Full wwPDB X-ray Structure Validation Report (i)

Dec 3, 2023 – 04:09 am GMT

PDB ID	:	1H78
Title	:	STRUCTURAL BASIS FOR ALLOSTERIC SUBSTRATE SPECIFICITY REGULATION IN CLASS III RIBONUCLEOTIDE REDUCTASES: NRDD IN COMPLEX WITH DCTP.
Authors	:	Larsson, K.-M.; Andersson, J.; Sjoeberg, B.-M.; Nordlund, P.; Logan, D.T.
Deposited on	:	2001-07-04
Resolution	:	2.50 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 (i) 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 (1)) were used in the production of this report:

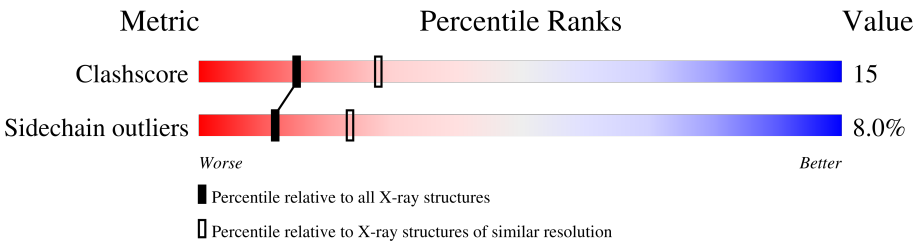
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5346 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	605	63% 21% • 12%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4371 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.

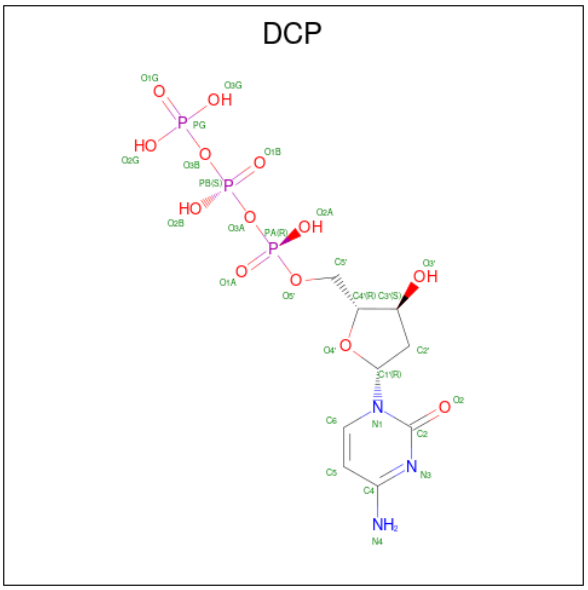
- Molecule 1 is a protein called ANAEROBIC RIBONUCLEOTIDE-TRIPHOSPHATE REDUCTASE LARGE CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	534	4218	2690	710	793	25	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 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: $C_9H_{16}N_3O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	28	9	3	13	3	0	0
2	A	1	28	9	3	13	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
			Total	O		
4	A	96	96	96	0	0

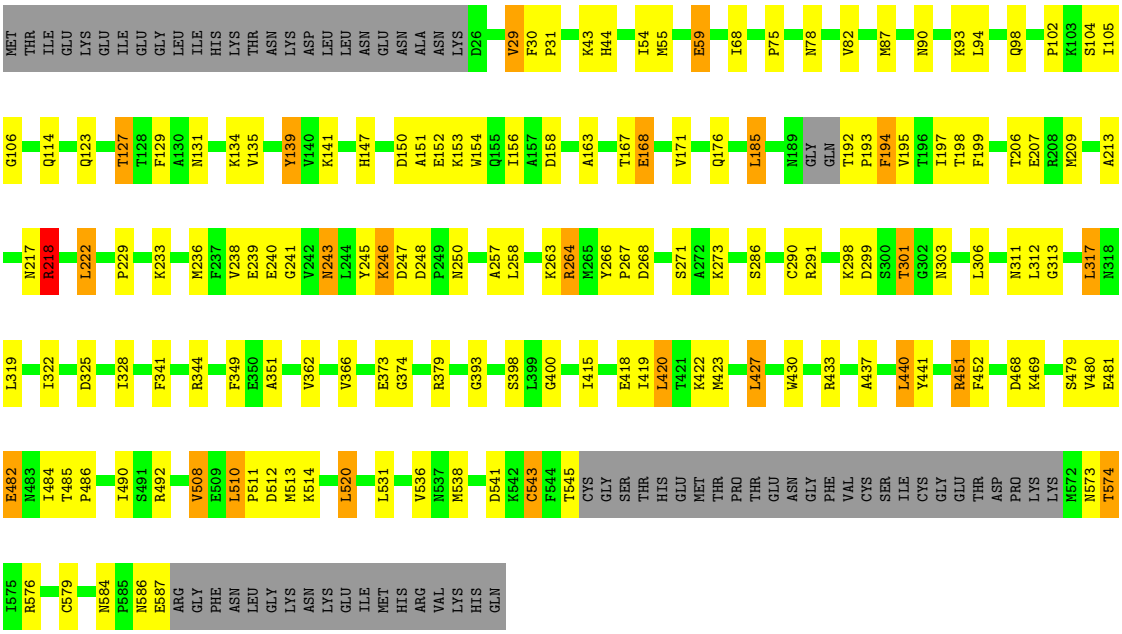
3 Residue-property plots (i)

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. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: ANAEROBIC RIBONUCLEOTIDE-TRIPHOSPHATE REDUCTASE LARGE CHAIN

Chain A: 63% 21% • 12%



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	97.94Å 97.94Å 242.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.50	Depositor
% Data completeness (in resolution range)	97.9 (19.96-2.50)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.254	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4371	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

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: MG, DCP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	1.04	3/4310 (0.1%)	1.03	14/5833 (0.2%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	543	CYS	CB-SG	16.64	2.10	1.82
1	A	579	CYS	CB-SG	7.57	1.95	1.82
1	A	451	ARG	CZ-NH1	5.54	1.40	1.33

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	543	CYS	CA-CB-SG	12.08	135.74	114.00
1	A	218	ARG	NE-CZ-NH2	-11.44	114.58	120.30
1	A	451	ARG	NE-CZ-NH2	-10.48	115.06	120.30
1	A	218	ARG	NE-CZ-NH1	10.40	125.50	120.30
1	A	379	ARG	NE-CZ-NH1	9.88	125.24	120.30
1	A	90	ASN	C-N-CA	-7.89	105.72	122.30
1	A	379	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	A	543	CYS	N-CA-C	-6.18	94.31	111.00
1	A	325	ASP	CB-CG-OD1	5.88	123.60	118.30
1	A	398	SER	N-CA-C	5.86	126.81	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	268	ASP	N-CA-C	-5.30	96.68	111.00
1	A	328	ILE	N-CA-C	-5.06	97.34	111.00
1	A	374	GLY	N-CA-C	5.06	125.75	113.10
1	A	451	ARG	NE-CZ-NH1	5.06	122.83	120.30

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 (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	4218	0	4177	127	1
2	A	56	0	24	2	1
3	A	1	0	0	0	0
4	A	96	0	0	5	0
All	All	4371	0	4201	127	1

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

All (127) 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:543:CYS:CB	1:A:543:CYS:SG	2.10	1.39
1:A:29:VAL:HG13	1:A:31:PRO:HD2	1.41	1.01
1:A:420:LEU:HD12	1:A:423:MET:CE	1.93	0.98
1:A:480:VAL:HG23	1:A:481:GLU:HG3	1.43	0.98
1:A:55:MET:O	1:A:59:GLU:HG2	1.69	0.91
1:A:167:THR:HG22	1:A:209:MET:CE	2.05	0.85
1:A:29:VAL:CG1	1:A:31:PRO:HD2	2.07	0.84
1:A:167:THR:HG22	1:A:209:MET:HE1	1.60	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:GLU:HG3	1:A:245:TYR:CE1	2.15	0.80
1:A:420:LEU:HD12	1:A:423:MET:HE3	1.69	0.75
1:A:236:MET:HE1	1:A:257:ALA:HB2	1.70	0.74
1:A:238:VAL:HA	1:A:243:ASN:HD21	1.54	0.70
1:A:78:ASN:HD22	1:A:311:ASN:HD22	1.41	0.69
1:A:341:PHE:CE1	1:A:419:ILE:HD11	2.29	0.67
1:A:240:GLU:HG3	1:A:245:TYR:HE1	1.59	0.67
1:A:78:ASN:HD22	1:A:311:ASN:ND2	1.94	0.65
1:A:167:THR:HG22	1:A:209:MET:HE3	1.79	0.64
1:A:141:LYS:HG3	1:A:206:THR:HG21	1.78	0.64
1:A:233:LYS:HE3	1:A:290:CYS:HA	1.79	0.64
1:A:520:LEU:HG	1:A:538:MET:HE1	1.80	0.63
1:A:301:THR:HB	4:A:2051:HOH:O	1.98	0.63
1:A:98:GLN:HG3	4:A:2016:HOH:O	1.97	0.63
1:A:241:GLY:N	1:A:248:ASP:OD1	2.30	0.63
1:A:168:GLU:HA	1:A:209:MET:CE	2.28	0.62
1:A:240:GLU:HG3	1:A:245:TYR:CD1	2.33	0.62
1:A:239:GLU:H	1:A:243:ASN:ND2	1.98	0.62
1:A:233:LYS:NZ	1:A:290:CYS:SG	2.72	0.62
1:A:480:VAL:HG23	1:A:481:GLU:N	2.16	0.61
1:A:245:TYR:N	1:A:248:ASP:OD2	2.34	0.60
1:A:233:LYS:CE	1:A:290:CYS:SG	2.89	0.60
1:A:349:PHE:HB2	1:A:430:TRP:CZ2	2.37	0.60
1:A:480:VAL:O	1:A:481:GLU:C	2.40	0.60
1:A:114:GLN:NE2	4:A:2019:HOH:O	2.34	0.59
1:A:258:LEU:HD23	1:A:520:LEU:HD13	1.84	0.59
1:A:301:THR:O	1:A:301:THR:HG23	2.02	0.59
1:A:246:LYS:HD2	1:A:246:LYS:H	1.67	0.59
1:A:480:VAL:O	1:A:482:GLU:N	2.36	0.59
1:A:451:ARG:HB2	2:A:1588:DCP:HN42	1.68	0.58
1:A:152:GLU:HG3	1:A:153:LYS:N	2.18	0.58
1:A:543:CYS:C	1:A:545:THR:H	2.06	0.58
1:A:541:ASP:HA	1:A:573:ASN:O	2.02	0.58
1:A:199:PHE:HE1	1:A:236:MET:HE2	1.69	0.58
1:A:192:THR:N	1:A:193:PRO:HD2	2.17	0.58
1:A:299:ASP:OD2	1:A:303:ASN:HB2	2.04	0.57
1:A:301:THR:HG22	1:A:303:ASN:OD1	2.04	0.57
1:A:222:LEU:HD22	1:A:229:PRO:HB3	1.86	0.57
1:A:298:LYS:HA	1:A:303:ASN:O	2.06	0.56
1:A:576:ARG:HG2	1:A:576:ARG:HH11	1.70	0.56
1:A:263:LYS:C	1:A:264:ARG:HG2	2.25	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:584:ASN:OD1	1:A:586:ASN:HB2	2.05	0.56
1:A:44:HIS:CD2	4:A:2003:HOH:O	2.59	0.56
1:A:151:ALA:HA	1:A:156:ILE:HD12	1.88	0.55
1:A:168:GLU:N	1:A:209:MET:HE3	2.21	0.55
1:A:82:VAL:CG1	1:A:87:MET:HE1	2.37	0.55
1:A:301:THR:O	1:A:301:THR:CG2	2.55	0.55
1:A:168:GLU:HA	1:A:209:MET:HE3	1.88	0.55
1:A:218:ARG:O	1:A:264:ARG:HD2	2.08	0.54
1:A:152:GLU:HG3	1:A:153:LYS:H	1.73	0.54
1:A:511:PRO:O	1:A:513:MET:HG2	2.07	0.54
1:A:102:PRO:HG2	1:A:139:TYR:CD1	2.43	0.54
1:A:322:ILE:HA	1:A:344:ARG:NH1	2.23	0.53
1:A:512:ASP:OD1	1:A:514:LYS:HE3	2.07	0.53
1:A:123:GLN:HE21	1:A:127:THR:HG22	1.74	0.53
1:A:480:VAL:CG2	1:A:481:GLU:HG3	2.30	0.53
1:A:258:LEU:CD2	1:A:520:LEU:HD13	2.39	0.52
1:A:131:ASN:O	1:A:135:VAL:HG23	2.09	0.52
1:A:311:ASN:ND2	1:A:313:GLY:H	2.08	0.52
1:A:171:VAL:HG12	1:A:213:ALA:CB	2.41	0.51
1:A:54:ILE:HD13	1:A:351:ALA:HA	1.93	0.51
1:A:194:PHE:CD1	1:A:194:PHE:N	2.77	0.51
1:A:134:LYS:HD3	1:A:207:GLU:OE2	2.11	0.50
1:A:266:TYR:HB3	1:A:267:PRO:HA	1.94	0.50
1:A:44:HIS:HD2	4:A:2003:HOH:O	1.94	0.49
1:A:317:LEU:HD13	1:A:319:LEU:HD23	1.92	0.49
1:A:199:PHE:HE1	1:A:236:MET:CE	2.25	0.49
1:A:168:GLU:CA	1:A:209:MET:HE3	2.43	0.49
1:A:479:SER:O	1:A:480:VAL:O	2.31	0.49
1:A:479:SER:C	1:A:480:VAL:O	2.52	0.48
1:A:198:THR:HG21	1:A:286:SER:HB3	1.94	0.48
1:A:43:LYS:HG2	1:A:68:ILE:HG23	1.95	0.48
1:A:576:ARG:HG2	1:A:576:ARG:NH1	2.29	0.48
1:A:400:GLY:HA2	1:A:441:TYR:O	2.14	0.47
1:A:512:ASP:OD1	1:A:514:LYS:HB2	2.13	0.47
1:A:102:PRO:HG2	1:A:139:TYR:CE1	2.48	0.47
1:A:82:VAL:HG13	1:A:87:MET:HE1	1.96	0.47
1:A:541:ASP:OD1	1:A:574:THR:HG22	2.15	0.47
1:A:168:GLU:HA	1:A:209:MET:HE2	1.96	0.47
1:A:239:GLU:H	1:A:243:ASN:HD21	1.62	0.46
1:A:468:ASP:OD1	1:A:469:LYS:N	2.48	0.46
1:A:420:LEU:HD12	1:A:423:MET:HE1	1.88	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:PHE:HB2	1:A:430:TRP:CE2	2.50	0.46
1:A:420:LEU:CD1	1:A:423:MET:CE	2.82	0.45
1:A:451:ARG:HB2	2:A:1588:DCP:N4	2.32	0.45
1:A:393:GLY:HA2	1:A:437:ALA:HB2	1.99	0.45
1:A:243:ASN:HB3	1:A:250:ASN:HB2	1.98	0.45
1:A:418:GLU:O	1:A:422:LYS:HG3	2.16	0.45
1:A:514:LYS:HE3	1:A:514:LYS:HB2	1.74	0.45
1:A:482:GLU:O	1:A:484:ILE:N	2.51	0.44
1:A:233:LYS:HE3	1:A:290:CYS:SG	2.58	0.44
1:A:484:ILE:HG22	1:A:485:THR:O	2.18	0.44
1:A:176:GLN:HG3	1:A:217:ASN:ND2	2.34	0.43
1:A:543:CYS:C	1:A:545:THR:N	2.71	0.43
1:A:129:PHE:HB2	1:A:197:ILE:HD13	2.01	0.43
1:A:59:GLU:HG2	1:A:59:GLU:H	1.67	0.43
1:A:75:PRO:CB	1:A:362:VAL:HG21	2.49	0.43
1:A:241:GLY:CA	1:A:248:ASP:OD1	2.66	0.43
1:A:105:ILE:HG23	1:A:106:GLY:N	2.34	0.42
1:A:147:HIS:HB3	1:A:163:ALA:HA	2.00	0.42
1:A:30:PHE:HB2	1:A:31:PRO:HD3	2.01	0.42
1:A:246:LYS:H	1:A:246:LYS:CD	2.27	0.42
1:A:427:LEU:HD12	1:A:427:LEU:HA	1.85	0.42
1:A:415:ILE:O	1:A:419:ILE:HG22	2.20	0.42
1:A:420:LEU:HG	1:A:440:LEU:HD11	2.01	0.42
1:A:427:LEU:HD12	1:A:430:TRP:CE3	2.55	0.42
1:A:480:VAL:HG23	1:A:481:GLU:H	1.85	0.42
1:A:185:LEU:HA	1:A:185:LEU:HD12	1.78	0.41
1:A:152:GLU:O	1:A:154:TRP:N	2.54	0.41
1:A:245:TYR:O	1:A:247:ASP:N	2.53	0.41
1:A:508:VAL:CG1	1:A:510:LEU:HD13	2.51	0.41
1:A:218:ARG:O	1:A:264:ARG:CD	2.68	0.41
1:A:301:THR:CG2	1:A:303:ASN:OD1	2.69	0.41
1:A:486:PRO:O	1:A:490:ILE:HG13	2.20	0.41
1:A:299:ASP:CG	1:A:303:ASN:HB2	2.40	0.40
1:A:341:PHE:CD1	1:A:419:ILE:HD11	2.56	0.40
1:A:93:LYS:O	1:A:373:GLU:HG3	2.21	0.40
1:A:536:VAL:HG11	1:A:538:MET:HE2	2.02	0.40
1:A:167:THR:C	1:A:209:MET:HE3	2.41	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:GLN:NE2	2:A:1589:DCP:O1B[8_665]	2.15	0.05

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

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	461/524 (88%)	424 (92%)	37 (8%)	12 23

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

Mol	Chain	Res	Type
1	A	29	VAL
1	A	59	GLU
1	A	94	LEU
1	A	104	SER
1	A	127	THR
1	A	150	ASP
1	A	158	ASP
1	A	168	GLU
1	A	185	LEU
1	A	194	PHE
1	A	195	VAL
1	A	218	ARG
1	A	222	LEU
1	A	243	ASN
1	A	246	LYS
1	A	264	ARG
1	A	271	SER
1	A	273	LYS

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Mol	Chain	Res	Type
1	A	291	ARG
1	A	301	THR
1	A	306	LEU
1	A	312	LEU
1	A	317	LEU
1	A	366	VAL
1	A	420	LEU
1	A	427	LEU
1	A	433	ARG
1	A	440	LEU
1	A	452	PHE
1	A	482	GLU
1	A	492	ARG
1	A	508	VAL
1	A	510	LEU
1	A	520	LEU
1	A	531	LEU
1	A	574	THR
1	A	587	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	176	GLN
1	A	217	ASN
1	A	243	ASN
1	A	311	ASN
1	A	335	GLN
1	A	405	HIS
1	A	474	ASN
1	A	516	ASN
1	A	586	ASN

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 3 ligands modelled in this entry, 1 is 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	DCP	A	1588	-	25,29,29	1.50	4 (16%)	37,45,45	1.73	9 (24%)
2	DCP	A	1589	3	25,29,29	1.32	2 (8%)	37,45,45	1.72	12 (32%)

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	DCP	A	1588	-	-	6/22/34/34	0/2/2/2
2	DCP	A	1589	3	-	7/22/34/34	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1588	DCP	PG-O1G	3.59	1.62	1.50
2	A	1588	DCP	C6-C5	3.32	1.42	1.35
2	A	1589	DCP	C6-C5	3.29	1.42	1.35
2	A	1589	DCP	O2-C2	3.03	1.29	1.23
2	A	1588	DCP	PG-O3G	2.53	1.64	1.54
2	A	1588	DCP	PB-O1B	2.19	1.58	1.50

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1588	DCP	O2-C2-N3	-4.81	114.51	122.33
2	A	1589	DCP	PB-O3A-PA	-4.23	118.30	132.83
2	A	1589	DCP	O2-C2-N3	-3.95	115.91	122.33
2	A	1589	DCP	PB-O3B-PG	-3.65	120.31	132.83
2	A	1588	DCP	C6-N1-C2	-3.15	115.03	120.49
2	A	1589	DCP	C1'-N1-C6	2.74	126.96	121.55
2	A	1588	DCP	O4'-C1'-N1	2.55	112.41	107.86
2	A	1588	DCP	PB-O3A-PA	-2.54	124.09	132.83
2	A	1589	DCP	C2'-C1'-N1	2.52	119.57	113.77
2	A	1588	DCP	O2A-PA-O5'	-2.39	96.64	107.75
2	A	1589	DCP	C5'-C4'-C3'	-2.33	101.06	114.74
2	A	1588	DCP	C5'-C4'-C3'	-2.30	101.25	114.74
2	A	1588	DCP	N1-C2-N3	2.29	122.97	118.81
2	A	1589	DCP	C6-C5-C4	-2.27	113.84	117.50
2	A	1589	DCP	C6-N1-C2	-2.22	116.65	120.49
2	A	1589	DCP	N4-C4-N3	-2.12	114.25	117.97
2	A	1588	DCP	O3G-PG-O3B	2.11	111.71	104.64
2	A	1589	DCP	N1-C2-N3	2.07	122.58	118.81
2	A	1589	DCP	C5-C4-N4	2.06	123.82	120.57
2	A	1589	DCP	O3G-PG-O3B	2.01	111.38	104.64
2	A	1588	DCP	O3G-PG-O2G	2.00	115.30	107.64

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1588	DCP	C3'-C4'-C5'-O5'
2	A	1588	DCP	O4'-C4'-C5'-O5'
2	A	1588	DCP	C5'-O5'-PA-O1A
2	A	1589	DCP	O4'-C4'-C5'-O5'
2	A	1589	DCP	C5'-O5'-PA-O1A
2	A	1589	DCP	C5'-O5'-PA-O2A
2	A	1589	DCP	C5'-O5'-PA-O3A
2	A	1589	DCP	C3'-C4'-C5'-O5'
2	A	1588	DCP	C5'-O5'-PA-O3A
2	A	1588	DCP	C5'-O5'-PA-O2A
2	A	1588	DCP	PG-O3B-PB-O2B
2	A	1589	DCP	PG-O3B-PB-O2B
2	A	1589	DCP	PG-O3B-PB-O1B

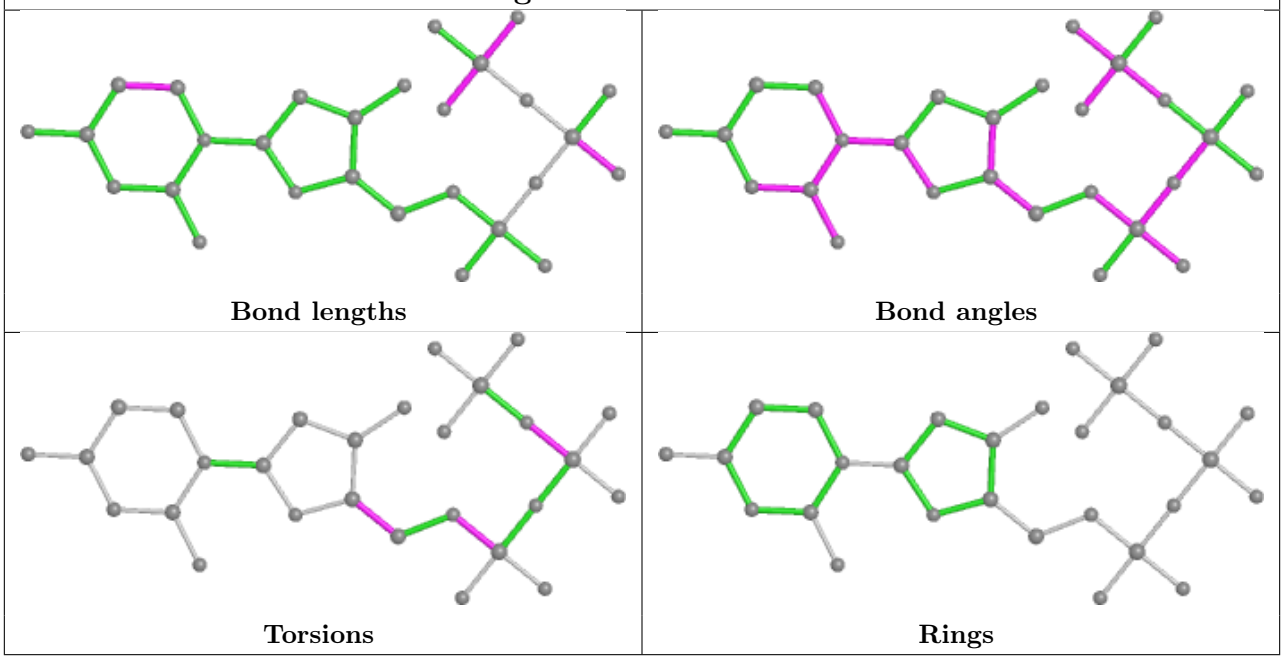
There are no ring outliers.

2 monomers are involved in 3 short contacts:

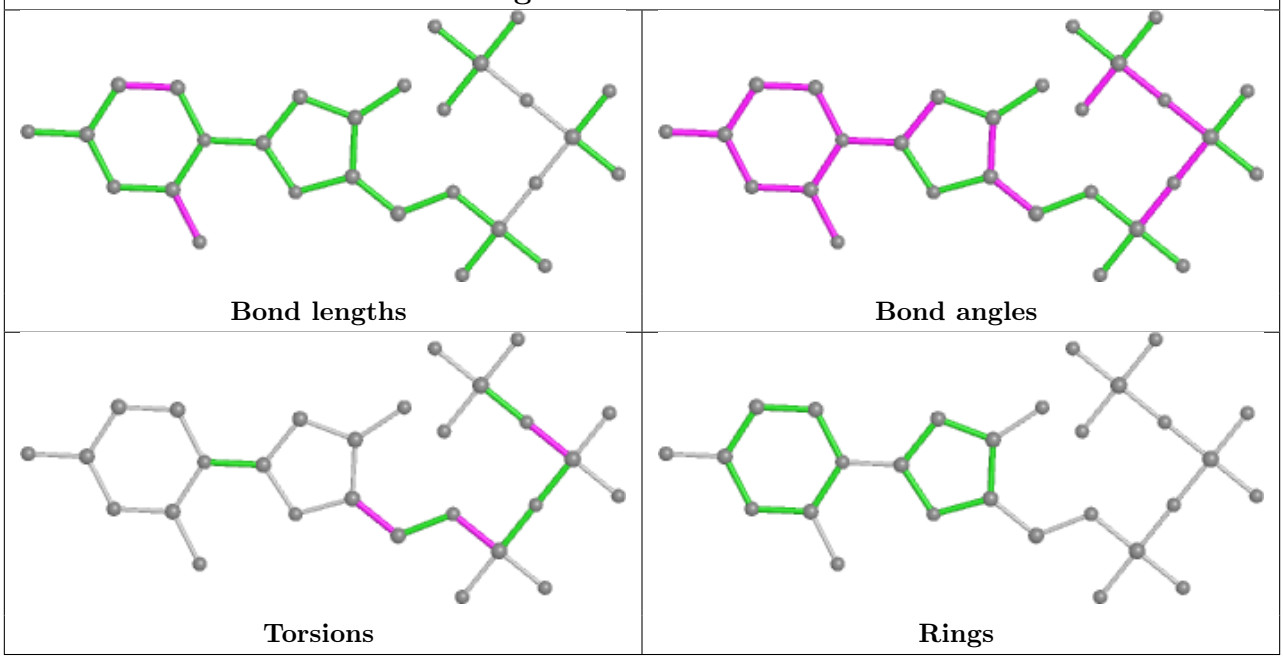
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1588	DCP	2	0
2	A	1589	DCP	0	1

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 then 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.

Ligand DCP A 1588



Ligand DCP A 1589



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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.