



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 10:50 am BST

PDB ID : 2XNS  
Title : Crystal Structure Of Human G alpha i1 Bound To A Designed Helical Peptide  
Derived From The Goloco Motif Of RGS14  
Authors : Bosch, D.; Sammond, D.W.; Butterfoss, G.L.; Machius, M.; Siderovski, D.P.;  
Kuhlman, B.  
Deposited on : 2010-08-05  
Resolution : 3.41 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

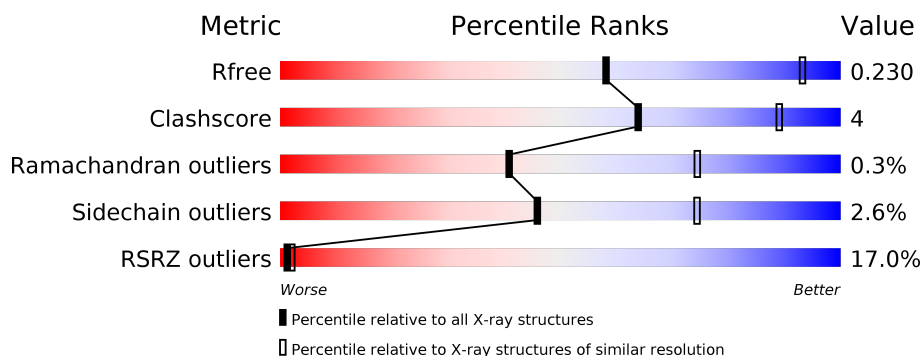
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.41 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1486 (3.50-3.34)
Clashscore	141614	1572 (3.50-3.34)
Ramachandran outliers	138981	1534 (3.50-3.34)
Sidechain outliers	138945	1535 (3.50-3.34)
RSRZ outliers	127900	1395 (3.50-3.34)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	327	<div> <div>16%</div> <div>86%</div> <div>10%</div> <div>••</div> </div>
1	B	327	<div> <div>16%</div> <div>87%</div> <div>9%</div> <div>••</div> </div>
2	C	40	<div> <div>23%</div> <div>83%</div> <div>15%</div> <div>•</div> </div>
2	D	40	<div> <div>18%</div> <div>83%</div> <div>15%</div> <div>•</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5862 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 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) SUB-UNIT ALPHA-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	0	1	0
			2553	1621	431	486	15			
1	B	316	Total	C	N	O	S	0	1	0
			2553	1621	431	486	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	SER	-	expression tag	UNP P63096
A	29	ASN	-	expression tag	UNP P63096
B	28	SER	-	expression tag	UNP P63096
B	29	ASN	-	expression tag	UNP P63096

- Molecule 2 is a protein called REGULATOR OF G-PROTEIN SIGNALING 14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	39	Total	C	N	O	0	1	0
			330	203	64	63			
2	D	39	Total	C	N	O	0	1	0
			330	203	64	63			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	517	GLY	-	expression tag	UNP O43566
C	518	LEU	-	expression tag	UNP O43566
C	519	LEU	-	expression tag	UNP O43566
C	520	SER	-	expression tag	UNP O43566
C	521	ASN	-	expression tag	UNP O43566
C	522	GLU	-	expression tag	UNP O43566
C	523	GLU	-	expression tag	UNP O43566

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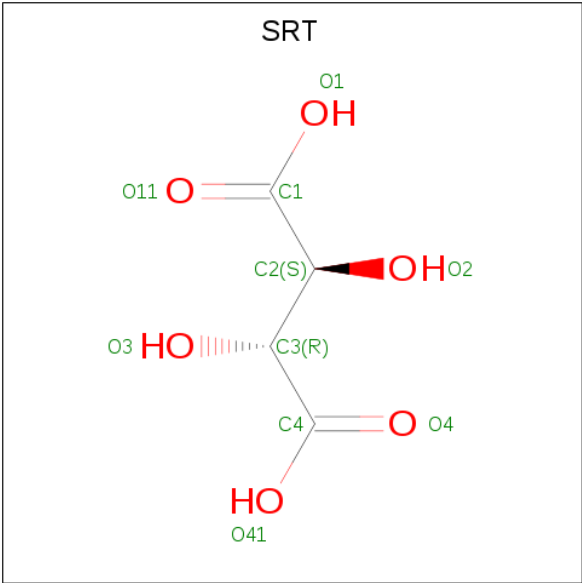
Chain	Residue	Modelled	Actual	Comment	Reference
C	524	VAL	-	expression tag	UNP O43566
C	525	PHE	-	expression tag	UNP O43566
C	526	ARG	-	expression tag	UNP O43566
C	527	ALA	-	expression tag	UNP O43566
C	528	LEU	-	expression tag	UNP O43566
C	529	ARG	-	expression tag	UNP O43566
C	530	ASP	-	expression tag	UNP O43566
C	531	PHE	-	expression tag	UNP O43566
C	532	ASP	-	expression tag	UNP O43566
C	533	ARG	-	expression tag	UNP O43566
C	534	TRP	-	expression tag	UNP O43566
C	535	PHE	-	expression tag	UNP O43566
D	517	GLY	-	expression tag	UNP O43566
D	518	LEU	-	expression tag	UNP O43566
D	519	LEU	-	expression tag	UNP O43566
D	520	SER	-	expression tag	UNP O43566
D	521	ASN	-	expression tag	UNP O43566
D	522	GLU	-	expression tag	UNP O43566
D	523	GLU	-	expression tag	UNP O43566
D	524	VAL	-	expression tag	UNP O43566
D	525	PHE	-	expression tag	UNP O43566
D	526	ARG	-	expression tag	UNP O43566
D	527	ALA	-	expression tag	UNP O43566
D	528	LEU	-	expression tag	UNP O43566
D	529	ARG	-	expression tag	UNP O43566
D	530	ASP	-	expression tag	UNP O43566
D	531	PHE	-	expression tag	UNP O43566
D	532	ASP	-	expression tag	UNP O43566
D	533	ARG	-	expression tag	UNP O43566
D	534	TRP	-	expression tag	UNP O43566
D	535	PHE	-	expression tag	UNP O43566

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:  $C_{10}H_{15}N_5O_{11}P_2$ ).



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

- Molecule 4 is S,R MESO-TARTARIC ACID (three-letter code: SRT) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>).



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

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	O	S	0	0
			5	4	1		
5	D	1	Total	O	S	0	0
			5	4	1		

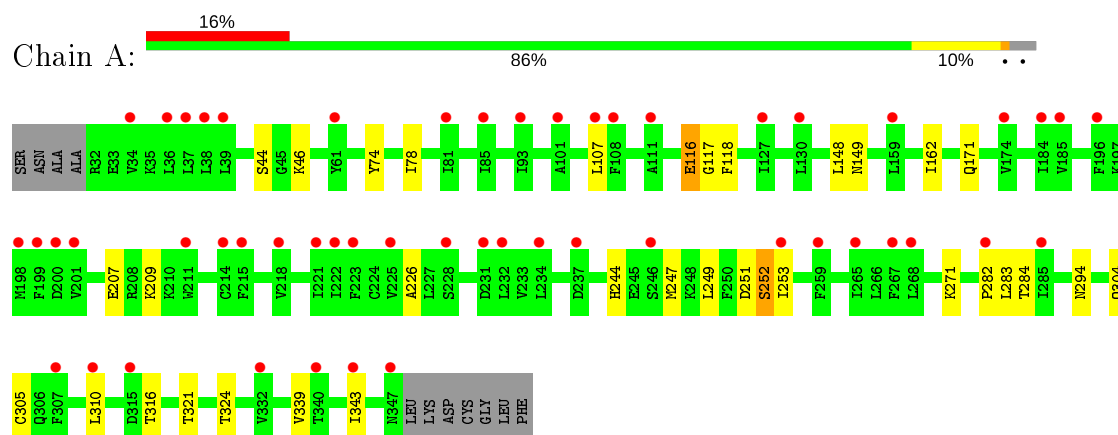
- Molecule 6 is water.

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

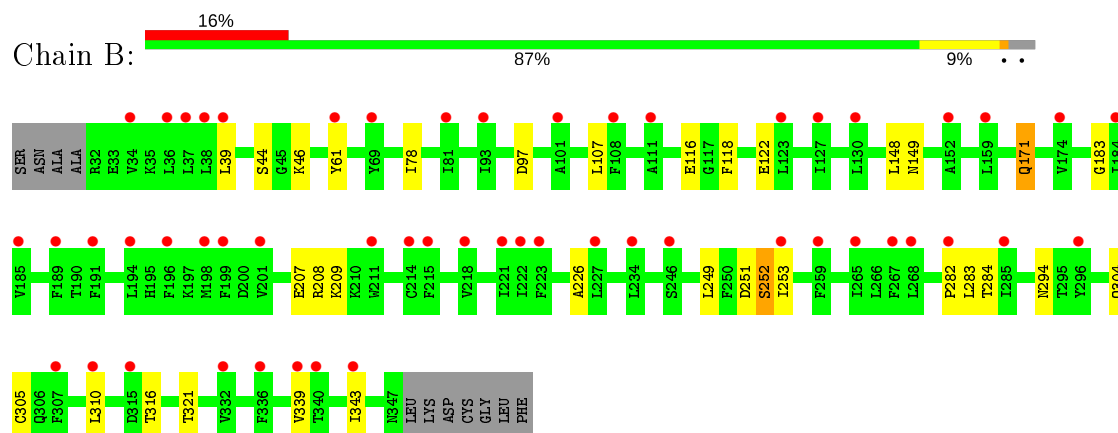
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

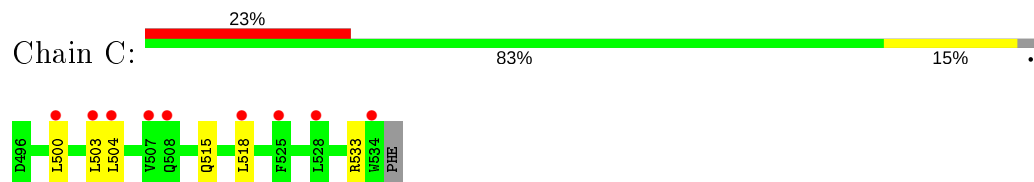
- Molecule 1: GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) SUBUNIT ALPHA-1



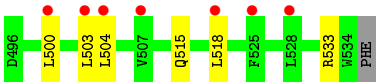
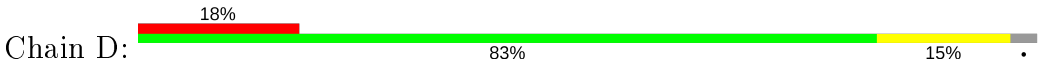
- Molecule 1: GUANINE NUCLEOTIDE-BINDING PROTEIN G(I) SUBUNIT ALPHA-1



- Molecule 2: REGULATOR OF G-PROTEIN SIGNALING 14



- Molecule 2: REGULATOR OF G-PROTEIN SIGNALING 14





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	265.26 Å   265.26 Å   265.26 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	39.99 – 3.41 39.99 – 3.41	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.99-3.41) 99.9 (39.99-3.41)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.68 (at 3.40 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.223 , 0.244 0.212 , 0.230	Depositor DCC
$R_{free}$ test set	1489 reflections (3.51%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	95.6	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 70.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.468 for -l,-k,-h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5862	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.87% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, SO4, SRT

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	0.34	0/2599	0.49	0/3501
1	B	0.34	0/2599	0.49	0/3501
2	C	0.36	0/335	0.62	0/450
2	D	0.36	0/335	0.62	0/450
All	All	0.35	0/5868	0.50	0/7902

There are no bond length outliers.

There are no bond angle outliers.

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	2553	0	2526	20	0
1	B	2553	0	2526	23	0
2	C	330	0	311	6	0
2	D	330	0	311	6	0
3	A	28	0	12	3	0
3	B	28	0	12	3	0
4	A	10	0	4	0	0
4	B	10	0	4	1	0
5	C	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	5	0	0	0	0
6	A	4	0	0	1	0
6	B	4	0	0	1	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
All	All	5862	0	5706	48	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 4.

All (48) 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:282:PRO:HB2	1:A:284:THR:HG22	1.57	0.86
1:A:304:GLN:HG3	1:A:321:THR:HG21	1.68	0.76
1:B:304:GLN:HG3	1:B:321:THR:HG21	1.75	0.69
1:B:282:PRO:HB2	1:B:284:THR:HG22	1.78	0.64
1:B:171[A]:GLN:HE21	1:B:171[A]:GLN:HA	1.64	0.63
3:B:1348:GDP:O1A	3:B:1348:GDP:H3'	2.01	0.61
3:A:1348:GDP:H3'	3:A:1348:GDP:O1A	1.99	0.61
1:A:116:GLU:HG3	2:C:518:LEU:HD22	1.83	0.60
1:B:171[A]:GLN:CA	1:B:171[A]:GLN:HE21	2.16	0.59
1:B:116:GLU:HG3	2:D:518:LEU:HD22	1.85	0.59
1:A:294:ASN:HB2	6:A:2004:HOH:O	2.03	0.57
1:A:253:ILE:HD13	2:C:500:LEU:HD11	1.87	0.56
1:B:149:ASN:HD22	2:D:515:GLN:HE21	1.53	0.56
1:A:339:VAL:O	1:A:343:ILE:HG12	2.06	0.55
1:A:249:LEU:HD11	2:C:504:LEU:HD13	1.88	0.55
1:B:171[A]:GLN:NE2	1:B:171[A]:GLN:HA	2.20	0.55
1:B:339:VAL:O	1:B:343:ILE:HG12	2.07	0.55
1:B:171[B]:GLN:H	1:B:171[B]:GLN:CD	2.11	0.54
1:A:252:SER:HB3	2:C:500:LEU:HD12	1.90	0.54
1:A:149:ASN:HD22	2:C:515:GLN:HE21	1.56	0.53
1:B:207:GLU:HG3	1:B:209:LYS:H	1.73	0.53
1:B:249:LEU:HD11	2:D:504:LEU:HD13	1.92	0.50
1:B:252:SER:HB3	2:D:500:LEU:HD12	1.92	0.50
1:A:171[B]:GLN:CD	1:A:171[B]:GLN:H	2.14	0.49
1:A:207:GLU:HG3	1:A:209:LYS:H	1.77	0.48
1:B:253:ILE:HD13	2:D:500:LEU:HD11	1.94	0.48
1:A:251:ASP:HB2	1:A:310:LEU:HD13	1.97	0.46
1:B:294:ASN:HB2	6:B:2004:HOH:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:LEU:HG	1:A:283:LEU:O	2.16	0.46
1:B:283:LEU:HG	1:B:283:LEU:O	2.16	0.45
3:A:1348:GDP:H5'	3:A:1348:GDP:H8	1.82	0.45
1:B:44:SER:HA	1:B:226:ALA:HB2	1.98	0.45
1:B:46:LYS:HB2	3:B:1348:GDP:O1B	2.16	0.44
1:B:61:TYR:HD1	1:B:171[A]:GLN:HE22	1.66	0.44
4:B:1349:SRT:O3	4:B:1349:SRT:O11	2.34	0.43
1:B:148:LEU:HA	2:D:515:GLN:HE22	1.84	0.43
1:A:148:LEU:HA	2:C:515:GLN:HE22	1.83	0.42
1:B:208:ARG:HG3	1:B:208:ARG:H	1.70	0.42
1:A:44:SER:HA	1:A:226:ALA:HB2	2.00	0.42
1:A:244:HIS:HA	1:A:247:MET:HB2	2.00	0.42
1:A:271:LYS:HG2	1:A:324:THR:O	2.20	0.42
1:A:74:TYR:HE1	1:A:162:ILE:HG22	1.84	0.42
1:B:39:LEU:HD13	1:B:253:ILE:HD12	2.02	0.42
1:B:251:ASP:HB2	1:B:310:LEU:HD13	2.01	0.42
1:A:46:LYS:HB2	3:A:1348:GDP:O1B	2.19	0.41
1:B:78:ILE:HG23	1:B:107:LEU:HD11	2.02	0.41
1:A:78:ILE:HG23	1:A:107:LEU:HD11	2.03	0.41
3:B:1348:GDP:H5'	3:B:1348:GDP:H8	1.86	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	315/327 (96%)	298 (95%)	16 (5%)	1 (0%)	41	74
1	B	315/327 (96%)	299 (95%)	15 (5%)	1 (0%)	41	74
2	C	38/40 (95%)	33 (87%)	5 (13%)	0	100	100
2	D	38/40 (95%)	33 (87%)	5 (13%)	0	100	100
All	All	706/734 (96%)	663 (94%)	41 (6%)	2 (0%)	41	74

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	183	GLY
1	A	117	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	276/283 (98%)	271 (98%)	5 (2%)	59	81
1	B	276/283 (98%)	268 (97%)	8 (3%)	42	72
2	C	35/35 (100%)	33 (94%)	2 (6%)	20	53
2	D	35/35 (100%)	33 (94%)	2 (6%)	20	53
All	All	622/636 (98%)	605 (97%)	17 (3%)	46	73

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

Mol	Chain	Res	Type
1	A	116	GLU
1	A	118	PHE
1	A	252	SER
1	A	305	CYS
1	A	316	THR
1	B	97	ASP
1	B	118	PHE
1	B	122	GLU
1	B	171[A]	GLN
1	B	171[B]	GLN
1	B	252	SER
1	B	305	CYS
1	B	316	THR
2	C	503	LEU
2	C	533	ARG
2	D	503	LEU
2	D	533	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	515	GLN
2	D	515	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates 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	$\# Z  > 2$
4	SRT	B	1349	-	3,9,9	0.45	0	6,12,12	0.75	0
4	SRT	A	1349	-	3,9,9	0.38	0	6,12,12	1.03	0
3	GDP	A	1348	-	24,30,30	1.10	2 (8%)	31,47,47	1.99	6 (19%)
5	SO4	C	1535	-	4,4,4	0.18	0	6,6,6	0.14	0
5	SO4	D	1535	-	4,4,4	0.16	0	6,6,6	0.16	0
3	GDP	B	1348	-	24,30,30	1.11	2 (8%)	31,47,47	1.99	6 (19%)

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
4	SRT	B	1349	-	-	3/4/12/12	-
4	SRT	A	1349	-	-	4/4/12/12	-
3	GDP	B	1348	-	-	6/12/32/32	0/3/3/3
3	GDP	A	1348	-	-	5/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1348	GDP	C6-C5	3.64	1.47	1.41
3	A	1348	GDP	C6-C5	3.62	1.47	1.41
3	B	1348	GDP	C5-C4	2.19	1.46	1.40
3	A	1348	GDP	C5-C4	2.13	1.46	1.40

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1348	GDP	C2-N3-C4	5.29	121.40	115.36
3	A	1348	GDP	C2-N3-C4	5.26	121.37	115.36
3	A	1348	GDP	C6-C5-C4	-4.27	116.72	120.80
3	B	1348	GDP	C6-C5-C4	-4.23	116.75	120.80
3	A	1348	GDP	C6-N1-C2	3.90	122.12	115.93
3	B	1348	GDP	C6-N1-C2	3.89	122.10	115.93
3	B	1348	GDP	N3-C2-N1	-3.68	122.31	127.22
3	A	1348	GDP	N3-C2-N1	-3.63	122.39	127.22
3	B	1348	GDP	PA-O3A-PB	-3.61	120.44	132.83
3	A	1348	GDP	C5-C6-N1	-3.58	118.53	123.43
3	B	1348	GDP	C5-C6-N1	-3.55	118.57	123.43
3	A	1348	GDP	PA-O3A-PB	-3.43	121.06	132.83

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1349	SRT	O2-C2-C3-O3
4	A	1349	SRT	C1-C2-C3-C4
4	A	1349	SRT	O2-C2-C3-O3
3	A	1348	GDP	PA-O3A-PB-O2B
3	A	1348	GDP	C5'-O5'-PA-O1A
3	B	1348	GDP	PA-O3A-PB-O2B
3	B	1348	GDP	C5'-O5'-PA-O1A

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Mol	Chain	Res	Type	Atoms
3	A	1348	GDP	C4'-C5'-O5'-PA
3	B	1348	GDP	C4'-C5'-O5'-PA
4	A	1349	SRT	O2-C2-C3-C4
4	B	1349	SRT	C1-C2-C3-C4
4	B	1349	SRT	C1-C2-C3-O3
3	A	1348	GDP	PA-O3A-PB-O3B
3	B	1348	GDP	PA-O3A-PB-O3B
4	A	1349	SRT	C1-C2-C3-O3
3	A	1348	GDP	O4'-C4'-C5'-O5'
3	B	1348	GDP	O4'-C4'-C5'-O5'
3	B	1348	GDP	PA-O3A-PB-O1B

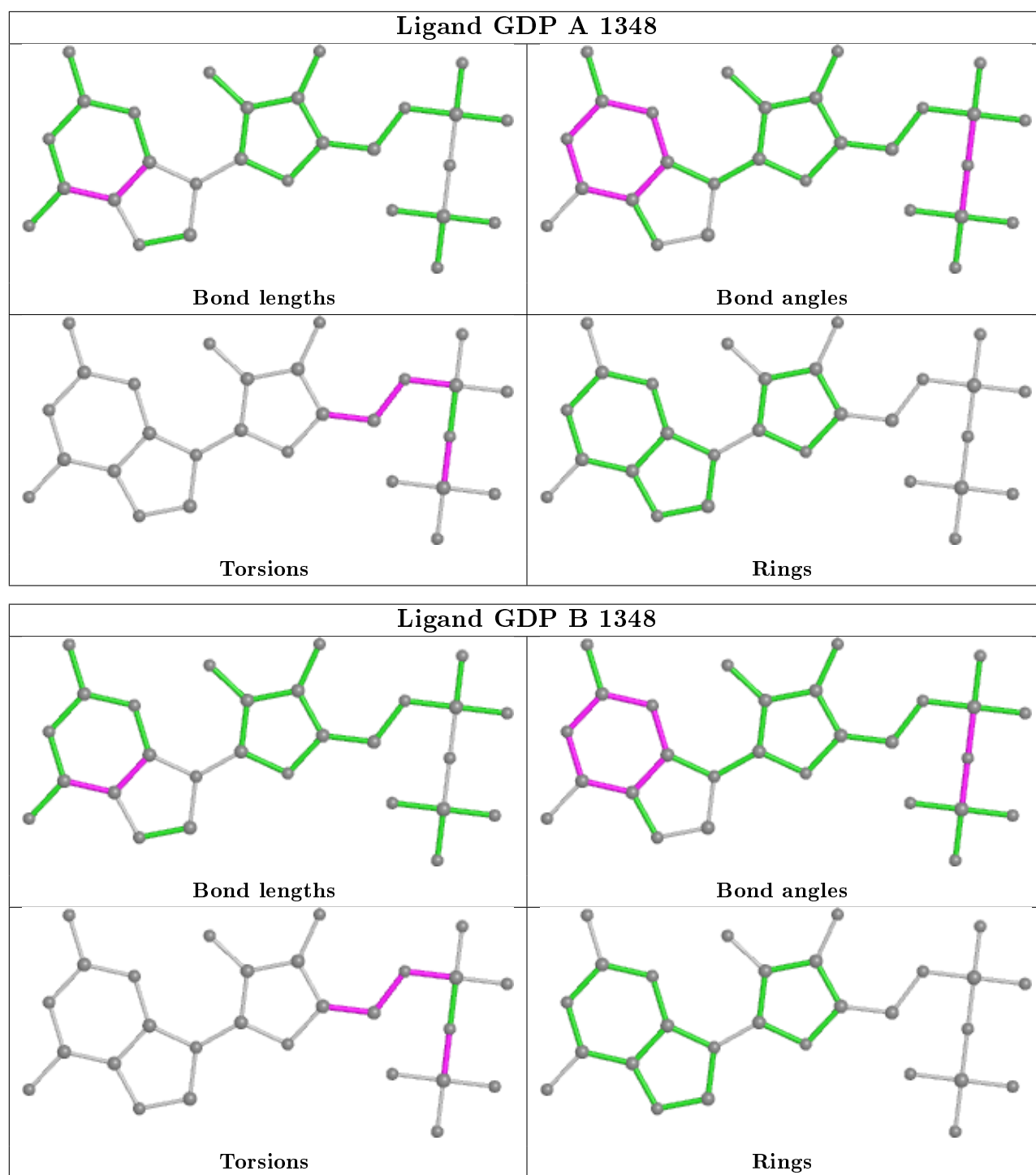
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1349	SRT	1	0
3	A	1348	GDP	3	0
3	B	1348	GDP	3	0

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





## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	316/327 (96%)	1.19	52 (16%)  	71, 102, 150, 176	0
1	B	316/327 (96%)	1.18	53 (16%)  	71, 102, 149, 177	0
2	C	39/40 (97%)	1.13	9 (23%)  	102, 113, 172, 181	0
2	D	39/40 (97%)	1.06	7 (17%)  	99, 110, 172, 178	0
All	All	710/734 (96%)	1.17	121 (17%)  	71, 104, 154, 181	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	196	PHE	4.0
1	A	199	PHE	3.8
1	A	211	TRP	3.8
1	B	211	TRP	3.7
1	B	196	PHE	3.7
1	B	199	PHE	3.6
1	B	222	ILE	3.4
1	A	222	ILE	3.2
1	A	37	LEU	3.1
1	B	37	LEU	3.0
1	B	221	ILE	2.9
1	B	265	ILE	2.9
1	B	108	PHE	2.9
1	A	221	ILE	2.9
1	B	315	ASP	2.9
1	A	265	ILE	2.9
1	A	215	PHE	2.9
1	B	184	ILE	2.8
1	A	282	PRO	2.8
1	A	268	LEU	2.7
2	C	500	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
2	D	500	LEU	2.7
1	B	268	LEU	2.7
1	A	108	PHE	2.7
1	B	282	PRO	2.7
1	B	223	PHE	2.6
1	B	253	ILE	2.6
1	A	307	PHE	2.6
1	B	214	CYS	2.6
2	D	503	LEU	2.6
2	C	504	LEU	2.5
1	A	253	ILE	2.5
1	B	39	LEU	2.5
1	B	310	LEU	2.5
1	A	39	LEU	2.5
2	C	518	LEU	2.5
1	A	246	SER	2.5
1	B	215	PHE	2.5
1	B	307	PHE	2.5
1	A	127	ILE	2.5
1	B	61	TYR	2.4
1	A	159	LEU	2.4
1	A	61	TYR	2.4
1	A	214	CYS	2.4
1	B	159	LEU	2.4
2	D	507	VAL	2.4
1	B	246	SER	2.4
1	B	198	MET	2.4
1	A	201	VAL	2.4
1	A	237	ASP	2.4
1	B	285	ILE	2.4
1	A	36	LEU	2.4
2	D	504	LEU	2.4
1	B	185	VAL	2.4
1	A	38	LEU	2.4
1	B	218	VAL	2.3
1	A	184	ILE	2.3
1	B	36	LEU	2.3
1	B	152	ALA	2.3
1	B	174	VAL	2.3
1	B	93	ILE	2.3
1	B	259	PHE	2.3
1	A	285	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	336	PHE	2.3
1	A	200	ASP	2.3
1	A	34	VAL	2.3
1	A	111	ALA	2.3
1	B	38	LEU	2.3
1	A	185	VAL	2.3
2	C	503	LEU	2.3
1	B	127	ILE	2.3
1	A	101	ALA	2.2
1	B	101	ALA	2.2
1	A	315	ASP	2.2
1	B	34	VAL	2.2
1	A	259	PHE	2.2
1	B	111	ALA	2.2
1	A	310	LEU	2.2
1	B	189	PHE	2.2
1	B	332	VAL	2.2
1	A	225	VAL	2.2
1	B	340	THR	2.2
1	A	218	VAL	2.2
1	B	130	LEU	2.2
1	A	81	ILE	2.2
1	A	343	ILE	2.2
1	B	201	VAL	2.2
1	B	234	LEU	2.2
1	B	343	ILE	2.1
1	A	232	LEU	2.1
1	B	69	TYR	2.1
1	A	174	VAL	2.1
2	D	528	LEU	2.1
2	C	525	PHE	2.1
2	C	508	GLN	2.1
1	A	198	MET	2.1
1	A	223	PHE	2.1
1	A	231	ASP	2.1
1	B	81	ILE	2.1
1	B	267	PHE	2.1
1	A	93	ILE	2.1
2	C	507	VAL	2.1
2	D	518	LEU	2.1
1	B	191	PHE	2.1
1	A	340	THR	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	525	PHE	2.1
1	A	267	PHE	2.1
1	A	107	LEU	2.1
1	B	227	LEU	2.0
2	C	528	LEU	2.0
1	A	332	VAL	2.0
1	B	123	LEU	2.0
2	C	534	TRP	2.0
1	B	296	TYR	2.0
1	A	130	LEU	2.0
1	A	228	SER	2.0
1	B	194	LEU	2.0
1	A	347	ASN	2.0
1	B	339	VAL	2.0
1	A	85	ILE	2.0
1	A	234	LEU	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

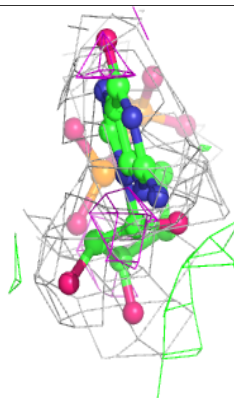
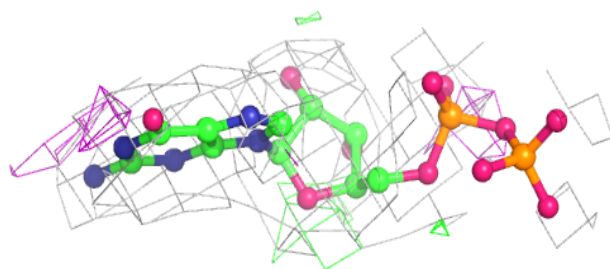
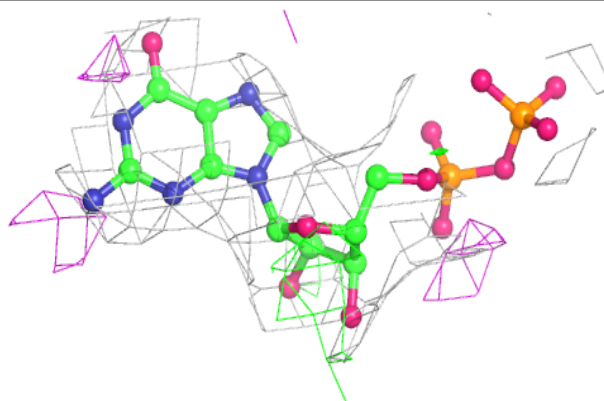
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
5	SO4	C	1535	5/5	0.73	0.22	131,132,132,132	0
5	SO4	D	1535	5/5	0.75	0.20	129,130,130,130	0
4	SRT	B	1349	10/10	0.93	0.37	81,82,82,83	0
4	SRT	A	1349	10/10	0.94	0.31	79,82,84,85	0
3	GDP	A	1348	28/28	0.96	0.28	86,90,96,96	0
3	GDP	B	1348	28/28	0.96	0.27	86,90,96,96	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.

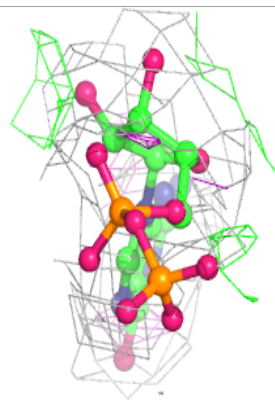
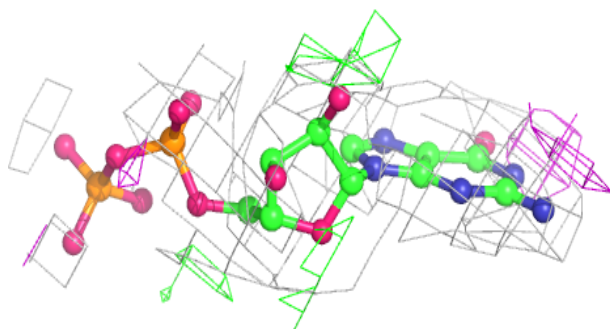
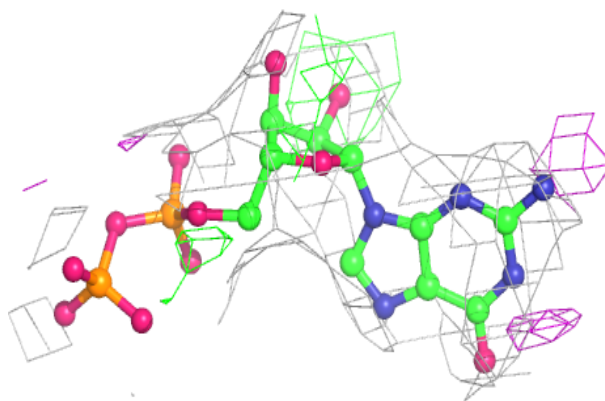
**Electron density around GDP A 1348:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around GDP B 1348:**

$2mF_o - DF_c$  (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.