



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 02:53 am BST

PDB ID : 3N1Y
Title : X-ray Crystal Structure of Toluene/o-Xylene Monooxygenase Hydroxylase T201G Mutant
Authors : McCormick, M.S.; Sazinsky, M.H.; Lippard, S.J.
Deposited on : 2010-05-17
Resolution : 2.10 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

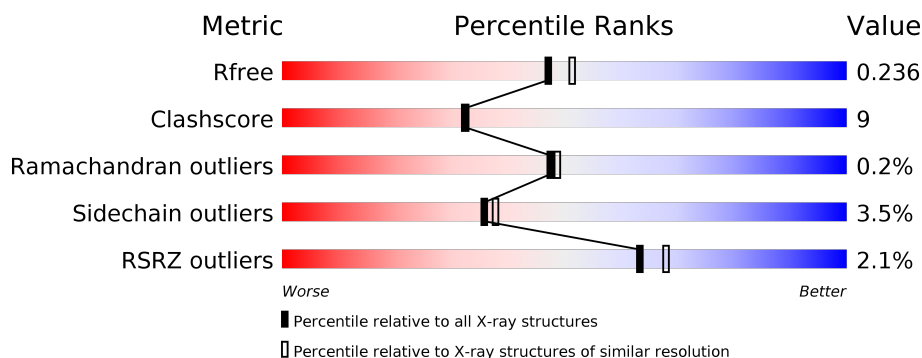
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	498	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>18%</div> <div>..</div> </div> </div>
2	B	330	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>..</div> </div> </div>
3	C	86	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>17%</div> <div>..</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	P6G	A	501	-	X	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7575 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 Toluene o-xylene monooxygenase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	0	0
			4013	2562	673	752	26			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	GLY	THR	ENGINEERED MUTATION	UNP Q6IV66

- Molecule 2 is a protein called Toluene o-xylene monooxygenase component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	322	Total	C	N	O	S	0	0	0
			2641	1674	467	490	10			

- Molecule 3 is a protein called Toluene o-xylene monooxygenase component.

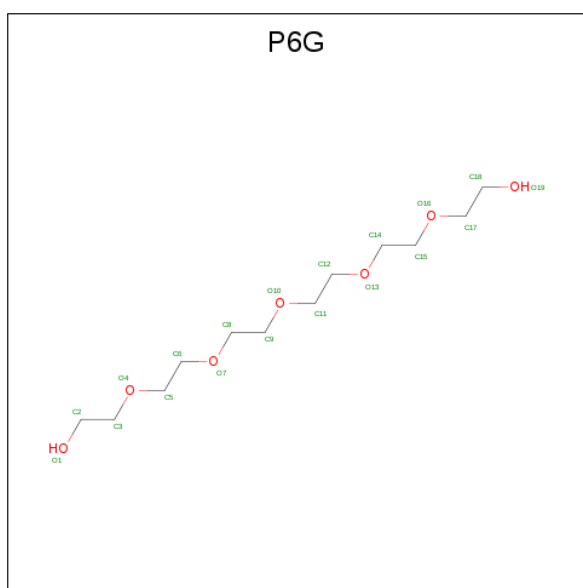
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	83	Total	C	N	O	S	0	0	0
			676	425	120	126	5			

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			19	12	7		
5	A	1	Total	C	O	0	0
			19	12	7		

- Molecule 6 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total 2	Fe 2	0	0

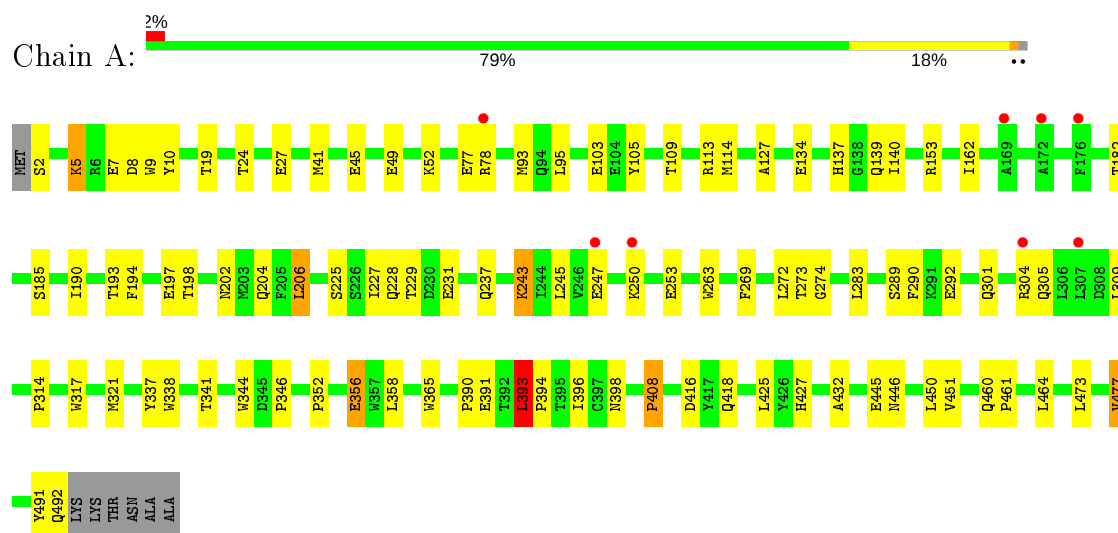
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	100	Total 100	O 100	0	0
7	B	79	Total 79	O 79	0	0
7	C	14	Total 14	O 14	0	0

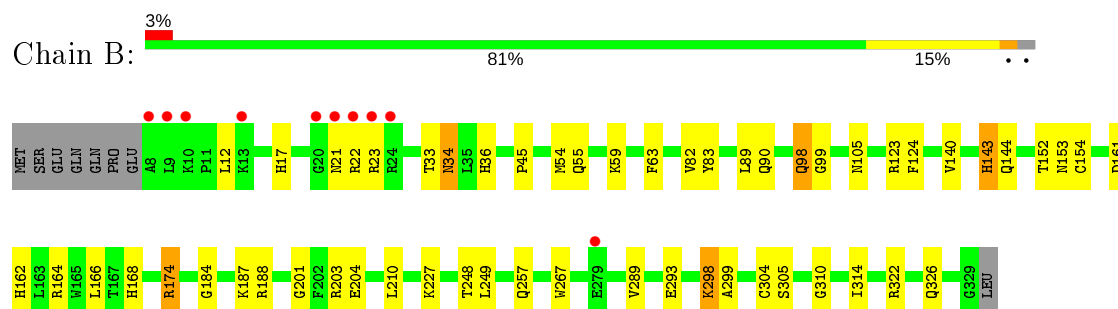
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

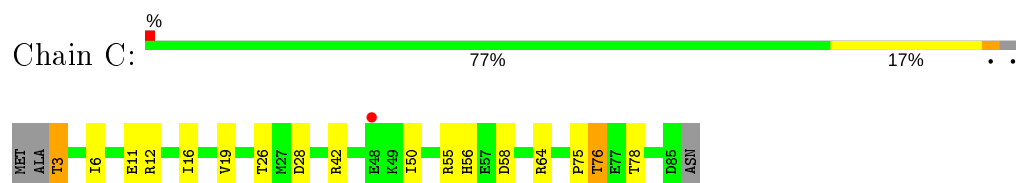
- Molecule 1: Toluene o-xylene monooxygenase component



- Molecule 2: Toluene o-xylene monooxygenase component



- Molecule 3: Toluene o-xylene monooxygenase component



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	182.97Å 182.97Å 68.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.10 45.74 – 2.10	Depositor EDS
% Data completeness (in resolution range)	96.7 (50.00-2.10) 96.4 (45.74-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.75 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.223 , 0.235 0.225 , 0.236	Depositor DCC
R_{free} test set	3768 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	1.126	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7575	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% 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: GOL, FE, P6G

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	0.37	0/4137	0.60	1/5622 (0.0%)
2	B	0.37	0/2713	0.59	0/3688
3	C	0.35	0/690	0.63	0/934
All	All	0.37	0/7540	0.60	1/10244 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	393	LEU	CA-CB-CG	5.55	128.06	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4013	0	3762	83	0
2	B	2641	0	2537	45	0
3	C	676	0	667	21	0
4	A	12	0	16	2	0
5	A	38	0	51	9	0
6	A	2	0	0	0	0
7	A	100	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	79	0	0	0	0
7	C	14	0	0	1	0
All	All	7575	0	7033	127	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 9.

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:9:TRP:HB3	2:B:174:ARG:HG3	1.55	0.87
3:C:26:THR:HG22	3:C:28:ASP:H	1.42	0.84
1:A:416:ASP:OD2	1:A:427:HIS:HD2	1.63	0.82
1:A:2:SER:N	2:B:105:ASN:HD22	1.80	0.79
1:A:427:HIS:CE1	3:C:76:THR:HG23	2.18	0.79
2:B:168:HIS:HD2	2:B:257:GLN:HE21	1.32	0.78
1:A:427:HIS:HE1	3:C:76:THR:HG23	1.48	0.76
1:A:113:ARG:HH11	2:B:144:GLN:HE21	1.32	0.74
1:A:19:THR:O	2:B:203:ARG:NH2	2.21	0.74
1:A:425:LEU:HD23	3:C:76:THR:HG22	1.68	0.73
1:A:243:LYS:O	1:A:247:GLU:HG3	1.89	0.72
1:A:204:GLN:NE2	5:A:501:P6G:H52	2.04	0.72
1:A:139:GLN:HE22	2:B:83:TYR:H	1.35	0.72
1:A:427:HIS:HE1	3:C:76:THR:CG2	2.03	0.71
1:A:398:ASN:HD22	1:A:427:HIS:H	1.40	0.69
1:A:416:ASP:H	3:C:56:HIS:CE1	2.12	0.68
1:A:338:TRP:CD1	1:A:390:PRO:HG3	2.29	0.68
2:B:305:SER:HB3	2:B:314:ILE:HD11	1.76	0.65
2:B:184:GLY:HA3	2:B:188:ARG:HD2	1.80	0.64
1:A:204:GLN:NE2	5:A:501:P6G:C5	2.62	0.62
2:B:59:LYS:HA	2:B:63:PHE:HD2	1.63	0.62
1:A:140:ILE:HG21	1:A:227:ILE:HD11	1.80	0.62
3:C:11:GLU:HG2	3:C:12:ARG:HG3	1.82	0.61
1:A:393:LEU:HD22	5:A:502:P6G:H111	1.83	0.60
1:A:9:TRP:CB	2:B:174:ARG:HG3	2.30	0.60
1:A:245:LEU:O	1:A:250:LYS:O	2.20	0.59
1:A:24:THR:OG1	1:A:27:GLU:HG3	2.03	0.58
2:B:168:HIS:CD2	2:B:257:GLN:HE21	2.17	0.58
1:A:394:PRO:HG3	5:A:502:P6G:H171	1.85	0.58
1:A:289:SER:OG	1:A:292:GLU:HG3	2.04	0.57
1:A:317:TRP:O	1:A:321:MET:HG2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:416:ASP:H	3:C:56:HIS:HE1	1.48	0.57
2:B:34:ASN:HD22	2:B:34:ASN:N	2.04	0.56
1:A:250:LYS:HB3	1:A:253:GLU:HB2	1.88	0.56
1:A:460:GLN:HA	1:A:461:PRO:C	2.25	0.56
1:A:182:THR:HA	2:B:54:MET:HG2	1.87	0.55
1:A:113:ARG:HH11	2:B:144:GLN:NE2	2.04	0.55
1:A:273:THR:HG23	5:A:501:P6G:O4	2.07	0.55
1:A:7:GLU:H	1:A:7:GLU:CD	2.09	0.54
1:A:418:GLN:HE22	3:C:78:THR:H	1.53	0.54
1:A:193:THR:HA	1:A:197:GLU:OE1	2.08	0.54
3:C:26:THR:HG22	3:C:28:ASP:N	2.20	0.53
1:A:352:PRO:O	1:A:356:GLU:HG2	2.08	0.53
1:A:41:MET:O	1:A:45:GLU:HG3	2.09	0.53
3:C:55:ARG:HD2	3:C:58:ASP:OD1	2.08	0.53
3:C:42:ARG:NH2	7:C:111:HOH:O	2.36	0.53
2:B:33:THR:HB	2:B:34:ASN:HD22	1.75	0.52
1:A:95:LEU:HD13	1:A:344:TRP:CZ3	2.45	0.52
2:B:162:HIS:HE1	2:B:227:LYS:HZ2	1.58	0.52
1:A:416:ASP:OD2	1:A:427:HIS:CD2	2.53	0.52
1:A:344:TRP:O	1:A:346:PRO:HD3	2.09	0.52
1:A:113:ARG:HD3	2:B:144:GLN:NE2	2.25	0.52
2:B:143:HIS:CD2	2:B:143:HIS:C	2.84	0.51
2:B:21:ASN:O	2:B:23:ARG:N	2.40	0.51
1:A:398:ASN:ND2	1:A:427:HIS:H	2.08	0.51
1:A:114:MET:HA	1:A:185:SER:OG	2.10	0.51
1:A:491:TYR:O	1:A:492:GLN:HB2	2.11	0.50
1:A:10:TYR:CZ	1:A:52:LYS:HB3	2.47	0.50
2:B:249:LEU:HD23	2:B:249:LEU:C	2.32	0.50
1:A:263:TRP:CE2	1:A:432:ALA:HB3	2.47	0.49
3:C:75:PRO:O	3:C:76:THR:HB	2.12	0.49
1:A:314:PRO:HD2	1:A:317:TRP:CE3	2.47	0.49
7:A:536:HOH:O	2:B:82:VAL:HG13	2.13	0.49
1:A:301:GLN:N	1:A:301:GLN:OE1	2.42	0.49
1:A:2:SER:N	2:B:105:ASN:ND2	2.57	0.49
1:A:153:ARG:HB3	1:A:477:VAL:HG12	1.94	0.49
3:C:26:THR:CG2	3:C:64:ARG:O	2.60	0.49
1:A:305:GLN:HE21	1:A:305:GLN:HA	1.77	0.49
1:A:49:GLU:HG2	1:A:49:GLU:O	2.13	0.49
3:C:6:ILE:HG13	3:C:19:VAL:O	2.13	0.48
1:A:204:GLN:HE21	5:A:501:P6G:C5	2.27	0.48
1:A:204:GLN:HG3	1:A:269:PHE:CZ	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ALA:HB2	1:A:237:GLN:HE22	1.78	0.48
2:B:201:GLY:HA3	2:B:299:ALA:HA	1.96	0.48
2:B:187:LYS:HB2	2:B:187:LYS:HE3	1.69	0.47
2:B:161:ASP:O	2:B:164:ARG:HB3	2.14	0.47
1:A:9:TRP:HB3	2:B:174:ARG:CG	2.37	0.47
1:A:253:GLU:OE1	1:A:253:GLU:N	2.49	0.46
3:C:75:PRO:O	3:C:76:THR:CB	2.63	0.46
1:A:274:GLY:HA2	1:A:290:PHE:CD1	2.50	0.46
1:A:105:TYR:HE1	2:B:153:ASN:HD21	1.64	0.46
1:A:206:LEU:HA	1:A:206:LEU:HD12	1.84	0.46
1:A:137:HIS:CD2	1:A:227:ILE:HD12	2.51	0.45
1:A:446:ASN:HD22	4:A:499:GOL:H2	1.82	0.45
2:B:34:ASN:ND2	2:B:34:ASN:N	2.65	0.45
1:A:337:TYR:O	1:A:390:PRO:HD3	2.16	0.45
1:A:93:MET:SD	4:A:500:GOL:H12	2.57	0.45
1:A:358:LEU:HD13	1:A:365:TRP:CZ2	2.52	0.45
2:B:36:HIS:HE1	2:B:152:THR:OG1	2.00	0.44
1:A:391:GLU:HA	1:A:464:LEU:HD11	1.98	0.44
1:A:393:LEU:HD22	5:A:502:P6G:C11	2.47	0.44
3:C:76:THR:HG23	3:C:76:THR:O	2.17	0.44
2:B:45:PRO:HG2	2:B:55:GLN:OE1	2.18	0.44
2:B:310:GLY:O	2:B:314:ILE:HG13	2.18	0.43
2:B:123:ARG:HD3	2:B:124:PHE:CE2	2.52	0.43
1:A:245:LEU:C	1:A:250:LYS:O	2.57	0.43
2:B:162:HIS:HE1	2:B:227:LYS:NZ	2.14	0.43
2:B:304:CYS:HB2	2:B:314:ILE:HG12	2.01	0.43
2:B:289:VAL:O	2:B:293:GLU:HB2	2.19	0.43
1:A:190:ILE:O	1:A:194:PHE:HB3	2.18	0.43
2:B:188:ARG:HH11	2:B:188:ARG:HG3	1.83	0.43
2:B:17:HIS:HE1	2:B:33:THR:OG1	2.02	0.43
1:A:162:ILE:HG22	1:A:162:ILE:O	2.18	0.42
1:A:5:LYS:HB2	1:A:8:ASP:OD2	2.18	0.42
1:A:341:THR:O	1:A:473:LEU:HD11	2.19	0.42
2:B:90:GLN:HA	2:B:90:GLN:OE1	2.19	0.42
2:B:322:ARG:HB3	2:B:326:GLN:HE21	1.83	0.42
2:B:98:GLN:HG3	2:B:99:GLY:N	2.33	0.42
1:A:225:SER:O	1:A:229:THR:HG23	2.19	0.42
2:B:21:ASN:O	2:B:22:ARG:HB3	2.20	0.42
1:A:231:GLU:OE1	7:A:505:HOH:O	2.21	0.42
1:A:427:HIS:CE1	3:C:76:THR:CG2	2.89	0.42
1:A:394:PRO:CG	5:A:502:P6G:H171	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:CYS:HB3	2:B:267:TRP:CE2	2.55	0.41
1:A:204:GLN:NE2	5:A:501:P6G:H51	2.35	0.41
1:A:134:GLU:HA	1:A:134:GLU:OE2	2.21	0.41
1:A:450:LEU:HA	1:A:450:LEU:HD12	1.82	0.41
1:A:103:GLU:HA	1:A:103:GLU:OE1	2.20	0.41
1:A:95:LEU:HD11	1:A:272:LEU:HD22	2.02	0.41
1:A:109:THR:HG23	2:B:144:GLN:HB2	2.01	0.41
2:B:204:GLU:OE1	2:B:298:LYS:HE3	2.20	0.41
2:B:210:LEU:HA	2:B:210:LEU:HD23	1.93	0.41
1:A:416:ASP:HB2	3:C:16:ILE:CD1	2.51	0.41
1:A:396:ILE:HG12	1:A:451:VAL:HG23	2.03	0.41
3:C:3:THR:HG22	3:C:3:THR:O	2.20	0.40
3:C:26:THR:HG23	3:C:64:ARG:O	2.22	0.40
1:A:194:PHE:O	1:A:198:THR:HB	2.21	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	489/498 (98%)	471 (96%)	16 (3%)	2 (0%)	34	32
2	B	320/330 (97%)	314 (98%)	6 (2%)	0	100	100
3	C	81/86 (94%)	75 (93%)	6 (7%)	0	100	100
All	All	890/914 (97%)	860 (97%)	28 (3%)	2 (0%)	47	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	408	PRO
1	A	445	GLU

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	415/421 (99%)	401 (97%)	14 (3%)	37	39
2	B	274/282 (97%)	264 (96%)	10 (4%)	35	36
3	C	77/79 (98%)	74 (96%)	3 (4%)	32	33
All	All	766/782 (98%)	739 (96%)	27 (4%)	36	38

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	77	GLU
1	A	78	ARG
1	A	202	ASN
1	A	206	LEU
1	A	228	GLN
1	A	243	LYS
1	A	283	LEU
1	A	304	ARG
1	A	309	LEU
1	A	356	GLU
1	A	393	LEU
1	A	408	PRO
1	A	477	VAL
2	B	12	LEU
2	B	34	ASN
2	B	89	LEU
2	B	98	GLN
2	B	140	VAL
2	B	143	HIS
2	B	166	LEU
2	B	174	ARG
2	B	248	THR
2	B	298	LYS
3	C	3	THR
3	C	50	ILE

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Mol	Chain	Res	Type
3	C	76	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	139	GLN
1	A	204	GLN
1	A	237	GLN
1	A	305	GLN
1	A	322	GLN
1	A	379	ASN
1	A	398	ASN
1	A	418	GLN
1	A	427	HIS
2	B	17	HIS
2	B	34	ASN
2	B	36	HIS
2	B	87	ASN
2	B	144	GLN
2	B	153	ASN
2	B	162	HIS
2	B	168	HIS
2	B	326	GLN
3	C	56	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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$
5	P6G	A	501	-	18,18,18	2.07	8 (44%)	17,17,17	3.79	14 (82%)
4	GOL	A	499	-	5,5,5	0.48	0	5,5,5	0.51	0
4	GOL	A	500	-	5,5,5	0.31	0	5,5,5	0.41	0
5	P6G	A	502	-	18,18,18	0.63	0	17,17,17	0.80	0

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
5	P6G	A	501	-	-	11/16/16/16	-
4	GOL	A	499	-	-	0/4/4/4	-
4	GOL	A	500	-	-	0/4/4/4	-
5	P6G	A	502	-	-	3/16/16/16	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	501	P6G	O16-C15	3.28	1.56	1.42
5	A	501	P6G	O10-C11	3.23	1.56	1.42
5	A	501	P6G	O19-C18	-3.02	1.26	1.42
5	A	501	P6G	C12-C11	2.98	1.64	1.49
5	A	501	P6G	O13-C14	2.74	1.53	1.42
5	A	501	P6G	O13-C12	2.67	1.53	1.42
5	A	501	P6G	C6-C5	2.64	1.62	1.49
5	A	501	P6G	O4-C5	2.21	1.51	1.42

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	501	P6G	C17-O16-C15	6.63	142.01	113.29
5	A	501	P6G	O13-C12-C11	5.72	136.20	110.39
5	A	501	P6G	O13-C14-C15	5.72	136.17	110.39
5	A	501	P6G	C5-O4-C3	4.41	132.42	113.29
5	A	501	P6G	O7-C6-C5	4.38	130.15	110.39
5	A	501	P6G	O10-C11-C12	4.33	129.90	110.39
5	A	501	P6G	O4-C5-C6	4.06	128.69	110.39
5	A	501	P6G	O16-C17-C18	3.50	125.44	110.07
5	A	501	P6G	C11-O10-C9	3.13	126.86	113.29
5	A	501	P6G	O10-C9-C8	3.11	124.41	110.39
5	A	501	P6G	O16-C15-C14	2.87	123.32	110.39
5	A	501	P6G	C8-O7-C6	2.44	123.88	113.29
5	A	501	P6G	C14-O13-C12	2.26	123.09	113.29
5	A	501	P6G	O4-C3-C2	2.17	119.61	110.07

There are no chirality outliers.

All (14) torsion outliers are listed below:

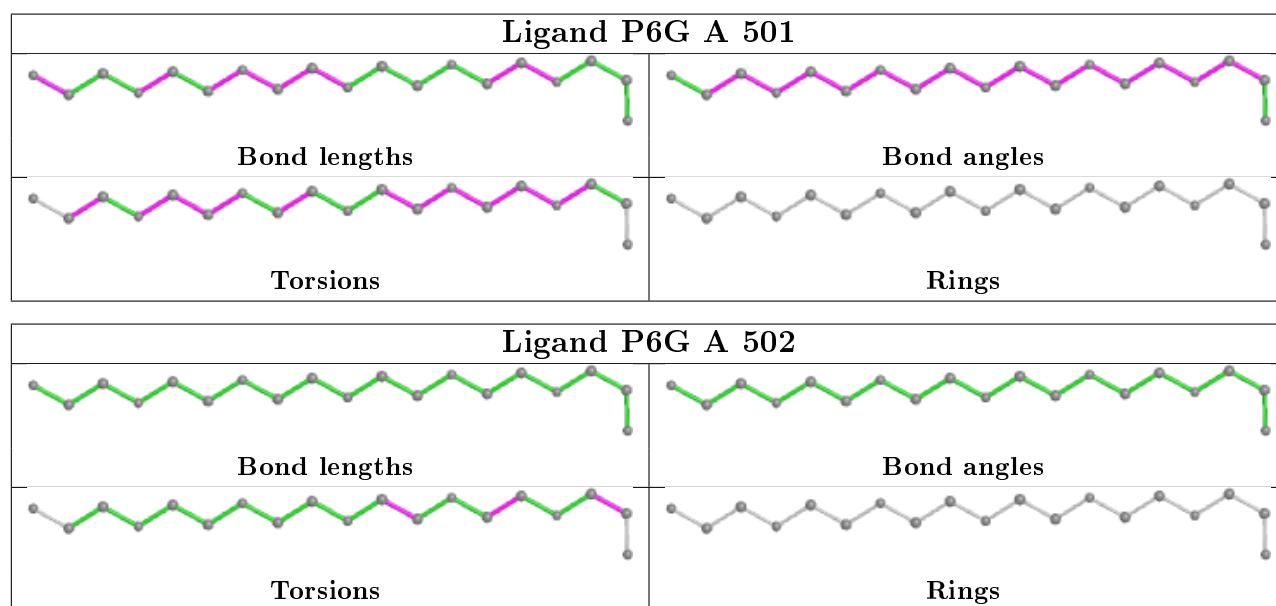
Mol	Chain	Res	Type	Atoms
5	A	501	P6G	O7-C8-C9-O10
5	A	501	P6G	O4-C5-C6-O7
5	A	502	P6G	O7-C8-C9-O10
5	A	501	P6G	O13-C14-C15-O16
5	A	502	P6G	O1-C2-C3-O4
5	A	501	P6G	C5-C6-O7-C8
5	A	502	P6G	O4-C5-C6-O7
5	A	501	P6G	O16-C17-C18-O19
5	A	501	P6G	O10-C11-C12-O13
5	A	501	P6G	C6-C5-O4-C3
5	A	501	P6G	C14-C15-O16-C17
5	A	501	P6G	C15-C14-O13-C12
5	A	501	P6G	C2-C3-O4-C5
5	A	501	P6G	C9-C8-O7-C6

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	501	P6G	5	0
4	A	499	GOL	1	0
4	A	500	GOL	1	0
5	A	502	P6G	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	491/498 (98%)	-0.05	8 (1%) 72 75	29, 38, 53, 70	0
2	B	322/330 (97%)	-0.18	10 (3%) 49 55	28, 37, 54, 84	0
3	C	83/86 (96%)	-0.24	1 (1%) 79 82	35, 44, 54, 67	0
All	All	896/914 (98%)	-0.12	19 (2%) 63 68	28, 38, 53, 84	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	22	ARG	5.4
2	B	23	ARG	4.2
2	B	8	ALA	3.7
2	B	20	GLY	3.7
2	B	9	LEU	3.5
2	B	24	ARG	3.2
1	A	250	LYS	3.1
2	B	21	ASN	3.0
1	A	304	ARG	2.7
1	A	307	LEU	2.5
1	A	172	ALA	2.3
1	A	247	GLU	2.3
1	A	176	PHE	2.2
2	B	10	LYS	2.2
2	B	13	LYS	2.2
1	A	169	ALA	2.1
3	C	48	GLU	2.1
1	A	78	ARG	2.0
2	B	279	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 carbohydrates in this entry.

6.4 Ligands [i](#)

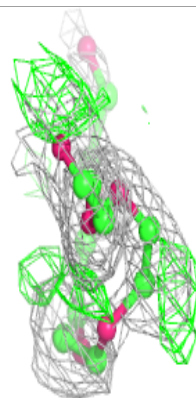
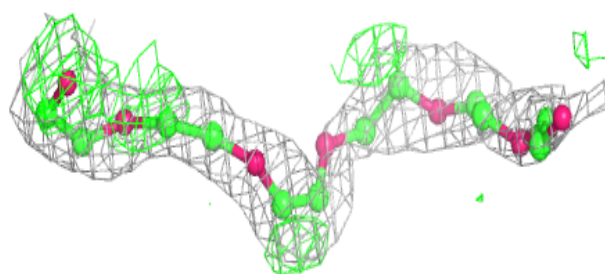
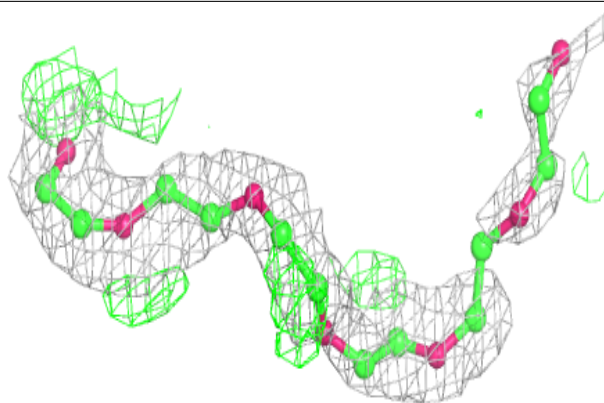
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	A	499	6/6	0.67	0.23	61,64,66,69	0
5	P6G	A	501	19/19	0.70	0.39	53,70,77,77	0
5	P6G	A	502	19/19	0.81	0.20	50,56,75,75	0
4	GOL	A	500	6/6	0.84	0.16	50,53,54,56	0
6	FE	A	504	1/1	0.99	0.16	37,37,37,37	0
6	FE	A	503	1/1	1.00	0.13	31,31,31,31	0

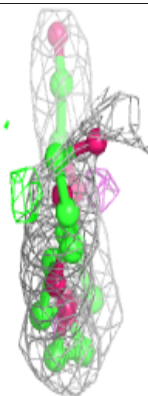
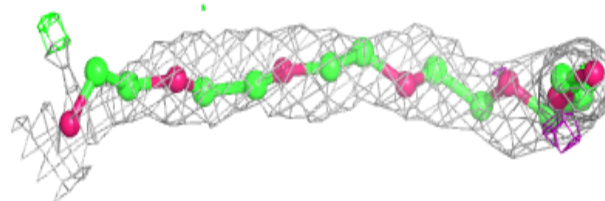
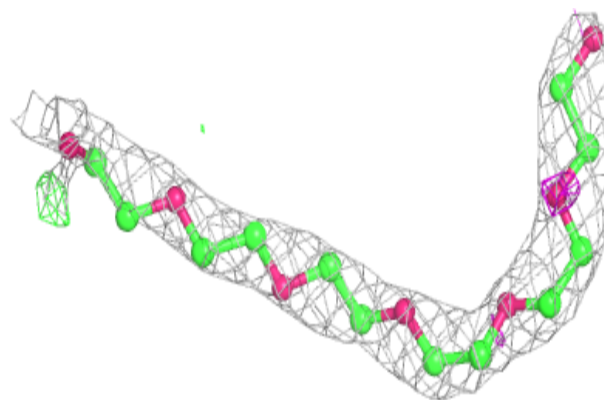
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around P6G A 501:

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

**Electron density around P6G A 502:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.