Full wwPDB X-ray Structure Validation Report ⓘ

Dec 10, 2022 – 08:57 PM EST

PDB ID	:	1F5A
Title	:	CRYSTAL STRUCTURE OF MAMMALIAN POLY(A) POLYMERASE
Authors	:	Martin, G.; Keller, W.; Doublie, S.
Deposited on	:	2000-06-13
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 ⓘ 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:

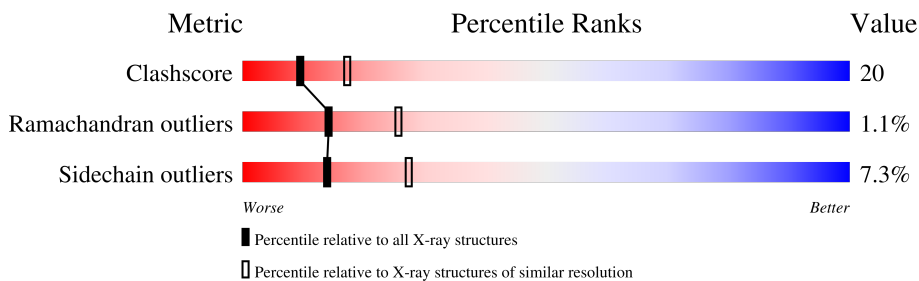|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 2.50 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	Percentile Ranks	Value
Clashscore		20
Ramachandran outliers		1.1%
Sidechain outliers		7.3%

Worse → *Better*

▊ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (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	513	58% 28% · 10%

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 3946 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 POLY(A) POLYMERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	463	Total 3730	C 2420	N 628	O 669	S 7	Se 6	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP P25500
A	251	MSE	MET	modified residue	UNP P25500
A	313	MSE	MET	modified residue	UNP P25500
A	335	MSE	MET	modified residue	UNP P25500
A	337	MSE	MET	modified residue	UNP P25500
A	436	MSE	MET	modified residue	UNP P25500
A	476	MSE	MET	modified residue	UNP P25500
A	481	MSE	MET	modified residue	UNP P25500
A	486	MSE	MET	modified residue	UNP P25500

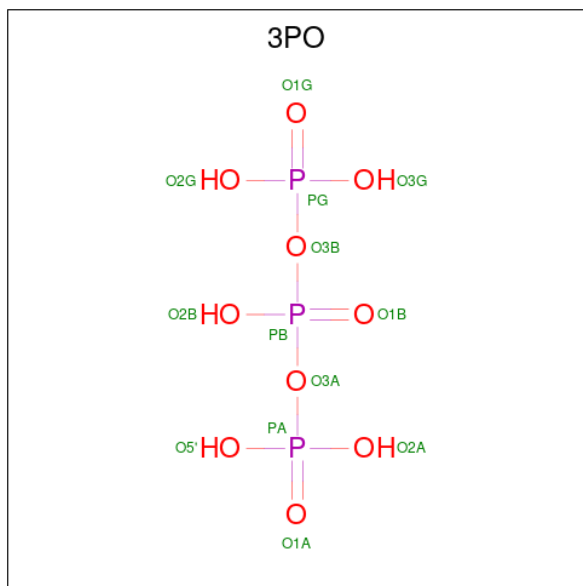- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is 3'-DEOXYADENOSINE-5'-TRIPHOSPHATE (three-letter code: 3AT) (formula: $C_{10}H_{16}N_5O_{12}P_3$).

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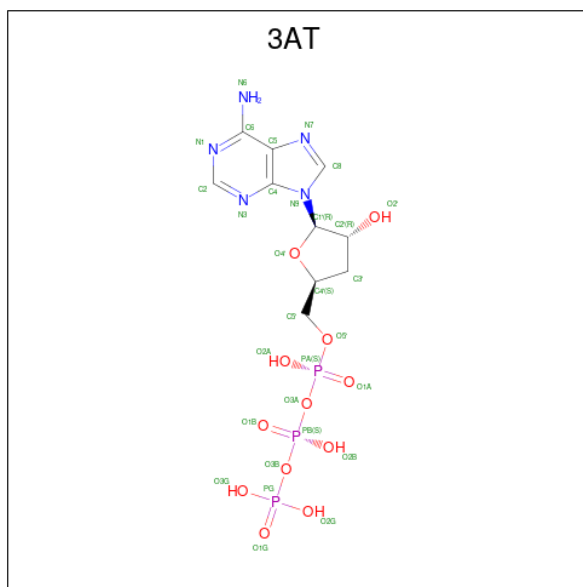
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			30	10	5	12	3		

- Molecule 4 is TRIPHOSPHATE (three-letter code: 3PO) (formula: $H_5O_{10}P_3$).

3PO

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			13	10	3		

- Molecule 5 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	170	Total 170	O 170	0	0

3 Residue-property plots ⓘ

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: POLY(A) POLYMERASE
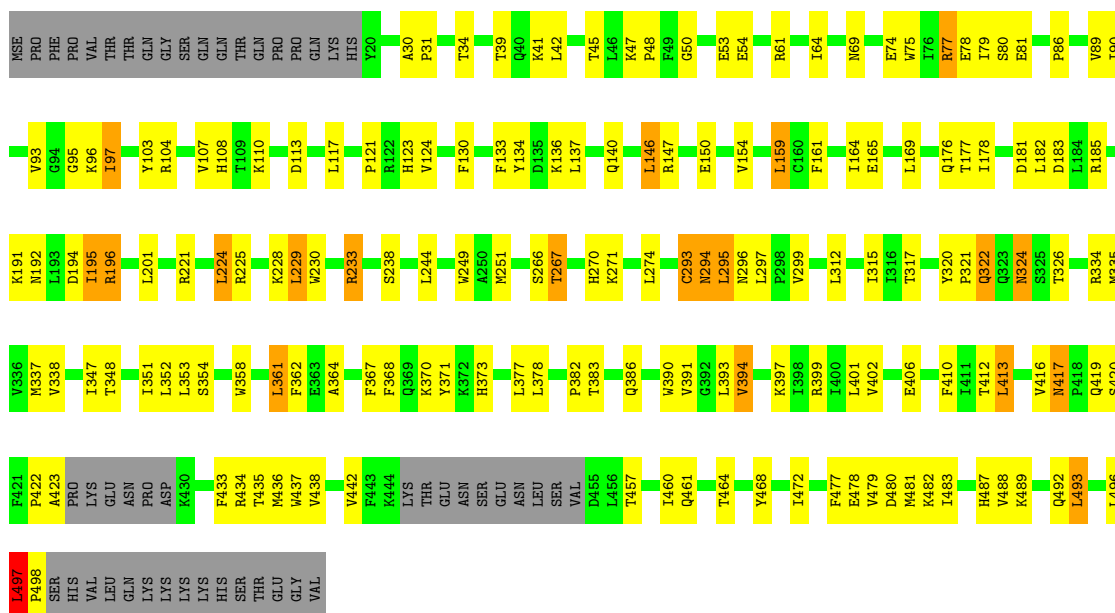
4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	57.55Å 62.72Å 179.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.50)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.219 , 0.261	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3946	wwPDB-VP
Average B, all atoms (Å^2)	29.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 3PO, 3AT, MN

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	0.38	0/3806	0.64	1/5152 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	159	LEU	CA-CB-CG	5.01	126.83	115.30

There are no chirality outliers.

There are no planarity outliers.

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	3730	0	3777	148	0
2	A	3	0	0	0	0
3	A	30	0	12	0	0
4	A	13	0	0	0	0
5	A	170	0	0	8	0
All	All	3946	0	3789	148	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 20.

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

All (148) 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:335:MSE:HE2	1:A:413:LEU:HD13	1.29	1.10
1:A:478:GLU:H	1:A:481:MSE:HE2	1.22	1.02
1:A:382:PRO:HG2	1:A:386:GLN:HE22	1.28	0.96
1:A:335:MSE:HE1	1:A:412:THR:HG22	1.53	0.88
1:A:61:ARG:NH1	1:A:164:ILE:HD12	1.89	0.87
1:A:399:ARG:HD3	5:A:2176:HOH:O	1.76	0.85
1:A:488:VAL:HG13	1:A:492:GLN:HG3	1.58	0.85
1:A:382:PRO:HG2	1:A:386:GLN:NE2	1.91	0.84
1:A:251:MSE:HE3	1:A:315:ILE:HG22	1.63	0.80
1:A:478:GLU:N	1:A:481:MSE:HE2	1.96	0.80
1:A:497:LEU:HB3	1:A:498:PRO:HD3	1.65	0.78
1:A:61:ARG:HH12	1:A:164:ILE:HD12	1.44	0.76
1:A:75:TRP:CE2	1:A:133:PHE:HB2	2.21	0.76
1:A:195:ILE:HD12	1:A:196:ARG:H	1.50	0.75
1:A:233:ARG:HH11	1:A:233:ARG:HB3	1.51	0.74
1:A:107:VAL:HG21	1:A:224:LEU:HD13	1.70	0.73
1:A:93:VAL:HA	1:A:177:THR:HG22	1.70	0.73
1:A:335:MSE:HE1	1:A:412:THR:CG2	2.21	0.71
1:A:64:ILE:HG23	1:A:161:PHE:CD1	2.26	0.70
1:A:294:ASN:O	1:A:296:ASN:N	2.23	0.70
1:A:39:THR:OG1	1:A:266:SER:HB2	1.92	0.69
1:A:417:ASN:C	1:A:417:ASN:HD22	1.96	0.69
1:A:312:LEU:HB3	1:A:334:ARG:HH21	1.58	0.68
1:A:69:ASN:ND2	1:A:97:ILE:H	1.91	0.68
1:A:47:LYS:HB2	1:A:48:PRO:HD3	1.75	0.68
1:A:417:ASN:ND2	1:A:419:GLN:H	1.92	0.68
1:A:493:LEU:HD22	1:A:497:LEU:HD13	1.76	0.67
1:A:477:PHE:HA	1:A:481:MSE:CE	2.24	0.66
1:A:233:ARG:NH1	1:A:364:ALA:HB2	2.12	0.65
1:A:417:ASN:HD22	1:A:419:GLN:H	1.44	0.64
1:A:270:HIS:HD2	1:A:348:THR:OG1	1.80	0.64
1:A:229:LEU:HD22	1:A:233:ARG:HG2	1.81	0.63
1:A:488:VAL:CG1	1:A:492:GLN:HG3	2.30	0.62
1:A:81:GLU:HG3	1:A:90:ILE:HD13	1.82	0.62
1:A:154:VAL:HG11	1:A:169:LEU:HD13	1.80	0.62
1:A:477:PHE:HA	1:A:481:MSE:HE2	1.82	0.62
1:A:134:TYR:CZ	1:A:146:LEU:HD13	2.35	0.61
1:A:478:GLU:O	1:A:481:MSE:HG3	2.01	0.60
1:A:402:VAL:O	1:A:406:GLU:HG3	2.01	0.60
1:A:30:ALA:HB1	1:A:31:PRO:HD2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:HIS:HB3	1:A:487:HIS:HE1	1.66	0.60
1:A:89:VAL:O	1:A:93:VAL:HG23	2.01	0.59
1:A:195:ILE:HD12	1:A:196:ARG:N	2.14	0.59
1:A:117:LEU:HD21	1:A:201:LEU:HD23	1.85	0.59
1:A:224:LEU:HD22	1:A:228:LYS:HG3	1.83	0.59
1:A:194:ASP:OD1	1:A:195:ILE:HD12	2.02	0.59
1:A:61:ARG:HG2	1:A:61:ARG:HH11	1.68	0.58
1:A:147:ARG:HA	5:A:2110:HOH:O	2.03	0.58
1:A:478:GLU:H	1:A:481:MSE:CE	2.08	0.57
1:A:312:LEU:HD22	1:A:334:ARG:NH2	2.19	0.57
1:A:390:TRP:O	1:A:394:VAL:HG12	2.03	0.57
1:A:367:PHE:CE2	1:A:417:ASN:HB2	2.40	0.57
1:A:324:ASN:ND2	1:A:326:THR:H	2.03	0.56
1:A:50:GLY:O	1:A:110:LYS:HD3	2.04	0.56
1:A:270:HIS:CG	1:A:352:LEU:HD11	2.41	0.56
1:A:244:LEU:HD13	1:A:337:MSE:HE1	1.87	0.56
1:A:383:THR:HA	1:A:433:PHE:CD2	2.41	0.55
1:A:295:LEU:HD12	1:A:320:TYR:CE2	2.42	0.55
1:A:221:ARG:HG2	1:A:225:ARG:NH1	2.22	0.54
1:A:251:MSE:HE3	1:A:315:ILE:CG2	2.36	0.54
1:A:244:LEU:HD13	1:A:337:MSE:SE	2.57	0.54
1:A:460:ILE:O	1:A:464:THR:HG23	2.09	0.53
1:A:221:ARG:HG2	1:A:225:ARG:HH12	1.73	0.53
1:A:378:LEU:O	1:A:483:ILE:HA	2.09	0.53
1:A:488:VAL:HG12	1:A:489:LYS:O	2.09	0.53
1:A:497:LEU:CB	1:A:498:PRO:HD3	2.37	0.52
1:A:413:LEU:HD23	1:A:442:VAL:HB	1.92	0.52
1:A:312:LEU:CB	1:A:334:ARG:HH21	2.23	0.52
1:A:477:PHE:HA	1:A:481:MSE:HE1	1.92	0.51
1:A:165:GLU:HG3	5:A:2123:HOH:O	2.10	0.51
1:A:422:PRO:HG3	5:A:2102:HOH:O	2.10	0.51
1:A:497:LEU:HB3	1:A:498:PRO:CD	2.31	0.51
1:A:230:TRP:CD1	1:A:361:LEU:HD22	2.45	0.51
1:A:399:ARG:HG3	5:A:2024:HOH:O	2.10	0.51
1:A:297:LEU:CD1	1:A:321:PRO:HG3	2.41	0.51
1:A:457:THR:O	1:A:461:GLN:HB2	2.12	0.50
1:A:334:ARG:O	1:A:338:VAL:HG23	2.12	0.49
1:A:353:LEU:O	1:A:354:SER:HB2	2.13	0.48
1:A:299:VAL:HG13	1:A:322:GLN:HG2	1.95	0.48
1:A:225:ARG:NH1	5:A:2054:HOH:O	2.47	0.48
1:A:416:VAL:HG23	5:A:2048:HOH:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:GLY:H	1:A:178:ILE:HB	1.79	0.48
1:A:74:GLU:O	1:A:78:GLU:HG3	2.13	0.48
1:A:31:PRO:HB3	5:A:2014:HOH:O	2.15	0.47
1:A:435:THR:HG22	1:A:436:MSE:N	2.29	0.47
1:A:391:VAL:HG13	1:A:437:TRP:CH2	2.50	0.47
1:A:103:TYR:HA	1:A:108:HIS:HB2	1.96	0.47
1:A:154:VAL:CG1	1:A:169:LEU:HD13	2.44	0.47
1:A:229:LEU:HD13	1:A:362:PHE:CD1	2.50	0.47
1:A:312:LEU:HB3	1:A:334:ARG:NH2	2.26	0.46
1:A:417:ASN:C	1:A:417:ASN:ND2	2.68	0.46
1:A:251:MSE:SE	1:A:317:THR:HA	2.65	0.46
1:A:297:LEU:HD12	1:A:320:TYR:CE2	2.50	0.45
1:A:393:LEU:O	1:A:397:LYS:HG2	2.16	0.45
1:A:322:GLN:NE2	1:A:322:GLN:H	2.14	0.45
1:A:391:VAL:HA	1:A:394:VAL:CG1	2.46	0.45
1:A:79:ILE:HG21	1:A:124:VAL:HG22	1.98	0.45
1:A:130:PHE:CD1	1:A:150:GLU:HB3	2.52	0.45
1:A:423:ALA:CB	1:A:434:ARG:HD3	2.46	0.45
1:A:130:PHE:CE1	1:A:150:GLU:HB3	2.51	0.45
1:A:267:THR:O	1:A:271:LYS:HG2	2.16	0.45
1:A:410:PHE:CD1	1:A:410:PHE:N	2.84	0.45
1:A:75:TRP:HB2	1:A:136:LYS:HE3	1.98	0.45
1:A:69:ASN:HD21	1:A:96:LYS:HA	1.82	0.44
1:A:136:LYS:O	1:A:140:GLN:HG2	2.18	0.44
1:A:233:ARG:HH12	1:A:364:ALA:N	2.15	0.44
1:A:45:THR:HG21	1:A:358:TRP:HB2	2.00	0.44
1:A:423:ALA:HB3	1:A:434:ARG:HD3	2.00	0.44
1:A:468:TYR:OH	1:A:482:LYS:HA	2.18	0.44
1:A:41:LYS:O	1:A:45:THR:HG23	2.19	0.43
1:A:322:GLN:H	1:A:322:GLN:CD	2.21	0.43
1:A:133:PHE:CE2	1:A:137:LEU:HD11	2.54	0.43
1:A:113:ASP:HB3	1:A:165:GLU:HG2	2.00	0.43
1:A:386:GLN:OE1	1:A:478:GLU:HG2	2.18	0.43
1:A:497:LEU:CB	1:A:498:PRO:CD	2.97	0.43
1:A:383:THR:HA	1:A:433:PHE:HD2	1.83	0.43
1:A:297:LEU:HD13	1:A:321:PRO:HG3	2.01	0.43
1:A:93:VAL:HG13	1:A:121:PRO:HG3	2.01	0.43
1:A:370:LYS:HG3	1:A:371:TYR:CD2	2.54	0.43
1:A:191:LYS:O	1:A:192:ASN:HB2	2.18	0.42
1:A:348:THR:O	1:A:352:LEU:HG	2.19	0.42
1:A:383:THR:HA	1:A:433:PHE:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:VAL:O	1:A:480:ASP:HB2	2.18	0.42
1:A:477:PHE:CA	1:A:481:MSE:HE2	2.49	0.42
1:A:347:ILE:O	1:A:351:ILE:HG13	2.19	0.42
1:A:368:PHE:CE1	1:A:438:VAL:HG21	2.55	0.42
1:A:468:TYR:O	1:A:472:ILE:HG13	2.21	0.41
1:A:61:ARG:HH11	1:A:61:ARG:CG	2.31	0.41
1:A:493:LEU:HD22	1:A:497:LEU:CD1	2.47	0.41
1:A:224:LEU:HD22	1:A:228:LYS:CG	2.49	0.41
1:A:483:ILE:HG23	1:A:483:ILE:O	2.20	0.41
1:A:93:VAL:CG1	1:A:121:PRO:HG3	2.51	0.41
1:A:293:CYS:O	1:A:294:ASN:C	2.59	0.41
1:A:183:ASP:OD1	1:A:185:ARG:HB2	2.20	0.41
1:A:249:TRP:CH2	1:A:337:MSE:HE3	2.55	0.41
1:A:320:TYR:CD1	1:A:321:PRO:HA	2.55	0.41
1:A:69:ASN:HD22	1:A:97:ILE:H	1.65	0.41
1:A:413:LEU:CD2	1:A:442:VAL:HB	2.50	0.41
1:A:86:PRO:HG2	1:A:89:VAL:CG2	2.51	0.41
1:A:64:ILE:HD12	1:A:164:ILE:HG13	2.02	0.41
1:A:368:PHE:HE1	1:A:438:VAL:HG21	1.86	0.41
1:A:244:LEU:HD13	1:A:337:MSE:CE	2.50	0.40
1:A:472:ILE:HG12	1:A:477:PHE:CD2	2.56	0.40
1:A:420:SER:HB3	1:A:437:TRP:NE1	2.37	0.40
1:A:496:LEU:O	1:A:497:LEU:HD12	2.21	0.40
1:A:77:ARG:O	1:A:80:SER:HB2	2.22	0.40
1:A:370:LYS:HG3	1:A:371:TYR:CE2	2.57	0.40
1:A:477:PHE:CD1	1:A:481:MSE:HE2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	457/513 (89%)	429 (94%)	23 (5%)	5 (1%)	14	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	295	LEU
1	A	497	LEU
1	A	294	ASN
1	A	123	HIS
1	A	238	SER

5.3.2 Protein sidechains ⓘ

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	411/459 (90%)	381 (93%)	30 (7%)	14	27

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	THR
1	A	42	LEU
1	A	53	GLU
1	A	54	GLU
1	A	77	ARG
1	A	97	ILE
1	A	104	ARG
1	A	146	LEU
1	A	159	LEU
1	A	176	GLN
1	A	181	ASP
1	A	182	LEU
1	A	195	ILE
1	A	196	ARG
1	A	224	LEU
1	A	229	LEU

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Mol	Chain	Res	Type
1	A	233	ARG
1	A	267	THR
1	A	274	LEU
1	A	293	CYS
1	A	322	GLN
1	A	324	ASN
1	A	361	LEU
1	A	377	LEU
1	A	394	VAL
1	A	401	LEU
1	A	413	LEU
1	A	417	ASN
1	A	493	LEU
1	A	497	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	87	GLN
1	A	140	GLN
1	A	202	ASN
1	A	234	HIS
1	A	270	HIS
1	A	296	ASN
1	A	322	GLN
1	A	323	GLN
1	A	324	ASN
1	A	386	GLN
1	A	417	ASN
1	A	461	GLN
1	A	487	HIS
1	A	492	GLN

5.3.3 RNA (i)

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 3 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	$\#|Z| > 2$
4	3PO	A	4000	2	8,12,12	1.19	0	15,20,20	1.22	2 (13%)
3	3AT	A	1000	2	25,32,32	1.19	5 (20%)	28,50,50	1.46	4 (14%)

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	3PO	A	4000	2	-	0/12/12/12	-
3	3AT	A	1000	2	-	4/18/34/34	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1000	3AT	C8-N7	-2.36	1.30	1.34
3	A	1000	3AT	PG-O2G	-2.33	1.45	1.54
3	A	1000	3AT	C4-N3	2.30	1.38	1.35
3	A	1000	3AT	PB-O2B	-2.19	1.45	1.55
3	A	1000	3AT	C2-N3	2.02	1.35	1.32

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1000	3AT	O2B-PB-O1B	3.70	130.51	112.24
3	A	1000	3AT	O4'-C1'-C2'	-3.41	101.94	106.93
3	A	1000	3AT	PA-O3A-PB	3.33	144.26	132.83
4	A	4000	3PO	O2A-PA-O1A	2.17	119.17	110.68
4	A	4000	3PO	O2A-PA-O3A	2.15	111.84	104.64
3	A	1000	3AT	C4-C5-N7	2.00	111.49	109.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1000	3AT	PB-O3B-PG-O2G
3	A	1000	3AT	PA-O3A-PB-O3B
3	A	1000	3AT	PB-O3B-PG-O1G
3	A	1000	3AT	PB-O3B-PG-O3G

There are no ring outliers.

No monomer is involved in short contacts.

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 3PO A 4000

Bond lengths

Bond angles

Torsions

Rings

Ligand 3AT A 1000

Bond lengths

Bond angles

Torsions

Rings
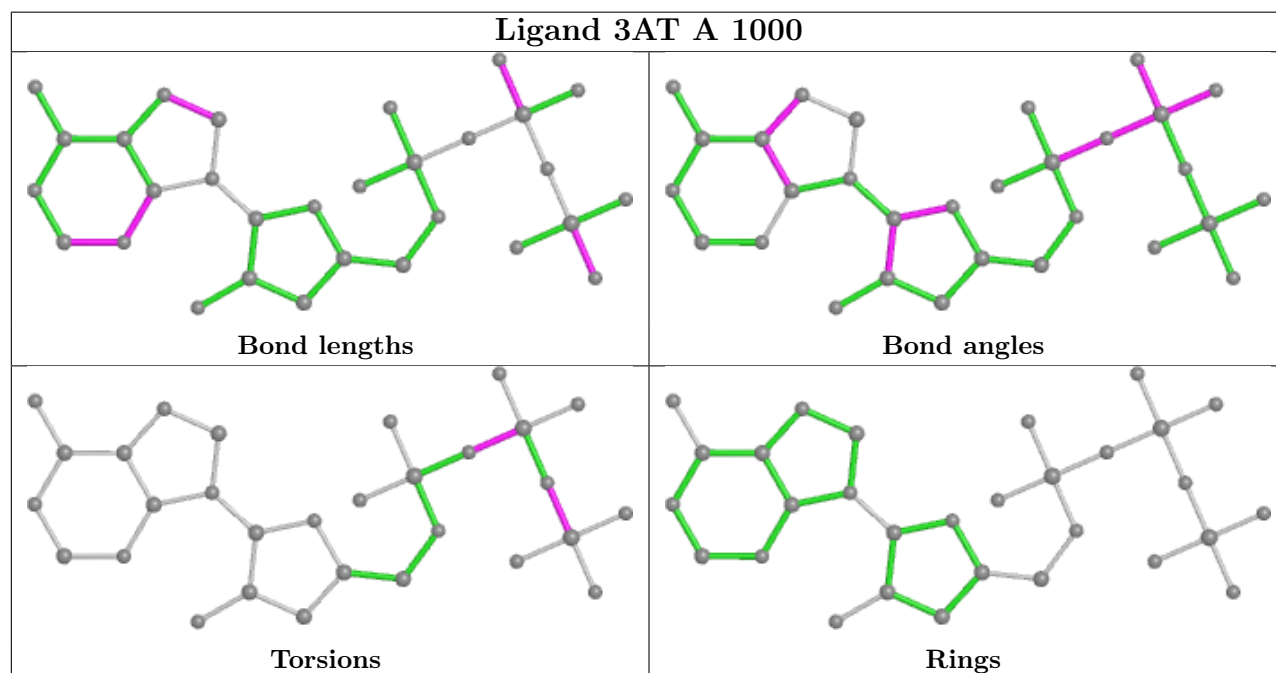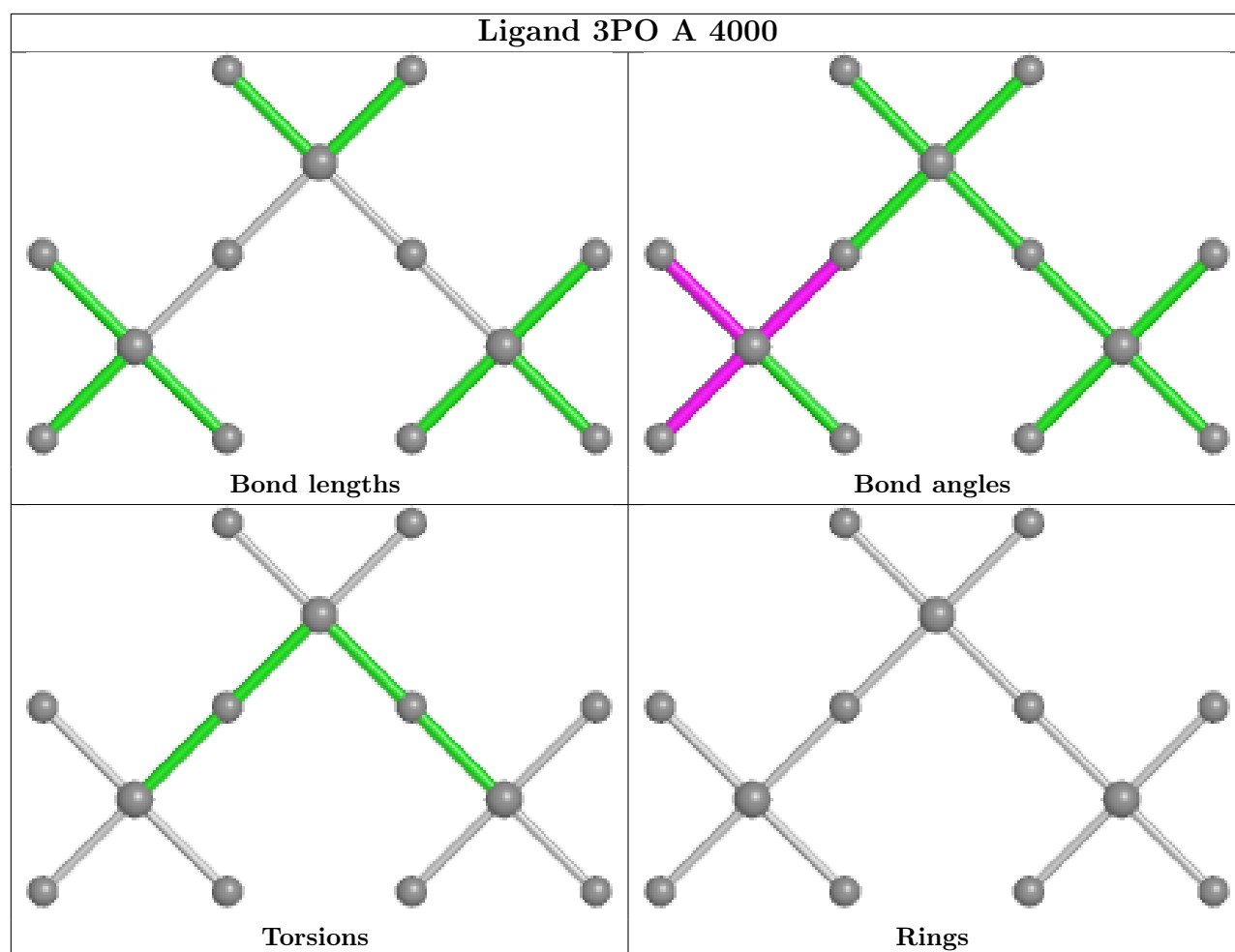
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.