



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 12:54 PM GMT

PDB ID : 1H6D  
Title : OXIDIZED PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE FROM ZYMOMONAS MOBILIS COMPLEXED WITH GLYCEROL  
Authors : Nurizzo, D.; Baker, E.N.  
Deposited on : 2001-06-12  
Resolution : 2.05 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>

---

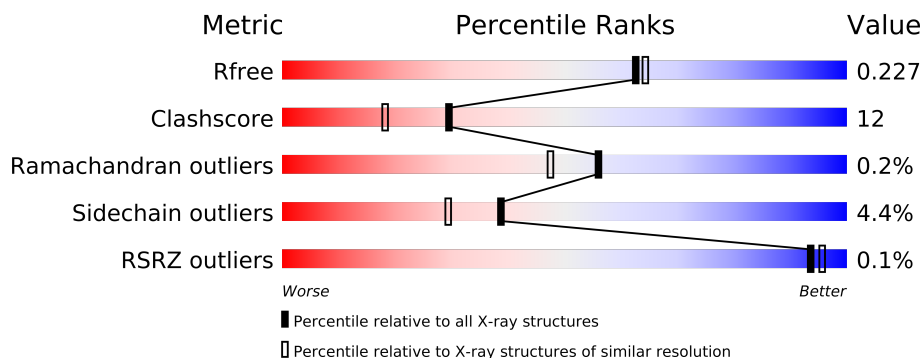
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.05 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	1380 (2.06-2.02)
Clashscore	79885	1577 (2.06-2.02)
Ramachandran outliers	78287	1565 (2.06-2.02)
Sidechain outliers	78261	1565 (2.06-2.02)
RSRZ outliers	66119	1381 (2.06-2.02)

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	433	
1	B	433	
1	C	433	
1	D	433	
1	E	433	
1	F	433	
1	G	433	
1	H	433	
1	I	433	
1	J	433	
1	K	433	
1	L	433	

The following table lists non-polymeric compounds that are outliers for geometric or electron-

density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	GOL	A	600[A]	-	X
3	GOL	A	600[B]	-	X
3	GOL	B	600[A]	-	X
3	GOL	B	600[B]	-	X
3	GOL	C	600[A]	-	X
3	GOL	C	600[B]	-	X
3	GOL	D	600[A]	-	X
3	GOL	D	600[B]	-	X
3	GOL	E	600[A]	-	X
3	GOL	E	600[B]	-	X
3	GOL	F	600[A]	-	X
3	GOL	F	600[B]	-	X
3	GOL	G	600[A]	-	X
3	GOL	G	600[B]	-	X
3	GOL	H	600[A]	-	X
3	GOL	H	600[B]	-	X
3	GOL	I	600[A]	-	X
3	GOL	I	600[B]	-	X
3	GOL	J	600[A]	-	X
3	GOL	J	600[B]	-	X
3	GOL	K	600[A]	-	X
3	GOL	K	600[B]	-	X
3	GOL	L	600[A]	-	X
3	GOL	L	600[B]	-	X

## 2 Entry composition

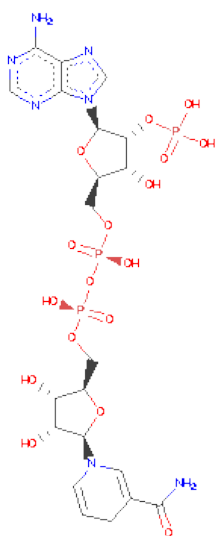
There are 4 unique types of molecules in this entry. The entry contains 40164 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	0	0
			2970	1862	532	556	20			
1	B	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			
1	C	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	D	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	E	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	F	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			
1	G	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			
1	H	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			
1	I	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	J	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			
1	K	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	L	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDEPHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	I	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	J	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	K	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	L	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	1
			7	3	4		
3	B	1	Total	C	O	0	1
			7	3	4		
3	C	1	Total	C	O	0	1
			7	3	4		
3	D	1	Total	C	O	0	1
			7	3	4		
3	E	1	Total	C	O	0	1
			7	3	4		
3	F	1	Total	C	O	0	1
			7	3	4		
3	G	1	Total	C	O	0	1
			7	3	4		
3	H	1	Total	C	O	0	1
			7	3	4		
3	I	1	Total	C	O	0	1
			7	3	4		
3	J	1	Total	C	O	0	1
			7	3	4		
3	K	1	Total	C	O	0	1
			7	3	4		
3	L	1	Total	C	O	0	1
			7	3	4		

- Molecule 4 is water.

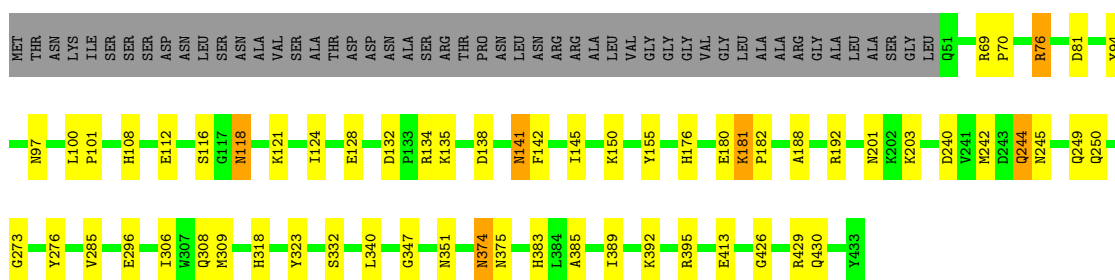
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	390	Total 390	O 390	0	0
4	B	295	Total 295	O 295	0	0
4	C	320	Total 320	O 320	0	0
4	D	213	Total 213	O 213	0	0
4	E	341	Total 341	O 341	0	0
4	F	219	Total 219	O 219	0	0
4	G	371	Total 371	O 371	0	0
4	H	289	Total 289	O 289	0	0
4	I	391	Total 391	O 391	0	0
4	J	377	Total 377	O 377	0	0
4	K	386	Total 386	O 386	0	0
4	L	357	Total 357	O 357	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.

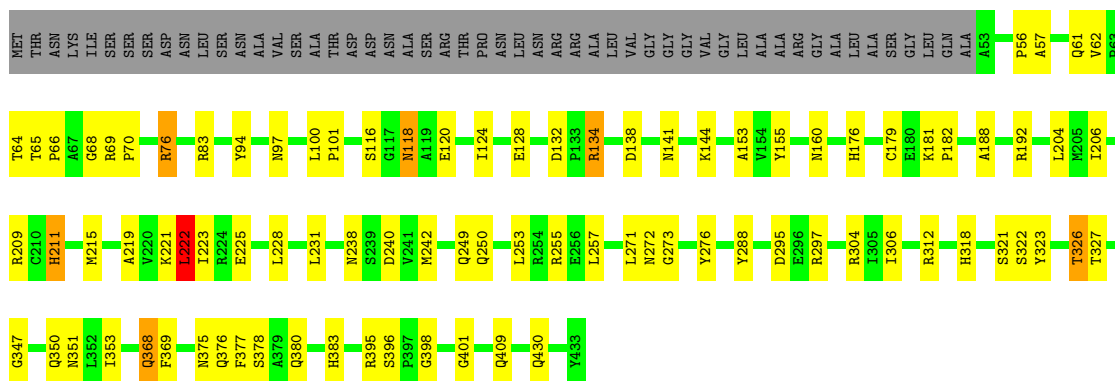
#### • Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain A:



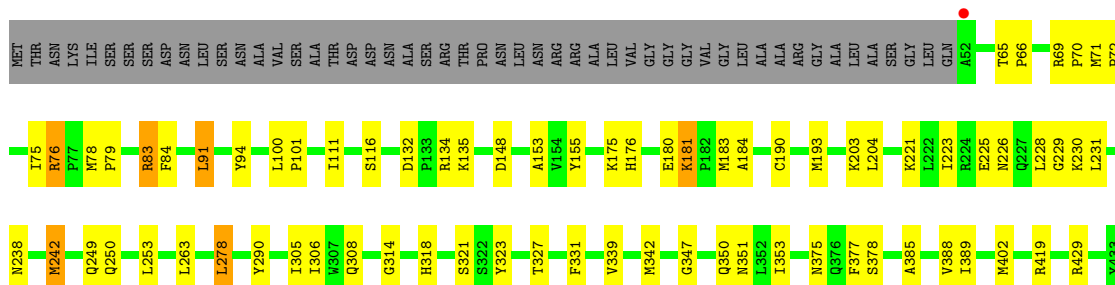
#### • Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain B:



#### • Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain C:

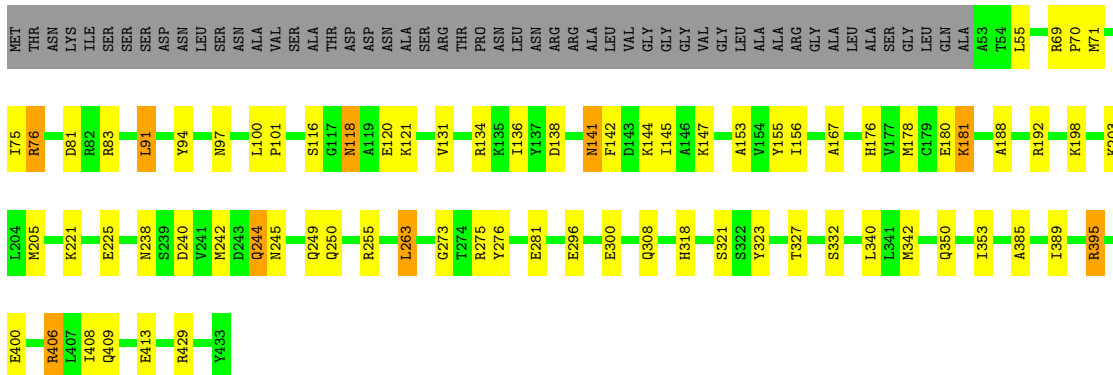






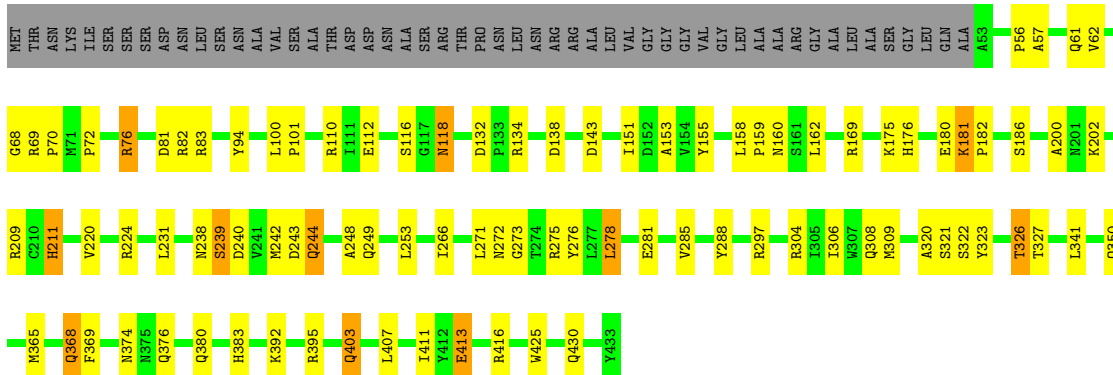
- Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain G:



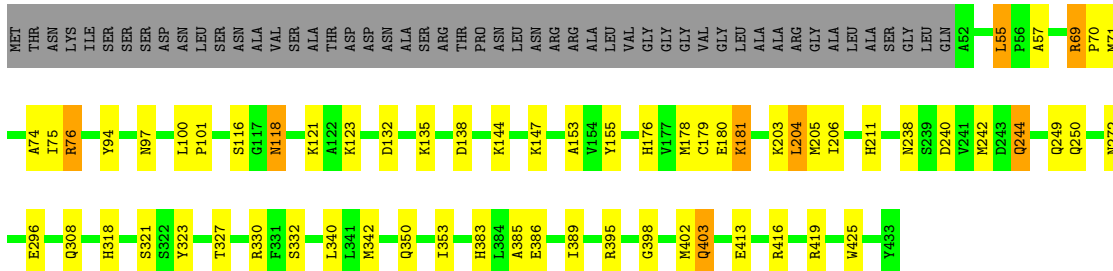
- Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain H:



- Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain I:



- Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain J:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.72Å 83.75Å 279.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.05 14.99 – 2.05	Depositor EDS
% Data completeness (in resolution range)	95.1 (15.00-2.05) 95.2 (14.99-2.05)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.05Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.197 , 0.228 0.197 , 0.227	Depositor DCC
$R_{free}$ test set	1557 reflections (0.49%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.6	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 49.1	EDS
Estimated twinning fraction	0.476 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	5 of 317882 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	40164	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	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 56.73 % 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 2.6219e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: GOL, NDP

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	0.35	0/3034	0.62	0/4107
1	B	0.31	0/3024	0.59	1/4093 (0.0%)
1	C	0.32	0/3029	0.59	0/4100
1	D	0.30	0/3029	0.58	1/4100 (0.0%)
1	E	0.33	0/3029	0.61	0/4100
1	F	0.30	0/3024	0.59	1/4093 (0.0%)
1	G	0.33	0/3024	0.62	0/4093
1	H	0.31	0/3024	0.59	0/4093
1	I	0.34	0/3029	0.61	0/4100
1	J	0.32	0/3024	0.60	0/4093
1	K	0.35	0/3029	0.62	0/4100
1	L	0.33	0/3024	0.62	0/4093
All	All	0.32	0/36323	0.60	3/49165 (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	B	222	LEU	CA-CB-CG	5.87	128.80	115.30
1	F	275	ARG	NE-CZ-NH2	5.20	122.90	120.30
1	D	275	ARG	NE-CZ-NH2	5.16	122.88	120.30

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	2970	0	2927	57	0
1	B	2960	0	2920	74	0
1	C	2965	0	2925	72	0
1	D	2965	0	2925	102	0
1	E	2965	0	2925	71	0
1	F	2960	0	2920	109	0
1	G	2960	0	2920	70	0
1	H	2960	0	2920	81	0
1	I	2965	0	2925	67	0
1	J	2960	0	2920	64	0
1	K	2965	0	2925	59	0
1	L	2960	0	2920	70	0
2	A	48	0	26	7	0
2	B	48	0	26	5	0
2	C	48	0	26	10	0
2	D	48	0	26	10	0
2	E	48	0	26	10	0
2	F	48	0	26	10	0
2	G	48	0	26	7	0
2	H	48	0	26	8	0
2	I	48	0	26	6	0
2	J	48	0	26	10	0
2	K	48	0	26	9	0
2	L	48	0	26	10	0
3	A	7	0	6	5	0
3	B	7	0	6	4	0
3	C	7	0	6	7	0
3	D	7	0	6	6	0
3	E	7	0	6	8	0
3	F	7	0	6	6	0
3	G	7	0	6	5	0
3	H	7	0	6	5	0
3	I	7	0	6	4	0
3	J	7	0	6	6	0
3	K	7	0	6	5	0
3	L	7	0	6	7	0
4	A	390	0	0	6	0
4	B	295	0	0	3	0
4	C	320	0	0	6	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	213	0	0	5	0
4	E	341	0	0	5	0
4	F	219	0	0	5	0
4	G	371	0	0	7	0
4	H	289	0	0	4	0
4	I	391	0	0	8	0
4	J	377	0	0	4	0
4	K	386	0	0	5	0
4	L	357	0	0	3	0
All	All	40164	0	35456	876	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 12.

The worst 5 of 876 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:K:500:NDP:H42N	3:K:600[B]:GOL:H31	1.20	1.16
2:G:500:NDP:H42N	3:G:600[B]:GOL:H31	1.27	1.15
2:K:500:NDP:H42N	3:K:600[A]:GOL:H32	1.14	1.13
2:A:500:NDP:H42N	3:A:600[B]:GOL:H31	1.25	1.13
2:B:500:NDP:H42N	3:B:600[A]:GOL:H31	1.15	1.13

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	381/433 (88%)	370 (97%)	11 (3%)	0	100	100
1	B	379/433 (88%)	366 (97%)	13 (3%)	0	100	100
1	C	380/433 (88%)	366 (96%)	13 (3%)	1 (0%)	50	39
1	D	380/433 (88%)	364 (96%)	15 (4%)	1 (0%)	50	39
1	E	380/433 (88%)	368 (97%)	11 (3%)	1 (0%)	50	39

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	379/433 (88%)	364 (96%)	15 (4%)	0	100	100
1	G	379/433 (88%)	367 (97%)	11 (3%)	1 (0%)	50	39
1	H	379/433 (88%)	365 (96%)	14 (4%)	0	100	100
1	I	380/433 (88%)	369 (97%)	10 (3%)	1 (0%)	50	39
1	J	379/433 (88%)	367 (97%)	12 (3%)	0	100	100
1	K	380/433 (88%)	367 (97%)	12 (3%)	1 (0%)	50	39
1	L	379/433 (88%)	366 (97%)	12 (3%)	1 (0%)	50	39
All	All	4555/5196 (88%)	4399 (97%)	149 (3%)	7 (0%)	56	47

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	327	THR
1	E	327	THR
1	G	327	THR
1	I	327	THR
1	K	327	THR

### 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	308/345 (89%)	297 (96%)	11 (4%)	47	38
1	B	308/345 (89%)	289 (94%)	19 (6%)	26	16
1	C	308/345 (89%)	299 (97%)	9 (3%)	55	48
1	D	308/345 (89%)	294 (96%)	14 (4%)	38	28
1	E	308/345 (89%)	297 (96%)	11 (4%)	47	38
1	F	308/345 (89%)	288 (94%)	20 (6%)	24	15
1	G	308/345 (89%)	294 (96%)	14 (4%)	38	28
1	H	308/345 (89%)	288 (94%)	20 (6%)	24	15
1	I	308/345 (89%)	297 (96%)	11 (4%)	47	38
1	J	308/345 (89%)	297 (96%)	11 (4%)	47	38

Continued on next page...



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	308/345 (89%)	299 (97%)	9 (3%)	55	48
1	L	308/345 (89%)	296 (96%)	12 (4%)	43	35
All	All	3696/4140 (89%)	3535 (96%)	161 (4%)	39	29

5 of 161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	255	ARG
1	G	181	LYS
1	K	374	ASN
1	F	271	LEU
1	F	384	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 212 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	227	GLN
1	G	308	GLN
1	L	160	ASN
1	F	308	GLN
1	F	403	GLN

### 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 ⓘ

Of 36 ligands modelled in this entry, 24 are modelled with single atom - leaving 12 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	NDP	A	500	-	52,52,52	1.71	12 (23%)	80,80,80	2.04	13 (16%)
2	NDP	B	500	-	52,52,52	1.66	10 (19%)	80,80,80	1.93	13 (16%)
2	NDP	C	500	-	52,52,52	1.66	11 (21%)	80,80,80	1.93	14 (17%)
2	NDP	D	500	-	52,52,52	1.69	12 (23%)	80,80,80	1.86	15 (18%)
2	NDP	E	500	-	52,52,52	1.68	12 (23%)	80,80,80	1.97	14 (17%)
2	NDP	F	500	-	52,52,52	1.69	12 (23%)	80,80,80	1.86	15 (18%)
2	NDP	G	500	-	52,52,52	1.70	10 (19%)	80,80,80	2.03	14 (17%)
2	NDP	H	500	-	52,52,52	1.65	11 (21%)	80,80,80	1.92	13 (16%)
2	NDP	I	500	-	52,52,52	1.68	11 (21%)	80,80,80	1.99	13 (16%)
2	NDP	J	500	-	52,52,52	1.68	11 (21%)	80,80,80	1.97	14 (17%)
2	NDP	K	500	-	52,52,52	1.68	11 (21%)	80,80,80	2.02	14 (17%)
2	NDP	L	500	-	52,52,52	1.67	11 (21%)	80,80,80	1.98	14 (17%)

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	NDP	A	500	-	-	0/35/77/77	0/3/5/5
2	NDP	B	500	-	-	0/35/77/77	0/3/5/5
2	NDP	C	500	-	-	0/35/77/77	0/3/5/5
2	NDP	D	500	-	-	0/35/77/77	0/3/5/5
2	NDP	E	500	-	-	0/35/77/77	0/3/5/5
2	NDP	F	500	-	-	0/35/77/77	0/3/5/5
2	NDP	G	500	-	-	0/35/77/77	0/3/5/5
2	NDP	H	500	-	-	0/35/77/77	0/3/5/5
2	NDP	I	500	-	-	0/35/77/77	0/3/5/5
2	NDP	J	500	-	-	0/35/77/77	0/3/5/5
2	NDP	K	500	-	-	0/35/77/77	0/3/5/5
2	NDP	L	500	-	-	0/35/77/77	0/3/5/5

The worst 5 of 134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	500	NDP	P2B-O2X	-4.85	1.37	1.54
2	A	500	NDP	P2B-O2X	-4.81	1.37	1.54
2	D	500	NDP	P2B-O2X	-4.79	1.37	1.54
2	K	500	NDP	P2B-O2X	-4.78	1.37	1.54
2	G	500	NDP	P2B-O2X	-4.72	1.37	1.54

The worst 5 of 166 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	500	NDP	N3A-C2A-N1A	-9.42	120.83	128.71
2	E	500	NDP	N3A-C2A-N1A	-9.35	120.89	128.71
2	H	500	NDP	N3A-C2A-N1A	-9.34	120.90	128.71
2	G	500	NDP	N3A-C2A-N1A	-9.32	120.92	128.71
2	A	500	NDP	N3A-C2A-N1A	-9.31	120.93	128.71

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	383/433 (88%)	-0.70	0 100 100	12, 18, 30, 48	0
1	B	381/433 (87%)	-0.57	0 100 100	13, 23, 38, 45	0
1	C	382/433 (88%)	-0.62	1 (0%) 91 94	14, 21, 32, 45	0
1	D	382/433 (88%)	-0.34	2 (0%) 88 91	16, 31, 44, 53	0
1	E	382/433 (88%)	-0.61	1 (0%) 91 94	14, 22, 32, 44	0
1	F	381/433 (87%)	-0.34	1 (0%) 91 94	16, 30, 46, 52	0
1	G	381/433 (87%)	-0.72	0 100 100	12, 18, 30, 40	0
1	H	381/433 (87%)	-0.59	0 100 100	14, 23, 39, 46	0
1	I	382/433 (88%)	-0.72	0 100 100	10, 16, 28, 39	0
1	J	381/433 (87%)	-0.69	0 100 100	11, 19, 30, 42	0
1	K	382/433 (88%)	-0.73	1 (0%) 91 94	10, 16, 27, 39	0
1	L	381/433 (87%)	-0.70	0 100 100	11, 19, 29, 40	0
All	All	4579/5196 (88%)	-0.61	6 (0%) 93 95	10, 21, 38, 53	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	52	ALA	2.6
1	D	52	ALA	2.5
1	C	52	ALA	2.3
1	D	389	ILE	2.3
1	F	147	LYS	2.2

### 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
3	GOL	I	600[B]	1/6	0.26	32.51	30,30,30,30	1
3	GOL	I	600[A]	1/6	0.26	30.49	29,29,29,29	1
3	GOL	L	600[A]	1/6	0.33	28.37	32,32,32,32	1
3	GOL	A	600[B]	1/6	0.23	27.47	25,25,25,25	1
3	GOL	A	600[A]	1/6	0.23	27.47	18,18,18,18	1
3	GOL	J	600[A]	1/6	0.27	26.52	30,30,30,30	1
3	GOL	K	600[B]	1/6	0.29	26.32	31,31,31,31	1
3	GOL	L	600[B]	1/6	0.33	23.54	31,31,31,31	1
3	GOL	J	600[B]	1/6	0.27	21.98	27,27,27,27	1
3	GOL	K	600[A]	1/6	0.29	21.70	29,29,29,29	1
3	GOL	E	600[B]	1/6	0.30	21.12	32,32,32,32	1
3	GOL	E	600[A]	1/6	0.30	21.12	33,33,33,33	1
3	GOL	B	600[B]	1/6	0.28	18.24	31,31,31,31	1
3	GOL	B	600[A]	1/6	0.28	17.26	34,34,34,34	1
3	GOL	G	600[A]	1/6	0.25	17.18	25,25,25,25	1
3	GOL	G	600[B]	1/6	0.25	17.18	30,30,30,30	1
3	GOL	C	600[A]	1/6	0.27	12.41	32,32,32,32	1
3	GOL	H	600[B]	1/6	0.26	11.08	36,36,36,36	1
3	GOL	H	600[A]	1/6	0.26	11.08	36,36,36,36	1
3	GOL	C	600[B]	1/6	0.27	10.41	31,31,31,31	1
3	GOL	D	600[A]	1/6	0.28	8.64	42,42,42,42	1
3	GOL	F	600[B]	1/6	0.23	8.23	42,42,42,42	1
3	GOL	D	600[B]	1/6	0.28	7.30	43,43,43,43	1
3	GOL	F	600[A]	1/6	0.23	7.24	42,42,42,42	1
2	NDP	A	500	48/48	0.09	1.29	12,15,17,17	0
2	NDP	I	500	48/48	0.09	1.15	10,15,18,18	0
2	NDP	B	500	48/48	0.10	1.15	18,23,26,26	0
2	NDP	F	500	48/48	0.12	1.13	28,33,42,43	0
2	NDP	J	500	48/48	0.09	1.12	15,19,22,22	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NDP	L	500	48/48	0.09	1.08	13,19,21,22	0
2	NDP	K	500	48/48	0.09	0.94	10,16,18,18	0
2	NDP	G	500	48/48	0.09	0.91	13,16,18,19	0
2	NDP	E	500	48/48	0.09	0.84	15,20,22,23	0
2	NDP	C	500	48/48	0.09	0.68	15,19,24,26	0
2	NDP	D	500	48/48	0.12	0.44	25,34,43,43	0
2	NDP	H	500	48/48	0.08	0.18	19,22,26,26	0

## 6.5 Other polymers

There are no such residues in this entry.