



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 05:34 PM GMT

PDB ID : 1G0R
Title : THE STRUCTURAL BASIS OF THE CATALYTIC MECHANISM AND
REGULATION OF GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSF
ERASE(RMLA). THYMIDINE/GLUCOSE-1-PHOSPHATECOMPLEX.
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Deposited on : 2000-10-07
Resolution : 1.87 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

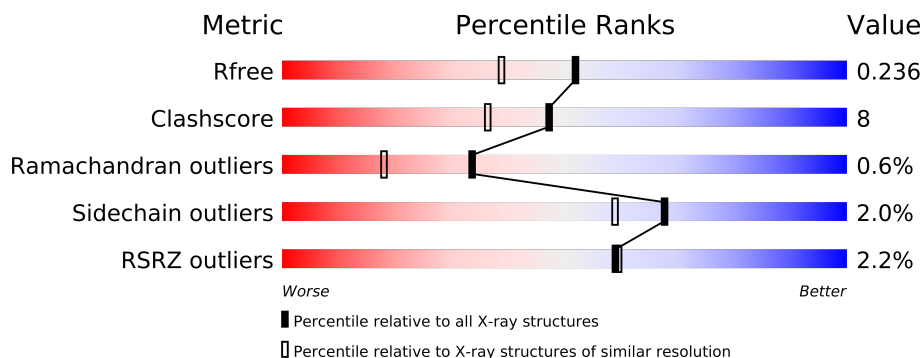
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.87 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	5260 (1.90-1.86)
Clashscore	79885	6268 (1.90-1.86)
Ramachandran outliers	78287	6195 (1.90-1.86)
Sidechain outliers	78261	6196 (1.90-1.86)
RSRZ outliers	66119	5262 (1.90-1.86)

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. 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	293	
1	B	293	
1	C	293	
1	D	293	
1	E	293	
1	F	293	
1	G	293	
1	H	293	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	G1P	B	2501	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	A	2507	-	X
3	SO4	B	2510	-	X
3	SO4	C	2515	-	X
3	SO4	E	2520	-	X
3	SO4	F	2522	-	X
3	SO4	G	2525	-	X
3	SO4	H	2529	-	X

2 Entry composition

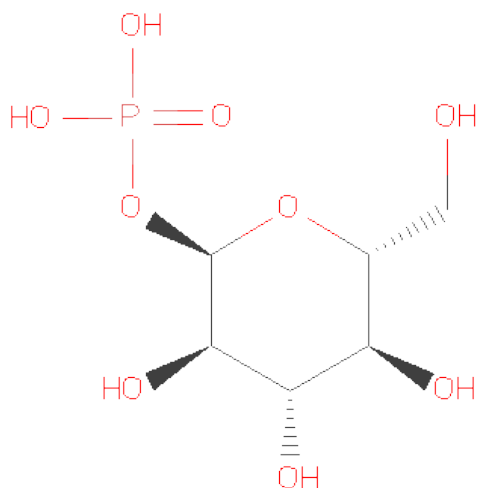
There are 5 unique types of molecules in this entry. The entry contains 21361 atoms, of which 0 are hydrogen and 0 are deuterium.

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 GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	292	Total	C	N	O	S	0	6	0
			2338	1493	396	444	5			
1	B	292	Total	C	N	O	S	0	8	0
			2350	1501	396	447	6			
1	C	292	Total	C	N	O	S	0	5	0
			2332	1491	395	441	5			
1	D	292	Total	C	N	O	S	0	5	0
			2325	1486	391	442	6			
1	E	292	Total	C	N	O	S	0	4	0
			2312	1477	389	440	6			
1	F	293	Total	C	N	O	S	0	5	0
			2340	1496	395	443	6			
1	G	292	Total	C	N	O	S	0	5	0
			2326	1487	390	443	6			
1	H	292	Total	C	N	O	S	0	2	0
			2303	1474	387	437	5			

- Molecule 2 is GLUCOSE-1-PHOSPHATE (three-letter code: G1P) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		
2	C	1	Total	C	O	P	0	0
			16	6	9	1		
2	D	1	Total	C	O	P	0	0
			16	6	9	1		
2	E	1	Total	C	O	P	0	0
			16	6	9	1		
2	G	1	Total	C	O	P	0	0
			16	6	9	1		
2	H	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



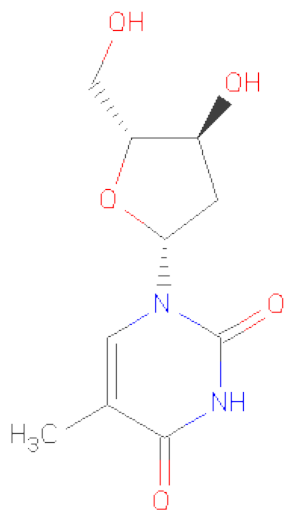
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is THYMIDINE (three-letter code: THM) (formula: C₁₀H₁₄N₂O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	10	2	5		
4	B	1	Total	C	N	O	0	0
			17	10	2	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	0	0
			17	10	2	5		
4	D	1	Total	C	N	O	0	0
			17	10	2	5		
4	E	1	Total	C	N	O	0	0
			17	10	2	5		
4	F	1	Total	C	N	O	0	0
			17	10	2	5		
4	G	1	Total	C	N	O	0	0
			17	10	2	5		
4	H	1	Total	C	N	O	0	0
			17	10	2	5		
4	A	1	Total	C	N	O	0	0
			17	10	2	5		
4	B	1	Total	C	N	O	0	0
			17	10	2	5		
4	C	1	Total	C	N	O	0	0
			17	10	2	5		
4	D	1	Total	C	N	O	0	0
			17	10	2	5		
4	E	1	Total	C	N	O	0	0
			17	10	2	5		
4	F	1	Total	C	N	O	0	0
			17	10	2	5		
4	G	1	Total	C	N	O	0	0
			17	10	2	5		
4	H	1	Total	C	N	O	0	0
			17	10	2	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	286	Total	O	0	0
			286	286		
5	B	307	Total	O	0	0
			307	307		
5	C	272	Total	O	0	0
			272	272		
5	D	266	Total	O	0	0
			266	266		
5	E	202	Total	O	0	0
			202	202		

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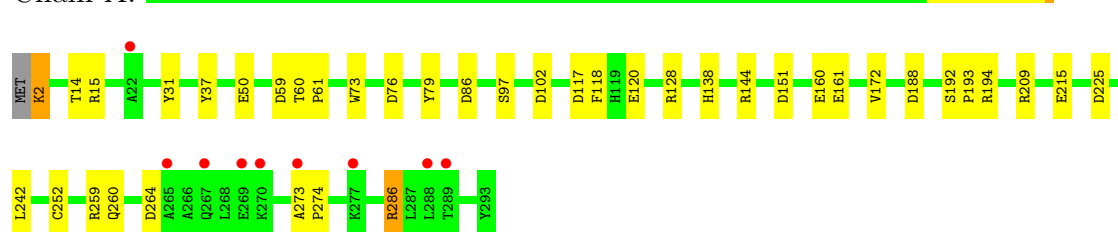
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	287	Total 287	O 287	0	0
5	G	327	Total 327	O 327	0	0
5	H	289	Total 289	O 289	0	0

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.

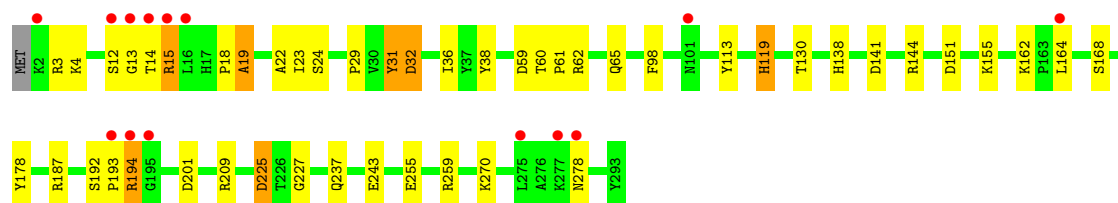
• Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE

Chain A:



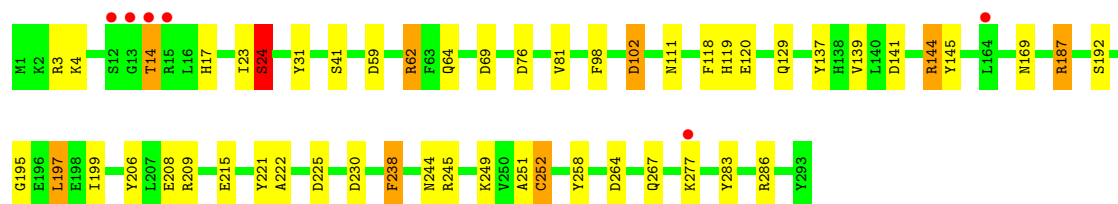
- Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE

Chain E:



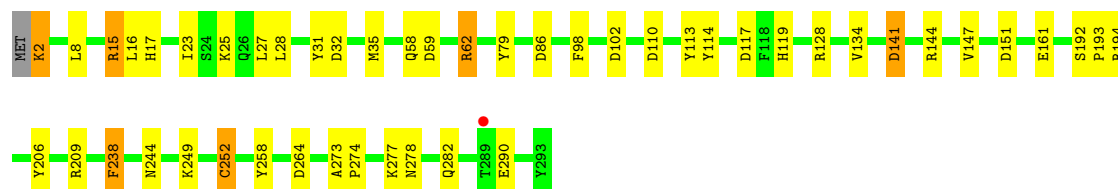
- Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE

Chain F:



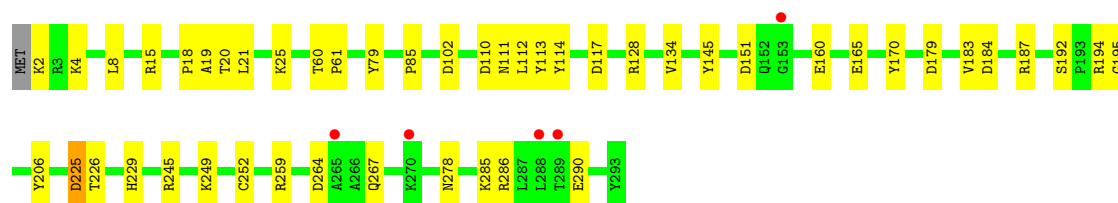
- Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE

Chain G:



- Molecule 1: GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE

Chain H:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.27Å 73.08Å 133.65Å 89.98° 81.42° 81.56°	Depositor
Resolution (Å)	73.00 – 1.87 36.27 – 1.87	Depositor EDS
% Data completeness (in resolution range)	84.0 (73.00-1.87) 84.7 (36.27-1.87)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.147 , 0.221 0.168 , 0.236	Depositor DCC
R_{free} test set	9145 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 183187 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21361	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: THM, SO4, G1P

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.44	10/2389 (0.4%)	1.17	16/3241 (0.5%)
1	B	1.46	13/2401 (0.5%)	1.19	16/3256 (0.5%)
1	C	1.43	7/2383 (0.3%)	1.20	14/3232 (0.4%)
1	D	1.40	10/2375 (0.4%)	1.19	12/3222 (0.4%)
1	E	1.31	7/2362 (0.3%)	1.14	10/3205 (0.3%)
1	F	1.49	17/2391 (0.7%)	1.25	14/3242 (0.4%)
1	G	1.53	20/2377 (0.8%)	1.32	22/3225 (0.7%)
1	H	1.42	10/2354 (0.4%)	1.15	11/3195 (0.3%)
All	All	1.44	94/19032 (0.5%)	1.20	115/25818 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2
1	E	0	1
All	All	0	3

The worst 5 of 94 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	114	TYR	CG-CD1	-10.11	1.26	1.39
1	F	81	VAL	CB-CG1	-9.19	1.33	1.52
1	C	137	TYR	CD1-CE1	-8.48	1.26	1.39
1	C	55	SER	CB-OG	8.20	1.52	1.42
1	C	223	TRP	CE3-CZ3	-7.56	1.25	1.38

The worst 5 of 115 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	209	ARG	NE-CZ-NH2	-13.04	113.78	120.30
1	D	188	ASP	CB-CG-OD2	10.32	127.58	118.30
1	G	141	ASP	CB-CG-OD2	10.29	127.56	118.30
1	G	35[A]	MET	CB-CG-SD	-10.18	81.86	112.40
1	G	35[B]	MET	CB-CG-SD	-10.18	81.86	112.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	119	HIS	Sidechain
1	D	16	LEU	Peptide
1	E	119	HIS	Sidechain

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	2338	0	0	12	0
1	B	2350	0	0	20	0
1	C	2332	0	0	26	0
1	D	2325	0	0	15	0
1	E	2312	0	0	25	0
1	F	2340	0	0	23	0
1	G	2326	0	0	17	0
1	H	2303	0	0	21	0
2	A	16	0	0	0	0
2	B	16	0	0	0	0
2	C	16	0	0	1	0
2	D	16	0	0	1	0
2	E	16	0	0	1	0
2	G	16	0	0	0	0
2	H	16	0	0	0	0
3	A	10	0	0	3	0
3	B	15	0	0	0	0
3	C	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	20	0	0	0	0
3	E	10	0	0	0	0
3	F	20	0	0	0	0
3	G	10	0	0	1	0
3	H	15	0	0	3	0
4	A	34	0	0	0	0
4	B	34	0	0	0	0
4	C	34	0	0	0	0
4	D	34	0	0	0	0
4	E	34	0	0	0	0
4	F	34	0	0	0	0
4	G	34	0	0	0	0
4	H	34	0	0	0	0
5	A	286	0	0	5	0
5	B	307	0	0	11	0
5	C	272	0	0	11	0
5	D	266	0	0	5	0
5	E	202	0	0	6	0
5	F	287	0	0	11	0
5	G	327	0	0	9	0
5	H	289	0	0	10	0
All	All	21361	0	0	153	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 8.

The worst 5 of 153 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:141:ASP:CB	5:B:2787:HOH:O	2.18	0.90
1:C:13:GLY:O	1:C:17:HIS:CD2	2.29	0.84
1:A:2:LYS:NZ	1:A:50:GLU:OE1	2.10	0.84
1:F:119:HIS:CE1	1:F:120:GLU:OE1	2.31	0.84
1:G:141:ASP:CB	5:G:2617:HOH:O	2.30	0.78

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	296/293 (101%)	290 (98%)	6 (2%)	0	100	100
1	B	298/293 (102%)	293 (98%)	3 (1%)	2 (1%)	30	14
1	C	295/293 (101%)	287 (97%)	6 (2%)	2 (1%)	30	14
1	D	295/293 (101%)	284 (96%)	7 (2%)	4 (1%)	16	4
1	E	294/293 (100%)	279 (95%)	12 (4%)	3 (1%)	22	8
1	F	296/293 (101%)	289 (98%)	5 (2%)	2 (1%)	30	14
1	G	295/293 (101%)	291 (99%)	3 (1%)	1 (0%)	50	36
1	H	292/293 (100%)	285 (98%)	7 (2%)	0	100	100
All	All	2361/2344 (101%)	2298 (97%)	49 (2%)	14 (1%)	33	18

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	14	THR
1	E	14	THR
1	B	23	ILE
1	F	31	TYR
1	B	31	TYR

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	245/240 (102%)	244 (100%)	1 (0%)	95	94
1	B	247/240 (103%)	241 (98%)	6 (2%)	61	50
1	C	244/240 (102%)	240 (98%)	4 (2%)	75	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	244/240 (102%)	239 (98%)	5 (2%)	68	59
1	E	243/240 (101%)	233 (96%)	10 (4%)	41	26
1	F	245/240 (102%)	240 (98%)	5 (2%)	68	59
1	G	244/240 (102%)	241 (99%)	3 (1%)	82	78
1	H	241/240 (100%)	236 (98%)	5 (2%)	66	56
All	All	1953/1920 (102%)	1914 (98%)	39 (2%)	68	59

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	23	ILE
1	E	164	LEU
1	H	112	LEU
1	E	24	SER
1	E	36	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

46 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	G1P	A	2500	-	16,16,16	1.85	2 (12%)	24,24,24	2.64	8 (33%)
3	SO4	A	2507	-	4,4,4	1.38	1 (25%)	6,6,6	0.82	0
3	SO4	A	2508	-	4,4,4	1.73	1 (25%)	6,6,6	1.47	1 (16%)
4	THM	A	2530	-	18,18,18	2.15	5 (27%)	21,26,26	3.36	12 (57%)
4	THM	A	2538	-	18,18,18	2.71	6 (33%)	21,26,26	1.89	8 (38%)
2	G1P	B	2501	-	16,16,16	2.13	4 (25%)	24,24,24	4.61	7 (29%)
3	SO4	B	2510	-	4,4,4	0.44	0	6,6,6	0.37	0
3	SO4	B	2511	-	4,4,4	1.66	0	6,6,6	1.15	1 (16%)
3	SO4	B	2528	-	4,4,4	1.49	1 (25%)	6,6,6	0.50	0
4	THM	B	2531	-	18,18,18	2.11	4 (22%)	21,26,26	2.50	9 (42%)
4	THM	B	2539	-	18,18,18	2.26	3 (16%)	21,26,26	2.29	8 (38%)
2	G1P	C	2502	-	16,16,16	2.02	5 (31%)	24,24,24	3.88	7 (29%)
3	SO4	C	2509	-	4,4,4	1.32	0	6,6,6	1.32	1 (16%)
3	SO4	C	2513	-	4,4,4	2.33	3 (75%)	6,6,6	0.77	0
3	SO4	C	2515	-	4,4,4	0.45	0	6,6,6	0.45	0
4	THM	C	2532	-	18,18,18	2.42	4 (22%)	21,26,26	3.21	12 (57%)
4	THM	C	2540	-	18,18,18	2.40	6 (33%)	21,26,26	2.40	5 (23%)
2	G1P	D	2503	-	16,16,16	1.99	5 (31%)	24,24,24	3.65	10 (41%)
3	SO4	D	2512	-	4,4,4	1.06	0	6,6,6	0.82	0
3	SO4	D	2514	-	4,4,4	0.73	0	6,6,6	0.80	0
3	SO4	D	2516	-	4,4,4	1.73	2 (50%)	6,6,6	0.12	0
3	SO4	D	2517	-	4,4,4	0.48	0	6,6,6	0.66	0
4	THM	D	2533	-	18,18,18	2.33	3 (16%)	21,26,26	2.17	7 (33%)
4	THM	D	2541	-	18,18,18	1.69	3 (16%)	21,26,26	3.03	8 (38%)
2	G1P	E	2504	-	16,16,16	1.90	3 (18%)	24,24,24	5.13	8 (33%)
3	SO4	E	2520	-	4,4,4	0.23	0	6,6,6	0.46	0
3	SO4	E	2527	-	4,4,4	2.13	2 (50%)	6,6,6	0.97	1 (16%)
4	THM	E	2534	-	18,18,18	2.28	4 (22%)	21,26,26	3.18	9 (42%)
4	THM	E	2542	-	18,18,18	2.51	8 (44%)	21,26,26	2.32	6 (28%)
3	SO4	F	2519	-	4,4,4	0.66	0	6,6,6	0.61	0
3	SO4	F	2521	-	4,4,4	1.38	1 (25%)	6,6,6	0.70	0
3	SO4	F	2522	-	4,4,4	0.65	0	6,6,6	0.65	0
3	SO4	F	2524	-	4,4,4	0.97	0	6,6,6	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	THM	F	2535	-	18,18,18	2.07	5 (27%)	21,26,26	3.07	14 (66%)
4	THM	F	2543	-	18,18,18	2.28	4 (22%)	21,26,26	2.33	6 (28%)
2	G1P	G	2505	-	16,16,16	1.63	2 (12%)	24,24,24	3.36	7 (29%)
3	SO4	G	2523	-	4,4,4	1.35	0	6,6,6	0.90	0
3	SO4	G	2525	-	4,4,4	0.69	0	6,6,6	1.07	1 (16%)
4	THM	G	2536	-	18,18,18	1.95	6 (33%)	21,26,26	2.84	9 (42%)
4	THM	G	2544	-	18,18,18	1.99	4 (22%)	21,26,26	1.97	4 (19%)
2	G1P	H	2506	-	16,16,16	1.73	4 (25%)	24,24,24	3.81	6 (25%)
3	SO4	H	2518	-	4,4,4	1.06	0	6,6,6	0.36	0
3	SO4	H	2526	-	4,4,4	0.50	0	6,6,6	0.26	0
3	SO4	H	2529	-	4,4,4	0.88	0	6,6,6	1.20	1 (16%)
4	THM	H	2537	-	18,18,18	2.83	7 (38%)	21,26,26	2.65	7 (33%)
4	THM	H	2545	-	18,18,18	2.13	7 (38%)	21,26,26	2.60	10 (47%)

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	G1P	A	2500	-	-	0/7/27/27	0/1/1/1
3	SO4	A	2507	-	-	0/0/0/0	0/0/0/0
3	SO4	A	2508	-	-	0/0/0/0	0/0/0/0
4	THM	A	2530	-	-	0/3/18/18	0/2/2/2
4	THM	A	2538	-	-	0/3/18/18	0/2/2/2
2	G1P	B	2501	-	-	0/7/27/27	0/1/1/1
3	SO4	B	2510	-	-	0/0/0/0	0/0/0/0
3	SO4	B	2511	-	-	0/0/0/0	0/0/0/0
3	SO4	B	2528	-	-	0/0/0/0	0/0/0/0
4	THM	B	2531	-	-	0/3/18/18	0/2/2/2
4	THM	B	2539	-	-	0/3/18/18	0/2/2/2
2	G1P	C	2502	-	-	0/7/27/27	0/1/1/1
3	SO4	C	2509	-	-	0/0/0/0	0/0/0/0
3	SO4	C	2513	-	-	0/0/0/0	0/0/0/0
3	SO4	C	2515	-	-	0/0/0/0	0/0/0/0
4	THM	C	2532	-	-	0/3/18/18	0/2/2/2
4	THM	C	2540	-	-	0/3/18/18	0/2/2/2
2	G1P	D	2503	-	-	0/7/27/27	0/1/1/1
3	SO4	D	2512	-	-	0/0/0/0	0/0/0/0
3	SO4	D	2514	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	D	2516	-	-	0/0/0/0	0/0/0/0
3	SO4	D	2517	-	-	0/0/0/0	0/0/0/0
4	THM	D	2533	-	-	0/3/18/18	0/2/2/2
4	THM	D	2541	-	-	0/3/18/18	0/2/2/2
2	G1P	E	2504	-	-	0/7/27/27	0/1/1/1
3	SO4	E	2520	-	-	0/0/0/0	0/0/0/0
3	SO4	E	2527	-	-	0/0/0/0	0/0/0/0
4	THM	E	2534	-	-	0/3/18/18	0/2/2/2
4	THM	E	2542	-	-	0/3/18/18	0/2/2/2
3	SO4	F	2519	-	-	0/0/0/0	0/0/0/0
3	SO4	F	2521	-	-	0/0/0/0	0/0/0/0
3	SO4	F	2522	-	-	0/0/0/0	0/0/0/0
3	SO4	F	2524	-	-	0/0/0/0	0/0/0/0
4	THM	F	2535	-	-	0/3/18/18	0/2/2/2
4	THM	F	2543	-	-	0/3/18/18	0/2/2/2
2	G1P	G	2505	-	-	0/7/27/27	0/1/1/1
3	SO4	G	2523	-	-	0/0/0/0	0/0/0/0
3	SO4	G	2525	-	-	0/0/0/0	0/0/0/0
4	THM	G	2536	-	-	0/3/18/18	0/2/2/2
4	THM	G	2544	-	-	0/3/18/18	0/2/2/2
2	G1P	H	2506	-	-	0/7/27/27	0/1/1/1
3	SO4	H	2518	-	-	0/0/0/0	0/0/0/0
3	SO4	H	2526	-	-	0/0/0/0	0/0/0/0
3	SO4	H	2529	-	-	0/0/0/0	0/0/0/0
4	THM	H	2537	-	-	0/3/18/18	0/2/2/2
4	THM	H	2545	-	-	0/3/18/18	0/2/2/2

The worst 5 of 115 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	2537	THM	C2-N1	-7.51	1.30	1.38
4	A	2538	THM	C2-N1	-7.10	1.30	1.38
4	C	2532	THM	C2-N1	-7.10	1.30	1.38
4	C	2540	THM	C2-N1	-6.58	1.31	1.38
4	F	2543	THM	C2-N1	-6.47	1.31	1.38

The worst 5 of 193 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2504	G1P	O5-C1-O1	-22.82	81.54	111.36
2	B	2501	G1P	O5-C1-O1	-18.25	87.50	111.36
2	H	2506	G1P	O5-C1-O1	-15.76	90.76	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2502	G1P	O5-C1-O1	-15.28	91.39	111.36
2	D	2503	G1P	O5-C1-O1	-14.59	92.29	111.36

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, 95th 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	292/293 (99%)	-0.13	9 (3%) 47 46	8, 16, 31, 40	0
1	B	292/293 (99%)	-0.23	3 (1%) 79 81	7, 14, 27, 34	0
1	C	292/293 (99%)	-0.18	4 (1%) 72 73	9, 16, 32, 49	0
1	D	292/293 (99%)	-0.04	9 (3%) 47 46	9, 18, 36, 57	0
1	E	292/293 (99%)	0.16	14 (4%) 29 29	11, 22, 42, 63	0
1	F	293/293 (100%)	-0.15	6 (2%) 62 63	7, 15, 33, 56	0
1	G	292/293 (99%)	-0.24	1 (0%) 91 93	7, 13, 26, 42	0
1	H	292/293 (99%)	-0.16	5 (1%) 67 68	11, 18, 30, 43	0
All	All	2337/2344 (99%)	-0.12	51 (2%) 59 59	7, 16, 33, 63	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	13	GLY	5.8
1	C	14	THR	5.7
1	F	13	GLY	5.4
1	E	195	GLY	5.4
1	F	14	THR	5.3

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, 95th 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 ²)	Q<0.9
3	SO4	H	2529	5/5	0.22	20.24	45,45,50,51	0
3	SO4	G	2525	5/5	0.32	4.59	45,46,47,52	0
3	SO4	E	2520	5/5	0.31	4.05	45,46,52,56	0
3	SO4	C	2515	5/5	0.24	3.82	40,48,51,52	0
3	SO4	A	2507	5/5	0.23	3.51	45,47,50,52	0
3	SO4	F	2522	5/5	0.26	2.87	39,45,48,53	0
2	G1P	B	2501	16/16	0.18	2.68	29,40,44,45	0
3	SO4	B	2510	5/5	0.22	2.23	40,48,51,53	0
2	G1P	E	2504	16/16	0.17	1.84	34,47,56,59	0
4	THM	C	2540	17/17	0.12	1.62	20,22,25,26	0
2	G1P	C	2502	16/16	0.15	1.06	30,42,48,49	0
4	THM	E	2542	17/17	0.13	1.04	26,30,32,32	0
4	THM	H	2537	17/17	0.11	0.90	20,26,33,39	0
4	THM	F	2543	17/17	0.14	0.89	19,23,26,27	0
4	THM	G	2544	17/17	0.13	0.88	17,22,25,27	0
4	THM	B	2539	17/17	0.12	0.88	21,24,25,28	0
3	SO4	B	2511	5/5	0.11	0.87	20,21,26,26	0
4	THM	F	2535	17/17	0.11	0.84	22,30,44,47	0
4	THM	B	2531	17/17	0.11	0.79	19,24,33,35	0
4	THM	E	2534	17/17	0.15	0.77	39,45,50,55	0
3	SO4	F	2519	5/5	0.15	0.68	55,56,57,60	0
4	THM	C	2532	17/17	0.10	0.63	24,30,38,45	0
4	THM	G	2536	17/17	0.10	0.62	20,24,29,29	0
4	THM	D	2541	17/17	0.11	0.55	19,21,24,24	0
4	THM	A	2538	17/17	0.12	0.48	19,22,25,27	0
2	G1P	G	2505	16/16	0.11	0.45	26,32,37,38	0
2	G1P	D	2503	16/16	0.12	0.43	30,37,41,42	0
4	THM	A	2530	17/17	0.10	0.30	24,29,32,38	0
4	THM	H	2545	17/17	0.12	0.28	19,25,27,31	0
3	SO4	D	2512	5/5	0.11	0.28	38,42,43,45	0
4	THM	D	2533	17/17	0.10	0.16	27,30,35,37	0
2	G1P	H	2506	16/16	0.11	0.06	29,34,41,42	0
3	SO4	A	2508	5/5	0.10	0.05	22,23,24,24	0
3	SO4	B	2528	5/5	0.09	-0.20	39,41,43,43	0
2	G1P	A	2500	16/16	0.09	-0.24	28,30,40,40	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	C	2509	5/5	0.09	-0.32	31,37,40,45	0
3	SO4	F	2524	5/5	0.07	-0.52	36,38,41,42	0
3	SO4	C	2513	5/5	0.09	-0.52	21,22,24,25	0
3	SO4	D	2514	5/5	0.09	-0.62	48,50,51,52	0
3	SO4	G	2523	5/5	0.09	-0.69	19,20,23,27	0
3	SO4	D	2516	5/5	0.09	-0.73	18,22,23,25	0
3	SO4	F	2521	5/5	0.10	-0.79	19,20,23,26	0
3	SO4	H	2518	5/5	0.08	-0.84	24,24,26,26	0
3	SO4	D	2517	5/5	0.17	-0.86	45,48,52,56	0
3	SO4	H	2526	5/5	0.07	-0.87	39,41,42,43	0
3	SO4	E	2527	5/5	0.08	-1.55	22,23,24,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.