



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 5, 2022 – 09:10 pm GMT

PDB ID : 7B9P
Title : Structure of Ribonucleotide reductase from Rhodobacter sphaeroides
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Deposited on : 2020-12-14
Resolution : 2.65 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.24
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.24

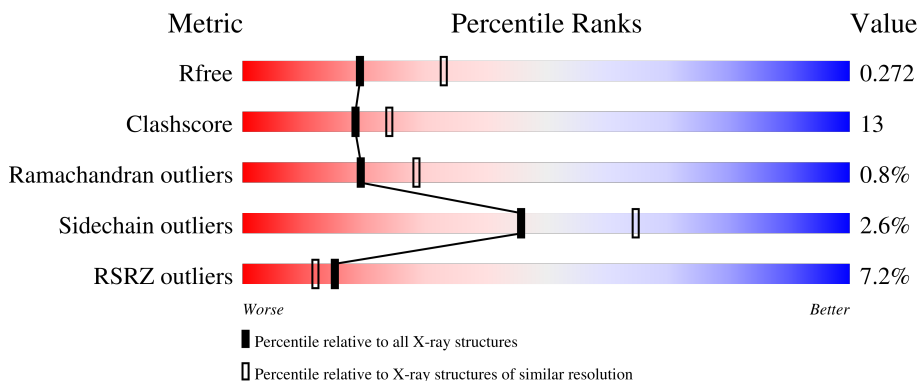
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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	925	 7% 71% 25% ..

2 Entry composition [i](#)

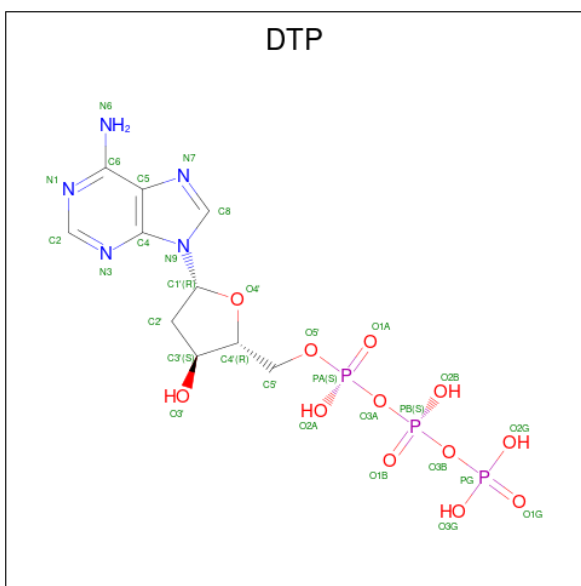
There are 4 unique types of molecules in this entry. The entry contains 7056 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Vitamin B12-dependent ribonucleotide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	899	6888	4338	1212	1303	35	1	0	0

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



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

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

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

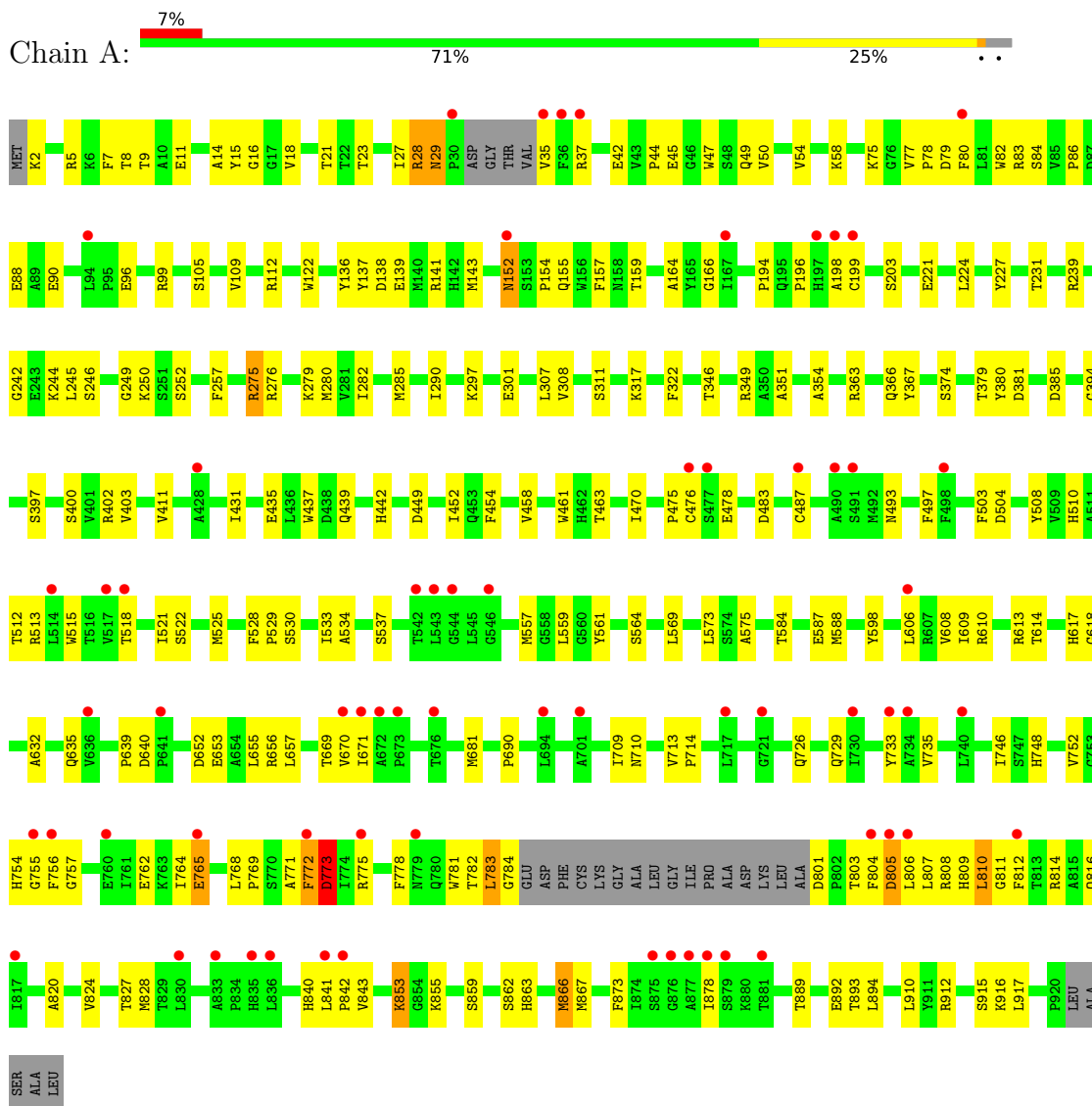
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	137	Total 137	O 137	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: Vitamin B12-dependent ribonucleotide reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	140.75Å 140.75Å 364.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.86 – 2.65 47.86 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.86-2.65) 99.8 (47.86-2.65)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.16	Depositor
R, R_{free}	0.230 , 0.272 0.230 , 0.272	Depositor DCC
R_{free} test set	2099 reflections (3.34%)	wwPDB-VP
Wilson B-factor (Å ²)	96.7	Xtriage
Anisotropy	0.109	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7056	wwPDB-VP
Average B, all atoms (Å ²)	114.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% 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: 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	0.26	0/7047	0.46	1/9544 (0.0%)

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	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	806	LEU	CA-CB-CG	6.13	129.39	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	765	GLU	Peptide
1	A	773	ASP	Peptide
1	A	805	ASP	Peptide

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	6888	0	6678	180	2
2	A	30	0	12	4	0
3	A	1	0	0	0	0
4	A	137	0	0	12	0
All	All	7056	0	6690	180	2

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 13.

All (180) 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:285:MET:CE	1:A:290:ILE:HD11	1.73	1.18
1:A:285:MET:HE2	1:A:290:ILE:HD11	1.35	1.03
1:A:285:MET:CE	1:A:290:ILE:CD1	2.38	1.01
1:A:285:MET:HA	1:A:290:ILE:HD13	1.42	1.01
1:A:285:MET:HE2	1:A:290:ILE:CD1	1.99	0.89
1:A:285:MET:HE1	1:A:290:ILE:CD1	2.04	0.86
1:A:96:GLU:HA	1:A:99:ARG:HG3	1.56	0.86
1:A:771:ALA:H	1:A:775:ARG:HH11	1.32	0.78
1:A:27:ILE:HD12	1:A:27:ILE:O	1.84	0.77
1:A:199:CYS:N	1:A:487:CYS:SG	2.61	0.74
1:A:515:TRP:HA	1:A:518:THR:HG22	1.70	0.74
1:A:772:PHE:HE1	1:A:828:MET:HE1	1.54	0.72
1:A:15:TYR:OH	4:A:1102:HOH:O	2.08	0.72
1:A:772:PHE:HE1	1:A:828:MET:CE	2.03	0.71
1:A:764:ILE:HG22	1:A:765:GLU:OE1	1.91	0.70
1:A:493:ASN:HB2	1:A:681:MET:HE2	1.75	0.69
1:A:765:GLU:OE1	1:A:765:GLU:N	2.26	0.68
1:A:280:MET:HB2	1:A:475:PRO:HA	1.77	0.67
1:A:893:THR:HG23	1:A:910:LEU:HD12	1.77	0.67
1:A:58:LYS:HE2	1:A:275:ARG:HH21	1.61	0.66
1:A:769:PRO:HB2	1:A:775:ARG:HH12	1.61	0.65
1:A:366:GLN:OE1	4:A:1103:HOH:O	2.14	0.65
1:A:889:THR:HG23	1:A:892:GLU:H	1.59	0.65
1:A:317:LYS:HD3	1:A:351:ALA:HA	1.78	0.64
1:A:15:TYR:HB3	1:A:18:VAL:HG22	1.79	0.64
1:A:518:THR:HA	1:A:521:ILE:HD12	1.80	0.63
1:A:772:PHE:CE1	1:A:828:MET:HE1	2.33	0.63
1:A:276:ARG:NH2	4:A:1114:HOH:O	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:GLN:HA	1:A:159:THR:HG23	1.81	0.62
1:A:772:PHE:CE1	1:A:828:MET:CE	2.83	0.62
1:A:83:ARG:NH1	4:A:1113:HOH:O	2.32	0.61
1:A:916:LYS:HD3	1:A:917:LEU:H	1.65	0.60
1:A:463:THR:HG22	1:A:608:VAL:HG11	1.83	0.60
1:A:138:ASP:OD1	1:A:141:ARG:NH2	2.35	0.59
1:A:141:ARG:HD2	4:A:1102:HOH:O	2.02	0.59
1:A:569:LEU:O	1:A:573:LEU:HD12	2.02	0.58
1:A:522:SER:HA	1:A:525:MET:HG2	1.85	0.58
1:A:285:MET:HA	1:A:290:ILE:CD1	2.26	0.58
1:A:224:LEU:HD21	1:A:529:PRO:HG3	1.83	0.58
1:A:618:GLY:HA2	1:A:632:ALA:HB1	1.85	0.58
1:A:782:THR:O	1:A:784:GLY:N	2.37	0.58
1:A:912:ARG:O	1:A:915:SER:OG	2.17	0.58
1:A:816:GLN:NE2	4:A:1107:HOH:O	2.24	0.57
1:A:152:ASN:HD22	1:A:154:PRO:HD2	1.69	0.57
1:A:136:TYR:OH	1:A:518:THR:HB	2.05	0.57
1:A:23:THR:HG21	1:A:49:GLN:OE1	2.05	0.56
1:A:311:SER:HB2	1:A:379:THR:HA	1.88	0.56
1:A:2:LYS:O	1:A:513:ARG:NH2	2.37	0.56
1:A:317:LYS:HE2	1:A:354:ALA:HB2	1.88	0.56
1:A:79:ASP:HA	1:A:82:TRP:CZ2	2.41	0.56
1:A:21:THR:HG22	1:A:45:GLU:HA	1.88	0.55
1:A:317:LYS:HE2	1:A:354:ALA:CB	2.36	0.55
1:A:461:TRP:HE3	1:A:608:VAL:HG23	1.71	0.55
1:A:285:MET:CE	1:A:290:ILE:HD13	2.33	0.55
1:A:748:HIS:O	1:A:752:VAL:HG12	2.07	0.55
1:A:437:TRP:CE2	1:A:894:LEU:HD22	2.42	0.55
1:A:221:GLU:HG2	1:A:231:THR:HG21	1.88	0.55
1:A:461:TRP:CE3	1:A:608:VAL:HG23	2.42	0.55
1:A:710:ASN:HB3	1:A:713:VAL:HG23	1.90	0.53
1:A:598:TYR:OH	1:A:606:LEU:HD11	2.08	0.53
1:A:640:ASP:OD2	4:A:1104:HOH:O	2.18	0.53
1:A:279:LYS:HD3	1:A:397:SER:HB3	1.90	0.53
1:A:726:GLN:HA	1:A:729:GLN:HG3	1.89	0.53
1:A:411:VAL:HG11	1:A:437:TRP:HB2	1.91	0.53
1:A:610:ARG:O	1:A:614:THR:HG23	2.09	0.53
1:A:86:PRO:HD2	1:A:166:GLY:HA3	1.91	0.53
1:A:139:GLU:OE1	1:A:510:HIS:NE2	2.40	0.52
1:A:653:GLU:O	1:A:657:LEU:HD12	2.10	0.52
1:A:282:ILE:HA	1:A:400:SER:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:ALA:HA	1:A:141:ARG:HH22	1.75	0.51
1:A:803:THR:O	1:A:803:THR:OG1	2.28	0.51
1:A:403:VAL:HG21	1:A:452:ILE:HD11	1.93	0.51
1:A:476:CYS:HB2	1:A:478:GLU:OE1	2.11	0.51
1:A:257:PHE:CZ	2:A:1001:DTP:H2'1	2.44	0.51
1:A:224:LEU:HD12	1:A:231:THR:HB	1.92	0.51
1:A:322:PHE:CE2	1:A:374:SER:HA	2.46	0.51
1:A:497:PHE:CE2	1:A:508:TYR:HA	2.45	0.51
1:A:28:ARG:HG2	1:A:35:VAL:HG23	1.92	0.50
1:A:257:PHE:CE2	2:A:1001:DTP:H2'1	2.45	0.50
1:A:613:ARG:HD2	1:A:652:ASP:HA	1.94	0.50
1:A:533:ILE:O	1:A:537:SER:OG	2.29	0.50
1:A:771:ALA:H	1:A:775:ARG:NH1	2.07	0.50
1:A:508:TYR:O	1:A:512:THR:HG23	2.12	0.50
1:A:561:TYR:CZ	1:A:866:MET:HE3	2.47	0.50
1:A:346:THR:HG23	1:A:349:ARG:HH12	1.77	0.50
1:A:308:VAL:HG12	1:A:380:TYR:HB2	1.92	0.49
1:A:454:PHE:O	1:A:458:VAL:HG23	2.12	0.49
1:A:733:TYR:CZ	1:A:827:THR:HG21	2.47	0.49
1:A:203:SER:HB3	1:A:483:ASP:HB3	1.95	0.49
1:A:557:MET:HB2	1:A:559:LEU:CD1	2.41	0.49
1:A:769:PRO:HB2	1:A:775:ARG:NH1	2.27	0.49
1:A:139:GLU:O	1:A:143:MET:HG3	2.12	0.49
1:A:154:PRO:HA	1:A:157:PHE:CZ	2.49	0.48
1:A:559:LEU:HD21	1:A:639:PRO:HG2	1.96	0.48
1:A:515:TRP:HA	1:A:518:THR:CG2	2.43	0.48
1:A:77:VAL:HG23	1:A:82:TRP:CD1	2.49	0.48
1:A:773:ASP:HB2	1:A:775:ARG:HG2	1.96	0.48
1:A:297:LYS:HD2	1:A:449:ASP:HB2	1.96	0.47
1:A:863:HIS:O	1:A:867:MET:HG3	2.14	0.47
1:A:5:ARG:NH1	1:A:8:THR:HG23	2.30	0.47
1:A:109:VAL:HA	1:A:112:ARG:HG2	1.97	0.47
1:A:561:TYR:CD1	1:A:690:PRO:HB3	2.49	0.47
1:A:28:ARG:HH11	1:A:29:ASN:H	1.62	0.47
1:A:402:ARG:NH1	1:A:470:ILE:O	2.47	0.47
1:A:820:ALA:O	1:A:824:VAL:HG12	2.14	0.47
1:A:810:LEU:HD12	1:A:811:GLY:N	2.29	0.47
1:A:497:PHE:HB2	1:A:503:PHE:CE1	2.50	0.47
1:A:559:LEU:C	1:A:843:VAL:HG23	2.35	0.47
1:A:80:PHE:HD1	1:A:80:PHE:H	1.63	0.46
1:A:285:MET:HE1	1:A:290:ILE:CG1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:ARG:HH12	1:A:9:THR:C	2.19	0.46
1:A:9:THR:OG1	1:A:11:GLU:HG2	2.15	0.46
1:A:242:GLY:O	1:A:250:LYS:HD2	2.15	0.46
1:A:7:PHE:N	4:A:1109:HOH:O	2.47	0.46
1:A:285:MET:HG3	1:A:403:VAL:HG12	1.96	0.46
1:A:613:ARG:HH21	1:A:617:HIS:HD2	1.63	0.46
1:A:772:PHE:CE1	1:A:828:MET:HE3	2.50	0.46
1:A:653:GLU:HG3	1:A:657:LEU:HD11	1.98	0.46
1:A:297:LYS:HE2	1:A:394:GLY:O	2.16	0.45
1:A:513:ARG:NH1	1:A:587:GLU:OE1	2.42	0.45
1:A:709:ILE:HB	1:A:735:VAL:HG21	1.98	0.45
1:A:805:ASP:OD2	1:A:805:ASP:N	2.49	0.45
1:A:78:PRO:HD3	1:A:122:TRP:NE1	2.32	0.45
1:A:808:ARG:HD2	1:A:808:ARG:C	2.37	0.45
1:A:613:ARG:HH21	1:A:617:HIS:CD2	2.34	0.45
1:A:617:HIS:C	1:A:635:GLN:HE22	2.20	0.45
1:A:159:THR:HG22	1:A:194:PRO:HB3	1.98	0.45
1:A:385:ASP:OD1	1:A:385:ASP:N	2.44	0.45
1:A:285:MET:HE2	1:A:290:ILE:HD13	1.94	0.45
1:A:713:VAL:HB	1:A:714:PRO:HD3	1.98	0.45
1:A:42:GLU:HB3	1:A:105:SER:HB2	1.99	0.45
1:A:252:SER:HB3	2:A:1001:DTP:H2	1.98	0.44
1:A:584:THR:O	1:A:588:MET:HG3	2.16	0.44
1:A:840:HIS:O	1:A:843:VAL:HG12	2.17	0.44
1:A:245:LEU:HG	1:A:249:GLY:O	2.17	0.44
1:A:808:ARG:HG3	1:A:814:ARG:HH11	1.82	0.44
1:A:669:THR:O	1:A:670:VAL:HG23	2.17	0.44
1:A:137:TYR:O	1:A:141:ARG:HG3	2.18	0.44
1:A:308:VAL:HA	1:A:311:SER:HG	1.83	0.43
1:A:769:PRO:HB2	1:A:775:ARG:HH22	1.83	0.43
1:A:841:LEU:N	1:A:842:PRO:HD2	2.33	0.43
1:A:50:VAL:O	1:A:54:VAL:HG12	2.18	0.43
1:A:90:GLU:OE2	4:A:1105:HOH:O	2.21	0.43
1:A:653:GLU:O	1:A:656:ARG:N	2.51	0.43
1:A:859:SER:OG	1:A:862:SER:N	2.48	0.43
1:A:154:PRO:HG2	1:A:198:ALA:HA	2.01	0.43
1:A:783:LEU:HD22	1:A:783:LEU:H	1.84	0.43
1:A:194:PRO:O	1:A:196:PRO:HD3	2.19	0.43
1:A:435:GLU:O	1:A:439:GLN:HG3	2.18	0.43
1:A:765:GLU:HA	1:A:768:LEU:HD12	2.01	0.43
1:A:246:SER:OG	2:A:1001:DTP:O3G	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:MET:HE1	1:A:290:ILE:HD13	1.94	0.43
1:A:801:ASP:N	4:A:1134:HOH:O	2.51	0.42
1:A:307:LEU:HD12	1:A:307:LEU:HA	1.85	0.42
1:A:528:PHE:HB2	1:A:534:ALA:HB2	2.01	0.42
1:A:84:SER:HB2	1:A:164:ALA:O	2.18	0.42
1:A:762:GLU:OE2	1:A:762:GLU:N	2.37	0.42
1:A:853:LYS:HB2	1:A:855:LYS:HZ1	1.85	0.42
1:A:606:LEU:HA	1:A:609:ILE:HB	2.02	0.42
1:A:754:HIS:O	1:A:756:PHE:N	2.48	0.41
1:A:610:ARG:HG2	1:A:655:LEU:HD11	2.02	0.41
1:A:773:ASP:HB2	1:A:775:ARG:CG	2.50	0.41
1:A:575:ALA:HA	1:A:873:PHE:HB3	2.02	0.41
1:A:804:PHE:HB3	1:A:805:ASP:OD2	2.21	0.41
1:A:346:THR:HG23	1:A:349:ARG:NH1	2.35	0.41
1:A:671:ILE:HD13	1:A:878:ILE:HG12	2.03	0.41
1:A:44:PRO:HB2	1:A:47:TRP:CD1	2.56	0.41
1:A:285:MET:HE1	1:A:290:ILE:HG12	2.02	0.41
1:A:559:LEU:HD21	1:A:639:PRO:CG	2.50	0.41
1:A:746:ILE:HG12	1:A:812:PHE:CD2	2.55	0.41
1:A:557:MET:HB2	1:A:559:LEU:HD12	2.02	0.40
1:A:14:ALA:HA	1:A:141:ARG:NH2	2.36	0.40
1:A:493:ASN:HB2	1:A:681:MET:CE	2.47	0.40
1:A:653:GLU:HG3	1:A:657:LEU:CD1	2.51	0.40
1:A:569:LEU:HG	1:A:573:LEU:CD1	2.52	0.40
1:A:239:ARG:NH1	1:A:245:LEU:HA	2.36	0.40
1:A:431:ILE:HD12	1:A:431:ILE:HA	2.00	0.40
1:A:801:ASP:HB3	4:A:1194:HOH:O	2.20	0.40
1:A:803:THR:HG22	4:A:1194:HOH:O	2.21	0.40
1:A:803:THR:H	1:A:807:LEU:HD11	1.87	0.40

All (2) 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)
1:A:367:TYR:OH	1:A:442:HIS:NE2[10_667]	2.14	0.06
1:A:301:GLU:OE1	1:A:363:ARG:NH2[10_667]	2.16	0.04

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	893/925 (96%)	850 (95%)	36 (4%)	7 (1%)	19 28

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	504	ASP
1	A	783	LEU
1	A	16	GLY
1	A	781	TRP
1	A	772	PHE
1	A	757	GLY
1	A	755	GLY

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	703/721 (98%)	685 (97%)	18 (3%)	46 65

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

Mol	Chain	Res	Type
1	A	28	ARG
1	A	29	ASN
1	A	37	ARG
1	A	75	LYS

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Mol	Chain	Res	Type
1	A	88	GLU
1	A	152	ASN
1	A	227	TYR
1	A	244	LYS
1	A	275	ARG
1	A	381	ASP
1	A	530	SER
1	A	564	SER
1	A	773	ASP
1	A	778	PHE
1	A	809	HIS
1	A	810	LEU
1	A	853	LYS
1	A	866	MET

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 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
2	DTP	A	1001	3	26,32,32	0.68	0	30,50,50	0.86	1 (3%)

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	DTP	A	1001	3	-	2/18/34/34	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	DTP	C5-C6-N6	2.30	123.85	120.35

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	DTP	C3'-C4'-C5'-O5'
2	A	1001	DTP	O4'-C4'-C5'-O5'

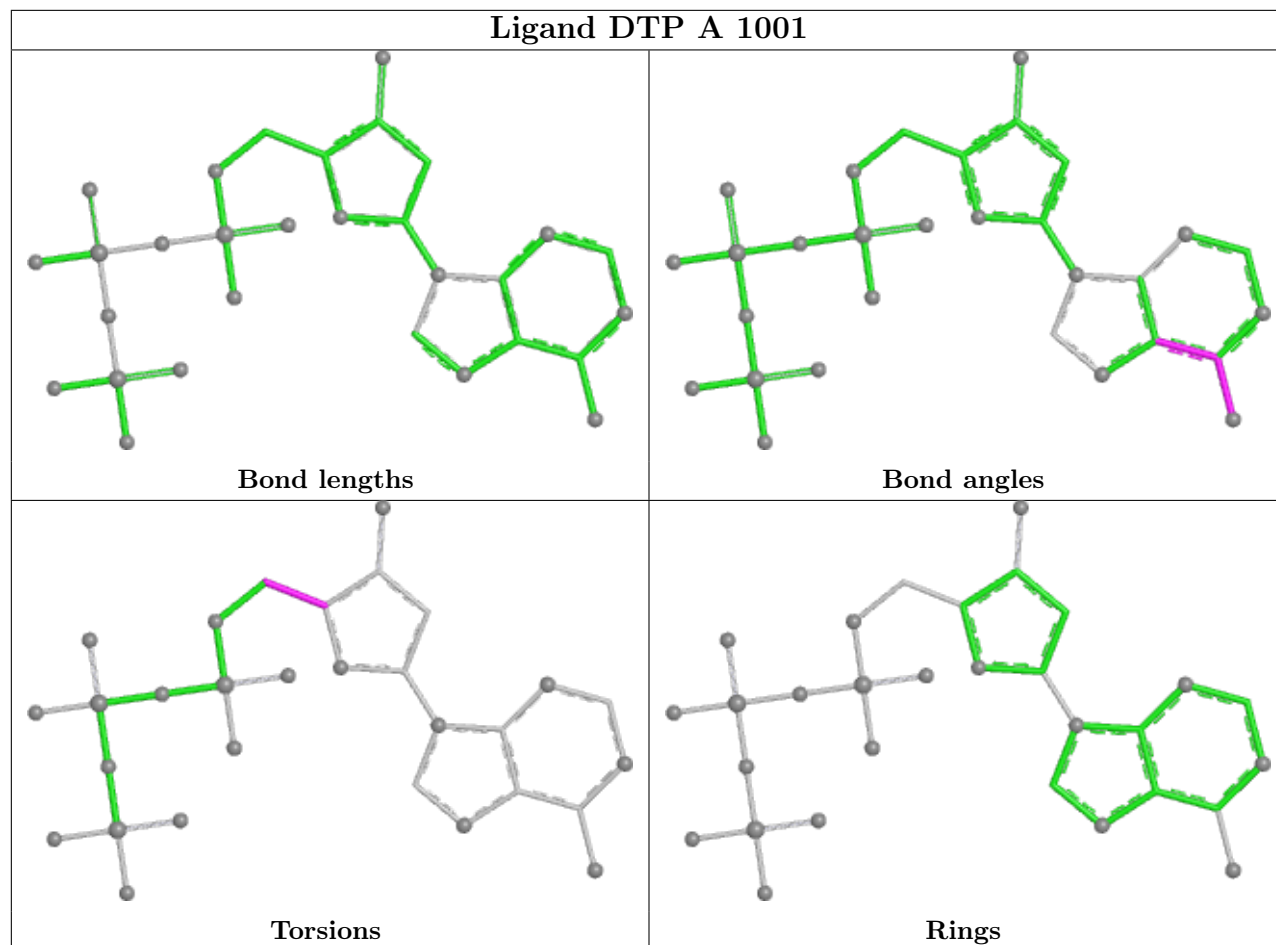
There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	DTP	4	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	899/925 (97%)	0.43	65 (7%) 15 12	68, 110, 159, 214	1 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	804	PHE	5.7
1	A	30	PRO	3.7
1	A	835	HIS	3.6
1	A	546	GLY	3.6
1	A	544	GLY	3.4
1	A	878	ILE	3.4
1	A	775	ARG	3.3
1	A	830	LEU	3.3
1	A	765	GLU	3.3
1	A	476	CYS	3.3
1	A	542	THR	3.1
1	A	94	LEU	3.0
1	A	491	SER	3.0
1	A	721	GLY	2.9
1	A	806	LEU	2.9
1	A	80	PHE	2.9
1	A	518	THR	2.9
1	A	514	LEU	2.9
1	A	836	LEU	2.9
1	A	490	ALA	2.8
1	A	879	SER	2.7
1	A	199	CYS	2.7
1	A	676	THR	2.7
1	A	198	ALA	2.7
1	A	779	ASN	2.6
1	A	740	LEU	2.6
1	A	670	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	671	ILE	2.6
1	A	730	ILE	2.5
1	A	36	PHE	2.5
1	A	805	ASP	2.5
1	A	543	LEU	2.5
1	A	756	PHE	2.5
1	A	701	ALA	2.5
1	A	197	HIS	2.4
1	A	734	ALA	2.4
1	A	152	ASN	2.4
1	A	694	LEU	2.4
1	A	498	PHE	2.4
1	A	672	ALA	2.3
1	A	881	THR	2.3
1	A	517	VAL	2.3
1	A	636	VAL	2.3
1	A	812	PHE	2.3
1	A	37	ARG	2.3
1	A	817	ILE	2.2
1	A	841	LEU	2.2
1	A	877	ALA	2.2
1	A	876	GLY	2.2
1	A	167	ILE	2.2
1	A	487	CYS	2.2
1	A	428	ALA	2.2
1	A	35	VAL	2.2
1	A	733	TYR	2.2
1	A	673	PRO	2.2
1	A	717	LEU	2.2
1	A	875	SER	2.1
1	A	760	GLU	2.1
1	A	477	SER	2.1
1	A	755	GLY	2.1
1	A	833	ALA	2.1
1	A	772	PHE	2.1
1	A	641	PRO	2.1
1	A	606	LEU	2.0
1	A	842	PRO	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](#)

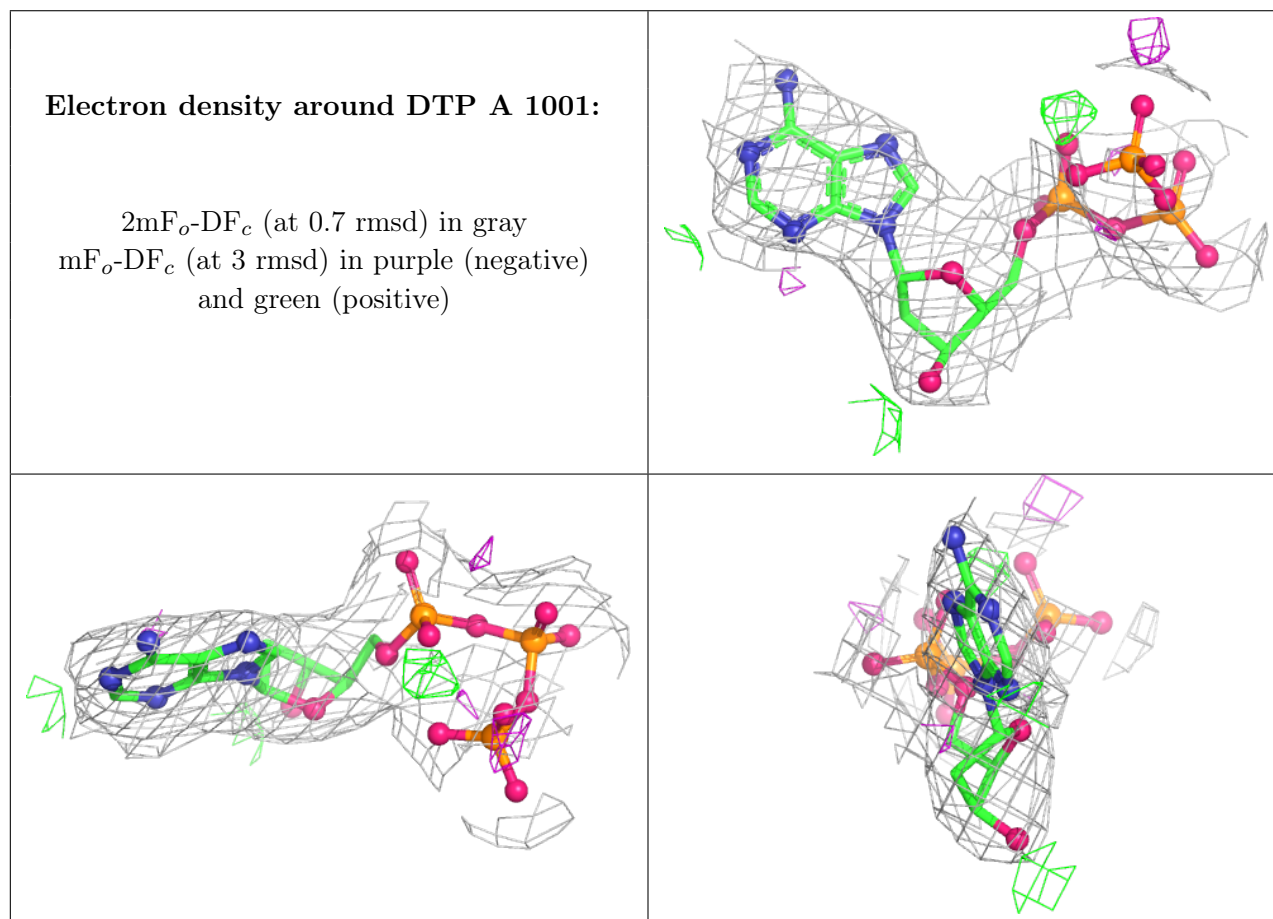
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
2	DTP	A	1001	30/30	0.95	0.12	78,101,146,147	30
3	MG	A	1002	1/1	0.98	0.15	121,121,121,121	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

There are no such residues in this entry.