



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:37 AM UTC

PDB ID : 1H79 / pdb_00001h79
Title : STRUCTURAL BASIS FOR ALLOSTERIC SUBSTRATE SPECIFICITY
REGULATION IN CLASS III RIBONUCLEOTIDE REDUCTASES: NRDD
IN COMPLEX WITH DTTP
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Deposited on : 2001-07-04
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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

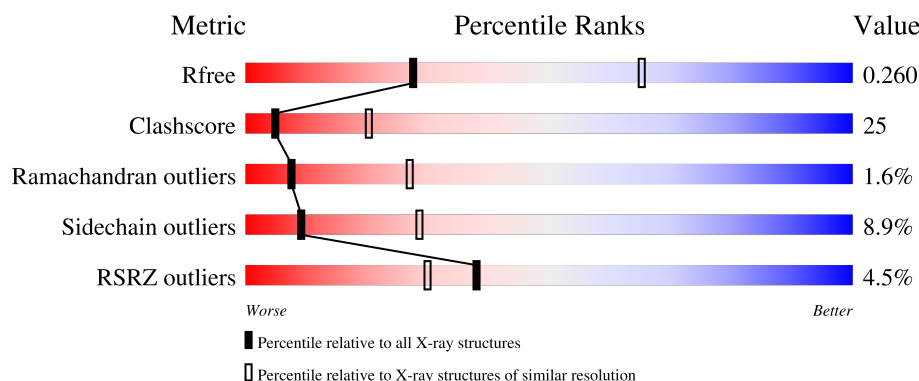
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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	605	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4479 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.

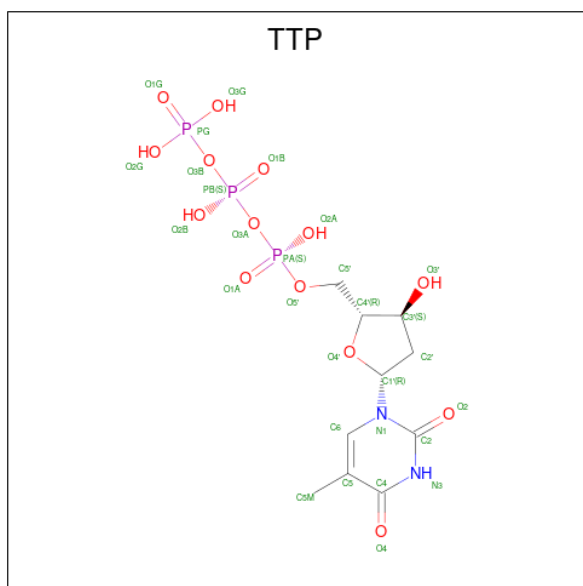
- Molecule 1 is a protein called ANAEROBIC RIBONUCLEOTIDE-TRIPHOSPHATE REDUCTASE LARGE CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	559	4395	2797	740	829	29	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	580	ALA	GLY	engineered mutation	UNP Q9T0V5

- Molecule 2 is THYMIDINE-5'-TRIPHOSPHATE (CCD ID: TTP) (formula: $C_{10}H_{17}N_2O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	29	10	2	14	3	0	0
2	A	1	29	10	2	14	3	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is FE (II) ION (CCD ID: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Fe	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	24	Total	O	0	0
			24	24		

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.10Å 98.10Å 243.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.90 19.99 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.99-2.90) 98.5 (19.99-2.90)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.14 (at 2.88Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.261 0.223 , 0.260	Depositor DCC
R_{free} test set	2270 reflections (8.47%)	wwPDB-VP
Wilson B-factor (Å ²)	59.7	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4479	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE2, MG, TTP

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	0.45	0/4493	0.95	16/6083 (0.3%)

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	1

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	187	SER	N-CA-C	-11.24	100.59	114.75
1	A	268	ASP	N-CA-C	-8.78	95.98	109.85
1	A	95	GLY	N-CA-C	-7.86	101.78	111.45
1	A	398	SER	N-CA-C	7.54	121.52	109.24
1	A	374	GLY	N-CA-C	7.46	123.91	114.66
1	A	328	ILE	N-CA-C	-7.17	97.16	107.77
1	A	266	TYR	N-CA-C	-6.27	102.92	110.13
1	A	530	HIS	N-CA-C	6.01	120.81	112.45
1	A	176	GLN	N-CA-C	-5.98	104.69	112.23
1	A	290	CYS	N-CA-C	5.71	117.19	110.97
1	A	422	LYS	N-CA-C	-5.59	105.29	111.71
1	A	96	ASN	N-CA-C	-5.50	106.56	113.72
1	A	393	GLY	N-CA-C	5.48	122.65	115.47
1	A	188	SER	N-CA-C	-5.42	104.79	111.40
1	A	190	GLY	N-CA-C	-5.28	100.68	113.18
1	A	77	THR	N-CA-C	-5.22	102.43	109.95

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	139	TYR	Sidechain

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	4395	0	4345	223	0
2	A	58	0	26	1	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	24	0	0	1	0
All	All	4479	0	4371	223	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 25.

All (223) 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:560:VAL:HG12	1:A:567:THR:HG22	1.44	0.97
1:A:492:ARG:HG2	1:A:492:ARG:HH11	1.29	0.95
1:A:240:GLU:HG3	1:A:244:LEU:HD23	1.48	0.95
1:A:29:VAL:HG12	1:A:31:PRO:HD2	1.53	0.89
1:A:559:PHE:HB2	1:A:572:MET:HE1	1.57	0.85
1:A:370:LEU:HA	1:A:375:ALA:HB3	1.61	0.82
1:A:478:VAL:HG11	1:A:489:LYS:HG3	1.61	0.81
1:A:118:GLN:HB3	1:A:369:ILE:HG12	1.63	0.81
1:A:486:PRO:O	1:A:490:ILE:HG23	1.80	0.81
1:A:236:MET:HE1	1:A:257:ALA:HB2	1.63	0.81
1:A:555:THR:HG22	1:A:557:ASN:H	1.47	0.80
1:A:518:LYS:H	1:A:518:LYS:HZ2	1.30	0.78
1:A:536:VAL:HG22	1:A:538:MET:HE3	1.69	0.74
1:A:490:ILE:HD12	1:A:527:ALA:HA	1.69	0.74
1:A:99:ILE:HG23	2:A:1586:TTP:H1'	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:LYS:NZ	1:A:290:CYS:SG	2.62	0.73
1:A:33:GLN:HE21	1:A:33:GLN:HA	1.53	0.73
1:A:518:LYS:H	1:A:518:LYS:NZ	1.86	0.72
1:A:240:GLU:CD	1:A:240:GLU:H	1.97	0.72
1:A:94:LEU:HD11	1:A:118:GLN:HG3	1.71	0.72
1:A:151:ALA:HA	1:A:156:ILE:CG1	2.22	0.69
1:A:233:LYS:HG3	1:A:266:TYR:CZ	2.28	0.69
1:A:276:LYS:HG2	1:A:281:SER:O	1.93	0.69
1:A:418:GLU:CD	1:A:418:GLU:H	2.00	0.68
1:A:546:CYS:HB3	1:A:564:CYS:HB2	1.74	0.68
1:A:536:VAL:CG2	1:A:538:MET:HE3	2.25	0.67
1:A:218:ARG:HD2	1:A:264:ARG:HG2	1.78	0.65
1:A:492:ARG:HG2	1:A:492:ARG:NH1	2.03	0.65
1:A:540:VAL:HG23	1:A:575:ILE:HB	1.78	0.65
1:A:420:LEU:HB3	1:A:499:ILE:HG21	1.78	0.65
1:A:359:LEU:O	1:A:362:VAL:HG13	1.97	0.65
1:A:369:ILE:HD12	1:A:370:LEU:H	1.60	0.65
1:A:28:ARG:H	1:A:28:ARG:CD	2.10	0.64
1:A:216:LYS:O	1:A:219:ILE:HG13	1.98	0.63
1:A:102:PRO:HG3	1:A:111:ILE:HD12	1.78	0.63
1:A:204:ASP:HB3	1:A:207:GLU:HG3	1.79	0.63
1:A:478:VAL:CG1	1:A:489:LYS:HG3	2.29	0.63
1:A:540:VAL:HG23	1:A:540:VAL:O	1.99	0.62
1:A:218:ARG:NH2	1:A:232:PRO:O	2.31	0.62
1:A:469:LYS:HE2	1:A:471:TRP:O	1.98	0.62
1:A:198:THR:HG22	1:A:235:VAL:HB	1.81	0.62
1:A:233:LYS:HE3	1:A:266:TYR:OH	1.99	0.62
1:A:299:ASP:HB3	1:A:305:ILE:HD12	1.81	0.62
1:A:151:ALA:HA	1:A:156:ILE:HG12	1.80	0.62
1:A:48:ASN:N	1:A:48:ASN:HD22	1.96	0.62
1:A:137:SER:HB3	1:A:138:PRO:HD3	1.80	0.62
1:A:372:GLN:NE2	1:A:382:PRO:HG3	2.14	0.61
1:A:285:VAL:HG22	1:A:306:LEU:HD21	1.83	0.61
1:A:184:THR:C	1:A:186:PHE:H	2.07	0.61
1:A:158:ASP:HB3	1:A:161:ASN:HB3	1.83	0.61
1:A:204:ASP:OD1	1:A:205:TRP:N	2.33	0.61
1:A:478:VAL:HG13	1:A:489:LYS:HE2	1.81	0.61
1:A:85:LYS:O	1:A:89:GLU:HG3	2.00	0.60
1:A:52:SER:O	1:A:56:LYS:HG2	2.02	0.60
1:A:28:ARG:HD3	1:A:28:ARG:N	2.17	0.60
1:A:28:ARG:H	1:A:28:ARG:HD3	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:ILE:HD12	1:A:220:LYS:N	2.16	0.59
1:A:345:MET:HE1	1:A:423:MET:CE	2.31	0.59
1:A:189:ASN:C	1:A:191:GLN:H	2.10	0.59
1:A:224:ARG:HG2	1:A:224:ARG:HH11	1.66	0.59
1:A:552:MET:HG2	1:A:559:PHE:HB3	1.83	0.59
1:A:509:GLU:C	1:A:510:LEU:HD12	2.29	0.58
1:A:29:VAL:HG12	1:A:31:PRO:CD	2.28	0.58
1:A:509:GLU:O	1:A:510:LEU:HD12	2.04	0.58
1:A:406:GLU:OE2	1:A:473:THR:HG23	2.04	0.58
1:A:47:LYS:C	1:A:48:ASN:HD22	2.11	0.58
1:A:258:LEU:HD12	1:A:520:LEU:HD13	1.84	0.58
1:A:402:ILE:HG13	1:A:403:GLY:N	2.18	0.58
1:A:555:THR:HB	1:A:558:GLY:O	2.04	0.57
1:A:539:PRO:HB2	1:A:576:ARG:HH21	1.69	0.57
1:A:312:LEU:HD13	1:A:395:SER:HB3	1.86	0.57
1:A:243:ASN:HD22	1:A:243:ASN:N	2.03	0.57
1:A:264:ARG:O	1:A:265:MET:HB3	2.04	0.57
1:A:424:ASN:O	1:A:428:LYS:HG2	2.04	0.57
1:A:539:PRO:CB	1:A:576:ARG:HH21	2.18	0.56
1:A:497:HIS:ND1	1:A:531:LEU:HB2	2.20	0.56
1:A:539:PRO:HA	1:A:576:ARG:HE	1.70	0.56
1:A:540:VAL:CG2	1:A:575:ILE:HB	2.36	0.56
1:A:468:ASP:OD1	1:A:469:LYS:N	2.39	0.56
1:A:490:ILE:HD11	1:A:526:TYR:CD2	2.41	0.55
1:A:82:VAL:CG1	1:A:87:MET:HE1	2.36	0.55
1:A:505:ILE:HG12	1:A:533:TYR:CD2	2.42	0.55
1:A:198:THR:HG21	1:A:286:SER:HB3	1.88	0.55
1:A:238:VAL:HA	1:A:243:ASN:HD21	1.72	0.55
1:A:314:VAL:HG22	1:A:398:SER:HB2	1.87	0.55
1:A:518:LYS:HZ2	1:A:518:LYS:N	2.02	0.55
1:A:158:ASP:CB	1:A:161:ASN:HB3	2.37	0.55
1:A:239:GLU:H	1:A:243:ASN:HD21	1.53	0.54
1:A:176:GLN:HB2	1:A:217:ASN:HD21	1.72	0.54
1:A:349:PHE:HB2	1:A:430:TRP:CZ2	2.43	0.54
1:A:349:PHE:CZ	1:A:353:MET:HG3	2.42	0.54
1:A:510:LEU:HB2	1:A:538:MET:HE2	1.90	0.54
1:A:59:GLU:HA	1:A:59:GLU:OE1	2.06	0.53
1:A:93:LYS:O	1:A:373:GLU:HG3	2.08	0.53
1:A:283:VAL:HG13	1:A:284:PRO:HD2	1.89	0.53
1:A:505:ILE:HD12	1:A:507:TYR:CE1	2.43	0.53
1:A:492:ARG:HH11	1:A:492:ARG:CG	2.12	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:PHE:HB2	1:A:373:GLU:HB3	1.90	0.52
1:A:299:ASP:OD1	1:A:303:ASN:N	2.40	0.52
1:A:218:ARG:O	1:A:264:ARG:HD3	2.09	0.52
1:A:514:LYS:NZ	1:A:549:THR:O	2.42	0.52
1:A:490:ILE:HD12	1:A:527:ALA:CA	2.40	0.52
1:A:188:SER:O	1:A:190:GLY:N	2.43	0.52
1:A:188:SER:C	1:A:190:GLY:H	2.18	0.52
1:A:564:CYS:SG	1:A:566:GLU:HB2	2.50	0.52
1:A:239:GLU:H	1:A:243:ASN:ND2	2.08	0.52
1:A:324:LEU:HB3	1:A:460:TYR:CE2	2.45	0.52
1:A:335:GLN:O	1:A:338:VAL:HG23	2.10	0.52
1:A:464:LYS:O	1:A:465:ASP:HB2	2.10	0.52
1:A:246:LYS:H	1:A:246:LYS:HD2	1.75	0.51
1:A:552:MET:HE2	1:A:572:MET:SD	2.50	0.51
1:A:158:ASP:O	1:A:159:ALA:C	2.53	0.51
1:A:176:GLN:O	1:A:180:TYR:HD1	1.93	0.51
1:A:511:PRO:O	1:A:513:MET:HG2	2.11	0.50
1:A:414:ASP:C	1:A:414:ASP:OD1	2.55	0.50
1:A:264:ARG:O	1:A:265:MET:CB	2.59	0.50
1:A:415:ILE:O	1:A:418:GLU:HG2	2.11	0.50
1:A:520:LEU:HD21	1:A:536:VAL:HG11	1.94	0.50
1:A:94:LEU:HD11	1:A:118:GLN:CG	2.41	0.49
1:A:48:ASN:N	1:A:48:ASN:ND2	2.60	0.49
1:A:319:LEU:HB2	1:A:320:PRO:HD3	1.94	0.49
1:A:369:ILE:HD12	1:A:370:LEU:N	2.25	0.49
1:A:448:LEU:HD12	1:A:451:ARG:HB3	1.94	0.49
1:A:345:MET:HE1	1:A:423:MET:HE2	1.94	0.49
1:A:176:GLN:HG3	1:A:217:ASN:HD21	1.78	0.48
1:A:466:VAL:HG12	1:A:467:THR:HG23	1.94	0.48
1:A:378:VAL:C	1:A:379:ARG:HG2	2.37	0.48
1:A:199:PHE:HE1	1:A:236:MET:CE	2.27	0.48
1:A:553:THR:HB	1:A:560:VAL:HG23	1.94	0.48
1:A:370:LEU:HA	1:A:375:ALA:CB	2.37	0.48
1:A:188:SER:C	1:A:190:GLY:N	2.68	0.48
1:A:199:PHE:HE1	1:A:236:MET:HE2	1.79	0.48
1:A:545:THR:HG23	1:A:571:LYS:HD2	1.95	0.48
1:A:413:ARG:HH11	1:A:413:ARG:HB2	1.79	0.47
1:A:418:GLU:CD	1:A:418:GLU:N	2.71	0.47
1:A:495:PRO:O	1:A:499:ILE:CD1	2.62	0.47
1:A:497:HIS:CE1	1:A:531:LEU:HB2	2.49	0.47
1:A:176:GLN:CB	1:A:217:ASN:HD21	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ASN:HB2	5:A:2009:HOH:O	2.14	0.47
1:A:81:LEU:HG	1:A:288:MET:HG2	1.96	0.47
1:A:218:ARG:HG3	1:A:264:ARG:HG2	1.96	0.47
1:A:545:THR:CG2	1:A:571:LYS:HD2	2.45	0.47
1:A:55:MET:HE1	1:A:68:ILE:HD11	1.97	0.47
1:A:400:GLY:HA2	1:A:441:TYR:O	2.15	0.47
1:A:485:THR:HG23	1:A:488:GLU:HB2	1.96	0.47
1:A:505:ILE:HG12	1:A:533:TYR:CG	2.50	0.46
1:A:28:ARG:CD	1:A:28:ARG:N	2.76	0.46
1:A:322:ILE:HA	1:A:344:ARG:NH1	2.30	0.46
1:A:410:LEU:HD21	1:A:466:VAL:HG21	1.98	0.46
1:A:369:ILE:O	1:A:375:ALA:HB3	2.15	0.46
1:A:576:ARG:HH11	1:A:576:ARG:HG3	1.81	0.46
1:A:372:GLN:HE22	1:A:382:PRO:HG3	1.80	0.46
1:A:33:GLN:HA	1:A:33:GLN:NE2	2.26	0.45
1:A:191:GLN:HE21	1:A:191:GLN:HB2	1.62	0.45
1:A:406:GLU:OE2	1:A:469:LYS:NZ	2.46	0.45
1:A:243:ASN:HD22	1:A:243:ASN:H	1.62	0.45
1:A:548:SER:HB2	1:A:563:ILE:HD11	1.97	0.45
1:A:189:ASN:C	1:A:191:GLN:N	2.70	0.45
1:A:269:ILE:HD13	1:A:524:TRP:CG	2.52	0.45
1:A:538:MET:HB2	1:A:539:PRO:HD2	1.98	0.45
1:A:133:ASP:HA	1:A:210:ILE:HG21	1.98	0.45
1:A:420:LEU:HD12	1:A:420:LEU:HA	1.82	0.45
1:A:496:TYR:HA	1:A:499:ILE:HD13	1.99	0.45
1:A:191:GLN:O	1:A:192:THR:C	2.60	0.45
1:A:507:TYR:HA	1:A:535:GLY:O	2.16	0.45
1:A:349:PHE:HB2	1:A:430:TRP:CE2	2.51	0.44
1:A:439:SER:OG	1:A:502:GLY:CA	2.65	0.44
1:A:205:TRP:CE2	1:A:206:THR:HG23	2.53	0.44
1:A:291:ARG:HD3	1:A:505:ILE:HB	1.98	0.44
1:A:545:THR:HG21	1:A:566:GLU:OE1	2.17	0.44
1:A:94:LEU:CD1	1:A:118:GLN:HG3	2.43	0.44
1:A:176:GLN:HG3	1:A:217:ASN:ND2	2.33	0.44
1:A:254:LYS:HE2	1:A:521:GLU:HG3	1.99	0.44
1:A:424:ASN:HB3	1:A:428:LYS:HE2	1.99	0.44
1:A:33:GLN:HE21	1:A:33:GLN:CA	2.20	0.44
1:A:53:PHE:HZ	1:A:350:GLU:HG2	1.83	0.44
1:A:234:LEU:HB2	1:A:266:TYR:HB3	2.00	0.44
1:A:443:THR:HG22	1:A:445:ALA:H	1.82	0.44
1:A:508:VAL:HG13	1:A:510:LEU:HD13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:563:ILE:O	1:A:563:ILE:HG13	2.17	0.44
1:A:156:ILE:HG21	1:A:162:TYR:CG	2.53	0.44
1:A:254:LYS:O	1:A:258:LEU:CD2	2.66	0.43
1:A:345:MET:HE1	1:A:423:MET:HE3	1.97	0.43
1:A:485:THR:HG23	1:A:488:GLU:CB	2.48	0.43
1:A:487:PHE:O	1:A:491:SER:HB2	2.19	0.43
1:A:499:ILE:N	1:A:499:ILE:HD12	2.34	0.43
1:A:225:ASP:O	1:A:226:GLY:C	2.60	0.43
1:A:519:GLY:O	1:A:522:ALA:HB3	2.17	0.43
1:A:87:MET:HE2	1:A:375:ALA:HA	2.01	0.43
1:A:138:PRO:O	1:A:141:LYS:HB2	2.19	0.43
1:A:265:MET:SD	1:A:537:ASN:HA	2.59	0.43
1:A:319:LEU:O	1:A:320:PRO:C	2.58	0.43
1:A:345:MET:CE	1:A:423:MET:HG2	2.49	0.43
1:A:481:GLU:O	1:A:482:GLU:C	2.62	0.43
1:A:487:PHE:HD2	1:A:526:TYR:CD2	2.37	0.43
1:A:185:LEU:HB3	1:A:193:PRO:HG2	2.01	0.43
1:A:265:MET:HE1	1:A:538:MET:O	2.19	0.42
1:A:546:CYS:SG	1:A:548:SER:HB3	2.60	0.42
1:A:439:SER:OG	1:A:502:GLY:HA3	2.19	0.42
1:A:54:ILE:HD13	1:A:351:ALA:HA	2.01	0.42
1:A:107:VAL:O	1:A:111:ILE:HG13	2.19	0.42
1:A:184:THR:O	1:A:186:PHE:N	2.52	0.42
1:A:179:GLU:CD	1:A:218:ARG:NH1	2.78	0.42
1:A:171:VAL:HG12	1:A:213:ALA:CB	2.50	0.42
1:A:471:TRP:CD1	1:A:471:TRP:C	2.97	0.42
1:A:254:LYS:O	1:A:258:LEU:HD23	2.20	0.42
1:A:243:ASN:HB3	1:A:250:ASN:HB2	2.02	0.41
1:A:266:TYR:HB3	1:A:267:PRO:HA	2.01	0.41
1:A:69:ASP:OD1	1:A:69:ASP:N	2.53	0.41
1:A:298:LYS:HA	1:A:303:ASN:O	2.20	0.41
1:A:487:PHE:HB3	1:A:526:TYR:CE2	2.56	0.41
1:A:153:LYS:HE3	1:A:154:TRP:CZ2	2.56	0.41
1:A:184:THR:C	1:A:186:PHE:N	2.73	0.41
1:A:336:LYS:HA	1:A:336:LYS:HD2	1.93	0.41
1:A:243:ASN:O	1:A:254:LYS:HD2	2.20	0.41
1:A:410:LEU:CD2	1:A:466:VAL:HG21	2.51	0.41
1:A:465:ASP:N	1:A:468:ASP:OD2	2.36	0.41
1:A:369:ILE:O	1:A:375:ALA:CB	2.69	0.41
1:A:153:LYS:HE3	1:A:154:TRP:CE2	2.56	0.41
1:A:357:SER:HA	1:A:360:LYS:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:VAL:HG12	1:A:493:GLU:OE2	2.21	0.41
1:A:79:CYS:O	1:A:310:ASN:HB2	2.21	0.41
1:A:135:VAL:O	1:A:138:PRO:HD2	2.21	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	557/605 (92%)	505 (91%)	43 (8%)	9 (2%)	7	27

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	189	ASN
1	A	564	CYS
1	A	157	ALA
1	A	246	LYS
1	A	185	LEU
1	A	192	THR
1	A	300	SER
1	A	475	SER
1	A	191	GLN

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	482/524 (92%)	439 (91%)	43 (9%)	9 28

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ARG
1	A	33	GLN
1	A	47	LYS
1	A	48	ASN
1	A	59	GLU
1	A	121	SER
1	A	127	THR
1	A	168	GLU
1	A	176	GLN
1	A	194	PHE
1	A	197	ILE
1	A	217	ASN
1	A	218	ARG
1	A	240	GLU
1	A	243	ASN
1	A	247	ASP
1	A	264	ARG
1	A	291	ARG
1	A	306	LEU
1	A	317	LEU
1	A	335	GLN
1	A	338	VAL
1	A	362	VAL
1	A	366	VAL
1	A	369	ILE
1	A	399	LEU
1	A	402	ILE
1	A	413	ARG
1	A	418	GLU
1	A	420	LEU
1	A	427	LEU
1	A	440	LEU
1	A	469	LYS
1	A	478	VAL
1	A	485	THR
1	A	490	ILE
1	A	492	ARG
1	A	505	ILE

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Mol	Chain	Res	Type
1	A	518	LYS
1	A	520	LEU
1	A	536	VAL
1	A	552	MET
1	A	581	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	48	ASN
1	A	98	GLN
1	A	118	GLN
1	A	176	GLN
1	A	189	ASN
1	A	191	GLN
1	A	217	ASN
1	A	243	ASN
1	A	255	GLN
1	A	274	ASN
1	A	342	ASN
1	A	372	GLN
1	A	392	ASN
1	A	426	HIS
1	A	429	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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
2	TTP	A	1586	3	29,30,30	2.14	9 (31%)	43,47,47	2.07	10 (23%)
2	TTP	A	1589	-	29,30,30	2.05	9 (31%)	43,47,47	2.12	10 (23%)

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	TTP	A	1586	3	-	8/22/34/34	0/2/2/2
2	TTP	A	1589	-	-	6/22/34/34	0/2/2/2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1586	TTP	C2'-C1'	-6.25	1.35	1.52
2	A	1589	TTP	C2'-C1'	-6.23	1.35	1.52
2	A	1586	TTP	PB-O3A	3.60	1.63	1.59
2	A	1589	TTP	C6-C5	3.56	1.40	1.34
2	A	1586	TTP	C6-N1	3.55	1.44	1.38
2	A	1589	TTP	C6-N1	3.41	1.43	1.38
2	A	1586	TTP	C6-C5	3.30	1.40	1.34
2	A	1586	TTP	PB-O3B	3.15	1.62	1.59
2	A	1589	TTP	C4-C5	-3.07	1.39	1.44
2	A	1586	TTP	PA-O3A	2.73	1.62	1.59
2	A	1586	TTP	C4-C5	-2.57	1.40	1.44
2	A	1586	TTP	C1'-N1	-2.56	1.41	1.48
2	A	1589	TTP	C2-N1	2.45	1.42	1.38
2	A	1589	TTP	PB-O3B	2.42	1.62	1.59
2	A	1589	TTP	PB-O3A	2.41	1.62	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1586	TTP	C2-N1	2.28	1.42	1.38
2	A	1589	TTP	C2-N3	2.23	1.41	1.38
2	A	1589	TTP	C1'-N1	-2.21	1.42	1.48

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1586	TTP	C5-C4-N3	6.43	120.92	115.32
2	A	1589	TTP	C5-C4-N3	6.40	120.89	115.32
2	A	1589	TTP	O4'-C1'-N1	6.30	119.04	107.86
2	A	1586	TTP	O4'-C1'-N1	5.55	117.71	107.86
2	A	1586	TTP	C4-N3-C2	-5.28	120.42	127.34
2	A	1589	TTP	C4-N3-C2	-5.26	120.44	127.34
2	A	1589	TTP	O4-C4-C5	-4.03	120.31	124.92
2	A	1586	TTP	O4-C4-C5	-3.98	120.36	124.92
2	A	1589	TTP	C3'-C2'-C1'	3.47	111.09	102.60
2	A	1589	TTP	N3-C2-N1	3.46	119.39	114.89
2	A	1586	TTP	N3-C2-N1	3.45	119.38	114.89
2	A	1586	TTP	C3'-C2'-C1'	3.18	110.37	102.60
2	A	1589	TTP	C6-N1-C2	-2.51	118.81	121.30
2	A	1586	TTP	C5-C6-N1	-2.33	120.78	123.31
2	A	1586	TTP	C4'-O4'-C1'	2.32	115.03	109.51
2	A	1589	TTP	C4'-O4'-C1'	2.27	114.90	109.51
2	A	1586	TTP	C5M-C5-C6	-2.24	119.82	122.85
2	A	1586	TTP	C6-N1-C2	-2.13	119.18	121.30
2	A	1589	TTP	C5-C6-N1	-2.04	121.10	123.31
2	A	1589	TTP	C5M-C5-C6	-2.02	120.11	122.85

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1586	TTP	C5'-O5'-PA-O1A
2	A	1586	TTP	C5'-O5'-PA-O2A
2	A	1586	TTP	C5'-O5'-PA-O3A
2	A	1589	TTP	PB-O3B-PG-O2G
2	A	1589	TTP	PB-O3B-PG-O3G
2	A	1589	TTP	O4'-C4'-C5'-O5'
2	A	1586	TTP	O4'-C4'-C5'-O5'
2	A	1589	TTP	C3'-C4'-C5'-O5'
2	A	1586	TTP	PA-O3A-PB-O3B
2	A	1586	TTP	C3'-C4'-C5'-O5'

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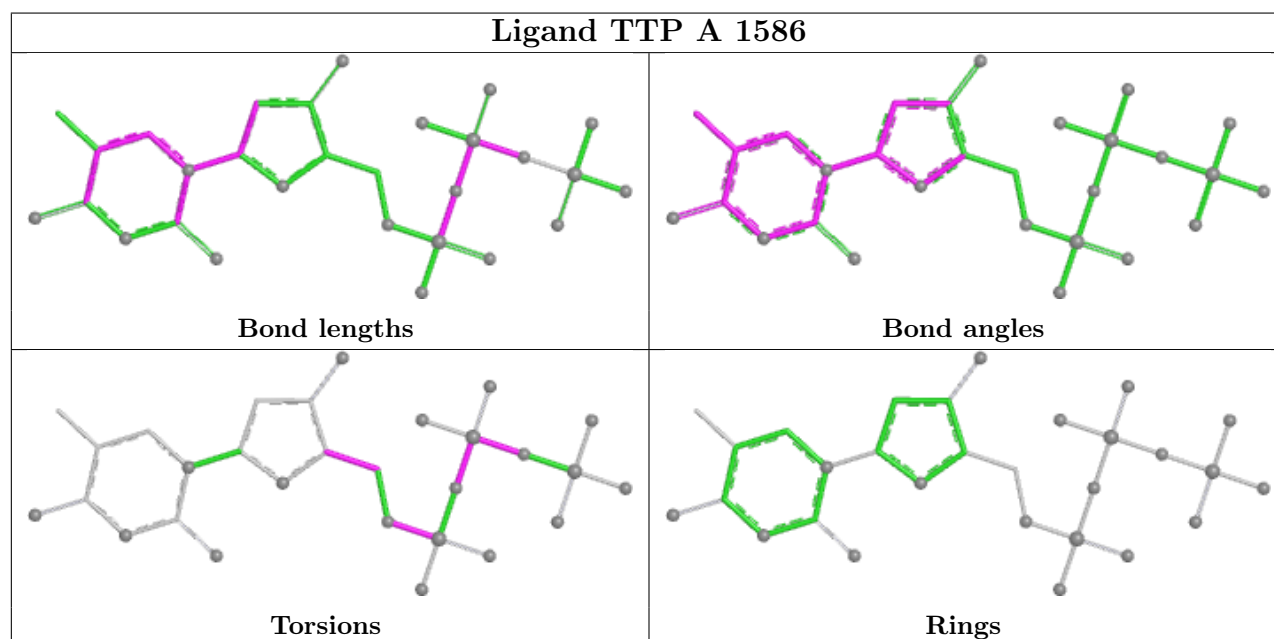
Mol	Chain	Res	Type	Atoms
2	A	1586	TTP	PG-O3B-PB-O2B
2	A	1586	TTP	PG-O3B-PB-O1B
2	A	1589	TTP	PG-O3B-PB-O1B
2	A	1589	TTP	PG-O3B-PB-O2B

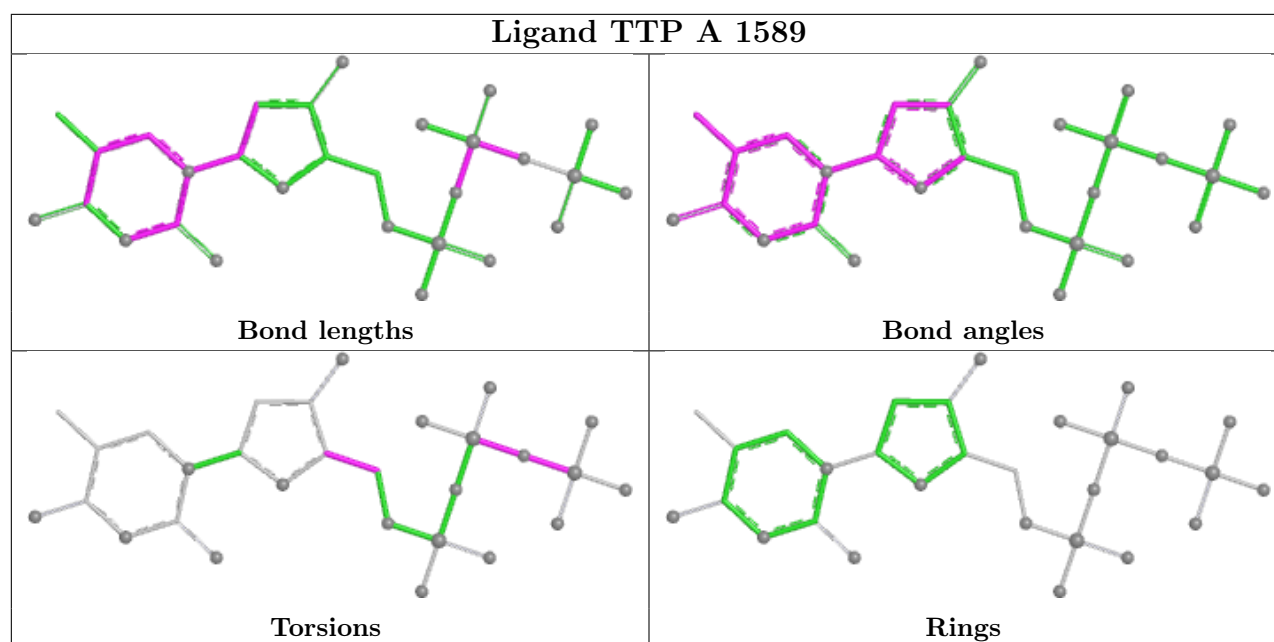
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1586	TTP	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	559/605 (92%)	-0.03	25 (4%) 38 30	26, 48, 92, 101	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	190	GLY	4.5
1	A	186	PHE	4.2
1	A	192	THR	4.0
1	A	556	GLU	4.0
1	A	159	ALA	3.8
1	A	27	SER	3.7
1	A	158	ASP	3.6
1	A	555	THR	3.6
1	A	554	PRO	3.2
1	A	191	GLN	3.1
1	A	188	SER	3.0
1	A	189	ASN	2.9
1	A	156	ILE	2.9
1	A	562	SER	2.8
1	A	247	ASP	2.7
1	A	541	ASP	2.7
1	A	240	GLU	2.6
1	A	193	PRO	2.5
1	A	157	ALA	2.5
1	A	219	ILE	2.4
1	A	154	TRP	2.2
1	A	168	GLU	2.2
1	A	563	ILE	2.1
1	A	553	THR	2.0
1	A	488	GLU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

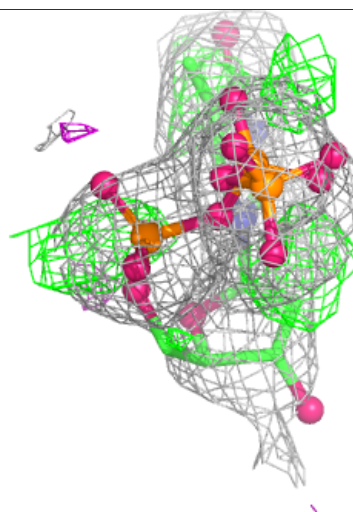
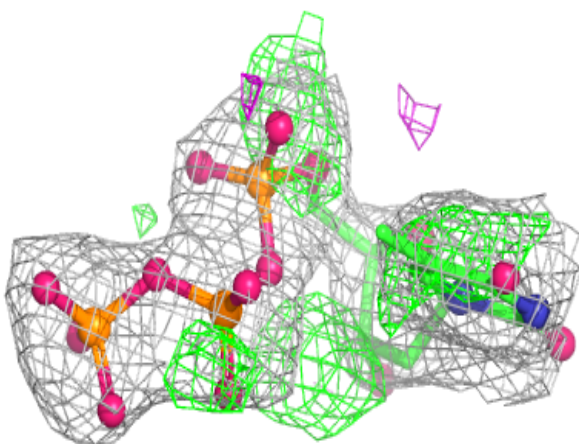
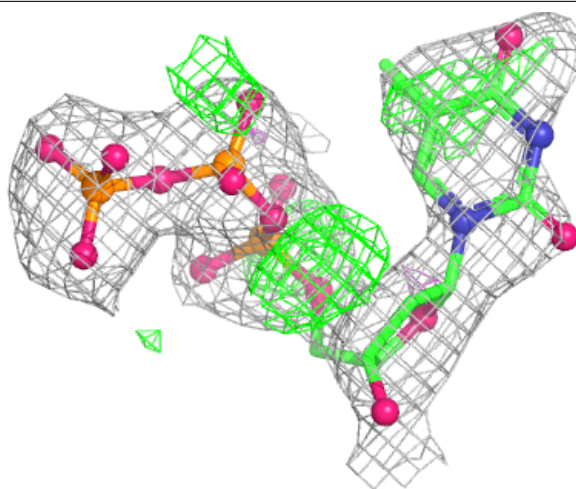
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

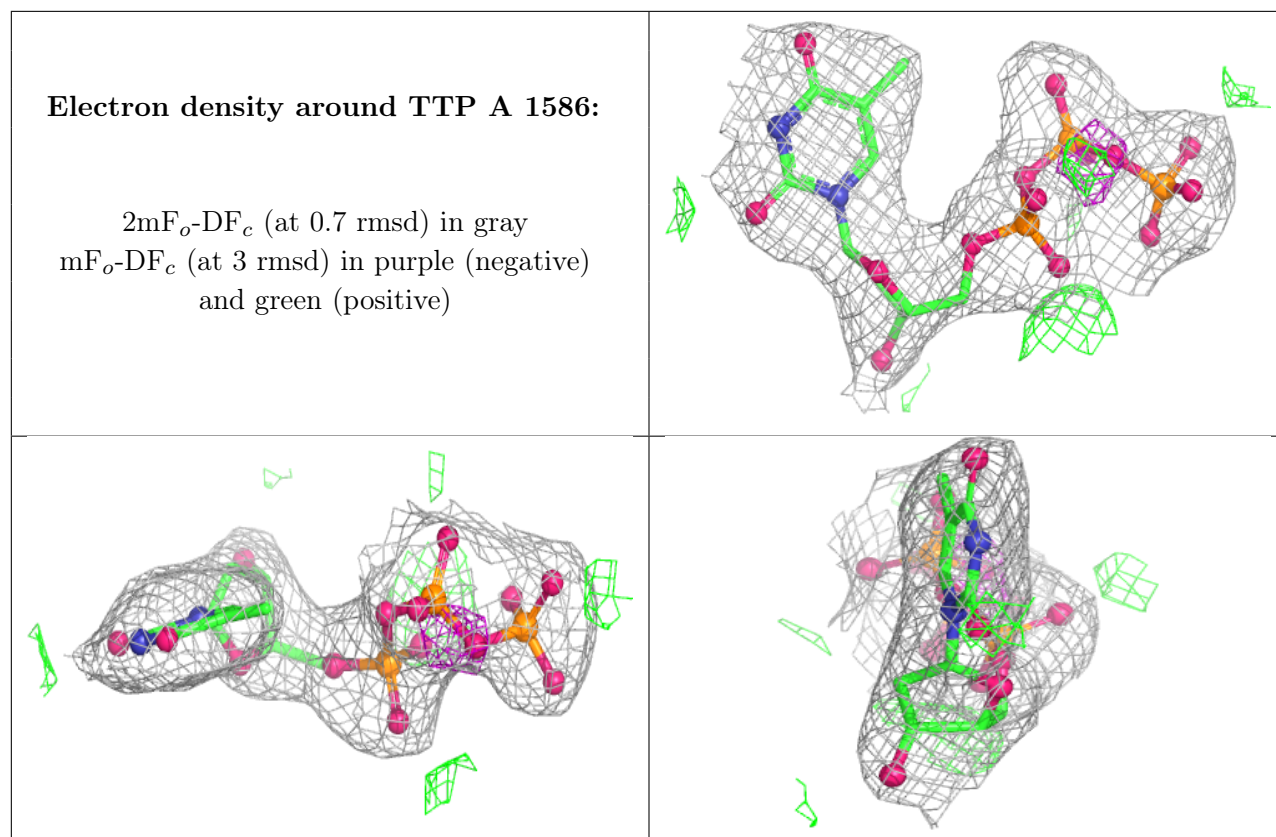
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	TTP	A	1589	29/29	0.93	0.17	45,66,79,80	29
3	MG	A	1587	1/1	0.94	0.06	23,23,23,23	0
2	TTP	A	1586	29/29	0.95	0.09	44,55,65,66	0
4	FE2	A	1588	1/1	0.98	0.09	74,74,74,74	0

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.

Electron density around TTP A 1589:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.