



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 17, 2022 – 02:01 PM EDT

PDB ID : 4Q2D
Title : Crystal Structure of CRISPR-Associated protein in complex with 2'-Deoxyadenosine 5'-Triphosphate
Authors : Gong, B.; Shin, M.; Sun, J.; van der Oost, J.; Kim, J.-S.
Deposited on : 2014-04-07
Resolution : 2.77 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 : 2.29
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) : 2.29

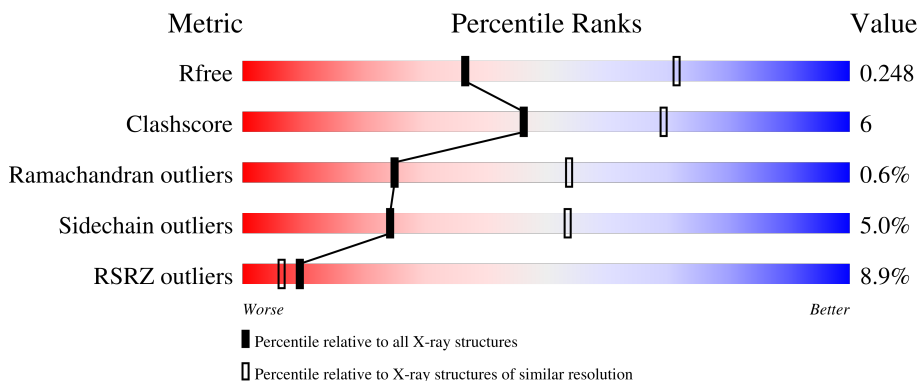
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.77 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	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)
RSRZ outliers	127900	4027 (2.80-2.76)

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	949	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7348 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 CRISPR-associated helicase Cas3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	927	7207	4575	1293	1313	7	19	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP D1CGD0
A	-3	GLY	-	expression tag	UNP D1CGD0
A	-2	GLY	-	expression tag	UNP D1CGD0
A	-1	GLY	-	expression tag	UNP D1CGD0
A	0	GLY	-	expression tag	UNP D1CGD0

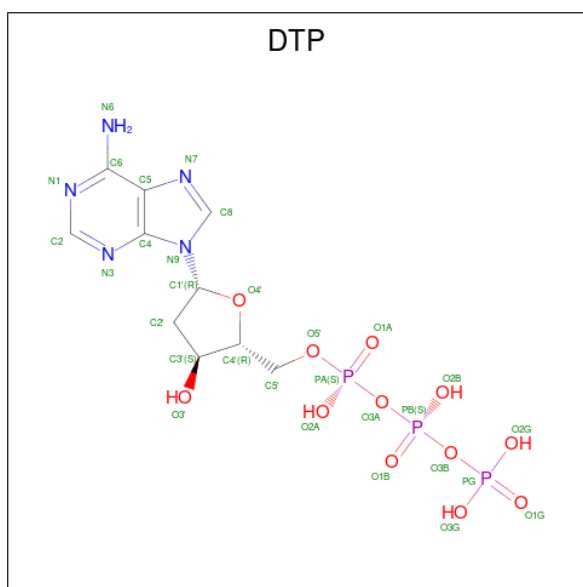
- Molecule 2 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Ni	0	0
			3	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2'-DEOXYADENOSINE 5'-TRIPHOSPHATE (three-letter code: DTP) (formula: C₁₀H₁₆N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	30	10	5	12	3	0	0

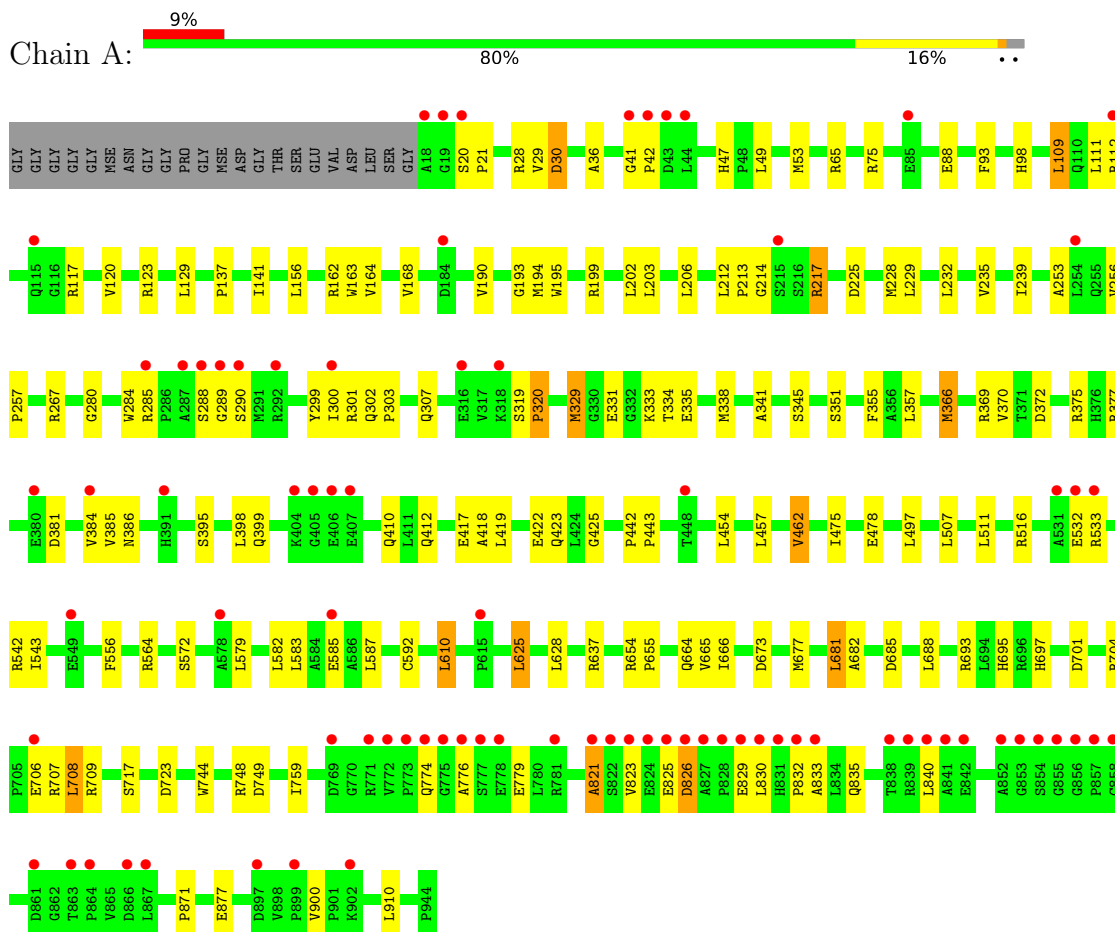
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	107	Total	O	0	0
			107	107		

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: CRISPR-associated helicase Cas3



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	105.68Å 211.63Å 104.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.66 – 2.77 45.66 – 2.77	Depositor EDS
% Data completeness (in resolution range)	95.5 (45.66-2.77) 95.5 (45.66-2.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.77Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.207 , 0.247 0.209 , 0.248	Depositor DCC
R_{free} test set	1438 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtrriage
Anisotropy	0.204	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7348	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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: NI, DTP, 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	0.22	0/7366	0.44	0/10007

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	7207	0	7161	90	0
2	A	3	0	0	0	0
3	A	1	0	0	0	0
4	A	30	0	12	3	0
5	A	107	0	0	3	0
All	All	7348	0	7173	91	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 6.

All (91) 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:701:ASP:OD1	1:A:704:ARG:NH1	2.19	0.76
1:A:829:GLU:HA	1:A:830:LEU:HB2	1.68	0.73
1:A:871:PRO:HG3	1:A:910:LEU:HD12	1.68	0.73
1:A:338:MSE:HE1	1:A:370:VAL:HA	1.71	0.71
1:A:137:PRO:HB3	1:A:417:GLU:HG2	1.73	0.70
1:A:28:ARG:O	1:A:30:ASP:N	2.29	0.65
1:A:825:GLU:N	1:A:826:ASP:OD1	2.29	0.64
1:A:357:LEU:HD21	1:A:366:MSE:HG3	1.78	0.63
1:A:98:HIS:HA	1:A:168:VAL:HG13	1.82	0.62
1:A:829:GLU:HG2	1:A:832:PRO:HB2	1.83	0.61
1:A:572:SER:HA	1:A:717:SER:HB3	1.83	0.59
1:A:688:LEU:HD13	1:A:759:ILE:HG23	1.85	0.59
1:A:109:LEU:O	1:A:117:ARG:NH1	2.35	0.59
1:A:748:ARG:NH1	1:A:774:GLN:OE1	2.31	0.58
1:A:419:LEU:HD13	1:A:425:GLY:HA2	1.85	0.58
1:A:162:ARG:NH1	5:A:1163:HOH:O	2.35	0.58
1:A:610:LEU:HB3	1:A:625:LEU:HD11	1.86	0.57
1:A:829:GLU:HB2	1:A:833:ALA:HB3	1.87	0.56
1:A:53:MSE:HE1	1:A:202:LEU:HB3	1.89	0.55
1:A:706:GLU:HA	1:A:709:ARG:HG3	1.88	0.55
1:A:341:ALA:HB2	1:A:475:ILE:HD11	1.90	0.54
1:A:190:VAL:O	1:A:199:ARG:NH2	2.40	0.53
1:A:75:ARG:NH2	1:A:225:ASP:OD1	2.41	0.53
1:A:681:LEU:HD11	1:A:744:TRP:HB2	1.89	0.53
1:A:289:GLY:HA3	1:A:377:ARG:HH12	1.74	0.53
1:A:307:GLN:OE1	4:A:1005:DTP:N6	2.42	0.53
1:A:821:ALA:H	1:A:823:VAL:HG23	1.73	0.53
1:A:299:TYR:OH	1:A:335:GLU:OE1	2.27	0.52
1:A:410:GLN:NE2	5:A:1136:HOH:O	2.41	0.52
1:A:835:GLN:HG3	1:A:840:LEU:HD22	1.90	0.51
1:A:319:SER:HB2	1:A:320:PRO:HD3	1.93	0.51
1:A:345:SER:HB2	1:A:351:SER:HA	1.92	0.51
1:A:93:PHE:CG	1:A:212:LEU:HD11	2.46	0.49
1:A:677:MSE:HE1	1:A:693:ARG:HB2	1.94	0.49
1:A:381:ASP:HA	1:A:384:VAL:HG22	1.95	0.48
1:A:454:LEU:HD23	1:A:457:LEU:HD12	1.94	0.48
1:A:457:LEU:O	1:A:462:VAL:HG11	2.14	0.48
1:A:685:ASP:N	1:A:685:ASP:OD1	2.44	0.48
1:A:36:ALA:HB2	1:A:49:LEU:HA	1.96	0.47
1:A:334:THR:O	1:A:338:MSE:HG3	2.13	0.47
1:A:267:ARG:NH2	5:A:1137:HOH:O	2.47	0.47
1:A:333:LYS:HB3	1:A:507:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ALA:CB	1:A:826:ASP:HB2	2.45	0.47
1:A:681:LEU:HD22	1:A:682:ALA:H	1.79	0.46
1:A:65:ARG:NE	1:A:88:GLU:OE2	2.42	0.46
1:A:582:LEU:HA	1:A:585:GLU:HG2	1.97	0.46
1:A:579:LEU:HA	1:A:582:LEU:HD12	1.97	0.46
1:A:592:CYS:SG	1:A:654:ARG:NH1	2.89	0.46
1:A:372:ASP:HA	1:A:375:ARG:HE	1.81	0.46
1:A:280:GLY:HA3	1:A:385:VAL:HG13	1.97	0.46
1:A:300:ILE:HD11	1:A:302:GLN:O	2.16	0.46
1:A:164:VAL:O	1:A:168:VAL:HB	2.16	0.45
1:A:695:HIS:HA	1:A:704:ARG:NH2	2.31	0.45
1:A:398:LEU:HD22	1:A:877:GLU:HG2	1.99	0.45
1:A:213:PRO:HA	1:A:214:GLY:HA2	1.63	0.45
1:A:123:ARG:NH2	1:A:253:ALA:O	2.42	0.45
1:A:723:ASP:OD2	1:A:776:ALA:HB1	2.16	0.45
1:A:129:LEU:HD22	1:A:195:TRP:CD2	2.52	0.44
1:A:516:ARG:NH1	1:A:542:ARG:HH21	2.15	0.44
1:A:677:MSE:HE2	1:A:677:MSE:HB2	1.94	0.44
1:A:300:ILE:HD13	4:A:1005:DTP:N1	2.33	0.44
1:A:288:SER:HA	1:A:289:GLY:HA3	1.71	0.44
1:A:235:VAL:O	1:A:239:ILE:HG12	2.18	0.44
1:A:141:ILE:HG23	1:A:190:VAL:HG22	2.00	0.43
1:A:300:ILE:HD12	1:A:301:ARG:N	2.33	0.43
1:A:329:MSE:H	1:A:329:MSE:SE	2.52	0.43
1:A:821:ALA:HA	1:A:823:VAL:H	1.82	0.43
1:A:111:LEU:HD23	1:A:111:LEU:HA	1.88	0.43
1:A:284:TRP:HH2	1:A:386:ASN:HB2	1.84	0.43
1:A:351:SER:O	1:A:351:SER:OG	2.33	0.42
1:A:20:SER:HB3	1:A:193:GLY:HA3	2.01	0.42
1:A:300:ILE:HD12	1:A:301:ARG:H	1.84	0.42
1:A:111:LEU:HD12	1:A:120:VAL:HG21	2.01	0.42
1:A:395:SER:O	1:A:399:GLN:HG2	2.20	0.42
1:A:41:GLY:HA3	1:A:42:PRO:HD3	1.91	0.41
1:A:338:MSE:HE3	1:A:355:PHE:CZ	2.55	0.41
1:A:418:ALA:HB3	1:A:826:ASP:HB2	2.03	0.41
1:A:610:LEU:HD12	1:A:610:LEU:HA	1.88	0.41
1:A:156:LEU:HD23	1:A:217:ARG:HB3	2.02	0.41
1:A:543:ILE:HG13	1:A:556:PHE:HE1	1.85	0.41
1:A:129:LEU:HG	1:A:194:MSE:HE3	2.02	0.41
1:A:442:PRO:HA	1:A:443:PRO:HD3	1.96	0.41
1:A:654:ARG:HA	1:A:655:PRO:HD2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:VAL:HG23	1:A:666:ILE:HD12	2.03	0.41
1:A:587:LEU:HD23	1:A:708:LEU:HD21	2.03	0.41
1:A:673:ASP:HB2	1:A:697:HIS:ND1	2.36	0.40
4:A:1005:DTP:H2'2	4:A:1005:DTP:H8	1.75	0.40
1:A:288:SER:HA	1:A:377:ARG:NH1	2.37	0.40
1:A:20:SER:HA	1:A:21:PRO:HD2	1.92	0.40
1:A:256:VAL:HA	1:A:257:PRO:HD3	1.97	0.40
1:A:302:GLN:HA	1:A:303:PRO:HD3	1.94	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	925/949 (98%)	891 (96%)	28 (3%)	6 (1%)	25 54

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	VAL
1	A	290	SER
1	A	320	PRO
1	A	478	GLU
1	A	821	ALA
1	A	30	ASP

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	745/736 (101%)	708 (95%)	37 (5%)	24	53

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	109	LEU
1	A	112	ARG
1	A	163	TRP
1	A	203	LEU
1	A	206	LEU
1	A	217	ARG
1	A	228	MSE
1	A	229	LEU
1	A	232	LEU
1	A	285	ARG
1	A	329	MSE
1	A	331	GLU
1	A	366	MSE
1	A	369	ARG
1	A	412	GLN
1	A	422	GLU
1	A	423	GLN
1	A	462	VAL
1	A	497	LEU
1	A	511	LEU
1	A	532	GLU
1	A	533	ARG
1	A	564	ARG
1	A	583	LEU
1	A	610	LEU
1	A	625	LEU
1	A	628	LEU
1	A	637	ARG
1	A	664	GLN
1	A	681	LEU
1	A	707	ARG
1	A	708	LEU
1	A	749	ASP
1	A	779	GLU

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Mol	Chain	Res	Type
1	A	826	ASP
1	A	900	VAL

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are 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
4	DTP	A	1005	3	26,32,32	1.36	4 (15%)	30,50,50	1.46	5 (16%)

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	DTP	A	1005	3	-	0/18/34/34	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1005	DTP	C2'-C3'	-3.13	1.44	1.52
4	A	1005	DTP	C2'-C1'	-3.11	1.43	1.52
4	A	1005	DTP	C6-N6	2.51	1.43	1.34
4	A	1005	DTP	C1'-N9	-2.19	1.42	1.49

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1005	DTP	PB-O3B-PG	-3.70	120.14	132.83
4	A	1005	DTP	PA-O3A-PB	-3.54	120.67	132.83
4	A	1005	DTP	N3-C2-N1	-3.24	123.62	128.68
4	A	1005	DTP	O5'-C5'-C4'	2.32	116.98	108.99
4	A	1005	DTP	C4-C5-N7	-2.07	107.24	109.40

There are no chirality outliers.

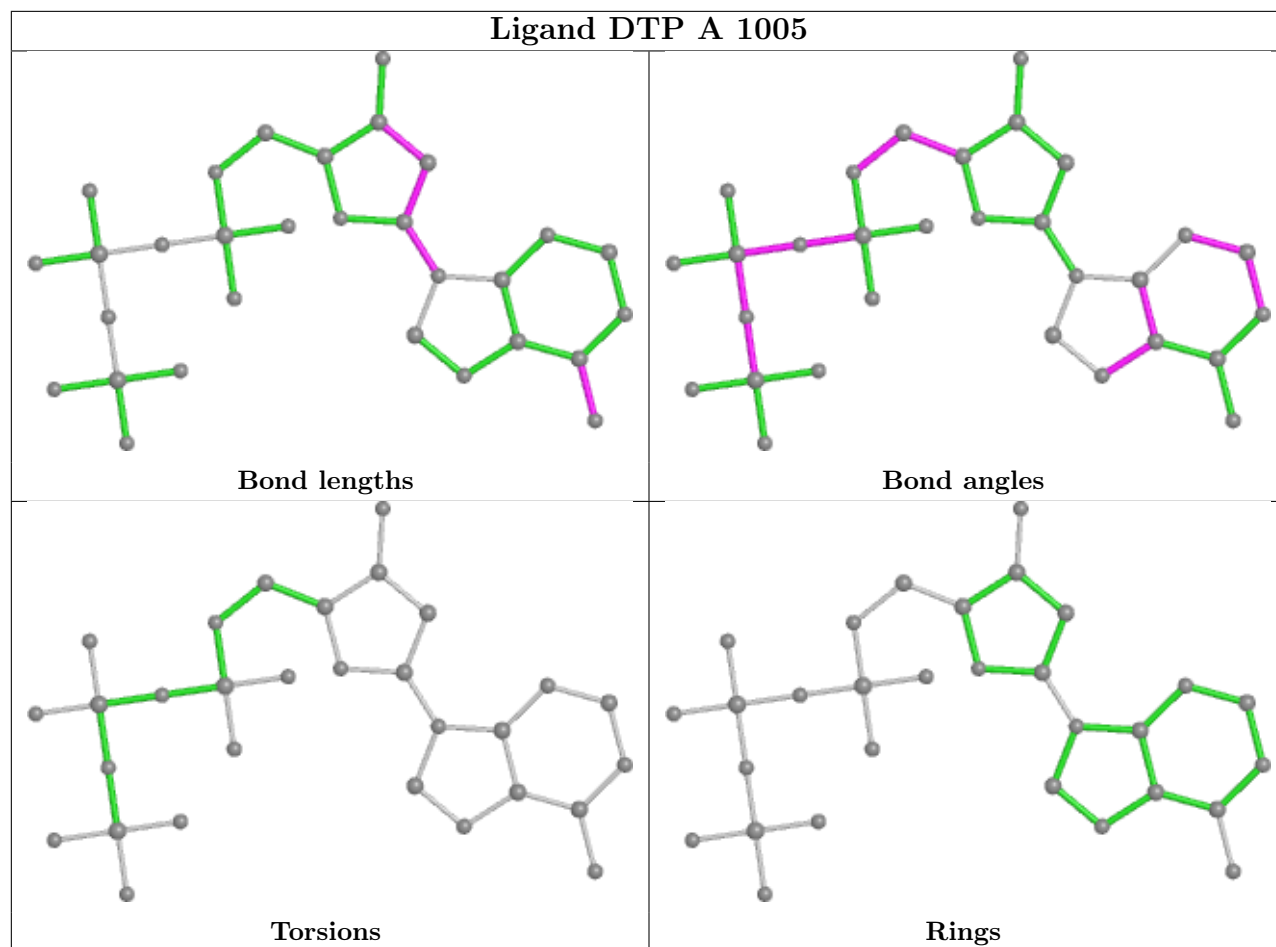
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1005	DTP	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, 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	908/949 (95%)	0.46	81 (8%) 9 6	21, 40, 96, 259	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	826	ASP	15.5
1	A	827	ALA	14.2
1	A	832	PRO	14.0
1	A	833	ALA	10.2
1	A	825	GLU	8.6
1	A	855	GLY	8.6
1	A	828	PRO	8.5
1	A	830	LEU	8.3
1	A	824	GLU	7.7
1	A	829	GLU	6.6
1	A	19	GLY	5.6
1	A	823	VAL	5.5
1	A	406	GLU	5.5
1	A	405	GLY	5.4
1	A	842	GLU	5.3
1	A	43	ASP	5.3
1	A	841	ALA	5.3
1	A	822	SER	5.1
1	A	42	PRO	4.7
1	A	384	VAL	4.7
1	A	112	ARG	4.4
1	A	404	LYS	4.4
1	A	864	PRO	4.1
1	A	831	HIS	4.0
1	A	838	THR	3.9
1	A	772	VAL	3.8
1	A	861	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	852	ALA	3.3
1	A	769	ASP	3.3
1	A	854	SER	3.1
1	A	285	ARG	3.1
1	A	821	ALA	3.1
1	A	20	SER	3.0
1	A	773	PRO	3.0
1	A	858	CYS	3.0
1	A	407	GLU	3.0
1	A	856	GLY	3.0
1	A	775	GLY	2.9
1	A	578	ALA	2.8
1	A	289	GLY	2.8
1	A	853	GLY	2.8
1	A	254	LEU	2.8
1	A	288	SER	2.8
1	A	18	ALA	2.8
1	A	300	ILE	2.7
1	A	41	GLY	2.7
1	A	615	PRO	2.7
1	A	771	ARG	2.7
1	A	863	THR	2.7
1	A	857	PRO	2.6
1	A	867	LEU	2.5
1	A	777	SER	2.5
1	A	549	GLU	2.5
1	A	897	ASP	2.5
1	A	776	ALA	2.5
1	A	44	LEU	2.4
1	A	115	GLN	2.3
1	A	533	ARG	2.3
1	A	585	GLU	2.2
1	A	316	GLU	2.2
1	A	778	GLU	2.2
1	A	531	ALA	2.2
1	A	292	ARG	2.2
1	A	380	GLU	2.1
1	A	532	GLU	2.1
1	A	840	LEU	2.1
1	A	215	SER	2.1
1	A	85	GLU	2.1
1	A	391	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	318	LYS	2.1
1	A	866	ASP	2.1
1	A	902	LYS	2.1
1	A	448	THR	2.1
1	A	184	ASP	2.1
1	A	899	PRO	2.1
1	A	839	ARG	2.0
1	A	774	GLN	2.0
1	A	706	GLU	2.0
1	A	287	ALA	2.0
1	A	290	SER	2.0
1	A	781	ARG	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](#)

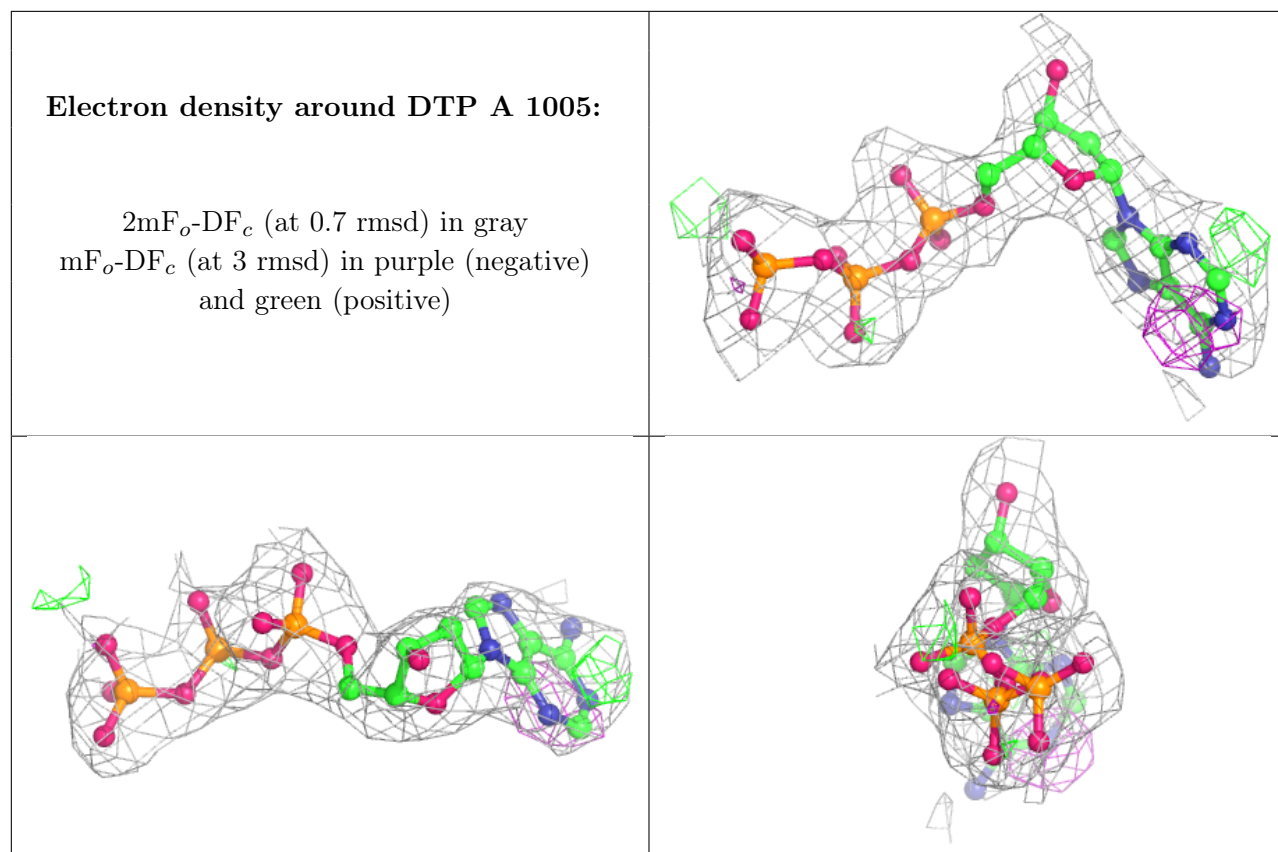
There are no monosaccharides in this entry.

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
3	MG	A	1004	1/1	0.93	0.28	24,24,24,24	0
4	DTP	A	1005	30/30	0.93	0.18	37,48,55,59	0
2	NI	A	1001	1/1	0.99	0.11	25,25,25,25	0
2	NI	A	1003	1/1	0.99	0.13	39,39,39,39	0
2	NI	A	1002	1/1	1.00	0.13	23,23,23,23	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.