



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:39 PM UTC

PDB ID : 5SUK / pdb_00005suk
Title : G6P bound activated state of yeast glycogen synthase 2
Authors : Baskaran, S.; Mahalingan, K.K.; Hurley, T.D.
Deposited on : 2016-08-03
Resolution : 2.88 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

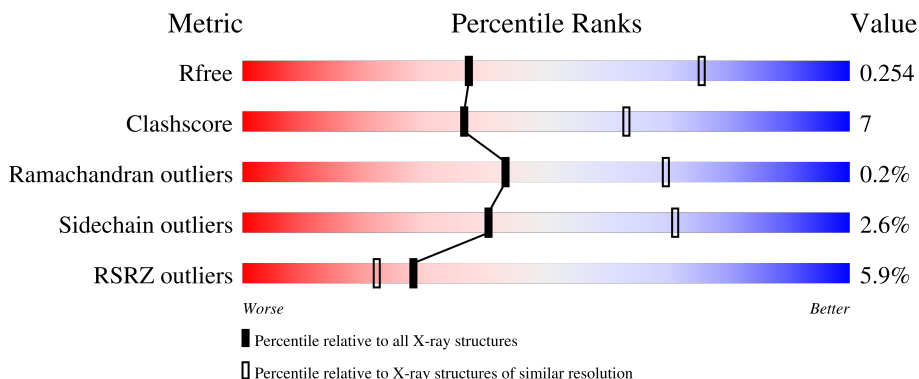
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.88 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}	180053	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)

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 of 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	725	4% 75% 12% • 12%
1	B	725	3% 76% 12% 12%
1	C	725	5% 75% 12% • 12%
1	D	725	8% 68% 14% 17%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19585 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 Glycogen [starch] synthase isoform 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	638	Total	C	N	O	S	0	0	0
			5020	3207	869	925	19			
1	B	637	Total	C	N	O	S	0	0	0
			5018	3198	877	925	18			
1	C	639	Total	C	N	O	S	0	0	0
			4869	3095	847	909	18			
1	D	604	Total	C	N	O	S	0	0	0
			4582	2921	797	847	17			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P27472
A	-18	GLY	-	expression tag	UNP P27472
A	-17	SER	-	expression tag	UNP P27472
A	-16	SER	-	expression tag	UNP P27472
A	-15	HIS	-	expression tag	UNP P27472
A	-14	HIS	-	expression tag	UNP P27472
A	-13	HIS	-	expression tag	UNP P27472
A	-12	HIS	-	expression tag	UNP P27472
A	-11	HIS	-	expression tag	UNP P27472
A	-10	HIS	-	expression tag	UNP P27472
A	-9	SER	-	expression tag	UNP P27472
A	-8	SER	-	expression tag	UNP P27472
A	-7	GLY	-	expression tag	UNP P27472
A	-6	LEU	-	expression tag	UNP P27472
A	-5	VAL	-	expression tag	UNP P27472
A	-4	PRO	-	expression tag	UNP P27472
A	-3	ARG	-	expression tag	UNP P27472
A	-2	GLY	-	expression tag	UNP P27472
A	-1	SER	-	expression tag	UNP P27472
A	0	HIS	-	expression tag	UNP P27472
A	535	SER	ALA	conflict	UNP P27472

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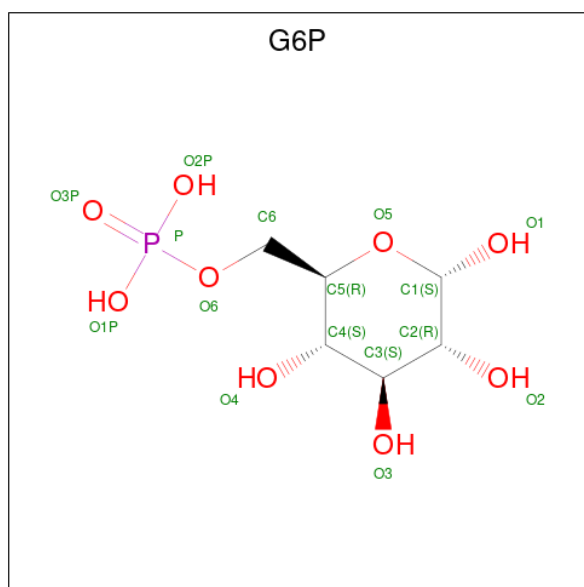
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	initiating methionine	UNP P27472
B	-18	GLY	-	expression tag	UNP P27472
B	-17	SER	-	expression tag	UNP P27472
B	-16	SER	-	expression tag	UNP P27472
B	-15	HIS	-	expression tag	UNP P27472
B	-14	HIS	-	expression tag	UNP P27472
B	-13	HIS	-	expression tag	UNP P27472
B	-12	HIS	-	expression tag	UNP P27472
B	-11	HIS	-	expression tag	UNP P27472
B	-10	HIS	-	expression tag	UNP P27472
B	-9	SER	-	expression tag	UNP P27472
B	-8	SER	-	expression tag	UNP P27472
B	-7	GLY	-	expression tag	UNP P27472
B	-6	LEU	-	expression tag	UNP P27472
B	-5	VAL	-	expression tag	UNP P27472
B	-4	PRO	-	expression tag	UNP P27472
B	-3	ARG	-	expression tag	UNP P27472
B	-2	GLY	-	expression tag	UNP P27472
B	-1	SER	-	expression tag	UNP P27472
B	0	HIS	-	expression tag	UNP P27472
B	535	SER	ALA	conflict	UNP P27472
C	-19	MET	-	initiating methionine	UNP P27472
C	-18	GLY	-	expression tag	UNP P27472
C	-17	SER	-	expression tag	UNP P27472
C	-16	SER	-	expression tag	UNP P27472
C	-15	HIS	-	expression tag	UNP P27472
C	-14	HIS	-	expression tag	UNP P27472
C	-13	HIS	-	expression tag	UNP P27472
C	-12	HIS	-	expression tag	UNP P27472
C	-11	HIS	-	expression tag	UNP P27472
C	-10	HIS	-	expression tag	UNP P27472
C	-9	SER	-	expression tag	UNP P27472
C	-8	SER	-	expression tag	UNP P27472
C	-7	GLY	-	expression tag	UNP P27472
C	-6	LEU	-	expression tag	UNP P27472
C	-5	VAL	-	expression tag	UNP P27472
C	-4	PRO	-	expression tag	UNP P27472
C	-3	ARG	-	expression tag	UNP P27472
C	-2	GLY	-	expression tag	UNP P27472
C	-1	SER	-	expression tag	UNP P27472
C	0	HIS	-	expression tag	UNP P27472
C	535	SER	ALA	conflict	UNP P27472

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	initiating methionine	UNP P27472
D	-18	GLY	-	expression tag	UNP P27472
D	-17	SER	-	expression tag	UNP P27472
D	-16	SER	-	expression tag	UNP P27472
D	-15	HIS	-	expression tag	UNP P27472
D	-14	HIS	-	expression tag	UNP P27472
D	-13	HIS	-	expression tag	UNP P27472
D	-12	HIS	-	expression tag	UNP P27472
D	-11	HIS	-	expression tag	UNP P27472
D	-10	HIS	-	expression tag	UNP P27472
D	-9	SER	-	expression tag	UNP P27472
D	-8	SER	-	expression tag	UNP P27472
D	-7	GLY	-	expression tag	UNP P27472
D	-6	LEU	-	expression tag	UNP P27472
D	-5	VAL	-	expression tag	UNP P27472
D	-4	PRO	-	expression tag	UNP P27472
D	-3	ARG	-	expression tag	UNP P27472
D	-2	GLY	-	expression tag	UNP P27472
D	-1	SER	-	expression tag	UNP P27472
D	0	HIS	-	expression tag	UNP P27472
D	535	SER	ALA	conflict	UNP P27472

- Molecule 2 is 6-O-phosphono-alpha-D-glucopyranose (CCD ID: G6P) (formula: $C_6H_{13}O_9P$).



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

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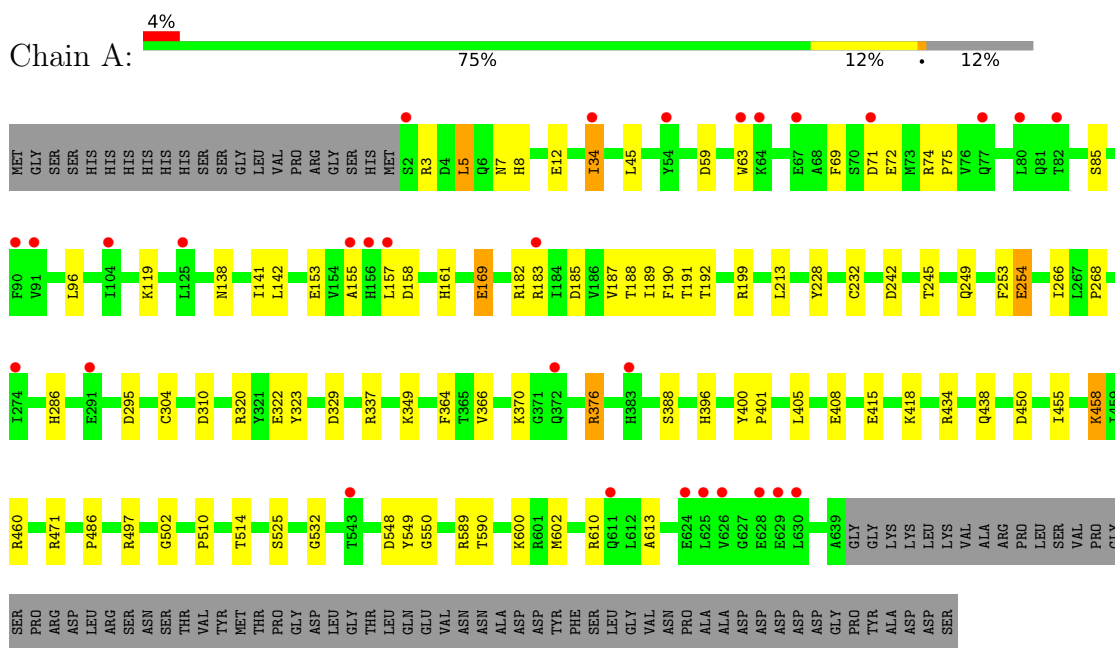
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		
2	C	1	Total	C	O	P	0	0
			16	6	9	1		
2	D	1	Total	C	O	P	0	0
			16	6	9	1		

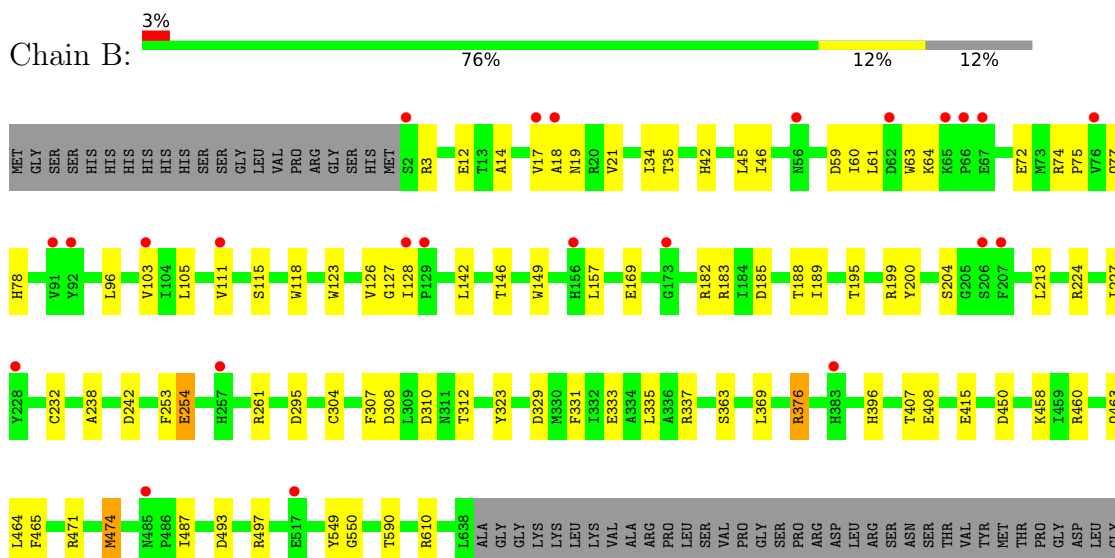
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

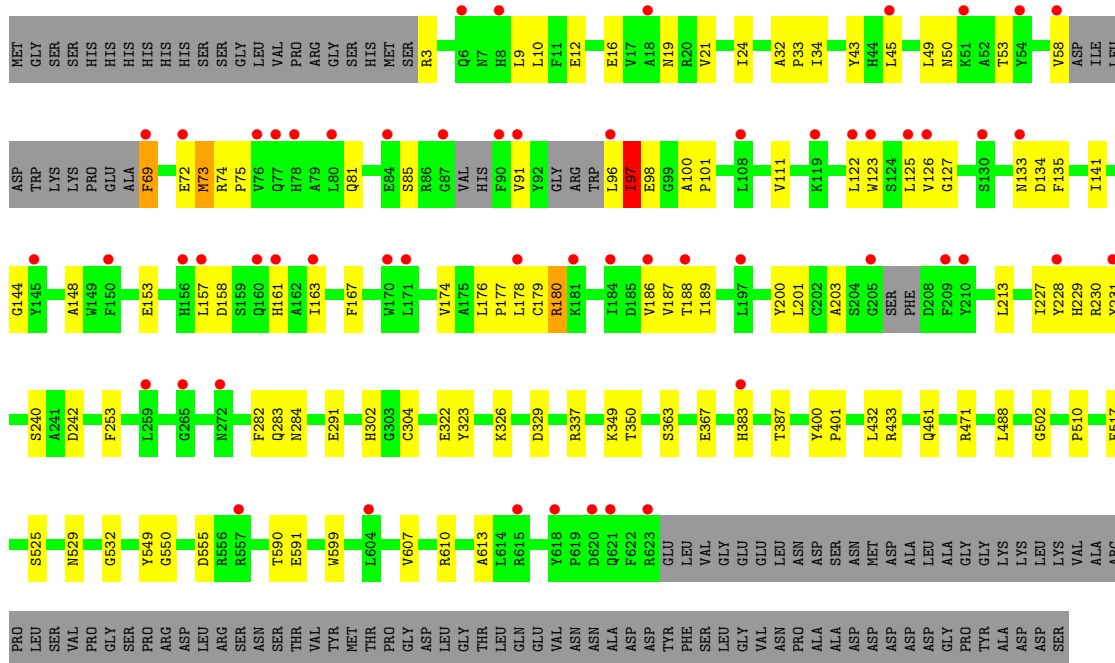
• Molecule 1: Glycogen [starch] synthase isoform 2



• Molecule 1: Glycogen [starch] synthase isoform 2



Chain C: 5% 75% 12% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	191.98Å 204.56Å 205.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	145.09 – 2.88 145.09 – 2.88	Depositor EDS
% Data completeness (in resolution range)	98.0 (145.09-2.88) 98.0 (145.09-2.88)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.219 , 0.260 0.217 , 0.254	Depositor DCC
R_{free} test set	4461 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	67.5	Xtriage
Anisotropy	0.687	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.9	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	19585	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: G6P

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	0.59	0/5140	0.84	0/6983
1	B	0.56	0/5136	0.85	0/6977
1	C	0.55	0/4975	0.86	0/6776
1	D	0.57	0/4677	0.88	1/6363 (0.0%)
All	All	0.57	0/19928	0.86	1/27099 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	97	ILE	N-CA-C	-6.71	98.92	108.65

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5020	0	4846	58	0
1	B	5018	0	4844	52	0
1	C	4869	0	4619	73	0
1	D	4582	0	4371	92	0
2	A	32	0	22	2	0
2	B	32	0	22	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	16	0	11	0	0
2	D	16	0	11	1	0
All	All	19585	0	18746	274	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 7.

All (274) 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:C:83:MET:C	1:C:88:VAL:HG22	1.73	1.13
1:D:167:PHE:CD2	1:D:176:LEU:HD21	1.87	1.09
1:C:83:MET:CA	1:C:88:VAL:HG22	1.92	0.98
1:D:176:LEU:HD11	1:D:188:THR:OG1	1.67	0.95
1:D:134:ASP:OD2	1:D:229:HIS:NE2	2.04	0.90
1:D:227:ILE:O	1:D:229:HIS:N	2.08	0.87
1:B:335:LEU:HD13	1:B:474:MET:HE1	1.57	0.85
1:C:280:HIS:CE1	1:D:283:GLN:HG2	2.13	0.84
1:C:82:THR:HG22	1:C:83:MET:H	1.41	0.83
2:B:902:G6P:O1P	2:B:902:G6P:O4	2.00	0.80
1:C:122:LEU:HD12	1:C:128:ILE:HB	1.64	0.79
1:C:42:HIS:HA	1:C:73:MET:HE1	1.64	0.79
1:C:83:MET:CB	1:C:88:VAL:CG2	2.62	0.77
1:A:7:ASN:ND2	1:A:72:GLU:OE2	2.17	0.77
1:D:148:ALA:HB1	1:D:178:LEU:HD11	1.67	0.77
1:C:83:MET:CA	1:C:88:VAL:CG2	2.63	0.76
1:C:83:MET:O	1:C:88:VAL:HG22	1.86	0.75
1:D:163:ILE:HB	1:D:186:VAL:HG22	1.68	0.75
1:D:167:PHE:CG	1:D:176:LEU:HD21	2.23	0.73
1:C:196:LEU:HD12	1:C:234:GLU:OE2	1.89	0.72
1:D:549:TYR:O	1:D:590:THR:HG22	1.89	0.72
1:D:176:LEU:CD1	1:D:188:THR:OG1	2.38	0.72
1:A:153:GLU:O	1:A:157:LEU:HD13	1.91	0.70
1:C:143:LEU:O	1:C:147:VAL:HG23	1.91	0.70
1:D:187:VAL:HG11	1:D:613:ALA:HB1	1.73	0.69
1:D:167:PHE:CD2	1:D:176:LEU:CD2	2.71	0.69
1:A:3:ARG:NH2	1:A:158:ASP:O	2.24	0.69
1:B:123:TRP:O	1:B:127:GLY:HA2	1.91	0.69
1:B:450:ASP:OD1	1:B:460:ARG:NH2	2.25	0.69
1:C:53:THR:O	1:C:55:GLN:N	2.24	0.69
1:A:549:TYR:O	1:A:590:THR:HG22	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:178:LEU:HD12	1:D:179:CYS:N	2.09	0.67
1:C:49:LEU:HD23	1:C:107:ASP:CB	2.25	0.66
1:A:5:LEU:O	1:A:8:HIS:HB3	1.95	0.66
1:B:74:ARG:NH1	1:B:77:GLN:OE1	2.29	0.66
1:D:302:HIS:HD2	1:D:432:LEU:O	1.79	0.65
1:C:179:CYS:HA	1:C:184:ILE:HD12	1.78	0.65
1:D:187:VAL:CG1	1:D:613:ALA:HB1	2.27	0.65
1:A:415:GLU:O	1:A:418:LYS:NZ	2.30	0.65
1:B:42:HIS:NE2	1:B:72:GLU:OE2	2.30	0.65
1:C:83:MET:O	1:C:88:VAL:N	2.27	0.65
1:A:71:ASP:HA	1:A:74:ARG:HG2	1.79	0.65
1:C:218:VAL:HG11	1:C:231:TYR:CZ	2.32	0.65
1:B:19:ASN:OD1	1:B:21:VAL:HG23	1.98	0.64
1:C:42:HIS:HA	1:C:73:MET:CE	2.28	0.64
1:C:284:ASN:HD21	1:D:284:ASN:HD21	1.45	0.64
1:C:122:LEU:CD1	1:C:128:ILE:HB	2.27	0.63
1:C:49:LEU:HB3	1:C:107:ASP:HA	1.81	0.63
1:C:77:GLN:HA	1:C:80:LEU:HB2	1.79	0.63
1:A:71:ASP:HA	1:A:74:ARG:CG	2.29	0.63
1:C:197:LEU:HD11	1:C:218:VAL:HG13	1.81	0.63
1:D:167:PHE:CG	1:D:176:LEU:CD2	2.82	0.63
1:C:12:GLU:HB3	1:C:45:LEU:HD23	1.79	0.62
1:C:83:MET:HA	1:C:88:VAL:HG22	1.81	0.62
1:C:510:PRO:O	1:C:532:GLY:HA3	2.00	0.62
1:C:77:GLN:O	1:C:81:GLN:N	2.32	0.62
1:C:196:LEU:HD12	1:C:234:GLU:CD	2.26	0.61
1:C:45:LEU:HB2	1:C:103:VAL:HG22	1.82	0.61
1:C:73:MET:C	1:C:75:PRO:HD2	2.26	0.60
1:C:406:THR:O	1:C:407:THR:OG1	2.15	0.60
1:D:227:ILE:HG23	1:D:230:ARG:CB	2.32	0.60
1:B:549:TYR:O	1:B:590:THR:HG22	2.01	0.59
1:D:188:THR:CG2	1:D:242:ASP:H	2.14	0.59
1:C:78:HIS:CB	1:C:157:LEU:HD13	2.33	0.59
1:D:97:ILE:HD13	1:D:97:ILE:H	1.67	0.59
1:D:148:ALA:CB	1:D:178:LEU:HD11	2.33	0.59
1:C:218:VAL:HG11	1:C:231:TYR:OH	2.03	0.58
1:A:187:VAL:HG12	1:A:613:ALA:HB1	1.83	0.58
1:C:450:ASP:OD1	1:C:460:ARG:NH2	2.36	0.58
1:A:12:GLU:HB3	1:A:45:LEU:HD23	1.85	0.58
1:C:78:HIS:CB	1:C:157:LEU:CD1	2.82	0.58
1:C:195:THR:OG1	1:C:254:GLU:OE1	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:ALA:HB2	1:B:105:LEU:CD2	2.34	0.57
1:D:176:LEU:N	1:D:177:PRO:HD2	2.19	0.57
1:C:550:GLY:HA3	1:C:590:THR:CG2	2.34	0.57
1:C:108:LEU:O	1:C:111:VAL:N	2.32	0.57
1:D:188:THR:HG23	1:D:242:ASP:H	1.70	0.57
1:A:158:ASP:OD2	1:A:161:HIS:ND1	2.30	0.56
1:C:83:MET:C	1:C:88:VAL:CG2	2.64	0.56
1:D:177:PRO:HA	1:D:240:SER:OG	2.05	0.55
1:A:187:VAL:CG1	1:A:613:ALA:HB1	2.36	0.55
1:C:82:THR:HA	1:C:85:SER:HB3	1.87	0.55
1:A:3:ARG:NH1	1:A:185:ASP:OD2	2.40	0.55
1:A:5:LEU:N	1:A:5:LEU:HD23	2.22	0.55
1:D:73:MET:HE3	1:D:73:MET:HA	1.87	0.55
1:D:510:PRO:O	1:D:532:GLY:HA3	2.07	0.55
1:D:74:ARG:N	1:D:75:PRO:HD2	2.21	0.54
1:D:3:ARG:NH2	1:D:158:ASP:O	2.40	0.54
1:B:63:TRP:H	1:B:63:TRP:CD1	2.23	0.54
1:A:213:LEU:HD21	1:A:254:GLU:HA	1.89	0.54
1:D:227:ILE:HG22	1:D:231:TYR:H	1.73	0.54
1:B:213:LEU:HD21	1:B:254:GLU:HA	1.90	0.54
1:B:60:ILE:C	1:B:61:LEU:HD12	2.33	0.54
1:D:12:GLU:HB3	1:D:45:LEU:HD23	1.90	0.54
1:B:12:GLU:HB3	1:B:45:LEU:HD23	1.89	0.54
1:C:82:THR:HG22	1:C:83:MET:N	2.15	0.53
1:C:122:LEU:HD11	1:C:128:ILE:HD12	1.91	0.53
1:A:434:ARG:NH1	1:A:438:GLN:OE1	2.42	0.52
1:D:96:LEU:N	1:D:100:ALA:HA	2.24	0.52
1:C:83:MET:CB	1:C:88:VAL:HG21	2.39	0.52
1:C:80:LEU:O	1:C:82:THR:O	2.27	0.52
1:A:199:ARG:NH2	2:A:902:G6P:O3P	2.33	0.52
1:C:14:ALA:O	1:C:17:VAL:HG23	2.09	0.52
1:B:323:TYR:OH	1:B:458:LYS:HG2	2.10	0.52
1:B:464:LEU:HD13	1:B:474:MET:HE3	1.92	0.52
1:B:115:SER:HB3	1:B:142:LEU:HD21	1.92	0.52
1:C:123:TRP:CD1	1:C:123:TRP:C	2.88	0.52
1:A:295:ASP:CG	1:A:376:ARG:HH22	2.19	0.51
1:D:123:TRP:O	1:D:127:GLY:HA2	2.10	0.51
1:D:73:MET:HA	1:D:73:MET:CE	2.39	0.51
1:B:308:ASP:O	1:B:312:THR:HG23	2.10	0.51
1:D:133:ASN:O	1:D:135:PHE:N	2.44	0.51
1:D:383:HIS:O	1:D:387:THR:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:ILE:HD11	1:A:610:ARG:HA	1.93	0.51
1:C:60:ILE:HG22	1:C:61:LEU:N	2.26	0.51
1:C:76:VAL:O	1:C:77:GLN:CB	2.58	0.51
1:D:187:VAL:HG11	1:D:613:ALA:C	2.36	0.50
1:A:74:ARG:N	1:A:75:PRO:CD	2.74	0.50
1:B:295:ASP:CG	1:B:376:ARG:HH22	2.19	0.50
1:D:227:ILE:HG22	1:D:231:TYR:N	2.27	0.50
1:C:323:TYR:CZ	1:C:329:ASP:HB3	2.46	0.50
1:D:34:ILE:HD13	1:D:599:TRP:HB3	1.94	0.50
1:B:126:VAL:HG12	1:B:128:ILE:HG13	1.93	0.50
1:A:188:THR:O	1:A:242:ASP:HB2	2.12	0.50
1:C:82:THR:O	1:C:83:MET:CB	2.60	0.50
1:B:45:LEU:HB2	1:B:103:VAL:HG12	1.94	0.50
1:B:333:GLU:OE1	1:B:458:LYS:NZ	2.45	0.49
1:B:369:LEU:HA	1:B:487:ILE:HD11	1.94	0.49
1:D:49:LEU:HD11	1:D:91:VAL:HG21	1.94	0.49
1:B:396:HIS:HE1	1:B:407:THR:O	1.94	0.49
1:C:83:MET:HA	1:C:88:VAL:CG2	2.40	0.49
1:C:218:VAL:CG1	1:C:231:TYR:CZ	2.95	0.49
1:B:63:TRP:O	1:B:77:GLN:NE2	2.44	0.49
1:C:213:LEU:HD21	1:C:254:GLU:HA	1.94	0.49
1:D:10:LEU:HD13	1:D:610:ARG:HD3	1.94	0.49
1:D:72:GLU:O	1:D:161:HIS:HE1	1.95	0.49
1:D:550:GLY:HA3	1:D:590:THR:CG2	2.43	0.49
1:A:450:ASP:OD1	1:A:460:ARG:NH2	2.44	0.48
1:C:196:LEU:CD1	1:C:234:GLU:CD	2.86	0.48
1:C:549:TYR:O	1:C:590:THR:HG22	2.12	0.48
1:D:97:ILE:HD13	1:D:97:ILE:N	2.28	0.48
1:C:189:ILE:HD11	1:C:610:ARG:HA	1.95	0.48
1:B:307:PHE:HD1	1:B:312:THR:HG21	1.78	0.48
1:A:510:PRO:O	1:A:532:GLY:HA3	2.14	0.48
1:B:18:ALA:HB2	1:B:105:LEU:HD22	1.96	0.48
1:A:34:ILE:CD1	1:A:600:LYS:HA	2.44	0.47
1:B:493:ASP:O	1:B:497:ARG:HG3	2.14	0.47
1:D:187:VAL:HG11	1:D:613:ALA:O	2.15	0.47
1:B:200:TYR:CD1	1:B:227:ILE:HD11	2.49	0.47
1:D:322:GLU:HB2	1:D:326:LYS:HG2	1.96	0.47
1:D:49:LEU:CD1	1:D:91:VAL:HG21	2.45	0.47
1:B:146:THR:O	1:B:149:TRP:HB3	2.15	0.47
1:B:396:HIS:HD2	1:B:415:GLU:OE2	1.97	0.47
1:D:49:LEU:CD1	1:D:91:VAL:CG2	2.92	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:GLU:HA	1:A:153:GLU:OE1	2.14	0.47
1:B:195:THR:OG1	1:B:254:GLU:OE2	2.29	0.47
1:D:97:ILE:HD13	1:D:101:PRO:HD2	1.95	0.47
1:D:126:VAL:HG12	1:D:126:VAL:O	2.15	0.47
1:C:49:LEU:HB3	1:C:107:ASP:CA	2.45	0.47
1:D:43:TYR:OH	1:D:45:LEU:HD21	2.15	0.47
1:D:189:ILE:HD11	1:D:610:ARG:HA	1.96	0.47
1:B:74:ARG:N	1:B:75:PRO:CD	2.78	0.47
1:B:463:GLN:HA	1:B:465:PHE:CE2	2.50	0.47
1:C:14:ALA:CB	1:C:28:LEU:HD11	2.45	0.47
1:C:19:ASN:OD1	1:C:21:VAL:HG23	2.15	0.47
1:D:187:VAL:HG12	1:D:188:THR:N	2.31	0.46
1:A:349:LYS:O	1:A:471:ARG:HD3	2.15	0.46
1:B:14:ALA:O	1:B:17:VAL:HG23	2.16	0.46
1:A:3:ARG:NH2	1:A:155:ALA:O	2.42	0.46
1:B:3:ARG:NH1	1:B:185:ASP:OD2	2.49	0.46
1:B:550:GLY:HA3	1:B:590:THR:CG2	2.45	0.46
1:D:49:LEU:HD12	1:D:91:VAL:CG2	2.45	0.46
1:A:169:GLU:HA	1:A:169:GLU:OE2	2.16	0.46
1:A:249:GLN:HG2	1:A:266:ILE:HD11	1.98	0.46
1:C:238:ALA:O	1:C:261:ARG:NH1	2.47	0.46
1:D:81:GLN:O	1:D:85:SER:N	2.44	0.46
1:D:9:LEU:CD2	1:D:73:MET:HE1	2.46	0.46
1:A:502:GLY:O	1:A:525:SER:HA	2.15	0.46
1:B:189:ILE:HD11	1:B:610:ARG:HA	1.97	0.46
1:B:331:PHE:CZ	1:B:335:LEU:HD11	2.50	0.46
1:C:60:ILE:CG2	1:C:61:LEU:N	2.79	0.46
1:C:357:MET:O	1:C:478:PRO:HA	2.16	0.46
1:C:283:GLN:NE2	1:C:584:ILE:HG23	2.31	0.45
1:A:400:TYR:CD1	1:A:401:PRO:HA	2.51	0.45
1:D:200:TYR:O	1:D:203:ALA:HB2	2.16	0.45
1:A:59:ASP:HB2	1:A:96:LEU:HD21	1.97	0.45
1:C:31:LYS:HD3	1:C:599:TRP:CH2	2.51	0.45
1:D:19:ASN:OD1	1:D:21:VAL:HG23	2.16	0.45
1:D:141:ILE:HA	1:D:174:VAL:HG11	1.97	0.45
1:D:187:VAL:HG11	1:D:613:ALA:CB	2.44	0.45
1:C:108:LEU:HD13	1:C:142:LEU:HB2	1.98	0.45
1:D:134:ASP:OD2	1:D:229:HIS:CD2	2.69	0.45
1:B:126:VAL:HG12	1:B:126:VAL:O	2.16	0.45
1:B:200:TYR:CE1	1:B:227:ILE:HD11	2.52	0.45
1:A:396:HIS:CE1	1:A:405:LEU:HD22	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:550:GLY:HA3	1:A:590:THR:CG2	2.48	0.44
1:B:323:TYR:CZ	1:B:329:ASP:HB3	2.52	0.44
1:D:283:GLN:HG3	2:D:901:G6P:O1	2.18	0.44
1:A:157:LEU:N	1:A:157:LEU:HD12	2.32	0.44
1:A:190:PHE:CE2	1:A:192:THR:HG23	2.52	0.44
1:A:514:THR:OG1	2:A:902:G6P:H1	2.17	0.44
1:C:550:GLY:HA3	1:C:590:THR:HG22	1.99	0.44
1:D:350:THR:OG1	1:D:471:ARG:NH1	2.50	0.44
1:D:69:PHE:CD2	1:D:69:PHE:N	2.86	0.44
1:D:213:LEU:HD23	1:D:253:PHE:CE2	2.52	0.44
1:C:177:PRO:HA	1:C:240:SER:OG	2.18	0.44
1:A:72:GLU:OE2	1:A:161:HIS:NE2	2.51	0.44
1:A:400:TYR:HA	1:A:405:LEU:HD12	1.99	0.44
1:C:209:PHE:O	1:C:213:LEU:HB2	2.18	0.43
1:D:73:MET:C	1:D:75:PRO:HD2	2.43	0.43
1:D:201:LEU:C	1:D:203:ALA:H	2.26	0.43
1:D:227:ILE:CG2	1:D:230:ARG:CB	2.96	0.43
1:B:111:VAL:HG11	1:B:118:TRP:CH2	2.53	0.43
1:A:268:PRO:HB2	1:A:602:MET:HE1	2.00	0.43
1:D:174:VAL:C	1:D:177:PRO:HD2	2.43	0.43
1:C:74:ARG:N	1:C:75:PRO:HD2	2.33	0.43
1:D:111:VAL:HG22	1:D:111:VAL:O	2.18	0.43
1:D:163:ILE:HG22	1:D:186:VAL:HG13	2.00	0.43
1:A:249:GLN:OE1	1:A:266:ILE:HD11	2.19	0.43
1:A:320:ARG:NH1	1:A:322:GLU:OE1	2.52	0.43
1:A:63:TRP:O	1:A:69:PHE:HE2	2.01	0.43
1:D:529:ASN:ND2	1:D:555:ASP:OD2	2.52	0.43
1:A:364:PHE:CE2	1:A:486:PRO:HD2	2.53	0.42
1:D:122:LEU:HA	1:D:125:LEU:HB2	2.01	0.42
1:A:34:ILE:HD11	1:A:600:LYS:HA	2.02	0.42
1:B:126:VAL:HG11	1:B:128:ILE:HD12	2.02	0.42
1:A:548:ASP:O	1:A:589:ARG:NH1	2.52	0.42
1:D:97:ILE:O	1:D:98:GLU:C	2.63	0.42
1:A:228:TYR:CE2	1:A:232:CYS:SG	3.12	0.42
1:B:78:HIS:HB2	1:B:157:LEU:HD13	2.01	0.42
1:C:333:GLU:OE1	1:C:458:LYS:NZ	2.52	0.42
1:D:122:LEU:CD1	1:D:141:ILE:HG12	2.50	0.42
1:A:182:ARG:O	1:A:183:ARG:C	2.63	0.42
1:A:323:TYR:CZ	1:A:329:ASP:HB3	2.54	0.42
1:A:323:TYR:OH	1:A:458:LYS:HG2	2.20	0.42
1:B:238:ALA:O	1:B:261:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:ASN:ND2	1:D:53:THR:OG1	2.53	0.42
1:D:180:ARG:HA	1:D:180:ARG:HD3	1.83	0.42
1:D:200:TYR:CE2	1:D:227:ILE:HD11	2.55	0.42
1:B:213:LEU:HD23	1:B:253:PHE:CE2	2.55	0.41
1:D:163:ILE:HG22	1:D:186:VAL:CG1	2.49	0.41
1:A:191:THR:HA	1:A:245:THR:O	2.19	0.41
1:D:32:ALA:HB3	1:D:33:PRO:HD3	2.02	0.41
1:D:302:HIS:HE1	1:D:367:GLU:OE2	2.02	0.41
1:A:295:ASP:OD1	1:A:376:ARG:NH2	2.53	0.41
1:D:323:TYR:CZ	1:D:329:ASP:HB3	2.55	0.41
1:A:119:LYS:NZ	1:A:138:ASN:OD1	2.53	0.41
1:B:128:ILE:HG12	1:B:232:CYS:HB3	2.03	0.41
1:D:174:VAL:O	1:D:177:PRO:HG2	2.21	0.41
1:A:187:VAL:HG11	1:A:613:ALA:C	2.46	0.41
1:C:323:TYR:OH	1:C:458:LYS:HG2	2.21	0.41
1:C:400:TYR:CD1	1:C:401:PRO:HA	2.55	0.41
1:D:16:GLU:HG3	1:D:24:ILE:HB	2.03	0.41
1:D:58:VAL:O	1:D:58:VAL:HG12	2.20	0.41
1:D:144:GLY:HA3	1:D:174:VAL:HB	2.02	0.41
1:D:400:TYR:CD1	1:D:401:PRO:HA	2.56	0.41
1:B:188:THR:O	1:B:242:ASP:HB2	2.21	0.41
1:B:369:LEU:HD23	1:B:487:ILE:HD11	2.03	0.41
1:D:349:LYS:O	1:D:471:ARG:HD3	2.21	0.41
1:A:213:LEU:HD23	1:A:253:PHE:CE1	2.56	0.41
1:D:282:PHE:CD1	1:D:591:GLU:OE1	2.73	0.41
1:A:366:VAL:O	1:A:370:LYS:HB2	2.21	0.41
1:B:199:ARG:HH22	2:B:902:G6P:P	2.44	0.41
1:B:17:VAL:HG21	1:B:46:ILE:O	2.21	0.40
1:B:59:ASP:HB2	1:B:96:LEU:HD21	2.03	0.40
1:B:182:ARG:O	1:B:183:ARG:C	2.64	0.40
1:D:97:ILE:CD1	1:D:101:PRO:HD2	2.51	0.40
1:D:502:GLY:O	1:D:525:SER:HA	2.21	0.40
1:D:607:VAL:HA	1:D:610:ARG:NH1	2.36	0.40
1:C:349:LYS:O	1:C:471:ARG:HG3	2.21	0.40
1:A:141:ILE:O	1:A:142:LEU:C	2.64	0.40
1:A:286:HIS:ND1	1:A:497:ARG:O	2.54	0.40
1:D:153:GLU:O	1:D:157:LEU:HG	2.21	0.40
1:C:3:ARG:NH1	1:C:185:ASP:OD2	2.53	0.40

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	636/725 (88%)	607 (95%)	29 (5%)	0	100	100
1	B	635/725 (88%)	612 (96%)	22 (4%)	1 (0%)	43	70
1	C	637/725 (88%)	605 (95%)	29 (5%)	3 (0%)	24	51
1	D	594/725 (82%)	570 (96%)	22 (4%)	2 (0%)	36	62
All	All	2502/2900 (86%)	2394 (96%)	102 (4%)	6 (0%)	43	70

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	54	TYR
1	D	228	TYR
1	D	363	SER
1	B	169	GLU
1	C	407	THR
1	C	77	GLN

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	524/625 (84%)	511 (98%)	13 (2%)	42	72
1	B	524/625 (84%)	510 (97%)	14 (3%)	39	70
1	C	494/625 (79%)	480 (97%)	14 (3%)	38	70
1	D	463/625 (74%)	452 (98%)	11 (2%)	43	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2005/2500 (80%)	1953 (97%)	52 (3%)	40 71

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	34	ILE
1	A	85	SER
1	A	169	GLU
1	A	254	GLU
1	A	304	CYS
1	A	310	ASP
1	A	337	ARG
1	A	376	ARG
1	A	388	SER
1	A	408	GLU
1	A	455	ILE
1	A	458	LYS
1	B	34	ILE
1	B	35	THR
1	B	64	LYS
1	B	204	SER
1	B	224	ARG
1	B	254	GLU
1	B	304	CYS
1	B	310	ASP
1	B	337	ARG
1	B	363	SER
1	B	376	ARG
1	B	408	GLU
1	B	471	ARG
1	B	474	MET
1	C	26	SER
1	C	34	ILE
1	C	35	THR
1	C	105	LEU
1	C	122	LEU
1	C	254	GLU
1	C	291	GLU
1	C	304	CYS
1	C	310	ASP
1	C	337	ARG

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Mol	Chain	Res	Type
1	C	420	SER
1	C	471	ARG
1	C	535	SER
1	C	581	ARG
1	D	69	PHE
1	D	73	MET
1	D	97	ILE
1	D	180	ARG
1	D	291	GLU
1	D	304	CYS
1	D	337	ARG
1	D	433	ARG
1	D	461	GLN
1	D	488	LEU
1	D	517	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	HIS
1	A	50	ASN
1	A	283	GLN
1	A	461	GLN
1	B	6	GLN
1	B	44	HIS
1	B	78	HIS
1	B	396	HIS
1	B	402	HIS
1	B	452	ASN
1	B	582	GLN
1	B	585	ASN
1	C	283	GLN
1	C	284	ASN
1	C	403	ASN
1	D	44	HIS
1	D	50	ASN
1	D	161	HIS
1	D	168	HIS
1	D	211	ASN
1	D	302	HIS
1	D	403	ASN
1	D	588	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

6 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	G6P	A	901	-	16,16,16	0.50	0	23,24,24	0.93	2 (8%)
2	G6P	B	902	-	16,16,16	0.66	0	23,24,24	1.72	8 (34%)
2	G6P	C	901	-	16,16,16	0.56	0	23,24,24	0.95	1 (4%)
2	G6P	A	902	-	16,16,16	0.58	0	23,24,24	1.20	3 (13%)
2	G6P	D	901	-	16,16,16	0.69	0	23,24,24	1.34	2 (8%)
2	G6P	B	901	-	16,16,16	0.54	0	23,24,24	0.83	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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	G6P	A	901	-	-	0/6/26/26	0/1/1/1
2	G6P	B	902	-	-	3/6/26/26	0/1/1/1
2	G6P	C	901	-	-	0/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	G6P	A	902	-	-	5/6/26/26	0/1/1/1
2	G6P	D	901	-	-	4/6/26/26	0/1/1/1
2	G6P	B	901	-	-	2/6/26/26	0/1/1/1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	901	G6P	O2P-P-O6	-4.09	96.00	106.67
2	B	902	G6P	O5-C5-C6	3.48	113.60	106.69
2	B	902	G6P	C4-C3-C2	-3.15	105.30	110.83
2	B	902	G6P	C3-C4-C5	-3.15	104.52	110.23
2	D	901	G6P	O2P-P-O1P	2.79	118.25	107.80
2	A	901	G6P	C1-O5-C5	2.52	118.52	113.65
2	A	902	G6P	O5-C5-C6	2.50	111.66	106.69
2	B	902	G6P	O5-C5-C4	-2.45	105.28	109.70
2	B	902	G6P	O4-C4-C3	2.36	115.94	110.38
2	B	902	G6P	O3-C3-C4	2.31	115.81	110.38
2	B	902	G6P	O1P-P-O6	-2.22	100.88	106.67
2	A	902	G6P	C6-C5-C4	-2.21	107.43	112.07
2	B	902	G6P	O5-C1-C2	2.20	114.16	110.30
2	C	901	G6P	O2P-P-O1P	2.19	116.02	107.80
2	A	901	G6P	O2P-P-O1P	2.09	115.64	107.80
2	A	902	G6P	C4-C3-C2	-2.01	107.31	110.83

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	902	G6P	C4-C5-C6-O6
2	A	902	G6P	O5-C5-C6-O6
2	A	902	G6P	C6-O6-P-O1P
2	A	902	G6P	C6-O6-P-O2P
2	A	902	G6P	C6-O6-P-O3P
2	B	901	G6P	C4-C5-C6-O6
2	B	901	G6P	O5-C5-C6-O6
2	B	902	G6P	C4-C5-C6-O6
2	B	902	G6P	O5-C5-C6-O6
2	D	901	G6P	C6-O6-P-O1P
2	D	901	G6P	C6-O6-P-O2P

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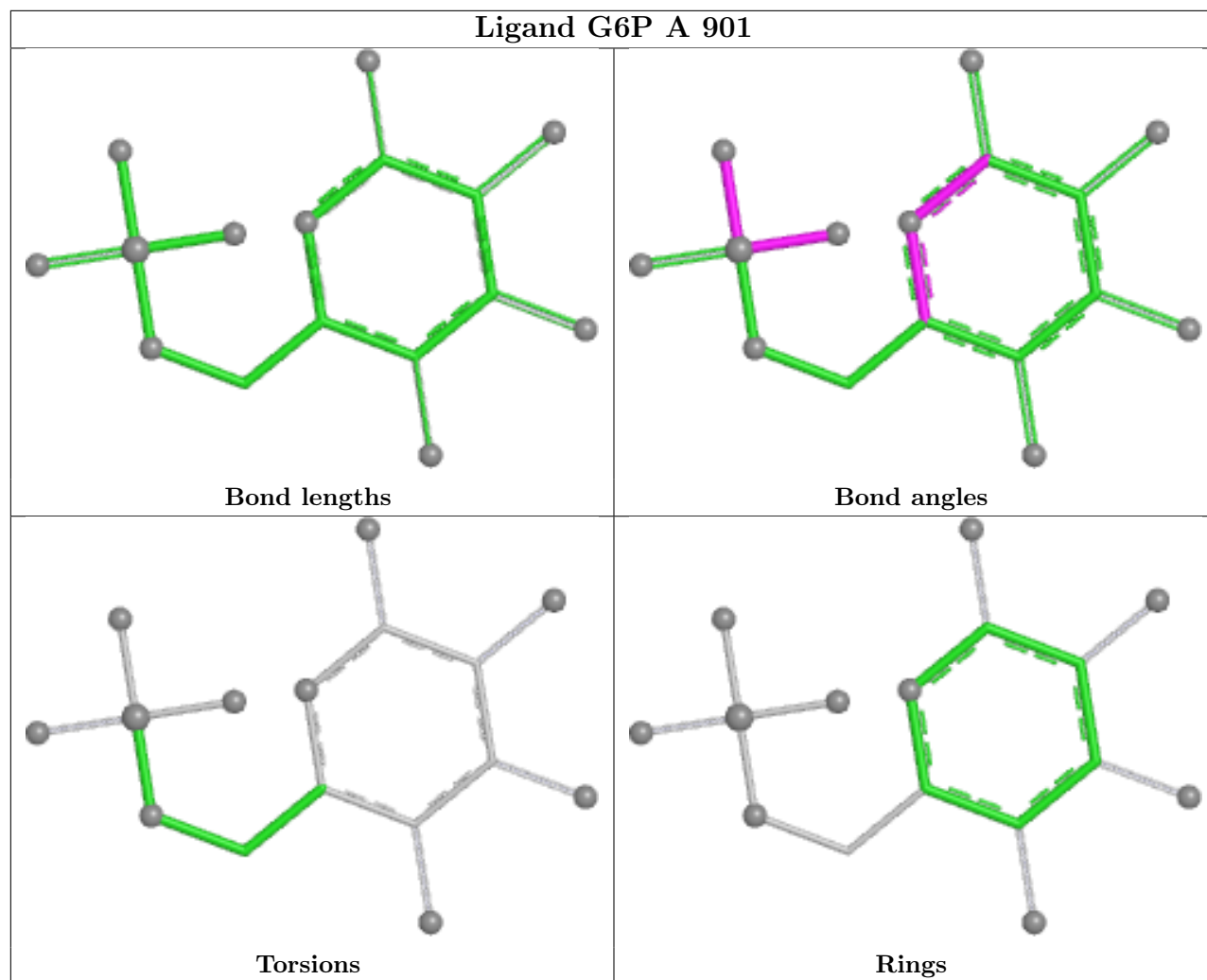
Mol	Chain	Res	Type	Atoms
2	D	901	G6P	C6-O6-P-O3P
2	B	902	G6P	C5-C6-O6-P
2	D	901	G6P	O5-C5-C6-O6

There are no ring outliers.

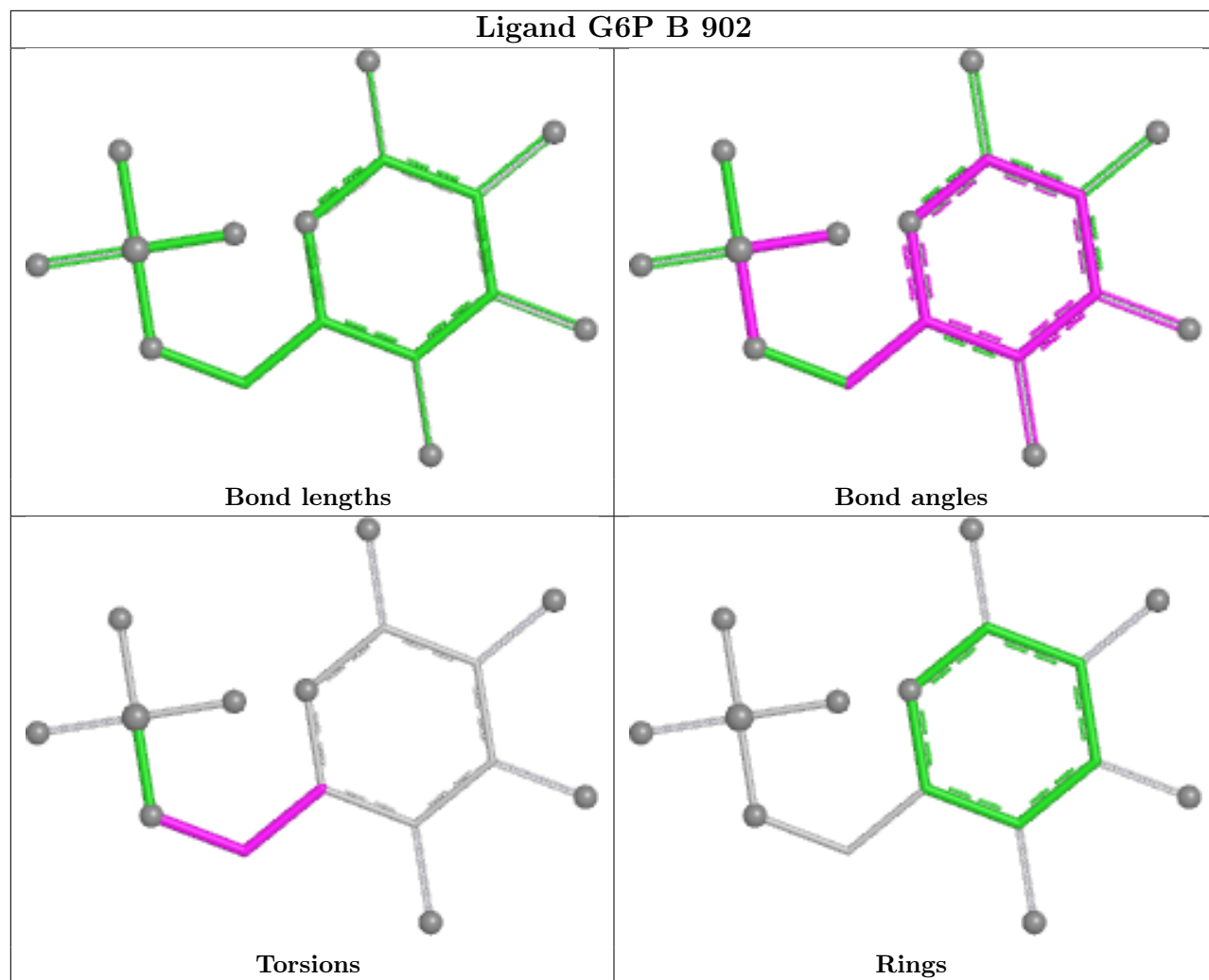
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	902	G6P	2	0
2	A	902	G6P	2	0
2	D	901	G6P	1	0

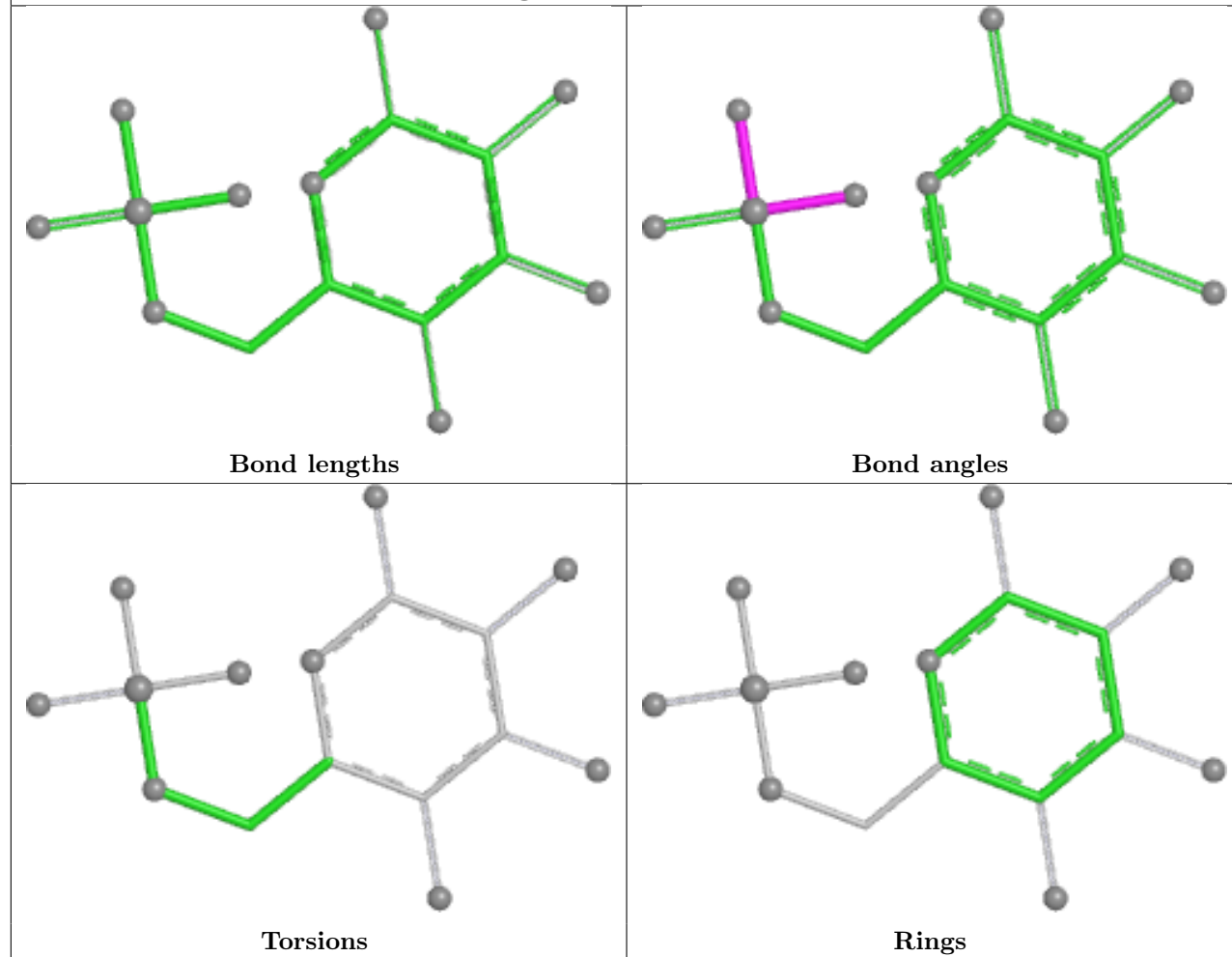
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



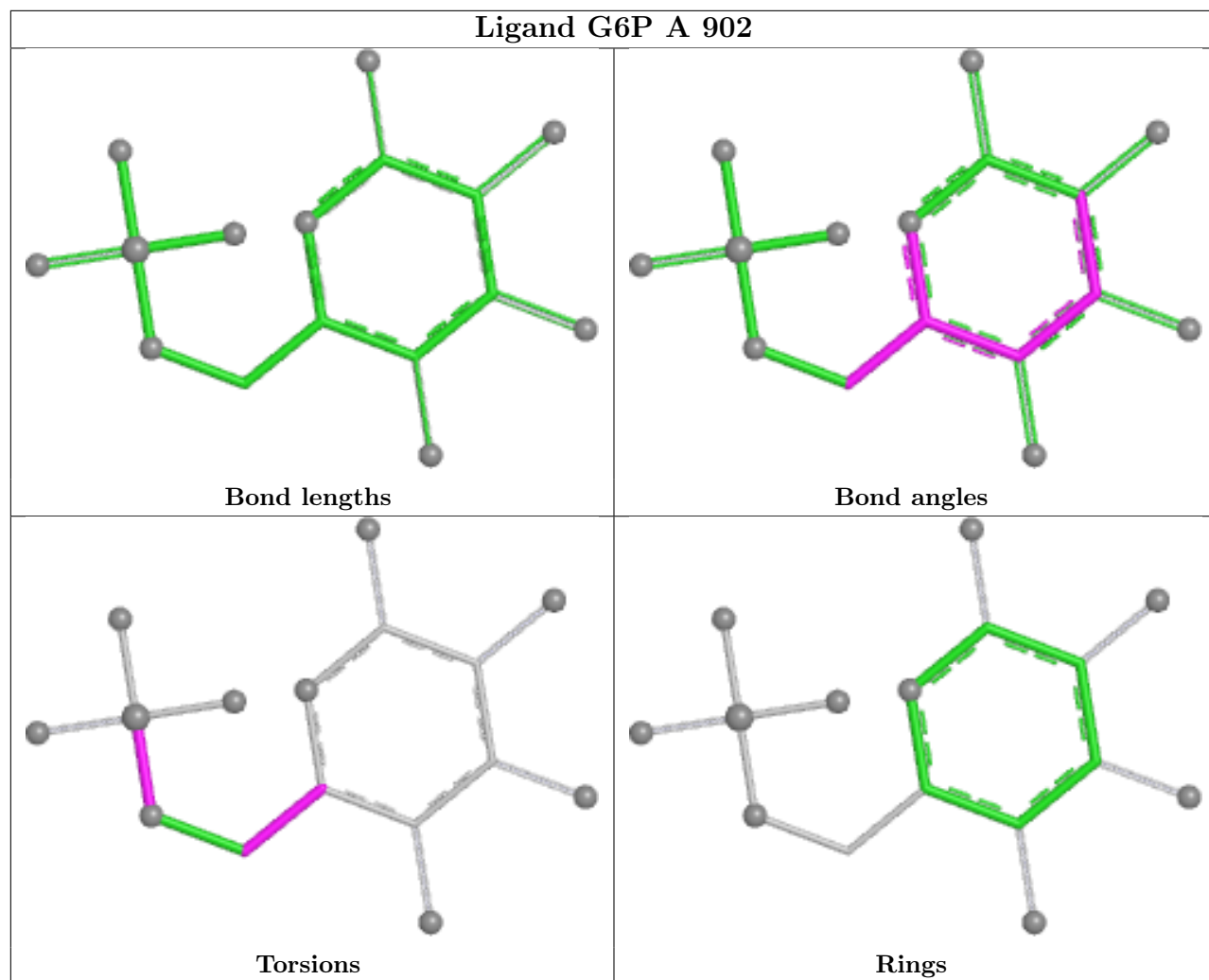
Ligand G6P B 902



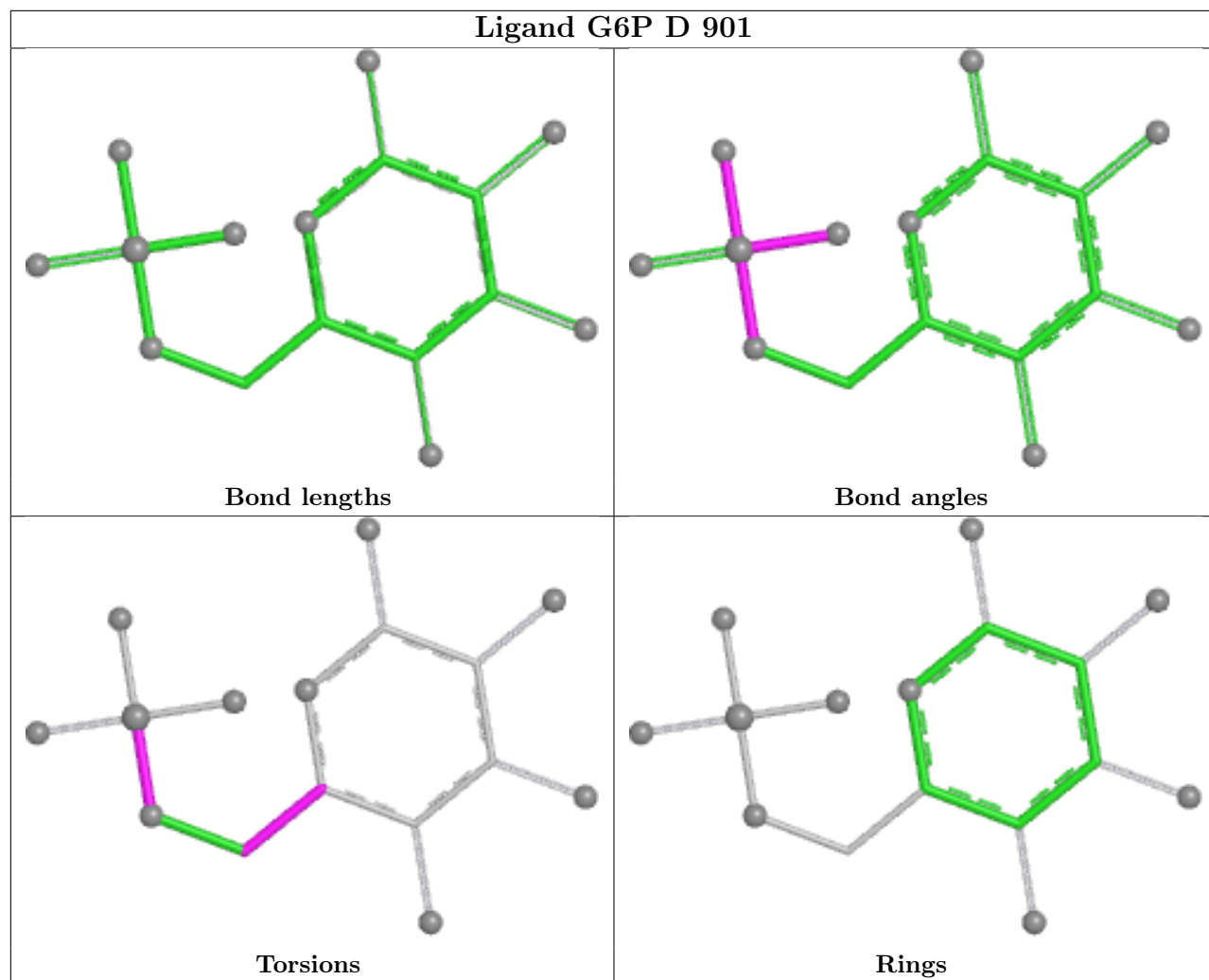
Ligand G6P C 901

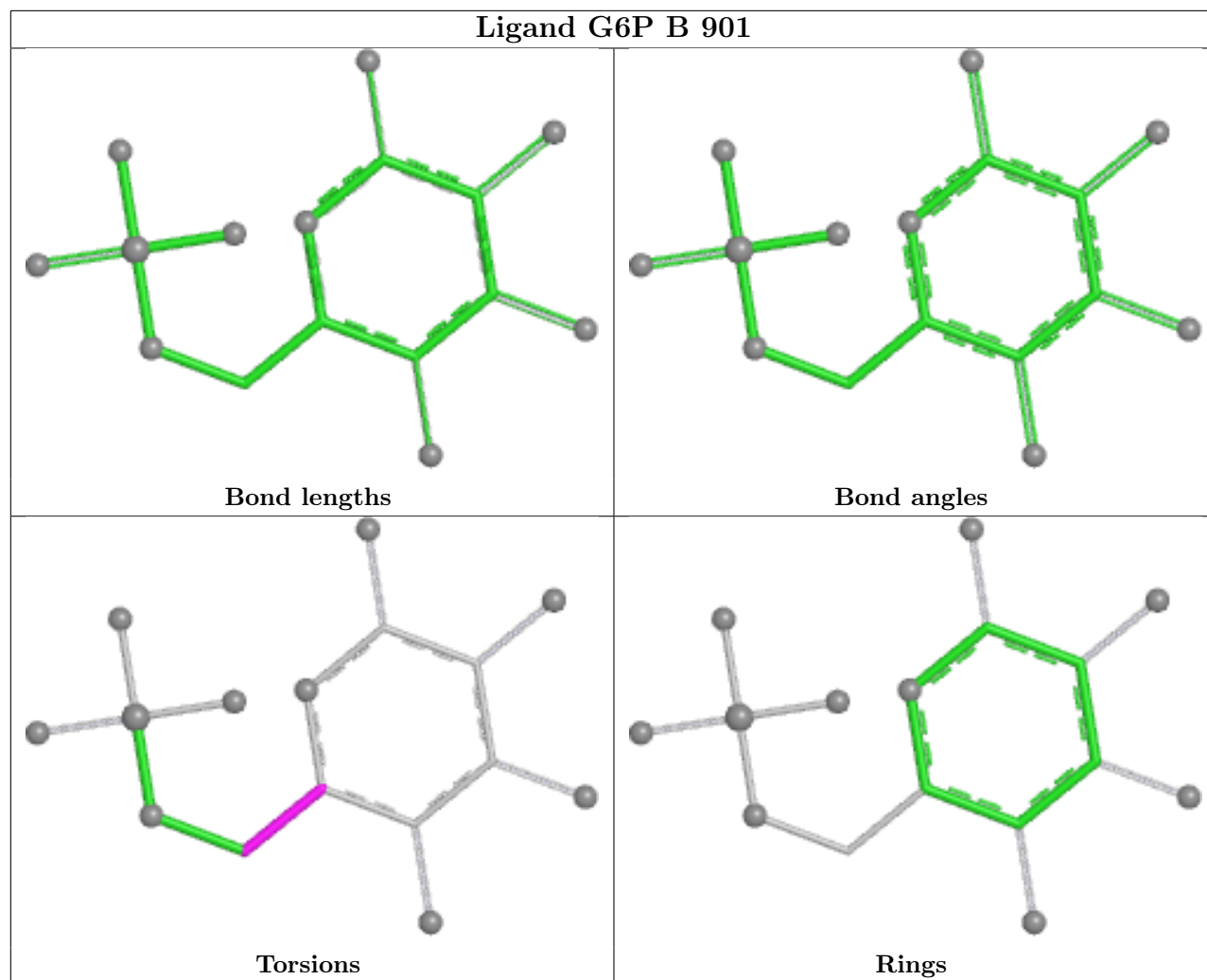


Ligand G6P A 902



Ligand G6P D 901





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	638/725 (88%)	0.21	30 (4%)	36	29	23, 67, 119, 145	4 (0%)
1	B	637/725 (87%)	0.32	24 (3%)	44	36	29, 75, 119, 137	3 (0%)
1	C	639/725 (88%)	0.51	38 (5%)	28	22	33, 81, 135, 160	2 (0%)
1	D	604/725 (83%)	0.53	57 (9%)	14	12	32, 80, 146, 168	1 (0%)
All	All	2518/2900 (86%)	0.39	149 (5%)	28	22	23, 77, 133, 168	10 (0%)

All (149) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	18	ALA	5.7
1	C	372	GLN	5.5
1	B	257	HIS	5.5
1	D	170	TRP	5.0
1	D	620	ASP	4.9
1	D	96	LEU	4.6
1	D	623	ARG	4.5
1	D	80	LEU	4.4
1	A	156	HIS	4.4
1	A	67	GLU	4.4
1	C	63	TRP	4.2
1	D	90	PHE	4.2
1	A	628	GLU	4.1
1	C	114	TYR	4.0
1	D	72	GLU	4.0
1	A	372	GLN	4.0
1	C	274	ILE	4.0
1	C	116	ASN	3.9
1	A	543	THR	3.8
1	D	618	TYR	3.7
1	A	383	HIS	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	630	LEU	3.7
1	D	58	VAL	3.7
1	D	171	LEU	3.6
1	D	205	GLY	3.6
1	C	145	TYR	3.6
1	D	621	GLN	3.5
1	D	108	LEU	3.5
1	C	89	HIS	3.4
1	D	156	HIS	3.4
1	A	625	LEU	3.4
1	B	2	SER	3.4
1	D	130	SER	3.4
1	C	62	ASP	3.4
1	B	485	ASN	3.4
1	C	543	THR	3.4
1	C	207	PHE	3.3
1	D	123	TRP	3.3
1	B	17	VAL	3.3
1	D	383	HIS	3.3
1	B	207	PHE	3.3
1	D	228	TYR	3.2
1	D	272	ASN	3.2
1	B	206	SER	3.2
1	C	542	GLU	3.2
1	C	57	GLU	3.1
1	B	383	HIS	3.1
1	D	184	ILE	3.1
1	B	66	PRO	3.1
1	D	8	HIS	3.1
1	A	90	PHE	3.0
1	D	181	LYS	3.0
1	D	160	GLN	3.0
1	B	67	GLU	2.9
1	B	91	VAL	2.9
1	D	76	VAL	2.9
1	B	62	ASP	2.9
1	C	97	ILE	2.9
1	D	77	GLN	2.9
1	C	383	HIS	2.8
1	C	92	TYR	2.8
1	D	150	PHE	2.7
1	A	291	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	111	VAL	2.7
1	C	54	TYR	2.7
1	C	95	TRP	2.7
1	D	145	TYR	2.7
1	A	624	GLU	2.6
1	D	186	VAL	2.6
1	D	78	HIS	2.6
1	B	65	LYS	2.6
1	A	157	LEU	2.6
1	D	91	VAL	2.6
1	D	126	VAL	2.6
1	D	69	PHE	2.6
1	C	156	HIS	2.6
1	D	54	TYR	2.6
1	A	91	VAL	2.6
1	B	129	PRO	2.5
1	B	92	TYR	2.5
1	C	106	PHE	2.5
1	A	2	SER	2.5
1	D	604	LEU	2.5
1	D	51	LYS	2.5
1	D	157	LEU	2.5
1	B	111	VAL	2.5
1	A	77	GLN	2.5
1	A	626	VAL	2.5
1	C	14	ALA	2.5
1	C	545	GLN	2.5
1	D	84	GLU	2.4
1	C	53	THR	2.4
1	C	117	GLU	2.4
1	D	133	ASN	2.4
1	B	128	ILE	2.4
1	C	131	PRO	2.4
1	C	91	VAL	2.4
1	C	180	ARG	2.4
1	A	80	LEU	2.4
1	A	71	ASP	2.4
1	D	6	GLN	2.4
1	C	99	GLY	2.3
1	D	125	LEU	2.3
1	D	231	TYR	2.3
1	A	183	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	557	ARG	2.3
1	D	18	ALA	2.3
1	D	87	GLY	2.3
1	D	45	LEU	2.2
1	A	611	GLN	2.2
1	B	517	GLU	2.2
1	D	178	LEU	2.2
1	A	82	THR	2.2
1	B	103	VAL	2.2
1	D	265	GLY	2.2
1	D	209	PHE	2.2
1	C	67	GLU	2.2
1	A	63	TRP	2.2
1	C	65	LYS	2.2
1	A	34	ILE	2.2
1	B	173	GLY	2.2
1	A	54	TYR	2.2
1	C	18	ALA	2.2
1	B	156	HIS	2.1
1	D	161	HIS	2.1
1	C	640	GLY	2.1
1	D	122	LEU	2.1
1	D	259	LEU	2.1
1	D	210	TYR	2.1
1	B	76	VAL	2.1
1	C	561	PRO	2.1
1	B	228	TYR	2.1
1	C	487	ILE	2.1
1	D	615	ARG	2.1
1	A	104	ILE	2.1
1	A	155	ALA	2.1
1	D	163	ILE	2.1
1	D	119	LYS	2.1
1	B	56	ASN	2.1
1	C	133	ASN	2.1
1	C	125	LEU	2.1
1	D	197	LEU	2.1
1	C	132	GLU	2.1
1	C	485	ASN	2.0
1	D	188	THR	2.0
1	A	629	GLU	2.0
1	A	125	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	274	ILE	2.0
1	A	64	LYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

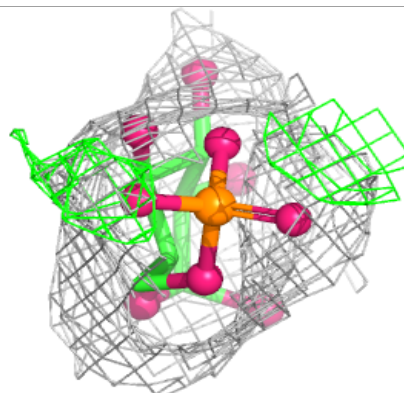
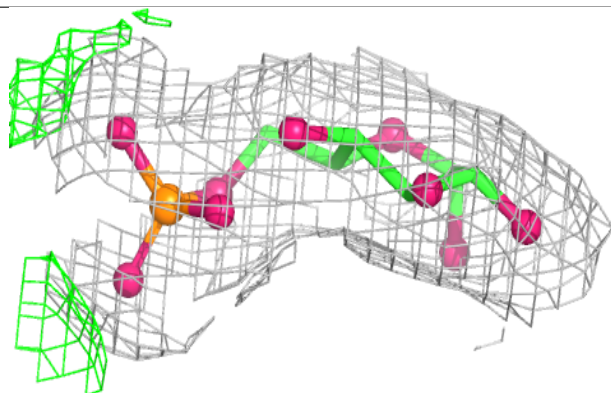
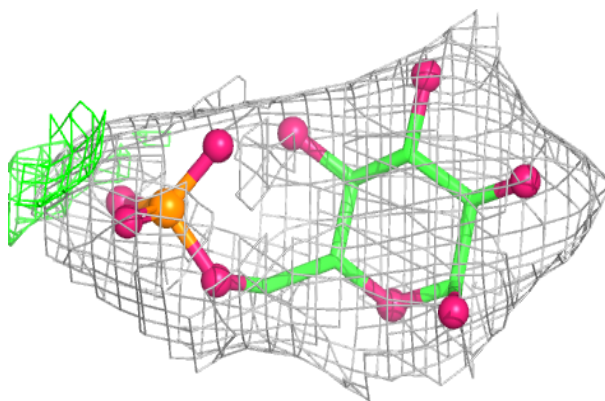
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	G6P	B	902	16/16	0.86	0.11	76,85,94,94	0
2	G6P	A	902	16/16	0.91	0.14	54,63,66,68	16
2	G6P	D	901	16/16	0.96	0.07	41,45,49,51	0
2	G6P	A	901	16/16	0.97	0.07	42,49,54,54	0
2	G6P	C	901	16/16	0.97	0.06	46,61,69,70	0
2	G6P	B	901	16/16	0.97	0.06	50,60,64,66	0

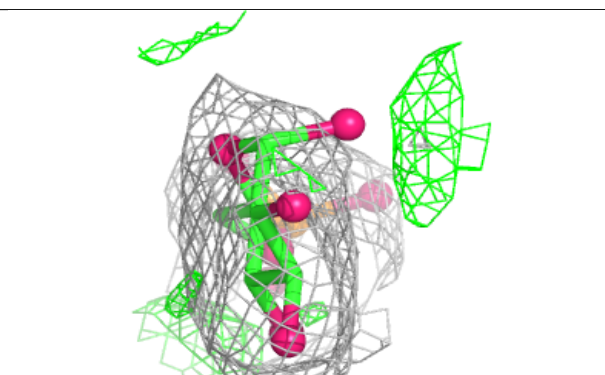
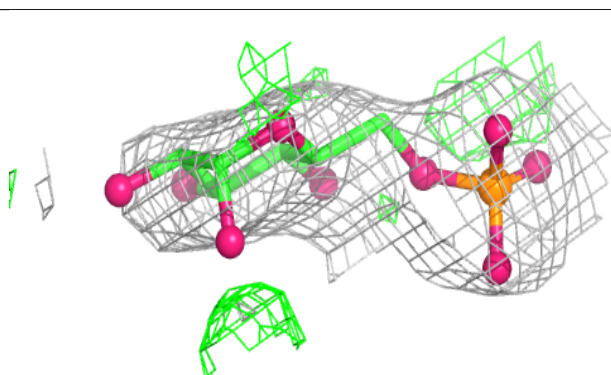
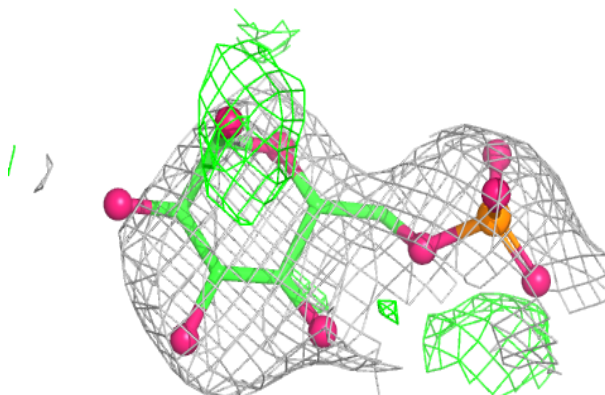
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around G6P B 902:

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

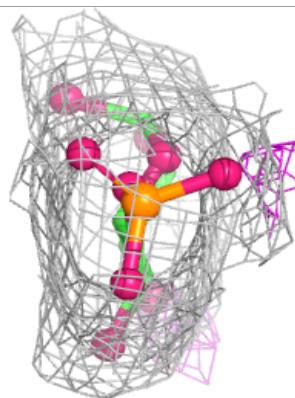
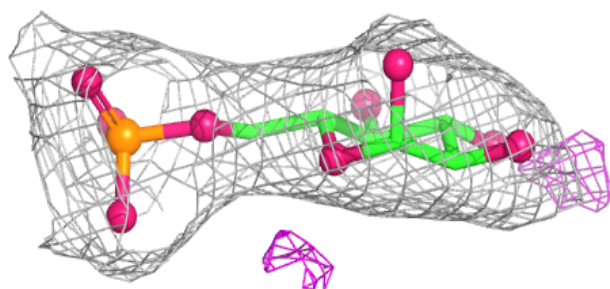
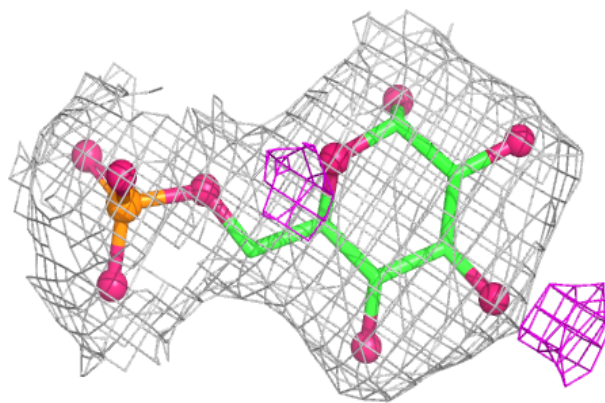
**Electron density around G6P A 902:**

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



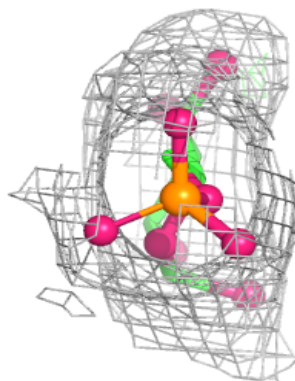
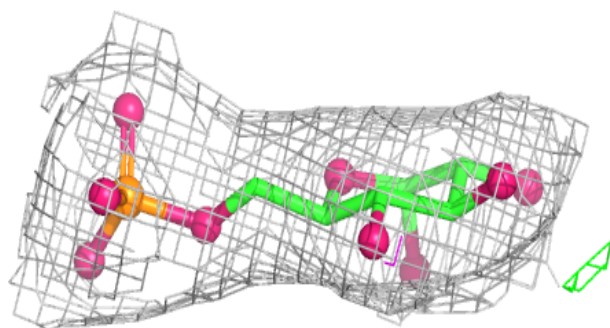
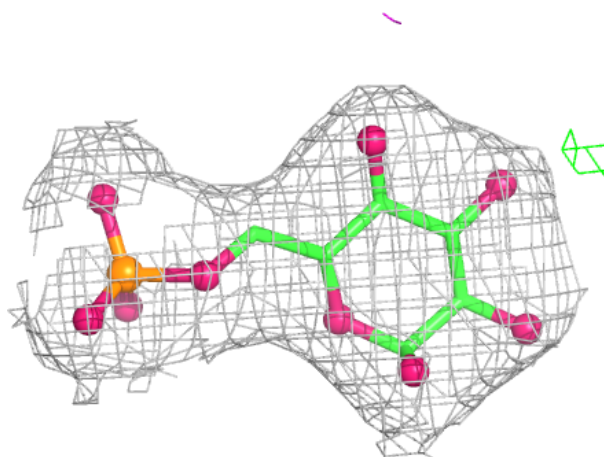
Electron density around G6P D 901:

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



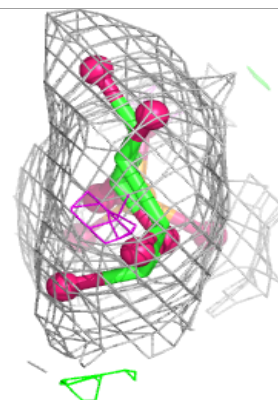
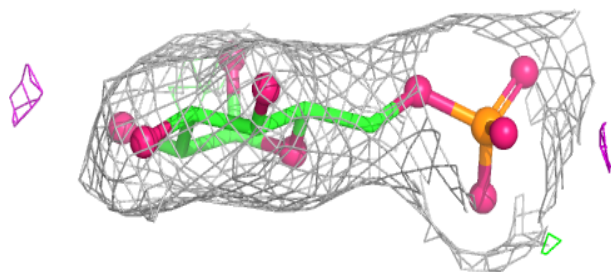
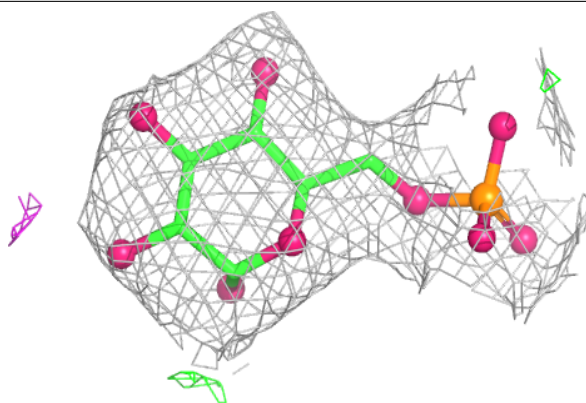
Electron density around G6P A 901:

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

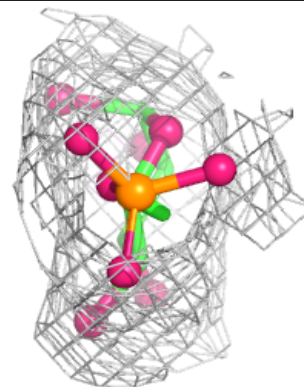
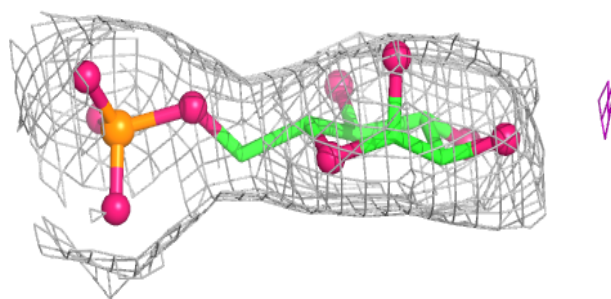
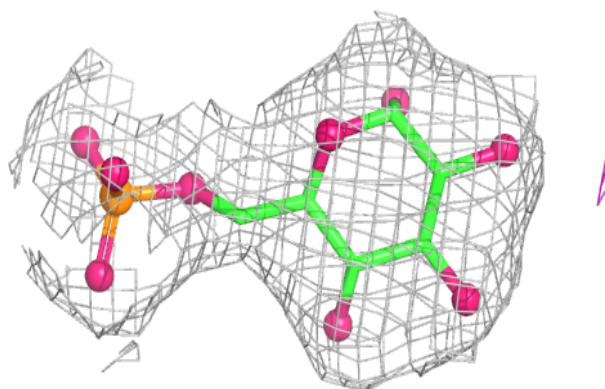


Electron density around G6P C 901:

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

**Electron density around G6P B 901:**

$2mF_o-DF_c$ (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.