



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2023 – 09:49 AM EDT

PDB ID : 1R5N
Title : Crystal Structure Analysis of sup35 complexed with GDP
Authors : Kong, C.; Song, H.
Deposited on : 2003-10-10
Resolution : 2.90 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

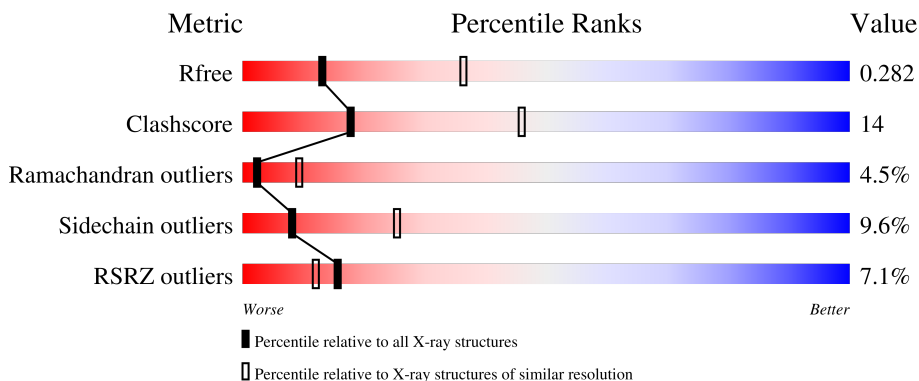
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	467	

2 Entry composition i

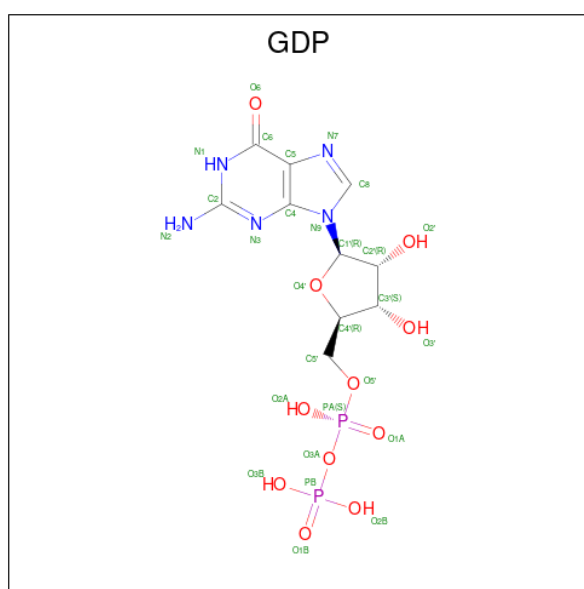
There are 3 unique types of molecules in this entry. The entry contains 3316 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Eukaryotic peptide chain release factor GTP-binding subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	408	3213	2019	556	619	19	0	0	0

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

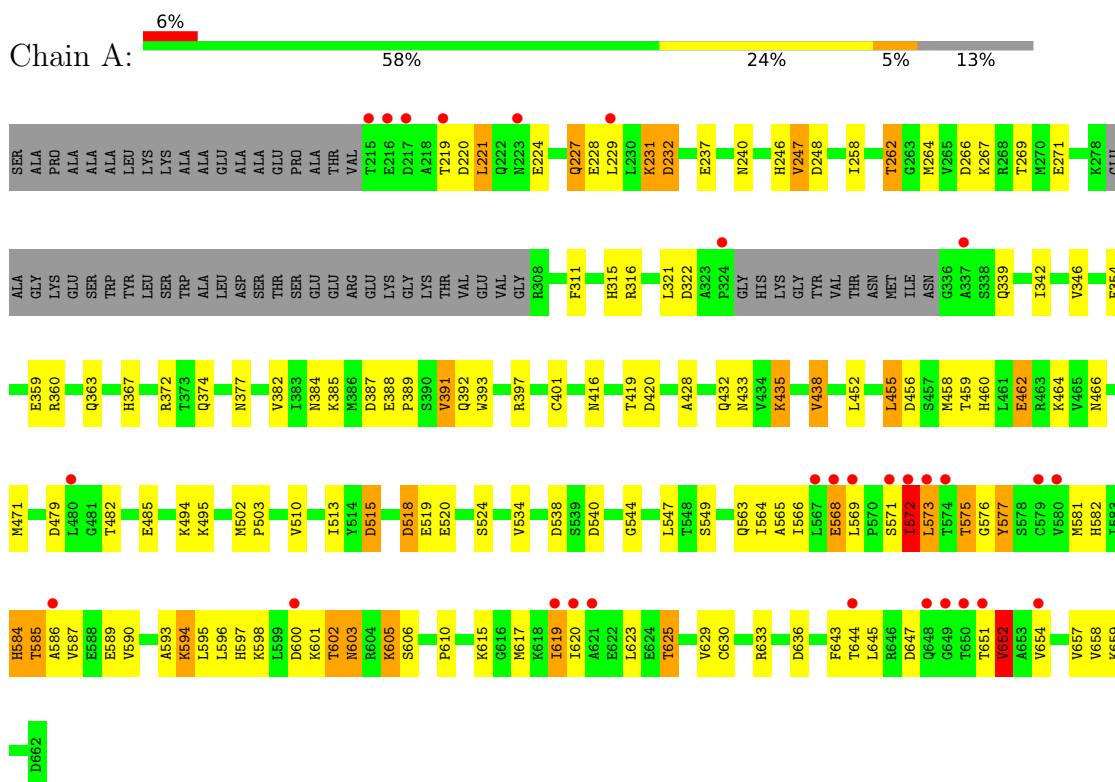
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total	O	0	0
			75	75		

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: Eukaryotic peptide chain release factor GTP-binding subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	82.76Å 82.76Å 169.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 46.61 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.90) 100.0 (46.61-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.256 , 0.284 0.257 , 0.282	Depositor DCC
R_{free} test set	852 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	63.8	Xtrriage
Anisotropy	0.228	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3316	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: 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	0.46	0/3264	0.76	9/4400 (0.2%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	647	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	538	ASP	CB-CG-OD2	6.20	123.88	118.30
1	A	232	ASP	CB-CG-OD2	5.69	123.42	118.30
1	A	387	ASP	CB-CG-OD2	5.55	123.30	118.30
1	A	540	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	518	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	322	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	515	ASP	CB-CG-OD2	5.07	122.86	118.30
1	A	636	ASP	CB-CG-OD2	5.05	122.84	118.30

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	3213	0	3228	88	0
2	A	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	75	0	0	10	0
All	All	3316	0	3240	88	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 14.

All (88) 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:598:LYS:HA	1:A:619:ILE:HG22	1.63	0.80
1:A:228:GLU:O	1:A:231:LYS:NZ	2.16	0.74
1:A:433:ASN:HB2	1:A:438:VAL:HG13	1.69	0.72
1:A:455:LEU:HA	1:A:458:MET:HE2	1.74	0.68
1:A:494:LYS:O	1:A:513:ILE:HD11	1.94	0.68
1:A:384:ASN:HD21	1:A:428:ALA:H	1.42	0.67
1:A:246:HIS:ND1	1:A:247:VAL:HG23	2.09	0.67
1:A:372:ARG:NH1	1:A:377:ASN:HD22	1.94	0.66
1:A:593:ALA:O	1:A:594:LYS:HB2	1.98	0.63
1:A:544:GLY:HA3	1:A:586:ALA:HA	1.81	0.61
1:A:392:GLN:N	3:A:24:HOH:O	2.27	0.60
1:A:393:TRP:CZ3	1:A:438:VAL:HG11	2.36	0.60
1:A:384:ASN:ND2	1:A:385:LYS:H	2.00	0.59
1:A:544:GLY:CA	1:A:586:ALA:HA	2.32	0.59
1:A:372:ARG:HH11	1:A:377:ASN:HD22	1.51	0.59
1:A:420:ASP:HB3	3:A:35:HOH:O	2.02	0.58
1:A:435:LYS:HA	1:A:452:LEU:HD12	1.84	0.58
1:A:581:MET:HE2	1:A:643:PHE:CG	2.39	0.58
1:A:510:VAL:HA	1:A:534:VAL:HG12	1.86	0.58
1:A:262:THR:HG21	1:A:311:PHE:HB2	1.85	0.58
1:A:644:THR:HG22	1:A:654:VAL:HG12	1.88	0.55
1:A:393:TRP:CH2	1:A:438:VAL:HG11	2.41	0.55
1:A:372:ARG:HH11	1:A:377:ASN:ND2	2.05	0.54
1:A:246:HIS:NE2	1:A:363:GLN:HG2	2.23	0.54
1:A:593:ALA:O	1:A:594:LYS:CB	2.55	0.54
1:A:602:THR:O	1:A:603:ASN:C	2.46	0.53
1:A:224:GLU:O	3:A:59:HOH:O	2.18	0.53
1:A:266:ASP:OD2	1:A:269:THR:N	2.34	0.53
1:A:246:HIS:CE1	1:A:363:GLN:HG2	2.44	0.52
1:A:240:ASN:HB3	1:A:321:LEU:HD11	1.90	0.52
1:A:460:HIS:HE1	1:A:462:GLU:OE2	1.94	0.51
1:A:597:HIS:HB2	1:A:620:ILE:HG12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:ILE:HD13	1:A:458:MET:HE1	1.93	0.50
1:A:267:LYS:O	1:A:271:GLU:HG3	2.11	0.50
1:A:363:GLN:HG3	1:A:367:HIS:CE1	2.47	0.50
1:A:633:ARG:HG3	3:A:41:HOH:O	2.12	0.50
1:A:584:HIS:O	1:A:585:THR:HB	2.11	0.50
1:A:582:HIS:O	1:A:643:PHE:HA	2.12	0.49
1:A:227:GLN:HE21	1:A:229:LEU:HB3	1.78	0.49
1:A:571:SER:O	1:A:572:ILE:HB	2.12	0.49
1:A:590:VAL:HG21	1:A:623:LEU:HD23	1.93	0.49
1:A:246:HIS:HE2	1:A:363:GLN:H	1.59	0.48
1:A:346:VAL:HA	1:A:382:VAL:HG12	1.95	0.48
1:A:416:ASN:ND2	1:A:419:THR:OG1	2.46	0.48
1:A:224:GLU:HG2	1:A:644:THR:CG2	2.44	0.48
1:A:566:ILE:HG22	1:A:615:LYS:HA	1.94	0.48
1:A:460:HIS:CE1	1:A:462:GLU:OE2	2.67	0.47
1:A:651:THR:O	1:A:652:VAL:HG13	2.14	0.47
1:A:315:HIS:HD2	1:A:456:ASP:OD2	1.98	0.47
1:A:372:ARG:NH1	1:A:377:ASN:ND2	2.62	0.47
1:A:339:GLN:NE2	1:A:374:GLN:O	2.48	0.46
1:A:590:VAL:CG2	1:A:623:LEU:HD23	2.45	0.46
1:A:581:MET:HE2	1:A:643:PHE:CD1	2.51	0.46
1:A:572:ILE:HG23	1:A:573:LEU:N	2.31	0.46
1:A:240:ASN:ND2	3:A:70:HOH:O	2.49	0.45
1:A:658:VAL:HB	3:A:32:HOH:O	2.17	0.45
1:A:471:MET:HE2	1:A:547:LEU:HD12	1.99	0.45
1:A:576:GLY:O	1:A:577:TYR:O	2.35	0.45
1:A:584:HIS:HE1	1:A:630:CYS:O	2.00	0.45
1:A:566:ILE:N	1:A:566:ILE:HD12	2.31	0.44
1:A:575:THR:HG23	1:A:593:ALA:HA	2.00	0.44
1:A:598:LYS:H	1:A:606:SER:HB2	1.83	0.44
1:A:388:GLU:O	1:A:391:VAL:O	2.36	0.44
1:A:572:ILE:HG23	1:A:573:LEU:HD13	1.99	0.44
1:A:258:ILE:O	1:A:262:THR:HB	2.17	0.44
1:A:589:GLU:O	1:A:625:THR:HG22	2.18	0.44
1:A:598:LYS:HG3	1:A:617:MET:HE3	2.00	0.44
1:A:582:HIS:HA	3:A:42:HOH:O	2.18	0.43
1:A:471:MET:CE	1:A:547:LEU:HD12	2.48	0.43
1:A:584:HIS:HD2	1:A:585:THR:HG22	1.83	0.43
1:A:566:ILE:HG21	3:A:33:HOH:O	2.18	0.43
1:A:462:GLU:OE2	3:A:28:HOH:O	2.21	0.43
1:A:495:LYS:NZ	1:A:520:GLU:HG2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:GLU:HB3	1:A:316:ARG:HG2	2.00	0.43
1:A:563:GLN:HG2	1:A:620:ILE:HG22	2.01	0.42
1:A:354:PHE:CZ	1:A:401:CYS:HA	2.55	0.42
1:A:502:MET:HB3	1:A:503:PRO:HA	2.01	0.42
1:A:221:LEU:CD1	1:A:644:THR:HG23	2.50	0.42
1:A:248:ASP:HB3	2:A:663:GDP:H5''	2.02	0.42
1:A:262:THR:CG2	1:A:264:MET:HG2	2.49	0.42
1:A:220:ASP:O	1:A:220:ASP:OD1	2.38	0.41
1:A:581:MET:HE2	1:A:643:PHE:CD2	2.55	0.41
1:A:359:GLU:O	1:A:360:ARG:C	2.59	0.41
1:A:564:ILE:HG22	1:A:565:ALA:N	2.35	0.41
1:A:432:GLN:HB3	1:A:438:VAL:HG12	2.02	0.41
1:A:455:LEU:HD12	1:A:458:MET:CE	2.51	0.41
1:A:237:GLU:OE2	1:A:464:LYS:NZ	2.42	0.40
1:A:610:PRO:HA	3:A:68:HOH:O	2.22	0.40

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	402/467 (86%)	339 (84%)	45 (11%)	18 (4%)	2 9

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	ASP
1	A	573	LEU
1	A	577	TYR
1	A	585	THR
1	A	594	LYS
1	A	601	LYS

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Mol	Chain	Res	Type
1	A	605	LYS
1	A	227	GLN
1	A	572	ILE
1	A	584	HIS
1	A	603	ASN
1	A	652	VAL
1	A	247	VAL
1	A	568	GLU
1	A	595	LEU
1	A	587	VAL
1	A	518	ASP
1	A	389	PRO

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	355/398 (89%)	321 (90%)	34 (10%)	8 25

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	219	THR
1	A	221	LEU
1	A	231	LYS
1	A	232	ASP
1	A	262	THR
1	A	391	VAL
1	A	397	ARG
1	A	435	LYS
1	A	438	VAL
1	A	455	LEU
1	A	459	THR
1	A	462	GLU
1	A	466	ASN
1	A	482	THR

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Mol	Chain	Res	Type
1	A	485	GLU
1	A	515	ASP
1	A	519	GLU
1	A	524	SER
1	A	549	SER
1	A	568	GLU
1	A	569	LEU
1	A	572	ILE
1	A	575	THR
1	A	596	LEU
1	A	600	ASP
1	A	602	THR
1	A	605	LYS
1	A	619	ILE
1	A	625	THR
1	A	629	VAL
1	A	645	LEU
1	A	652	VAL
1	A	657	VAL
1	A	659	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	222	GLN
1	A	227	GLN
1	A	240	ASN
1	A	315	HIS
1	A	377	ASN
1	A	378	HIS
1	A	384	ASN
1	A	416	ASN
1	A	460	HIS
1	A	466	ASN
1	A	506	GLN
1	A	542	GLN
1	A	563	GLN
1	A	584	HIS

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](#)

1 ligand is 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
2	GDP	A	663	-	24,30,30	1.14	2 (8%)	30,47,47	1.37	4 (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
2	GDP	A	663	-	-	3/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	663	GDP	C5-C6	-3.77	1.39	1.47
2	A	663	GDP	C2-N3	2.25	1.38	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	663	GDP	PA-O3A-PB	-3.97	119.20	132.83
2	A	663	GDP	C5-C6-N1	2.97	119.20	113.95
2	A	663	GDP	C8-N7-C5	2.89	108.49	102.99
2	A	663	GDP	C2-N1-C6	-2.38	120.71	125.10

There are no chirality outliers.

All (3) torsion outliers are listed below:

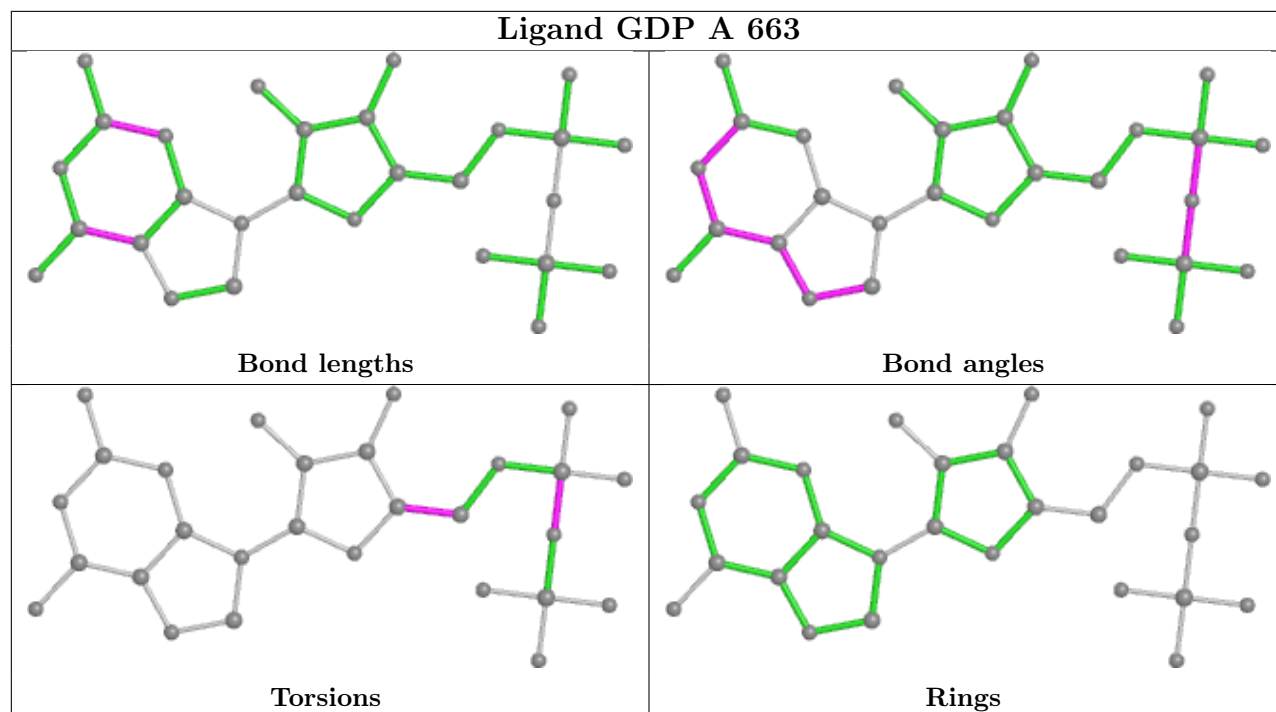
Mol	Chain	Res	Type	Atoms
2	A	663	GDP	O4'-C4'-C5'-O5'
2	A	663	GDP	C3'-C4'-C5'-O5'
2	A	663	GDP	PB-O3A-PA-O2A

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	663	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 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	408/467 (87%)	0.29	29 (7%) 16 12	28, 60, 99, 111	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	573	LEU	8.4
1	A	569	LEU	6.4
1	A	568	GLU	4.7
1	A	571	SER	4.1
1	A	580	VAL	3.9
1	A	572	ILE	3.9
1	A	621	ALA	3.9
1	A	217	ASP	3.8
1	A	567	LEU	3.6
1	A	337	ALA	3.4
1	A	619	ILE	3.4
1	A	215	THR	3.3
1	A	648	GLN	2.9
1	A	644	THR	2.9
1	A	651	THR	2.8
1	A	579	CYS	2.8
1	A	586	ALA	2.6
1	A	229	LEU	2.5
1	A	650	THR	2.5
1	A	600	ASP	2.4
1	A	216	GLU	2.4
1	A	574	THR	2.3
1	A	620	ILE	2.3
1	A	219	THR	2.2
1	A	223	ASN	2.1
1	A	324	PRO	2.1
1	A	649	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	654	VAL	2.0
1	A	480	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](#)

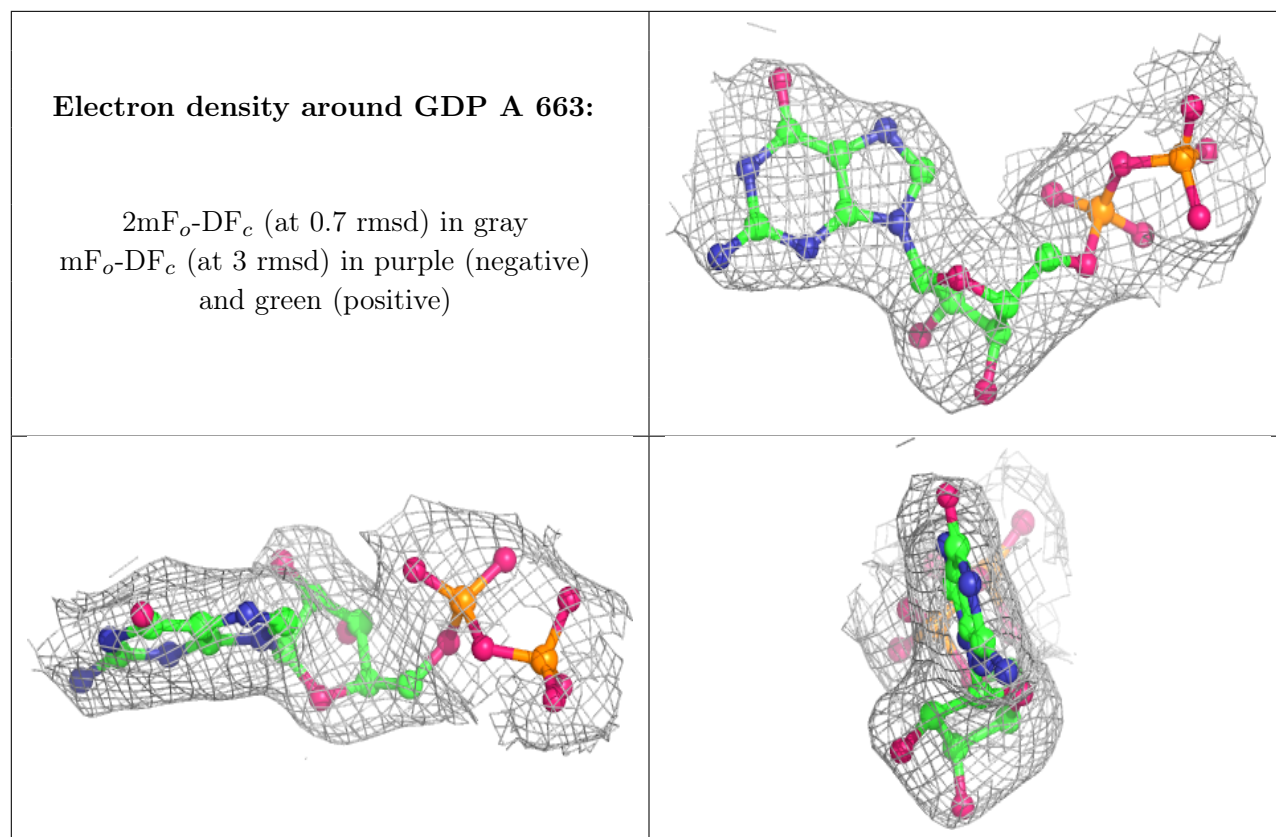
There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GDP	A	663	28/28	0.97	0.16	63,65,66,67	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.