Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 10:25 AM EST

PDB ID	:	1QG4
Title	:	CANINE GDP-RAN F72Y MUTANT
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Deposited on	:	1999-04-20
Resolution	:	2.50 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 (i) 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 (1)) were used in the production of this report:

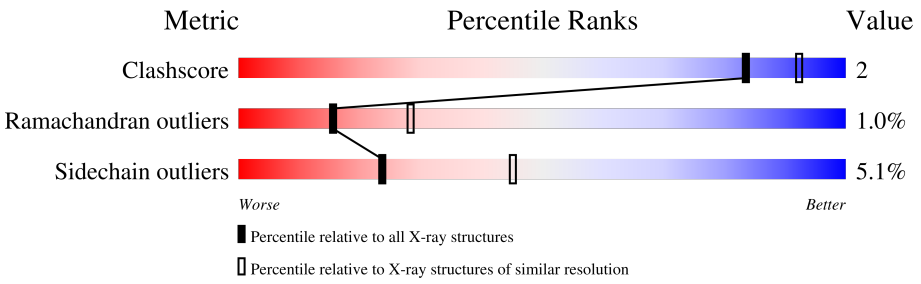
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	216	83% 10% • 6%
1	B	216	82% 14% • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3559 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 PROTEIN (RAN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	202	1613	1045	278	284	6	0	0	0
1	B	215	1703	1098	291	308	6	0	0	0

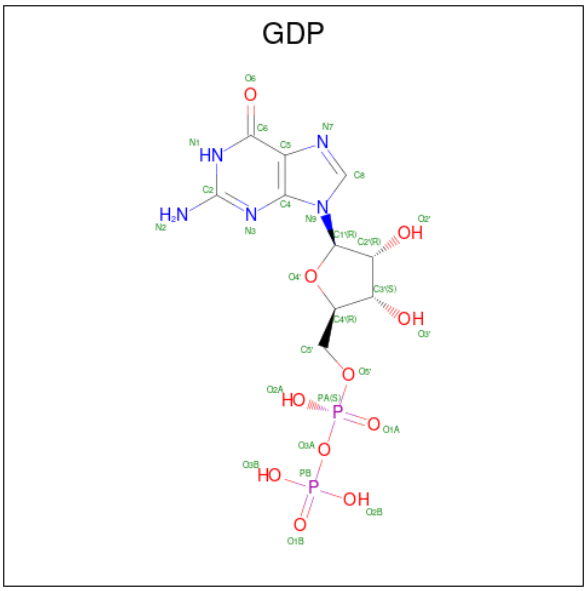
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	TYR	PHE	engineered mutation	UNP P62825
B	72	TYR	PHE	engineered mutation	UNP P62825

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- 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
			Total	C	N	O	P		
3	A	1	28	10	5	11	2	0	0
			Total	C	N	O	P		
3	B	1	28	10	5	11	2	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	96	96	96	0	0
			Total	O		
4	B	89	89	89	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. 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. 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.

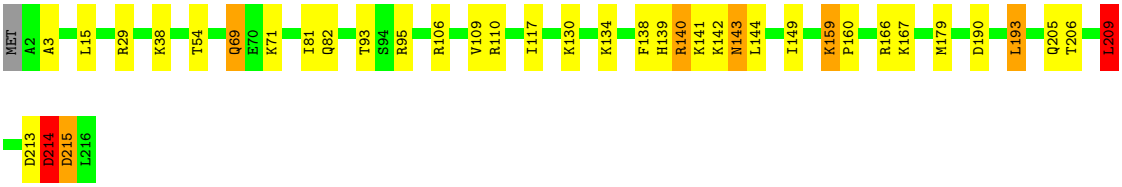
Note EDS was not executed.

• Molecule 1: PROTEIN (RAN)

Chain A:

• Molecule 1: PROTEIN (RAN)

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	60.52Å 60.17Å 61.44Å 90.00° 101.77° 90.00°	Depositor
Resolution (Å)	6.00 – 2.50	Depositor
% Data completeness (in resolution range)	94.7 (6.00-2.50)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.174 , 0.237	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3559	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

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: MG, GDP

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	0.56	0/1654	1.37	8/2245 (0.4%)
1	B	0.58	0/1745	1.39	10/2370 (0.4%)
All	All	0.57	0/3399	1.38	18/4615 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
All	All	0	8

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	29	ARG	NE-CZ-NH1	-9.99	115.31	120.30
1	A	129	ARG	CD-NE-CZ	8.38	135.33	123.60
1	B	209	LEU	CA-CB-CG	7.26	132.01	115.30
1	A	91	ASP	CB-CG-OD1	6.30	123.97	118.30
1	B	190	ASP	CB-CG-OD1	6.12	123.81	118.30
1	A	148	ASP	CB-CG-OD1	5.73	123.45	118.30
1	B	95	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	B	110	ARG	CD-NE-CZ	5.52	131.33	123.60
1	B	166	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	A	190	ASP	CB-CG-OD1	5.48	123.23	118.30
1	B	179	MET	CA-CB-CG	5.46	122.58	113.30
1	B	69	GLN	CA-CB-CG	5.38	125.24	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	109	VAL	O-C-N	-5.38	114.09	122.70
1	A	77	ASP	CB-CG-OD1	5.27	123.05	118.30
1	A	197	TYR	CB-CG-CD2	-5.18	117.89	121.00
1	A	129	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	A	18	ASP	CB-CG-OD1	5.06	122.86	118.30
1	B	193	LEU	CA-CB-CG	5.05	126.92	115.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	116	PRO	Mainchain
1	A	171	ASP	Mainchain
1	A	27	VAL	Mainchain
1	A	54	THR	Mainchain
1	B	3	ALA	Mainchain
1	B	54	THR	Mainchain
1	B	69	GLN	Mainchain
1	B	71	LYS	Mainchain

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	1613	0	1615	7	0
1	B	1703	0	1688	10	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	28	0	12	1	0
3	B	28	0	12	0	0
4	A	96	0	0	0	0
4	B	89	0	0	0	0
All	All	3559	0	3327	16	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 2.

All (16) 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:139:HIS:O	1:B:140:ARG:HB2	1.93	0.68
1:A:134:LYS:HD2	1:B:215:ASP:HB3	1.84	0.59
1:B:143:ASN:HD21	1:B:167:LYS:HE2	1.67	0.58
1:B:140:ARG:HA	1:B:144:LEU:HD22	1.88	0.56
1:B:213:ASP:O	1:B:214:ASP:HB2	2.08	0.54
1:B:81:ILE:O	1:B:82:GLN:HB2	2.11	0.49
1:B:206:THR:HA	1:B:209:LEU:HD22	1.97	0.46
1:A:137:VAL:HG22	1:A:205:GLN:HE22	1.80	0.46
1:A:158:GLU:H	1:A:158:GLU:HG3	1.53	0.45
1:A:103:ASN:O	1:A:106:ARG:HD3	2.17	0.45
1:B:117:ILE:O	1:B:144:LEU:HA	2.19	0.43
1:B:159:LYS:HB2	1:B:160:PRO:HD3	2.01	0.43
1:A:183:ALA:HA	1:A:184:PRO:HD3	1.94	0.42
1:A:123:LYS:HE2	3:A:220:GDP:N9	2.35	0.41
1:A:103:ASN:HB3	1:A:106:ARG:HH11	1.84	0.41
1:B:93:THR:HA	1:B:130:LYS:HG2	2.02	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	200/216 (93%)	192 (96%)	8 (4%)	0	100 100
1	B	213/216 (99%)	197 (92%)	12 (6%)	4 (2%)	8 13
All	All	413/432 (96%)	389 (94%)	20 (5%)	4 (1%)	15 28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	140	ARG

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Mol	Chain	Res	Type
1	B	214	ASP
1	B	215	ASP
1	B	142	LYS

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	171/185 (92%)	166 (97%)	5 (3%)	42	69
1	B	180/185 (97%)	167 (93%)	13 (7%)	14	28
All	All	351/370 (95%)	333 (95%)	18 (5%)	24	45

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	106	ARG
1	A	143	ASN
1	A	158	GLU
1	A	196	GLN
1	B	15	LEU
1	B	38	LYS
1	B	106	ARG
1	B	134	LYS
1	B	138	PHE
1	B	141	LYS
1	B	143	ASN
1	B	149	ILE
1	B	159	LYS
1	B	193	LEU
1	B	205	GLN
1	B	209	LEU
1	B	214	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	62	ASN
1	A	103	ASN
1	B	10	GLN
1	B	62	ASN
1	B	103	ASN
1	B	143	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
3	GDP	A	220	2	24,30,30	1.31	4 (16%)	30,47,47	1.47	6 (20%)
3	GDP	B	220	2	24,30,30	1.33	3 (12%)	30,47,47	1.85	6 (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
3	GDP	A	220	2	-	0/12/32/32	0/3/3/3
3	GDP	B	220	2	-	1/12/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	220	GDP	PB-O3B	-3.18	1.42	1.54
3	A	220	GDP	C2'-C1'	3.05	1.58	1.53
3	A	220	GDP	C5-C6	-2.55	1.42	1.47
3	A	220	GDP	PB-O3B	-2.29	1.46	1.54
3	B	220	GDP	O4'-C1'	2.25	1.44	1.41
3	A	220	GDP	C8-N7	-2.17	1.31	1.35
3	B	220	GDP	C5-C6	-2.14	1.43	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	220	GDP	PA-O3A-PB	4.91	149.69	132.83
3	A	220	GDP	O4'-C1'-C2'	-4.29	100.66	106.93
3	B	220	GDP	O2B-PB-O3A	4.07	118.29	104.64
3	B	220	GDP	O6-C6-N1	-3.90	116.04	120.65
3	B	220	GDP	O6-C6-C5	3.41	131.04	124.37
3	A	220	GDP	O3B-PB-O3A	2.87	114.25	104.64
3	A	220	GDP	O6-C6-C5	2.71	129.66	124.37
3	B	220	GDP	O4'-C1'-C2'	-2.55	103.20	106.93
3	A	220	GDP	O6-C6-N1	-2.52	117.68	120.65
3	A	220	GDP	O2'-C2'-C1'	2.33	119.46	110.85
3	B	220	GDP	O2'-C2'-C1'	2.15	118.81	110.85
3	A	220	GDP	C5-C6-N1	-2.10	110.25	113.95

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	220	GDP	PB-O3A-PA-O2A

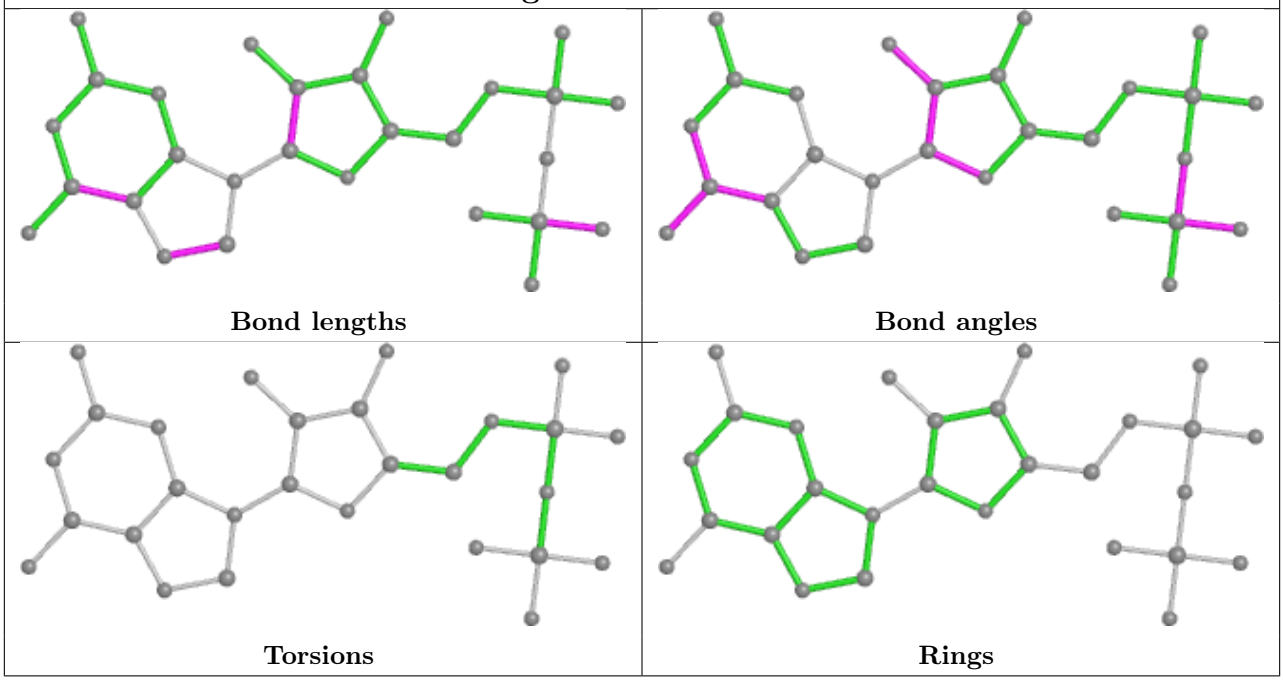
There are no ring outliers.

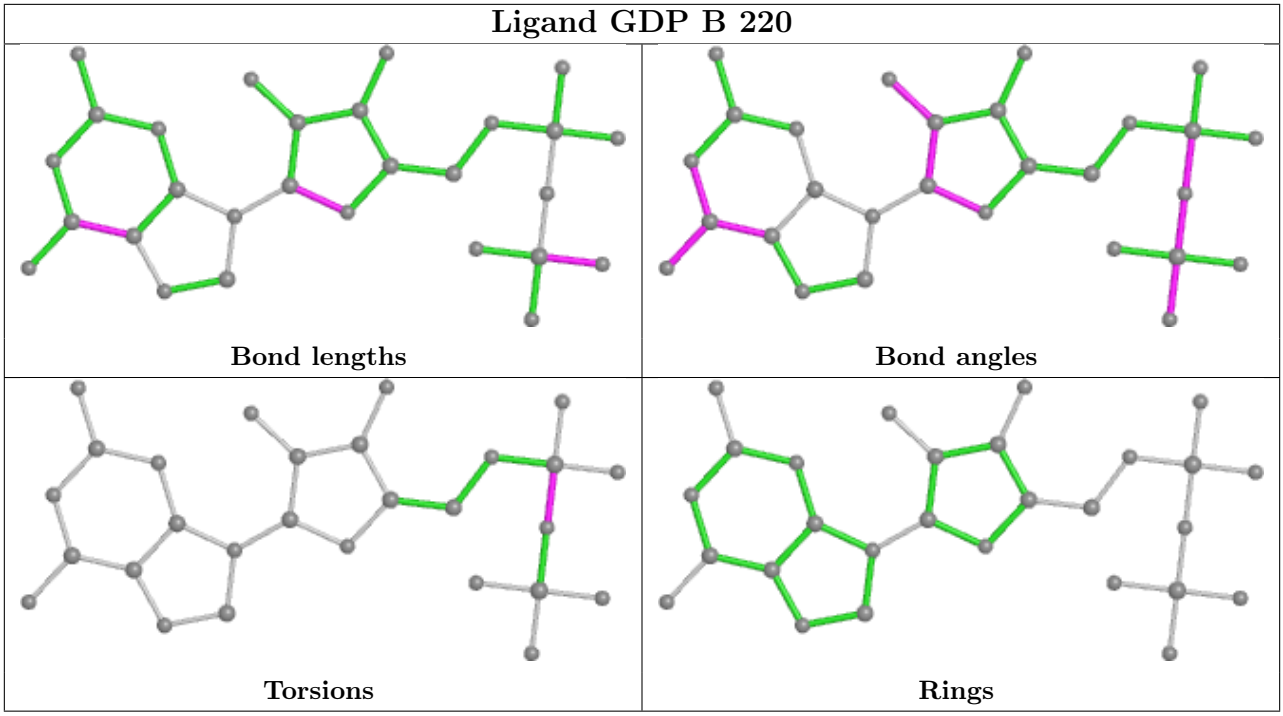
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	220	GDP	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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GDP A 220





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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.