



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 26, 2026 – 12:19 AM UTC

PDB ID : 3MOH / pdb_00003moh
Title : The structure of rat cytosolic PEPCK mutant A467G in complex with phosphoglycolate and GDP
Authors : Johnson, T.A.; Holyoak, T.
Deposited on : 2010-04-22
Resolution : 2.10 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

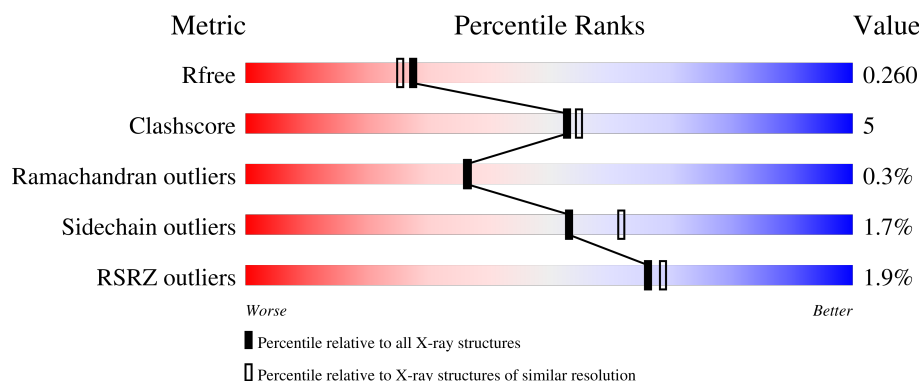
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

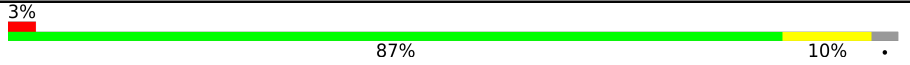
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	624	
1	B	624	

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10430 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.

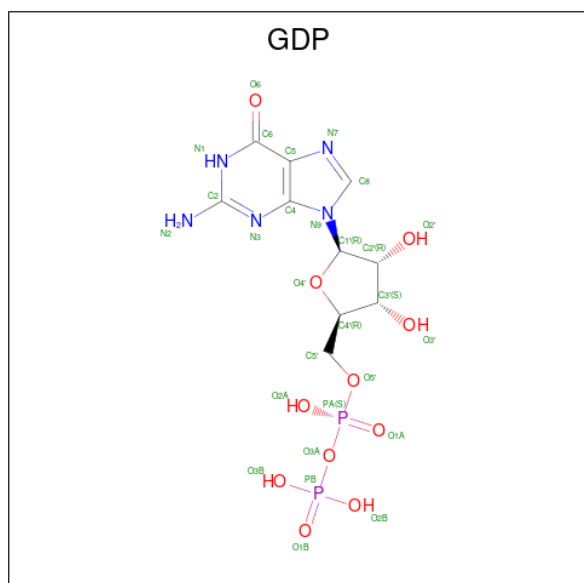
- Molecule 1 is a protein called Phosphoenolpyruvate carboxykinase, cytosolic [GTP].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	604	Total	C	N	O	S	0	10	0
			4811	3079	820	881	31			
1	B	613	Total	C	N	O	S	0	6	0
			4852	3104	828	887	33			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P07379
A	0	SER	-	expression tag	UNP P07379
A	467	GLY	ALA	engineered mutation	UNP P07379
B	-1	GLY	-	expression tag	UNP P07379
B	0	SER	-	expression tag	UNP P07379
B	467	GLY	ALA	engineered mutation	UNP P07379

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).

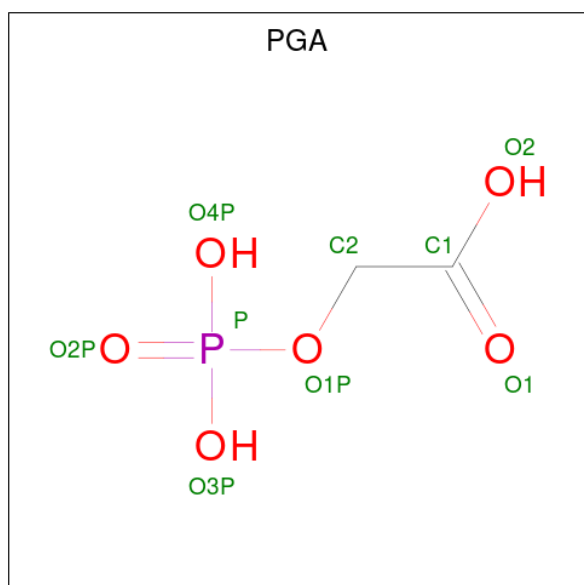


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
2	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mn	0	0
			2	2		
3	B	2	Total	Mn	0	0
			2	2		

- Molecule 4 is 2-PHOSPHOGLYCOLIC ACID (CCD ID: PGA) (formula: C₂H₅O₆P).



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

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		

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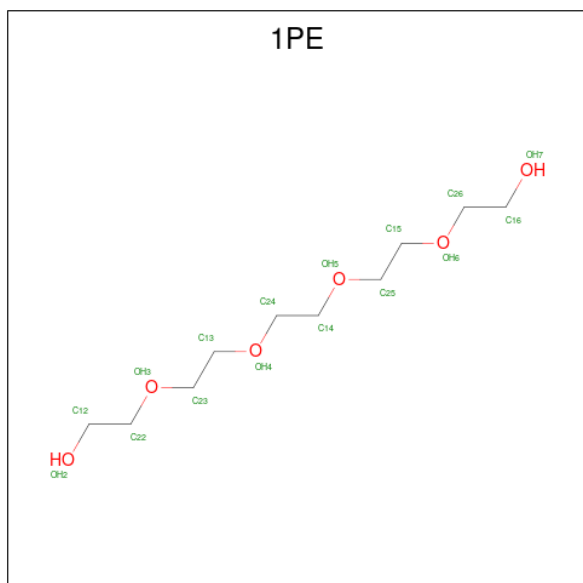
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			5	3	2		
7	B	1	Total	C	O	0	0
			10	6	4		

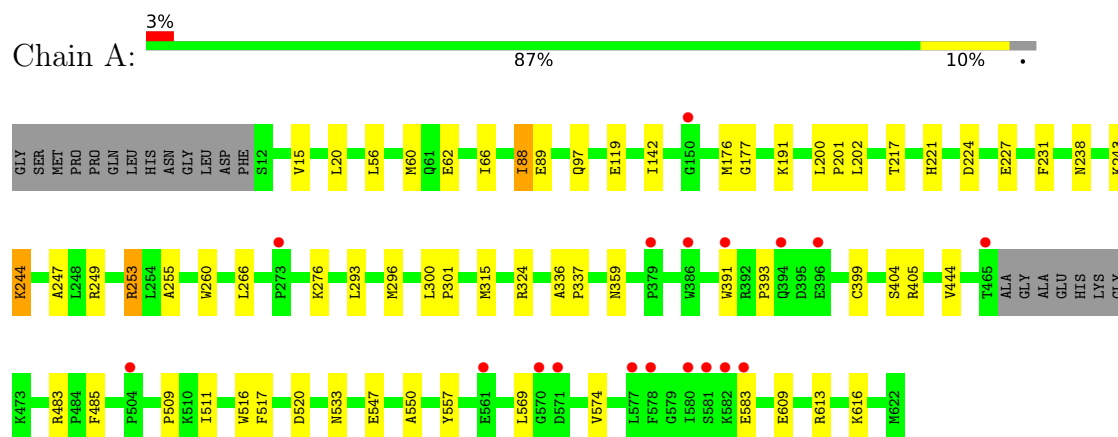
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	370	Total	O	0	0
			370	370		
8	B	298	Total	O	0	0
			298	298		

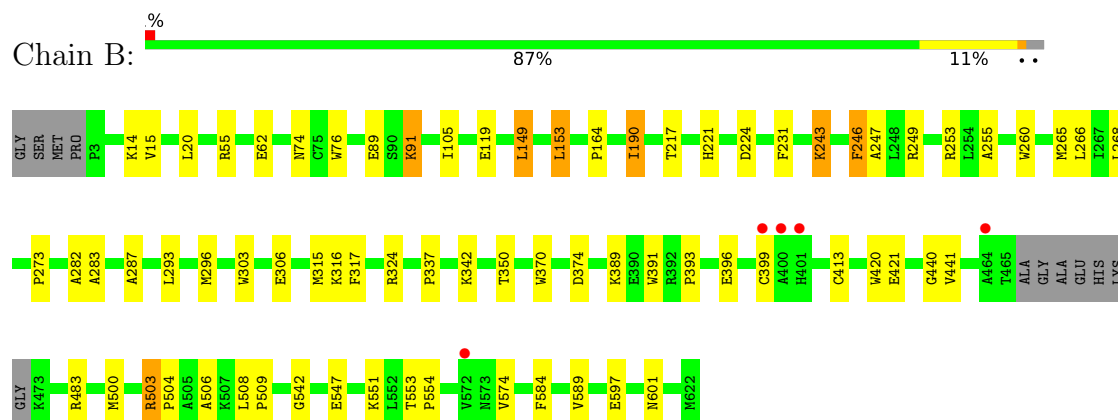
3 Residue-property plots

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: Phosphoenolpyruvate carboxykinase, cytosolic [GTP]



- Molecule 1: Phosphoenolpyruvate carboxykinase, cytosolic [GTP]



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.08Å 119.52Å 87.02Å 90.00° 107.15° 90.00°	Depositor
Resolution (Å)	35.93 – 2.10 35.93 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.8 (35.93-2.10) 97.2 (35.93-2.10)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.190 , 0.247 0.205 , 0.260	Depositor DCC
R_{free} test set	3483 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 32.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10430	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.98 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1384e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GDP, 1PE, EDO, MN, NA, PGA

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	0.83	1/4965 (0.0%)	0.94	1/6717 (0.0%)
1	B	0.80	0/4997	0.96	3/6765 (0.0%)
All	All	0.82	1/9962 (0.0%)	0.95	4/13482 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	444	VAL	CA-CB	5.66	1.61	1.55

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	177	GLY	N-CA-C	5.98	119.02	110.46
1	B	503	ARG	CA-C-N	5.81	125.67	119.28
1	B	503	ARG	C-N-CA	5.81	125.67	119.28
1	B	441	VAL	N-CA-C	5.28	113.09	107.76

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	4811	0	4787	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4852	0	4812	48	0
2	A	28	0	12	0	0
2	B	28	0	12	3	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	9	0	2	1	0
4	B	9	0	2	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	4	0	6	0	0
7	A	5	0	5	2	0
7	B	10	0	13	2	0
8	A	370	0	0	5	0
8	B	298	0	0	8	0
All	All	10430	0	9651	97	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 5.

All (97) 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:119[B]:GLU:HG3	8:A:916:HOH:O	1.86	0.74
2:B:1000:GDP:O1B	8:B:746:HOH:O	2.11	0.69
1:B:293:LEU:HD12	1:B:296:MET:HE3	1.76	0.67
1:B:89:GLU:OE2	1:B:483:ARG:NH1	2.28	0.66
1:B:224:ASP:OD2	8:B:626:HOH:O	2.14	0.65
1:A:296:MET:HE2	1:A:533:ASN:HB2	1.79	0.64
1:B:190:ILE:HG21	1:B:246:PHE:CE2	2.36	0.60
1:B:287:ALA:HA	2:B:1000:GDP:H5'	1.83	0.60
1:B:317:PHE:HE2	1:B:500[B]:MET:HE3	1.67	0.60
1:A:509:PRO:O	7:A:1300:1PE:H122	2.02	0.60
1:A:511:ILE:H	7:A:1300:1PE:C23	2.14	0.59
1:A:62[B]:GLU:HA	1:A:62[B]:GLU:OE1	2.03	0.58
1:B:91:LYS:HD3	1:B:217:THR:O	2.03	0.58
1:A:217:THR:HA	1:A:231:PHE:O	2.04	0.58
1:B:14:LYS:NZ	7:B:1300:1PE:H122	2.20	0.57
1:A:315:MET:HA	1:A:324:ARG:O	2.05	0.57
1:A:296:MET:CE	1:A:533:ASN:HB2	2.35	0.56
1:B:62[B]:GLU:HG2	8:B:796:HOH:O	2.05	0.56
1:A:89:GLU:OE1	1:A:483:ARG:NH2	2.28	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:PHE:CE2	1:B:500[B]:MET:HE3	2.39	0.56
1:B:224:ASP:OD1	1:B:253:ARG:NH2	2.39	0.56
1:B:14:LYS:HZ1	7:B:1300:1PE:H122	1.70	0.56
1:A:243:LYS:HG2	1:A:244:LYS:HD2	1.89	0.55
1:B:55:ARG:NH2	8:B:665:HOH:O	2.39	0.55
1:A:97[B]:GLN:OE1	1:A:119[B]:GLU:OE1	2.25	0.55
1:A:224:ASP:OD1	1:A:253:ARG:NH2	2.40	0.54
1:A:293:LEU:HD12	1:A:296:MET:HE3	1.89	0.54
1:B:420:TRP:CE2	1:B:421:GLU:HG3	2.42	0.54
1:A:62[B]:GLU:HG2	8:A:664:HOH:O	2.08	0.54
1:B:293:LEU:CD1	1:B:296:MET:HE3	2.39	0.53
1:A:244:LYS:HE2	1:A:485:PHE:CZ	2.44	0.53
1:A:255:ALA:HB1	1:A:260:TRP:O	2.10	0.52
1:B:503:ARG:HG2	1:B:506:ALA:HB2	1.91	0.52
1:A:244:LYS:HE2	1:A:485:PHE:CE1	2.44	0.52
1:B:217:THR:HA	1:B:231:PHE:O	2.10	0.51
1:A:266:LEU:C	1:A:266:LEU:HD12	2.35	0.51
1:A:609:GLU:OE1	1:A:613:ARG:HD2	2.10	0.51
1:B:243:LYS:O	1:B:247:ALA:HB3	2.11	0.51
1:B:153:LEU:HD11	1:B:316:LYS:HD3	1.93	0.51
1:B:391:TRP:CD2	1:B:399:CYS:HB3	2.46	0.51
1:A:391:TRP:CD2	1:A:399:CYS:HB3	2.47	0.50
1:B:89:GLU:CD	1:B:483:ARG:HH12	2.19	0.50
1:B:164:PRO:HD2	8:B:705:HOH:O	2.12	0.49
1:A:391:TRP:CE2	1:A:399:CYS:HB3	2.47	0.49
1:B:105:ILE:O	1:B:601[B]:ASN:ND2	2.46	0.47
1:A:200:LEU:HA	1:A:201:PRO:C	2.38	0.47
1:A:276:LYS:HE3	8:B:658:HOH:O	2.14	0.47
1:B:15:VAL:HG21	1:B:20:LEU:HG	1.97	0.47
2:B:1000:GDP:PB	8:B:746:HOH:O	2.73	0.47
1:B:350:THR:OG1	1:B:413:CYS:HA	2.15	0.47
1:A:202:LEU:HD22	8:A:682:HOH:O	2.15	0.47
1:A:293:LEU:CD1	1:A:296:MET:HE3	2.45	0.46
1:A:88:ILE:H	1:A:238:ASN:HD21	1.63	0.46
1:B:553:THR:HB	1:B:554:PRO:HD2	1.98	0.46
1:A:15:VAL:HG21	1:A:20:LEU:HG	1.98	0.46
1:B:265:MET:HA	1:B:282:ALA:O	2.16	0.45
1:A:244:LYS:HG3	1:A:485:PHE:CE1	2.51	0.45
1:B:342:LYS:HE2	1:B:374:ASP:OD2	2.16	0.45
1:B:246:PHE:C	1:B:246:PHE:CD1	2.95	0.45
1:B:391:TRP:CE2	1:B:399:CYS:HB3	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:LEU:HA	1:B:509:PRO:HD2	1.88	0.44
1:A:336:ALA:HB3	1:A:337:PRO:HD3	1.98	0.44
1:A:547[A]:GLU:OE1	8:A:890:HOH:O	2.21	0.44
1:B:266:LEU:C	1:B:266:LEU:HD12	2.43	0.44
1:A:255:ALA:HB1	1:A:260:TRP:C	2.43	0.44
1:B:273:PRO:HD3	1:B:303:TRP:CE2	2.52	0.44
1:A:191:LYS:HB2	1:A:227:GLU:HG2	2.00	0.44
1:B:74:ASN:ND2	1:B:76:TRP:HE1	2.16	0.44
4:B:900:PGA:P	8:B:845:HOH:O	2.76	0.44
1:A:516:TRP:HB2	1:A:517:PHE:CE2	2.53	0.43
1:A:520:ASP:OD1	1:A:520:ASP:C	2.59	0.43
1:B:389:LYS:HA	1:B:389:LYS:HD3	1.84	0.43
1:B:255:ALA:HB1	1:B:260:TRP:C	2.44	0.43
1:B:260:TRP:HB3	1:B:316:LYS:HD2	1.99	0.43
1:B:268:LEU:HD12	1:B:268:LEU:C	2.44	0.43
1:B:260:TRP:HB2	1:B:315:MET:O	2.19	0.43
1:A:89:GLU:OE2	1:A:483:ARG:NH1	2.40	0.42
1:A:221:HIS:CE1	1:A:249:ARG:HD2	2.55	0.42
1:B:503:ARG:HA	1:B:504:PRO:HD3	1.78	0.42
1:A:89:GLU:HB2	8:A:862:HOH:O	2.18	0.42
1:A:300:LEU:HA	1:A:301:PRO:HD3	1.95	0.42
1:A:616:LYS:HB2	1:A:616:LYS:HE3	1.79	0.42
1:A:550:ALA:HB1	1:A:557:TYR:HB3	2.02	0.42
1:B:315:MET:HA	1:B:324:ARG:O	2.20	0.42
1:B:221:HIS:CE1	1:B:249:ARG:HE	2.37	0.42
1:B:597:GLU:O	1:B:601[B]:ASN:HB3	2.20	0.41
1:A:56:LEU:HD12	1:A:56:LEU:HA	1.89	0.41
1:A:359:ASN:O	1:A:404:SER:HB3	2.21	0.41
1:B:265:MET:HG2	1:B:283:ALA:HB2	2.03	0.41
1:A:405:ARG:NH1	4:A:900:PGA:O2P	2.40	0.41
1:B:542:GLY:O	1:B:547:GLU:HB2	2.21	0.41
1:B:246:PHE:C	1:B:246:PHE:HD1	2.29	0.41
1:A:142:ILE:HG23	1:A:176:MET:CG	2.51	0.40
1:B:440:GLY:HA3	1:B:584:PHE:CZ	2.57	0.40
1:B:337:PRO:HA	1:B:370:TRP:CD1	2.56	0.40
1:A:60:MET:HB3	1:A:66:ILE:HG12	2.02	0.40
1:A:243:LYS:O	1:A:247:ALA:HB3	2.22	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	610/624 (98%)	590 (97%)	19 (3%)	1 (0%)	43	44
1	B	615/624 (99%)	587 (95%)	25 (4%)	3 (0%)	24	22
All	All	1225/1248 (98%)	1177 (96%)	44 (4%)	4 (0%)	36	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	149	LEU
1	B	243	LYS
1	B	393	PRO
1	A	393	PRO

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	516/520 (99%)	510 (99%)	6 (1%)	63	72
1	B	520/520 (100%)	509 (98%)	11 (2%)	47	54
All	All	1036/1040 (100%)	1019 (98%)	17 (2%)	53	64

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	ILE
1	A	244	LYS

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Mol	Chain	Res	Type
1	A	253	ARG
1	A	569	LEU
1	A	574	VAL
1	A	583	GLU
1	B	91	LYS
1	B	119	GLU
1	B	149	LEU
1	B	153	LEU
1	B	190	ILE
1	B	246	PHE
1	B	306	GLU
1	B	396	GLU
1	B	551	LYS
1	B	574	VAL
1	B	589	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	25	GLN
1	A	238	ASN
1	A	346	ASN
1	A	352	GLN
1	B	25	GLN
1	B	59	HIS
1	B	74	ASN
1	B	322	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

Of 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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
7	1PE	A	1300	-	4,4,15	0.65	0	3,3,14	0.66	0
6	EDO	A	1200	-	3,3,3	0.90	0	2,2,2	0.43	0
2	GDP	B	1000	3	29,30,30	1.43	3 (10%)	45,47,47	2.00	13 (28%)
4	PGA	B	900	3	8,8,8	0.85	0	10,11,11	1.05	0
4	PGA	A	900	3	8,8,8	1.05	1 (12%)	10,11,11	1.22	1 (10%)
7	1PE	B	1300	-	9,9,15	0.69	0	8,8,14	0.59	0
2	GDP	A	1000	3	29,30,30	1.08	2 (6%)	45,47,47	1.85	9 (20%)

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
7	1PE	A	1300	-	-	1/2/2/13	-
6	EDO	A	1200	-	-	0/1/1/1	-
2	GDP	B	1000	3	-	0/16/32/32	0/3/3/3
4	PGA	B	900	3	-	0/6/6/6	-
4	PGA	A	900	3	-	0/6/6/6	-
7	1PE	B	1300	-	-	4/7/7/13	-
2	GDP	A	1000	3	-	0/16/32/32	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1000	GDP	PA-O3A	4.30	1.64	1.59
2	B	1000	GDP	C5-C4	3.78	1.49	1.38
2	A	1000	GDP	C5-C4	2.68	1.46	1.38
4	A	900	PGA	O1P-C2	-2.20	1.41	1.43
2	B	1000	GDP	O6-C6	2.15	1.27	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	GDP	C6-N1	-2.07	1.35	1.38

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1000	GDP	C5-C4-N3	-6.00	118.84	128.39
2	A	1000	GDP	C5-C4-N3	-5.78	119.18	128.39
2	B	1000	GDP	N9-C4-N3	5.60	137.14	125.95
2	A	1000	GDP	C2-N3-C4	5.04	120.97	112.30
2	B	1000	GDP	C2-N3-C4	4.35	119.80	112.30
2	A	1000	GDP	N9-C4-N3	4.11	134.18	125.95
2	B	1000	GDP	O6-C6-C5	-3.54	117.18	126.53
2	B	1000	GDP	O4'-C1'-C2'	-3.52	99.08	106.62
2	A	1000	GDP	O6-C6-C5	-3.15	118.21	126.53
2	A	1000	GDP	O2A-PA-O3A	3.00	115.38	107.27
2	A	1000	GDP	C6-C5-N7	2.84	135.46	130.29
2	B	1000	GDP	O3'-C3'-C2'	-2.54	103.67	111.82
2	B	1000	GDP	O6-C6-N1	2.39	124.60	120.11
2	B	1000	GDP	C2'-C1'-N9	-2.36	106.67	113.25
2	B	1000	GDP	O2B-PB-O3A	2.35	112.50	104.64
2	B	1000	GDP	O3B-PB-O3A	2.31	112.39	104.64
2	A	1000	GDP	C4-C5-N7	-2.25	107.11	110.67
2	A	1000	GDP	C2-N1-C6	-2.22	121.08	125.11
2	B	1000	GDP	C8-N9-C4	2.12	110.00	106.03
2	B	1000	GDP	C1'-N9-C8	-2.08	120.82	126.73
4	A	900	PGA	O4P-P-O3P	2.07	115.58	107.80
2	B	1000	GDP	C2-N1-C6	-2.05	121.39	125.11
2	A	1000	GDP	N2-C2-N1	2.05	121.09	116.76

There are no chirality outliers.

All (5) torsion outliers are listed below:

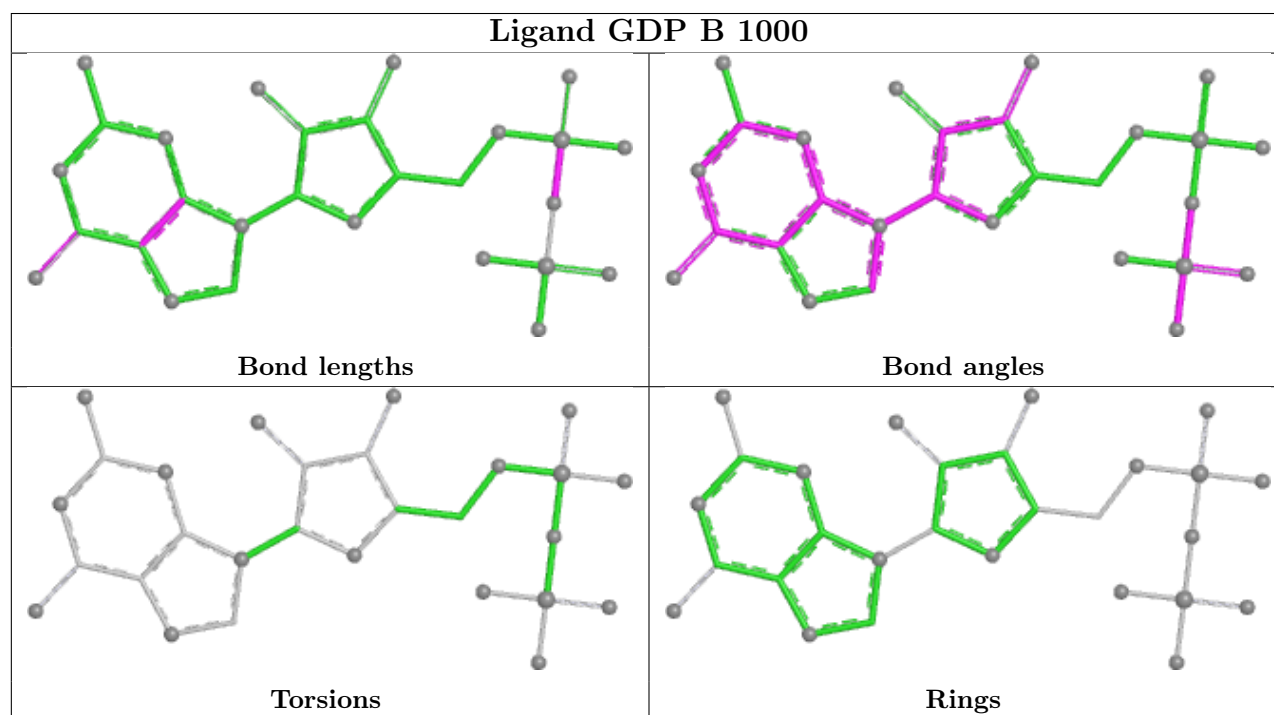
Mol	Chain	Res	Type	Atoms
7	B	1300	1PE	OH4-C13-C23-OH3
7	B	1300	1PE	OH5-C14-C24-OH4
7	A	1300	1PE	OH2-C12-C22-OH3
7	B	1300	1PE	C12-C22-OH3-C23
7	B	1300	1PE	C14-C24-OH4-C13

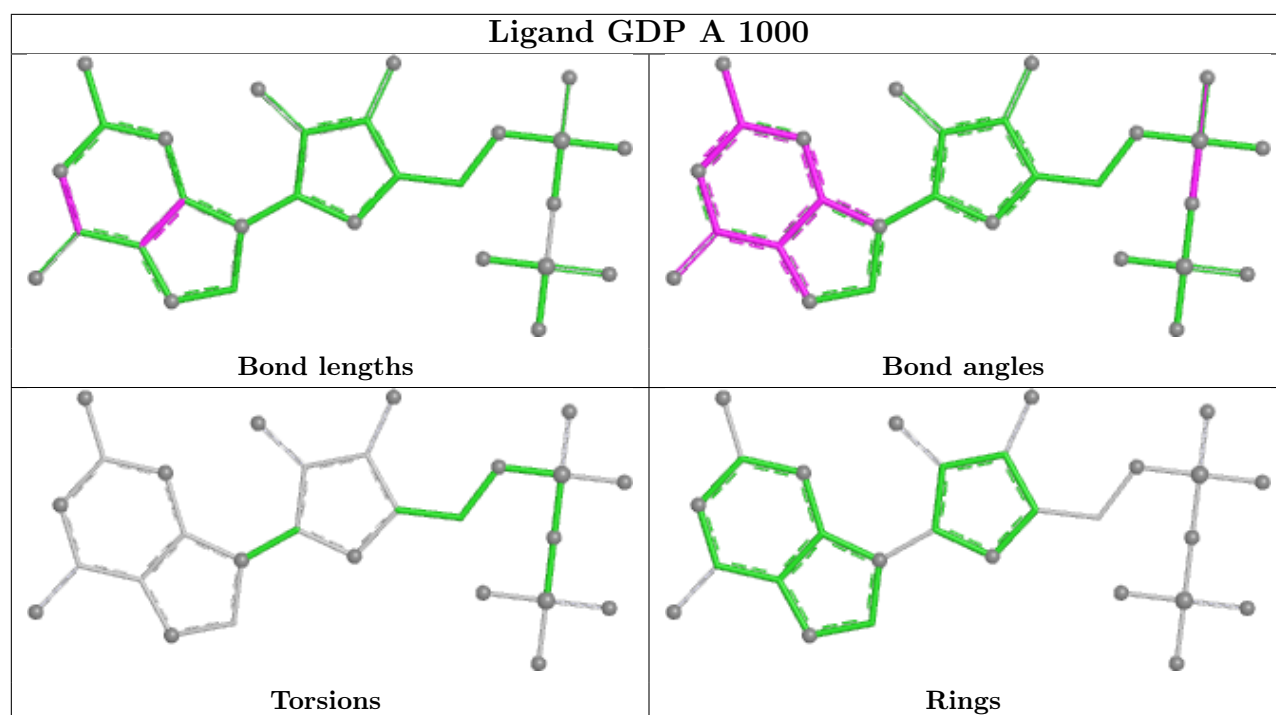
There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1300	1PE	2	0
2	B	1000	GDP	3	0
4	B	900	PGA	1	0
4	A	900	PGA	1	0
7	B	1300	1PE	2	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

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	604/624 (96%)	0.01	18 (2%) 52 55	6, 12, 16, 21	10 (1%)
1	B	613/624 (98%)	-0.11	5 (0%) 82 84	7, 13, 17, 21	6 (0%)
All	All	1217/1248 (97%)	-0.05	23 (1%) 66 69	6, 12, 17, 21	16 (1%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	580	ILE	4.9
1	A	581	SER	4.7
1	A	394	GLN	4.4
1	A	578	PHE	3.8
1	A	582	LYS	3.6
1	A	577	LEU	3.6
1	A	571	ASP	3.5
1	A	386	TRP	3.3
1	B	399	CYS	2.9
1	A	396	GLU	2.8
1	A	391	TRP	2.8
1	A	465	THR	2.6
1	A	150	GLY	2.5
1	B	464	ALA	2.4
1	B	401	HIS	2.4
1	A	504	PRO	2.2
1	B	400	ALA	2.2
1	B	572	VAL	2.2
1	A	570	GLY	2.2
1	A	273	PRO	2.1
1	A	561	GLU	2.1
1	A	583	GLU	2.1
1	A	379	PRO	2.1

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](#)

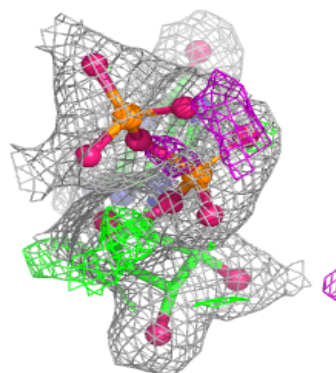
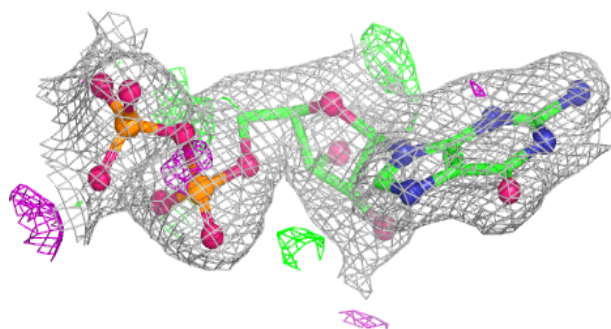
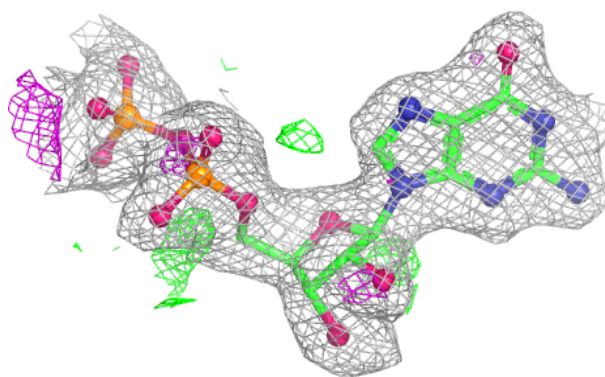
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	A	1200	4/4	0.78	0.11	25,27,28,28	0
7	1PE	B	1300	10/16	0.84	0.14	23,28,29,30	0
7	1PE	A	1300	5/16	0.87	0.16	17,20,24,25	0
5	NA	B	1100	1/1	0.91	0.08	24,24,24,24	0
5	NA	A	1100	1/1	0.91	0.04	22,22,22,22	0
4	PGA	B	900	9/9	0.94	0.11	19,20,21,21	0
2	GDP	B	1000	28/28	0.94	0.07	15,18,21,22	0
2	GDP	A	1000	28/28	0.97	0.05	14,17,19,23	0
4	PGA	A	900	9/9	0.97	0.06	15,16,18,18	0
3	MN	B	700	1/1	0.98	0.06	19,19,19,19	0
3	MN	A	700	1/1	0.99	0.07	18,18,18,18	0
3	MN	B	701	1/1	0.99	0.09	20,20,20,20	0
3	MN	A	701	1/1	0.99	0.04	19,19,19,19	0

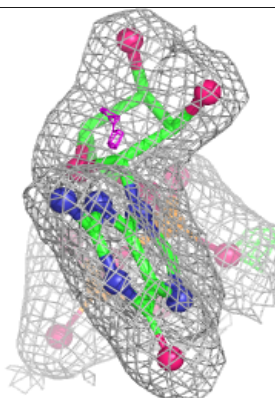
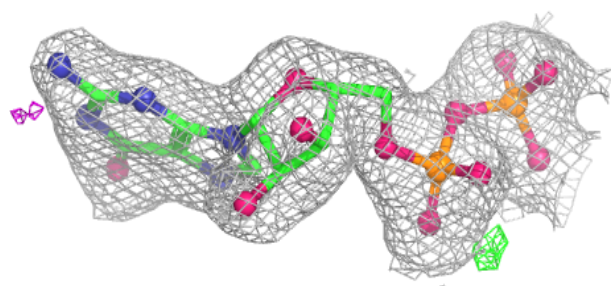
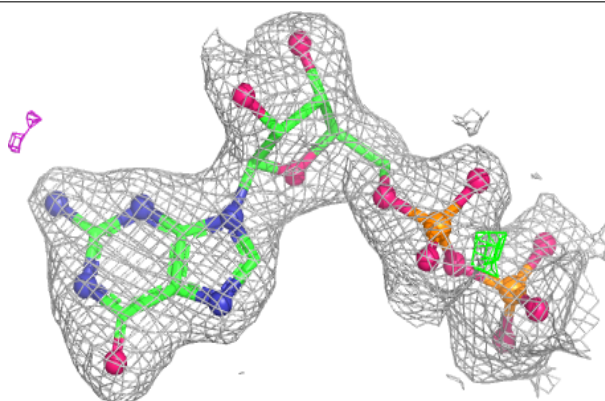
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GDP B 1000:

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

**Electron density around GDP A 1000:**

$2mF_o-DF_c$ (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.