



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 02:02 am GMT

PDB ID : 1A9Z  
Title : UDP-GALACTOSE 4-EPIMERASE MUTANT S124A/Y149F COM-  
PLEXED WITH UDP-GALACTOSE  
Authors : Thoden, J.B.; Holden, H.M.  
Deposited on : 1998-04-14  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

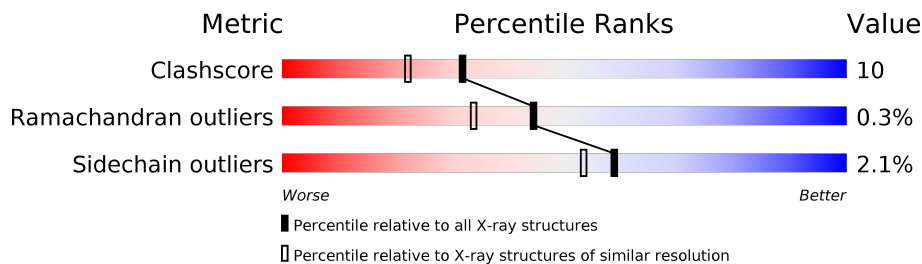
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	338	

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
4	UPG	A	341	X	-	-	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3257 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 UDP-GALACTOSE 4-EPIMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2623	1655	463	493	12			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	124	ALA	SER	ENGINEERED	UNP P09147
A	131	ASN	GLN	CONFLICT	UNP P09147
A	149	PHE	TYR	ENGINEERED	UNP P09147

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

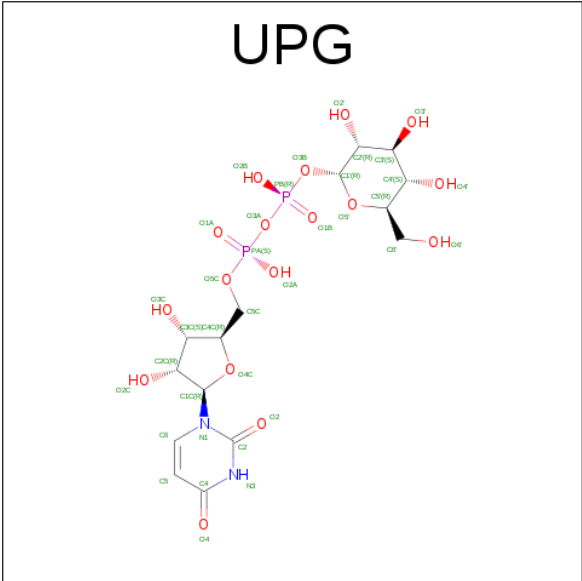
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Na	0	0
			3	3		

- 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>).



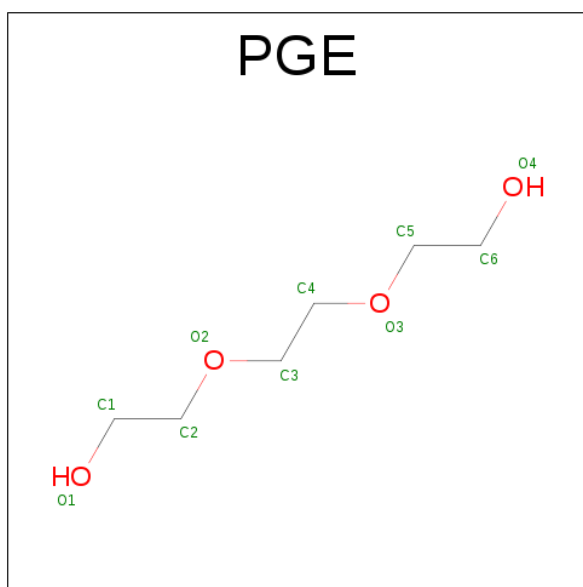
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is URIDINE-5'-DIPHOSPHATE-GLUCOSE (three-letter code: UPG) (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
4	A	1	Total	C	N	O	P	0	0
			36	15	2	17	2		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 6 is water.

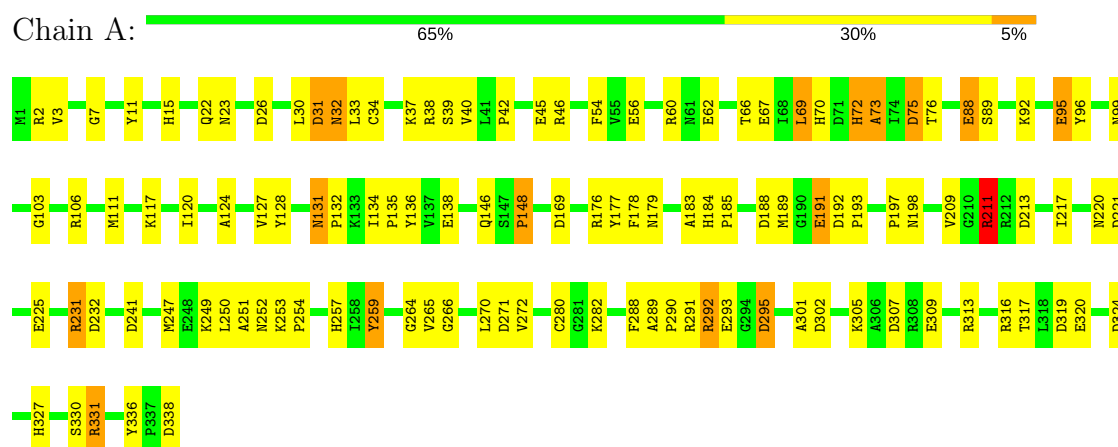
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	541	Total	O	0	0
			541	541		

### 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 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.

Note EDS was not executed.

#### • Molecule 1: UDP-GALACTOSE 4-EPIMERASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.90Å 83.90Å 108.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.90	Depositor
% Data completeness (in resolution range)	91.0 (30.00-1.90)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	TNT V. 5-E	Depositor
R, $R_{free}$	0.188 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3257	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UPG, PGE, NAD, NA

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	0.80	13/2689 (0.5%)	1.61	65/3659 (1.8%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	249	LYS	CE-NZ	-9.39	1.25	1.49
1	A	62	GLU	CD-OE1	6.28	1.32	1.25
1	A	225	GLU	CD-OE2	6.22	1.32	1.25
1	A	191	GLU	CD-OE1	6.00	1.32	1.25
1	A	293	GLU	CD-OE1	5.97	1.32	1.25
1	A	56	GLU	CD-OE2	5.88	1.32	1.25
1	A	225	GLU	CD-OE1	-5.86	1.19	1.25
1	A	138	GLU	CD-OE1	5.68	1.31	1.25
1	A	88	GLU	CD-OE2	5.62	1.31	1.25
1	A	95	GLU	CD-OE1	5.62	1.31	1.25
1	A	45	GLU	CD-OE1	5.35	1.31	1.25
1	A	309	GLU	CD-OE1	5.31	1.31	1.25
1	A	67	GLU	CD-OE1	5.15	1.31	1.25

All (65) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	291	ARG	NE-CZ-NH1	12.30	126.45	120.30
1	A	211	ARG	NE-CZ-NH1	10.96	125.78	120.30
1	A	292	ARG	NE-CZ-NH2	-10.21	115.20	120.30
1	A	292	ARG	NE-CZ-NH1	9.75	125.17	120.30
1	A	324	ASP	CB-CG-OD2	-8.90	110.29	118.30
1	A	106	ARG	NE-CZ-NH2	-8.65	115.97	120.30
1	A	295	ASP	CB-CG-OD2	-8.57	110.58	118.30
1	A	307	ASP	CB-CG-OD1	-8.05	111.05	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	241	ASP	CB-CG-OD2	-7.98	111.12	118.30
1	A	76	THR	CA-CB-CG2	-7.90	101.34	112.40
1	A	38	ARG	NE-CZ-NH1	7.83	124.21	120.30
1	A	188	ASP	CB-CG-OD1	-7.66	111.41	118.30
1	A	26	ASP	CB-CG-OD1	-7.61	111.45	118.30
1	A	302	ASP	CB-CG-OD2	7.60	125.14	118.30
1	A	54	PHE	CB-CG-CD2	-7.47	115.57	120.80
1	A	31	ASP	CB-CG-OD2	7.46	125.02	118.30
1	A	136	TYR	CB-CG-CD1	7.34	125.41	121.00
1	A	259	TYR	CB-CG-CD2	-7.12	116.73	121.00
1	A	131	ASN	N-CA-CB	6.98	123.16	110.60
1	A	136	TYR	CB-CG-CD2	-6.94	116.84	121.00
1	A	31	ASP	CB-CG-OD1	-6.80	112.18	118.30
1	A	192	ASP	CB-CG-OD2	-6.76	112.21	118.30
1	A	46	ARG	NE-CZ-NH2	-6.75	116.92	120.30
1	A	176	ARG	NE-CZ-NH2	-6.59	117.00	120.30
1	A	259	TYR	CB-CG-CD1	6.52	124.91	121.00
1	A	313	ARG	NE-CZ-NH1	6.37	123.49	120.30
1	A	221	ASP	CB-CG-OD2	6.37	124.03	118.30
1	A	271	ASP	CB-CG-OD1	6.36	124.02	118.30
1	A	46	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	A	324	ASP	CB-CG-OD1	6.25	123.92	118.30
1	A	319	ASP	CB-CG-OD2	-6.21	112.71	118.30
1	A	319	ASP	CB-CG-OD1	6.13	123.82	118.30
1	A	60	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	A	231	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	A	307	ASP	CB-CG-OD2	5.98	123.69	118.30
1	A	251	ALA	N-CA-CB	5.93	118.41	110.10
1	A	26	ASP	CB-CG-OD2	5.91	123.62	118.30
1	A	272	VAL	CA-CB-CG1	5.88	119.72	110.90
1	A	128	TYR	CB-CG-CD2	-5.88	117.47	121.00
1	A	75	ASP	CB-CG-OD1	-5.82	113.07	118.30
1	A	197	PRO	N-CA-CB	5.78	110.23	103.30
1	A	54	PHE	CB-CA-C	-5.77	98.87	110.40
1	A	178	PHE	CB-CG-CD2	5.76	124.83	120.80
1	A	317	THR	CA-CB-CG2	-5.72	104.39	112.40
1	A	69	LEU	CB-CG-CD1	-5.67	101.36	111.00
1	A	66	THR	CA-CB-CG2	-5.67	104.47	112.40
1	A	178	PHE	CB-CA-C	5.67	121.73	110.40
1	A	221	ASP	CB-CG-OD1	-5.59	113.27	118.30
1	A	232	ASP	CB-CG-OD2	5.53	123.27	118.30
1	A	225	GLU	CB-CA-C	-5.52	99.35	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	54	PHE	CB-CG-CD1	5.49	124.64	120.80
1	A	177	TYR	CB-CA-C	-5.46	99.49	110.40
1	A	177	TYR	CB-CG-CD2	-5.44	117.73	121.00
1	A	213	ASP	CB-CG-OD1	5.41	123.17	118.30
1	A	257	HIS	N-CA-CB	-5.34	100.98	110.60
1	A	192	ASP	CB-CG-OD1	5.29	123.06	118.30
1	A	331	ARG	NE-CZ-NH1	5.27	122.93	120.30
1	A	111	MET	CA-CB-CG	-5.25	104.38	113.30
1	A	73	ALA	N-CA-CB	-5.24	102.76	110.10
1	A	169	ASP	CB-CG-OD1	-5.23	113.59	118.30
1	A	148	PRO	N-CA-CB	5.23	109.57	103.30
1	A	330	SER	CB-CA-C	5.19	119.95	110.10
1	A	96	TYR	CA-CB-CG	-5.17	103.57	113.40
1	A	211	ARG	NH1-CZ-NH2	-5.13	113.76	119.40
1	A	72	HIS	CA-CB-CG	-5.05	105.01	113.60

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	2623	0	2555	54	0
2	A	3	0	0	0	0
3	A	44	0	26	0	0
4	A	36	0	22	0	0
5	A	10	0	14	5	0
6	A	541	0	0	9	3
All	All	3257	0	2617	54	3

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 10.

All (54) 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:253:LYS:NZ	5:A:410:PGE:H22	1.80	0.95
1:A:253:LYS:HZ3	5:A:410:PGE:H22	1.41	0.82
1:A:327:HIS:O	1:A:331:ARG:HG3	1.83	0.79
1:A:23:ASN:OD1	6:A:846:HOH:O	2.10	0.68
1:A:95:GLU:HG3	6:A:917:HOH:O	1.94	0.67
1:A:179:ASN:HB3	6:A:435:HOH:O	1.95	0.66
1:A:259:TYR:CE1	1:A:305:LYS:HE2	2.36	0.61
1:A:292:ARG:HB3	1:A:295:ASP:OD2	2.01	0.61
1:A:70:HIS:ND1	6:A:857:HOH:O	2.31	0.60
1:A:198:ASN:ND2	6:A:891:HOH:O	2.32	0.59
1:A:184:HIS:CG	1:A:185:PRO:HD2	2.38	0.59
1:A:264:GLY:HA2	1:A:301:ALA:O	2.03	0.58
1:A:265:VAL:HG22	1:A:266:GLY:N	2.19	0.57
1:A:32:ASN:ND2	1:A:34:CYS:H	2.02	0.57
1:A:39:SER:O	1:A:42:PRO:HD2	2.05	0.57
1:A:131:ASN:OD1	1:A:132:PRO:HD2	2.05	0.57
1:A:292:ARG:NH1	6:A:820:HOH:O	2.32	0.56
1:A:32:ASN:C	1:A:32:ASN:HD22	2.09	0.56
1:A:22:GLN:NE2	6:A:760:HOH:O	2.37	0.56
1:A:30:LEU:C	1:A:30:LEU:HD13	2.29	0.53
1:A:253:LYS:HZ2	5:A:410:PGE:H22	1.70	0.52
1:A:211:ARG:NH1	6:A:587:HOH:O	2.42	0.52
1:A:88:GLU:HG3	1:A:92:LYS:CE	2.41	0.50
1:A:253:LYS:HZ3	5:A:410:PGE:C2	2.21	0.49
1:A:289:ALA:HB1	1:A:290:PRO:HD2	1.93	0.49
1:A:15:HIS:CE1	1:A:189:MET:HE3	2.48	0.49
1:A:183:ALA:HB1	1:A:189:MET:O	2.12	0.49
1:A:191:GLU:HG2	1:A:193:PRO:HD3	1.95	0.49
1:A:72:HIS:O	1:A:73:ALA:HB3	2.12	0.49
1:A:88:GLU:HG3	1:A:92:LYS:HE2	1.95	0.48
1:A:120:ILE:HD11	1:A:247:MET:HA	1.96	0.48
1:A:252:ASN:O	1:A:254:PRO:HD3	2.16	0.46
1:A:265:VAL:CG2	1:A:266:GLY:N	2.79	0.46
1:A:220:ASN:HB3	1:A:288:PHE:CD1	2.52	0.45
1:A:32:ASN:ND2	1:A:32:ASN:C	2.69	0.45
1:A:2:ARG:HG3	1:A:75:ASP:OD2	2.17	0.45
1:A:189:MET:HG2	1:A:336:TYR:OH	2.17	0.45
1:A:211:ARG:HD3	6:A:751:HOH:O	2.17	0.44
1:A:316:ARG:HA	1:A:320:GLU:OE1	2.17	0.44
1:A:217:ILE:HD13	1:A:217:ILE:HG21	1.60	0.44
1:A:280:CYS:SG	1:A:282:LYS:HG2	2.57	0.44
1:A:32:ASN:HD22	1:A:33:LEU:N	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:GLY:HA2	1:A:31:ASP:OD2	2.19	0.43
1:A:250:LEU:HA	1:A:250:LEU:HD23	1.81	0.43
1:A:37:LYS:O	1:A:40:VAL:HG12	2.19	0.42
1:A:99:ASN:O	1:A:103:GLY:HA3	2.20	0.42
1:A:253:LYS:CE	5:A:410:PGE:H22	2.46	0.42
1:A:134:ILE:HA	1:A:135:PRO:C	2.40	0.41
1:A:270:LEU:HD23	1:A:270:LEU:HA	1.85	0.41
1:A:231:ARG:O	1:A:266:GLY:HA2	2.19	0.41
1:A:89:SER:O	1:A:148:PRO:HG2	2.19	0.41
1:A:124:ALA:O	1:A:127:VAL:HG22	2.21	0.41
1:A:117:LYS:NZ	1:A:252:ASN:OD1	2.54	0.40
1:A:69:LEU:HD23	1:A:69:LEU:HA	1.89	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:853:HOH:O	6:A:853:HOH:O[6_555]	0.40	1.80
6:A:830:HOH:O	6:A:830:HOH:O[4_556]	0.73	1.47
6:A:663:HOH:O	6:A:663:HOH:O[6_555]	2.10	0.10

## 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	336/338 (99%)	327 (97%)	8 (2%)	1 (0%)	44 34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	TYR

### 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	281/281 (100%)	275 (98%)	6 (2%)	59	53

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	VAL
1	A	32	ASN
1	A	146	GLN
1	A	209	VAL
1	A	211	ARG
1	A	338	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	158	GLN
1	A	274	ASN
1	A	323	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

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	NAD	A	340	-	41,48,48	1.90	6 (14%)	43,73,73	1.61	5 (11%)
4	UPG	A	341	-	31,38,38	1.26	4 (12%)	40,58,58	2.85	13 (32%)
5	PGE	A	410	-	9,9,9	0.80	0	8,8,8	1.54	2 (25%)

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	NAD	A	340	-	-	0/22/62/62	0/5/5/5
4	UPG	A	341	-	1/1/11/11	0/19/59/59	0/3/3/3
5	PGE	A	410	-	-	0/7/7/7	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	341	UPG	C6-C5	-3.27	1.31	1.38
3	A	340	NAD	C6N-C5N	-2.43	1.33	1.38
4	A	341	UPG	PB-O3B	-2.36	1.54	1.60
3	A	340	NAD	C2A-N1A	2.02	1.37	1.33
3	A	340	NAD	C6N-N1N	2.47	1.41	1.35
4	A	341	UPG	C6-N1	2.61	1.39	1.35
4	A	341	UPG	C4-N3	3.93	1.40	1.33
3	A	340	NAD	C5N-C4N	5.95	1.50	1.38
3	A	340	NAD	C2N-C3N	6.12	1.48	1.39
3	A	340	NAD	C4N-C3N	6.26	1.49	1.39

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	340	NAD	C5N-C4N-C3N	-6.43	112.78	120.35
4	A	341	UPG	O5'-C1'-O3B	-5.13	104.65	111.36
3	A	340	NAD	O7N-C7N-C3N	-3.35	115.70	119.62
4	A	341	UPG	C5-C4-N3	-3.17	115.55	123.12
4	A	341	UPG	O5'-C5'-C6'	-3.14	98.89	106.41
4	A	341	UPG	O5'-C5'-C4'	-2.69	104.70	109.66
4	A	341	UPG	O6'-C6'-C5'	-2.54	102.78	111.34
4	A	341	UPG	O2C-C2C-C3C	-2.31	104.43	111.83
3	A	340	NAD	C5A-C6A-N6A	2.12	124.78	120.47
5	A	410	PGE	O2-C2-C1	2.31	120.81	110.15
4	A	341	UPG	O2B-PB-O3B	2.40	116.12	106.49
4	A	341	UPG	O4C-C1C-N1	2.61	113.31	108.08
3	A	340	NAD	C6N-C5N-C4N	2.66	123.45	119.44
5	A	410	PGE	C5-O3-C4	2.69	124.96	113.30
4	A	341	UPG	C4C-O4C-C1C	3.14	113.11	109.77
4	A	341	UPG	O3B-C1'-C2'	3.50	114.80	108.38
4	A	341	UPG	C1'-C2'-C3'	3.93	117.28	109.98
3	A	340	NAD	C3N-C7N-N7N	4.09	122.44	117.77
4	A	341	UPG	O2'-C2'-C1'	4.12	118.64	110.03
4	A	341	UPG	C4-N3-C2	13.02	125.32	114.13

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	341	UPG	C4'

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	410	PGE	5	0

## 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.