



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 09:22 PM GMT

PDB ID : 1OF6  
Title : crystal structure of the tyrosine-regulated 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase from saccharomyces cerevisiae complexed with tyrosine and manganese  
Authors : Koenig, V.; Pfeil, A.; Heinrich, G.; Braus, G.; Schneider, T.R.  
Deposited on : 2003-04-08  
Resolution : 2.10 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

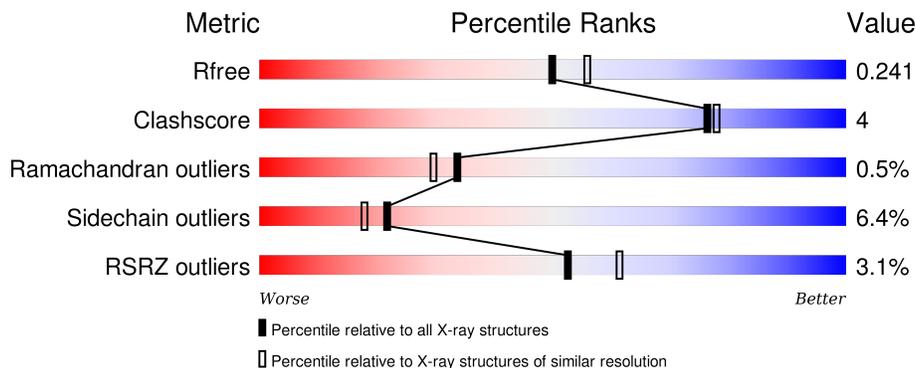
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	370	 3% 81% 12% • 5%
1	B	370	 2% 78% 12% • 6%
1	C	370	 2% 79% 14% •• 5%
1	D	370	 2% 81% 11% • 6%
1	E	370	 4% 77% 14% • 8%

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Mol	Chain	Length	Quality of chain
1	F	370	<p>2% 82% 11% • 6%</p>
1	G	370	<p>4% 71% 18% • 8%</p>
1	H	370	<p>5% 78% 15% • 6%</p>

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	DTY	A	1370	X	-	-	-
3	DTY	B	1370	X	-	-	-
3	DTY	C	1371	X	-	-	-
3	DTY	D	1370	X	-	-	-
3	DTY	E	1370	X	-	-	-
3	DTY	F	1370	X	-	-	-
3	DTY	G	1369	X	-	-	-
3	DTY	H	1369	X	-	-	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 21605 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 PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2630	1635	473	512	10			
1	B	346	Total	C	N	O	S	0	0	0
			2608	1623	466	509	10			
1	C	350	Total	C	N	O	S	0	0	0
			2634	1639	472	513	10			
1	D	349	Total	C	N	O	S	0	0	0
			2617	1627	468	512	10			
1	E	339	Total	C	N	O	S	0	0	0
			2559	1590	459	500	10			
1	F	347	Total	C	N	O	S	0	0	0
			2607	1622	467	508	10			
1	G	342	Total	C	N	O	S	0	0	0
			2572	1601	459	502	10			
1	H	347	Total	C	N	O	S	0	0	0
			2599	1615	465	509	10			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

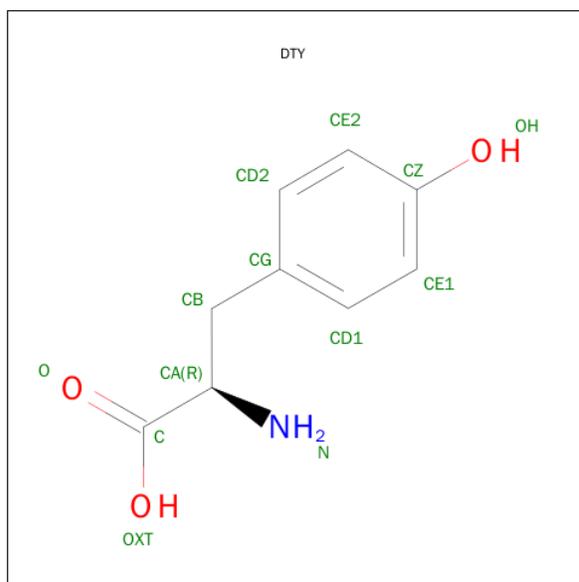
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		
2	E	1	Total	Mn	0	0
			1	1		
2	H	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	F	1	Total	Mn	0	0
			1	1		

- Molecule 3 is D-TYROSINE (three-letter code: DTY) (formula: C<sub>9</sub>H<sub>11</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			13	9	1	3		
3	B	1	Total	C	N	O	0	0
			13	9	1	3		
3	C	1	Total	C	N	O	0	0
			13	9	1	3		
3	D	1	Total	C	N	O	0	0
			13	9	1	3		
3	E	1	Total	C	N	O	0	0
			13	9	1	3		
3	F	1	Total	C	N	O	0	0
			13	9	1	3		
3	G	1	Total	C	N	O	0	0
			13	9	1	3		
3	H	1	Total	C	N	O	0	0
			13	9	1	3		

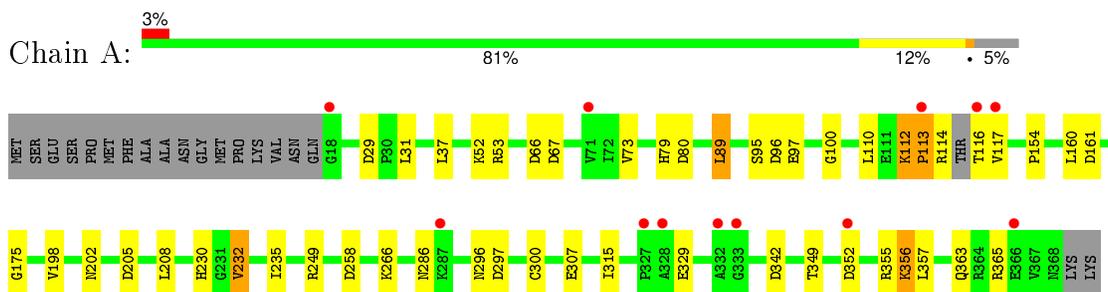
- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	106	Total 106	O 106	0	0
4	B	91	Total 91	O 91	0	0
4	C	83	Total 83	O 83	0	0
4	D	113	Total 113	O 113	0	0
4	E	63	Total 63	O 63	0	0
4	F	88	Total 88	O 88	0	0
4	G	58	Total 58	O 58	0	0
4	H	65	Total 65	O 65	0	0

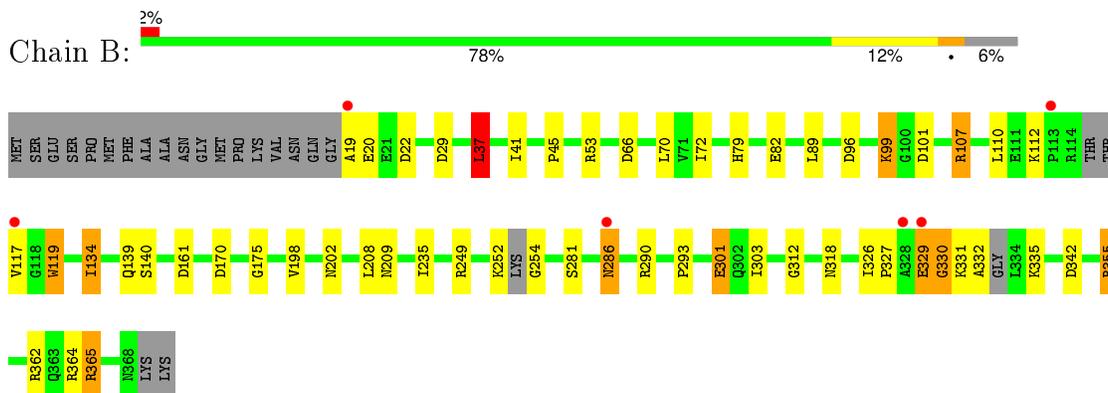
### 3 Residue-property plots [i](#)

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

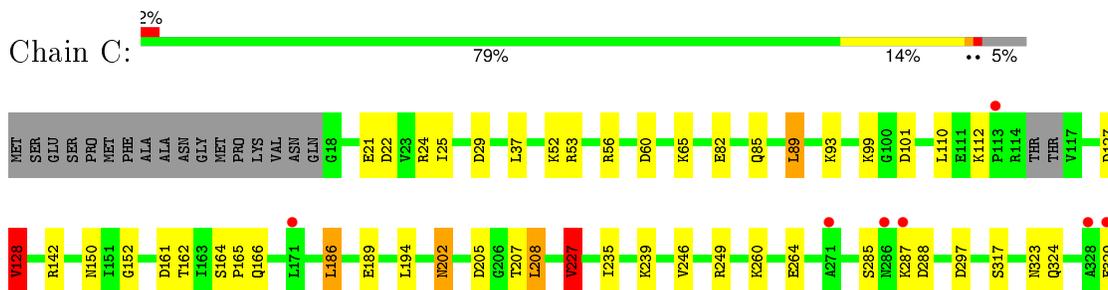
- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED



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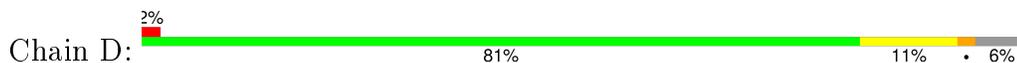


- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED

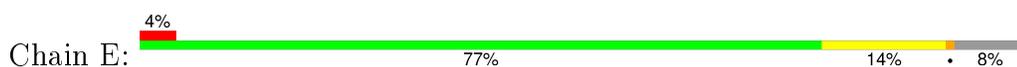




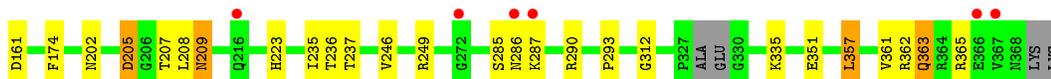
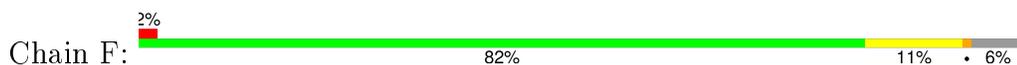
- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED



- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED

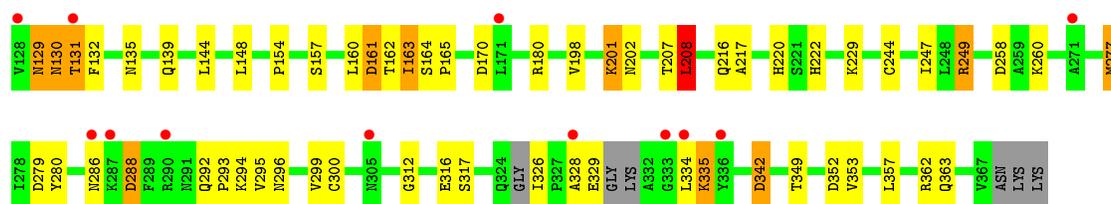


- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED

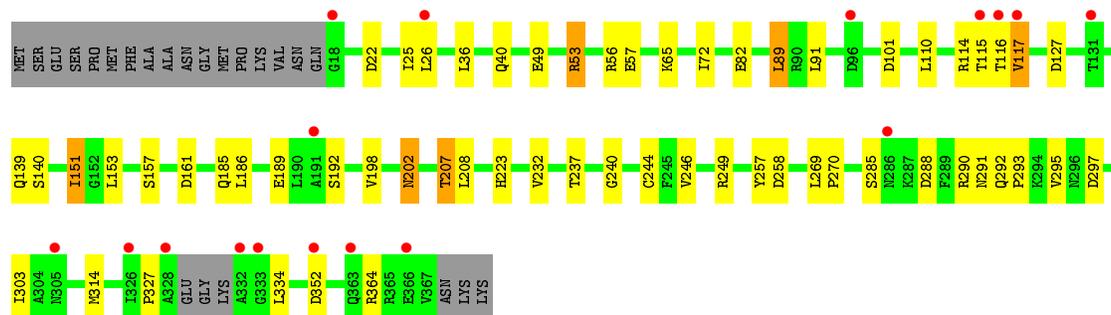
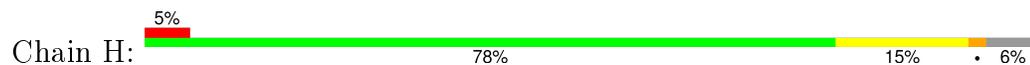


- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED





• Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, TYROSINE-INHIBITED



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.13Å 94.70Å 104.84Å 64.71° 85.51° 75.61°	Depositor
Resolution (Å)	20.00 – 2.10 19.99 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.2 (20.00-2.10) 83.4 (19.99-2.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.35 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.195 , 0.237 0.201 , 0.241	Depositor DCC
$R_{free}$ test set	4949 reflections (3.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.0	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 38.9	EDS
Estimated twinning fraction	0.001 for -h,-k,-k+l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 156678 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21605	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.70 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.6318e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: DTY, MN

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	1.12	0/2668	1.08	12/3612 (0.3%)
1	B	1.18	7/2644 (0.3%)	1.07	12/3577 (0.3%)
1	C	1.08	4/2672 (0.1%)	1.11	15/3615 (0.4%)
1	D	1.15	4/2655 (0.2%)	1.06	7/3596 (0.2%)
1	E	1.06	0/2595	1.10	11/3512 (0.3%)
1	F	1.04	1/2644 (0.0%)	1.06	6/3578 (0.2%)
1	G	1.11	4/2608 (0.2%)	1.12	17/3531 (0.5%)
1	H	1.05	1/2637 (0.0%)	1.08	8/3576 (0.2%)
All	All	1.10	21/21123 (0.1%)	1.08	88/28597 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	301	GLU	CD-OE2	8.84	1.35	1.25
1	D	301	GLU	CG-CD	8.67	1.65	1.51
1	G	201	LYS	CE-NZ	8.42	1.70	1.49
1	B	301	GLU	CD-OE1	7.46	1.33	1.25
1	B	301	GLU	CG-CD	7.08	1.62	1.51

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	161	ASP	CB-CG-OD2	10.21	127.49	118.30
1	F	161	ASP	CB-CG-OD2	8.86	126.28	118.30
1	E	161	ASP	CB-CG-OD2	8.86	126.27	118.30
1	H	161	ASP	CB-CG-OD2	8.67	126.11	118.30
1	G	279	ASP	CB-CG-OD1	8.34	125.80	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	207	THR	Peptide

## 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	2630	0	2628	17	0
1	B	2608	0	2604	18	0
1	C	2634	0	2638	21	0
1	D	2617	0	2603	23	0
1	E	2559	0	2557	20	0
1	F	2607	0	2602	17	0
1	G	2572	0	2558	36	0
1	H	2599	0	2578	21	0
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
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	13	0	9	0	0
3	B	13	0	9	0	0
3	C	13	0	9	1	0
3	D	13	0	9	0	0
3	E	13	0	9	0	0
3	F	13	0	9	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	13	0	9	0	0
3	H	13	0	9	0	0
4	A	106	0	0	1	0
4	B	91	0	0	1	0
4	C	83	0	0	0	0
4	D	113	0	0	1	0
4	E	63	0	0	0	0
4	F	88	0	0	1	0
4	G	58	0	0	2	0
4	H	65	0	0	1	0
All	All	21605	0	20840	158	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 4.

The worst 5 of 158 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:G:201:LYS:CE	1:G:201:LYS:NZ	1.70	1.53
1:D:208:LEU:HD11	1:D:246:VAL:HG11	1.56	0.88
1:A:97:GLU:OE2	1:A:355:ARG:NH1	2.08	0.86
1:D:303:ILE:O	1:D:364:ARG:HB2	1.80	0.81
1:C:208:LEU:HD21	1:C:246:VAL:HG11	1.64	0.80

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	346/370 (94%)	331 (96%)	13 (4%)	2 (1%)	30 24
1	B	338/370 (91%)	324 (96%)	11 (3%)	3 (1%)	21 15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	346/370 (94%)	334 (96%)	11 (3%)	1 (0%)	46	45
1	D	345/370 (93%)	332 (96%)	12 (4%)	1 (0%)	46	45
1	E	333/370 (90%)	314 (94%)	18 (5%)	1 (0%)	46	45
1	F	341/370 (92%)	324 (95%)	16 (5%)	1 (0%)	46	45
1	G	334/370 (90%)	311 (93%)	20 (6%)	3 (1%)	21	15
1	H	343/370 (93%)	328 (96%)	13 (4%)	2 (1%)	30	24
All	All	2726/2960 (92%)	2598 (95%)	114 (4%)	14 (0%)	34	30

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	329	GLU
1	F	286	ASN
1	G	335	LYS
1	A	329	GLU
1	B	286	ASN

### 5.3.2 Protein sidechains [i](#)

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	279/298 (94%)	261 (94%)	18 (6%)	21	17
1	B	278/298 (93%)	260 (94%)	18 (6%)	21	17
1	C	280/298 (94%)	260 (93%)	20 (7%)	18	14
1	D	277/298 (93%)	264 (95%)	13 (5%)	32	30
1	E	274/298 (92%)	256 (93%)	18 (7%)	21	17
1	F	277/298 (93%)	261 (94%)	16 (6%)	25	21
1	G	273/298 (92%)	254 (93%)	19 (7%)	19	15
1	H	275/298 (92%)	256 (93%)	19 (7%)	19	15
All	All	2213/2384 (93%)	2072 (94%)	141 (6%)	22	18

5 of 141 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	232	VAL
1	E	204	THR
1	H	117	VAL
1	D	281	SER
1	E	89	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	222	HIS
1	D	243	HIS
1	G	222	HIS
1	B	286	ASN
1	G	220	HIS

### 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 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	DTY	A	1370	-	10,13,13	1.35	1 (10%)	11,17,17	1.11	1 (9%)
3	DTY	B	1370	-	10,13,13	1.99	2 (20%)	11,17,17	0.70	0
3	DTY	C	1371	-	10,13,13	1.14	1 (10%)	11,17,17	0.48	0
3	DTY	D	1370	-	10,13,13	1.73	4 (40%)	11,17,17	1.44	2 (18%)
3	DTY	E	1370	-	10,13,13	1.05	1 (10%)	11,17,17	0.84	0
3	DTY	F	1370	-	10,13,13	1.35	1 (10%)	11,17,17	0.95	1 (9%)
3	DTY	G	1369	-	10,13,13	1.09	1 (10%)	11,17,17	0.85	0
3	DTY	H	1369	-	10,13,13	1.78	1 (10%)	11,17,17	1.09	1 (9%)

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	DTY	A	1370	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	B	1370	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	C	1371	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	D	1370	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	E	1370	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	F	1370	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	G	1369	-	1/1/2/2	0/4/8/8	0/1/1/1
3	DTY	H	1369	-	1/1/2/2	0/4/8/8	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1370	DTY	OH-CZ	-5.49	1.24	1.37
3	H	1369	DTY	OH-CZ	-4.64	1.26	1.37
3	F	1370	DTY	OH-CZ	-4.12	1.27	1.37
3	A	1370	DTY	OH-CZ	-3.89	1.27	1.37
3	E	1370	DTY	OH-CZ	-3.02	1.29	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1370	DTY	CE2-CZ-CE1	-3.19	115.24	119.79
3	A	1370	DTY	CD2-CE2-CZ	-2.20	117.32	119.87
3	F	1370	DTY	CG-CB-CA	-2.17	109.32	114.34
3	H	1369	DTY	CE1-CD1-CG	-2.07	118.20	121.04

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Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	D	1370	DTY	CD2-CE2-CZ	2.62	122.89	119.87

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	1371	DTY	CA
3	F	1370	DTY	CA
3	B	1370	DTY	CA
3	E	1370	DTY	CA
3	G	1369	DTY	CA

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1371	DTY	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 [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	350/370 (94%)	0.00	12 (3%) 49 58	31, 43, 60, 77	0
1	B	346/370 (93%)	-0.03	6 (1%) 73 78	29, 42, 56, 81	0
1	C	350/370 (94%)	0.02	9 (2%) 59 66	33, 45, 63, 83	0
1	D	349/370 (94%)	-0.03	6 (1%) 73 78	31, 40, 55, 70	0
1	E	339/370 (91%)	0.19	15 (4%) 38 47	34, 51, 66, 79	0
1	F	347/370 (93%)	0.05	9 (2%) 59 66	35, 46, 61, 71	0
1	G	342/370 (92%)	0.22	13 (3%) 44 53	35, 50, 66, 80	0
1	H	347/370 (93%)	0.10	17 (4%) 33 42	35, 46, 62, 78	0
All	All	2770/2960 (93%)	0.07	87 (3%) 52 61	29, 45, 63, 83	0

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	117	VAL	5.0
1	A	328	ALA	4.7
1	C	328	ALA	4.6
1	C	113	PRO	4.6
1	H	115	THR	4.6

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

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

### 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. 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
3	DTY	A	1370	13/13	0.96	0.13	0.50	28,33,34,34	0
3	DTY	H	1369	13/13	0.96	0.12	0.15	35,38,40,41	0
3	DTY	C	1371	13/13	0.97	0.11	-0.18	33,34,38,39	0
3	DTY	G	1369	13/13	0.97	0.11	-0.27	35,40,41,41	0
3	DTY	B	1370	13/13	0.97	0.10	-0.42	33,35,37,38	0
3	DTY	D	1370	13/13	0.96	0.09	-0.55	30,33,35,35	0
3	DTY	F	1370	13/13	0.96	0.10	-0.65	33,38,41,43	0
2	MN	H	1368	1/1	0.96	0.05	-1.51	37,37,37,37	0
2	MN	E	1369	1/1	0.99	0.05	-1.58	45,45,45,45	0
3	DTY	E	1370	13/13	0.97	0.07	-1.71	31,34,37,38	0
2	MN	A	1369	1/1	0.98	0.04	-1.83	33,33,33,33	0
2	MN	C	1370	1/1	0.96	0.03	-1.91	38,38,38,38	0
2	MN	D	1369	1/1	0.99	0.03	-1.93	30,30,30,30	0
2	MN	G	1368	1/1	0.98	0.04	-2.01	45,45,45,45	0
2	MN	B	1369	1/1	1.00	0.02	-	31,31,31,31	0
2	MN	F	1369	1/1	1.00	0.02	-	33,33,33,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.