wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 07:50 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 X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

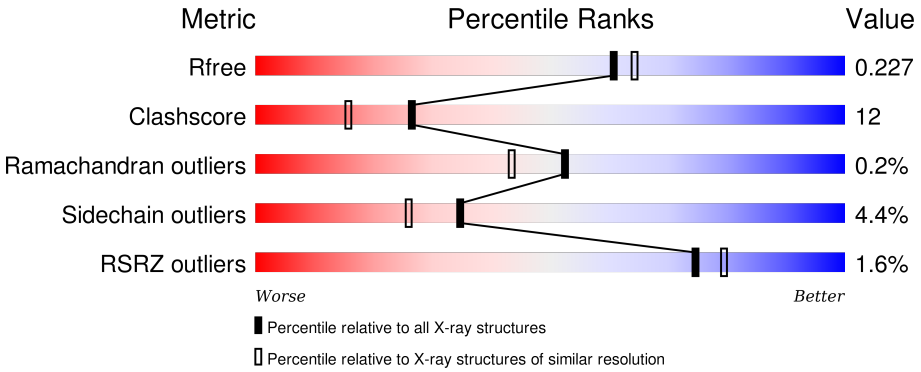
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

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}	91344	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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 >=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 <=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	433	74% 13% • 12%
1	B	433	2% 67% 19% • 12%
1	C	433	71% 16% • 12%
1	D	433	5% 62% 24% • 12%
1	E	433	72% 15% • 12%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	433	3% 59% 26% • 12%
1	G	433	% 71% 15% • 12%
1	H	433	2% 67% 19% • 12%
1	I	433	73% 13% • 12%
1	J	433	75% 11% • 12%
1	K	433	75% 12% • 12%
1	L	433	71% 15% • 12%

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	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	X
3	GOL	C	600[B]	-	-	-	X
3	GOL	D	600[A]	-	-	-	X
3	GOL	D	600[B]	-	-	X	X
3	GOL	E	600[A]	-	-	X	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	X
3	GOL	L	600[B]	-	-	-	X

2 Entry composition (i)

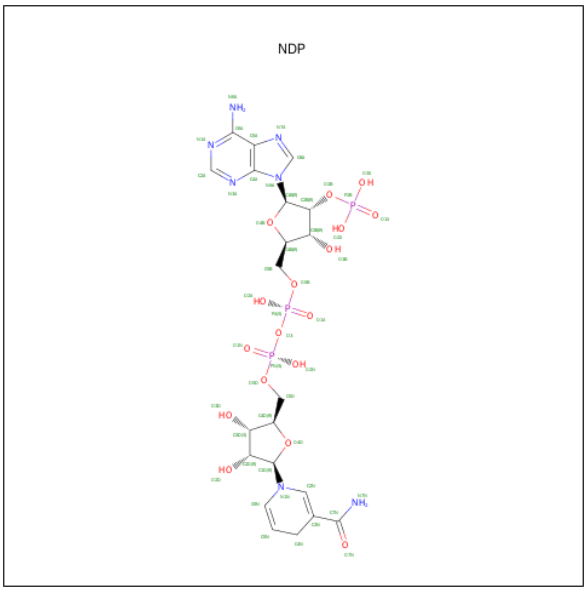
There are 4 unique types of molecules in this entry. The entry contains 40164 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE.

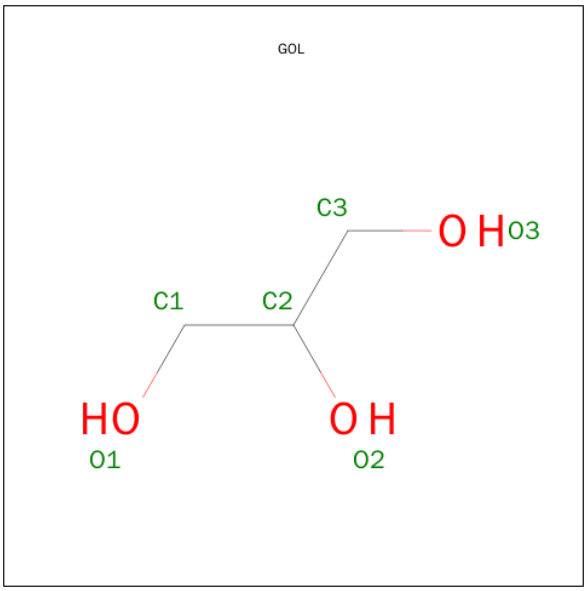
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	383	Total	C	N	O	S	0	0	0
			2970	1862	532	556	20			
1	B	381	Total	C	N	O	S	0	0	0
			2960	1856	530	554	20			
1	C	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	D	382	Total	C	N	O	S	0	0	0
			2965	1859	531	555	20			
1	E	382	Total	C	N	O	S	0	0	0
			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-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



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: $C_3H_8O_3$).



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.

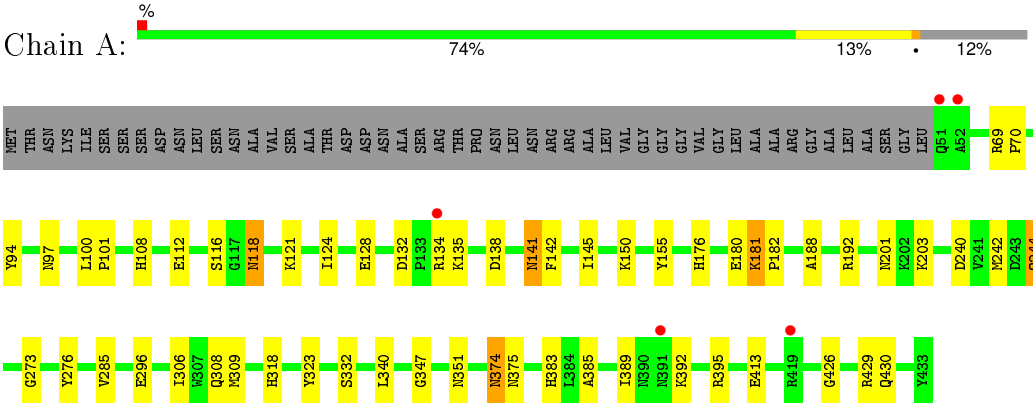
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	390	Total O 390 390	0	0
4	B	295	Total O 295 295	0	0
4	C	320	Total O 320 320	0	0
4	D	213	Total O 213 213	0	0
4	E	341	Total O 341 341	0	0
4	F	219	Total O 219 219	0	0
4	G	371	Total O 371 371	0	0
4	H	289	Total O 289 289	0	0
4	I	391	Total O 391 391	0	0
4	J	377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

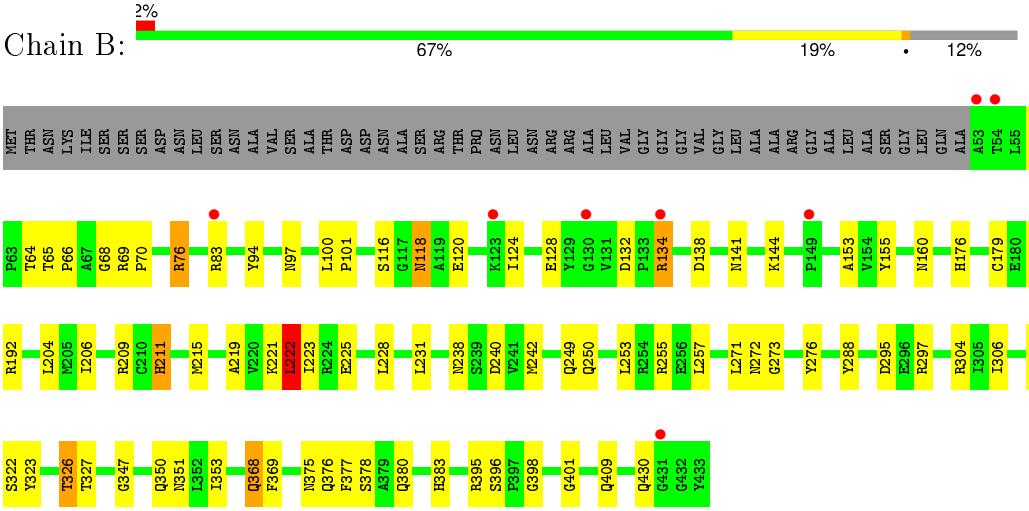
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain A:



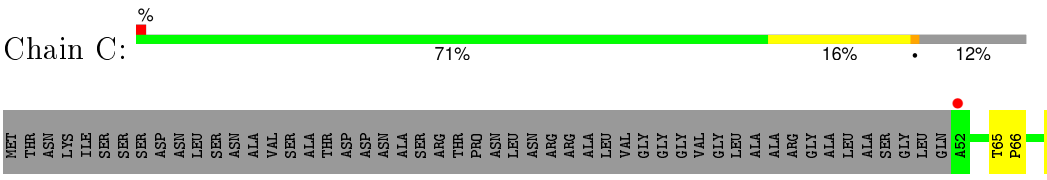
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

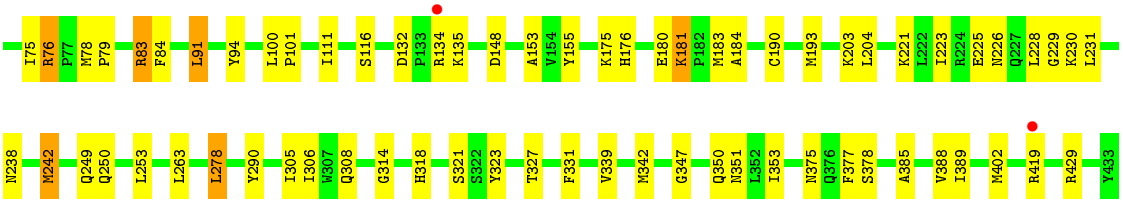
Chain B:



• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

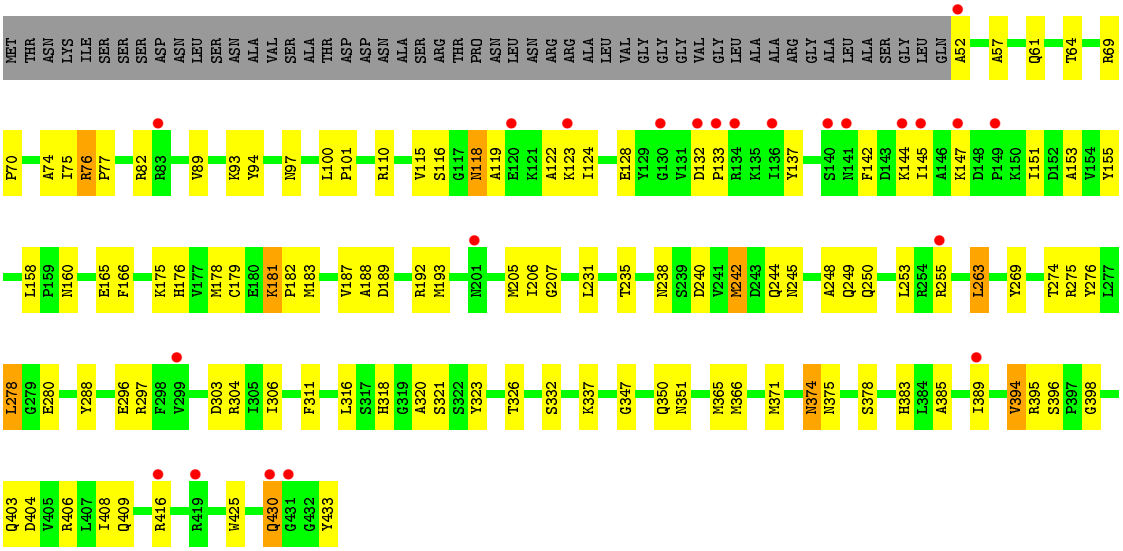
Chain C:





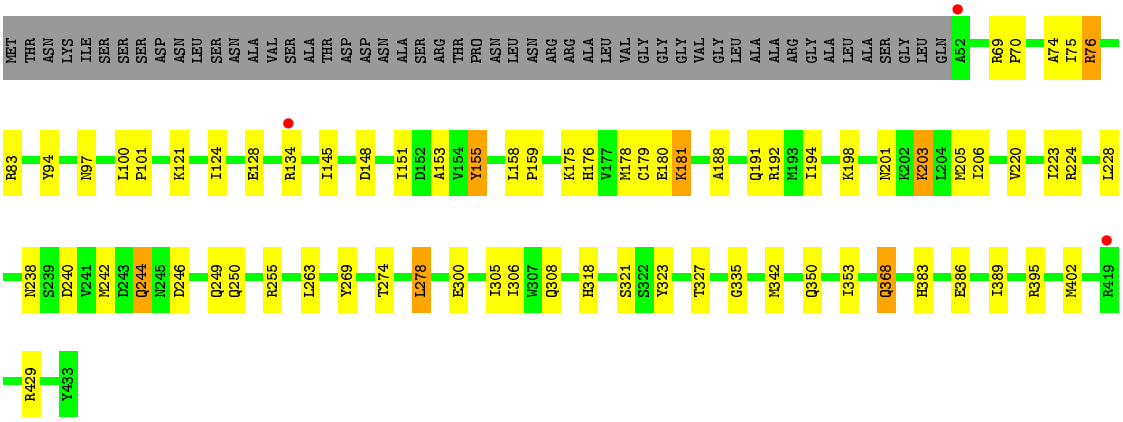
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain D:



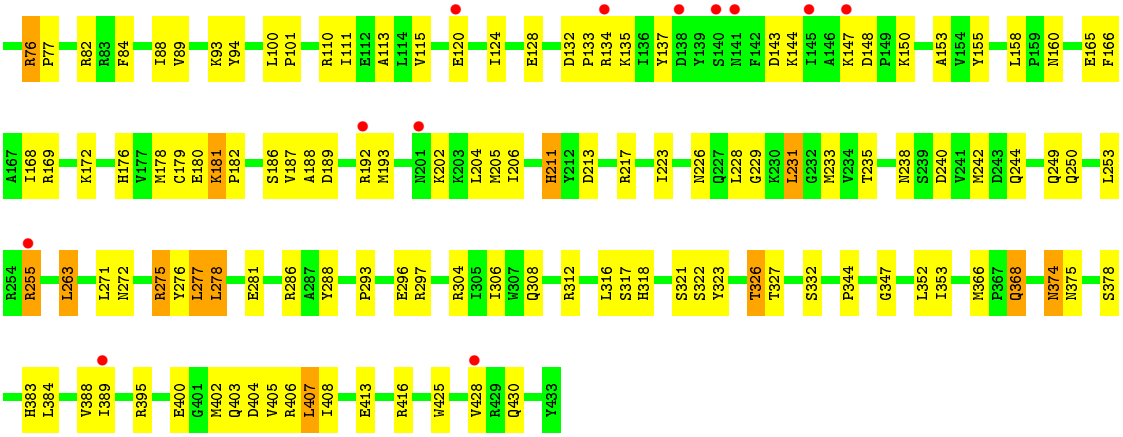
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain E:



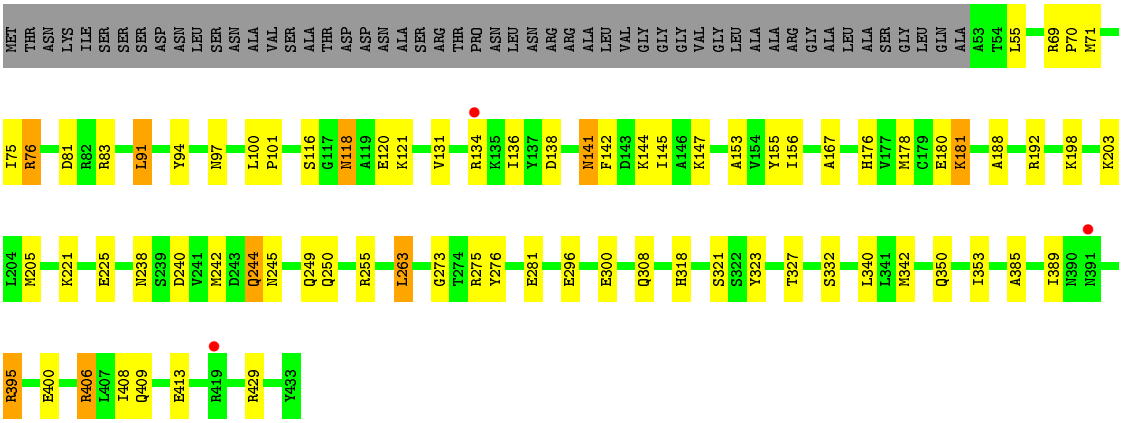
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain F:



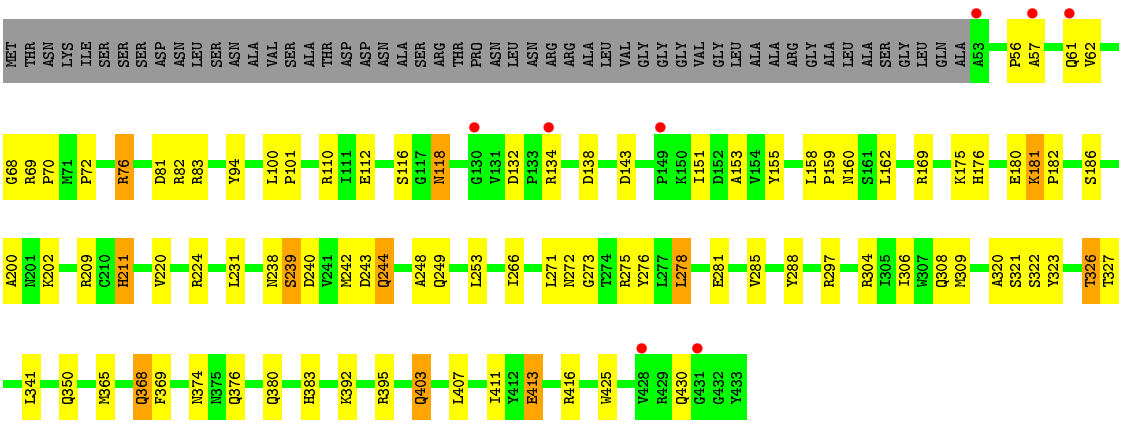
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain G:



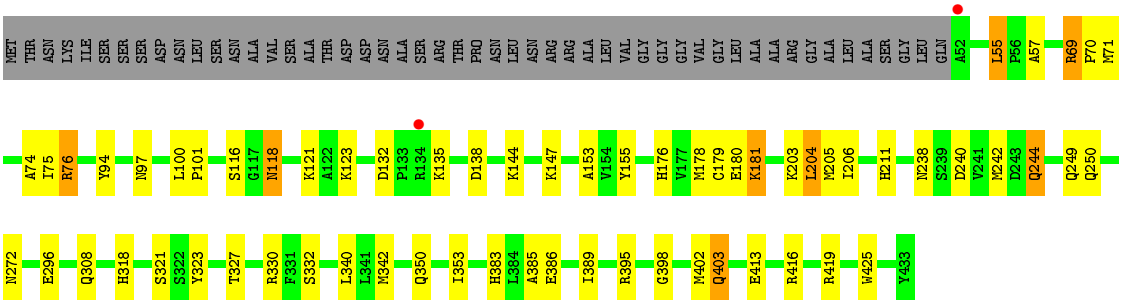
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain H:



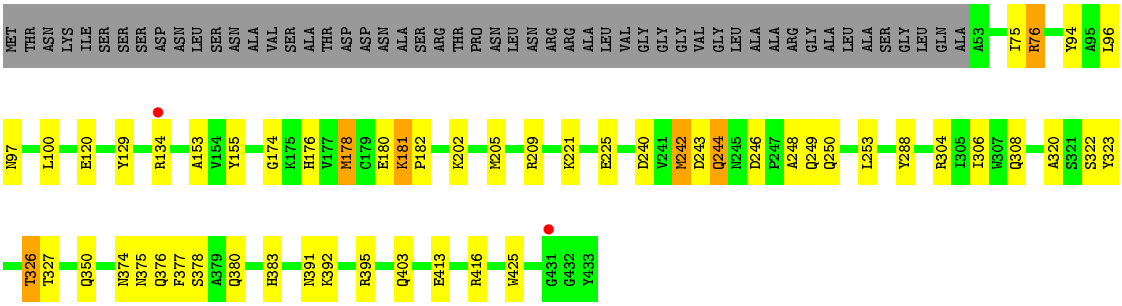
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain I:



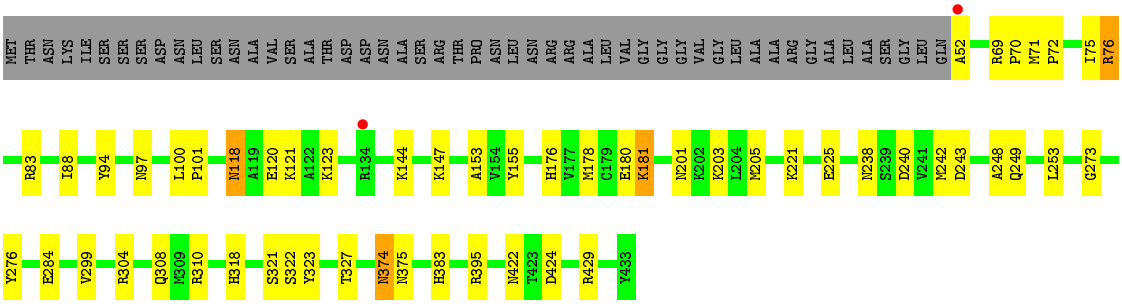
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain J:



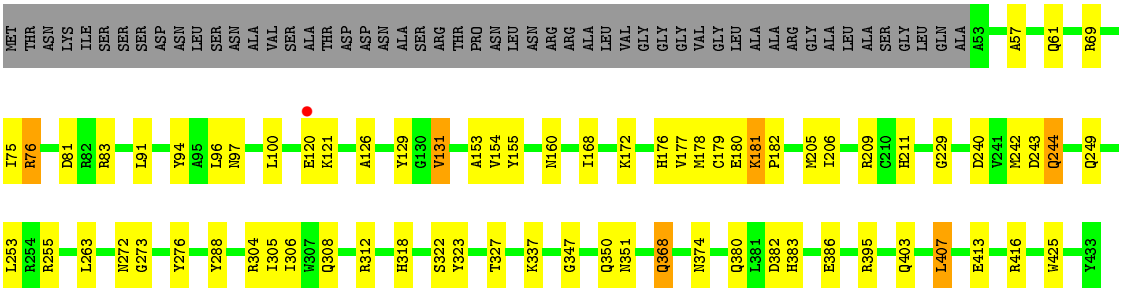
• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain K:



• Molecule 1: PRECURSOR FORM OF GLUCOSE-FRUCTOSE OXIDOREDUCTASE

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	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
$< I/\sigma(I) >$ [1]	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^2)	21.6	Xtriage
Anisotropy	0.317	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 62.3	EDS
Estimated twinning fraction	0.476 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	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^2)	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.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: 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(^{o})	Ideal(^{o})
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 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	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
4	D	213	0	0	5	0
4	E	341	0	0	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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

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 12.

The worst 5 of 876 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)
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 (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	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%)	46	36
1	D	380/433 (88%)	364 (96%)	15 (4%)	1 (0%)	46	36

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	E	380/433 (88%)	368 (97%)	11 (3%)	1 (0%)	46 36
1	F	379/433 (88%)	364 (96%)	15 (4%)	0	100 100
1	G	379/433 (88%)	367 (97%)	11 (3%)	1 (0%)	46 36
1	H	379/433 (88%)	365 (96%)	14 (4%)	0	100 100
1	I	380/433 (88%)	369 (97%)	10 (3%)	1 (0%)	46 36
1	J	379/433 (88%)	367 (97%)	12 (3%)	0	100 100
1	K	380/433 (88%)	367 (97%)	12 (3%)	1 (0%)	46 36
1	L	379/433 (88%)	366 (97%)	12 (3%)	1 (0%)	46 36
All	All	4555/5196 (88%)	4399 (97%)	149 (3%)	7 (0%)	52 43

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 (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	308/345 (89%)	297 (96%)	11 (4%)	42 34
1	B	308/345 (89%)	289 (94%)	19 (6%)	23 13
1	C	308/345 (89%)	299 (97%)	9 (3%)	50 42
1	D	308/345 (89%)	294 (96%)	14 (4%)	34 25
1	E	308/345 (89%)	297 (96%)	11 (4%)	42 34
1	F	308/345 (89%)	288 (94%)	20 (6%)	21 11
1	G	308/345 (89%)	294 (96%)	14 (4%)	34 25
1	H	308/345 (89%)	288 (94%)	20 (6%)	21 11

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	308/345 (89%)	297 (96%)	11 (4%)	42	34
1	J	308/345 (89%)	297 (96%)	11 (4%)	42	34
1	K	308/345 (89%)	299 (97%)	9 (3%)	50	42
1	L	308/345 (89%)	296 (96%)	12 (4%)	39	30
All	All	3696/4140 (89%)	3535 (96%)	161 (4%)	35	26

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 (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)

36 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	$\#\|Z\| > 2$
2	NDP	A	500	-	42,52,52	1.66	8 (19%)	55,80,80	2.08	10 (18%)
3	GOL	A	600[A]	-	5,5,5	1.05	0	5,5,5	0.52	0
3	GOL	A	600[B]	-	5,5,5	1.04	0	5,5,5	0.52	0
2	NDP	B	500	-	42,52,52	1.61	7 (16%)	55,80,80	2.03	9 (16%)
3	GOL	B	600[A]	-	5,5,5	1.04	0	5,5,5	0.52	0
3	GOL	B	600[B]	-	5,5,5	1.03	0	5,5,5	0.52	0
2	NDP	C	500	-	42,52,52	1.58	8 (19%)	55,80,80	2.04	10 (18%)
3	GOL	C	600[A]	-	5,5,5	1.04	0	5,5,5	0.53	0
3	GOL	C	600[B]	-	5,5,5	1.04	0	5,5,5	0.53	0
2	NDP	D	500	-	42,52,52	1.63	10 (23%)	55,80,80	1.99	11 (20%)
3	GOL	D	600[A]	-	5,5,5	1.03	0	5,5,5	0.53	0
3	GOL	D	600[B]	-	5,5,5	1.02	0	5,5,5	0.53	0
2	NDP	E	500	-	42,52,52	1.59	9 (21%)	55,80,80	2.05	10 (18%)
3	GOL	E	600[A]	-	5,5,5	1.01	0	5,5,5	0.53	0
3	GOL	E	600[B]	-	5,5,5	1.01	0	5,5,5	0.53	0
2	NDP	F	500	-	42,52,52	1.63	10 (23%)	55,80,80	1.99	11 (20%)
3	GOL	F	600[A]	-	5,5,5	1.02	0	5,5,5	0.53	0
3	GOL	F	600[B]	-	5,5,5	1.01	0	5,5,5	0.53	0
2	NDP	G	500	-	42,52,52	1.65	8 (19%)	55,80,80	2.06	9 (16%)
3	GOL	G	600[A]	-	5,5,5	1.02	0	5,5,5	0.53	0
3	GOL	G	600[B]	-	5,5,5	1.01	0	5,5,5	0.53	0
2	NDP	H	500	-	42,52,52	1.60	8 (19%)	55,80,80	2.03	9 (16%)
3	GOL	H	600[A]	-	5,5,5	1.00	0	5,5,5	0.53	0
3	GOL	H	600[B]	-	5,5,5	1.00	0	5,5,5	0.53	0
2	NDP	I	500	-	42,52,52	1.63	9 (21%)	55,80,80	2.07	9 (16%)
3	GOL	I	600[A]	-	5,5,5	0.99	0	5,5,5	0.52	0
3	GOL	I	600[B]	-	5,5,5	0.99	0	5,5,5	0.52	0
2	NDP	J	500	-	42,52,52	1.63	7 (16%)	55,80,80	2.05	10 (18%)
3	GOL	J	600[A]	-	5,5,5	0.98	0	5,5,5	0.52	0
3	GOL	J	600[B]	-	5,5,5	0.97	0	5,5,5	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NDP	K	500	-	42,52,52	1.66	9 (21%)	55,80,80	2.08	10 (18%)
3	GOL	K	600[A]	-	5,5,5	0.97	0	5,5,5	0.52	0
3	GOL	K	600[B]	-	5,5,5	0.96	0	5,5,5	0.52	0
2	NDP	L	500	-	42,52,52	1.61	7 (16%)	55,80,80	2.05	10 (18%)
3	GOL	L	600[A]	-	5,5,5	0.97	0	5,5,5	0.52	0
3	GOL	L	600[B]	-	5,5,5	0.96	0	5,5,5	0.52	0

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	-	-	0/30/77/77	0/5/5/5
3	GOL	A	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	A	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	B	500	-	-	0/30/77/77	0/5/5/5
3	GOL	B	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	B	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	C	500	-	-	0/30/77/77	0/5/5/5
3	GOL	C	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	C	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	D	500	-	-	0/30/77/77	0/5/5/5
3	GOL	D	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	D	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	E	500	-	-	0/30/77/77	0/5/5/5
3	GOL	E	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	E	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	F	500	-	-	0/30/77/77	0/5/5/5
3	GOL	F	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	F	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	G	500	-	-	0/30/77/77	0/5/5/5
3	GOL	G	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	G	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	H	500	-	-	0/30/77/77	0/5/5/5
3	GOL	H	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	H	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	I	500	-	-	0/30/77/77	0/5/5/5
3	GOL	I	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	I	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	J	500	-	-	0/30/77/77	0/5/5/5
3	GOL	J	600[A]	-	-	0/4/4/4	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	J	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	K	500	-	-	0/30/77/77	0/5/5/5
3	GOL	K	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	K	600[B]	-	-	0/4/4/4	0/0/0/0
2	NDP	L	500	-	-	0/30/77/77	0/5/5/5
3	GOL	L	600[A]	-	-	0/4/4/4	0/0/0/0
3	GOL	L	600[B]	-	-	0/4/4/4	0/0/0/0

The worst 5 of 100 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	500	NDP	P2B-O2X	-4.94	1.37	1.54
2	A	500	NDP	P2B-O2X	-4.90	1.37	1.54
2	D	500	NDP	P2B-O2X	-4.88	1.37	1.54
2	K	500	NDP	P2B-O2X	-4.86	1.37	1.54
2	G	500	NDP	P2B-O2X	-4.81	1.37	1.54

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	500	NDP	N3A-C2A-N1A	-10.53	120.83	128.89
2	E	500	NDP	N3A-C2A-N1A	-10.46	120.89	128.89
2	H	500	NDP	N3A-C2A-N1A	-10.44	120.90	128.89
2	G	500	NDP	N3A-C2A-N1A	-10.42	120.92	128.89
2	A	500	NDP	N3A-C2A-N1A	-10.40	120.93	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

36 monomers are involved in 104 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	NDP	7	0
3	A	600[A]	GOL	2	0
3	A	600[B]	GOL	3	0
2	B	500	NDP	5	0
3	B	600[A]	GOL	2	0
3	B	600[B]	GOL	2	0
2	C	500	NDP	10	0
3	C	600[A]	GOL	4	0
3	C	600[B]	GOL	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	500	NDP	10	0
3	D	600[A]	GOL	2	0
3	D	600[B]	GOL	4	0
2	E	500	NDP	10	0
3	E	600[A]	GOL	5	0
3	E	600[B]	GOL	3	0
2	F	500	NDP	10	0
3	F	600[A]	GOL	3	0
3	F	600[B]	GOL	3	0
2	G	500	NDP	7	0
3	G	600[A]	GOL	2	0
3	G	600[B]	GOL	3	0
2	H	500	NDP	8	0
3	H	600[A]	GOL	3	0
3	H	600[B]	GOL	2	0
2	I	500	NDP	6	0
3	I	600[A]	GOL	2	0
3	I	600[B]	GOL	2	0
2	J	500	NDP	10	0
3	J	600[A]	GOL	3	0
3	J	600[B]	GOL	3	0
2	K	500	NDP	9	0
3	K	600[A]	GOL	2	0
3	K	600[B]	GOL	3	0
2	L	500	NDP	10	0
3	L	600[A]	GOL	4	0
3	L	600[B]	GOL	3	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^{th} 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^2)	Q<0.9
1	A	383/433 (88%)	-0.47	5 (1%)	79 83	12, 18, 30, 48	0
1	B	381/433 (87%)	-0.21	9 (2%)	62 68	13, 23, 38, 45	0
1	C	382/433 (88%)	-0.36	3 (0%)	87 90	14, 21, 32, 45	0
1	D	382/433 (88%)	0.11	23 (6%)	25 28	16, 31, 44, 53	0
1	E	382/433 (88%)	-0.34	3 (0%)	87 90	14, 22, 32, 44	0
1	F	381/433 (87%)	0.09	12 (3%)	52 60	16, 30, 46, 52	0
1	G	381/433 (87%)	-0.47	3 (0%)	87 90	12, 18, 30, 40	0
1	H	381/433 (87%)	-0.17	8 (2%)	67 72	14, 23, 39, 46	0
1	I	382/433 (88%)	-0.54	2 (0%)	91 93	10, 16, 28, 39	0
1	J	381/433 (87%)	-0.44	2 (0%)	91 93	11, 19, 30, 42	0
1	K	382/433 (88%)	-0.54	2 (0%)	91 93	10, 16, 27, 39	0
1	L	381/433 (87%)	-0.43	1 (0%)	94 95	11, 19, 29, 40	0
All	All	4579/5196 (88%)	-0.31	73 (1%)	74 79	10, 21, 38, 53	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	52	ALA	7.0
1	C	52	ALA	6.0
1	K	52	ALA	5.7
1	E	52	ALA	5.4
1	I	52	ALA	5.0

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 (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^{th} 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^2)	Q<0.9
3	GOL	I	600[B]	6/6	0.63	0.31	20.04	30,30,32,33	1
3	GOL	I	600[A]	6/6	0.63	0.31	20.04	29,30,32,33	1
3	GOL	L	600[B]	6/6	0.41	0.40	16.46	31,34,35,35	1
3	GOL	L	600[A]	6/6	0.41	0.40	16.46	32,34,35,35	1
3	GOL	K	600[B]	6/6	0.56	0.32	15.29	31,31,32,33	1
3	GOL	K	600[A]	6/6	0.56	0.32	15.29	29,31,32,33	1
3	GOL	E	600[B]	6/6	0.46	0.34	14.46	32,34,34,35	1
3	GOL	E	600[A]	6/6	0.46	0.34	14.46	33,34,34,35	1
3	GOL	C	600[B]	6/6	0.56	0.31	13.91	31,33,33,33	1
3	GOL	C	600[A]	6/6	0.56	0.31	13.91	32,33,33,33	1
3	GOL	J	600[A]	6/6	0.41	0.34	13.90	30,30,31,31	1
3	GOL	H	600[B]	6/6	0.45	0.33	12.60	36,37,38,38	1
3	GOL	H	600[A]	6/6	0.45	0.33	12.60	36,37,38,38	1
3	GOL	G	600[B]	6/6	0.48	0.28	11.85	28,29,30,31	1
3	GOL	G	600[A]	6/6	0.48	0.28	11.85	25,28,29,31	1
3	GOL	A	600[B]	6/6	0.59	0.28	11.61	21,23,25,25	1
3	GOL	A	600[A]	6/6	0.59	0.28	11.61	18,22,23,25	1
3	GOL	J	600[B]	6/6	0.41	0.34	11.22	27,30,31,31	1
3	GOL	B	600[B]	6/6	0.50	0.33	10.06	31,33,35,35	1
3	GOL	B	600[A]	6/6	0.50	0.33	9.60	33,34,35,35	1
3	GOL	F	600[A]	6/6	0.37	0.29	8.27	42,43,43,43	1
3	GOL	F	600[B]	6/6	0.37	0.29	8.27	42,43,43,43	1
3	GOL	D	600[B]	6/6	0.47	0.30	7.29	43,44,44,44	1
3	GOL	D	600[A]	6/6	0.47	0.30	7.29	42,44,44,44	1
2	NDP	C	500	48/48	0.96	0.10	0.46	15,19,24,26	0
2	NDP	A	500	48/48	0.96	0.10	0.42	12,15,17,17	0
2	NDP	K	500	48/48	0.97	0.09	0.33	10,16,18,18	0
2	NDP	L	500	48/48	0.97	0.09	0.17	13,19,21,22	0
2	NDP	I	500	48/48	0.97	0.09	0.15	10,15,18,18	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	NDP	G	500	48/48	0.97	0.09	0.15	13,16,18,19	0
2	NDP	F	500	48/48	0.91	0.13	0.14	28,33,42,43	0
2	NDP	J	500	48/48	0.96	0.09	0.13	15,19,22,22	0
2	NDP	E	500	48/48	0.96	0.10	0.13	15,20,22,23	0
2	NDP	B	500	48/48	0.96	0.10	-0.12	18,23,26,26	0
2	NDP	D	500	48/48	0.93	0.12	-0.27	25,34,43,43	0
2	NDP	H	500	48/48	0.96	0.09	-0.27	19,22,26,26	0

6.5 Other polymers

There are no such residues in this entry.