



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 11:16 AM BST

PDB ID : 4KQ2
Title : Glucose1,2cyclic phosphate bound activated state of Yeast Glycogen Synthase
Authors : Chikwana, V.M.; Hurley, T.D.
Deposited on : 2013-05-14
Resolution : 2.95 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

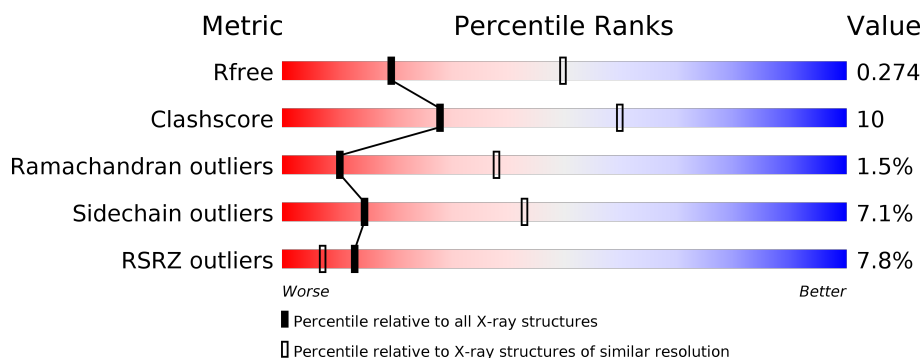
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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}	130704	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 respectively. 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.

Mol	Chain	Length	Quality of chain
1	A	724	<div> <div>7%</div> <div> <div></div> <div>66%</div> <div>20%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	724	<div> <div>3%</div> <div> <div></div> <div>67%</div> <div>18%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	724	<div> <div>11%</div> <div> <div></div> <div>64%</div> <div>21%</div> <div>•</div> <div>12%</div> </div> </div>
1	D	724	<div> <div>7%</div> <div> <div></div> <div>64%</div> <div>22%</div> <div>•</div> <div>12%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20806 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 Gsy2p.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	638	Total	C	N	O	S	0	0	0
			5145	3286	896	944	19			
1	B	638	Total	C	N	O	S	0	3	0
			5163	3298	900	946	19			
1	C	638	Total	C	N	O	S	0	1	0
			5154	3291	898	946	19			
1	D	636	Total	C	N	O	S	0	2	0
			5146	3284	897	946	19			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP E7NKU1
A	-17	GLY	-	expression tag	UNP E7NKU1
A	-16	SER	-	expression tag	UNP E7NKU1
A	-15	SER	-	expression tag	UNP E7NKU1
A	-14	HIS	-	expression tag	UNP E7NKU1
A	-13	HIS	-	expression tag	UNP E7NKU1
A	-12	HIS	-	expression tag	UNP E7NKU1
A	-11	HIS	-	expression tag	UNP E7NKU1
A	-10	HIS	-	expression tag	UNP E7NKU1
A	-9	HIS	-	expression tag	UNP E7NKU1
A	-8	SER	-	expression tag	UNP E7NKU1
A	-7	SER	-	expression tag	UNP E7NKU1
A	-6	GLY	-	expression tag	UNP E7NKU1
A	-5	LEU	-	expression tag	UNP E7NKU1
A	-4	VAL	-	expression tag	UNP E7NKU1
A	-3	PRO	-	expression tag	UNP E7NKU1
A	-2	ARG	-	expression tag	UNP E7NKU1
A	-1	GLY	-	expression tag	UNP E7NKU1
A	0	SER	-	expression tag	UNP E7NKU1
A	589	ALA	ARG	engineered mutation	UNP E7NKU1
A	592	ALA	ARG	engineered mutation	UNP E7NKU1

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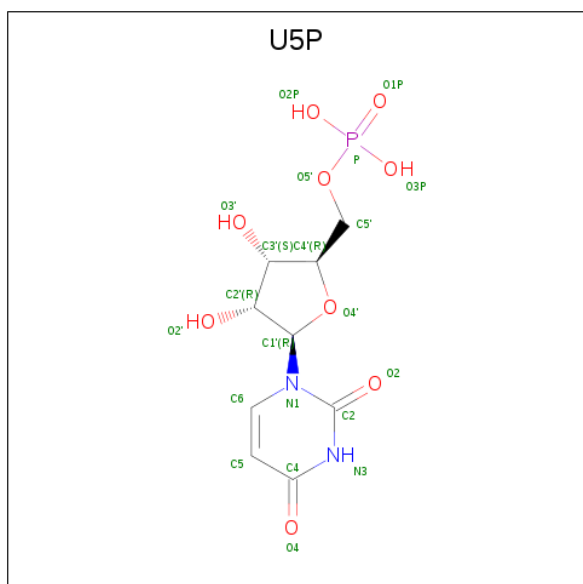
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	MET	-	initiating methionine	UNP E7NKU1
B	-17	GLY	-	expression tag	UNP E7NKU1
B	-16	SER	-	expression tag	UNP E7NKU1
B	-15	SER	-	expression tag	UNP E7NKU1
B	-14	HIS	-	expression tag	UNP E7NKU1
B	-13	HIS	-	expression tag	UNP E7NKU1
B	-12	HIS	-	expression tag	UNP E7NKU1
B	-11	HIS	-	expression tag	UNP E7NKU1
B	-10	HIS	-	expression tag	UNP E7NKU1
B	-9	HIS	-	expression tag	UNP E7NKU1
B	-8	SER	-	expression tag	UNP E7NKU1
B	-7	SER	-	expression tag	UNP E7NKU1
B	-6	GLY	-	expression tag	UNP E7NKU1
B	-5	LEU	-	expression tag	UNP E7NKU1
B	-4	VAL	-	expression tag	UNP E7NKU1
B	-3	PRO	-	expression tag	UNP E7NKU1
B	-2	ARG	-	expression tag	UNP E7NKU1
B	-1	GLY	-	expression tag	UNP E7NKU1
B	0	SER	-	expression tag	UNP E7NKU1
B	589	ALA	ARG	engineered mutation	UNP E7NKU1
B	592	ALA	ARG	engineered mutation	UNP E7NKU1
C	-18	MET	-	initiating methionine	UNP E7NKU1
C	-17	GLY	-	expression tag	UNP E7NKU1
C	-16	SER	-	expression tag	UNP E7NKU1
C	-15	SER	-	expression tag	UNP E7NKU1
C	-14	HIS	-	expression tag	UNP E7NKU1
C	-13	HIS	-	expression tag	UNP E7NKU1
C	-12	HIS	-	expression tag	UNP E7NKU1
C	-11	HIS	-	expression tag	UNP E7NKU1
C	-10	HIS	-	expression tag	UNP E7NKU1
C	-9	HIS	-	expression tag	UNP E7NKU1
C	-8	SER	-	expression tag	UNP E7NKU1
C	-7	SER	-	expression tag	UNP E7NKU1
C	-6	GLY	-	expression tag	UNP E7NKU1
C	-5	LEU	-	expression tag	UNP E7NKU1
C	-4	VAL	-	expression tag	UNP E7NKU1
C	-3	PRO	-	expression tag	UNP E7NKU1
C	-2	ARG	-	expression tag	UNP E7NKU1
C	-1	GLY	-	expression tag	UNP E7NKU1
C	0	SER	-	expression tag	UNP E7NKU1
C	589	ALA	ARG	engineered mutation	UNP E7NKU1
C	592	ALA	ARG	engineered mutation	UNP E7NKU1

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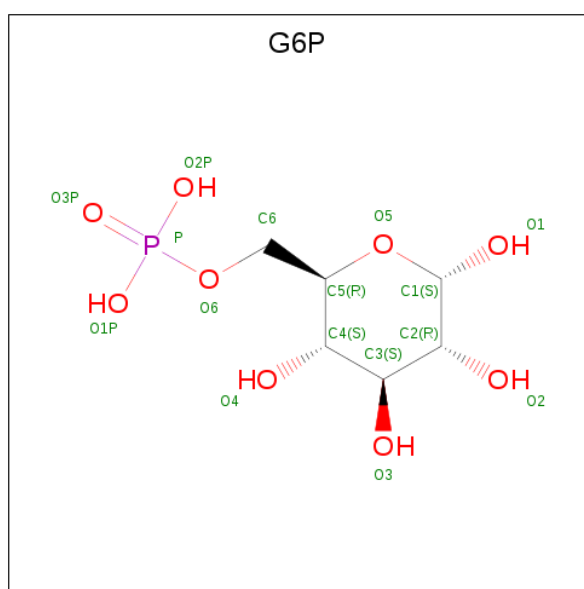
Chain	Residue	Modelled	Actual	Comment	Reference
D	-18	MET	-	initiating methionine	UNP E7NKU1
D	-17	GLY	-	expression tag	UNP E7NKU1
D	-16	SER	-	expression tag	UNP E7NKU1
D	-15	SER	-	expression tag	UNP E7NKU1
D	-14	HIS	-	expression tag	UNP E7NKU1
D	-13	HIS	-	expression tag	UNP E7NKU1
D	-12	HIS	-	expression tag	UNP E7NKU1
D	-11	HIS	-	expression tag	UNP E7NKU1
D	-10	HIS	-	expression tag	UNP E7NKU1
D	-9	HIS	-	expression tag	UNP E7NKU1
D	-8	SER	-	expression tag	UNP E7NKU1
D	-7	SER	-	expression tag	UNP E7NKU1
D	-6	GLY	-	expression tag	UNP E7NKU1
D	-5	LEU	-	expression tag	UNP E7NKU1
D	-4	VAL	-	expression tag	UNP E7NKU1
D	-3	PRO	-	expression tag	UNP E7NKU1
D	-2	ARG	-	expression tag	UNP E7NKU1
D	-1	GLY	-	expression tag	UNP E7NKU1
D	0	SER	-	expression tag	UNP E7NKU1
D	589	ALA	ARG	engineered mutation	UNP E7NKU1
D	592	ALA	ARG	engineered mutation	UNP E7NKU1

- Molecule 2 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U5P) (formula: $C_9H_{13}N_2O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	B	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	C	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
2	D	1	Total	C	N	O	P	0	0
			21	9	2	9	1		

- Molecule 3 is 6-O-phosphono-alpha-D-glucopyranose (three-letter code: G6P) (formula: $C_6H_{13}O_9P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			16	6	9	1		
3	B	1	Total	C	O	P	0	0
			16	6	9	1		
3	C	1	Total	C	O	P	0	0
			16	6	9	1		
3	D	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).

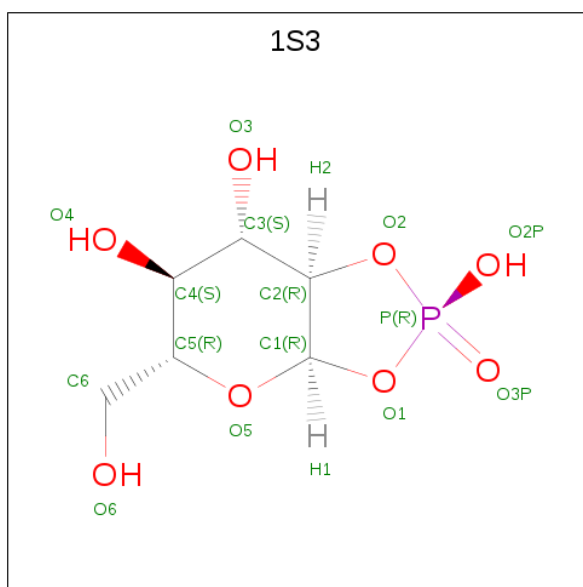


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		

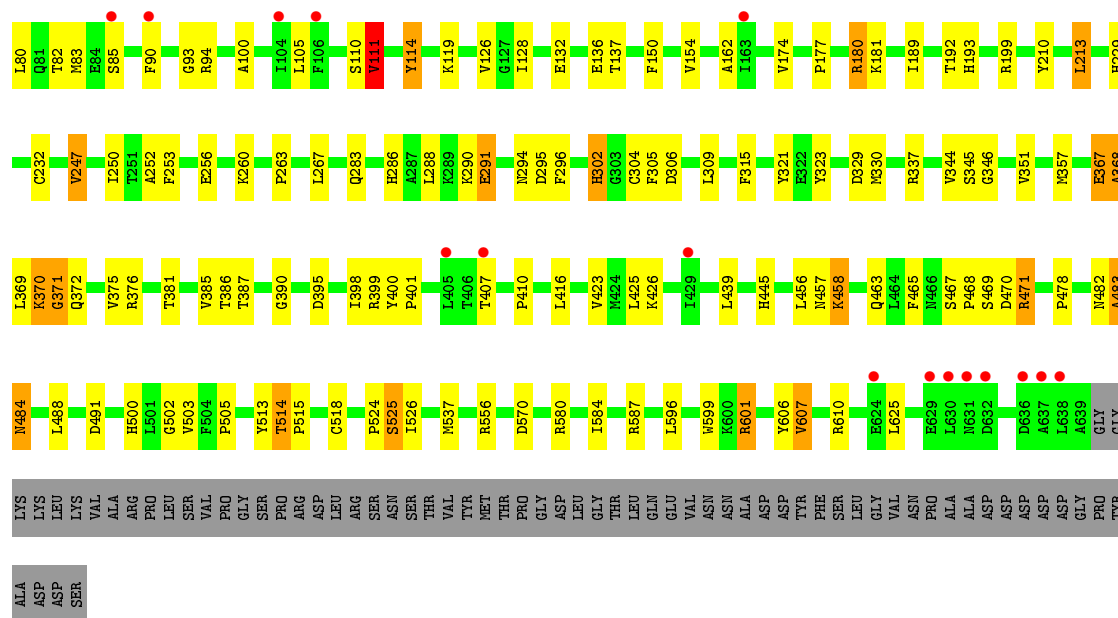
- Molecule 5 is BARIUM ION (three-letter code: BA) (formula: Ba).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ba	0	0
			2	2		
5	A	2	Total	Ba	0	0
			2	2		
5	D	2	Total	Ba	0	0
			2	2		
5	C	1	Total	Ba	0	0
			1	1		

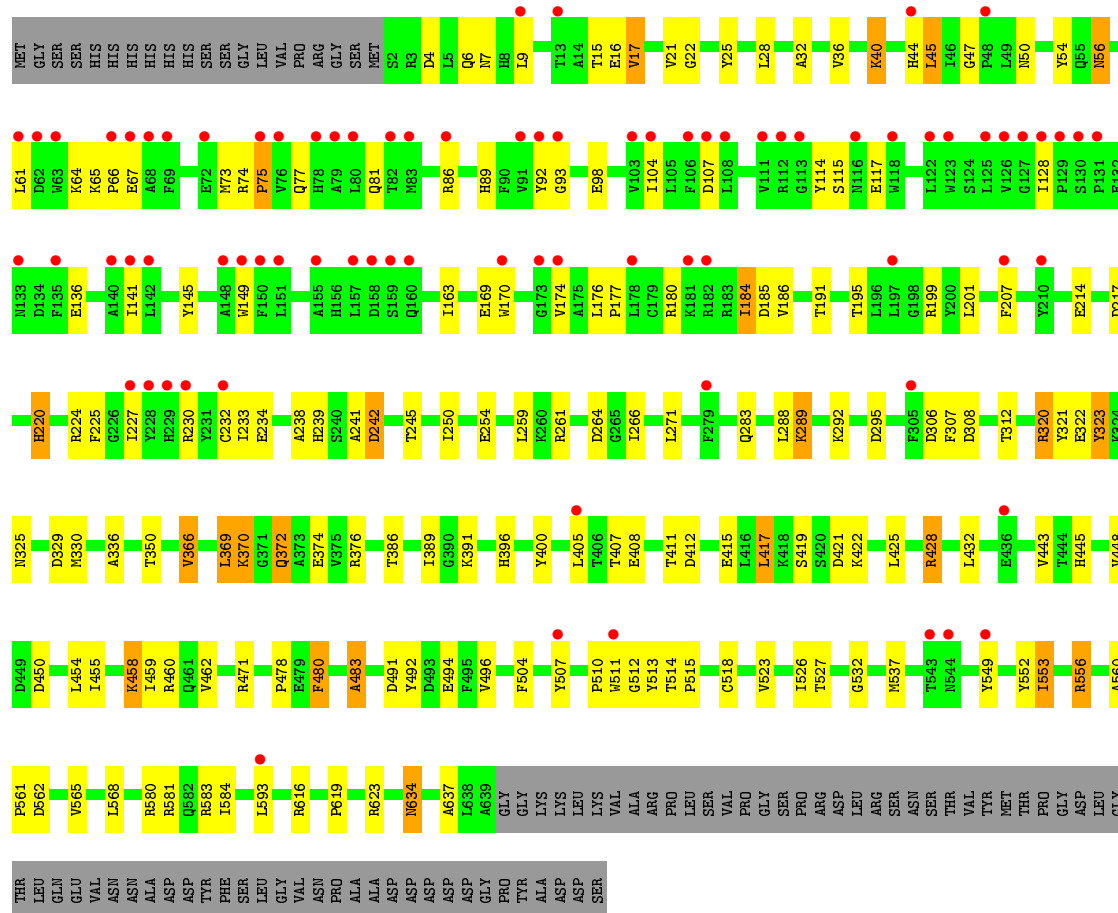
- Molecule 6 is (2R,3aR,5R,6S,7S,7aR)-5-(hydroxymethyl)tetrahydro-3aH-[1,3,2]dioxaphospholo[4,5-b]pyran-2,6,7-triol 2-oxide (three-letter code: 1S3) (formula: C₆H₁₁O₈P).



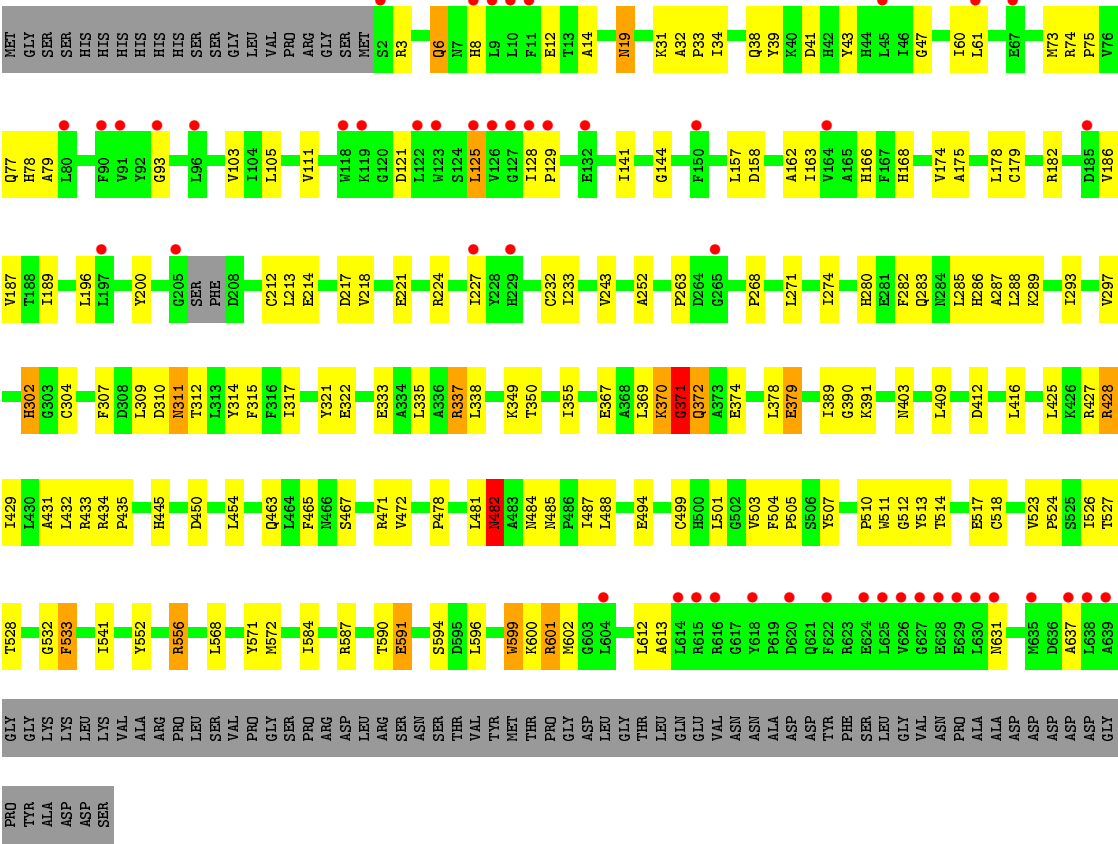
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	O	P	0	0
			15	6	8	1		



• Molecule 1: Gsy2p



• Molecule 1: Gsy2p



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	193.49Å 203.98Å 206.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.46 – 2.95 48.41 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.46-2.95) 99.8 (48.41-2.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.22 (at 2.96Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.224 , 0.271 0.223 , 0.274	Depositor DCC
R_{free} test set	4240 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	76.3	Xtriage
Anisotropy	0.416	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 74.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	20806	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: 1S3, G6P, PEG, BA, U5P

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	0.36	0/5270	0.56	0/7141
1	B	0.44	0/5298	0.63	0/7180
1	C	0.35	0/5279	0.56	0/7153
1	D	0.42	1/5269 (0.0%)	0.62	2/7138 (0.0%)
All	All	0.39	1/21116 (0.0%)	0.60	2/28612 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	371	GLY	C-O	5.58	1.32	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	372[A]	GLN	CA-CB-CG	5.01	124.43	113.40
1	D	372[B]	GLN	CA-CB-CG	5.01	124.43	113.40

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	5145	0	5054	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5163	0	5075	101	0
1	C	5154	0	5061	105	0
1	D	5146	0	5051	117	0
2	A	21	0	11	0	0
2	B	21	0	11	0	0
2	C	21	0	11	0	0
2	D	21	0	11	0	0
3	A	16	0	11	2	0
3	B	16	0	11	0	0
3	C	16	0	11	3	0
3	D	16	0	11	1	0
4	A	7	0	10	0	0
4	B	7	0	10	0	0
4	C	7	0	10	3	0
4	D	7	0	10	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	1	0	0	0	0
5	D	2	0	0	0	0
6	C	15	0	11	1	0
All	All	20806	0	20380	407	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 10.

All (407) 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:336:ALA:HB2	1:A:462:VAL:HG11	1.32	1.08
1:D:428:ARG:HH11	1:D:428:ARG:HG2	0.86	1.00
1:A:336:ALA:HB2	1:A:462:VAL:CG1	1.92	0.98
1:D:428:ARG:HH11	1:D:428:ARG:CG	1.78	0.96
1:D:428:ARG:NH1	1:D:428:ARG:HG2	1.65	0.95
1:B:471:ARG:HH11	1:B:471:ARG:HG2	1.30	0.93
1:A:283:GLN:HG2	1:D:280:HIS:CE1	2.07	0.90
1:C:336:ALA:HB2	1:C:462:VAL:HG11	1.54	0.88
1:A:336:ALA:CB	1:A:462:VAL:CG1	2.56	0.83
1:B:439:LEU:HD22	1:B:467:SER:HA	1.60	0.83
1:B:445[B]:HIS:ND1	1:B:478:PRO:HD2	1.93	0.83
1:B:445[A]:HIS:ND1	1:B:478:PRO:HD2	1.93	0.82
1:D:482:ASN:HD22	1:D:484:ASN:H	1.24	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:GLN:HG2	1:D:280:HIS:HE1	1.42	0.82
1:C:312:THR:HG22	1:C:350:THR:HB	1.59	0.81
1:A:323:TYR:OH	1:A:458:LYS:HG3	1.83	0.79
1:B:180:ARG:HH11	1:B:180:ARG:HG3	1.48	0.78
1:D:3:ARG:NH2	1:D:158:ASP:O	2.17	0.77
1:C:330:MET:HG3	1:C:565:VAL:HG22	1.65	0.76
1:A:280:HIS:CE1	1:D:283:GLN:HG2	2.21	0.76
1:B:503:VAL:HG22	1:B:526:ILE:HD12	1.67	0.75
1:C:336:ALA:HB2	1:C:462:VAL:CG1	2.16	0.75
1:D:429:ILE:HA	1:D:432:LEU:HD12	1.67	0.75
1:D:74:ARG:N	1:D:75:PRO:HD2	2.01	0.74
1:D:482:ASN:ND2	1:D:484:ASN:H	1.86	0.72
1:A:299:GLY:HA2	1:A:375:VAL:HG21	1.69	0.72
1:A:369:LEU:HB3	1:C:369:LEU:HD22	1.72	0.72
1:A:501:LEU:HD21	1:A:526:ILE:HD12	1.71	0.71
1:A:177:PRO:HA	1:A:240:SER:OG	1.90	0.70
1:D:221:GLU:OE2	1:D:224:ARG:NH1	2.24	0.70
1:C:32:ALA:O	1:C:36:VAL:HG23	1.90	0.70
1:A:510:PRO:O	1:A:532:GLY:HA3	1.91	0.70
1:B:74:ARG:N	1:B:75:PRO:HD2	2.07	0.69
1:C:307:PHE:HD2	1:C:312:THR:HG21	1.56	0.69
1:D:471:ARG:HA	1:D:471:ARG:NE	2.06	0.69
1:C:391:LYS:HZ3	4:C:804:PEG:H22	1.57	0.69
1:B:367:GLU:O	1:B:369:LEU:N	2.24	0.69
1:D:471:ARG:HE	1:D:471:ARG:HA	1.59	0.68
1:C:163:ILE:HB	1:C:186:VAL:HG12	1.76	0.68
1:D:526:ILE:HG21	1:D:568:LEU:HD13	1.76	0.68
1:B:193:HIS:HD2	1:B:247:VAL:HG11	1.59	0.67
1:B:463:GLN:CG	1:B:465:PHE:HE2	2.07	0.67
1:D:481:LEU:O	1:D:482:ASN:HB2	1.94	0.67
1:B:514:THR:HB	1:B:515:PRO:CD	2.25	0.67
1:A:283:GLN:HG3	3:A:802:G6P:O1	1.95	0.66
1:D:511:TRP:HA	1:D:532:GLY:HA3	1.78	0.66
1:B:463:GLN:HG2	1:B:465:PHE:HE2	1.61	0.66
1:C:583:ARG:NH1	3:C:803:G6P:O1P	2.29	0.65
1:A:463:GLN:HG2	1:A:465:PHE:HE1	1.62	0.65
1:C:50:ASN:O	1:C:54:TYR:HB3	1.96	0.65
1:B:471:ARG:NH1	1:B:471:ARG:HG2	2.04	0.65
1:B:8:HIS:HB2	1:B:162:ALA:O	1.98	0.64
1:D:485:ASN:OD1	1:D:488:LEU:N	2.26	0.64
1:D:283:GLN:HG3	3:D:802:G6P:O1	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:527:THR:O	1:C:553:ILE:HA	1.98	0.64
1:B:180:ARG:NH1	1:B:180:ARG:HG3	2.05	0.63
1:C:217:ASP:HB3	1:C:220:HIS:HB2	1.78	0.63
1:D:463:GLN:HA	1:D:465:PHE:CE2	2.32	0.63
1:B:330:MET:HE2	1:B:505:PRO:HB2	1.81	0.63
1:C:336:ALA:CB	1:C:462:VAL:CG1	2.76	0.63
1:B:180:ARG:HH11	1:B:180:ARG:CG	2.12	0.62
1:B:580:ARG:O	1:B:584:ILE:HG13	1.99	0.62
1:D:309:LEU:C	1:D:311:ASN:H	2.03	0.62
1:A:580:ARG:HA	1:A:583:ARG:NH1	2.14	0.62
1:C:510:PRO:O	1:C:532:GLY:HA3	1.99	0.62
1:A:586:GLN:O	1:A:590:THR:HG22	2.00	0.62
1:B:482:ASN:O	1:B:484:ASN:N	2.30	0.61
1:C:307:PHE:CD2	1:C:312:THR:HG21	2.35	0.61
1:D:378:LEU:HA	1:D:428:ARG:HG3	1.81	0.61
1:C:16:GLU:HG2	1:C:22:GLY:H	1.65	0.61
1:A:357:MET:O	1:A:478:PRO:HA	1.99	0.61
1:B:6:GLN:HE21	1:B:625:LEU:HD23	1.66	0.61
1:C:458:LYS:O	1:C:462:VAL:HG23	2.01	0.60
1:A:144:GLY:HA3	1:A:174:VAL:HB	1.81	0.60
1:B:128:ILE:HG12	1:B:232:CYS:HB3	1.82	0.60
1:C:201:LEU:HB3	1:C:207:PHE:HE1	1.67	0.60
1:A:372:GLN:HE21	1:A:376:ARG:HH21	1.49	0.60
1:C:391:LYS:NZ	4:C:804:PEG:H22	2.17	0.60
1:D:141:ILE:HA	1:D:174:VAL:HG11	1.84	0.60
1:A:264:ASP:OD1	1:A:616:ARG:NH1	2.34	0.59
1:C:323:TYR:OH	1:C:458:LYS:HG3	2.01	0.59
1:B:370:LYS:O	1:B:371:GLY:C	2.39	0.59
1:A:587:ARG:HA	1:A:590:THR:HG23	1.84	0.59
1:D:485:ASN:OD1	1:D:487:ILE:N	2.36	0.58
1:A:443:VAL:HG13	1:A:456:LEU:HD21	1.85	0.58
1:D:507:TYR:HB2	1:D:556:ARG:NH2	2.19	0.58
1:C:396:HIS:NE2	1:C:405:LEU:HD12	2.19	0.58
1:D:599:TRP:HA	1:D:599:TRP:CE3	2.38	0.58
1:C:61:LEU:HB2	1:C:93:GLY:HA2	1.85	0.58
1:B:213:LEU:HD21	1:B:253:PHE:CE1	2.39	0.58
1:C:322:GLU:HB3	1:C:325:ASN:HB2	1.86	0.57
1:D:335:LEU:HD22	1:D:472:VAL:HG11	1.87	0.57
1:A:336:ALA:CB	1:A:462:VAL:HG11	2.16	0.57
1:A:283:GLN:NE2	1:A:588:ASN:OD1	2.38	0.57
1:C:400:TYR:CD2	1:C:408:GLU:HA	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ASN:O	1:A:343:LYS:HG3	2.04	0.57
1:D:14:ALA:HB2	1:D:168:HIS:HB2	1.87	0.57
1:C:264:ASP:O	1:C:634:ASN:HB2	2.03	0.57
1:B:110:SER:O	1:B:111:VAL:HG13	2.05	0.57
1:B:502:GLY:O	1:B:525:SER:HA	2.05	0.57
1:C:619:PRO:O	1:C:623:ARG:HB2	2.05	0.57
1:A:319:GLY:HA3	1:A:326:LYS:HE3	1.87	0.56
1:B:193:HIS:HD2	1:B:247:VAL:CG1	2.17	0.56
1:A:505:PRO:HA	1:A:528:THR:HG23	1.87	0.56
1:B:302:HIS:C	1:B:302:HIS:HD1	2.08	0.56
1:B:193:HIS:CD2	1:B:247:VAL:HG11	2.40	0.56
1:B:467:SER:O	1:B:470:ASP:HB2	2.05	0.56
1:C:238:ALA:O	1:C:261:ARG:NH1	2.37	0.56
1:D:307:PHE:HD1	1:D:307:PHE:H	1.53	0.56
1:C:445:HIS:ND1	1:C:478:PRO:HD2	2.21	0.56
1:D:349:LYS:O	1:D:471:ARG:HD3	2.06	0.56
1:D:163:ILE:HB	1:D:186:VAL:HG12	1.88	0.56
1:C:4:ASP:OD2	1:C:7:ASN:HB3	2.06	0.55
1:A:336:ALA:CB	1:A:462:VAL:HG13	2.36	0.55
1:D:428:ARG:NH1	1:D:428:ARG:CG	2.49	0.55
1:B:395:ASP:O	1:B:398:ILE:HG22	2.07	0.55
1:C:239:HIS:NE2	1:C:259:LEU:O	2.38	0.55
1:C:239:HIS:CE1	1:C:261:ARG:HB2	2.42	0.55
1:B:213:LEU:HD21	1:B:253:PHE:HE1	1.72	0.55
1:A:236:ALA:O	1:A:240:SER:HB2	2.07	0.55
1:B:357:MET:O	1:B:478:PRO:HA	2.06	0.55
1:B:482:ASN:C	1:B:484:ASN:H	2.10	0.54
1:D:503:VAL:O	1:D:505:PRO:HD3	2.07	0.54
1:C:450:ASP:OD1	1:C:460:ARG:NH2	2.37	0.54
1:D:631:ASN:HB3	1:D:637:ALA:HB1	1.89	0.54
1:A:587:ARG:HA	1:A:590:THR:CG2	2.38	0.54
1:D:61:LEU:HB2	1:D:93:GLY:HA2	1.90	0.54
1:C:308:ASP:O	1:C:312:THR:HG23	2.08	0.54
1:C:443:VAL:HG22	1:C:445:HIS:H	1.73	0.54
1:D:314:TYR:O	1:D:315:PHE:HD1	1.91	0.54
1:D:599:TRP:C	1:D:601:ARG:H	2.11	0.53
1:A:327:GLY:HA3	1:A:505:PRO:O	2.08	0.53
1:C:396:HIS:CD2	1:C:405:LEU:HD12	2.44	0.53
1:D:315:PHE:HE2	1:D:572:MET:HG2	1.74	0.53
1:D:283:GLN:HE21	1:D:584:ILE:HG23	1.72	0.53
1:C:225:PHE:O	1:C:227:ILE:HG12	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:333:GLU:OE2	1:D:337:ARG:NH1	2.39	0.53
4:C:804:PEG:H31	1:D:379:GLU:HG3	1.90	0.53
1:C:526:ILE:HG12	1:C:552:TYR:HB2	1.91	0.53
1:A:300:HIS:HD2	1:A:301:PHE:CE1	2.27	0.53
1:D:217:ASP:O	1:D:221:GLU:HG2	2.08	0.53
1:D:187:VAL:HG11	1:D:613:ALA:O	2.08	0.52
1:D:309:LEU:O	1:D:311:ASN:N	2.39	0.52
1:D:591:GLU:O	1:D:594:SER:HB3	2.09	0.52
1:A:565:VAL:O	1:A:569:VAL:HG23	2.08	0.52
1:B:385:VAL:HG21	1:B:425:LEU:HD11	1.92	0.52
1:C:336:ALA:CB	1:C:462:VAL:HG13	2.38	0.52
1:D:74:ARG:N	1:D:75:PRO:CD	2.72	0.52
1:A:95:TRP:HB3	1:A:101:PRO:HD2	1.91	0.52
1:B:39:TYR:HB2	1:B:43:TYR:HB2	1.92	0.52
1:C:141:ILE:HA	1:C:174:VAL:HG11	1.92	0.52
1:B:295:ASP:OD1	1:B:295:ASP:C	2.48	0.52
1:B:607:VAL:HG23	1:B:610:ARG:HH21	1.75	0.52
1:B:80:LEU:HD22	1:B:90:PHE:CE2	2.45	0.51
1:A:141:ILE:HA	1:A:174:VAL:HG11	1.92	0.51
1:C:201:LEU:HB3	1:C:207:PHE:CE1	2.44	0.51
1:D:482:ASN:HD22	1:D:484:ASN:N	2.01	0.51
1:A:366:VAL:O	1:A:370:LYS:HB2	2.11	0.51
1:B:456:LEU:O	1:B:458:LYS:N	2.43	0.51
1:B:463:GLN:HA	1:B:465:PHE:CE2	2.45	0.51
1:D:282:PHE:CD2	1:D:591:GLU:HG3	2.46	0.51
1:B:367:GLU:O	1:B:368:ALA:C	2.48	0.51
1:B:31:LYS:HE2	1:B:606:TYR:CE2	2.45	0.51
1:C:283:GLN:HB3	3:C:803:G6P:O1	2.11	0.51
1:A:304:CYS:HB2	1:A:434:ARG:HD3	1.93	0.51
1:A:239:HIS:CE1	1:A:259:LEU:O	2.64	0.51
1:A:29:LYS:HG3	1:A:97:ILE:HD13	1.93	0.51
1:A:302:HIS:HB2	1:A:432:LEU:HD22	1.92	0.50
1:B:290:LYS:HG2	1:B:290:LYS:O	2.10	0.50
1:C:176:LEU:HB2	1:C:177:PRO:HD3	1.93	0.50
1:D:289:LYS:HE3	1:D:494:GLU:HG2	1.93	0.50
1:A:19:ASN:HD22	1:A:19:ASN:H	1.60	0.50
1:A:509:GLU:OE2	1:A:531:SER:HB2	2.11	0.50
1:B:513:TYR:N	1:B:513:TYR:CD1	2.79	0.50
1:C:323:TYR:CZ	1:C:329:ASP:HB3	2.46	0.50
1:B:286:HIS:HD2	1:B:587:ARG:NH2	2.10	0.50
1:D:128:ILE:HG12	1:D:232:CYS:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:ARG:HD3	1:B:100:ALA:HB1	1.94	0.49
1:D:374[B]:GLU:O	1:D:374[B]:GLU:CD	2.51	0.49
1:B:189:ILE:HD11	1:B:610:ARG:HA	1.93	0.49
1:D:282:PHE:CE2	1:D:591:GLU:HG3	2.47	0.49
1:B:315:PHE:CD2	1:B:351:VAL:HG11	2.46	0.49
1:C:512:GLY:O	1:C:515:PRO:HD2	2.12	0.49
1:B:193:HIS:CD2	1:B:247:VAL:CG1	2.96	0.49
1:D:302:HIS:O	1:D:434:ARG:HD2	2.12	0.49
1:D:19:ASN:HD22	1:D:19:ASN:N	2.11	0.49
1:C:16:GLU:HB3	1:C:25:TYR:HB2	1.95	0.49
1:A:128:ILE:HG12	1:A:232:CYS:HB3	1.93	0.49
1:A:399:ARG:HD3	1:A:403:ASN:OD1	2.13	0.49
1:C:128:ILE:HG12	1:C:232:CYS:HB3	1.95	0.49
1:A:283:GLN:CG	1:D:280:HIS:CE1	2.89	0.49
1:D:309:LEU:HA	1:D:312:THR:OG1	2.12	0.49
1:B:513:TYR:H	1:B:513:TYR:HD1	1.61	0.49
1:C:56:ASN:ND2	1:C:56:ASN:H	2.10	0.49
1:D:178:LEU:O	1:D:182:ARG:HB2	2.12	0.49
1:A:314:TYR:CD1	1:A:354:PHE:HE2	2.31	0.49
1:C:264:ASP:CG	1:C:616:ARG:HH12	2.15	0.49
1:D:315:PHE:CE2	1:D:572:MET:HG2	2.48	0.49
1:B:500:HIS:O	1:B:524:PRO:HD2	2.12	0.48
1:C:580:ARG:NE	3:C:803:G6P:O1P	2.40	0.48
1:D:513:TYR:CD1	1:D:513:TYR:N	2.81	0.48
1:D:596:LEU:HA	1:D:601:ARG:HD3	1.95	0.48
1:A:518:CYS:SG	1:A:523:VAL:HB	2.53	0.48
1:D:121:ASP:O	1:D:125:LEU:HB2	2.13	0.48
1:D:144:GLY:HA3	1:D:174:VAL:HB	1.95	0.48
1:A:403:ASN:N	1:A:403:ASN:ND2	2.60	0.48
1:D:31:LYS:O	1:D:34:ILE:HG22	2.14	0.48
1:D:587:ARG:HA	1:D:590:THR:HG22	1.95	0.48
1:C:560:ALA:C	1:C:562:ASP:H	2.15	0.48
1:A:61:LEU:HB2	1:A:93:GLY:HA2	1.95	0.48
1:A:628:GLU:HG3	1:A:630:LEU:HD23	1.95	0.48
1:B:344:VAL:C	1:B:346:GLY:H	2.16	0.48
1:C:65:LYS:HE2	1:C:67:GLU:HB3	1.96	0.48
1:D:612:LEU:O	1:D:612:LEU:HG	2.13	0.48
1:D:283:GLN:NE2	1:D:584:ILE:HG23	2.29	0.48
1:A:264:ASP:CG	1:A:616:ARG:HH12	2.18	0.47
1:B:150:PHE:O	1:B:154:VAL:HG23	2.14	0.47
1:B:514:THR:HB	1:B:515:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:GLU:HG3	1:C:21:VAL:HB	1.96	0.47
1:A:440:PRO:O	1:A:441:PRO:O	2.32	0.47
1:B:11:PHE:HD1	1:B:46:ILE:HD11	1.79	0.47
1:D:370:LYS:O	1:D:371:GLY:C	2.53	0.47
1:D:425:LEU:O	1:D:429:ILE:HG13	2.14	0.47
1:D:374[A]:GLU:HG2	1:D:431:ALA:HB1	1.95	0.47
1:B:463:GLN:CG	1:B:465:PHE:CE2	2.94	0.47
1:B:306:ASP:OD2	1:B:468:PRO:HB3	2.15	0.47
1:D:268:PRO:HB2	1:D:602:MET:CE	2.45	0.47
1:D:39:TYR:HB2	1:D:43:TYR:HB2	1.95	0.47
1:B:82:THR:O	1:B:85:SER:HB2	2.15	0.47
1:C:145:TYR:O	1:C:149:TRP:HB2	2.15	0.47
1:C:374:GLU:HB3	1:C:432:LEU:HD23	1.97	0.47
1:D:12:GLU:HG3	1:D:166:HIS:HB3	1.97	0.47
1:C:74:ARG:N	1:C:75:PRO:HD2	2.29	0.47
1:D:510:PRO:O	1:D:532:GLY:HA3	2.15	0.47
1:C:306:ASP:HA	1:D:403:ASN:HD21	1.80	0.47
1:D:513:TYR:O	1:D:517:GLU:HG3	2.15	0.47
1:A:287:ALA:HB2	3:A:802:G6P:H2	1.97	0.47
1:C:336:ALA:HB1	1:C:462:VAL:HG13	1.96	0.46
1:C:458:LYS:HE2	1:C:462:VAL:CG2	2.44	0.46
1:C:184:ILE:HG22	1:C:185:ASP:H	1.81	0.46
1:C:28:LEU:HD22	1:C:45:LEU:HD21	1.98	0.46
1:D:79:ALA:HB2	1:D:157:LEU:HD12	1.98	0.46
1:B:302:HIS:C	1:B:302:HIS:ND1	2.69	0.46
1:A:409:LEU:HD12	1:B:426:LYS:HE3	1.97	0.46
1:B:385:VAL:O	1:B:387:THR:N	2.49	0.46
1:B:323:TYR:CZ	1:B:329:ASP:HB3	2.51	0.46
1:C:176:LEU:HD22	1:C:241:ALA:HB2	1.98	0.46
1:C:483:ALA:N	1:C:491:ASP:OD1	2.38	0.46
1:A:150:PHE:O	1:A:154:VAL:HG23	2.16	0.46
1:D:428:ARG:HD3	1:D:428:ARG:HA	1.57	0.46
1:A:60:ILE:HD12	1:A:60:ILE:H	1.81	0.46
1:B:286:HIS:CD2	1:B:587:ARG:CZ	2.99	0.46
1:B:39:TYR:HB3	1:B:42:HIS:HB2	1.98	0.45
1:C:170:TRP:HB3	1:C:234:GLU:HG3	1.96	0.45
1:C:307:PHE:HD2	1:C:312:THR:CG2	2.26	0.45
1:D:463:GLN:HA	1:D:465:PHE:HE2	1.79	0.45
1:D:501:LEU:HD21	1:D:526:ILE:CD1	2.46	0.45
1:D:528:THR:HG21	1:D:556:ARG:HG3	1.96	0.45
1:D:47:GLY:O	1:D:105:LEU:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:471:ARG:HE	1:D:471:ARG:CA	2.29	0.45
1:D:227:ILE:HG22	1:D:227:ILE:O	2.16	0.45
1:A:195:THR:OG1	1:A:254:GLU:OE1	2.34	0.45
1:D:501:LEU:HD21	1:D:526:ILE:HD12	1.99	0.45
1:D:599:TRP:HA	1:D:599:TRP:HE3	1.79	0.45
1:A:213:LEU:O	1:A:216:VAL:HG22	2.17	0.45
1:A:471:ARG:NE	1:A:471:ARG:HA	2.30	0.45
1:B:11:PHE:CD1	1:B:46:ILE:HD11	2.51	0.45
1:C:320:ARG:NH2	1:C:322:GLU:OE1	2.49	0.45
1:B:210:TYR:CE1	1:B:250:ILE:HD11	2.51	0.45
1:B:305:PHE:HZ	1:B:309:LEU:HG	1.82	0.45
1:C:560:ALA:O	1:C:562:ASP:N	2.49	0.45
1:A:302:HIS:O	1:A:302:HIS:CG	2.70	0.45
1:B:267:LEU:HB3	1:B:606:TYR:CE1	2.51	0.45
1:D:523:VAL:HA	1:D:524:PRO:HD3	1.81	0.45
1:B:47:GLY:O	1:B:105:LEU:HA	2.17	0.45
1:B:410:PRO:HG2	1:B:416:LEU:HD21	1.99	0.45
1:C:417:LEU:HD22	1:C:422:LYS:HG3	1.99	0.45
1:C:17:VAL:HG13	1:C:45:LEU:HD22	1.99	0.45
1:D:41:ASP:OD2	1:D:73:MET:HG3	2.17	0.45
1:C:634:ASN:ND2	1:C:637:ALA:H	2.15	0.44
1:C:386:THR:HG21	1:D:390:GLY:CA	2.47	0.44
1:A:386:THR:HG21	1:B:390:GLY:CA	2.47	0.44
1:C:191:THR:HA	1:C:245:THR:O	2.17	0.44
1:D:482:ASN:ND2	1:D:484:ASN:HB2	2.32	0.44
1:A:450:ASP:CG	1:A:460:ARG:HH22	2.20	0.44
1:B:491:ASP:OD1	1:D:427:ARG:NH2	2.33	0.44
1:C:366:VAL:O	1:C:370:LYS:HB2	2.17	0.44
1:C:65:LYS:HA	1:C:66:PRO:HD3	1.88	0.44
1:B:17:VAL:C	1:B:19:ASN:H	2.21	0.44
1:D:286:HIS:O	1:D:287:ALA:C	2.55	0.44
1:A:25:TYR:CE2	1:A:95:TRP:HZ2	2.35	0.44
1:A:386:THR:HA	1:A:389:ILE:HD12	1.99	0.44
1:B:286:HIS:CD2	1:B:587:ARG:NH2	2.86	0.44
1:A:176:LEU:HB2	1:A:177:PRO:HD3	1.99	0.44
1:A:447:MET:HB2	1:A:450:ASP:HB2	2.00	0.44
1:A:51:LYS:HA	1:A:54:TYR:CD1	2.53	0.44
1:C:114:TYR:O	1:C:117:GLU:HG2	2.18	0.44
1:C:396:HIS:HE1	1:C:407:THR:O	2.01	0.44
1:A:322:GLU:HG2	1:A:325:ASN:HB2	1.99	0.44
1:D:144:GLY:O	1:D:175:ALA:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:434:ARG:HB2	1:D:435:PRO:HD2	2.00	0.44
1:D:285:LEU:HA	1:D:285:LEU:HD23	1.78	0.44
1:C:518:CYS:SG	1:C:523:VAL:HB	2.58	0.43
1:A:294:ASN:O	1:A:295:ASP:C	2.56	0.43
1:A:527:THR:O	1:A:553:ILE:HA	2.18	0.43
1:A:549:TYR:HD2	1:A:593:LEU:HG	1.82	0.43
1:A:386:THR:HG21	1:B:390:GLY:HA2	2.00	0.43
1:B:80:LEU:HB3	1:B:90:PHE:CZ	2.53	0.43
1:C:511:TRP:HB3	6:C:801:1S3:O4	2.18	0.43
1:D:32:ALA:HB3	1:D:33:PRO:HD3	2.01	0.43
1:D:367:GLU:HA	1:D:367:GLU:OE1	2.18	0.43
1:A:410:PRO:HG2	1:A:416:LEU:HD21	1.99	0.43
1:B:114:TYR:N	1:B:114:TYR:CD1	2.85	0.43
1:B:302:HIS:CD2	1:B:371:GLY:HA2	2.53	0.43
1:B:283:GLN:O	1:B:286:HIS:HB3	2.19	0.43
1:D:293:ILE:O	1:D:297:VAL:HG23	2.19	0.43
1:D:309:LEU:C	1:D:311:ASN:N	2.70	0.43
1:D:317:ILE:HG22	1:D:355:ILE:HA	1.99	0.43
1:B:76:VAL:O	1:B:80:LEU:HG	2.18	0.43
1:C:372[A]:GLN:HE21	1:C:372[A]:GLN:HB3	1.67	0.43
1:A:634:ASN:HB2	1:A:637:ALA:H	1.84	0.43
1:B:256:GLU:O	1:B:260:LYS:HA	2.17	0.43
1:C:507:TYR:HB2	1:C:556:ARG:NH2	2.34	0.43
1:D:445:HIS:ND1	1:D:478:PRO:HD2	2.33	0.43
1:B:596:LEU:HA	1:B:601:ARG:HD3	2.00	0.42
1:C:17:VAL:HG21	1:C:47:GLY:HA3	2.01	0.42
1:D:338:LEU:HD22	1:D:572:MET:HB3	2.00	0.42
1:A:450:ASP:OD1	1:A:460:ARG:NH2	2.51	0.42
1:D:189:ILE:HG23	1:D:243:VAL:HB	2.01	0.42
1:C:455:ILE:O	1:C:459:ILE:HG13	2.19	0.42
1:C:526:ILE:HG12	1:C:552:TYR:CB	2.49	0.42
1:C:580:ARG:O	1:C:584:ILE:HG13	2.19	0.42
1:A:467:SER:O	1:A:469:SER:N	2.53	0.42
1:C:227:ILE:HG23	1:C:230:ARG:HD2	2.00	0.42
1:C:44:HIS:HE1	1:C:73:MET:HE1	1.84	0.42
1:D:335:LEU:HD22	1:D:472:VAL:CG1	2.47	0.42
1:B:291:GLU:O	1:B:294:ASN:HB2	2.19	0.42
1:C:492:TYR:O	1:C:496:VAL:HG23	2.19	0.42
1:D:389:ILE:HG23	1:D:416:LEU:HD13	2.02	0.42
1:A:273:VAL:HG13	1:A:520:VAL:HG13	2.01	0.42
1:B:39:TYR:O	1:B:41:ASP:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:242:ASP:N	1:C:242:ASP:OD1	2.53	0.42
1:C:89:HIS:O	1:C:107:ASP:HB3	2.20	0.42
1:A:250:ILE:HD12	1:A:250:ILE:HA	1.80	0.42
1:B:514:THR:HB	1:B:515:PRO:HD3	2.00	0.42
1:C:174:VAL:HG22	1:C:233:ILE:HG21	2.01	0.42
1:C:396:HIS:HD2	1:C:415:GLU:OE2	2.02	0.42
1:C:289:LYS:HG3	1:C:494:GLU:HB3	2.01	0.42
1:C:549:TYR:HD2	1:C:593:LEU:HD21	1.84	0.42
1:D:252:ALA:HB1	1:D:263:PRO:HG2	2.01	0.42
1:D:552:TYR:HB3	1:D:571:TYR:CD2	2.55	0.42
1:A:463:GLN:HA	1:A:465:PHE:CE1	2.55	0.42
1:C:195:THR:OG1	1:C:254:GLU:OE2	2.30	0.42
1:A:198:GLY:HA2	1:A:209:PHE:CE2	2.54	0.42
1:A:262:LYS:HA	1:A:263:PRO:HD3	1.88	0.42
1:B:119:LYS:HE2	1:B:132:GLU:OE2	2.20	0.42
1:B:296:PHE:HA	1:B:372[B]:GLN:NE2	2.35	0.42
1:D:75:PRO:CB	1:D:158:ASP:HB2	2.50	0.42
1:A:351:VAL:HG12	1:A:351:VAL:O	2.20	0.42
1:A:523:VAL:HA	1:A:524:PRO:HD3	1.93	0.42
1:C:417:LEU:HD23	1:C:421:ASP:HB2	2.01	0.42
1:B:599:TRP:HA	1:B:599:TRP:CE3	2.55	0.41
1:B:61:LEU:HB2	1:B:93:GLY:HA2	2.01	0.41
1:C:526:ILE:HG21	1:C:568:LEU:CD1	2.51	0.41
1:A:19:ASN:ND2	1:A:19:ASN:H	2.19	0.41
1:B:252:ALA:HA	1:B:263:PRO:HG2	2.02	0.41
1:B:400:TYR:CD2	1:B:401:PRO:HA	2.55	0.41
1:C:580:ARG:O	1:C:581:ARG:C	2.59	0.41
1:D:78:HIS:HB2	1:D:157:LEU:HD13	2.02	0.41
1:A:238:ALA:O	1:A:261:ARG:NH1	2.52	0.41
1:A:403:ASN:HD22	1:A:403:ASN:N	2.17	0.41
1:C:428:ARG:HD3	1:C:428:ARG:HA	1.70	0.41
1:A:247:VAL:O	1:A:268:PRO:HA	2.21	0.41
1:B:114:TYR:N	1:B:114:TYR:HD1	2.18	0.41
1:D:369:LEU:HD23	1:D:487:ILE:HG23	2.03	0.41
1:B:375:VAL:O	1:B:375:VAL:CG1	2.69	0.41
1:C:92:TYR:HD1	1:C:104:ILE:HG12	1.85	0.41
1:C:480:PHE:HA	1:C:480:PHE:HD1	1.80	0.41
1:D:533:PHE:CD1	1:D:533:PHE:C	2.94	0.41
1:A:115:SER:O	1:A:119:LYS:HG3	2.20	0.41
1:A:455:ILE:O	1:A:459:ILE:HG13	2.20	0.41
1:B:337:ARG:HD2	1:B:337:ARG:HH11	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:527:THR:OG1	1:D:528:THR:N	2.54	0.41
1:A:10:LEU:HD13	1:A:610:ARG:HD3	2.02	0.41
1:D:174:VAL:HG22	1:D:233:ILE:HG21	2.03	0.41
1:A:125:LEU:HD22	1:A:181:LYS:HG2	2.03	0.41
1:D:128:ILE:HA	1:D:129:PRO:HD2	1.98	0.41
1:A:30:SER:O	1:A:272:ASN:ND2	2.54	0.41
1:B:323:TYR:OH	1:B:458:LYS:HG2	2.20	0.41
1:B:483:ALA:HB2	1:B:491:ASP:N	2.36	0.41
1:D:196:LEU:O	1:D:200:TYR:HD2	2.04	0.41
1:A:357:MET:HA	1:A:358:PRO:HD3	1.93	0.40
1:B:471:ARG:NH1	1:B:471:ARG:CG	2.75	0.40
1:B:74:ARG:N	1:B:75:PRO:CD	2.79	0.40
1:D:38:GLN:HB3	1:D:39:TYR:CD1	2.57	0.40
1:A:269:ASN:HB2	1:A:511:TRP:CD1	2.57	0.40
1:B:439:LEU:HD22	1:B:467:SER:CA	2.40	0.40
1:C:425:LEU:HB3	1:D:409:LEU:HD21	2.04	0.40
1:C:74:ARG:NH1	1:C:77:GLN:OE1	2.54	0.40
1:A:606:TYR:HB3	1:A:610:ARG:NH2	2.37	0.40
1:B:137:THR:HG21	1:B:229:HIS:HD2	1.86	0.40
1:C:386:THR:HA	1:C:389:ILE:HD12	2.02	0.40
1:B:174:VAL:O	1:B:177:PRO:HD2	2.22	0.40
1:D:8:HIS:HB2	1:D:162:ALA:O	2.21	0.40
1:A:314:TYR:HD1	1:A:354:PHE:HE2	1.69	0.40
1:C:289:LYS:O	1:C:292:LYS:HB2	2.21	0.40
1:C:64:LYS:HG2	1:C:81:GLN:NE2	2.35	0.40

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	636/724 (88%)	574 (90%)	53 (8%)	9 (1%)	11 39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	639/724 (88%)	569 (89%)	59 (9%)	11 (2%)	9	34
1	C	637/724 (88%)	576 (90%)	52 (8%)	9 (1%)	11	39
1	D	634/724 (88%)	567 (89%)	57 (9%)	10 (2%)	9	36
All	All	2546/2896 (88%)	2286 (90%)	221 (9%)	39 (2%)	10	38

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	17	VAL
1	A	441	PRO
1	B	111	VAL
1	B	304	CYS
1	B	367	GLU
1	B	368	ALA
1	B	457	ASN
1	B	483	ALA
1	D	111	VAL
1	D	482	ASN
1	D	600	LYS
1	B	17	VAL
1	B	371	GLY
1	B	386	THR
1	C	6	GLN
1	C	17	VAL
1	D	310	ASP
1	D	311	ASN
1	D	601	ARG
1	A	419	SER
1	A	435	PRO
1	B	40	LYS
1	C	40	LYS
1	C	169	GLU
1	C	561	PRO
1	B	345	SER
1	C	115	SER
1	A	169	GLU
1	A	413	LEU
1	A	561	PRO
1	C	323	TYR
1	C	483	ALA
1	D	6	GLN

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Mol	Chain	Res	Type
1	D	499	CYS
1	C	75	PRO
1	A	273	VAL
1	D	512	GLY
1	A	33	PRO
1	D	371	GLY

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	551/622 (89%)	518 (94%)	33 (6%)	19	50
1	B	554/622 (89%)	515 (93%)	39 (7%)	15	43
1	C	552/622 (89%)	506 (92%)	46 (8%)	11	35
1	D	551/622 (89%)	511 (93%)	40 (7%)	14	41
All	All	2208/2488 (89%)	2050 (93%)	158 (7%)	14	42

All (158) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	35	THR
1	A	45	LEU
1	A	60	ILE
1	A	61	LEU
1	A	111	VAL
1	A	181	LYS
1	A	212	CYS
1	A	240	SER
1	A	272	ASN
1	A	283	GLN
1	A	304	CYS
1	A	310	ASP
1	A	321	TYR
1	A	322	GLU

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Mol	Chain	Res	Type
1	A	403	ASN
1	A	406	THR
1	A	420	SER
1	A	454	LEU
1	A	469	SER
1	A	471	ARG
1	A	479	GLU
1	A	485	ASN
1	A	513	TYR
1	A	521	MET
1	A	535	SER
1	A	541	ILE
1	A	553	ILE
1	A	556	ARG
1	A	581	ARG
1	A	590	THR
1	A	622	PHE
1	A	630	LEU
1	B	16	GLU
1	B	17	VAL
1	B	34	ILE
1	B	60	ILE
1	B	67	GLU
1	B	83	MET
1	B	111	VAL
1	B	114	TYR
1	B	126	VAL
1	B	136	GLU
1	B	180	ARG
1	B	181	LYS
1	B	192	THR
1	B	199	ARG
1	B	213	LEU
1	B	247	VAL
1	B	288	LEU
1	B	291	GLU
1	B	302	HIS
1	B	321	TYR
1	B	370	LYS
1	B	376	ARG
1	B	381	THR
1	B	399	ARG

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Mol	Chain	Res	Type
1	B	407	THR
1	B	423	VAL
1	B	458	LYS
1	B	469	SER
1	B	471	ARG
1	B	484	ASN
1	B	488	LEU
1	B	514	THR
1	B	518	CYS
1	B	525	SER
1	B	537	MET
1	B	556	ARG
1	B	570	ASP
1	B	601	ARG
1	B	607	VAL
1	C	9	LEU
1	C	15	THR
1	C	40	LYS
1	C	45	LEU
1	C	56	ASN
1	C	86	ARG
1	C	98	GLU
1	C	136	GLU
1	C	180	ARG
1	C	184	ILE
1	C	199	ARG
1	C	214	GLU
1	C	220	HIS
1	C	224	ARG
1	C	242	ASP
1	C	250	ILE
1	C	266	ILE
1	C	271	LEU
1	C	288	LEU
1	C	289	LYS
1	C	295	ASP
1	C	320	ARG
1	C	321	TYR
1	C	366	VAL
1	C	369	LEU
1	C	370	LYS
1	C	372[A]	GLN

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Mol	Chain	Res	Type
1	C	372[B]	GLN
1	C	376	ARG
1	C	411	THR
1	C	412	ASP
1	C	417	LEU
1	C	419	SER
1	C	428	ARG
1	C	448	VAL
1	C	454	LEU
1	C	458	LYS
1	C	471	ARG
1	C	480	PHE
1	C	504	PHE
1	C	513	TYR
1	C	514	THR
1	C	537	MET
1	C	553	ILE
1	C	556	ARG
1	C	634	ASN
1	D	6	GLN
1	D	19	ASN
1	D	60	ILE
1	D	77	GLN
1	D	103	VAL
1	D	125	LEU
1	D	179	CYS
1	D	212	CYS
1	D	213	LEU
1	D	214	GLU
1	D	218	VAL
1	D	271	LEU
1	D	274	ILE
1	D	288	LEU
1	D	302	HIS
1	D	304	CYS
1	D	321	TYR
1	D	322	GLU
1	D	337	ARG
1	D	350	THR
1	D	370	LYS
1	D	372[A]	GLN
1	D	372[B]	GLN

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Mol	Chain	Res	Type
1	D	379	GLU
1	D	391	LYS
1	D	412	ASP
1	D	428	ARG
1	D	433	ARG
1	D	450	ASP
1	D	454	LEU
1	D	467	SER
1	D	482	ASN
1	D	504	PHE
1	D	514	THR
1	D	518	CYS
1	D	533	PHE
1	D	541	ILE
1	D	556	ARG
1	D	591	GLU
1	D	599	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	272	ASN
1	A	300	HIS
1	A	372	GLN
1	A	477	HIS
1	A	585	ASN
1	A	586	GLN
1	B	6	GLN
1	B	193	HIS
1	B	286	HIS
1	B	403	ASN
1	B	621	GLN
1	C	6	GLN
1	C	44	HIS
1	C	56	ASN
1	C	362	ASN
1	C	396	HIS
1	C	621	GLN
1	C	634	ASN
1	D	19	ASN
1	D	168	HIS

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Mol	Chain	Res	Type
1	D	211	ASN
1	D	280	HIS
1	D	403	ASN
1	D	482	ASN
1	D	621	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 7 are monoatomic - leaving 13 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	$\# Z > 2$
6	1S3	C	801	-	14,16,16	0.63	0	19,25,25	1.31	4 (21%)
2	U5P	B	801	-	18,22,22	0.82	0	21,33,33	1.15	0
2	U5P	A	801	-	18,22,22	0.82	0	21,33,33	1.21	1 (4%)
3	G6P	C	803	-	16,16,16	0.56	0	24,24,24	0.80	0
3	G6P	D	802	-	16,16,16	0.47	0	24,24,24	0.97	2 (8%)
2	U5P	C	802	-	18,22,22	0.82	0	21,33,33	1.28	1 (4%)
3	G6P	B	802	-	16,16,16	0.46	0	24,24,24	1.07	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	G6P	A	802	-	16,16,16	0.58	0	24,24,24	1.10	2 (8%)
4	PEG	B	803	-	6,6,6	0.45	0	5,5,5	0.44	0
4	PEG	D	803	-	6,6,6	0.42	0	5,5,5	0.41	0
4	PEG	A	803	-	6,6,6	0.60	0	5,5,5	0.34	0
4	PEG	C	804	-	6,6,6	0.49	0	5,5,5	0.27	0
2	U5P	D	801	-	18,22,22	0.82	0	21,33,33	1.10	1 (4%)

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
6	1S3	C	801	-	-	0/2/32/32	0/2/2/2
2	U5P	B	801	-	-	3/8/26/26	0/2/2/2
2	U5P	A	801	-	-	5/8/26/26	0/2/2/2
3	G6P	C	803	-	-	2/6/26/26	0/1/1/1
3	G6P	D	802	-	-	3/6/26/26	0/1/1/1
2	U5P	C	802	-	-	4/8/26/26	0/2/2/2
3	G6P	B	802	-	-	2/6/26/26	0/1/1/1
3	G6P	A	802	-	-	3/6/26/26	0/1/1/1
4	PEG	B	803	-	-	2/4/4/4	-
4	PEG	D	803	-	-	3/4/4/4	-
4	PEG	A	803	-	-	3/4/4/4	-
4	PEG	C	804	-	-	3/4/4/4	-
2	U5P	D	801	-	-	5/8/26/26	0/2/2/2

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	802	U5P	C3'-C2'-C1'	3.61	106.41	100.98
2	A	801	U5P	C3'-C2'-C1'	3.18	105.77	100.98
3	A	802	G6P	O2P-P-O1P	2.88	118.66	107.64
3	B	802	G6P	C1-O5-C5	2.77	118.89	113.66
6	C	801	1S3	O5-C1-O1	2.54	113.93	109.34
2	D	801	U5P	C3'-C2'-C1'	2.33	104.48	100.98
3	D	802	G6P	O2P-P-O1P	2.22	116.14	107.64
6	C	801	1S3	P-O1-C1	-2.20	106.80	111.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	G6P	O2P-P-O6	-2.20	100.89	106.73
6	C	801	1S3	O2-P-O3P	-2.15	110.08	115.76
6	C	801	1S3	O1-P-O3P	-2.07	110.31	115.76
3	D	802	G6P	O5-C1-C2	-2.06	106.62	110.28

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	801	U5P	C5'-O5'-P-O2P
2	B	801	U5P	C5'-O5'-P-O3P
2	A	801	U5P	C2'-C1'-N1-C6
2	A	801	U5P	O4'-C1'-N1-C6
2	A	801	U5P	O4'-C4'-C5'-O5'
3	C	803	G6P	C4-C5-C6-O6
3	D	802	G6P	C6-O6-P-O2P
2	C	802	U5P	C2'-C1'-N1-C6
2	C	802	U5P	O4'-C1'-N1-C6
3	B	802	G6P	C4-C5-C6-O6
3	B	802	G6P	O5-C5-C6-O6
3	A	802	G6P	C6-O6-P-O3P
2	D	801	U5P	C2'-C1'-N1-C6
2	D	801	U5P	O4'-C1'-N1-C6
2	D	801	U5P	O4'-C4'-C5'-O5'
4	D	803	PEG	O1-C1-C2-O2
4	B	803	PEG	O2-C3-C4-O4
4	A	803	PEG	O1-C1-C2-O2
4	C	804	PEG	O2-C3-C4-O4
2	B	801	U5P	C5'-O5'-P-O1P
3	D	802	G6P	C6-O6-P-O3P
3	C	803	G6P	O5-C5-C6-O6
2	D	801	U5P	C4'-C5'-O5'-P
4	A	803	PEG	O2-C3-C4-O4
3	D	802	G6P	C6-O6-P-O1P
4	A	803	PEG	C1-C2-O2-C3
4	D	803	PEG	C1-C2-O2-C3
4	D	803	PEG	C4-C3-O2-C2
2	D	801	U5P	C3'-C4'-C5'-O5'
2	C	802	U5P	C4'-C5'-O5'-P
2	A	801	U5P	C3'-C4'-C5'-O5'
4	C	804	PEG	C4-C3-O2-C2
3	A	802	G6P	C6-O6-P-O1P

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Mol	Chain	Res	Type	Atoms
3	A	802	G6P	C6-O6-P-O2P
2	C	802	U5P	O4'-C4'-C5'-O5'
4	B	803	PEG	O1-C1-C2-O2
4	C	804	PEG	C1-C2-O2-C3
2	A	801	U5P	C4'-C5'-O5'-P

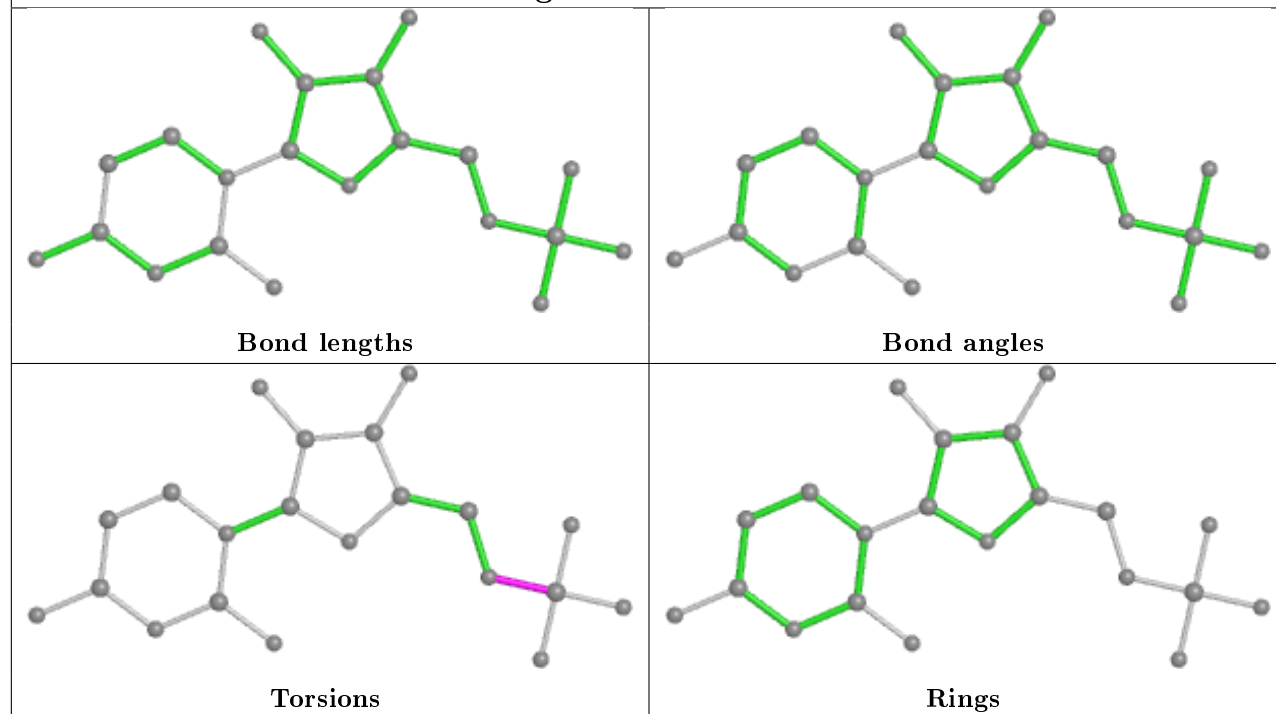
There are no ring outliers.

5 monomers are involved in 10 short contacts:

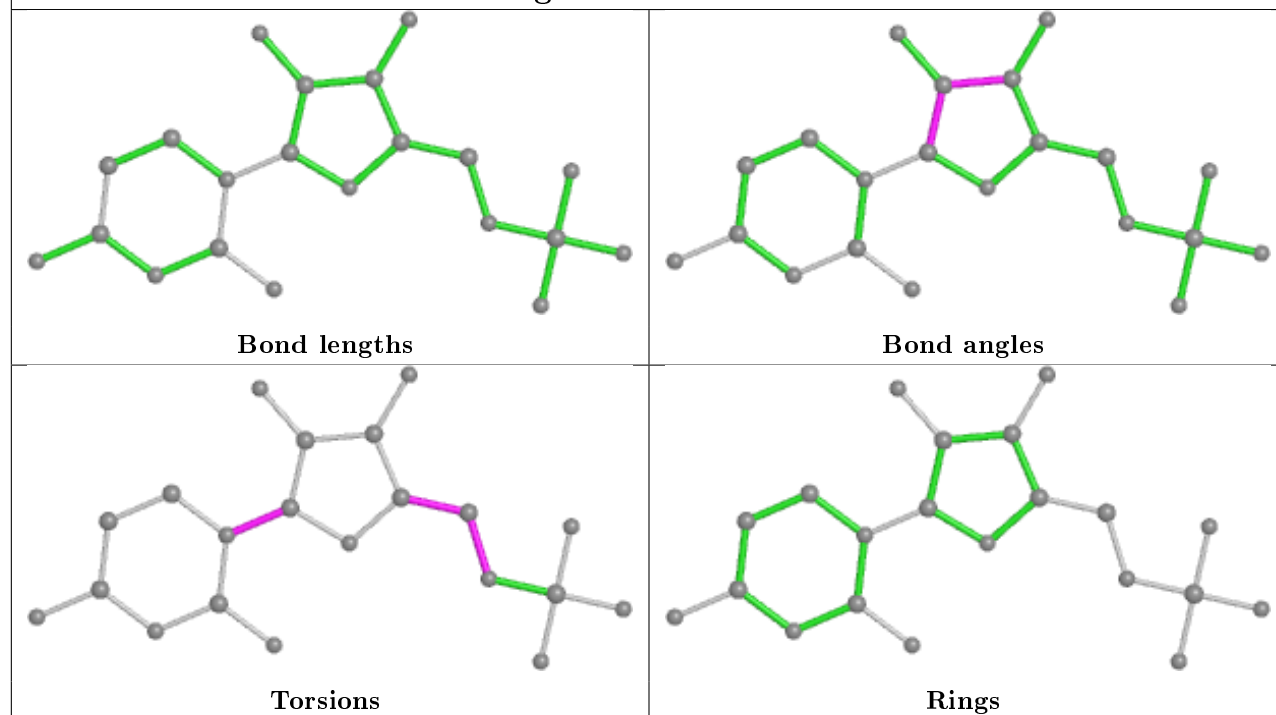
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	801	1S3	1	0
3	C	803	G6P	3	0
3	D	802	G6P	1	0
3	A	802	G6P	2	0
4	C	804	PEG	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

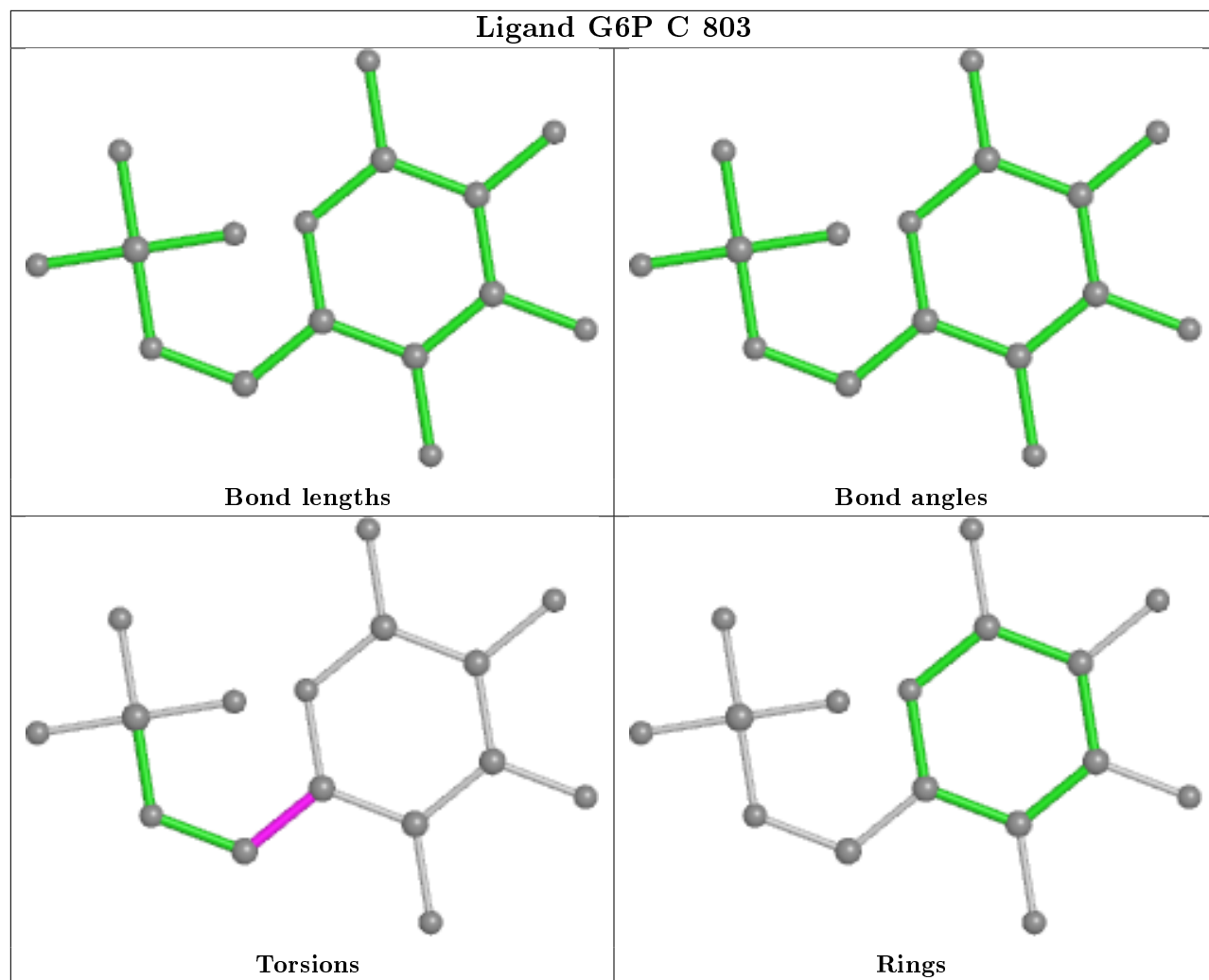
Ligand U5P B 801



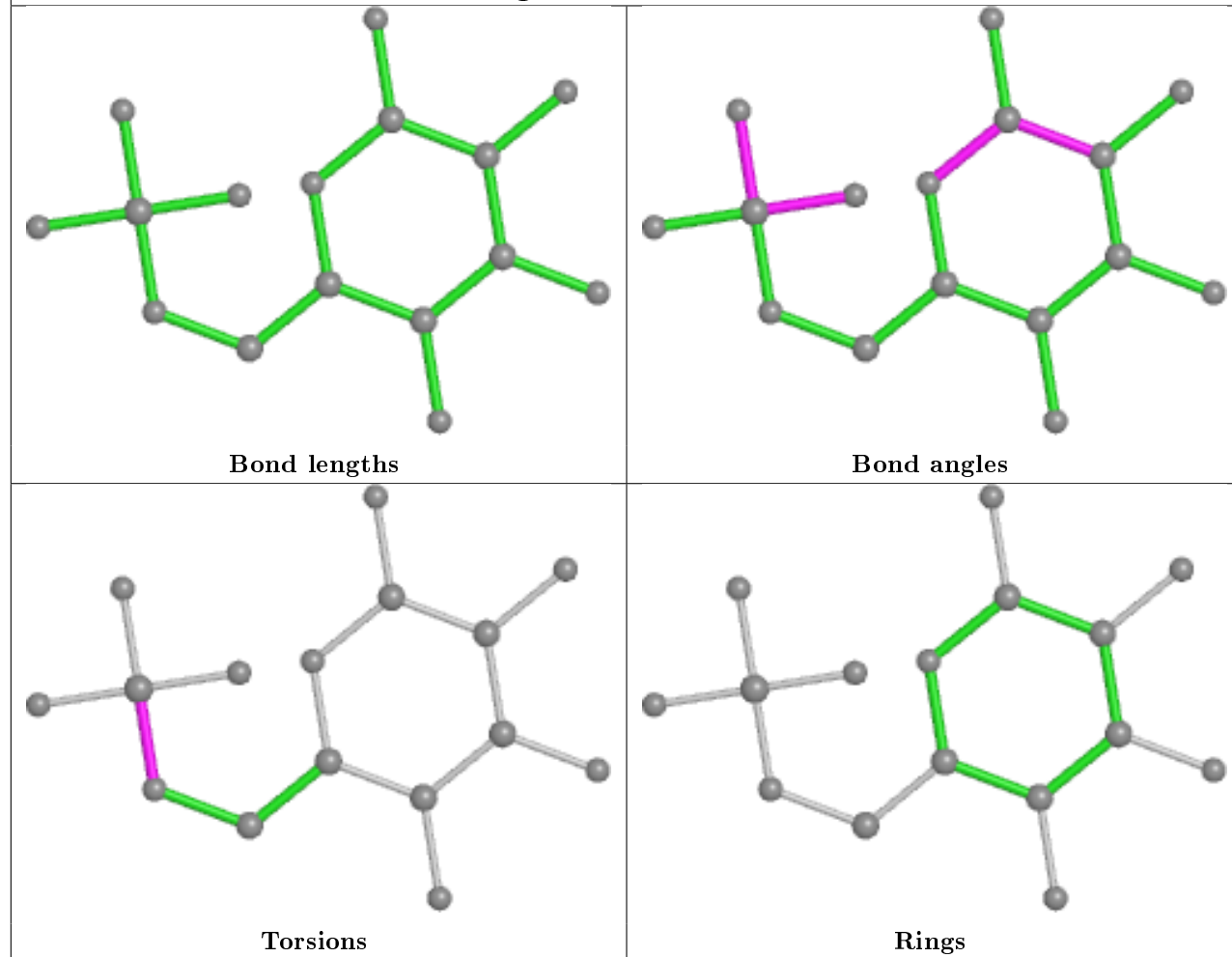
Ligand U5P A 801



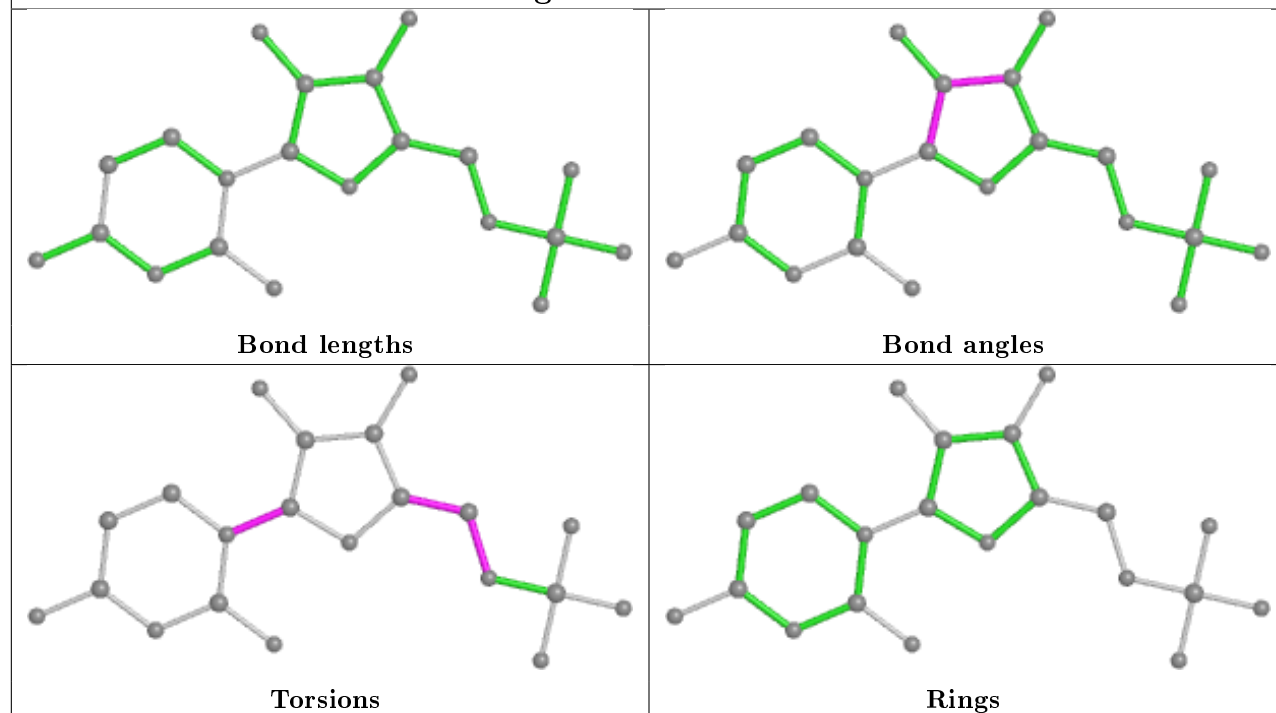
Ligand G6P C 803

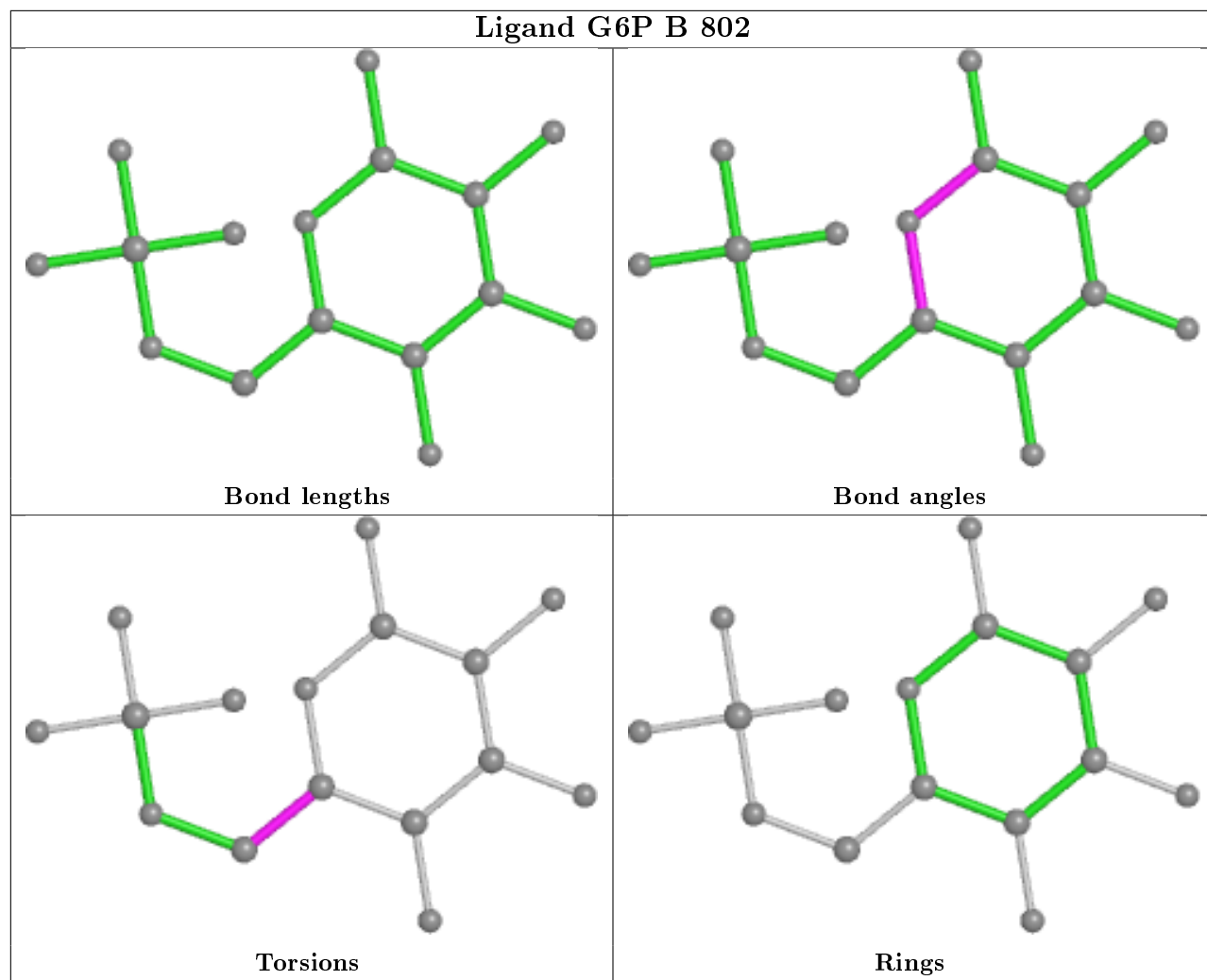


Ligand G6P D 802

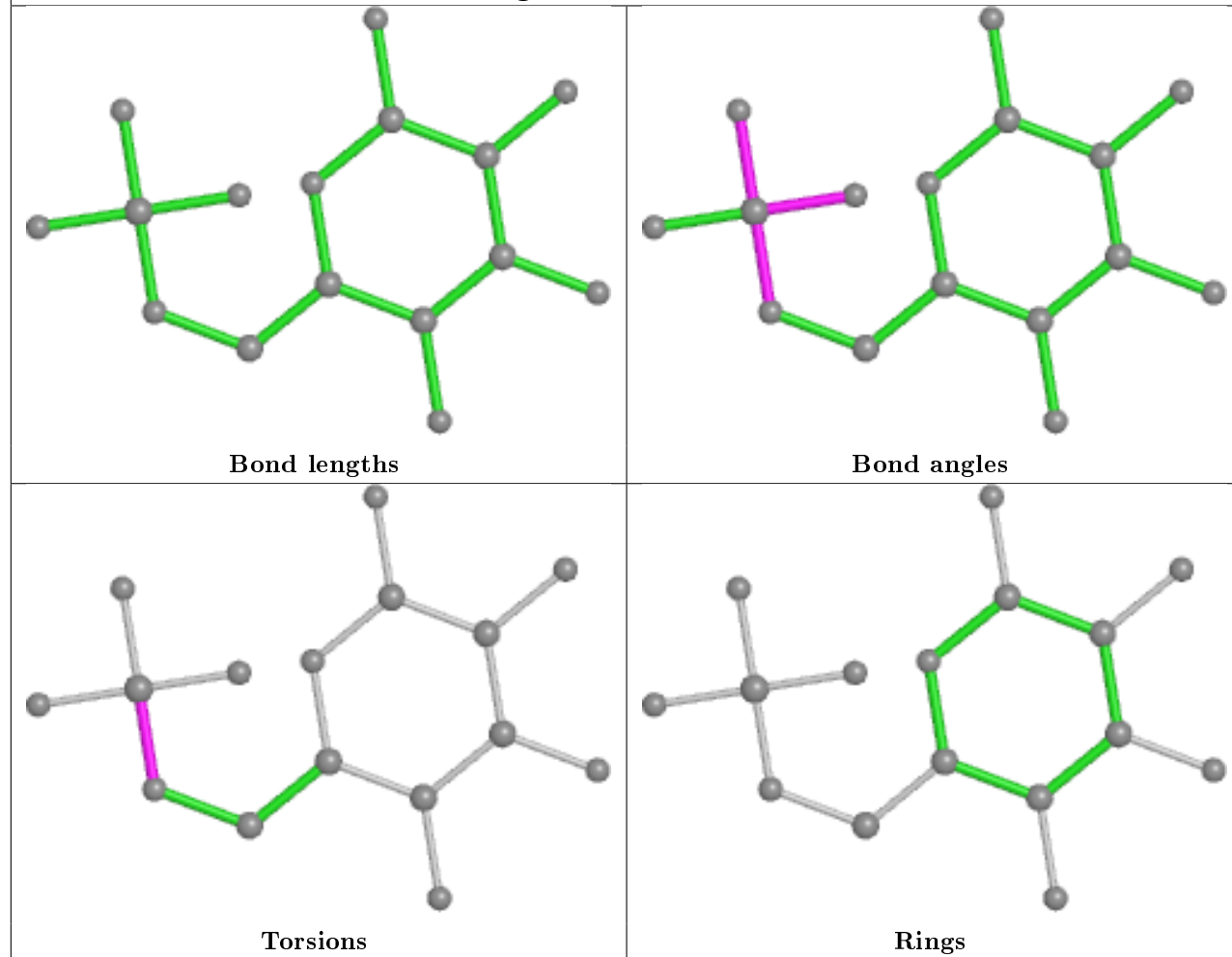


Ligand U5P C 802

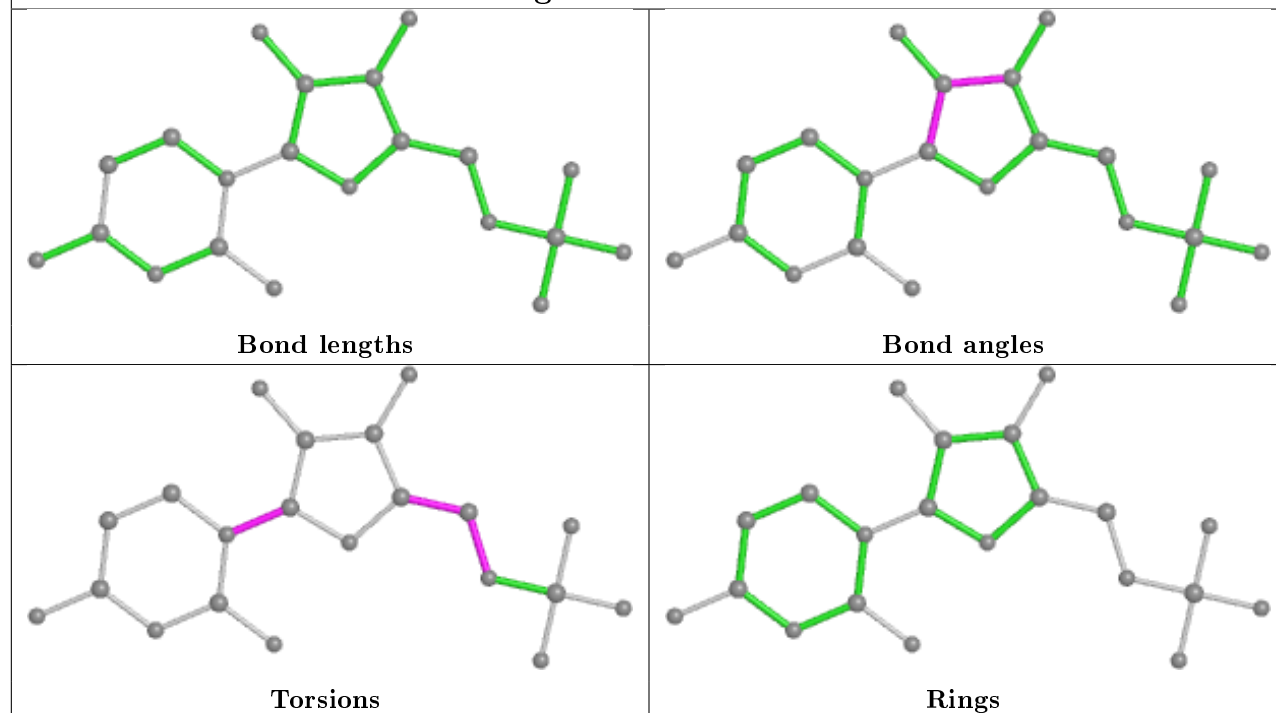




Ligand G6P A 802



Ligand U5P D 801



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, 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	638/724 (88%)	0.41	49 (7%) 13 7	53, 103, 165, 226	0
1	B	638/724 (88%)	0.17	21 (3%) 46 30	24, 86, 150, 198	0
1	C	638/724 (88%)	0.70	80 (12%) 3 2	45, 108, 183, 247	0
1	D	636/724 (87%)	0.45	50 (7%) 12 7	30, 104, 190, 223	0
All	All	2550/2896 (88%)	0.43	200 (7%) 13 7	24, 101, 179, 247	0

All (200) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	638	LEU	9.9
1	C	141	ILE	8.3
1	C	111	VAL	7.6
1	C	63	TRP	7.2
1	B	630	LEU	7.1
1	C	108	LEU	7.0
1	C	91	VAL	7.0
1	D	630	LEU	6.8
1	D	125	LEU	6.6
1	C	127	GLY	6.4
1	A	91	VAL	6.2
1	C	103	VAL	6.1
1	C	106	PHE	6.1
1	C	155	ALA	5.9
1	D	626	VAL	5.7
1	C	129	PRO	5.6
1	C	131	PRO	5.5
1	D	627	GLY	5.3
1	A	77	GLN	5.3
1	B	624	GLU	5.2
1	C	128	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
1	A	63	TRP	5.0
1	C	92	TYR	5.0
1	C	83	MET	5.0
1	A	61	LEU	4.9
1	D	622	PHE	4.8
1	A	92	TYR	4.8
1	C	181	LYS	4.7
1	D	639	ALA	4.4
1	C	76	VAL	4.4
1	D	631	ASN	4.4
1	C	126	VAL	4.3
1	D	129	PRO	4.3
1	A	80	LEU	4.3
1	D	122	LEU	4.2
1	A	104	ILE	4.2
1	C	68	ALA	4.2
1	D	123	TRP	4.2
1	D	126	VAL	4.2
1	D	618	TYR	4.2
1	D	635	MET	4.1
1	D	2	SER	4.1
1	D	10	LEU	4.1
1	D	629	GLU	4.1
1	C	157	LEU	4.1
1	C	107	ASP	4.0
1	D	205	GLY	4.0
1	D	614	LEU	4.0
1	D	628	GLU	4.0
1	D	625	LEU	4.0
1	C	170	TRP	3.9
1	D	637	ALA	3.9
1	A	76	VAL	3.8
1	A	305	PHE	3.8
1	C	544	ASN	3.7
1	C	279	PHE	3.7
1	D	91	VAL	3.6
1	B	67	GLU	3.6
1	A	90	PHE	3.6
1	D	604	LEU	3.5
1	C	142	LEU	3.4
1	A	197	LEU	3.4
1	A	64	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	624	GLU	3.4
1	A	5	LEU	3.4
1	A	78	HIS	3.4
1	C	118	TRP	3.4
1	C	123	TRP	3.3
1	D	45	LEU	3.3
1	C	86	ARG	3.3
1	D	127	GLY	3.3
1	A	106	PHE	3.3
1	C	149	TRP	3.3
1	D	128	ILE	3.2
1	C	62	ASP	3.2
1	D	229	HIS	3.2
1	C	133	ASN	3.2
1	B	632	ASP	3.2
1	D	61	LEU	3.1
1	A	79	ALA	3.1
1	C	80	LEU	3.1
1	B	405	LEU	3.1
1	C	79	ALA	3.1
1	B	629	GLU	3.1
1	C	78	HIS	3.1
1	D	67	GLU	3.1
1	D	132	GLU	3.0
1	C	125	LEU	3.0
1	C	227	ILE	3.0
1	A	88	VAL	3.0
1	D	150	PHE	3.0
1	C	549	TYR	2.9
1	B	106	PHE	2.9
1	C	66	PRO	2.9
1	D	265	GLY	2.9
1	C	69	PHE	2.9
1	C	173	GLY	2.9
1	C	67	GLU	2.9
1	C	229	HIS	2.9
1	C	116	ASN	2.9
1	A	507	TYR	2.8
1	C	104	ILE	2.8
1	C	210	TYR	2.8
1	D	9	LEU	2.8
1	C	151	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	140	ALA	2.8
1	C	543	THR	2.8
1	A	89	HIS	2.8
1	B	71	ASP	2.8
1	D	616	ARG	2.7
1	A	214	GLU	2.7
1	C	135	PHE	2.7
1	C	228	TYR	2.7
1	A	543	THR	2.7
1	A	62	ASP	2.6
1	D	620	ASP	2.6
1	B	163	ILE	2.6
1	A	158	ASP	2.6
1	A	83	MET	2.6
1	A	151	LEU	2.6
1	A	464	LEU	2.6
1	C	174	VAL	2.6
1	C	48	PRO	2.6
1	C	178	LEU	2.6
1	B	631	ASN	2.6
1	A	108	LEU	2.6
1	B	638	LEU	2.5
1	D	164	VAL	2.5
1	C	207	PHE	2.5
1	A	129	PRO	2.5
1	D	118	TRP	2.5
1	C	112	ARG	2.5
1	A	103	VAL	2.5
1	C	182	ARG	2.5
1	C	93	GLY	2.5
1	A	149	TRP	2.5
1	B	85	SER	2.4
1	B	637	ALA	2.4
1	B	636	ASP	2.4
1	C	230	ARG	2.4
1	B	9	LEU	2.4
1	A	565	VAL	2.4
1	C	44	HIS	2.4
1	A	448	VAL	2.4
1	D	615	ARG	2.4
1	A	66	PRO	2.4
1	C	61	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	130	SER	2.3
1	D	8	HIS	2.3
1	A	544	ASN	2.3
1	C	305	PHE	2.3
1	C	160	GLN	2.3
1	C	197	LEU	2.3
1	D	227	ILE	2.3
1	C	113	GLY	2.3
1	D	93	GLY	2.3
1	D	185	ASP	2.3
1	A	157	LEU	2.3
1	A	69	PHE	2.3
1	C	82	THR	2.3
1	C	593	LEU	2.3
1	D	197	LEU	2.2
1	A	465	PHE	2.2
1	B	407	THR	2.2
1	D	90	PHE	2.2
1	B	68	ALA	2.2
1	C	507	TYR	2.2
1	A	417	LEU	2.2
1	A	593	LEU	2.2
1	A	46	ILE	2.2
1	C	148	ALA	2.2
1	D	80	LEU	2.2
1	C	159	SER	2.2
1	C	158	ASP	2.2
1	C	122	LEU	2.2
1	B	429	ILE	2.2
1	A	82	THR	2.2
1	A	11	PHE	2.1
1	A	253	PHE	2.1
1	D	96	LEU	2.1
1	C	13	THR	2.1
1	A	613	ALA	2.1
1	B	90	PHE	2.1
1	C	75	PRO	2.1
1	C	232	CYS	2.1
1	C	72	GLU	2.1
1	A	49	LEU	2.0
1	D	11	PHE	2.1
1	A	59	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	159	SER	2.0
1	A	111	VAL	2.0
1	A	94	ARG	2.0
1	C	511	TRP	2.0
1	C	436	GLU	2.0
1	C	9	LEU	2.0
1	C	150	PHE	2.0
1	B	104	ILE	2.0
1	D	119	LYS	2.0
1	B	66	PRO	2.0
1	C	405	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides 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. 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	BA	B	805	1/1	0.64	0.06	245,245,245,245	0
5	BA	D	805	1/1	0.78	0.07	227,227,227,227	0
6	1S3	C	801	15/15	0.82	0.21	107,130,156,156	0
4	PEG	C	804	7/7	0.84	0.34	88,89,96,96	0
4	PEG	B	803	7/7	0.85	0.25	98,103,115,115	0
2	U5P	C	802	21/21	0.87	0.26	95,123,162,163	0
5	BA	A	805	1/1	0.88	0.17	212,212,212,212	0
4	PEG	A	803	7/7	0.92	0.19	71,74,82,85	0
5	BA	B	804	1/1	0.92	0.26	149,149,149,149	0
4	PEG	D	803	7/7	0.92	0.23	90,90,95,96	0
2	U5P	A	801	21/21	0.93	0.23	89,103,120,123	0
5	BA	D	804	1/1	0.93	0.22	159,159,159,159	0

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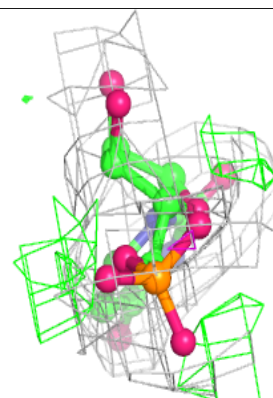
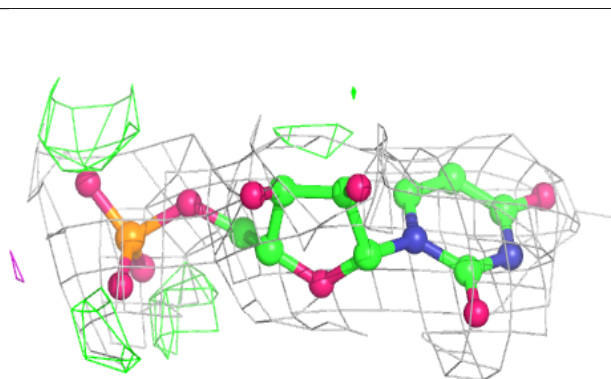
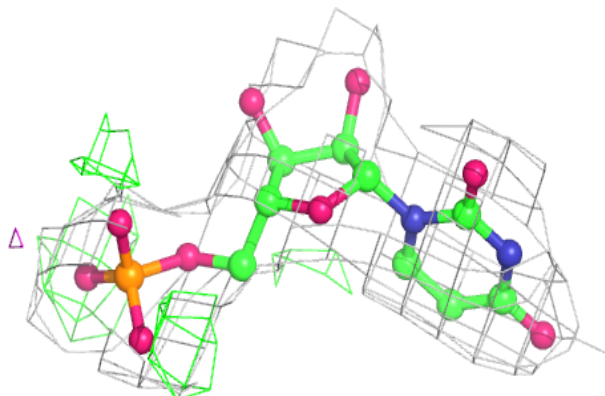
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	U5P	D	801	21/21	0.94	0.15	93,105,112,127	0
2	U5P	B	801	21/21	0.96	0.15	82,91,100,105	0
3	G6P	C	803	16/16	0.98	0.15	66,77,83,84	0
3	G6P	B	802	16/16	0.98	0.19	56,74,80,80	0
3	G6P	A	802	16/16	0.98	0.16	80,92,98,102	0
3	G6P	D	802	16/16	0.98	0.16	55,67,75,78	0
5	BA	A	804	1/1	0.98	0.22	135,135,135,135	0
5	BA	C	805	1/1	0.99	0.23	145,145,145,145	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

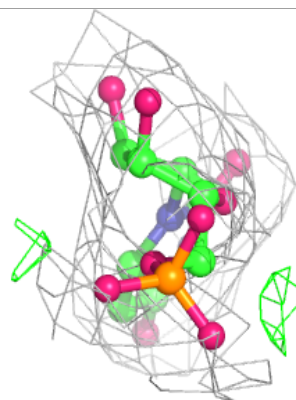
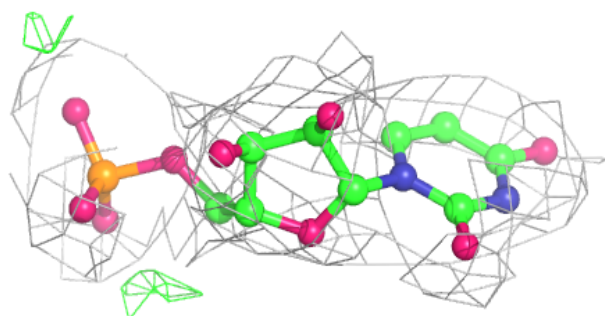
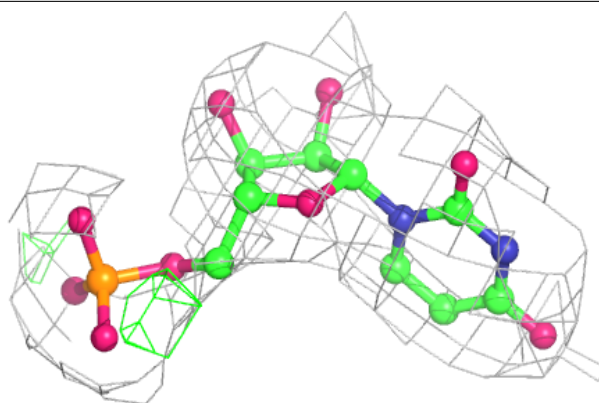
Electron density around U5P C 802:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

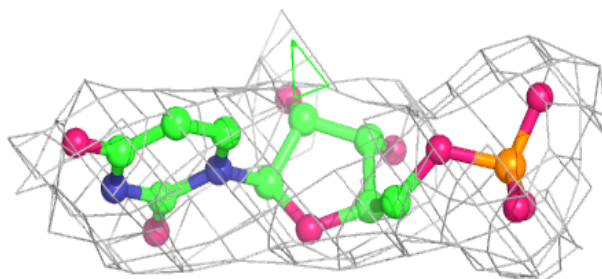
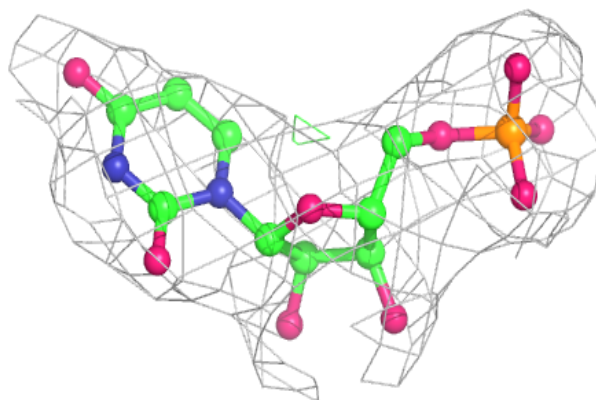


Electron density around U5P A 801:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

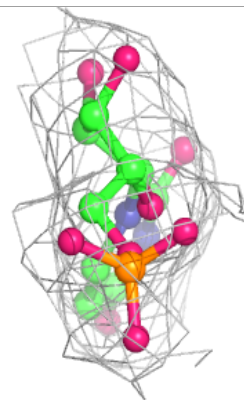
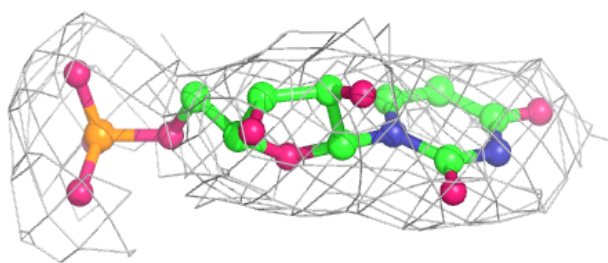
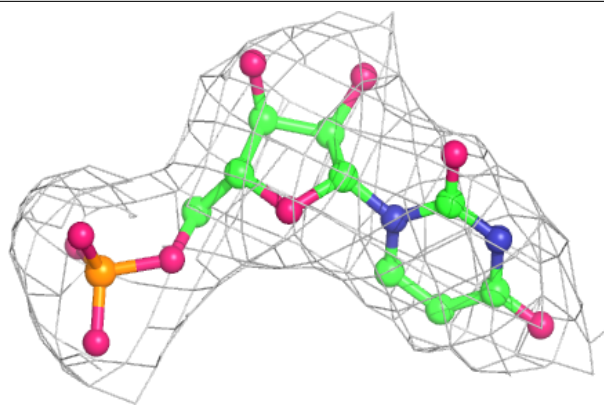
**Electron density around U5P D 801:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

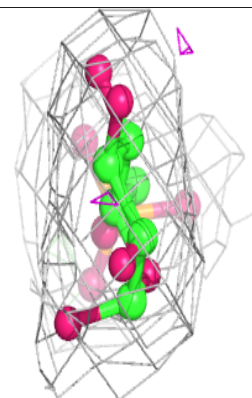
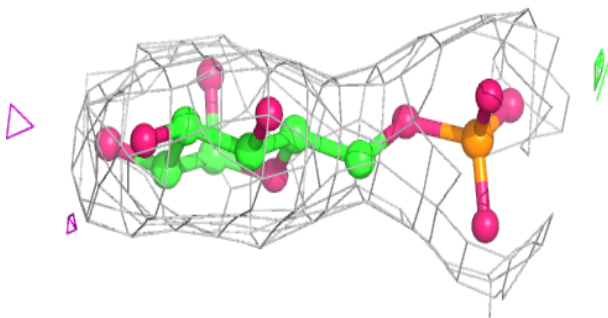
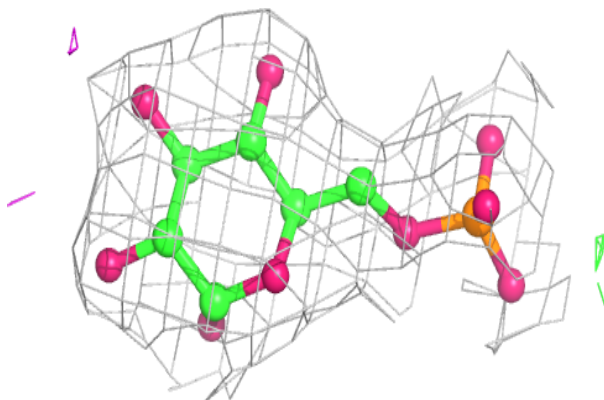


Electron density around U5P B 801:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

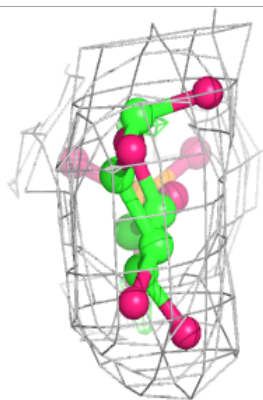
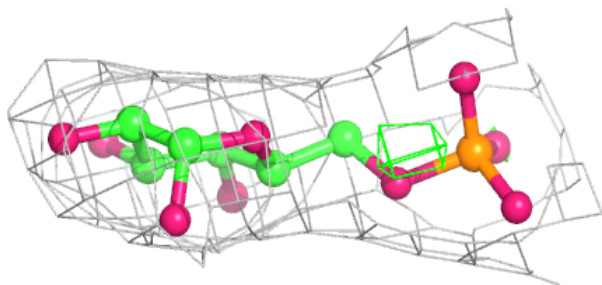
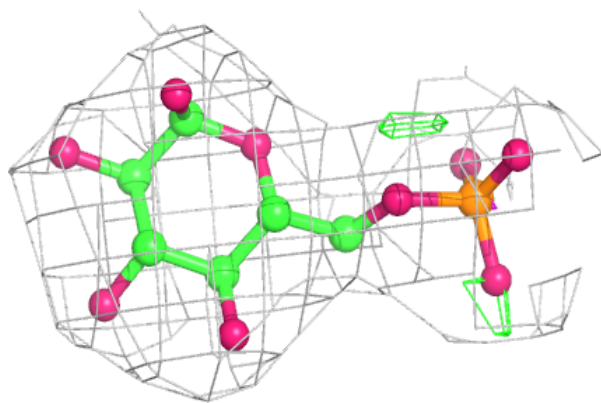
**Electron density around G6P C 803:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

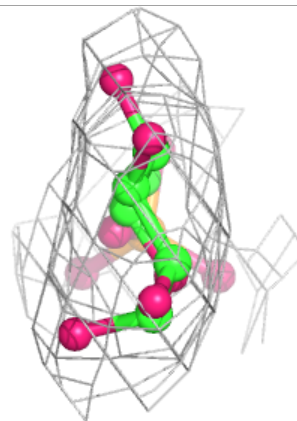
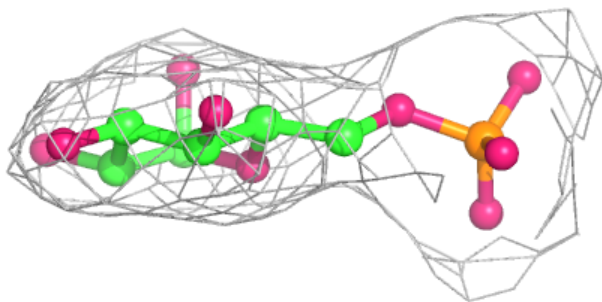
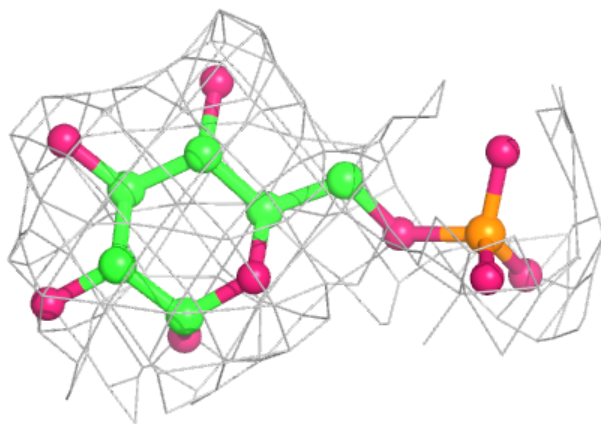


Electron density around G6P B 802:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

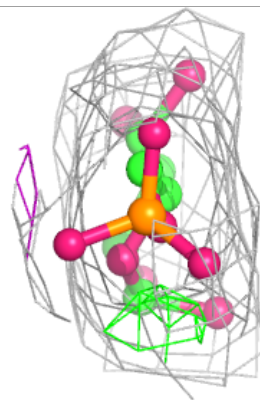
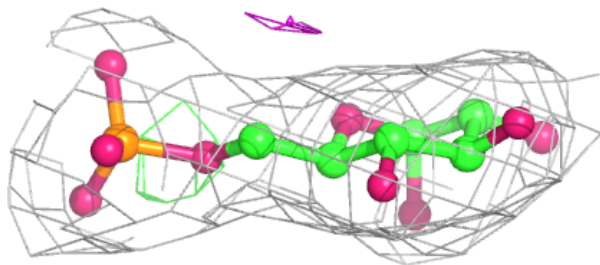
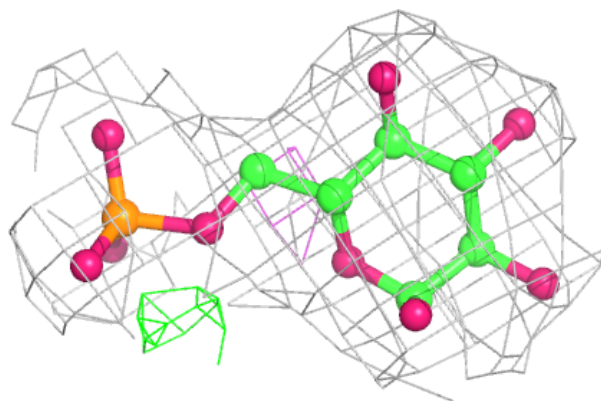
**Electron density around G6P A 802:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around G6P D 802:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.