



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 1FTN / pdb_00001ftn
Title : CRYSTAL STRUCTURE OF THE HUMAN RHOA/GDP COMPLEX
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Deposited on : 1997-03-13
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

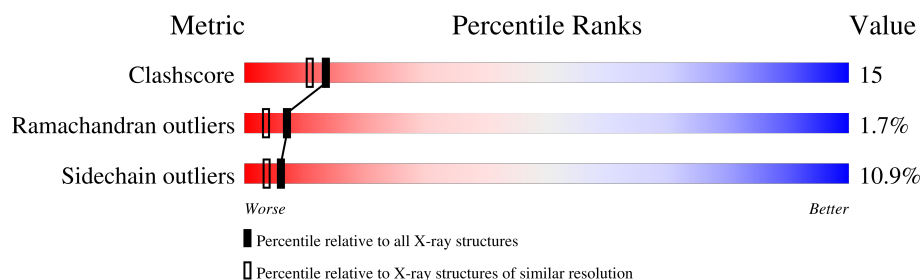
1 Overall quality at a glance

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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	193	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1653 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 TRANSFORMING PROTEIN RHOA (H12).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	26	0	0
			1405	886	239	270	10			

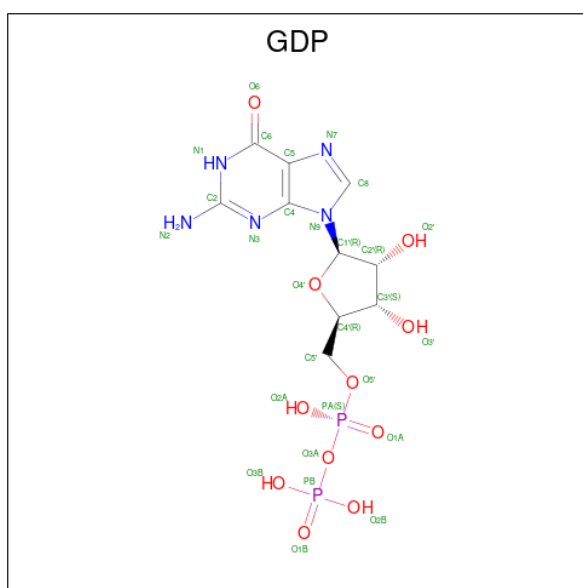
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	ASN	PHE	engineered mutation	UNP P61586

- 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		

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	219	Total	O	0	0
			219	219		

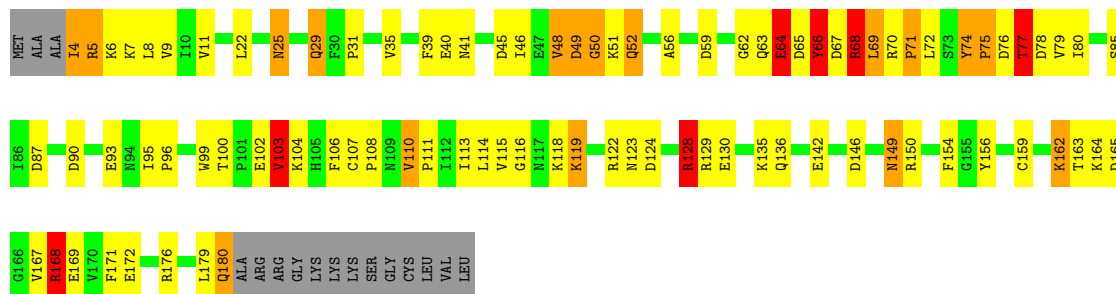
3 Residue-property plots [i](#)

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: TRANSFORMING PROTEIN RHOA (H12)

Chain A: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	31.92Å 65.96Å 83.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.10)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
Refinement program	SHELX-90	Depositor
R, R_{free}	0.186 , 0.304	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1653	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG

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	1.26	1/1432 (0.1%)	2.42	95/1937 (4.9%)

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	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	GLY	N-CA	5.45	1.52	1.44

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	ARG	CD-NE-CZ	14.48	144.68	124.40
1	A	5	ARG	CD-NE-CZ	13.99	143.99	124.40
1	A	65	ASP	CA-C-O	-10.31	108.65	120.20
1	A	65	ASP	CA-CB-CG	-9.34	103.26	112.60
1	A	49	ASP	CA-CB-CG	-9.33	103.27	112.60
1	A	11	VAL	CA-C-O	-8.50	112.74	121.67
1	A	78	ASP	CA-CB-CG	-8.45	104.15	112.60
1	A	122	ARG	NH1-CZ-NH2	8.30	130.09	119.30
1	A	106	PHE	CA-C-N	8.10	131.96	122.89
1	A	106	PHE	C-N-CA	8.10	131.96	122.89
1	A	122	ARG	NE-CZ-NH2	-7.83	112.16	119.20
1	A	35	VAL	CA-C-O	7.82	124.01	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	156	TYR	CA-C-O	-7.72	112.02	120.36
1	A	25	ASN	CA-CB-CG	-7.67	104.93	112.60
1	A	90	ASP	N-CA-CB	7.63	121.08	110.01
1	A	4	ILE	N-CA-CB	7.47	124.21	111.50
1	A	176	ARG	NE-CZ-NH2	-7.36	112.58	119.20
1	A	46	ILE	CB-CG1-CD1	7.31	129.15	113.80
1	A	150	ARG	NE-CZ-NH2	-7.27	112.65	119.20
1	A	77	THR	CA-CB-OG1	7.20	120.40	109.60
1	A	39	PHE	CA-CB-CG	7.12	120.92	113.80
1	A	129	ARG	N-CA-C	7.08	119.66	111.02
1	A	29	GLN	OE1-CD-NE2	7.02	129.62	122.60
1	A	154	PHE	CA-CB-CG	6.98	120.78	113.80
1	A	149	ASN	CA-CB-CG	-6.94	105.66	112.60
1	A	5	ARG	NE-CZ-NH2	-6.94	112.95	119.20
1	A	130	GLU	CA-C-O	-6.84	113.63	120.82
1	A	56	ALA	CA-C-N	-6.83	113.41	123.11
1	A	56	ALA	C-N-CA	-6.83	113.41	123.11
1	A	63	GLN	N-CA-C	-6.76	104.08	112.47
1	A	65	ASP	CA-C-N	6.71	134.35	121.54
1	A	65	ASP	C-N-CA	6.71	134.35	121.54
1	A	52	GLN	OE1-CD-NE2	-6.68	115.92	122.60
1	A	65	ASP	N-CA-C	6.64	120.25	111.75
1	A	113	ILE	N-CA-CB	6.63	118.97	111.21
1	A	6	LYS	O-C-N	-6.62	115.10	123.24
1	A	45	ASP	CA-CB-CG	-6.58	106.02	112.60
1	A	114	LEU	CA-C-N	-6.48	114.65	123.14
1	A	114	LEU	C-N-CA	-6.48	114.65	123.14
1	A	136	GLN	OE1-CD-NE2	-6.43	116.17	122.60
1	A	67	ASP	N-CA-C	-6.31	104.40	111.28
1	A	142	GLU	CB-CA-C	-6.19	100.51	110.79
1	A	6	LYS	CA-C-N	6.17	131.69	123.05
1	A	6	LYS	C-N-CA	6.17	131.69	123.05
1	A	50	GLY	N-CA-C	-6.11	102.14	111.24
1	A	171	PHE	CA-CB-CG	-6.09	107.71	113.80
1	A	63	GLN	CA-C-O	6.04	128.29	120.55
1	A	129	ARG	CD-NE-CZ	6.03	132.84	124.40
1	A	111	PRO	CA-C-N	6.00	130.62	123.19
1	A	111	PRO	C-N-CA	6.00	130.62	123.19
1	A	76	ASP	CA-C-N	-5.98	111.47	121.39
1	A	76	ASP	C-N-CA	-5.98	111.47	121.39
1	A	118	LYS	CG-CD-CE	5.98	125.04	111.30
1	A	167	VAL	N-CA-C	5.95	116.12	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	79	VAL	CA-C-O	-5.91	115.41	120.96
1	A	103	VAL	CA-CB-CG2	5.88	120.39	110.40
1	A	5	ARG	NE-CZ-NH1	5.86	127.36	121.50
1	A	176	ARG	CD-NE-CZ	5.86	132.60	124.40
1	A	31	PRO	O-C-N	-5.83	114.78	122.64
1	A	128	ARG	CB-CG-CD	5.80	124.64	111.30
1	A	75	PRO	CA-C-O	-5.77	115.03	121.32
1	A	74	TYR	O-C-N	-5.76	114.70	121.32
1	A	124	ASP	CA-C-O	5.76	127.61	121.16
1	A	119	LYS	CA-C-N	5.75	130.33	120.72
1	A	119	LYS	C-N-CA	5.75	130.33	120.72
1	A	162	LYS	N-CA-CB	5.73	118.64	110.16
1	A	49	ASP	N-CA-C	5.67	118.40	109.96
1	A	180	GLN	CG-CD-NE2	-5.65	107.92	116.40
1	A	68	ARG	NH1-CZ-NH2	-5.65	111.96	119.30
1	A	113	ILE	CA-C-O	-5.59	114.49	120.59
1	A	39	PHE	CA-C-O	-5.57	114.62	120.58
1	A	52	GLN	CA-C-O	-5.56	114.20	120.32
1	A	115	VAL	CA-C-N	-5.49	117.40	122.29
1	A	115	VAL	C-N-CA	-5.49	117.40	122.29
1	A	87	ASP	O-C-N	-5.49	115.31	122.39
1	A	163	THR	N-CA-C	-5.46	106.66	113.38
1	A	176	ARG	NE-CZ-NH1	5.38	126.88	121.50
1	A	68	ARG	NE-CZ-NH1	5.37	126.87	121.50
1	A	180	GLN	OE1-CD-NE2	5.37	127.97	122.60
1	A	77	THR	CB-CA-C	5.32	119.25	109.46
1	A	146	ASP	CA-CB-CG	-5.31	107.29	112.60
1	A	25	ASN	N-CA-CB	5.31	118.40	110.22
1	A	180	GLN	CB-CA-C	-5.30	100.03	110.10
1	A	128	ARG	CA-CB-CG	-5.26	103.58	114.10
1	A	154	PHE	N-CA-CB	-5.26	101.67	110.39
1	A	114	LEU	CA-C-O	-5.18	114.63	120.43
1	A	68	ARG	N-CA-C	-5.16	105.72	112.23
1	A	115	VAL	CA-C-O	-5.14	114.99	120.39
1	A	162	LYS	CA-C-O	-5.04	115.08	120.42
1	A	66	TYR	CA-C-O	5.02	127.68	120.51
1	A	52	GLN	CA-C-N	-5.01	116.63	123.10
1	A	52	GLN	C-N-CA	-5.01	116.63	123.10
1	A	103	VAL	N-CA-CB	5.01	119.84	110.77
1	A	102	GLU	N-CA-CB	5.00	117.26	110.01
1	A	159	CYS	CA-C-O	5.00	126.66	121.36

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	48	VAL	Peptide
1	A	49	ASP	Peptide
1	A	50	GLY	Peptide
1	A	62	GLY	Mainchain
1	A	64	GLU	Peptide

5.2 Too-close contacts ⓘ

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	1405	0	1396	41	0
2	A	1	0	0	0	0
3	A	28	0	12	0	0
4	A	219	0	0	16	1
All	All	1653	0	1408	41	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

All (41) 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:107:CYS:HB3	1:A:110:VAL:HG13	1.56	0.87
1:A:40:GLU:HG2	4:A:398:HOH:O	1.86	0.75
1:A:128:ARG:HH11	1:A:128:ARG:HG2	1.54	0.71
1:A:149:ASN:ND2	4:A:392:HOH:O	2.23	0.71
1:A:66:TYR:HA	4:A:370:HOH:O	1.90	0.70
1:A:68:ARG:NH2	4:A:463:HOH:O	2.26	0.68
1:A:66:TYR:OH	4:A:522:HOH:O	2.09	0.66
1:A:4:ILE:HG22	1:A:52:GLN:O	1.96	0.65
1:A:68:ARG:HD3	4:A:464:HOH:O	1.96	0.65
1:A:107:CYS:HB3	1:A:110:VAL:CG1	2.27	0.63
1:A:128:ARG:HG2	1:A:128:ARG:NH1	2.13	0.62
1:A:95:ILE:HB	1:A:96:PRO:HD3	1.81	0.61
1:A:168:ARG:HG2	4:A:403:HOH:O	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:ASN:ND2	4:A:491:HOH:O	2.33	0.60
1:A:135:LYS:NZ	4:A:442:HOH:O	2.30	0.60
1:A:7:LYS:HE2	1:A:77:THR:HG22	1.88	0.55
1:A:72:LEU:HD22	1:A:72:LEU:H	1.72	0.54
1:A:74:TYR:N	1:A:75:PRO:CD	2.72	0.53
1:A:128:ARG:HG3	4:A:443:HOH:O	2.08	0.52
1:A:119:LYS:NZ	1:A:165:ASP:OD2	2.26	0.51
1:A:100:THR:O	1:A:104:LYS:HG2	2.13	0.48
1:A:168:ARG:HE	1:A:168:ARG:CA	2.27	0.48
1:A:169:GLU:OE1	1:A:169:GLU:N	2.45	0.47
1:A:5:ARG:HD2	4:A:509:HOH:O	2.14	0.47
1:A:93:GLU:O	1:A:96:PRO:HD2	2.14	0.47
1:A:9:VAL:HB	1:A:80:ILE:HD13	1.97	0.46
1:A:8:LEU:C	1:A:8:LEU:HD23	2.41	0.46
1:A:99:TRP:O	1:A:103:VAL:HG13	2.16	0.46
1:A:74:TYR:O	1:A:75:PRO:C	2.59	0.45
1:A:22:LEU:CD1	1:A:59:ASP:HB2	2.46	0.44
1:A:40:GLU:HA	4:A:386:HOH:O	2.17	0.43
1:A:74:TYR:O	1:A:77:THR:HG23	2.19	0.43
1:A:172:GLU:HB3	4:A:485:HOH:O	2.19	0.43
1:A:95:ILE:HB	1:A:96:PRO:CD	2.49	0.42
1:A:70:ARG:HB3	1:A:71:PRO:HD3	2.01	0.42
1:A:108:PRO:HG3	4:A:503:HOH:O	2.19	0.42
1:A:69:LEU:HA	1:A:72:LEU:HD23	2.01	0.41
1:A:66:TYR:CA	4:A:370:HOH:O	2.59	0.41
1:A:68:ARG:HB2	4:A:525:HOH:O	2.21	0.40
1:A:51:LYS:CG	1:A:52:GLN:H	2.33	0.40
1:A:9:VAL:HG21	1:A:77:THR:HG21	2.02	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:368:HOH:O	4:A:422:HOH:O[4_455]	2.06	0.14

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	175/193 (91%)	164 (94%)	8 (5%)	3 (2%)	7 3

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	66	TYR
1	A	64	GLU

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	156/167 (93%)	139 (89%)	17 (11%)	6 4

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

Mol	Chain	Res	Type
1	A	29	GLN
1	A	48	VAL
1	A	64	GLU
1	A	68	ARG
1	A	69	LEU
1	A	71	PRO
1	A	77	THR
1	A	85	SER

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Mol	Chain	Res	Type
1	A	103	VAL
1	A	110	VAL
1	A	123	ASN
1	A	128	ARG
1	A	162	LYS
1	A	164	LYS
1	A	168	ARG
1	A	179	LEU
1	A	180	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	200	2	29,30,30	1.33	3 (10%)	45,47,47	1.29	6 (13%)

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	200	2	-	0/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	200	GDP	PA-O3A	3.29	1.63	1.59
3	A	200	GDP	C5-C4	-2.99	1.30	1.38
3	A	200	GDP	PB-O1B	2.76	1.59	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	200	GDP	O2'-C2'-C1'	-3.26	98.87	110.10
3	A	200	GDP	O3B-PB-O1B	2.85	121.93	110.83
3	A	200	GDP	O2B-PB-O3A	-2.54	96.10	104.64
3	A	200	GDP	O2A-PA-O1A	2.06	122.02	112.44
3	A	200	GDP	O4'-C1'-C2'	-2.06	102.21	106.62
3	A	200	GDP	C6-C5-N7	-2.00	126.65	130.29

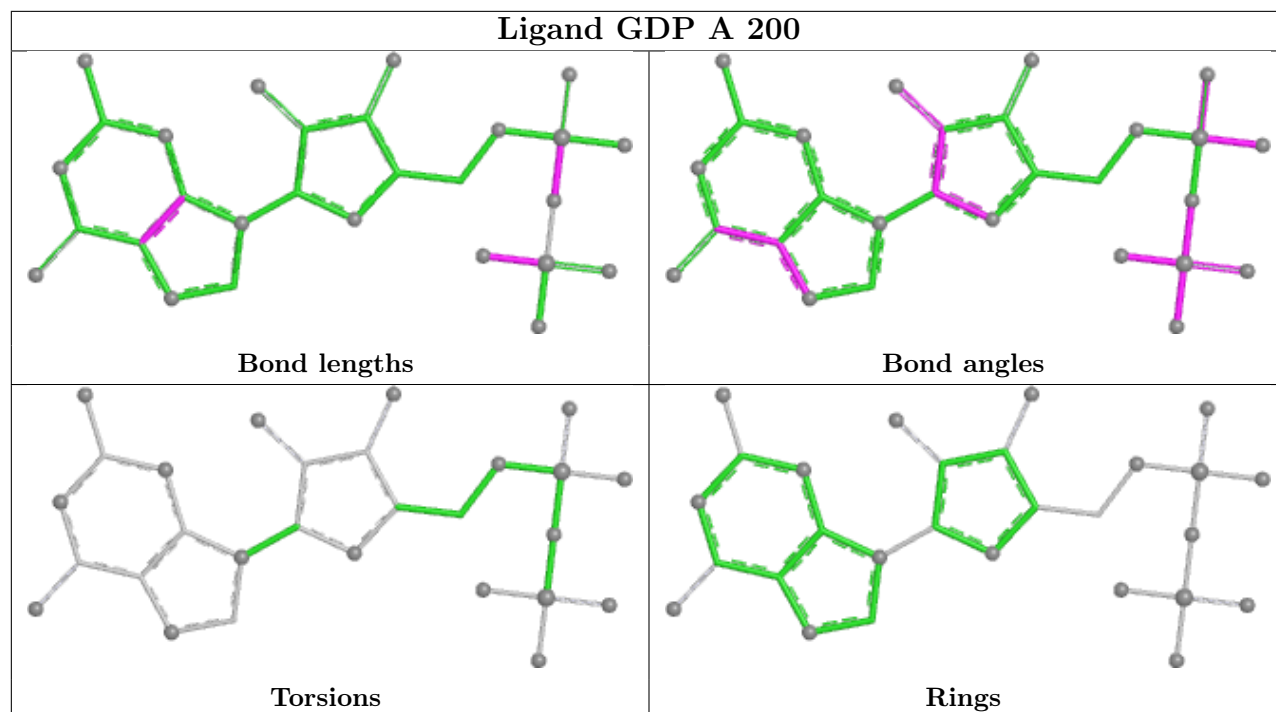
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.