



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 01:21 PM GMT

PDB ID : 3HDQ  
Title : Crystal structure of UDP-galactopyranose mutase (oxidized form) in complex with substrate  
Authors : Partha, S.K.; van Straaten, K.E.; Sanders, D.A.  
Deposited on : 2009-05-07  
Resolution : 2.36 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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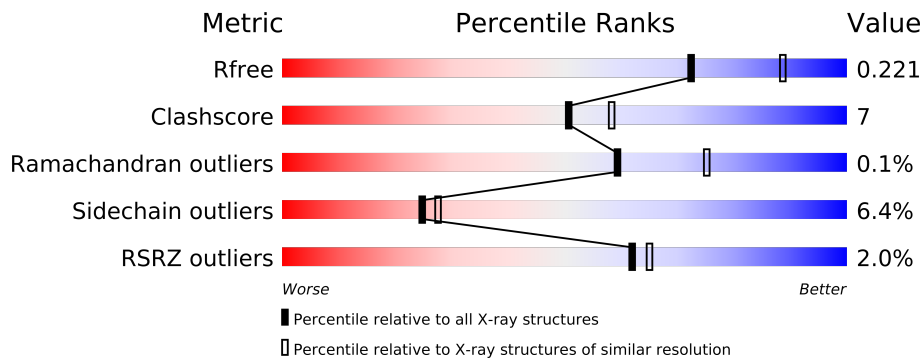
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.36 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	3327 (2.40-2.32)
Clashscore	79885	1064 (2.38-2.34)
Ramachandran outliers	78287	1048 (2.38-2.34)
Sidechain outliers	78261	1049 (2.38-2.34)
RSRZ outliers	66119	3330 (2.40-2.32)

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	397	
1	B	397	
1	C	397	
1	D	397	
1	E	397	
1	F	397	
1	G	397	
1	H	397	
1	I	397	
1	J	397	

## 2 Entry composition

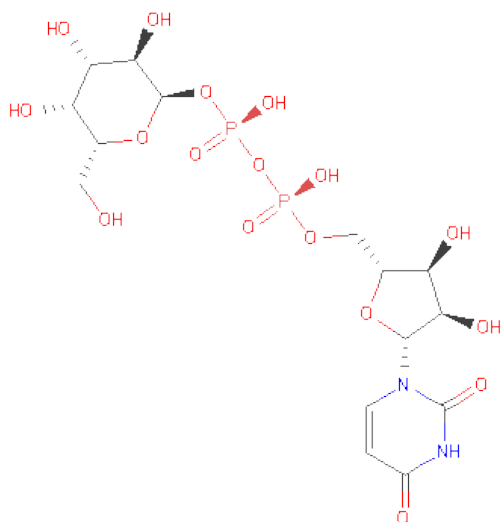
There are 4 unique types of molecules in this entry. The entry contains 31875 atoms, of which 0 are hydrogen and 0 are deuterium.

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 UDP-galactopyranose mutase.

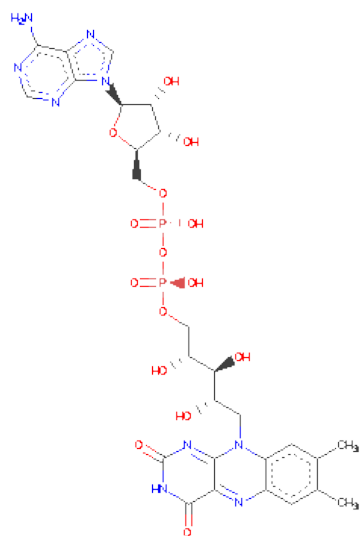
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	365	Total	C	N	O	S	0	1	0
			2992	1909	521	554	8			
1	B	364	Total	C	N	O	S	4	2	0
			2990	1909	522	551	8			
1	C	361	Total	C	N	O	S	23	1	0
			2964	1894	516	546	8			
1	D	360	Total	C	N	O	S	0	1	0
			2955	1888	514	545	8			
1	E	364	Total	C	N	O	S	8	0	0
			2975	1899	516	552	8			
1	F	363	Total	C	N	O	S	4	1	0
			2977	1901	519	549	8			
1	G	363	Total	C	N	O	S	4	1	0
			2974	1899	518	549	8			
1	H	364	Total	C	N	O	S	0	1	0
			2983	1904	520	551	8			
1	I	363	Total	C	N	O	S	4	1	0
			2975	1899	517	551	8			
1	J	361	Total	C	N	O	S	4	1	0
			2959	1890	515	546	8			

- Molecule 2 is SUGAR (GALACTOSE-URIDINE-5'-DIPHOSPHATE) (three-letter code: GDU) (formula: C<sub>15</sub>H<sub>24</sub>N<sub>2</sub>O<sub>17</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	B	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	C	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	D	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	E	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	F	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	G	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	H	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	I	1	Total	C	N	O	P	0	0
			36	15	2	17	2		
2	J	1	Total	C	N	O	P	0	0
			36	15	2	17	2		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	I	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	J	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	164	Total	O	0	0
			164	164		
4	B	104	Total	O	0	0
			104	104		

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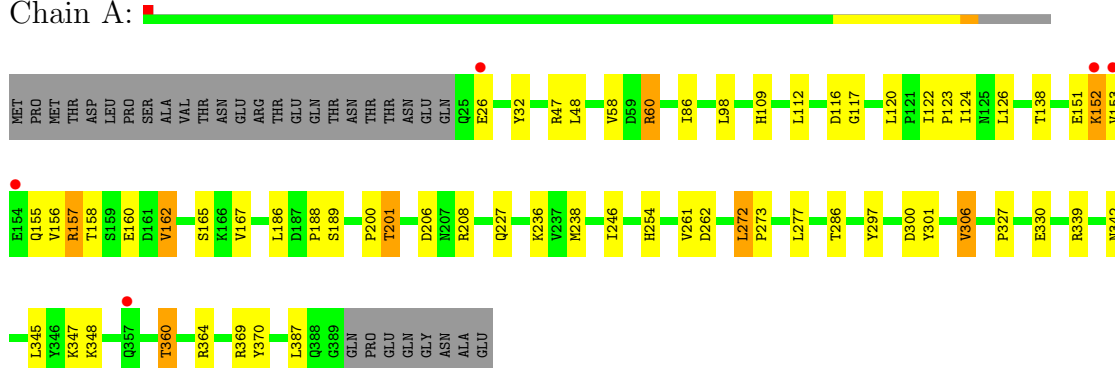
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	88	Total 88	O 88	0	0
4	D	86	Total 86	O 86	0	0
4	E	110	Total 110	O 110	0	0
4	F	143	Total 143	O 143	0	0
4	G	116	Total 116	O 116	0	0
4	H	143	Total 143	O 143	0	0
4	I	160	Total 160	O 160	0	0
4	J	127	Total 127	O 127	0	0

### 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.

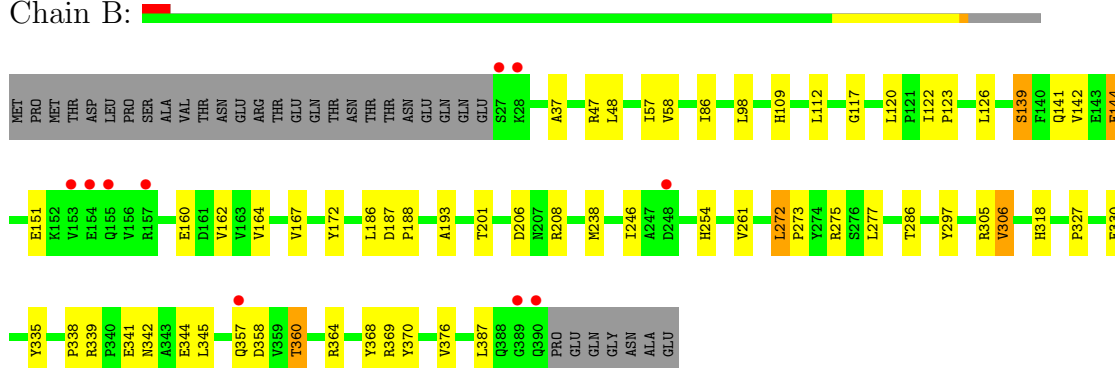
#### • Molecule 1: UDP-galactopyranose mutase

Chain A:



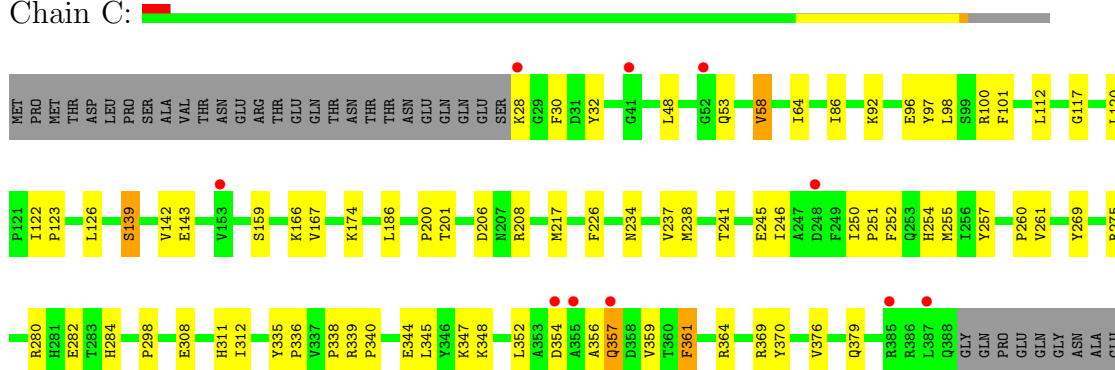
#### • Molecule 1: UDP-galactopyranose mutase

Chain B:



#### • Molecule 1: UDP-galactopyranose mutase

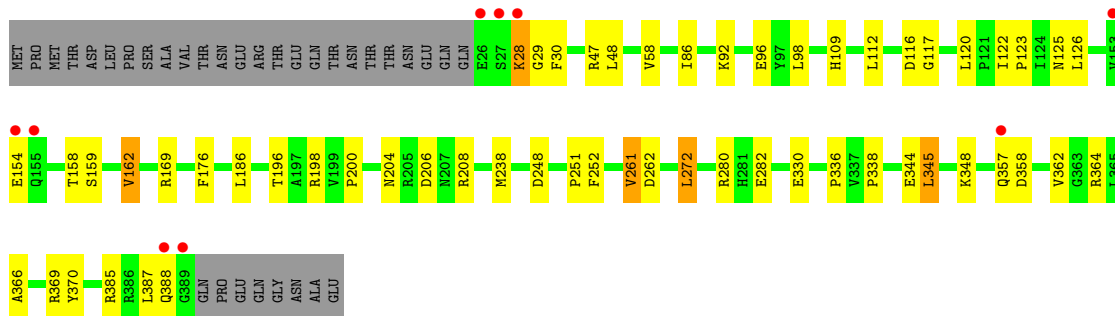
Chain C:



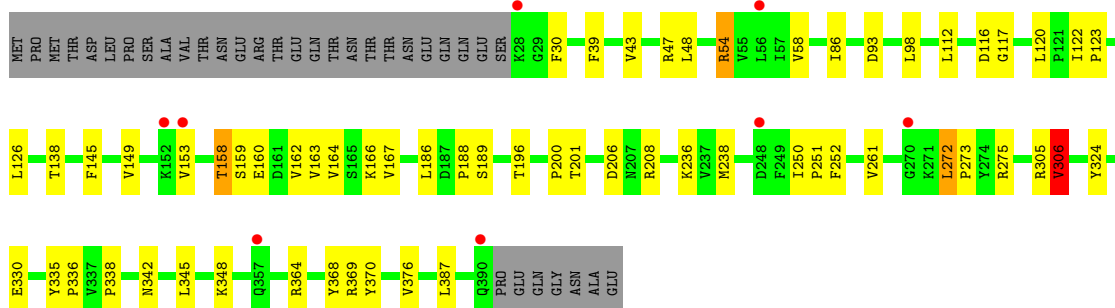
Chain D: 



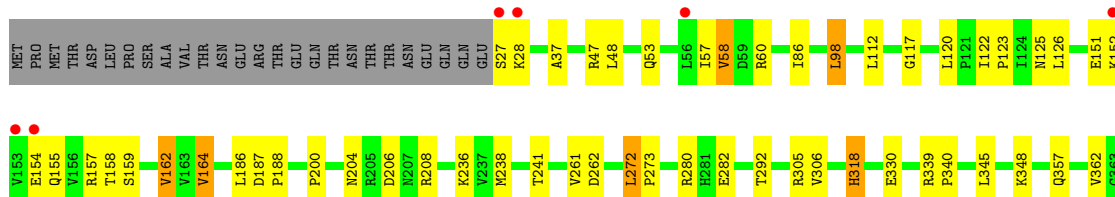
Chain E: 

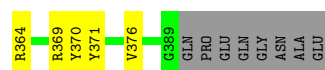


Chain F:



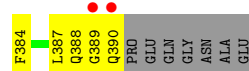
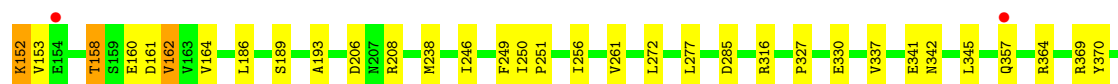
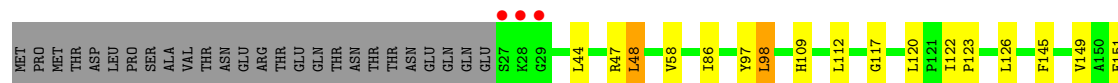
Chain G: 





• Molecule 1: UDP-galactopyranose mutase

Chain H:



• Molecule 1: UDP-galactopyranose mutase

Chain I:



• Molecule 1: UDP-galactopyranose mutase

Chain J:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.02Å 176.65Å 220.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 2.36 19.88 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.88-2.36) 97.8 (19.88-2.30)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.50 (at 2.30Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.177 , 0.226 0.177 , 0.221	Depositor DCC
$R_{free}$ test set	11274 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.7	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 29.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 225489 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	31875	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.70% 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: GDU, FAD

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	0.43	0/3079	0.58	0/4185
1	B	0.39	0/3081	0.56	0/4188
1	C	0.35	0/3051	0.54	0/4148
1	D	0.40	0/3042	0.54	0/4137
1	E	0.34	0/3059	0.52	0/4159
1	F	0.38	0/3064	0.56	1/4165 (0.0%)
1	G	0.41	0/3061	0.54	0/4161
1	H	0.39	0/3070	0.54	0/4173
1	I	0.41	0/3059	0.57	1/4159 (0.0%)
1	J	0.39	0/3046	0.55	1/4142 (0.0%)
All	All	0.39	0/30612	0.55	3/41617 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	306	VAL	CB-CA-C	-5.47	101.01	111.40
1	F	306	VAL	CB-CA-C	-5.33	101.27	111.40
1	J	306	VAL	CB-CA-C	-5.05	101.81	111.40

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	2992	0	2867	50	0
1	B	2990	0	2868	44	0
1	C	2964	0	2845	56	0
1	D	2955	0	2832	45	0
1	E	2975	0	2846	36	0
1	F	2977	0	2856	41	0
1	G	2974	0	2853	36	0
1	H	2983	0	2861	47	0
1	I	2975	0	2847	50	0
1	J	2959	0	2835	67	0
2	A	36	0	22	0	0
2	B	36	0	22	3	0
2	C	36	0	22	1	0
2	D	36	0	22	3	0
2	E	36	0	22	1	0
2	F	36	0	22	2	0
2	G	36	0	22	3	0
2	H	36	0	22	1	0
2	I	36	0	22	4	0
2	J	36	0	22	2	0
3	A	53	0	30	1	0
3	B	53	0	31	2	0
3	C	53	0	30	1	0
3	D	53	0	31	0	0
3	E	53	0	31	0	0
3	F	53	0	29	1	0
3	G	53	0	31	3	0
3	H	53	0	31	0	0
3	I	53	0	31	1	0
3	J	53	0	30	1	0
4	A	164	0	0	2	0
4	B	104	0	0	3	0
4	C	88	0	0	2	0
4	D	86	0	0	1	0
4	E	110	0	0	3	0
4	F	143	0	0	0	0
4	G	116	0	0	1	0
4	H	143	0	0	0	0
4	I	160	0	0	2	0
4	J	127	0	0	0	0
All	All	31875	0	29035	438	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 7.

The worst 5 of 438 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:152:LYS:CD	1:A:153:VAL:H	1.54	1.18
1:J:357:GLN:HA	1:J:357:GLN:HE21	1.15	1.10
1:A:152:LYS:HD3	1:A:153:VAL:N	1.72	1.04
1:E:58:VAL:HG22	1:E:238:MET:HB3	1.42	1.01
1:H:152:LYS:HA	1:H:152:LYS:HE2	1.38	1.01

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	364/397 (92%)	355 (98%)	9 (2%)	0	100	100
1	B	364/397 (92%)	352 (97%)	12 (3%)	0	100	100
1	C	360/397 (91%)	347 (96%)	13 (4%)	0	100	100
1	D	359/397 (90%)	345 (96%)	13 (4%)	1 (0%)	50	62
1	E	362/397 (91%)	353 (98%)	9 (2%)	0	100	100
1	F	362/397 (91%)	356 (98%)	6 (2%)	0	100	100
1	G	362/397 (91%)	355 (98%)	6 (2%)	1 (0%)	50	62
1	H	363/397 (91%)	353 (97%)	10 (3%)	0	100	100
1	I	362/397 (91%)	353 (98%)	9 (2%)	0	100	100
1	J	360/397 (91%)	353 (98%)	7 (2%)	0	100	100
All	All	3618/3970 (91%)	3522 (97%)	94 (3%)	2 (0%)	59	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	340	PRO

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Mol	Chain	Res	Type
1	G	154	GLU

### 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	318/346 (92%)	292 (92%)	26 (8%)	17	18
1	B	318/346 (92%)	299 (94%)	19 (6%)	27	32
1	C	315/346 (91%)	294 (93%)	21 (7%)	23	26
1	D	314/346 (91%)	294 (94%)	20 (6%)	25	27
1	E	316/346 (91%)	298 (94%)	18 (6%)	29	34
1	F	316/346 (91%)	296 (94%)	20 (6%)	25	29
1	G	316/346 (91%)	294 (93%)	22 (7%)	21	23
1	H	317/346 (92%)	301 (95%)	16 (5%)	34	42
1	I	316/346 (91%)	294 (93%)	22 (7%)	21	23
1	J	314/346 (91%)	295 (94%)	19 (6%)	26	31
All	All	3160/3460 (91%)	2957 (94%)	203 (6%)	25	27

5 of 203 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	126	LEU
1	F	159	SER
1	J	120	LEU
1	E	186	LEU
1	E	387	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	388	GLN
1	F	390	GLN
1	H	388	GLN

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Mol	Chain	Res	Type
1	E	357	GLN
1	H	284	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 ⓘ

20 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	FAD	A	450	-	58,58,58	1.78	17 (29%)	85,89,89	2.13	15 (17%)
2	GDU	A	500	-	38,38,38	2.76	5 (13%)	54,58,58	4.07	14 (25%)
3	FAD	B	450	-	58,58,58	1.69	14 (24%)	85,89,89	2.02	17 (20%)
2	GDU	B	500	-	38,38,38	2.72	4 (10%)	54,58,58	4.14	16 (29%)
3	FAD	C	450	-	58,58,58	1.82	18 (31%)	85,89,89	2.04	22 (25%)
2	GDU	C	500	-	38,38,38	2.75	6 (15%)	54,58,58	4.15	16 (29%)
3	FAD	D	450	-	58,58,58	1.70	14 (24%)	85,89,89	2.15	20 (23%)
2	GDU	D	500	-	38,38,38	2.76	6 (15%)	54,58,58	4.23	19 (35%)
3	FAD	E	450	-	58,58,58	1.68	12 (20%)	85,89,89	1.95	17 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	GDU	E	500	-	38,38,38	2.75	5 (13%)	54,58,58	4.14	16 (29%)
3	FAD	F	450	-	58,58,58	1.76	16 (27%)	85,89,89	1.87	14 (16%)
2	GDU	F	500	-	38,38,38	2.76	5 (13%)	54,58,58	4.18	18 (33%)
3	FAD	G	450	-	58,58,58	1.59	11 (18%)	85,89,89	1.88	16 (18%)
2	GDU	G	500	-	38,38,38	2.70	5 (13%)	54,58,58	4.20	18 (33%)
3	FAD	H	450	-	58,58,58	1.77	15 (25%)	85,89,89	1.74	14 (16%)
2	GDU	H	500	-	38,38,38	2.82	6 (15%)	54,58,58	4.03	14 (25%)
3	FAD	I	450	-	58,58,58	1.73	16 (27%)	85,89,89	1.92	15 (17%)
2	GDU	I	500	-	38,38,38	2.73	5 (13%)	54,58,58	4.31	17 (31%)
3	FAD	J	450	-	58,58,58	1.78	13 (22%)	85,89,89	1.85	14 (16%)
2	GDU	J	500	-	38,38,38	2.77	5 (13%)	54,58,58	4.22	15 (27%)

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	FAD	A	450	-	-	0/34/50/50	0/1/6/6
2	GDU	A	500	-	-	0/21/59/59	0/3/3/3
3	FAD	B	450	-	-	0/34/50/50	0/1/6/6
2	GDU	B	500	-	-	0/21/59/59	0/3/3/3
3	FAD	C	450	-	-	0/34/50/50	0/1/6/6
2	GDU	C	500	-	-	0/21/59/59	0/3/3/3
3	FAD	D	450	-	-	0/34/50/50	0/1/6/6
2	GDU	D	500	-	-	0/21/59/59	0/3/3/3
3	FAD	E	450	-	-	0/34/50/50	0/1/6/6
2	GDU	E	500	-	-	0/21/59/59	0/3/3/3
3	FAD	F	450	-	-	0/34/50/50	0/1/6/6
2	GDU	F	500	-	-	0/21/59/59	0/3/3/3
3	FAD	G	450	-	-	0/34/50/50	0/1/6/6
2	GDU	G	500	-	-	0/21/59/59	0/3/3/3
3	FAD	H	450	-	-	0/34/50/50	0/1/6/6
2	GDU	H	500	-	-	0/21/59/59	0/3/3/3
3	FAD	I	450	-	-	0/34/50/50	0/1/6/6
2	GDU	I	500	-	-	0/21/59/59	0/3/3/3
3	FAD	J	450	-	-	0/34/50/50	0/1/6/6
2	GDU	J	500	-	-	0/21/59/59	0/3/3/3

The worst 5 of 198 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	GDU	C2-N1	-11.82	1.25	1.38
2	J	500	GDU	C2-N1	-11.65	1.25	1.38
2	H	500	GDU	C2-N1	-11.57	1.25	1.38
2	F	500	GDU	C2-N1	-11.38	1.26	1.38
2	I	500	GDU	C2-N1	-11.37	1.26	1.38

The worst 5 of 327 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	500	GDU	N3-C2-N1	25.17	136.98	115.97
2	A	500	GDU	N3-C2-N1	25.11	136.93	115.97
2	J	500	GDU	N3-C2-N1	25.09	136.91	115.97
2	F	500	GDU	N3-C2-N1	24.79	136.66	115.97
2	B	500	GDU	N3-C2-N1	24.76	136.64	115.97

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	365/397 (91%)	-0.45	5 (1%) 72 76	20, 30, 46, 75	0
1	B	364/397 (91%)	-0.33	10 (2%) 52 55	23, 34, 54, 80	1 (0%)
1	C	361/397 (90%)	-0.08	10 (2%) 50 54	25, 39, 64, 82	6 (1%)
1	D	360/397 (90%)	-0.17	10 (2%) 50 54	20, 41, 65, 81	0
1	E	364/397 (91%)	-0.32	9 (2%) 54 58	24, 37, 57, 98	2 (0%)
1	F	363/397 (91%)	-0.39	8 (2%) 59 62	20, 32, 51, 75	1 (0%)
1	G	363/397 (91%)	-0.32	6 (1%) 67 70	20, 35, 55, 78	1 (0%)
1	H	364/397 (91%)	-0.37	7 (1%) 64 66	20, 32, 52, 76	0
1	I	363/397 (91%)	-0.41	3 (0%) 83 86	20, 32, 47, 70	1 (0%)
1	J	361/397 (90%)	-0.26	5 (1%) 72 76	20, 35, 59, 81	1 (0%)
All	All	3628/3970 (91%)	-0.31	73 (2%) 62 65	20, 34, 58, 98	13 (0%)

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	26	GLU	7.2
1	D	357	GLN	5.7
1	D	153	VAL	5.7
1	H	27	SER	5.4
1	F	153	VAL	5.2

### 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(Å <sup>2</sup> )	Q<0.9
2	GDU	I	500	36/36	0.15	1.92	29,34,54,58	0
2	GDU	B	500	36/36	0.15	1.68	31,39,57,61	0
2	GDU	D	500	36/36	0.15	1.43	35,44,65,69	0
2	GDU	H	500	36/36	0.14	1.40	25,31,48,52	0
2	GDU	E	500	36/36	0.14	1.33	28,36,55,58	0
2	GDU	J	500	36/36	0.14	1.25	25,32,54,57	0
2	GDU	G	500	36/36	0.13	0.95	31,36,40,43	11
2	GDU	F	500	36/36	0.13	0.83	26,35,50,53	0
2	GDU	A	500	36/36	0.12	0.70	25,29,32,34	12
2	GDU	C	500	36/36	0.13	0.41	29,39,63,64	0
3	FAD	C	450	53/53	0.13	-0.06	23,29,36,51	0
3	FAD	E	450	53/53	0.10	-0.35	23,29,36,51	0
3	FAD	D	450	53/53	0.10	-0.46	23,29,36,51	0
3	FAD	J	450	53/53	0.11	-0.48	23,29,36,51	0
3	FAD	G	450	53/53	0.10	-0.59	23,29,36,51	0
3	FAD	B	450	53/53	0.08	-0.73	23,29,36,51	0
3	FAD	H	450	53/53	0.09	-0.78	23,29,36,51	0
3	FAD	F	450	53/53	0.08	-1.02	23,29,36,51	0
3	FAD	I	450	53/53	0.08	-1.15	23,29,36,51	0
3	FAD	A	450	53/53	0.08	-1.17	23,29,36,51	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.