



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:25 AM UTC

PDB ID : 2XTZ / pdb_00002xtz
Title : Crystal structure of the G alpha protein AtGPA1 from Arabidopsis thaliana
Authors : Jones, J.C.; Duffy, J.W.; Machius, M.; Temple, B.R.S.; Dohlman, H.G.; Jones, A.M.
Deposited on : 2010-10-13
Resolution : 2.34 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

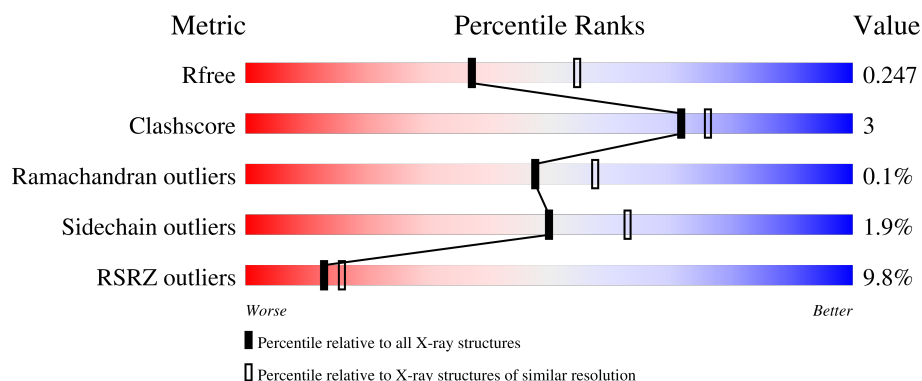
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	354	
1	B	354	
1	C	354	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7909 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 ALPHA-1 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	3	0
			2838	1818	479	528	13			
1	B	291	Total	C	N	O	S	0	0	0
			2431	1573	405	444	9			
1	C	270	Total	C	N	O	S	0	0	0
			2263	1470	378	406	9			

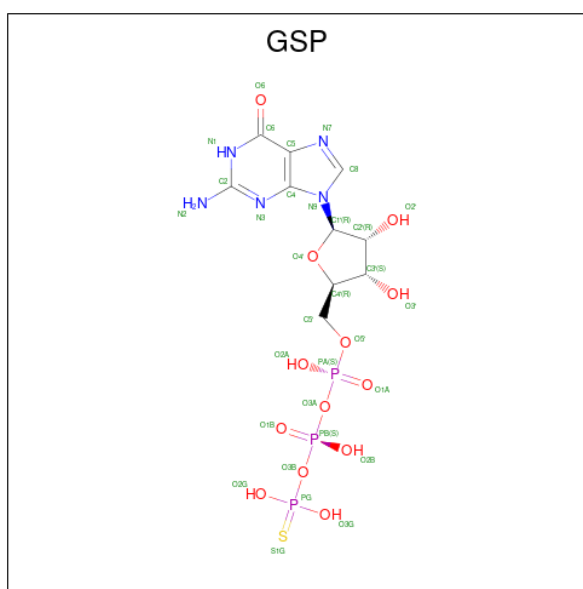
There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	GLY	-	expression tag	UNP P18064
A	31	ALA	-	expression tag	UNP P18064
A	32	MET	-	expression tag	UNP P18064
A	33	GLY	-	expression tag	UNP P18064
A	34	SER	-	expression tag	UNP P18064
A	35	GLY	-	expression tag	UNP P18064
A	36	ILE	-	expression tag	UNP P18064
B	30	GLY	-	expression tag	UNP P18064
B	31	ALA	-	expression tag	UNP P18064
B	32	MET	-	expression tag	UNP P18064
B	33	GLY	-	expression tag	UNP P18064
B	34	SER	-	expression tag	UNP P18064
B	35	GLY	-	expression tag	UNP P18064
B	36	ILE	-	expression tag	UNP P18064
C	30	GLY	-	expression tag	UNP P18064
C	31	ALA	-	expression tag	UNP P18064
C	32	MET	-	expression tag	UNP P18064
C	33	GLY	-	expression tag	UNP P18064
C	34	SER	-	expression tag	UNP P18064
C	35	GLY	-	expression tag	UNP P18064
C	36	ILE	-	expression tag	UNP P18064

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 5'-GUANOSINE-DIPHOSPHATE-MONOTHIOPHOSPHATE (CCD ID: GSP) (formula: C₁₀H₁₆N₅O₁₃P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			32	10	5	13	3	1		
3	B	1	Total	C	N	O	P	S	0	0
			32	10	5	13	3	1		
3	C	1	Total	C	N	O	P	S	0	0
			32	10	5	13	3	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		
4	B	2	Total	Cl	0	0
			2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total Cl 1 1	0	0

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



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

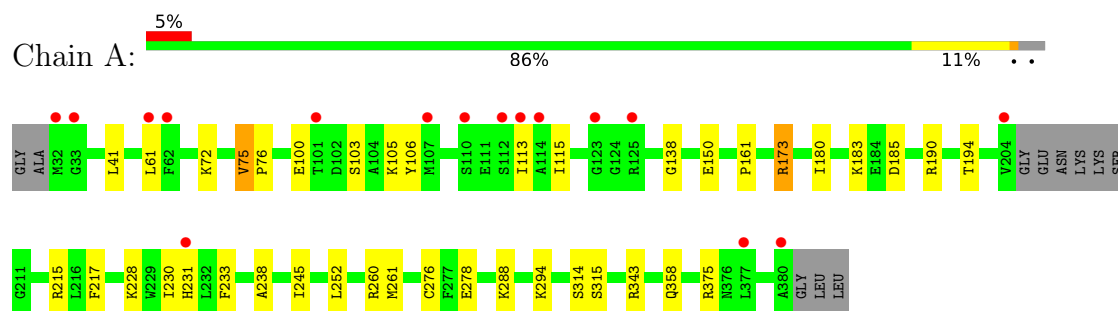
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	139	Total O 139 139	0	0
6	B	69	Total O 69 69	0	0
6	C	41	Total O 41 41	0	0

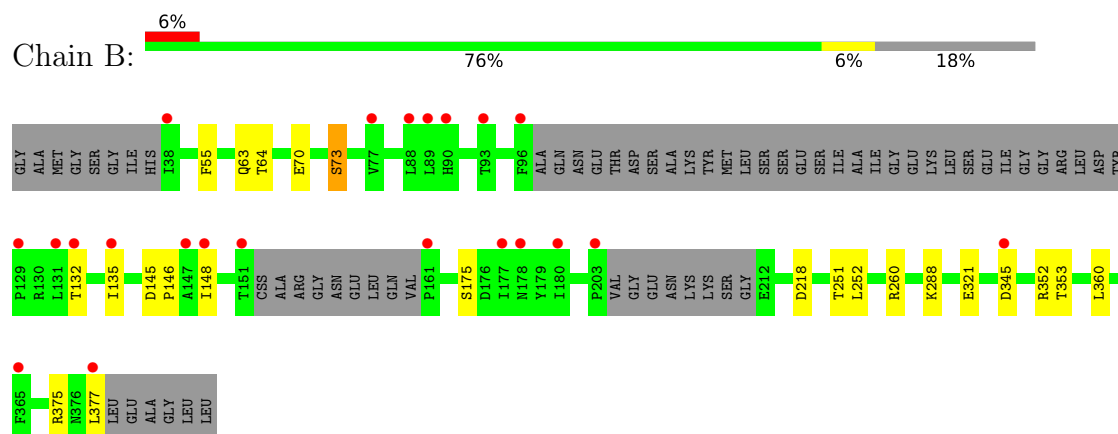
3 Residue-property plots [i](#)

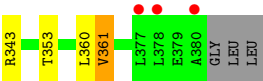
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT



• Molecule 1: GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.13Å 119.35Å 161.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	96.03 – 2.34 96.03 – 2.34	Depositor EDS
% Data completeness (in resolution range)	99.9 (96.03-2.34) 94.1 (96.03-2.34)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.211 , 0.254 0.204 , 0.247	Depositor DCC
R_{free} test set	1520 reflections (2.73%)	wwPDB-VP
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7909	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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: SO4, CSS, MG, CL, GSP

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	0.66	1/2878 (0.0%)	0.87	0/3872
1	B	0.62	0/2473	0.82	0/3325
1	C	0.59	1/2300 (0.0%)	0.86	0/3094
All	All	0.63	2/7651 (0.0%)	0.85	0/10291

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	75	VAL	CA-CB	6.33	1.57	1.54
1	A	75	VAL	CA-CB	6.04	1.57	1.54

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	2838	0	2837	22	0
1	B	2431	0	2450	15	0
1	C	2263	0	2296	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	32	0	12	1	0
3	B	32	0	12	1	0
3	C	32	0	12	1	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	15	0	0	0	0
6	A	139	0	0	2	0
6	B	69	0	0	0	0
6	C	41	0	0	0	0
All	All	7909	0	7619	51	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 3.

All (51) 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:63:GLN:HG3	1:B:64:THR:H	1.23	1.03
1:C:305:GLU:O	1:C:308:ARG:HG3	1.73	0.87
1:B:63:GLN:HG3	1:B:64:THR:N	2.03	0.70
1:A:105:LYS:HG2	1:A:150:GLU:HG2	1.73	0.69
1:B:251:THR:O	1:B:260:ARG:HD2	1.95	0.66
1:A:245:ILE:HA	1:A:261:MET:HE1	1.86	0.57
1:C:134:ASP:C	1:C:136:ALA:H	2.13	0.56
1:A:215[A]:ARG:HG2	1:A:217:PHE:CE2	2.41	0.55
1:C:245:ILE:HA	1:C:261:MET:HE1	1.89	0.54
1:C:134:ASP:CG	1:C:135:ILE:N	2.65	0.52
1:A:115:ILE:HG21	1:A:138:GLY:O	2.10	0.51
1:A:288:LYS:HG2	3:A:1382:GSP:C6	2.45	0.51
1:A:100:GLU:HG3	1:A:106:TYR:CE1	2.45	0.51
1:C:278:GLU:HA	1:C:343:ARG:HG2	1.92	0.51
1:C:57:GLN:HB3	1:C:361:VAL:HG21	1.92	0.51
1:B:132:THR:H	1:B:135:ILE:HG22	1.76	0.50
1:A:278:GLU:HA	1:A:343:ARG:HG2	1.94	0.49
1:A:230:ILE:HG13	6:A:2056:HOH:O	2.13	0.49
1:B:288:LYS:HG2	3:B:1379:GSP:C6	2.48	0.49
1:A:375:ARG:NH2	6:A:2134:HOH:O	2.47	0.48
1:A:103:SER:OG	1:A:105:LYS:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:GLU:OE2	1:B:352:ARG:NH2	2.35	0.48
1:B:375:ARG:O	1:B:375:ARG:HD3	2.15	0.47
1:C:86:ILE:HA	1:C:89:LEU:HD12	1.97	0.47
1:A:100:GLU:HG3	1:A:106:TYR:HE1	1.80	0.47
1:C:314:SER:OG	1:C:315:SER:N	2.48	0.46
1:A:161:PRO:HB3	1:A:190:ARG:NH1	2.31	0.46
1:A:194:THR:O	1:A:228:LYS:NZ	2.48	0.46
1:B:63:GLN:CG	1:B:64:THR:H	2.08	0.46
1:B:353:THR:HA	1:B:360:LEU:HD21	1.97	0.45
1:C:86:ILE:H	1:C:86:ILE:HG13	1.39	0.45
1:A:252:LEU:HD23	1:A:260:ARG:HG2	1.98	0.45
1:C:353:THR:HA	1:C:360:LEU:HD21	1.98	0.45
1:A:314:SER:OG	1:A:315:SER:N	2.49	0.44
1:C:57:GLN:CB	1:C:361:VAL:HG21	2.47	0.44
1:A:115:ILE:HG21	1:A:138:GLY:C	2.42	0.44
1:C:200:GLN:OE1	1:C:215:ARG:NH1	2.51	0.43
1:A:41:LEU:HD22	1:A:238:ALA:HB3	2.00	0.43
1:A:72:LYS:HE2	1:A:180:ILE:HG12	2.00	0.43
1:A:173:ARG:NH1	1:A:185:ASP:OD1	2.40	0.42
1:B:70:GLU:O	1:B:73:SER:HB3	2.19	0.42
1:B:252:LEU:HD23	1:B:260:ARG:HG2	2.01	0.42
1:B:55:PHE:CD1	1:B:218:ASP:HB2	2.55	0.42
1:B:345:ASP:O	1:B:375:ARG:NH2	2.53	0.42
1:C:310:TYR:OH	1:C:319:GLU:OE2	2.31	0.41
1:C:288:LYS:HG2	3:C:1382:GSP:C6	2.55	0.41
1:A:233:PHE:HB3	1:A:276[A]:CYS:SG	2.61	0.41
1:B:145:ASP:HA	1:B:146:PRO:HD3	1.94	0.41
1:A:75:VAL:N	1:A:76:PRO:HD2	2.36	0.41
1:B:375:ARG:C	1:B:377:LEU:H	2.29	0.41
1:A:61:LEU:HD12	1:A:358:GLN:HE21	1.85	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	340/354 (96%)	335 (98%)	5 (2%)	0	100	100
1	B	282/354 (80%)	278 (99%)	4 (1%)	0	100	100
1	C	259/354 (73%)	250 (96%)	8 (3%)	1 (0%)	30	32
All	All	881/1062 (83%)	863 (98%)	17 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	135	ILE

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	308/313 (98%)	303 (98%)	5 (2%)	55	67
1	B	267/313 (85%)	264 (99%)	3 (1%)	65	77
1	C	249/313 (80%)	241 (97%)	8 (3%)	34	44
All	All	824/939 (88%)	808 (98%)	16 (2%)	50	63

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	ILE
1	A	173	ARG
1	A	183	LYS
1	A	231	HIS
1	A	294	LYS
1	B	73	SER
1	B	148	ILE
1	B	175	SER
1	C	42	LEU

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Mol	Chain	Res	Type
1	C	86	ILE
1	C	141	THR
1	C	176	ASP
1	C	178	ASN
1	C	291	ILE
1	C	303	VAL
1	C	361	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	156	ASN
1	A	311	GLN
1	C	63	GLN
1	C	318	GLN
1	C	358	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSS	B	163	1	4,6,7	1.00	0	2,6,8	1.26	0
1	CSS	C	163	1	4,6,7	0.90	0	2,6,8	0.83	0
1	CSS	A	152	1	4,6,7	0.70	0	2,6,8	1.15	0
1	CSS	A	163	1	4,6,7	0.94	0	2,6,8	1.05	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 Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSS	B	163	1	-	1/1/5/7	-
1	CSS	C	163	1	-	0/1/5/7	-
1	CSS	A	152	1	-	1/1/5/7	-
1	CSS	A	163	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	163	CSS	N-CA-CB-SG
1	A	152	CSS	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 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	$\# Z > 2$
5	SO4	A	1384	-	4,4,4	0.14	0	6,6,6	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	B	1381	-	4,4,4	0.27	0	6,6,6	0.12	0
5	SO4	C	1385	-	4,4,4	0.26	0	6,6,6	0.39	0
3	GSP	B	1379	2	33,34,34	1.44	2 (6%)	47,54,54	1.64	11 (23%)
5	SO4	C	1383	-	4,4,4	0.26	0	6,6,6	0.22	0
3	GSP	C	1382	2	33,34,34	1.78	4 (12%)	47,54,54	1.77	10 (21%)
3	GSP	A	1382	2	33,34,34	1.49	3 (9%)	47,54,54	1.72	9 (19%)
5	SO4	C	1384	-	4,4,4	0.22	0	6,6,6	0.20	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 Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GSP	C	1382	2	-	2/21/38/38	0/3/3/3
3	GSP	A	1382	2	-	2/21/38/38	0/3/3/3
3	GSP	B	1379	2	-	2/21/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1382	GSP	PG-S1G	-8.34	1.72	1.90
3	B	1379	GSP	PG-S1G	-6.38	1.76	1.90
3	A	1382	GSP	PG-S1G	-5.57	1.78	1.90
3	A	1382	GSP	PB-O3B	4.47	1.64	1.59
3	B	1379	GSP	PB-O3B	2.60	1.62	1.59
3	C	1382	GSP	C2-N3	2.58	1.39	1.33
3	A	1382	GSP	C2-N3	2.24	1.38	1.33
3	C	1382	GSP	PB-O3B	2.20	1.61	1.59
3	C	1382	GSP	PA-O3A	2.06	1.61	1.59

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1382	GSP	C5-C4-N3	-5.13	120.23	128.39
3	A	1382	GSP	C5-C4-N3	-4.95	120.52	128.39
3	A	1382	GSP	C2-N3-C4	4.89	120.72	112.30
3	C	1382	GSP	C2-N3-C4	4.81	120.58	112.30
3	B	1379	GSP	C2-N3-C4	4.23	119.58	112.30
3	B	1379	GSP	C5-C4-N3	-4.01	122.02	128.39
3	C	1382	GSP	N9-C4-N3	3.58	133.10	125.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1382	GSP	N9-C4-N3	3.54	133.03	125.95
3	B	1379	GSP	N9-C8-N7	-3.42	107.07	113.40
3	C	1382	GSP	C2-N1-C6	-3.17	119.36	125.11
3	A	1382	GSP	C2-N1-C6	-3.06	119.56	125.11
3	C	1382	GSP	N9-C8-N7	-2.98	107.88	113.40
3	A	1382	GSP	C5-C6-N1	2.93	120.71	113.25
3	A	1382	GSP	N9-C8-N7	-2.93	107.97	113.40
3	B	1379	GSP	N9-C4-N3	2.85	131.66	125.95
3	C	1382	GSP	O6-C6-C5	-2.85	119.02	126.53
3	C	1382	GSP	C5-C6-N1	2.83	120.44	113.25
3	B	1379	GSP	C8-N7-C5	2.81	109.27	104.26
3	C	1382	GSP	C8-N7-C5	2.67	109.02	104.26
3	A	1382	GSP	C8-N7-C5	2.64	108.96	104.26
3	C	1382	GSP	O2B-PB-O3B	2.45	113.90	107.27
3	B	1379	GSP	C2-N1-C6	-2.42	120.72	125.11
3	B	1379	GSP	O6-C6-C5	-2.35	120.34	126.53
3	A	1382	GSP	O6-C6-C5	-2.25	120.60	126.53
3	B	1379	GSP	C5-C6-N1	2.25	118.97	113.25
3	B	1379	GSP	O3'-C3'-C4'	-2.24	104.64	111.08
3	B	1379	GSP	O2B-PB-O3B	2.17	113.14	107.27
3	C	1382	GSP	O3G-PG-O3B	2.16	111.86	104.64
3	A	1382	GSP	O2A-PA-O3A	2.09	112.92	107.27
3	B	1379	GSP	O2B-PB-O3A	2.08	112.90	107.27

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1382	GSP	PA-O3A-PB-O1B
3	B	1379	GSP	PA-O3A-PB-O2B
3	C	1382	GSP	PA-O3A-PB-O2B
3	B	1379	GSP	PA-O3A-PB-O1B
3	A	1382	GSP	PA-O3A-PB-O2B
3	C	1382	GSP	PA-O3A-PB-O1B

There are no ring outliers.

3 monomers are involved in 3 short contacts:

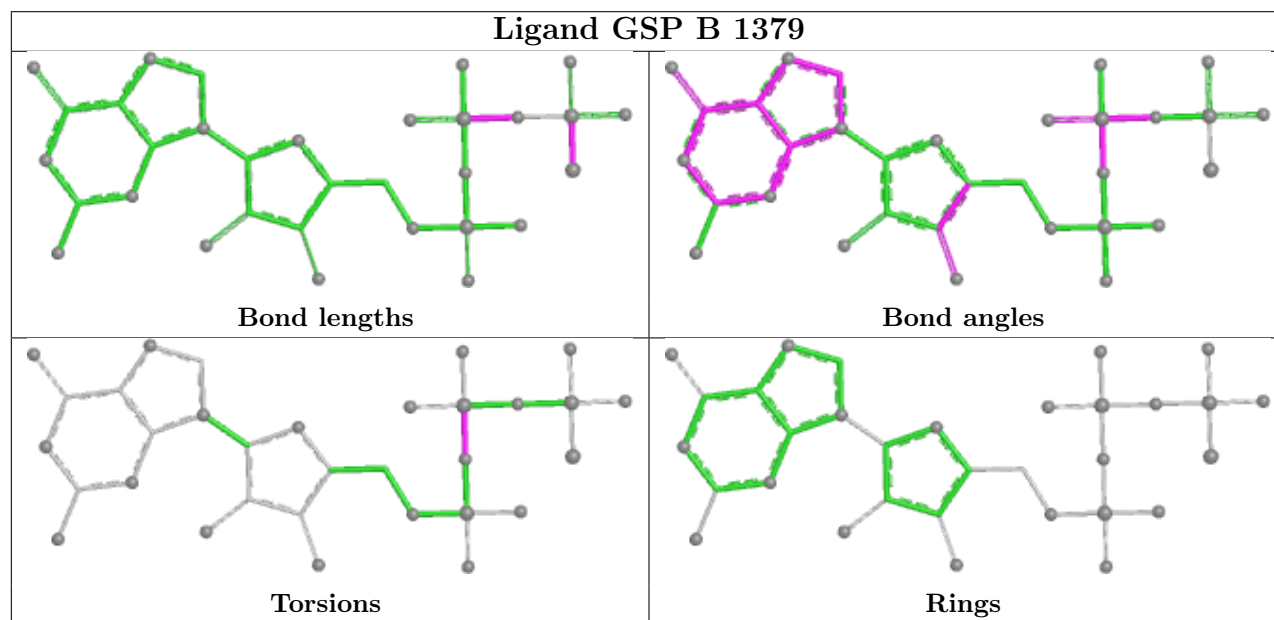
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1379	GSP	1	0
3	C	1382	GSP	1	0

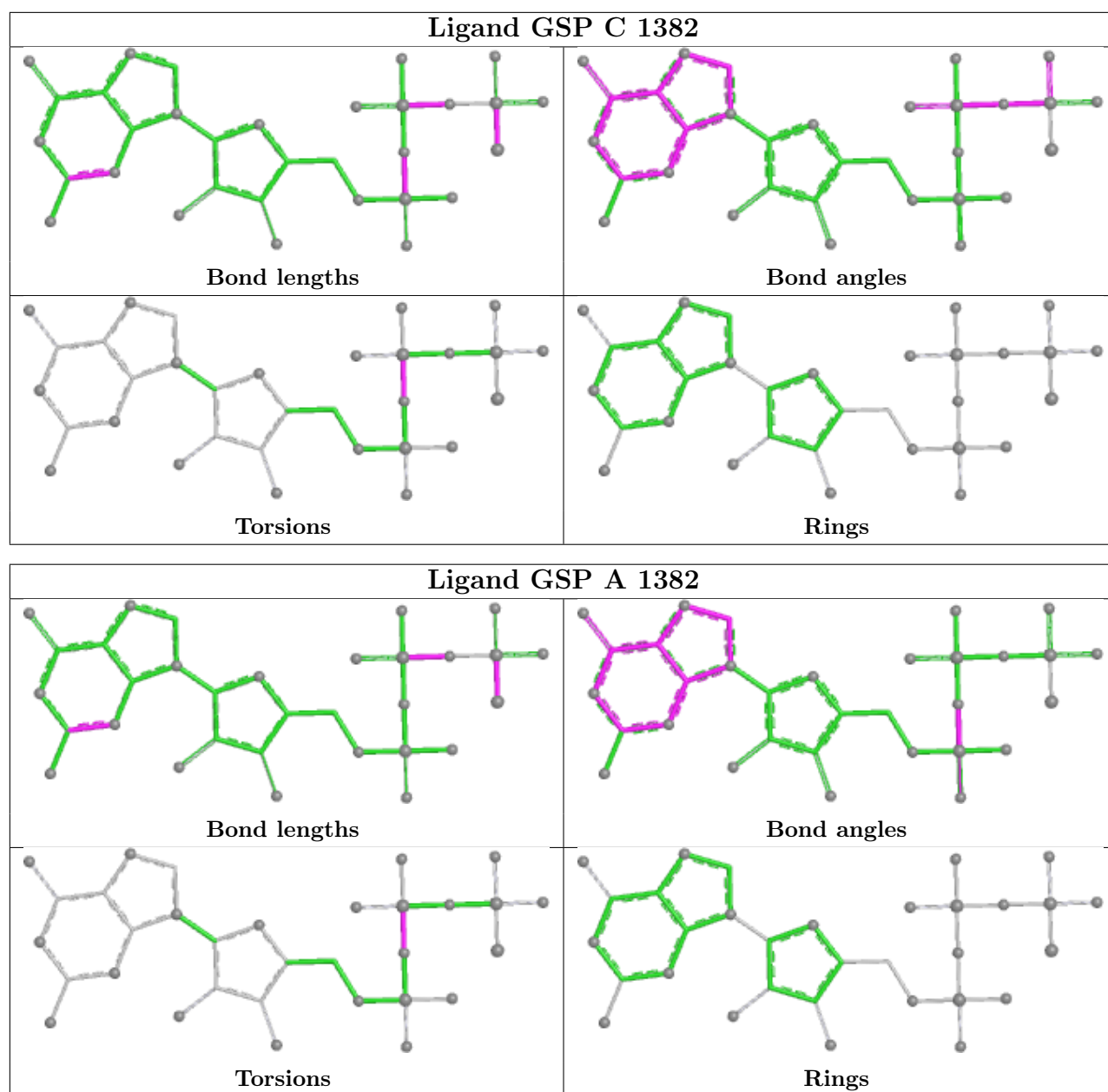
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1382	GSP	1	0

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

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	341/354 (96%)	0.03	16 (4%) 36 42	14, 31, 68, 86	3 (0%)
1	B	290/354 (81%)	0.26	22 (7%) 20 24	18, 36, 88, 105	0
1	C	269/354 (75%)	0.80	50 (18%) 3 3	20, 51, 105, 122	0
All	All	900/1062 (84%)	0.33	88 (9%) 13 16	14, 38, 92, 122	3 (0%)

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	158	LEU	7.0
1	C	380	ALA	5.6
1	B	129	PRO	5.6
1	A	204	VAL	5.2
1	C	73	SER	5.1
1	C	160	VAL	5.0
1	B	161	PRO	4.7
1	B	96	PHE	4.5
1	A	380	ALA	4.4
1	B	151	THR	4.4
1	C	135	ILE	4.3
1	B	377	LEU	4.2
1	C	88	LEU	4.2
1	C	377	LEU	4.2
1	C	141	THR	4.2
1	C	143	TRP	4.1
1	C	165	LYS	4.0
1	C	90	HIS	3.8
1	C	180	ILE	3.7
1	C	75	VAL	3.6
1	A	113	ILE	3.6
1	C	177	ILE	3.6
1	A	101	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	74	TYR	3.5
1	C	89	LEU	3.5
1	C	159	GLN	3.4
1	C	179	TYR	3.3
1	C	203	PRO	3.2
1	C	164	THR	3.2
1	A	112	SER	3.2
1	C	60	LEU	3.1
1	C	144	LYS	3.1
1	A	114	ALA	3.1
1	C	172	LYS	3.1
1	C	139	ILE	3.0
1	C	62	PHE	3.0
1	C	64	THR	3.0
1	A	377	LEU	2.9
1	C	134	ASP	2.9
1	C	378	LEU	2.9
1	A	123	GLY	2.8
1	A	107	MET	2.8
1	C	38	ILE	2.8
1	C	196	VAL	2.8
1	B	180	ILE	2.7
1	C	199	ILE	2.7
1	B	88	LEU	2.6
1	C	181	PRO	2.6
1	C	136	ALA	2.5
1	B	177	ILE	2.5
1	B	89	LEU	2.5
1	B	147	ALA	2.5
1	C	142	LEU	2.5
1	C	83	TYR	2.5
1	B	345	ASP	2.5
1	B	77	VAL	2.4
1	A	33	GLY	2.4
1	B	135	ILE	2.4
1	B	203	PRO	2.4
1	C	85	THR	2.4
1	A	61	LEU	2.4
1	A	231	HIS	2.4
1	A	32	MET	2.3
1	B	148	ILE	2.3
1	C	84	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	162	ASP	2.3
1	C	194	THR	2.3
1	B	131	LEU	2.3
1	A	125	ARG	2.3
1	C	86	ILE	2.3
1	A	62	PHE	2.2
1	C	174	LEU	2.2
1	B	178	ASN	2.2
1	B	90	HIS	2.2
1	C	171	LEU	2.2
1	C	61	LEU	2.1
1	C	313	VAL	2.1
1	B	132	THR	2.1
1	C	167	LEU	2.1
1	C	297	LEU	2.1
1	C	197	VAL	2.1
1	C	231	HIS	2.1
1	C	173	ARG	2.1
1	B	365	PHE	2.1
1	C	257	GLN	2.1
1	B	93	THR	2.0
1	A	110	SER	2.0
1	B	38	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSS	C	163	7/8	0.85	0.14	82,84,87,87	0
1	CSS	B	163	7/8	0.89	0.12	59,61,63,63	0
1	CSS	A	152	7/8	0.91	0.10	42,43,46,48	0
1	CSS	A	163	7/8	0.95	0.07	34,35,36,37	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

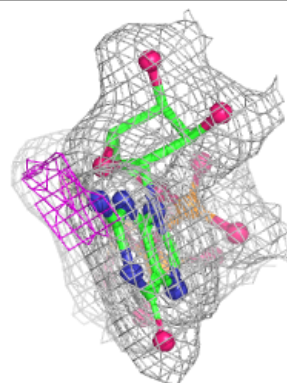
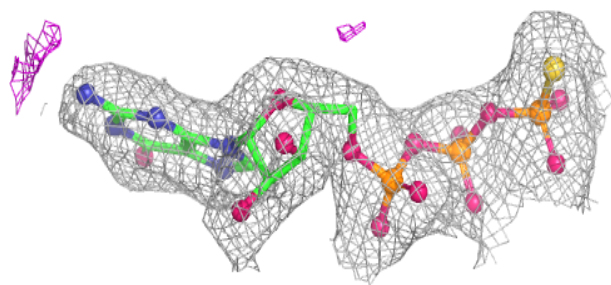
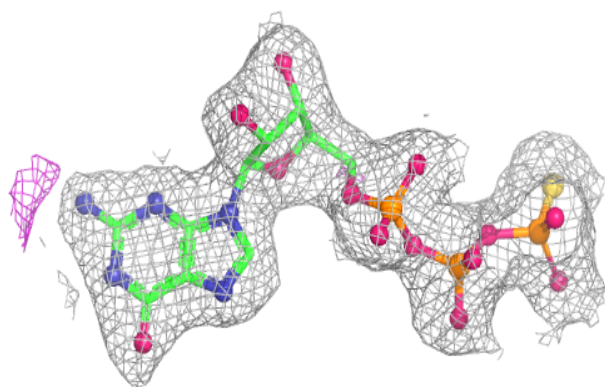
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	B	1381	5/5	0.77	0.13	79,79,79,80	0
5	SO4	C	1383	5/5	0.80	0.11	81,82,82,83	0
5	SO4	C	1385	5/5	0.84	0.21	71,72,72,72	0
4	CL	C	1386	1/1	0.86	0.22	85,85,85,85	0
5	SO4	C	1384	5/5	0.89	0.14	65,66,67,67	0
4	CL	B	1382	1/1	0.91	0.14	68,68,68,68	0
4	CL	B	1380	1/1	0.91	0.12	76,76,76,76	0
5	SO4	A	1384	5/5	0.95	0.13	45,45,46,46	0
4	CL	A	1383	1/1	0.96	0.17	49,49,49,49	0
2	MG	C	1381	1/1	0.97	0.04	44,44,44,44	0
2	MG	A	1381	1/1	0.98	0.03	18,18,18,18	0
3	GSP	A	1382	32/32	0.98	0.05	20,26,35,38	0
3	GSP	C	1382	32/32	0.98	0.06	34,38,44,48	0
2	MG	B	1378	1/1	0.99	0.01	25,25,25,25	0
3	GSP	B	1379	32/32	0.99	0.04	20,23,31,34	0

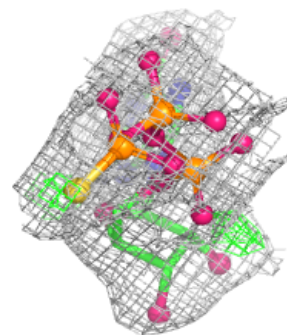
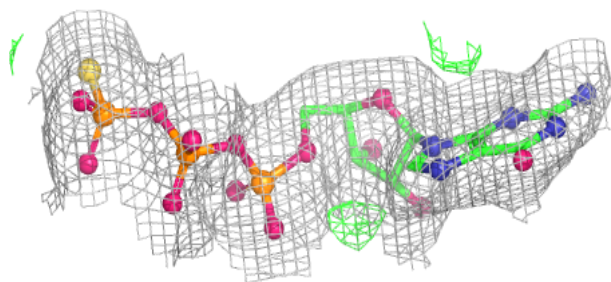
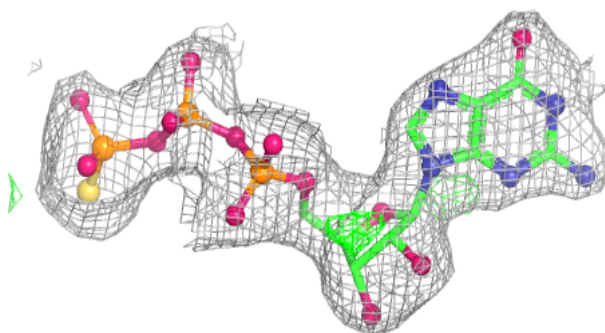
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

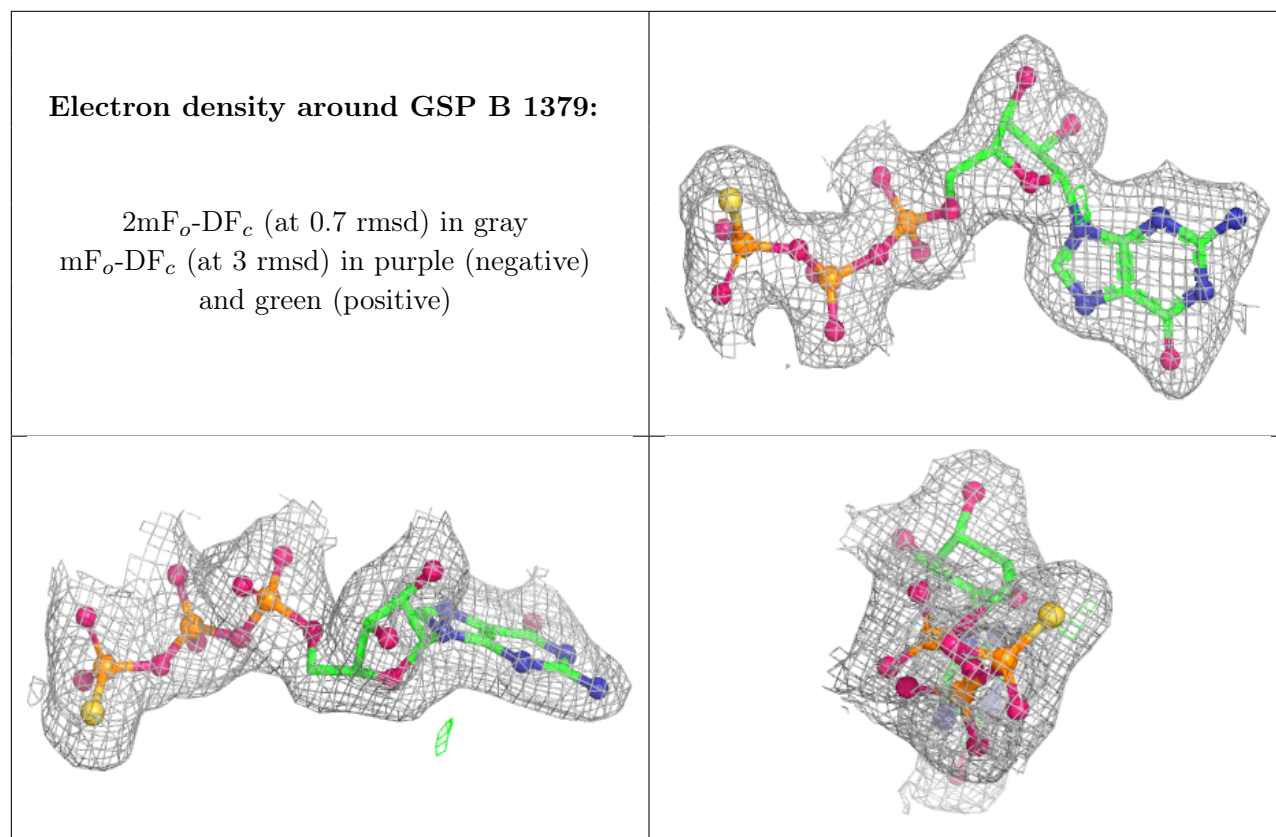
Electron density around GSP A 1382:

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

**Electron density around GSP C 1382:**

$2mF_o-DF_c$ (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.