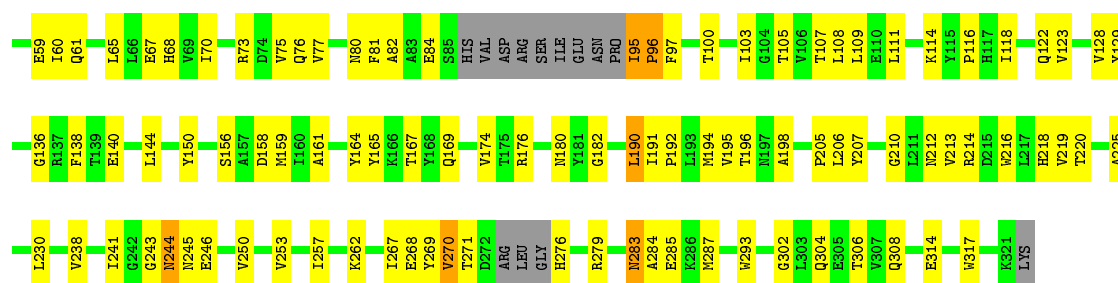


#### • Molecule 1: dTDP-glucose 4,6-dehydratase

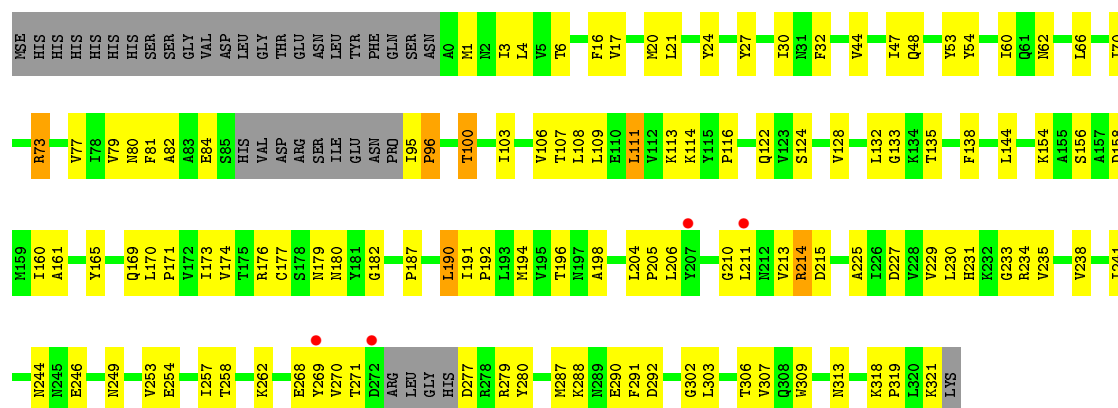


#### • Molecule 1: dTDP-glucose 4,6-dehydratase

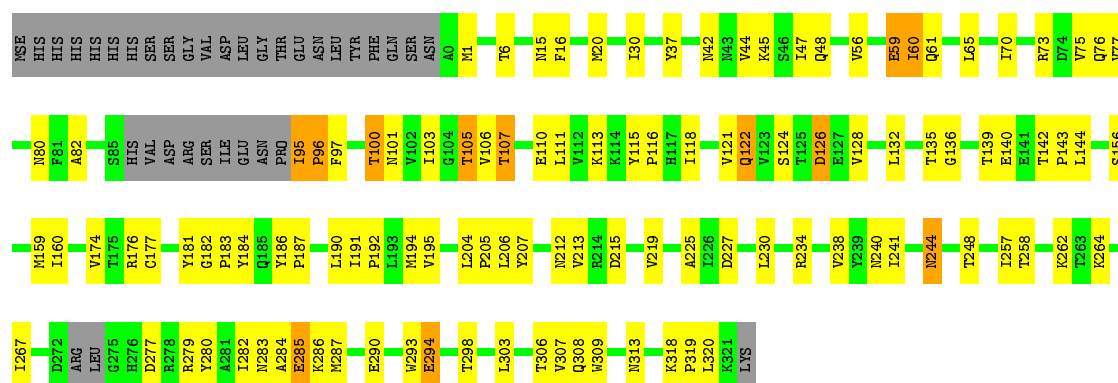




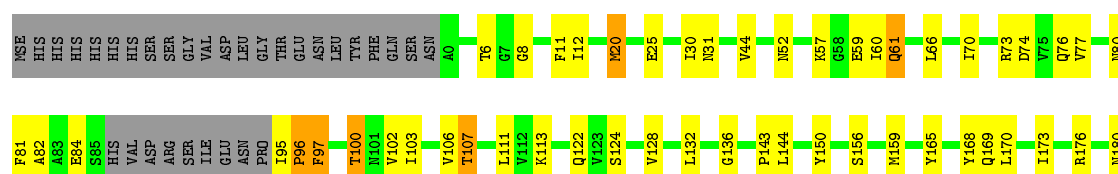
• Molecule 1: dTDP-glucose 4,6-dehydratase

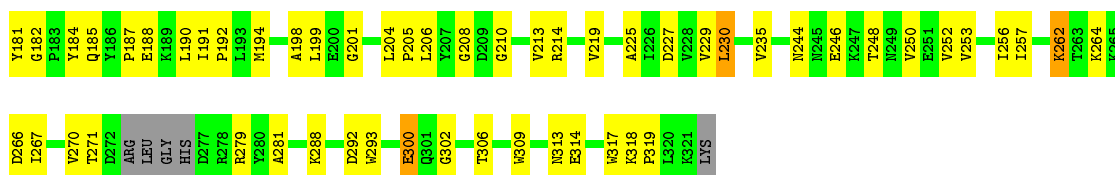


• Molecule 1: dTDP-glucose 4,6-dehydratase

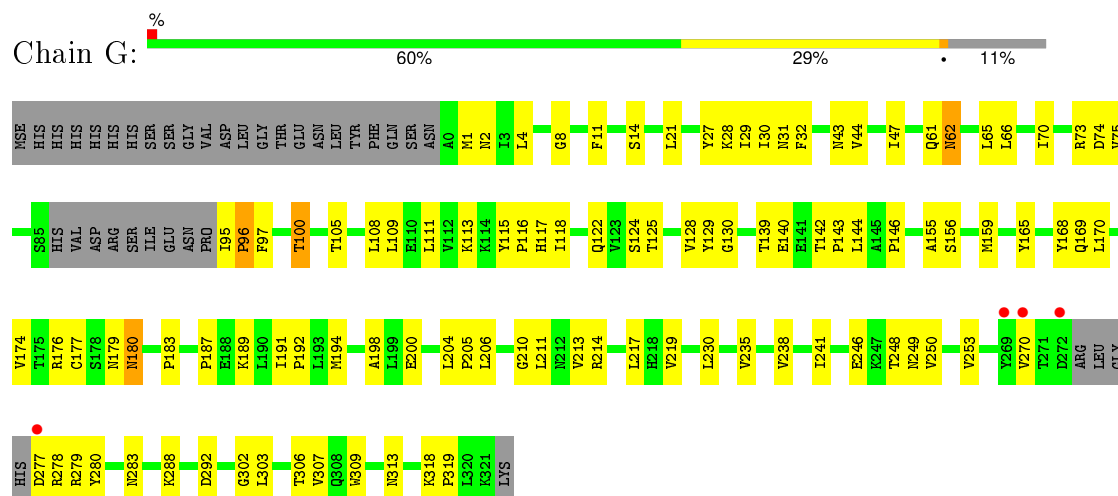


• Molecule 1: dTDP-glucose 4,6-dehydratase

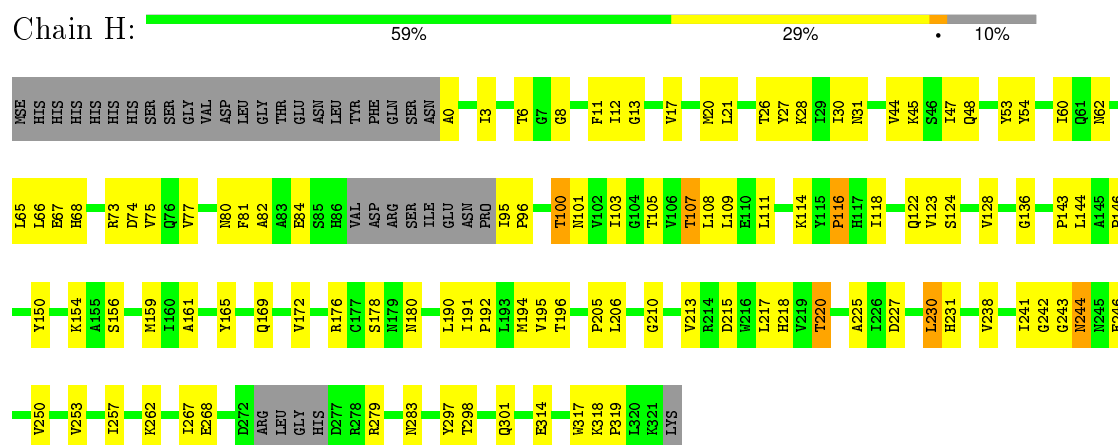




• Molecule 1: dTDP-glucose 4,6-dehydratase



• Molecule 1: dTDP-glucose 4,6-dehydratase





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	165.59Å 165.59Å 292.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.96 – 3.00 29.96 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.9 (29.96-3.00) 98.9 (29.96-3.00)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.81 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.168 , 0.228 0.176 , 0.232	Depositor DCC
$R_{free}$ test set	3872 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	60.1	Xtriage
Anisotropy	0.352	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.439 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 77084 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20705	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NI, SUC, SO4, NAD

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	0.62	0/2561	0.86	2/3469 (0.1%)
1	B	0.66	0/2540	0.90	2/3441 (0.1%)
1	C	0.61	1/2557 (0.0%)	0.87	4/3464 (0.1%)
1	D	0.61	0/2546	0.84	3/3449 (0.1%)
1	E	0.63	0/2561	0.88	5/3469 (0.1%)
1	F	0.62	0/2546	0.90	4/3449 (0.1%)
1	G	0.61	0/2546	0.84	1/3449 (0.0%)
1	H	0.62	0/2566	0.88	2/3476 (0.1%)
All	All	0.62	1/20423 (0.0%)	0.87	23/27666 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	84	GLU	CG-CD	5.78	1.60	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	230	LEU	CA-CB-CG	9.20	136.47	115.30
1	C	230	LEU	CA-CB-CG	7.97	133.64	115.30
1	D	230	LEU	CB-CA-C	-6.41	98.02	110.20
1	G	230	LEU	CA-CB-CG	6.38	129.98	115.30
1	C	230	LEU	CB-CA-C	-6.34	98.15	110.20

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	2507	0	2464	130	0
1	B	2487	0	2449	112	0
1	C	2503	0	2461	117	0
1	D	2493	0	2454	117	0
1	E	2507	0	2464	128	0
1	F	2493	0	2454	107	0
1	G	2493	0	2454	121	0
1	H	2512	0	2468	112	0
2	A	15	0	0	1	0
2	B	20	0	0	0	0
2	C	30	0	0	0	0
2	D	15	0	0	1	0
2	E	25	0	0	0	0
2	F	15	0	0	0	0
2	G	20	0	0	1	0
2	H	15	0	0	0	0
3	A	44	0	26	1	0
3	B	44	0	26	5	0
3	C	44	0	26	1	0
3	D	44	0	26	3	0
3	E	44	0	26	2	0
3	F	44	0	26	3	0
3	G	44	0	26	1	0
3	H	44	0	26	1	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	H	1	0	0	0	0
5	B	23	0	22	2	0
5	E	23	0	22	4	0
5	F	23	0	22	3	0
5	H	23	0	22	5	0
6	A	19	0	0	3	0
6	B	13	0	0	3	0
6	C	12	0	0	0	0
6	D	9	0	0	0	0
6	E	16	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	16	0	0	3	0
6	G	11	0	0	0	0
6	H	11	0	0	1	0
All	All	20705	0	19964	887	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 22.

The worst 5 of 887 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:C:128:VAL:CG1	1:C:144:LEU:HD22	1.68	1.22
1:A:70:ILE:CD1	1:A:111:LEU:HD21	1.67	1.21
1:E:128:VAL:CG1	1:E:144:LEU:HD22	1.73	1.18
1:E:95:ILE:HB	1:E:96:PRO:CD	1.75	1.17
1:G:95:ILE:HB	1:G:96:PRO:HD2	1.27	1.16

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	305/346 (88%)	282 (92%)	22 (7%)	1 (0%)	46 84
1	B	302/346 (87%)	276 (91%)	23 (8%)	3 (1%)	19 61
1	C	304/346 (88%)	283 (93%)	16 (5%)	5 (2%)	12 48
1	D	303/346 (88%)	280 (92%)	21 (7%)	2 (1%)	26 70
1	E	305/346 (88%)	276 (90%)	26 (8%)	3 (1%)	19 61
1	F	303/346 (88%)	280 (92%)	18 (6%)	5 (2%)	11 46
1	G	303/346 (88%)	274 (90%)	24 (8%)	5 (2%)	11 46

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	305/346 (88%)	283 (93%)	18 (6%)	4 (1%)	15	53
All	All	2430/2768 (88%)	2234 (92%)	168 (7%)	28 (1%)	16	56

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	96	PRO
1	E	96	PRO
1	E	285	GLU
1	F	96	PRO
1	G	96	PRO

### 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	275/302 (91%)	265 (96%)	10 (4%)	42	79
1	B	273/302 (90%)	266 (97%)	7 (3%)	54	85
1	C	275/302 (91%)	270 (98%)	5 (2%)	66	91
1	D	274/302 (91%)	267 (97%)	7 (3%)	54	85
1	E	275/302 (91%)	268 (98%)	7 (2%)	55	86
1	F	274/302 (91%)	265 (97%)	9 (3%)	45	82
1	G	274/302 (91%)	269 (98%)	5 (2%)	66	91
1	H	276/302 (91%)	272 (99%)	4 (1%)	74	93
All	All	2196/2416 (91%)	2142 (98%)	54 (2%)	55	86

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	100	THR
1	E	95	ILE
1	G	219	VAL
1	D	111	LEU

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Mol	Chain	Res	Type
1	D	180	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	244	ASN
1	D	180	ASN
1	G	313	ASN
1	C	283	ASN
1	D	48	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 47 ligands modelled in this entry, 4 are monoatomic - leaving 43 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	$\# Z  > 2$
2	SO4	A	401[B]	-	4,4,4	0.22	0	6,6,6	0.19	0
2	SO4	A	402[A]	-	4,4,4	0.07	0	6,6,6	0.18	0
2	SO4	A	403[A]	-	4,4,4	0.23	0	6,6,6	0.29	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAD	A	404	-	38,48,48	0.81	2 (5%)	47,73,73	1.92	5 (10%)
2	SO4	B	402[A]	-	4,4,4	0.17	0	6,6,6	0.18	0
2	SO4	B	403[B]	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	B	404	-	4,4,4	0.25	0	6,6,6	0.39	0
2	SO4	B	405[B]	-	4,4,4	0.18	0	6,6,6	0.19	0
5	SUC	B	406	-	24,24,24	0.37	0	36,36,36	0.99	2 (5%)
3	NAD	B	407	-	38,48,48	0.82	2 (5%)	47,73,73	2.00	6 (12%)
2	SO4	C	402[A]	-	4,4,4	0.22	0	6,6,6	0.18	0
2	SO4	C	403	-	4,4,4	0.21	0	6,6,6	0.45	0
2	SO4	C	404[B]	-	4,4,4	0.14	0	6,6,6	0.13	0
2	SO4	C	405	-	4,4,4	0.15	0	6,6,6	0.28	0
2	SO4	C	406	-	4,4,4	0.17	0	6,6,6	0.19	0
2	SO4	C	407	-	4,4,4	0.19	0	6,6,6	0.21	0
3	NAD	C	408	-	38,48,48	0.88	3 (7%)	47,73,73	2.23	7 (14%)
2	SO4	D	402[A]	-	4,4,4	0.19	0	6,6,6	0.18	0
2	SO4	D	403[B]	-	4,4,4	0.17	0	6,6,6	0.23	0
2	SO4	D	404	-	4,4,4	0.23	0	6,6,6	0.26	0
3	NAD	D	405	-	38,48,48	0.77	1 (2%)	47,73,73	2.13	6 (12%)
2	SO4	E	401[A]	-	4,4,4	0.12	0	6,6,6	0.36	0
2	SO4	E	402[B]	-	4,4,4	0.14	0	6,6,6	0.11	0
2	SO4	E	403	-	4,4,4	0.27	0	6,6,6	0.16	0
2	SO4	E	404[A]	-	4,4,4	0.14	0	6,6,6	0.11	0
2	SO4	E	405	-	4,4,4	0.14	0	6,6,6	0.08	0
5	SUC	E	406	-	24,24,24	0.49	0	36,36,36	1.22	2 (5%)
3	NAD	E	407	-	38,48,48	0.79	0	47,73,73	2.12	6 (12%)
2	SO4	F	401[B]	-	4,4,4	0.18	0	6,6,6	0.26	0
2	SO4	F	402[A]	-	4,4,4	0.13	0	6,6,6	0.22	0
2	SO4	F	403	-	4,4,4	0.17	0	6,6,6	0.44	0
5	SUC	F	404	-	24,24,24	0.39	0	36,36,36	1.37	4 (11%)
3	NAD	F	405	-	38,48,48	0.77	1 (2%)	47,73,73	1.99	7 (14%)
2	SO4	G	401[A]	-	4,4,4	0.22	0	6,6,6	0.31	0
2	SO4	G	402	-	4,4,4	0.17	0	6,6,6	0.24	0
2	SO4	G	403[B]	-	4,4,4	0.14	0	6,6,6	0.25	0
2	SO4	G	404	-	4,4,4	0.19	0	6,6,6	0.08	0
3	NAD	G	405	-	38,48,48	0.83	1 (2%)	47,73,73	1.98	5 (10%)
2	SO4	H	402[A]	-	4,4,4	0.16	0	6,6,6	0.24	0
2	SO4	H	403	-	4,4,4	0.21	0	6,6,6	0.49	0
2	SO4	H	404[B]	-	4,4,4	0.19	0	6,6,6	0.15	0
5	SUC	H	405	-	24,24,24	0.42	0	36,36,36	1.26	4 (11%)
3	NAD	H	406	-	38,48,48	0.80	1 (2%)	47,73,73	1.91	7 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	401[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	A	402[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	A	403[A]	-	-	0/0/0/0	0/0/0/0
3	NAD	A	404	-	-	0/22/62/62	0/5/5/5
2	SO4	B	402[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	B	403[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	B	404	-	-	0/0/0/0	0/0/0/0
2	SO4	B	405[B]	-	-	0/0/0/0	0/0/0/0
5	SUC	B	406	-	-	0/12/51/51	0/2/2/2
3	NAD	B	407	-	-	0/22/62/62	0/5/5/5
2	SO4	C	402[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	C	403	-	-	0/0/0/0	0/0/0/0
2	SO4	C	404[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	C	405	-	-	0/0/0/0	0/0/0/0
2	SO4	C	406	-	-	0/0/0/0	0/0/0/0
2	SO4	C	407	-	-	0/0/0/0	0/0/0/0
3	NAD	C	408	-	-	0/22/62/62	0/5/5/5
2	SO4	D	402[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	D	403[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	D	404	-	-	0/0/0/0	0/0/0/0
3	NAD	D	405	-	-	0/22/62/62	0/5/5/5
2	SO4	E	401[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	E	402[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	E	403	-	-	0/0/0/0	0/0/0/0
2	SO4	E	404[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	E	405	-	-	0/0/0/0	0/0/0/0
5	SUC	E	406	-	-	0/12/51/51	0/2/2/2
3	NAD	E	407	-	-	0/22/62/62	0/5/5/5
2	SO4	F	401[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	F	402[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	F	403	-	-	0/0/0/0	0/0/0/0
5	SUC	F	404	-	-	0/12/51/51	0/2/2/2
3	NAD	F	405	-	-	0/22/62/62	0/5/5/5
2	SO4	G	401[A]	-	-	0/0/0/0	0/0/0/0
2	SO4	G	402	-	-	0/0/0/0	0/0/0/0
2	SO4	G	403[B]	-	-	0/0/0/0	0/0/0/0
2	SO4	G	404	-	-	0/0/0/0	0/0/0/0
3	NAD	G	405	-	-	0/22/62/62	0/5/5/5
2	SO4	H	402[A]	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	H	403	-	-	0/0/0/0	0/0/0/0
2	SO4	H	404[B]	-	-	0/0/0/0	0/0/0/0
5	SUC	H	405	-	-	0/12/51/51	0/2/2/2
3	NAD	H	406	-	-	0/22/62/62	0/5/5/5

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	408	NAD	C5A-C4A	-2.01	1.36	1.40
3	A	404	NAD	C6N-N1N	2.05	1.41	1.35
3	B	407	NAD	O4D-C1D	2.08	1.43	1.41
3	B	407	NAD	C6N-N1N	2.10	1.41	1.35
3	G	405	NAD	C6N-N1N	2.25	1.41	1.35

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	405	NAD	N3A-C2A-N1A	-11.82	119.85	128.89
3	E	407	NAD	N3A-C2A-N1A	-11.71	119.93	128.89
3	C	408	NAD	N3A-C2A-N1A	-11.37	120.19	128.89
3	B	407	NAD	N3A-C2A-N1A	-10.92	120.53	128.89
3	G	405	NAD	N3A-C2A-N1A	-10.83	120.61	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

15 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401[B]	SO4	1	0
3	A	404	NAD	1	0
5	B	406	SUC	2	0
3	B	407	NAD	5	0
3	C	408	NAD	1	0
2	D	402[A]	SO4	1	0
3	D	405	NAD	3	0
5	E	406	SUC	4	0
3	E	407	NAD	2	0
5	F	404	SUC	3	0
3	F	405	NAD	3	0
2	G	401[A]	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	405	NAD	1	0
5	H	405	SUC	5	0
3	H	406	NAD	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	306/346 (88%)	0.04	0 100 100	31, 53, 80, 97	0
1	B	303/346 (87%)	0.08	1 (0%) 94 84	29, 48, 84, 106	0
1	C	305/346 (88%)	0.04	1 (0%) 94 84	31, 50, 76, 95	0
1	D	304/346 (87%)	0.13	4 (1%) 79 53	34, 53, 91, 122	0
1	E	306/346 (88%)	0.05	0 100 100	32, 52, 77, 93	0
1	F	304/346 (87%)	0.09	0 100 100	27, 48, 83, 106	0
1	G	304/346 (87%)	0.10	4 (1%) 79 53	34, 53, 89, 124	0
1	H	305/346 (88%)	0.06	0 100 100	34, 51, 75, 93	0
All	All	2437/2768 (88%)	0.07	10 (0%) 93 80	27, 51, 81, 124	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	269	TYR	3.8
1	B	204	LEU	2.7
1	D	269	TYR	2.3
1	G	272	ASP	2.3
1	D	272	ASP	2.3

### 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	SUC	E	406	23/23	0.87	0.35	3.83	63,69,81,82	23
5	SUC	H	405	23/23	0.89	0.34	3.37	67,73,76,77	23
5	SUC	B	406	23/23	0.91	0.31	2.98	74,79,86,90	23
5	SUC	F	404	23/23	0.91	0.26	1.60	67,71,73,75	23
3	NAD	H	406	44/44	0.97	0.27	0.73	41,50,55,55	0
3	NAD	A	404	44/44	0.98	0.27	0.73	44,54,63,64	0
3	NAD	F	405	44/44	0.98	0.27	0.54	48,55,64,65	0
3	NAD	D	405	44/44	0.98	0.27	0.50	40,54,62,63	0
3	NAD	C	408	44/44	0.98	0.27	0.49	38,47,55,55	0
3	NAD	E	407	44/44	0.97	0.26	0.45	41,50,63,64	0
3	NAD	G	405	44/44	0.98	0.27	0.45	47,55,61,61	0
3	NAD	B	407	44/44	0.98	0.25	0.02	49,54,62,64	0
2	SO4	A	401[B]	5/5	0.94	0.27	-0.05	36,36,38,38	5
2	SO4	A	402[A]	5/5	0.90	0.22	-0.28	60,60,63,63	5
2	SO4	C	402[A]	5/5	0.90	0.23	-0.92	36,38,40,41	5
2	SO4	D	402[A]	5/5	0.80	0.19	-1.11	87,88,88,89	5
2	SO4	E	401[A]	5/5	0.92	0.21	-1.20	41,43,44,46	5
2	SO4	B	402[A]	5/5	0.92	0.14	-4.80	51,52,53,53	5
2	SO4	F	401[B]	5/5	0.90	0.17	-	47,47,49,49	5
4	NI	H	401	1/1	0.98	0.09	-	78,78,78,78	1
2	SO4	C	405	5/5	0.91	0.19	-	66,67,68,69	5
2	SO4	F	402[A]	5/5	0.87	0.20	-	55,56,57,58	5
2	SO4	B	403[B]	5/5	0.87	0.19	-	61,61,63,64	5
2	SO4	G	403[B]	5/5	0.87	0.20	-	60,60,61,62	5
2	SO4	F	403	5/5	0.96	0.21	-	24,25,28,28	5
2	SO4	H	404[B]	5/5	0.94	0.17	-	53,54,55,55	5
2	SO4	G	402	5/5	0.89	0.17	-	59,60,62,63	5
4	NI	D	401	1/1	0.99	0.08	-	66,66,66,66	1
2	SO4	E	403	5/5	0.94	0.21	-	54,57,57,58	5
2	SO4	C	403	5/5	0.95	0.20	-	48,51,54,54	5
4	NI	B	401	1/1	0.99	0.12	-	65,65,65,65	1
2	SO4	B	404	5/5	0.97	0.17	-	47,47,49,51	5
2	SO4	D	404	5/5	0.91	0.15	-	64,67,68,68	5
2	SO4	C	404[B]	5/5	0.82	0.35	-	54,54,54,55	5
2	SO4	E	405	5/5	0.92	0.16	-	80,80,82,83	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	E	404[A]	5/5	0.86	0.30	-	64,65,66,66	5
2	SO4	E	402[B]	5/5	0.85	0.30	-	76,76,78,78	5
2	SO4	C	407	5/5	0.88	0.25	-	75,75,76,76	5
2	SO4	B	405[B]	5/5	0.89	0.37	-	60,61,62,63	5
2	SO4	D	403[B]	5/5	0.93	0.17	-	61,61,64,64	5
2	SO4	C	406	5/5	0.82	0.28	-	68,68,70,70	5
2	SO4	H	402[A]	5/5	0.92	0.20	-	36,38,39,42	5
2	SO4	G	404	5/5	0.80	0.28	-	78,78,80,80	5
2	SO4	H	403	5/5	0.95	0.23	-	47,48,50,52	5
2	SO4	G	401[A]	5/5	0.91	0.23	-	48,48,51,52	5
2	SO4	A	403[A]	5/5	0.97	0.17	-	50,51,53,53	5
4	NI	C	401	1/1	0.98	0.07	-	70,70,70,70	1

## 6.5 Other polymers

There are no such residues in this entry.