



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:03 PM UTC

PDB ID : 3A22 / pdb_00003a22
Title : Crystal Structure of beta-L-Arabinopyranosidase complexed with L-arabinose
Authors : Fujimoto, Z.; Ichinose, H.; Kaneko, S.
Deposited on : 2009-04-27
Resolution : 1.90 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

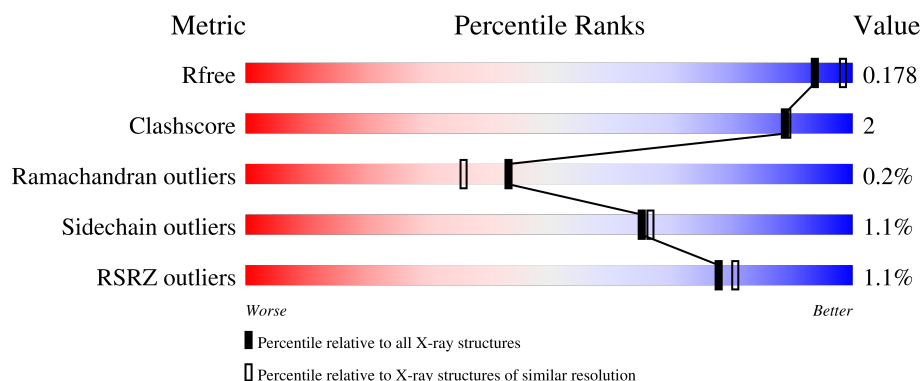
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	614	% 96% .
1	B	614	% 95% .

2 Entry composition [i](#)

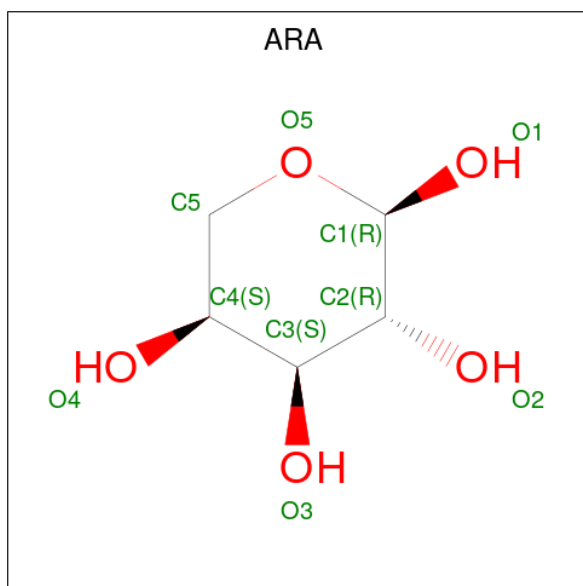
There are 7 unique types of molecules in this entry. The entry contains 10788 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Putative secreted alpha-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	614	Total	C	N	O	S	0	13	0
			4568	2835	785	928	20			
1	B	612	Total	C	N	O	S	0	12	0
			4568	2833	787	928	20			

- Molecule 2 is alpha-L-arabinopyranose (CCD ID: ARA) (formula: C₅H₁₀O₅).



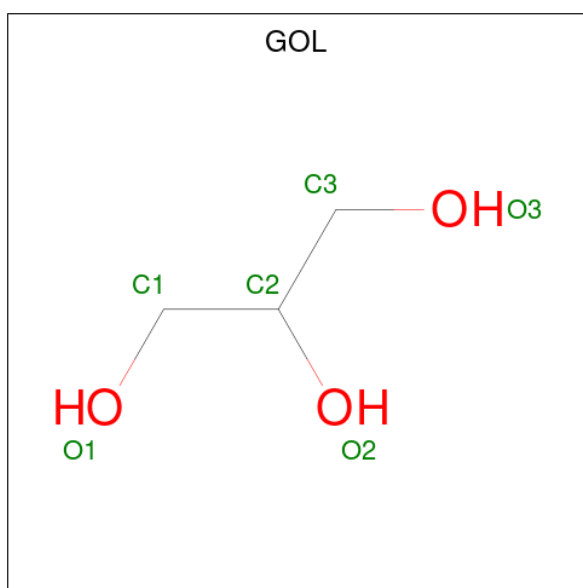
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



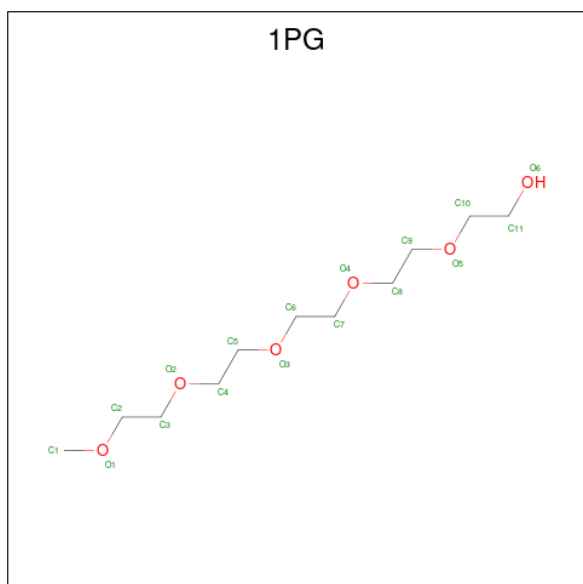
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

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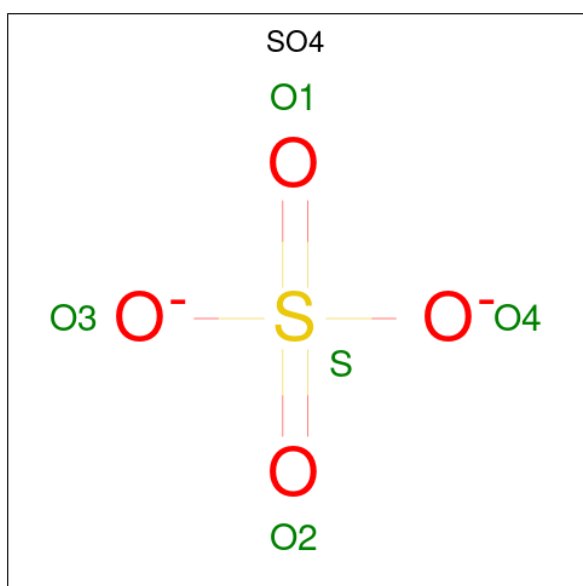
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is 2-(2-{2-[2-(2-METHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHANOL (CCD ID: 1PG) (formula: C₁₁H₂₄O₆).



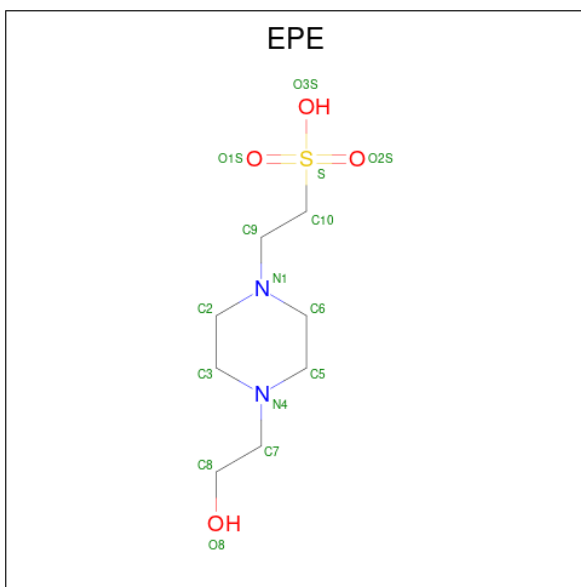
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			16	10	6		
4	A	1	Total	C	O	0	0
			16	10	6		
4	B	1	Total	C	O	0	0
			16	10	6		
4	B	1	Total	C	O	0	0
			16	10	6		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	702	Total	O	0	0
			702	702		
7	B	658	Total	O	0	0
			658	658		

3 Residue-property plots [i](#)

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: Putative secreted alpha-galactosidase



- Molecule 1: Putative secreted alpha-galactosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.34Å 99.28Å 182.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.27 – 1.90 41.27 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.6 (41.27-1.90) 97.6 (41.27-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.162 , 0.207 (Not available) , 0.178	Depositor DCC
R_{free} test set	4799 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	12.2	Xtriage
Anisotropy	0.066	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10788	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% 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: GOL, EPE, ARA, 1PG, SO4

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	0.68	0/4708	0.77	0/6444
1	B	0.66	0/4684	0.77	1/6410 (0.0%)
All	All	0.67	0/9392	0.77	1/12854 (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	B	63	TRP	N-CA-C	5.29	116.85	111.14

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	4568	0	4348	12	0
1	B	4568	0	4347	19	0
2	A	50	0	50	0	0
2	B	40	0	40	0	0
3	A	60	0	80	6	0
3	B	48	0	64	3	0
4	A	32	0	42	0	0
4	B	32	0	42	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	10	0	0	0	0
5	B	5	0	0	0	0
6	B	15	0	17	0	0
7	A	702	0	0	3	1
7	B	658	0	0	4	0
All	All	10788	0	9030	35	1

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 2.

All (35) 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:B:633:ASN:ND2	4:B:966:1PG:H42	1.38	1.39
1:B:633:ASN:ND2	4:B:966:1PG:C4	2.23	1.01
1:B:633:ASN:HD21	4:B:966:1PG:H42	0.91	0.91
7:A:723:HOH:O	4:B:966:1PG:H92	1.78	0.84
1:A:271:THR:OG1	3:A:914:GOL:H31	1.82	0.79
1:B:633:ASN:HD21	4:B:966:1PG:C4	1.84	0.79
4:B:966:1PG:H72	7:B:1007:HOH:O	1.92	0.69
3:A:926:GOL:H31	7:A:1038:HOH:O	2.04	0.58
1:B:139:ILE:HG13	1:B:140:TYR:H	1.68	0.58
1:B:133:LYS:HE3	7:B:1129:HOH:O	2.05	0.57
1:A:494:ALA:H	3:A:930:GOL:H12	1.73	0.53
1:A:403:ARG:NH1	7:A:776:HOH:O	2.37	0.52
1:B:256:SER:HA	3:B:934:GOL:H11	1.91	0.52
3:A:926:GOL:H11	1:B:591:LEU:HD22	1.91	0.51
1:B:321:SER:N	3:B:916:GOL:H32	2.26	0.50
1:A:539[A]:GLN:HE22	1:A:634:ALA:HB1	1.76	0.50
1:A:139:ILE:HG13	1:A:140:TYR:H	1.78	0.49
1:B:400:LEU:HD12	1:B:424[B]:MET:HE3	1.97	0.47
1:B:220:THR:HG23	1:B:240:PRO:HG2	1.97	0.47
1:B:335:VAL:HG11	1:B:424[B]:MET:HE1	1.97	0.47
1:B:442[A]:SER:O	1:B:443[A]:THR:C	2.58	0.47
1:A:231:PRO:HA	1:A:234:TRP:CE2	2.51	0.45
1:B:260:LEU:C	1:B:260:LEU:HD23	2.42	0.45
1:B:321:SER:H	3:B:916:GOL:H32	1.82	0.44
1:B:474:THR:O	1:B:513:LEU:HA	2.17	0.44
4:B:966:1PG:H52	7:B:1005:HOH:O	2.17	0.43
1:A:152:TYR:CD2	3:A:919:GOL:H32	2.54	0.42
1:A:350:ASP:HB2	3:A:915:GOL:H12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:463:TYR:CE2	1:B:487:PHE:HB3	2.54	0.42
1:B:379:HIS:HB3	7:B:1029:HOH:O	2.18	0.42
1:A:87:LEU:N	1:A:88:PRO:CD	2.83	0.41
1:A:139:ILE:HD12	1:A:139:ILE:HA	1.95	0.41
1:B:120:PRO:HG2	4:B:963:1PG:H52	2.02	0.41
1:A:542:ARG:HD2	1:A:636:THR:O	2.21	0.41
1:A:463:TYR:CE2	1:A:487:PHE:HB3	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1024:HOH:O	7:A:1319:HOH:O[1_655]	2.09	0.11

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	625/614 (102%)	608 (97%)	16 (3%)	1 (0%)	43	36
1	B	622/614 (101%)	607 (98%)	14 (2%)	1 (0%)	43	36
All	All	1247/1228 (102%)	1215 (97%)	30 (2%)	2 (0%)	43	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	ASP
1	B	282	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	479/468 (102%)	475 (99%)	4 (1%)	73	75
1	B	475/468 (102%)	469 (99%)	6 (1%)	61	61
All	All	954/936 (102%)	944 (99%)	10 (1%)	65	70

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	ASN
1	A	226	TRP
1	A	267	THR
1	A	385	TRP
1	B	225	ASN
1	B	226	TRP
1	B	267	THR
1	B	291	PHE
1	B	385	TRP
1	B	633	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	366	ASN
1	A	392	ASN
1	A	607	GLN
1	A	624	ASN
1	B	366	ASN
1	B	405	ASN
1	B	548	ASN
1	B	633	ASN

5.3.3 RNA [i](#)

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 ⓘ

35 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	$\# Z > 2$
3	GOL	A	925	-	5,5,5	0.46	0	5,5,5	0.51	0
3	GOL	A	926	-	5,5,5	0.38	0	5,5,5	0.36	0
2	ARA	B	781	-	10,10,10	0.61	0	14,14,14	0.76	1 (7%)
2	ARA	A	731	-	10,10,10	0.62	0	14,14,14	0.51	0
3	GOL	A	914	-	5,5,5	0.41	0	5,5,5	0.75	0
3	GOL	B	916	-	5,5,5	0.47	0	5,5,5	0.32	0
3	GOL	B	934	-	5,5,5	0.38	0	5,5,5	0.53	0
4	1PG	B	963	-	15,15,16	0.47	0	14,14,15	0.24	0
5	SO4	B	972	-	4,4,4	0.22	0	6,6,6	0.26	0
3	GOL	A	917	-	5,5,5	0.38	0	5,5,5	0.41	0
3	GOL	B	922	-	5,5,5	0.31	0	5,5,5	0.92	0
4	1PG	B	966	-	15,15,16	0.47	0	14,14,15	0.35	0
5	SO4	A	971	-	4,4,4	0.34	0	6,6,6	0.17	0
3	GOL	B	920	-	5,5,5	0.38	0	5,5,5	0.46	0
3	GOL	A	927	-	5,5,5	0.36	0	5,5,5	0.12	0
2	ARA	B	771	-	10,10,10	0.65	0	14,14,14	0.45	0
3	GOL	B	918	-	5,5,5	0.47	0	5,5,5	0.59	0
3	GOL	B	932	-	5,5,5	0.29	0	5,5,5	0.77	0
3	GOL	A	912	-	5,5,5	0.32	0	5,5,5	0.62	0
2	ARA	B	761	-	10,10,10	0.38	0	14,14,14	0.83	0
2	ARA	A	741	-	10,10,10	0.83	0	14,14,14	1.27	1 (7%)
6	EPE	B	951	-	15,15,15	0.80	1 (6%)	19,20,20	1.83	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	A	911	-	5,5,5	0.38	0	5,5,5	0.51	0
4	1PG	A	962	-	15,15,16	0.50	0	14,14,15	0.42	0
3	GOL	B	928	-	5,5,5	0.33	0	5,5,5	0.77	0
3	GOL	A	915	-	5,5,5	0.43	0	5,5,5	0.31	0
3	GOL	A	930	-	5,5,5	0.35	0	5,5,5	0.18	0
4	1PG	A	964	-	15,15,16	0.48	0	14,14,15	0.26	0
2	ARA	A	701	-	10,10,10	0.67	0	14,14,14	0.83	1 (7%)
3	GOL	B	913	-	5,5,5	0.41	0	5,5,5	0.29	0
2	ARA	A	711	-	10,10,10	0.69	0	14,14,14	0.66	0
5	SO4	A	973	-	4,4,4	0.24	0	6,6,6	0.28	0
2	ARA	A	721	-	10,10,10	0.46	0	14,14,14	0.38	0
3	GOL	A	919	-	5,5,5	0.35	0	5,5,5	0.72	0
2	ARA	B	751	-	10,10,10	0.51	0	14,14,14	0.85	1 (7%)

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
3	GOL	A	925	-	-	2/4/4/4	-
3	GOL	A	926	-	-	2/4/4/4	-
2	ARA	B	781	-	-	-	0/1/1/1
3	GOL	B	934	-	-	2/4/4/4	-
3	GOL	A	914	-	-	2/4/4/4	-
3	GOL	B	916	-	-	2/4/4/4	-
4	1PG	B	963	-	-	5/13/13/14	-
2	ARA	A	731	-	-	-	0/1/1/1
3	GOL	A	917	-	-	1/4/4/4	-
3	GOL	B	922	-	-	4/4/4/4	-
4	1PG	B	966	-	-	5/13/13/14	-
3	GOL	B	920	-	-	0/4/4/4	-
3	GOL	B	918	-	-	2/4/4/4	-
3	GOL	A	927	-	-	2/4/4/4	-
2	ARA	B	771	-	-	-	0/1/1/1
2	ARA	B	751	-	-	-	0/1/1/1
3	GOL	A	912	-	-	0/4/4/4	-
2	ARA	B	761	-	-	-	0/1/1/1
2	ARA	A	741	-	-	-	0/1/1/1
6	EPE	B	951	-	-	1/9/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	911	-	-	2/4/4/4	-
4	1PG	A	962	-	-	6/13/13/14	-
3	GOL	B	928	-	-	2/4/4/4	-
3	GOL	A	915	-	-	0/4/4/4	-
3	GOL	A	930	-	-	0/4/4/4	-
4	1PG	A	964	-	-	2/13/13/14	-
3	GOL	B	913	-	-	0/4/4/4	-
2	ARA	A	701	-	-	-	0/1/1/1
2	ARA	A	711	-	-	-	0/1/1/1
2	ARA	A	721	-	-	-	0/1/1/1
3	GOL	A	919	-	-	2/4/4/4	-
3	GOL	B	932	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	951	EPE	C10-S	2.54	1.81	1.77

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	951	EPE	C5-N4-C3	4.75	119.07	108.84
6	B	951	EPE	C7-N4-C3	3.90	121.63	111.24
2	A	741	ARA	C5-C4-C3	3.45	114.67	109.64
6	B	951	EPE	O1S-S-C10	2.75	110.88	106.73
2	B	751	ARA	C4-C3-C2	-2.27	106.86	110.86
2	B	781	ARA	C5-O5-C1	2.10	116.82	112.46
6	B	951	EPE	C9-N1-C6	-2.02	105.86	111.24
2	A	701	ARA	C4-C3-C2	-2.02	107.31	110.86

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	914	GOL	O1-C1-C2-O2
3	A	914	GOL	O1-C1-C2-C3
3	A	919	GOL	C1-C2-C3-O3
3	A	927	GOL	O1-C1-C2-C3
3	B	922	GOL	O1-C1-C2-C3
3	B	922	GOL	C1-C2-C3-O3

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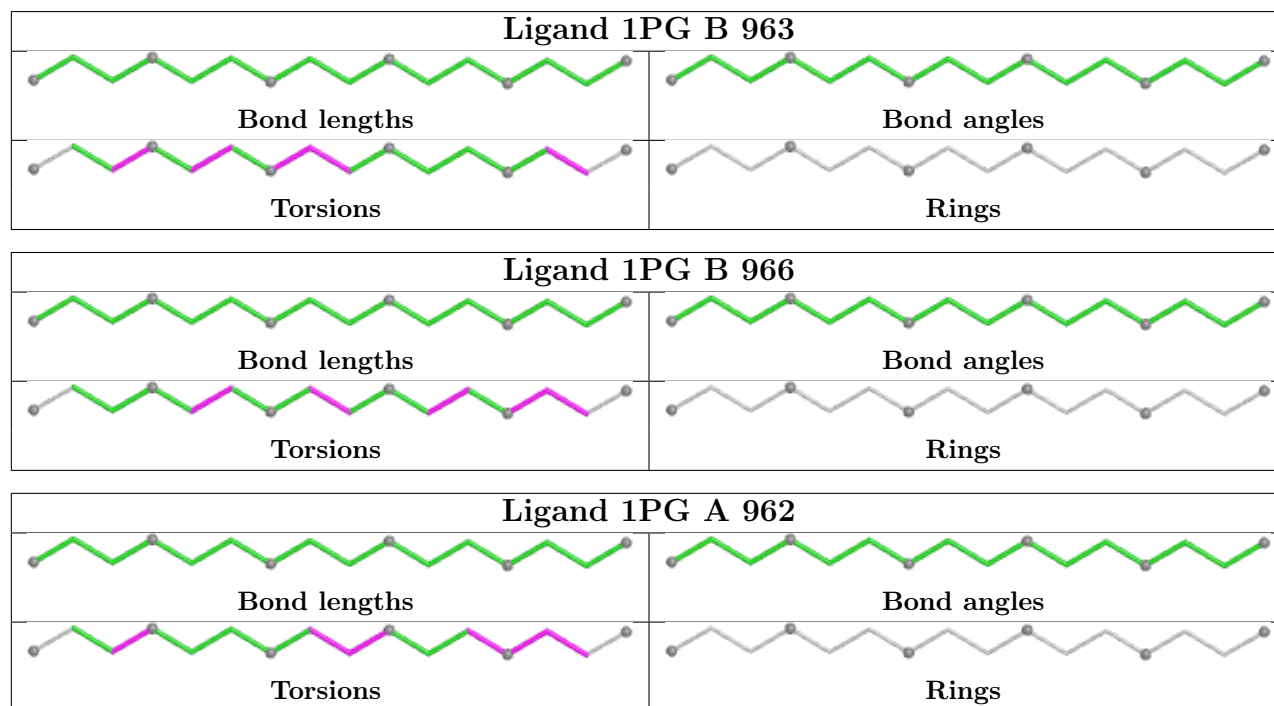
Mol	Chain	Res	Type	Atoms
3	B	928	GOL	O1-C1-C2-C3
3	B	932	GOL	O1-C1-C2-C3
6	B	951	EPE	C8-C7-N4-C3
4	B	966	1PG	O1-C2-C3-O2
4	A	962	1PG	O1-C2-C3-O2
4	B	963	1PG	O1-C2-C3-O2
3	A	911	GOL	C1-C2-C3-O3
3	A	925	GOL	C1-C2-C3-O3
3	A	926	GOL	C1-C2-C3-O3
3	B	916	GOL	C1-C2-C3-O3
3	B	934	GOL	C1-C2-C3-O3
3	A	911	GOL	O2-C2-C3-O3
3	A	919	GOL	O2-C2-C3-O3
3	A	927	GOL	O1-C1-C2-O2
3	B	916	GOL	O2-C2-C3-O3
3	B	922	GOL	O2-C2-C3-O3
3	B	928	GOL	O1-C1-C2-O2
4	B	966	1PG	O4-C8-C9-O5
4	B	966	1PG	O2-C4-C5-O3
4	A	964	1PG	O5-C10-C11-O6
4	A	962	1PG	O3-C6-C7-O4
3	A	925	GOL	O2-C2-C3-O3
3	B	922	GOL	O1-C1-C2-O2
3	B	932	GOL	O1-C1-C2-O2
4	B	963	1PG	O4-C8-C9-O5
3	A	917	GOL	O2-C2-C3-O3
3	B	918	GOL	O2-C2-C3-O3
3	B	934	GOL	O2-C2-C3-O3
4	B	963	1PG	C6-C7-O4-C8
4	B	966	1PG	C2-C3-O2-C4
4	A	964	1PG	C4-C5-O3-C6
4	B	963	1PG	C11-C10-O5-C9
3	B	918	GOL	O1-C1-C2-O2
4	A	962	1PG	C5-C4-O2-C3
3	A	926	GOL	O2-C2-C3-O3
4	A	962	1PG	C11-C10-O5-C9
4	A	962	1PG	C7-C6-O3-C5
4	B	963	1PG	O3-C6-C7-O4
4	A	962	1PG	C2-C3-O2-C4
4	B	966	1PG	O3-C6-C7-O4

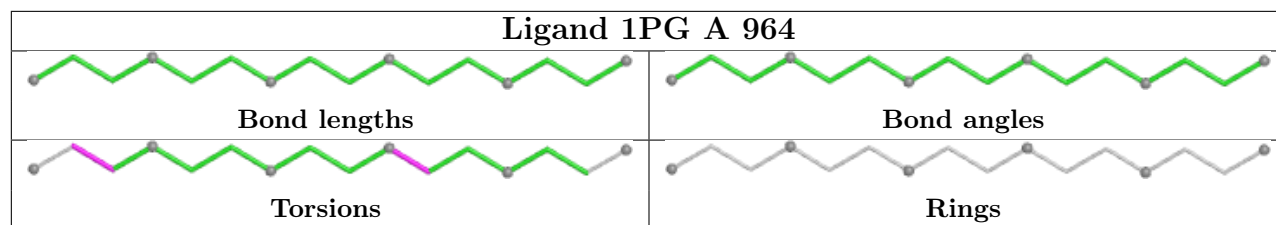
There are no ring outliers.

9 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	926	GOL	2	0
3	A	914	GOL	1	0
3	B	916	GOL	2	0
3	B	934	GOL	1	0
4	B	963	1PG	1	0
4	B	966	1PG	7	0
3	A	915	GOL	1	0
3	A	930	GOL	1	0
3	A	919	GOL	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.





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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	614/614 (100%)	-0.55	4 (0%) 84 86	6, 10, 16, 34	13 (2%)
1	B	612/614 (99%)	-0.46	9 (1%) 72 75	6, 11, 19, 31	12 (1%)
All	All	1226/1228 (99%)	-0.50	13 (1%) 78 80	6, 10, 18, 34	25 (2%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	649[A]	THR	4.9
1	B	443[A]	THR	4.0
1	A	46	VAL	3.8
1	B	441[A]	THR	3.7
1	A	45	ALA	3.6
1	B	47	THR	3.5
1	B	657	VAL	3.1
1	A	649[A]	THR	3.1
1	B	439[A]	ALA	3.0
1	B	492	ALA	2.6
1	B	440[A]	ALA	2.6
1	A	251	TYR	2.1
1	B	442[A]	SER	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

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.

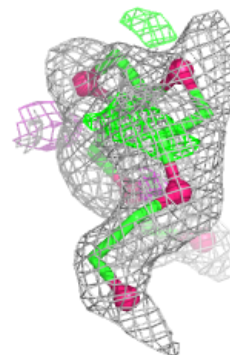
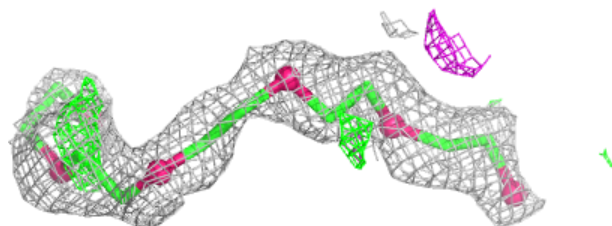
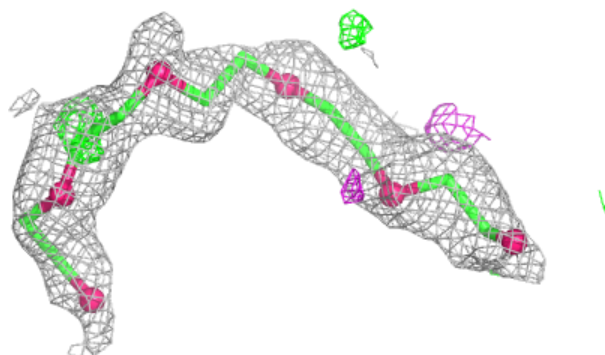
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ARA	A	741	10/10	0.78	0.16	42,44,45,45	0
3	GOL	A	930	6/6	0.80	0.16	38,39,40,42	0
4	1PG	B	966	16/17	0.80	0.15	31,33,38,40	0
4	1PG	A	964	16/17	0.81	0.15	38,43,52,53	0
4	1PG	A	962	16/17	0.83	0.16	34,37,42,42	0
3	GOL	A	919	6/6	0.83	0.13	29,30,30,32	0
3	GOL	B	922	6/6	0.83	0.15	22,28,30,33	0
3	GOL	B	934	6/6	0.84	0.13	27,29,31,34	0
5	SO4	A	973	5/5	0.84	0.13	50,50,51,51	0
4	1PG	B	963	16/17	0.85	0.14	43,44,50,51	0
3	GOL	B	932	6/6	0.85	0.14	21,27,28,31	0
3	GOL	A	927	6/6	0.85	0.13	24,32,33,36	0
5	SO4	B	972	5/5	0.87	0.10	48,48,49,49	0
3	GOL	A	914	6/6	0.88	0.16	15,22,24,27	0
3	GOL	A	926	6/6	0.88	0.16	34,35,35,36	0
3	GOL	B	918	6/6	0.88	0.12	24,28,29,30	0
3	GOL	B	920	6/6	0.90	0.11	20,25,26,27	0
3	GOL	B	928	6/6	0.90	0.11	28,30,31,31	0
3	GOL	A	911	6/6	0.92	0.08	20,22,24,24	0
3	GOL	A	915	6/6	0.92	0.13	21,25,25,25	0
3	GOL	A	925	6/6	0.93	0.11	18,26,28,31	0
3	GOL	A	917	6/6	0.93	0.09	26,27,27,28	0
3	GOL	B	916	6/6	0.93	0.10	12,19,20,22	0
2	ARA	B	761	10/10	0.94	0.06	8,10,13,18	0
2	ARA	B	781	10/10	0.94	0.06	15,18,20,22	0
5	SO4	A	971	5/5	0.94	0.10	23,24,26,27	0
3	GOL	B	913	6/6	0.94	0.09	20,23,24,24	0
2	ARA	A	731	10/10	0.94	0.07	11,15,17,23	0
3	GOL	A	912	6/6	0.95	0.07	21,22,23,23	0
2	ARA	A	711	10/10	0.95	0.06	8,10,14,20	0
2	ARA	B	771	10/10	0.96	0.06	13,14,15,16	0
6	EPE	B	951	15/15	0.96	0.07	18,19,23,26	0
2	ARA	B	751	10/10	0.97	0.05	6,9,11,11	0
2	ARA	A	721	10/10	0.97	0.05	10,10,12,13	0
2	ARA	A	701	10/10	0.98	0.04	8,11,11,12	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.

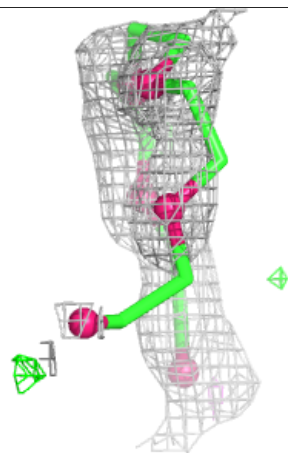
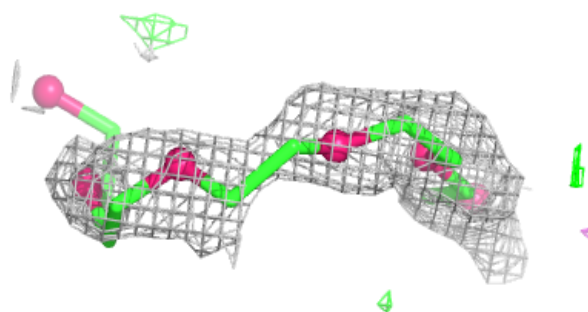
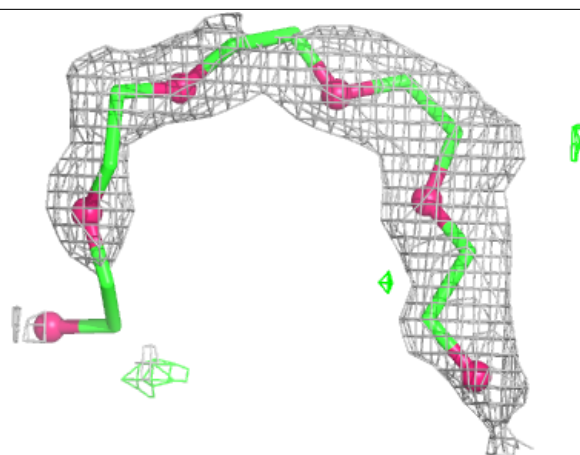
Electron density around 1PG B 966:

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



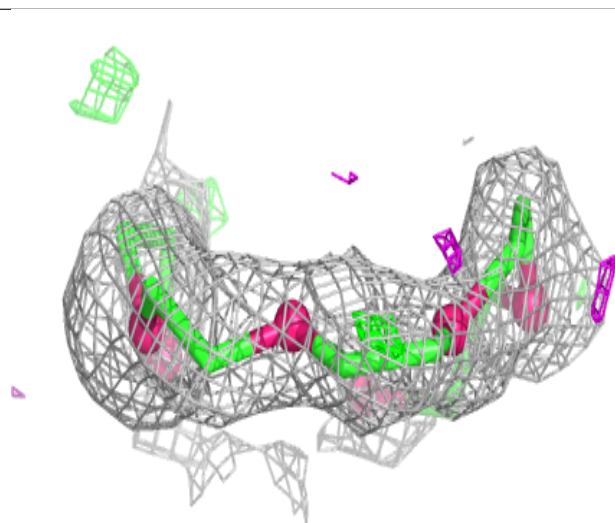
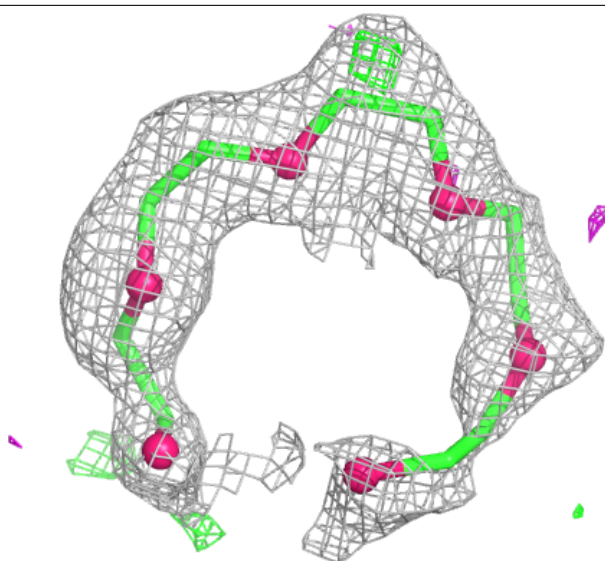
Electron density around 1PG A 964:

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



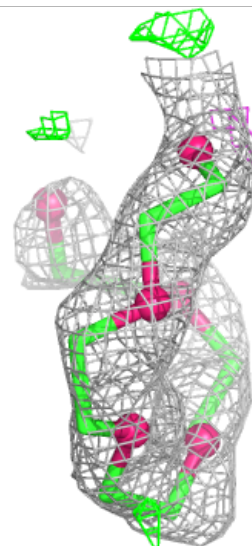
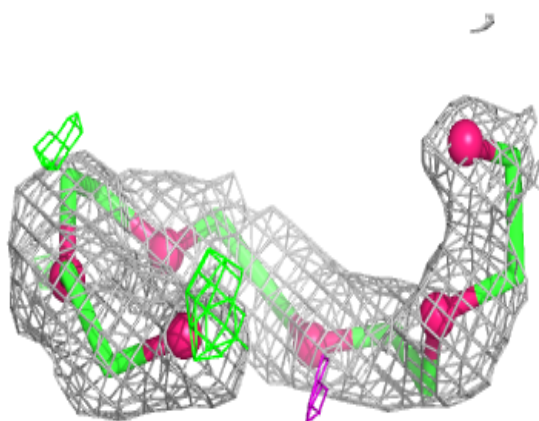
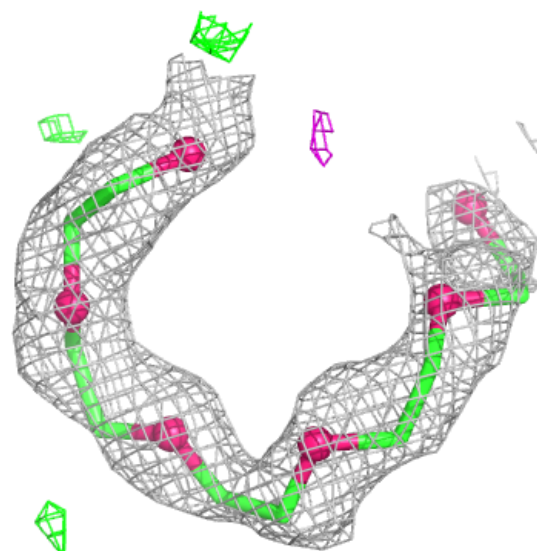
Electron density around 1PG A 962:

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



Electron density around 1PG B 963:

$2mF_o-DF_c$ (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.