



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 11:04 am BST

PDB ID : 5C53
Title : Probing the Structural and Molecular Basis of Nucleotide Selectivity by Human Mitochondrial DNA Polymerase gamma
Authors : Sohl, C.D.; Szymanski, M.R.; Mislak, A.C.; Shumate, C.K.; Amiralaie, S.; Schinazi, R.F.; Anderson, K.S.; Yin, Y.W.
Deposited on : 2015-06-19
Resolution : 3.57 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

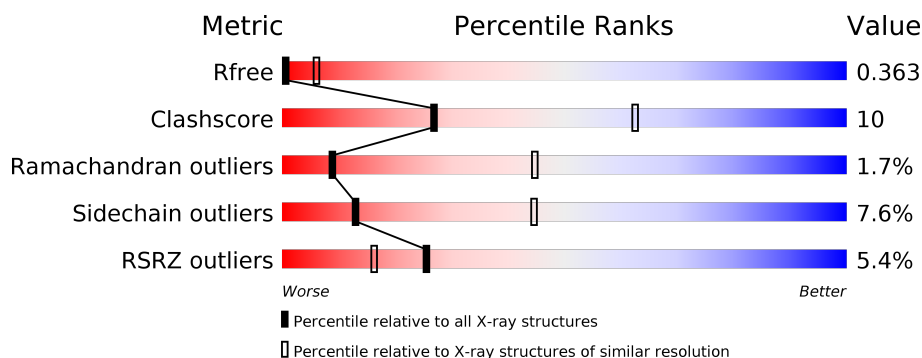
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.57 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	1020 (3.62-3.50)
Clashscore	141614	1100 (3.62-3.50)
Ramachandran outliers	138981	1065 (3.62-3.50)
Sidechain outliers	138945	1066 (3.62-3.50)
RSRZ outliers	127900	1009 (3.64-3.48)

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	1205	<div> <div>5%</div> <div> <div></div> <div>56%</div> <div>21%</div> <div>•</div> <div>18%</div> </div> </div>
2	B	903	<div> <div>%</div> <div> <div></div> <div>31%</div> <div>8%</div> <div>•</div> <div>60%</div> </div> </div>
2	C	903	<div> <div>3%</div> <div> <div></div> <div>29%</div> <div>9%</div> <div>•</div> <div>60%</div> </div> </div>
3	T	26	<div> <div>12%</div> <div> <div></div> <div>62%</div> <div>38%</div> </div> </div>
4	P	22	<div> <div></div> <div> <div></div> <div>68%</div> <div>27%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14634 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 DNA polymerase subunit gamma-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	983	Total	C	N	O	S	0	0	0
			7799	4966	1371	1413	49			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098

- Molecule 2 is a protein called Pol gamma B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	363	Total	C	N	O	S	0	0	0
			2942	1885	520	521	16			
2	C	358	Total	C	N	O	S	0	0	0
			2883	1850	506	511	16			

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	26	Total	C	N	O	P	0	0	0
			529	251	93	159	26			

- Molecule 4 is a DNA chain called DNA (5'-D(*AP*AP*AP*AP*CP*GP*AP*GP*GP*GP*

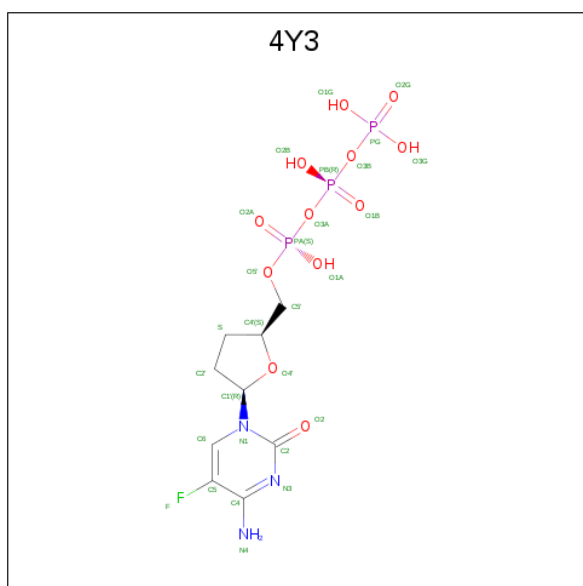
CP*CP*AP*GP*TP*GP*CP*CP*GP*TP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	P	21	Total	C	N	O	P	0	0	0
			433	205	89	119	20			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

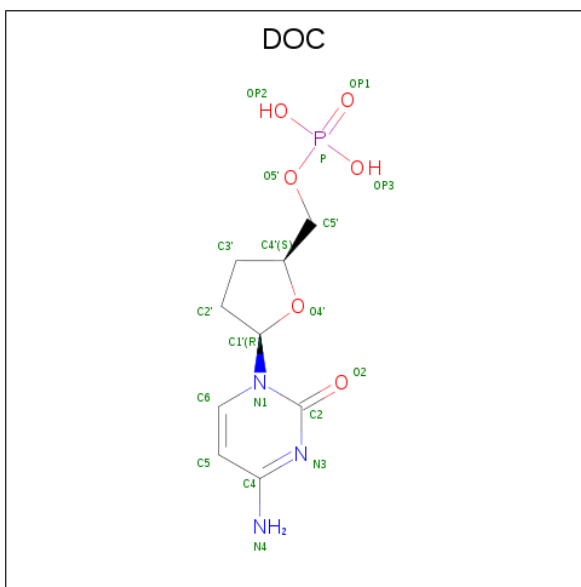
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is [[[(2S,5R)-5-(4-azanyl-5-fluoranyl-2-oxidanylidene-pyrimidin-1-yl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] phosphono hydrogen phosphate (three-letter code: 4Y3) (formula: C₉H₁₅FN₃O₁₂P₃).

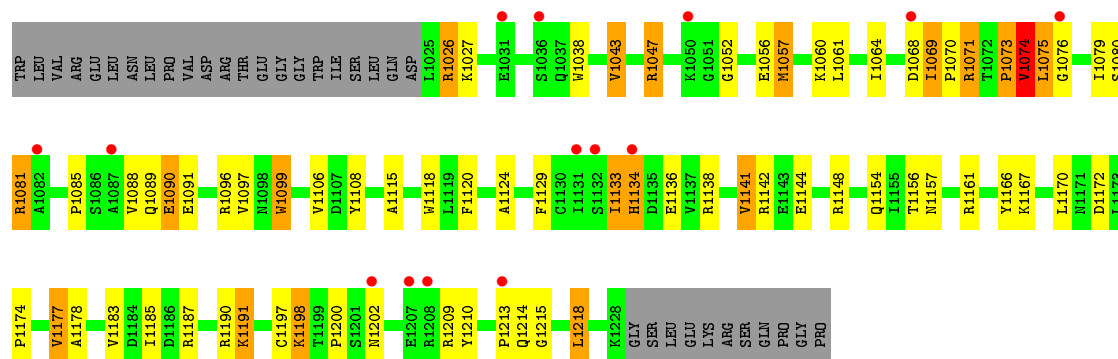


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	F	N	O	P	0	0
			28	9	1	3	12	3		

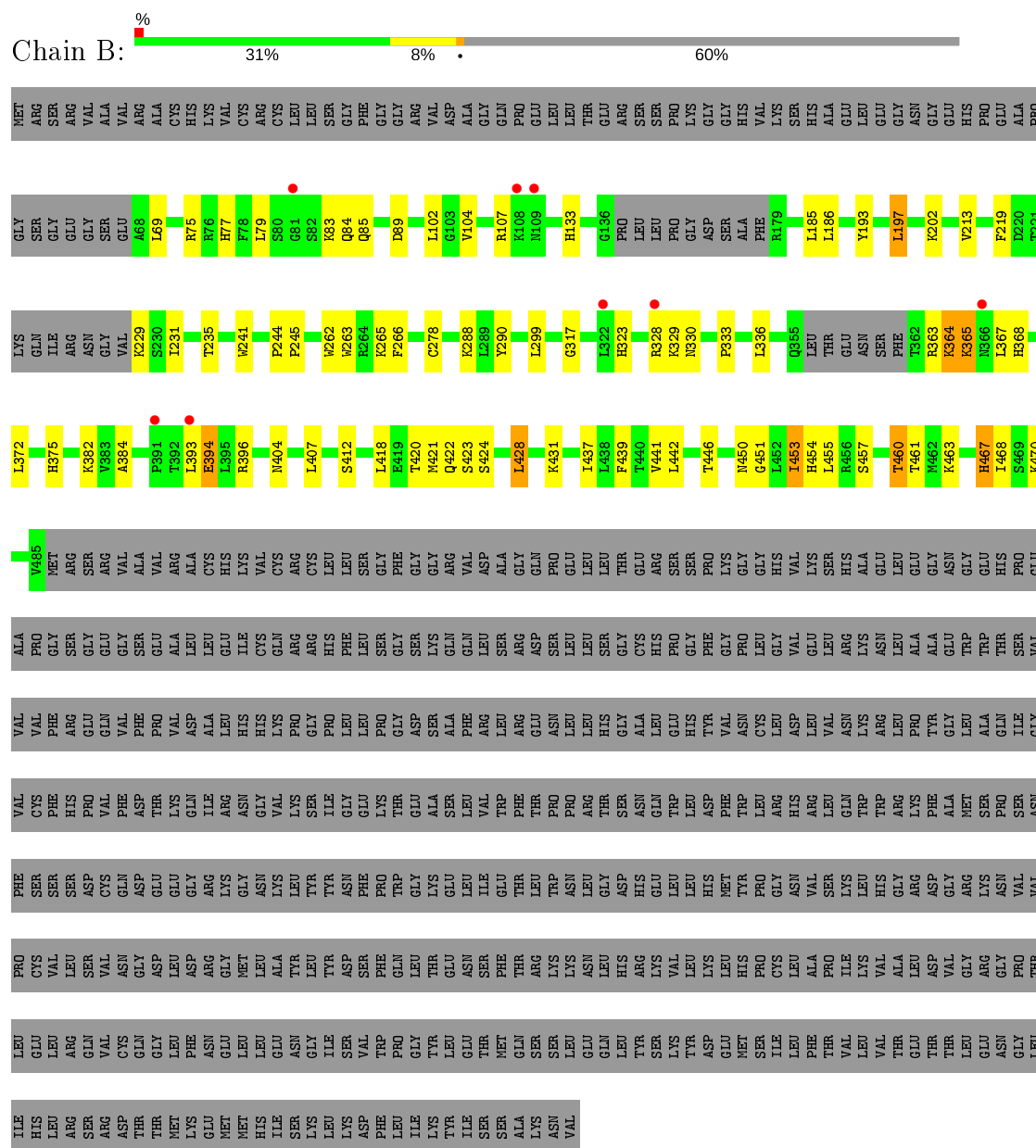
- Molecule 7 is 2',3'-DIDEOXYCYTIDINE-5'-MONOPHOSPHATE (three-letter code: DOC) (formula: C₉H₁₄N₃O₆P).



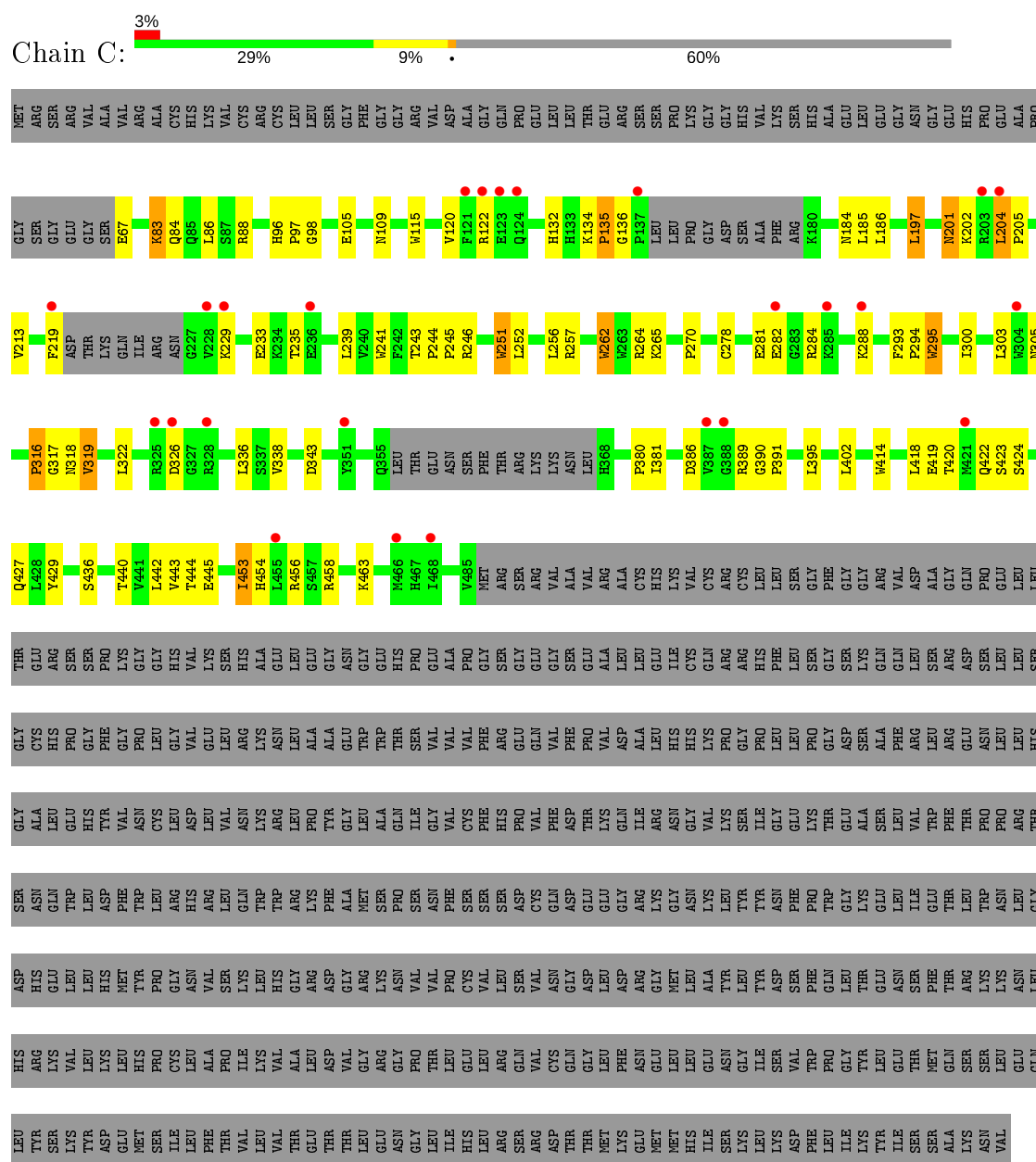
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	P	1	Total	C	N	O	P	0	0
			18	9	3	5	1		



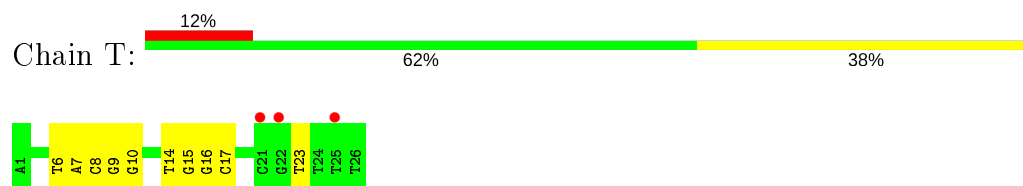
• Molecule 2: Pol gamma B



• Molecule 2: Pol gamma B



- Molecule 3: DNA (26-MER)



- Molecule 4: DNA (5'-D(*AP*AP*AP*AP*CP*GP*AP*GP*GP*GP*CP*CP*AP*GP*TP*GP*CP*CP*GP*TP*AP*C)-3')



A3	G12	G21
C13	C13	T22
C14	C14	A23
A15	A15	DC

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	217.45Å 217.45Å 163.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 3.57 48.91 – 3.57	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.91-3.57) 85.1 (48.91-3.57)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 3.57Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.300 , 0.338 0.333 , 0.363	Depositor DCC
R_{free} test set	2000 reflections (4.24%)	wwPDB-VP
Wilson B-factor (Å ²)	135.3	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 7.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	14634	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.41% 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: DOC, MG, 4Y3

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	0.22	0/7999	0.43	1/10852 (0.0%)
2	B	0.22	0/3015	0.39	0/4074
2	C	0.23	0/2956	0.42	2/3997 (0.1%)
3	T	0.51	0/591	0.88	0/909
4	P	0.49	0/488	0.75	0/752
All	All	0.25	0/15049	0.47	3/20584 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	135	PRO	CA-N-CD	-8.64	99.41	111.50
2	C	96	HIS	C-N-CD	-7.46	104.20	120.60
1	A	752	LEU	C-N-CD	-6.44	106.44	120.60

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	7799	0	7692	184	0
2	B	2942	0	2937	44	0
2	C	2883	0	2858	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	T	529	0	291	10	0
4	P	433	0	234	6	0
5	A	2	0	0	0	0
6	A	28	0	11	4	0
7	P	18	0	12	1	0
All	All	14634	0	14035	292	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 10.

All (292) 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)
2:C:134:LYS:CD	2:C:135:PRO:HD3	1.82	1.08
2:C:135:PRO:HD2	2:C:136:GLY:H	1.11	1.06
2:C:134:LYS:HD2	2:C:135:PRO:CD	1.92	1.00
2:C:134:LYS:HD2	2:C:135:PRO:HD3	1.01	1.00
2:C:419:GLU:H	2:C:420:THR:HA	1.35	0.92
2:C:135:PRO:HD2	2:C:136:GLY:N	1.88	0.86
2:C:134:LYS:NZ	2:C:135:PRO:HD2	1.92	0.85
2:C:134:LYS:CD	2:C:135:PRO:CD	2.57	0.78
2:C:443:VAL:HG22	2:C:453:ILE:HD11	1.66	0.77
1:A:243:ASP:HB3	1:A:279:ARG:HE	1.49	0.77
2:C:135:PRO:CD	2:C:136:GLY:H	1.94	0.74
2:C:442:LEU:HB3	2:C:454:HIS:HB2	1.69	0.73
1:A:464:MET:HB2	1:A:589:PRO:HG2	1.71	0.73
1:A:487:ASP:OD2	1:A:601:LYS:NZ	2.22	0.72
1:A:849:THR:HG22	1:A:850:ILE:HD13	1.71	0.72
1:A:1068:ASP:HA	1:A:1085:PRO:HG2	1.72	0.71
2:C:134:LYS:HZ2	2:C:135:PRO:HD2	1.56	0.70
1:A:153:ALA:HB1	1:A:194:ALA:HB2	1.74	0.69
2:C:134:LYS:NZ	2:C:135:PRO:CD	2.55	0.69
1:A:938:THR:H	1:A:939:VAL:HA	1.61	0.66
1:A:1161:ARG:HE	1:A:1177:VAL:HG22	1.61	0.65
1:A:533:CYS:SG	1:A:534:SER:N	2.69	0.65
2:B:77:HIS:HE1	2:B:431:LYS:HG3	1.61	0.65
2:C:213:VAL:HG22	2:C:235:THR:HG22	1.77	0.65
1:A:856:GLU:OE1	1:A:859:TRP:N	2.26	0.65
2:B:197:LEU:HD22	2:B:202:LYS:HA	1.79	0.64
1:A:800:PHE:HB2	1:A:869:ARG:HE	1.63	0.64
1:A:896:LEU:HD21	1:A:931:LEU:HD23	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:83:LYS:HG2	2:C:84:GLN:HG2	1.79	0.64
2:C:134:LYS:HZ3	2:C:135:PRO:CD	2.11	0.63
1:A:230:GLU:OE2	1:A:386:ARG:NH1	2.32	0.62
1:A:1057:MET:SD	1:A:1057:MET:N	2.73	0.62
2:B:442:LEU:HB3	2:B:454:HIS:HB2	1.82	0.62
1:A:884:TYR:HA	1:A:1142:ARG:HA	1.80	0.62
1:A:850:ILE:HG22	3:T:6:DT:H4'	1.81	0.61
1:A:79:LEU:H	1:A:83:LEU:HG	1.65	0.61
2:C:135:PRO:CD	2:C:136:GLY:N	2.56	0.61
2:C:429:TYR:HE1	2:C:463:LYS:HZ3	1.47	0.60
1:A:963:GLU:HG3	1:A:981:LYS:HZ3	1.66	0.60
1:A:978:ALA:HA	1:A:981:LYS:HD2	1.83	0.60
1:A:1142:ARG:NH1	1:A:1144:GLU:OE1	2.34	0.59
1:A:502:LYS:HB3	1:A:503:VAL:HB	1.83	0.59
1:A:1069:ILE:O	1:A:1071:ARG:N	2.35	0.59
1:A:1108:TYR:OH	1:A:1161:ARG:NH1	2.34	0.59
1:A:744:ILE:HG23	1:A:745:PRO:HD3	1.83	0.59
1:A:743:ASP:OD1	1:A:743:ASP:N	2.36	0.59
2:B:75:ARG:NH1	2:B:84:GLN:OE1	2.35	0.59
1:A:134:ASN:ND2	1:A:1166:TYR:OH	2.32	0.59
1:A:938:THR:N	1:A:939:VAL:HA	2.16	0.59
1:A:463:LEU:HD21	1:A:594:LEU:HD23	1.84	0.58
2:C:219:PHE:HD1	2:C:229:LYS:HG2	1.69	0.58
1:A:107:LEU:O	1:A:112:LEU:N	2.36	0.57
1:A:921:LEU:HD22	1:A:1174:PRO:HG2	1.86	0.57
1:A:208:CYS:SG	1:A:227:ARG:NH2	2.77	0.57
2:C:197:LEU:HD12	2:C:202:LYS:HG2	1.86	0.57
1:A:831:TYR:H	1:A:832:ASP:HA	1.69	0.57
1:A:951:TYR:CD2	6:A:4003:4Y3:H7	2.40	0.57
2:B:363:ARG:HD3	2:B:364:LYS:H	1.70	0.56
2:B:428:LEU:HD13	2:B:428:LEU:H	1.70	0.56
1:A:887:VAL:HG22	1:A:1185:ILE:HG23	1.87	0.56
1:A:488:LEU:H	1:A:488:LEU:HD13	1.69	0.55
2:B:185:LEU:H	2:B:185:LEU:HD23	1.71	0.55
2:C:319:VAL:HA	2:C:322:LEU:HD13	1.88	0.55
1:A:1079:ILE:HG12	1:A:1099:TRP:CZ3	2.42	0.55
2:B:104:VAL:HG23	2:B:107:ARG:HH21	1.72	0.54
1:A:869:ARG:NH1	4:P:22:DT:OP1	2.41	0.54
1:A:1073:PRO:HA	1:A:1074:VAL:HG13	1.89	0.54
1:A:162:LEU:HG	1:A:401:TRP:CZ3	2.42	0.54
1:A:1096:ARG:HA	1:A:1099:TRP:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:278:CYS:SG	2:C:288:LYS:NZ	2.81	0.54
1:A:239:LEU:O	1:A:279:ARG:NH1	2.41	0.54
2:B:241:TRP:HB3	2:B:336:LEU:HB3	1.90	0.54
1:A:466:LEU:HB3	1:A:602:LEU:HD21	1.89	0.53
2:B:323:HIS:HB3	2:B:330:ASN:HB2	1.90	0.53
2:C:424:SER:HB3	2:C:427:GLN:HG2	1.90	0.53
1:A:861:THR:HG21	3:T:8:DC:H1'	1.91	0.52
2:B:262:TRP:HA	2:B:265:LYS:HE2	1.91	0.52
2:C:184:ASN:OD1	2:C:185:LEU:N	2.41	0.52
1:A:1089:GLN:N	1:A:1090:GLU:HA	2.24	0.52
1:A:911:HIS:NE2	1:A:1172:ASP:O	2.37	0.52
1:A:761:ASN:N	1:A:761:ASN:OD1	2.43	0.52
1:A:977:GLU:HB3	1:A:981:LYS:HZ2	1.74	0.52
1:A:549:LEU:HD11	2:B:468:ILE:HG21	1.92	0.52
1:A:353:VAL:HG13	1:A:355:SER:H	1.75	0.52
1:A:752:LEU:HB2	1:A:753:PRO:HA	1.90	0.52
1:A:834:GLU:HG3	2:B:328:ARG:HH21	1.75	0.52
1:A:895:GLU:CG	6:A:4003:4Y3:H4	2.23	0.52
2:C:419:GLU:N	2:C:420:THR:HA	2.07	0.52
1:A:196:VAL:HG22	1:A:215:ILE:HG12	1.93	0.51
2:B:83:LYS:HG2	2:B:85:GLN:H	1.74	0.51
1:A:866:ARG:HH21	1:A:869:ARG:HD2	1.75	0.51
1:A:562:ARG:HH11	1:A:563:PRO:HD2	1.74	0.51
1:A:622:TYR:HB2	1:A:770:PHE:HE2	1.75	0.51
1:A:93:GLU:HA	1:A:94:MET:HB2	1.93	0.51
1:A:212:ALA:HB3	1:A:223:TRP:HB3	1.92	0.51
1:A:296:SER:HB2	1:A:847:ALA:HB3	1.93	0.51
1:A:1061:LEU:HB3	1:A:1097:VAL:HG13	1.92	0.51
1:A:495:PHE:HB3	1:A:496:LYS:HB2	1.92	0.51
2:B:407:LEU:HD13	2:C:120:VAL:HG12	1.92	0.51
2:C:262:TRP:HA	2:C:265:LYS:HE2	1.93	0.51
1:A:299:MET:HG2	1:A:848:GLY:HA2	1.93	0.51
2:B:365:LYS:H	2:B:365:LYS:HD2	1.75	0.50
2:B:219:PHE:HA	2:B:229:LYS:N	2.27	0.50
2:C:444:THR:OG1	2:C:445:GLU:OE2	2.28	0.50
1:A:963:GLU:HG3	1:A:981:LYS:NZ	2.27	0.50
1:A:1200:PRO:O	1:A:1202:ASN:N	2.44	0.50
2:C:252:LEU:HD22	2:C:305:ASN:HB2	1.93	0.50
2:C:389:ARG:HD3	2:C:395:LEU:HD11	1.93	0.50
2:B:404:ASN:HA	2:B:407:LEU:HG	1.93	0.50
2:C:444:THR:OG1	2:C:445:GLU:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:GLN:HB2	1:A:263:GLU:HG2	1.94	0.49
2:B:393:LEU:HD12	2:B:394:GLU:HG2	1.93	0.49
2:C:134:LYS:HZ3	2:C:135:PRO:HD2	1.70	0.49
2:C:201:ASN:ND2	2:C:201:ASN:O	2.42	0.49
1:A:608:ASP:OD1	1:A:778:THR:OG1	2.29	0.49
1:A:750:PHE:HD1	1:A:751:LYS:HG2	1.76	0.49
2:C:134:LYS:CG	2:C:135:PRO:CD	2.91	0.49
1:A:1088:VAL:HG12	1:A:1090:GLU:HA	1.94	0.49
1:A:556:THR:HA	1:A:559:LEU:HD13	1.95	0.49
2:C:205:PRO:HB3	2:C:243:THR:HA	1.95	0.49
2:C:241:TRP:HD1	2:C:336:LEU:HD22	1.77	0.49
1:A:1115:ALA:HB3	1:A:1156:THR:HG23	1.95	0.49
1:A:94:MET:HG3	1:A:1170:LEU:HD11	1.95	0.49
1:A:953:ARG:HG3	1:A:957:ALA:HB2	1.93	0.49
1:A:987:ALA:HB1	1:A:1056:GLU:HG2	1.95	0.49
1:A:275:ARG:NH2	1:A:433:SER:O	2.42	0.49
2:B:441:VAL:HG23	2:B:453:ILE:HG13	1.94	0.48
1:A:1075:LEU:HD23	1:A:1075:LEU:H	1.78	0.48
1:A:856:GLU:H	1:A:860:LEU:HD12	1.78	0.48
2:C:436:SER:OG	2:C:458:ARG:NH1	2.46	0.48
1:A:1154:GLN:HG3	1:A:1218:LEU:HD21	1.95	0.48
2:B:457:SER:OG	2:B:460:THR:O	2.32	0.48
2:B:213:VAL:HA	2:B:235:THR:HA	1.95	0.48
2:C:134:LYS:HG3	2:C:135:PRO:HD2	1.96	0.48
2:B:384:ALA:HB2	2:B:437:ILE:HD13	1.94	0.48
2:C:105:GLU:O	2:C:109:ASN:ND2	2.43	0.48
1:A:825:VAL:HG13	1:A:882:PRO:HG2	1.95	0.48
1:A:869:ARG:HB2	1:A:872:SER:HB2	1.96	0.48
1:A:991:GLY:HA2	1:A:1052:GLY:HA2	1.96	0.48
1:A:175:TRP:CD2	1:A:223:TRP:HB2	2.48	0.48
1:A:1134:HIS:HD2	7:P:101:DOC:H1'	1.78	0.48
1:A:616:GLU:HB2	1:A:617:ARG:HD3	1.96	0.48
2:C:317:GLY:HA3	2:C:318:ASN:HA	1.58	0.48
1:A:803:ASN:HA	3:T:10:DG:H4'	1.95	0.47
1:A:849:THR:OG1	3:T:7:DA:OP1	2.23	0.47
1:A:887:VAL:HG13	1:A:1185:ILE:HG12	1.95	0.47
1:A:178:TYR:O	1:A:219:ALA:HB1	2.14	0.47
1:A:1183:VAL:HB	1:A:1214:GLN:HB3	1.96	0.47
1:A:1183:VAL:N	1:A:1214:GLN:O	2.47	0.47
1:A:475:SER:HA	1:A:476:GLY:HA2	1.49	0.47
1:A:1090:GLU:O	1:A:1091:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:611:PRO:HG3	1:A:652:ILE:HD13	1.97	0.47
2:C:235:THR:OG1	2:C:343:ASP:OD1	2.29	0.47
1:A:804:ALA:O	1:A:808:ILE:HG12	2.14	0.46
1:A:272:SER:HB3	1:A:843:GLN:HA	1.97	0.46
1:A:642:SER:HA	1:A:643:ALA:HA	1.58	0.46
1:A:765:PRO:HA	1:A:766:PHE:HA	1.58	0.46
2:C:246:ARG:NH2	2:C:326:ASP:OD2	2.46	0.46
2:B:428:LEU:HA	2:B:431:LYS:HB3	1.96	0.46
1:A:593:SER:HB2	1:A:596:MET:HB2	1.97	0.46
1:A:939:VAL:HA	1:A:940:GLY:HA3	1.71	0.46
1:A:135:LEU:H	1:A:135:LEU:HD23	1.79	0.46
1:A:866:ARG:HE	1:A:869:ARG:HD2	1.79	0.46
1:A:977:GLU:HB3	1:A:981:LYS:NZ	2.31	0.46
4:P:14:DC:H2'	4:P:15:DA:C8	2.50	0.46
1:A:302:SER:HB2	1:A:1081:ARG:HD3	1.96	0.46
1:A:636:THR:OG1	1:A:637:GLY:N	2.49	0.46
1:A:888:GLY:HA3	1:A:1138:ARG:HD2	1.97	0.46
1:A:897:TRP:CD1	1:A:1177:VAL:HG21	2.50	0.46
2:B:193:TYR:OH	2:B:333:PRO:HG3	2.15	0.46
1:A:606:THR:HB	1:A:612:LEU:HD13	1.97	0.46
2:B:266:PHE:HA	2:B:375:HIS:CD2	2.51	0.46
2:B:197:LEU:HA	2:B:197:LEU:HD23	1.84	0.45
2:B:364:LYS:HB2	2:B:364:LYS:HE2	1.65	0.45
1:A:618:HIS:CD2	1:A:619:GLY:H	2.34	0.45
2:C:381:ILE:HG21	2:C:414:TRP:HB2	1.97	0.45
3:T:16:DG:H1	4:P:13:DC:H42	1.63	0.45
1:A:942:SER:HA	1:A:943:ARG:HA	1.58	0.45
2:B:278:CYS:SG	2:B:288:LYS:NZ	2.87	0.45
2:B:420:THR:HG23	2:B:421:MET:HG2	1.99	0.45
2:B:467:HIS:HB3	2:B:470:LYS:HB2	1.97	0.45
1:A:617:ARG:HB2	1:A:763:GLY:HA3	1.99	0.45
1:A:384:ASP:OD1	1:A:384:ASP:N	2.42	0.45
1:A:894:GLN:HG3	1:A:895:GLU:H	1.81	0.45
1:A:262:GLN:HA	1:A:263:GLU:HA	1.51	0.45
1:A:110:HIS:HB3	1:A:111:GLY:HA2	1.98	0.45
1:A:435:LEU:HD22	1:A:878:VAL:HG11	1.98	0.45
1:A:778:THR:HA	1:A:779:LEU:HA	1.61	0.45
2:B:244:PRO:HA	2:B:245:PRO:HD3	1.86	0.45
1:A:895:GLU:CD	6:A:4003:4Y3:H4	2.21	0.45
1:A:976:GLN:O	1:A:980:GLU:HG2	2.17	0.45
2:C:67:GLU:N	2:C:88:ARG:HH21	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1124:ALA:O	1:A:1148:ARG:NH2	2.44	0.44
2:C:389:ARG:HB3	2:C:395:LEU:HD11	1.98	0.44
1:A:1214:GLN:HA	1:A:1215:GLY:HA3	1.58	0.44
1:A:307:PHE:O	1:A:310:SER:OG	2.34	0.44
1:A:268:GLY:HA2	1:A:403:THR:HG21	1.99	0.44
2:C:293:PHE:HB3	2:C:295:TRP:H	1.82	0.44
1:A:372:GLU:HG3	1:A:375:GLU:H	1.82	0.44
1:A:612:LEU:HA	1:A:612:LEU:HD12	1.76	0.44
1:A:808:ILE:HD12	1:A:874:LEU:HG	1.99	0.44
2:B:454:HIS:ND1	2:B:463:LYS:HE3	2.33	0.44
1:A:162:LEU:HD22	1:A:163:PRO:HD2	1.99	0.44
1:A:582:ASP:HA	1:A:583:PRO:HD3	1.90	0.44
1:A:856:GLU:HA	1:A:857:PRO:HD3	1.85	0.44
2:B:421:MET:HA	2:B:422:GLN:HB3	1.99	0.44
2:C:239:LEU:HB3	2:C:338:VAL:HB	1.99	0.44
1:A:1133:ILE:HG12	1:A:1136:GLU:HB3	1.98	0.44
2:B:365:LYS:HG2	2:B:367:LEU:H	1.82	0.44
2:C:303:LEU:HD22	2:C:338:VAL:HG22	2.00	0.44
1:A:579:ARG:NH1	4:P:12:DG:OP1	2.51	0.44
1:A:1187:ARG:HH11	1:A:1209:ARG:HH12	1.66	0.44
1:A:267:VAL:HG12	1:A:292:LEU:HB3	1.98	0.44
1:A:536:GLU:HG3	2:C:257:ARG:HH12	1.82	0.43
1:A:773:LYS:HD2	1:A:773:LYS:HA	1.89	0.43
1:A:892:ASP:HA	1:A:893:SER:HA	1.66	0.43
1:A:566:LEU:HD13	1:A:566:LEU:H	1.81	0.43
1:A:856:GLU:N	1:A:860:LEU:HD12	2.33	0.43
1:A:973:LEU:HD21	1:A:976:GLN:HG3	1.99	0.43
1:A:1047:ARG:H	1:A:1047:ARG:HG3	1.64	0.43
1:A:895:GLU:HG3	6:A:4003:4Y3:H4	1.81	0.43
1:A:505:LYS:HD3	1:A:505:LYS:HA	1.78	0.43
1:A:831:TYR:N	1:A:832:ASP:HA	2.30	0.43
2:C:134:LYS:CE	2:C:135:PRO:HD3	2.47	0.43
2:C:419:GLU:OE2	2:C:422:GLN:HB2	2.18	0.43
3:T:9:DG:H2'	3:T:10:DG:C8	2.53	0.43
2:C:316:PRO:HA	2:C:317:GLY:HA2	1.57	0.43
2:C:134:LYS:HG3	2:C:135:PRO:CD	2.49	0.43
4:P:21:DG:H2'	4:P:22:DT:C6	2.53	0.43
1:A:1079:ILE:HG12	1:A:1099:TRP:CE3	2.54	0.43
1:A:1198:LYS:HB3	1:A:1198:LYS:HE3	1.81	0.43
2:B:418:LEU:HD22	2:C:204:LEU:HD12	1.99	0.43
3:T:17:DC:H42	4:P:12:DG:H1	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1026:ARG:HD2	1:A:1026:ARG:O	2.20	0.42
1:A:498:LYS:HD3	3:T:23:DT:OP1	2.19	0.42
1:A:782:GLY:HA2	1:A:784:GLY:HA2	2.01	0.42
1:A:864:ASN:HB3	1:A:1191:LYS:HD3	2.01	0.42
1:A:1060:LYS:HE2	1:A:1064:ILE:HD11	2.01	0.42
2:C:205:PRO:HB3	2:C:244:PRO:HD3	2.01	0.42
1:A:155:ASN:O	1:A:159:GLN:HG2	2.20	0.42
1:A:963:GLU:HA	1:A:981:LYS:HE2	2.02	0.42
2:C:243:THR:HG1	2:C:251:TRP:HE3	1.64	0.42
1:A:206:GLY:HA3	1:A:207:THR:HA	1.82	0.42
1:A:299:MET:SD	1:A:849:THR:HG23	2.59	0.42
2:B:133:HIS:ND1	2:C:233:GLU:OE2	2.51	0.42
1:A:828:HIS:O	1:A:830:ASP:N	2.45	0.41
1:A:87:ILE:HD13	1:A:127:LEU:HD22	2.01	0.41
1:A:176:THR:OG1	1:A:222:SER:OG	2.36	0.41
1:A:288:ARG:HA	1:A:288:ARG:HE	1.86	0.41
1:A:79:LEU:HD13	1:A:80:SER:H	1.84	0.41
1:A:818:ARG:H	1:A:818:ARG:HE	1.68	0.41
1:A:298:HIS:HB2	1:A:410:GLN:HE22	1.85	0.41
1:A:371:LYS:HA	1:A:371:LYS:HD2	1.97	0.41
1:A:595:GLN:OE1	1:A:795:ASN:ND2	2.37	0.41
2:B:213:VAL:HG11	2:C:132:HIS:CE1	2.55	0.41
1:A:247:LEU:H	1:A:247:LEU:HD13	1.85	0.41
3:T:14:DT:H2''	3:T:15:DG:C8	2.55	0.41
1:A:78:MET:HA	1:A:79:LEU:HA	1.77	0.41
2:C:389:ARG:HG2	2:C:390:GLY:N	2.35	0.41
2:C:418:LEU:N	2:C:419:GLU:HA	2.36	0.41
1:A:1074:VAL:HB	1:A:1167:LYS:HB3	2.01	0.41
1:A:499:LYS:H	1:A:499:LYS:HG3	1.59	0.41
1:A:850:ILE:HA	1:A:851:THR:HA	1.76	0.41
2:B:439:PHE:HB3	2:B:455:LEU:HD11	2.03	0.41
3:T:6:DT:H2'	3:T:7:DA:O4'	2.20	0.41
1:A:1075:LEU:HB2	1:A:1076:GLY:HA3	2.02	0.41
1:A:851:THR:O	1:A:1106:VAL:HG21	2.21	0.41
2:C:440:THR:OG1	2:C:456:ARG:HB3	2.20	0.41
1:A:864:ASN:O	1:A:872:SER:OG	2.38	0.41
2:B:79:LEU:HG	2:B:102:LEU:HB2	2.03	0.41
1:A:1064:ILE:HG22	1:A:1071:ARG:HB3	2.03	0.41
1:A:749:PHE:HB2	1:A:750:PHE:H	1.60	0.41
2:C:264:ARG:HG3	2:C:270:PRO:HB3	2.02	0.41
1:A:1213:PRO:O	1:A:1214:GLN:NE2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:LEU:HD12	1:A:377:PHE:HZ	1.86	0.40
1:A:225:SER:HB3	1:A:227:ARG:NH2	2.35	0.40
1:A:502:LYS:HA	1:A:503:VAL:HA	1.94	0.40
2:B:382:LYS:H	2:B:412:SER:HB2	1.86	0.40
2:C:293:PHE:N	2:C:294:PRO:HA	2.37	0.40
1:A:1157:ASN:ND2	1:A:1178:ALA:O	2.55	0.40
1:A:151:LEU:HA	1:A:151:LEU:HD23	1.95	0.40
1:A:304:LEU:HD13	1:A:309:ARG:HG2	2.02	0.40
1:A:771:LEU:HD21	1:A:792:LEU:HB3	2.02	0.40
1:A:299:MET:HG3	1:A:849:THR:HG23	2.03	0.40
1:A:175:TRP:CE3	1:A:223:TRP:HB2	2.57	0.40
1:A:631:LEU:HB3	1:A:633:LYS:NZ	2.35	0.40
2:B:446:THR:O	2:B:450:ASN:ND2	2.53	0.40
1:A:1136:GLU:OE2	1:A:1138:ARG:NH1	2.55	0.40
1:A:151:LEU:HD21	1:A:424:LEU:HD11	2.04	0.40
2:B:290:TYR:HD1	2:B:299:LEU:HA	1.87	0.40
2:B:423:SER:OG	2:B:424:SER:N	2.54	0.40
2:C:244:PRO:HA	2:C:245:PRO:HD3	1.81	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	969/1205 (80%)	835 (86%)	114 (12%)	20 (2%)	7	40
2	B	355/903 (39%)	326 (92%)	27 (8%)	2 (1%)	25	64
2	C	350/903 (39%)	325 (93%)	18 (5%)	7 (2%)	7	42
All	All	1674/3011 (56%)	1486 (89%)	159 (10%)	29 (2%)	9	45

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	752	LEU
1	A	1070	PRO
2	C	97	PRO
1	A	749	PHE
1	A	1177	VAL
2	C	98	GLY
2	C	423	SER
1	A	642	SER
1	A	767	ALA
1	A	1073	PRO
1	A	1080	SER
1	A	1134	HIS
2	C	316	PRO
2	C	319	VAL
2	C	391	PRO
1	A	95	PRO
1	A	610	PHE
1	A	618	HIS
1	A	811	GLN
1	A	927	ARG
1	A	1074	VAL
1	A	743	ASP
1	A	765	PRO
2	B	317	GLY
2	C	380	PRO
2	B	451	GLY
1	A	560	PRO
1	A	1043	VAL
1	A	1141	VAL

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	823/1017 (81%)	749 (91%)	74 (9%)	9	39
2	B	325/791 (41%)	307 (94%)	18 (6%)	21	56
2	C	316/791 (40%)	297 (94%)	19 (6%)	19	54

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1464/2599 (56%)	1353 (92%)	111 (8%)	13	44

All (111) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	LEU
1	A	101	ARG
1	A	118	VAL
1	A	130	LEU
1	A	133	ASP
1	A	195	LEU
1	A	197	PHE
1	A	201	VAL
1	A	227	ARG
1	A	236	THR
1	A	245	ILE
1	A	247	LEU
1	A	292	LEU
1	A	304	LEU
1	A	311	LEU
1	A	316	LYS
1	A	424	LEU
1	A	488	LEU
1	A	499	LYS
1	A	548	CYS
1	A	558	LEU
1	A	565	HIS
1	A	566	LEU
1	A	595	GLN
1	A	596	MET
1	A	613	HIS
1	A	617	ARG
1	A	636	THR
1	A	639	THR
1	A	640	LEU
1	A	655	LEU
1	A	743	ASP
1	A	744	ILE
1	A	748	TRP
1	A	751	LYS
1	A	761	ASN
1	A	768	LYS

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Mol	Chain	Res	Type
1	A	774	MET
1	A	779	LEU
1	A	816	LEU
1	A	818	ARG
1	A	821	LEU
1	A	841	LEU
1	A	851	THR
1	A	927	ARG
1	A	941	ILE
1	A	964	ARG
1	A	970	ASN
1	A	973	LEU
1	A	977	GLU
1	A	1026	ARG
1	A	1027	LYS
1	A	1038	TRP
1	A	1043	VAL
1	A	1047	ARG
1	A	1057	MET
1	A	1069	ILE
1	A	1071	ARG
1	A	1074	VAL
1	A	1075	LEU
1	A	1081	ARG
1	A	1090	GLU
1	A	1099	TRP
1	A	1118	TRP
1	A	1120	PHE
1	A	1129	PHE
1	A	1133	ILE
1	A	1141	VAL
1	A	1190	ARG
1	A	1191	LYS
1	A	1197	CYS
1	A	1198	LYS
1	A	1210	TYR
1	A	1218	LEU
2	B	69	LEU
2	B	89	ASP
2	B	186	LEU
2	B	197	LEU
2	B	231	ILE

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Mol	Chain	Res	Type
2	B	263	TRP
2	B	329	LYS
2	B	364	LYS
2	B	365	LYS
2	B	368	HIS
2	B	372	LEU
2	B	394	GLU
2	B	396	ARG
2	B	428	LEU
2	B	453	ILE
2	B	460	THR
2	B	461	THR
2	B	467	HIS
2	C	83	LYS
2	C	86	LEU
2	C	115	TRP
2	C	122	ARG
2	C	186	LEU
2	C	197	LEU
2	C	201	ASN
2	C	204	LEU
2	C	251	TRP
2	C	256	LEU
2	C	262	TRP
2	C	281	GLU
2	C	282	GLU
2	C	284	ARG
2	C	295	TRP
2	C	300	ILE
2	C	386	ASP
2	C	402	LEU
2	C	453	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	264	GLN
1	A	1134	HIS
2	C	96	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 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	$\# Z > 2$
6	4Y3	A	4003	5	22,29,29	3.40	7 (31%)	27,45,45	1.61	5 (18%)
7	DOC	P	101	4	14,19,20	0.78	0	13,26,29	1.09	1 (7%)

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
6	4Y3	A	4003	5	-	5/19/31/31	0/2/2/2
7	DOC	P	101	4	-	0/4/18/19	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	4003	4Y3	O4'-C1'	8.78	1.62	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	4003	4Y3	C2'-C1'	-8.15	1.33	1.51
6	A	4003	4Y3	O4'-C4'	-7.63	1.29	1.44
6	A	4003	4Y3	C4-N4	4.74	1.46	1.34
6	A	4003	4Y3	C4-C5	2.54	1.42	1.40
6	A	4003	4Y3	C2-N3	-2.36	1.33	1.38
6	A	4003	4Y3	C1'-N1	-2.07	1.43	1.49

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	4003	4Y3	C2-N3-C4	4.22	121.12	116.02
7	P	101	DOC	C2-N3-C4	3.61	120.00	116.34
6	A	4003	4Y3	S-C2'-C1'	3.26	106.55	102.78
6	A	4003	4Y3	PB-O3A-PA	-2.79	123.25	132.83
6	A	4003	4Y3	PB-O3B-PG	-2.52	124.19	132.83
6	A	4003	4Y3	N4-C4-N3	2.42	120.46	117.03

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	4003	4Y3	C5'-O5'-PA-O1A
6	A	4003	4Y3	C5'-O5'-PA-O2A
6	A	4003	4Y3	PA-O3A-PB-O2B
6	A	4003	4Y3	C5'-O5'-PA-O3A
6	A	4003	4Y3	PG-O3B-PB-O2B

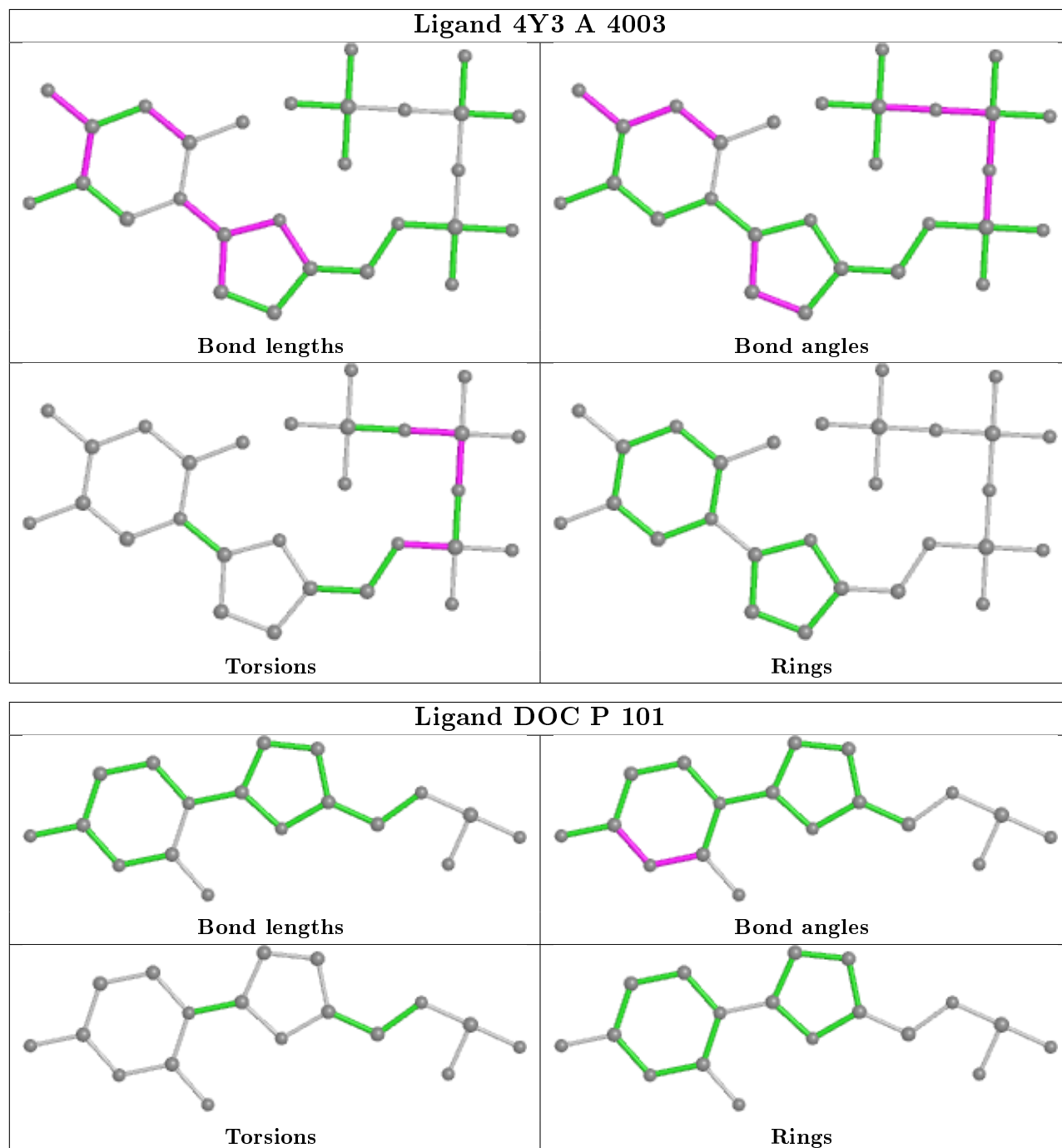
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	4003	4Y3	4	0
7	P	101	DOC	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 ⓘ

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

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	983/1205 (81%)	0.32	59 (6%) 21 13	44, 73, 91, 163	0
2	B	363/903 (40%)	0.21	8 (2%) 62 45	47, 65, 87, 101	0
2	C	358/903 (39%)	0.33	25 (6%) 16 10	54, 73, 86, 96	0
3	T	26/26 (100%)	0.75	3 (11%) 4 4	84, 107, 126, 131	0
4	P	21/22 (95%)	0.17	0 100 100	92, 105, 127, 166	0
All	All	1751/3059 (57%)	0.30	95 (5%) 25 16	44, 72, 94, 166	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	745	PRO	11.0
1	A	630	ASN	9.6
1	A	746	GLY	9.0
1	A	747	CYS	7.9
1	A	632	ALA	6.9
2	C	282	GLU	5.9
1	A	501	LYS	5.7
1	A	631	LEU	5.5
1	A	744	ILE	5.0
2	C	228	VAL	5.0
1	A	500	ALA	4.5
1	A	509	THR	4.5
2	B	366	ASN	4.4
1	A	741	ASP	4.4
1	A	622	TYR	4.3
1	A	508	ALA	4.1
1	A	619	GLY	4.1
2	C	121	PHE	3.9
1	A	865	ALA	3.8
1	A	640	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	1202	ASN	3.7
1	A	1031	GLU	3.5
1	A	1087	ALA	3.5
1	A	230	GLU	3.4
1	A	759	SER	3.4
1	A	506	GLU	3.4
1	A	102	ARG	3.4
2	C	123	GLU	3.3
1	A	214	ALA	3.1
1	A	760	CYS	3.1
1	A	94	MET	3.1
1	A	1207	GLU	3.1
2	C	325	ARG	3.1
1	A	507	PRO	3.0
1	A	431	GLY	3.0
1	A	764	SER	2.9
2	B	328	ARG	2.9
2	C	288	LYS	2.9
1	A	633	LYS	2.8
2	C	421	MET	2.8
1	A	601	LYS	2.8
1	A	969	PHE	2.8
2	C	229	LYS	2.8
1	A	173	GLU	2.7
2	C	124	GLN	2.7
2	B	322	LEU	2.7
2	C	328	ARG	2.7
2	C	204	LEU	2.7
2	B	108	LYS	2.7
2	C	304	TRP	2.7
2	C	388	GLY	2.6
1	A	1213	PRO	2.6
2	C	137	PRO	2.6
2	C	351	TYR	2.6
2	C	455	LEU	2.6
1	A	502	LYS	2.5
1	A	893	SER	2.5
2	C	468	ILE	2.5
3	T	25	DT	2.5
2	C	285	LYS	2.5
1	A	1208	ARG	2.4
2	B	81	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	1082	ALA	2.4
2	C	466	MET	2.4
1	A	846	THR	2.4
2	C	122	ARG	2.4
1	A	1076	GLY	2.4
1	A	342	ILE	2.3
1	A	927	ARG	2.3
1	A	832	ASP	2.3
1	A	890	ASP	2.3
1	A	1134	HIS	2.3
1	A	942	SER	2.3
2	C	219	PHE	2.3
1	A	348	LEU	2.3
2	C	203	ARG	2.2
1	A	1050	LYS	2.2
2	B	109	ASN	2.2
2	B	391	PRO	2.2
1	A	304	LEU	2.2
2	C	387	VAL	2.2
1	A	1036	SER	2.2
3	T	22	DG	2.2
1	A	122	ASP	2.1
1	A	1068	ASP	2.1
2	C	326	ASP	2.1
2	C	236	GLU	2.1
2	B	393	LEU	2.1
1	A	93	GLU	2.1
1	A	912	GLY	2.1
3	T	21	DC	2.1
1	A	1131	ILE	2.1
1	A	892	ASP	2.0
1	A	563	PRO	2.0
1	A	1132	SER	2.0

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

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

6.3 Carbohydrates ⓘ

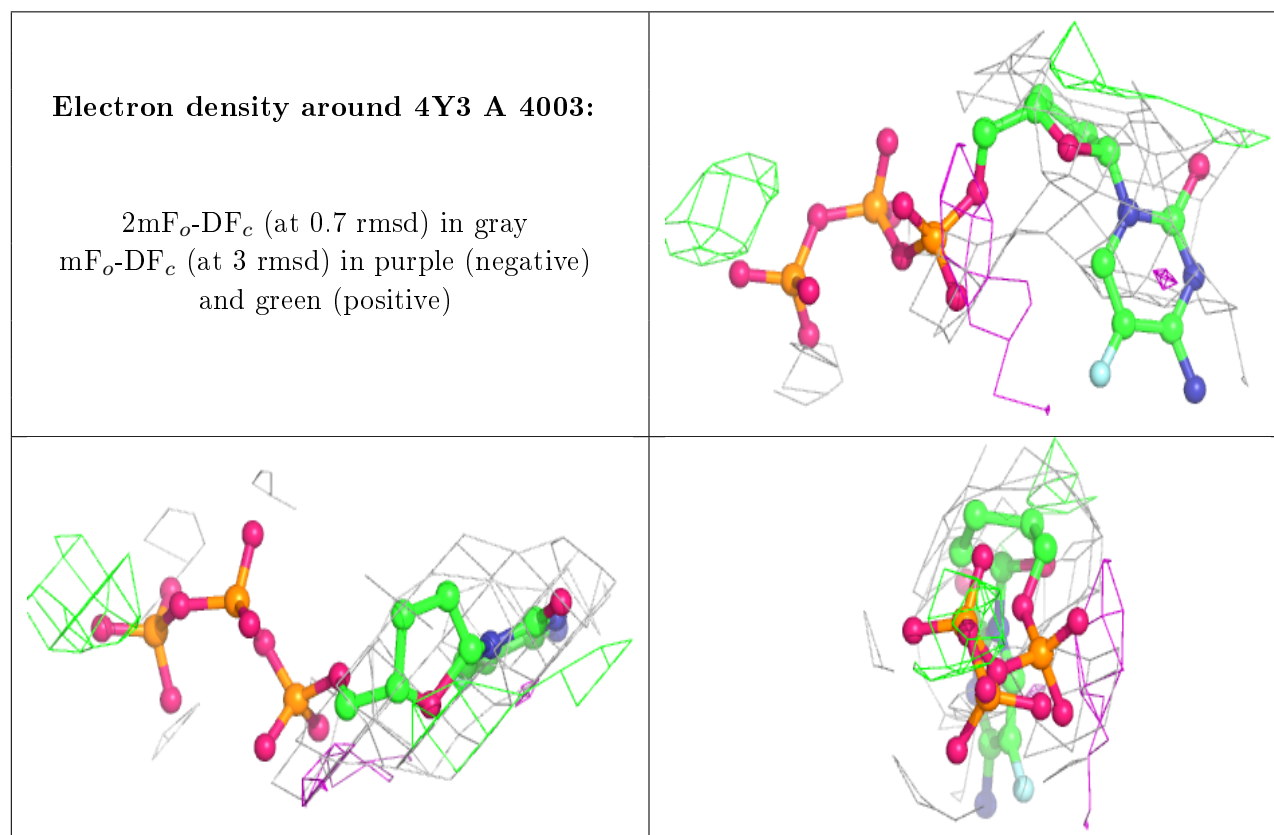
There are no carbohydrates in this entry.

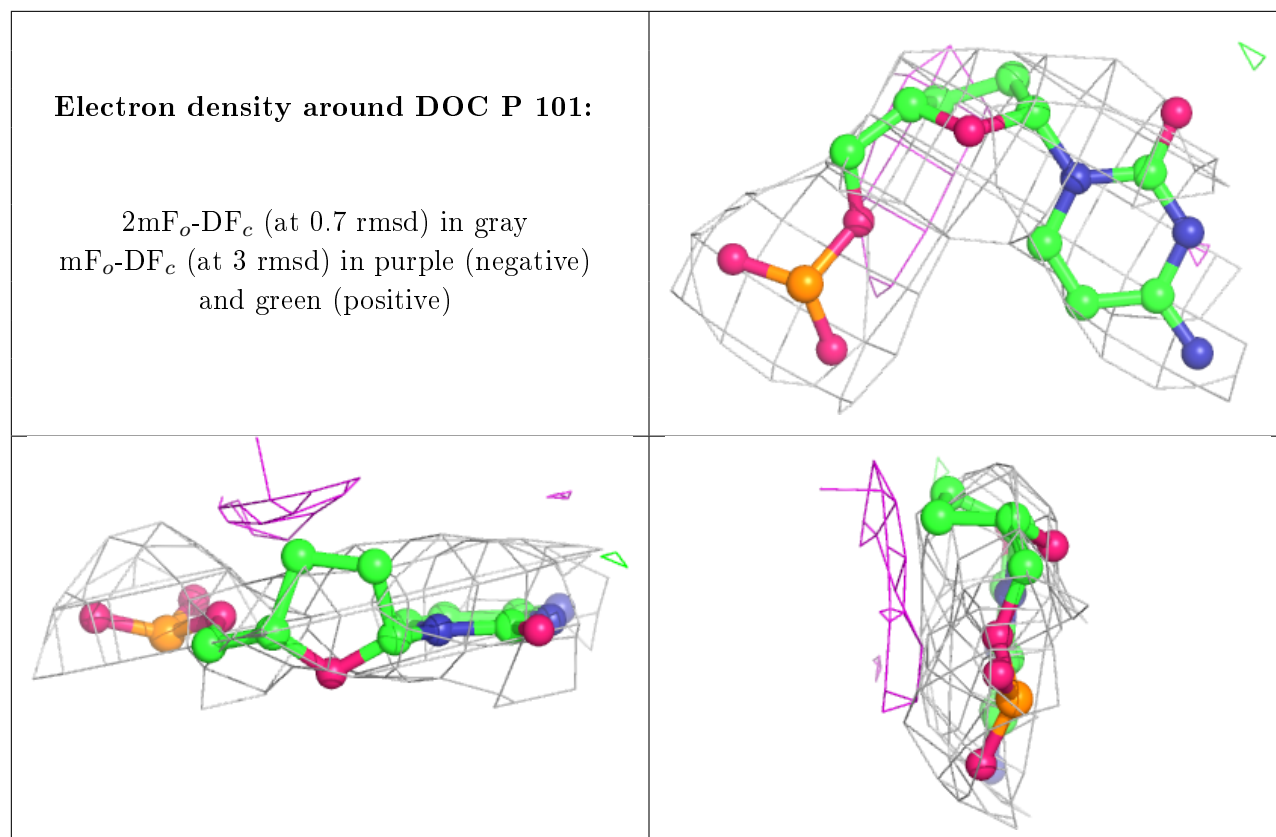
6.4 Ligands ⓘ

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(Å ²)	Q<0.9
6	4Y3	A	4003	28/28	0.83	0.42	80,100,106,107	0
7	DOC	P	101	18/19	0.84	0.35	91,94,98,99	0
5	MG	A	4002	1/1	0.88	0.34	60,60,60,60	0
5	MG	A	4001	1/1	0.92	0.20	70,70,70,70	0

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





6.5 Other polymers [i](#)

There are no such residues in this entry.