



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 06:30 pm BST

PDB ID : 3TH1  
Title : Crystal structure of chlorocatechol 1,2-dioxygenase from *Pseudomonas putida*  
Authors : Rustiguel, J.K.; Nonato, M.C.  
Deposited on : 2011-08-18  
Resolution : 3.40 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](mailto: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.

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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

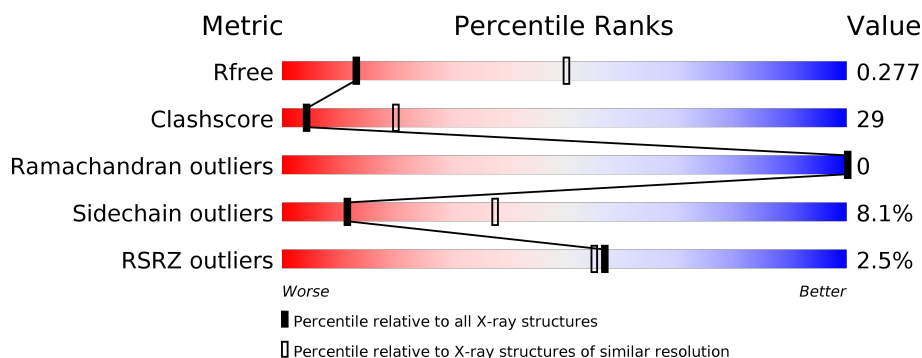
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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  $\geq 3$ , 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	260	<div> <div>56%</div> <div>37%</div> <div>• 5%</div> </div>
1	B	260	<div> <div>3%</div> <div>51%</div> <div>40%</div> <div>• 7%</div> </div>
1	C	260	<div> <div>4%</div> <div>63%</div> <div>28%</div> <div>• 8%</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
3	DTD	A	301	-	-	X	X
4	3PH	B	302	-	-	X	-

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5462 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.

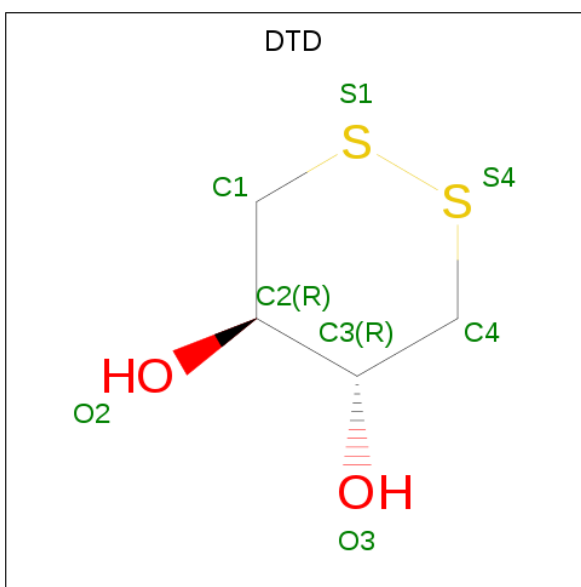
- Molecule 1 is a protein called Chlorocatechol 1,2-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	2	0
			1927	1226	329	366	6			
1	B	243	Total	C	N	O	S	14	1	0
			1749	1107	300	337	5			
1	C	238	Total	C	N	O	S	4	0	0
			1630	1024	281	321	4			

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

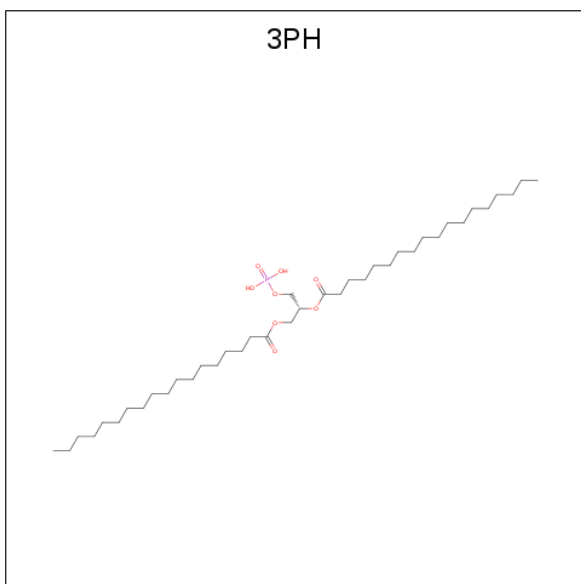
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Fe	0	0
			1	1		
2	A	1	Total	Fe	0	0
			1	1		
2	C	1	Total	Fe	0	0
			1	1		

- Molecule 3 is DITHIANE DIOL (three-letter code: DTD) (formula: C<sub>4</sub>H<sub>8</sub>O<sub>2</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			8	4	2	2		
3	B	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 4 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula:  $C_{39}H_{77}O_8P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	5	0
			48	39	8	1		

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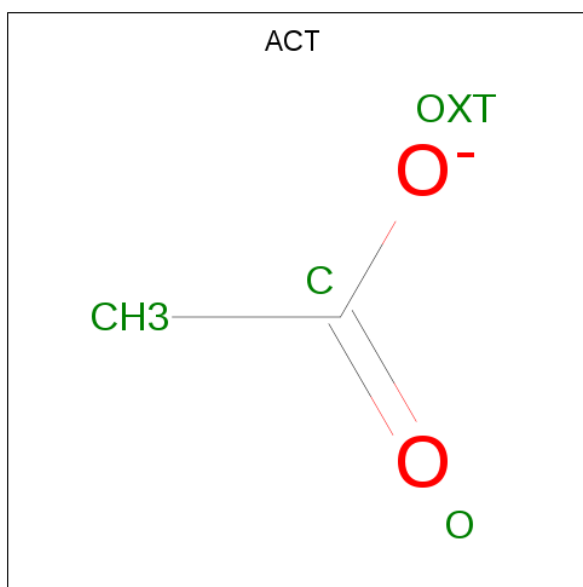
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	P	1	0
			48	39	8	1		

- 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 ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	1
			12	6	6		
7	B	1	Total	C	O	0	0
			6	3	3		

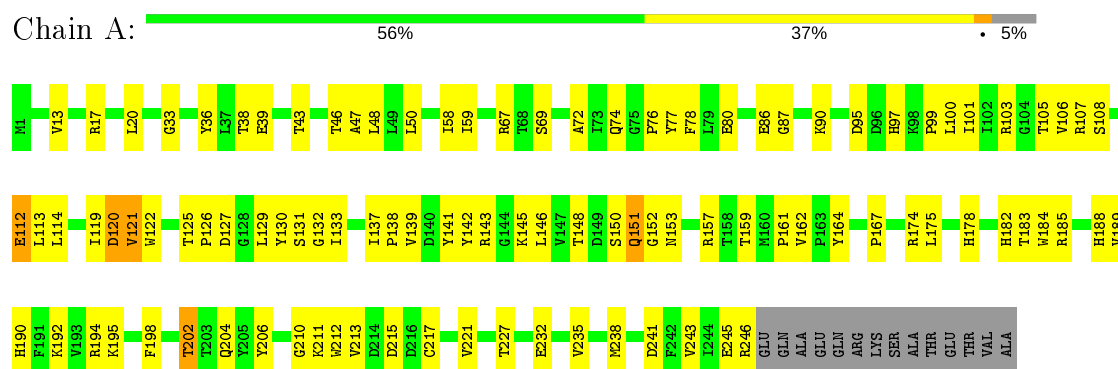
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total	O	0	0
			8	8		
8	B	3	Total	O	0	0
			3	3		
8	C	6	Total	O	0	0
			6	6		

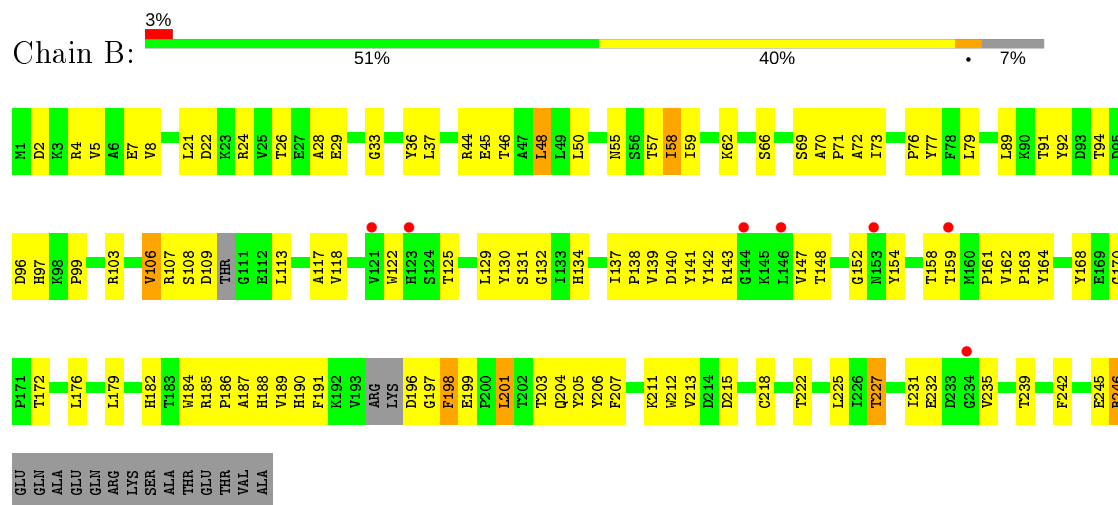
### 3 Residue-property plots

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.

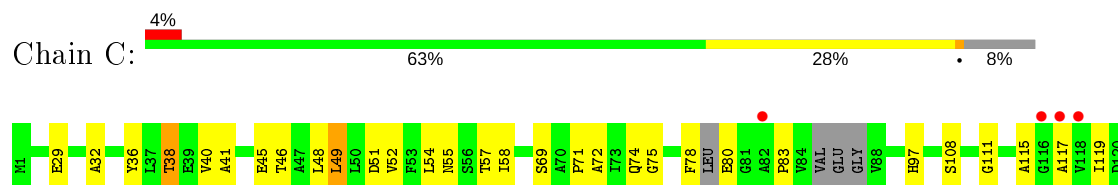
#### • Molecule 1: Chlorocatechol 1,2-dioxygenase



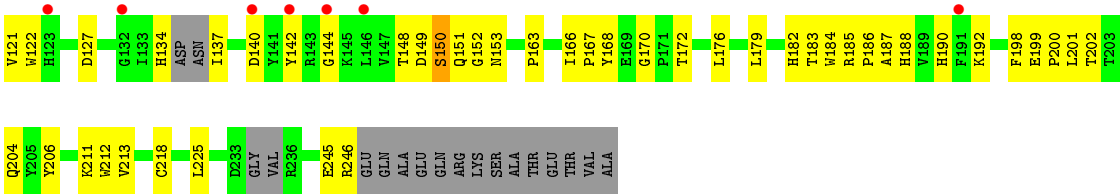
#### • Molecule 1: Chlorocatechol 1,2-dioxygenase



#### • Molecule 1: Chlorocatechol 1,2-dioxygenase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.57Å 97.57Å 423.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	54.18 – 3.40 54.18 – 3.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.18-3.40) 96.1 (54.18-3.40)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	0.21	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.46 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.227 , 0.279 0.223 , 0.277	Depositor DCC
$R_{free}$ test set	1747 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.7	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 91.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	5462	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, MG, DTD, 3PH, FE, ACT

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	0.27	0/1972	0.54	0/2689
1	B	0.23	0/1792	0.50	0/2453
1	C	0.24	0/1668	0.48	0/2291
All	All	0.25	0/5432	0.51	0/7433

There are no bond length outliers.

There are no bond angle outliers.

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	1927	0	1872	94	0
1	B	1749	0	1504	127	0
1	C	1630	0	1304	63	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	8	0	8	4	0
3	B	8	0	8	1	0
4	A	48	0	75	10	0
4	B	48	0	75	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
6	A	4	0	3	0	0
7	B	18	0	24	0	0
8	A	8	0	0	1	0
8	B	3	0	0	0	0
8	C	6	0	0	0	0
All	All	5462	0	4873	299	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 29.

All (299) 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)
4:A:302:3PH:H3D2	4:A:302:3PH:C39	1.38	1.38
1:C:134:HIS:C	1:C:137:ILE:CB	2.08	1.22
1:B:197:GLY:C	1:B:198:PHE:HD1	1.43	1.19
4:A:302:3PH:C3D	4:A:302:3PH:H391	1.82	1.09
4:A:302:3PH:C3D	4:A:302:3PH:C39	2.30	1.07
1:B:197:GLY:C	1:B:198:PHE:CD1	2.32	1.01
1:B:50:LEU:HD21	4:B:302:3PH:H3F1	1.42	1.00
1:B:246:ARG:CG	1:B:246:ARG:HH21	1.77	0.97
1:A:182:HIS:HE1	1:A:215:ASP:HB3	1.30	0.97
1:B:198:PHE:N	1:B:198:PHE:HD1	1.62	0.96
4:B:302:3PH:H241	4:B:302:3PH:O21	1.65	0.95
1:C:152:GLY:N	1:C:153:ASN:CB	2.29	0.95
1:B:50:LEU:CD2	4:B:302:3PH:H3F1	1.98	0.94
1:B:190:HIS:HD2	1:B:204:GLN:HB3	1.36	0.90
1:B:198:PHE:CD1	1:B:198:PHE:N	2.37	0.89
1:A:76:PRO:HD2	3:A:301:DTD:H21	1.55	0.88
4:A:302:3PH:H3D2	4:A:302:3PH:H391	0.89	0.88
1:B:198:PHE:HA	1:B:246:ARG:CG	2.04	0.87
1:B:50:LEU:CD2	4:B:302:3PH:C3F	2.54	0.85
1:B:50:LEU:HD21	4:B:302:3PH:C3F	2.07	0.83
4:A:302:3PH:H3D2	4:A:302:3PH:H392	1.58	0.83
4:B:302:3PH:O22	4:B:302:3PH:H12	1.76	0.83
1:B:246:ARG:HG3	1:B:246:ARG:HH21	1.45	0.81
1:B:154:TYR:CE2	1:B:242:PHE:HE2	2.00	0.79
1:B:198:PHE:HB3	1:B:246:ARG:HB3	1.63	0.78
1:A:178:HIS:HD2	1:B:168:TYR:OH	1.67	0.77
1:A:77:TYR:HD1	1:A:133:ILE:HD13	1.50	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:PRO:HB2	1:A:141:TYR:HD2	1.51	0.75
1:B:246:ARG:NH2	1:B:246:ARG:CG	2.45	0.75
1:B:182:HIS:HD2	1:B:184:TRP:H	1.33	0.75
4:B:302:3PH:H261	4:B:302:3PH:O32	1.88	0.74
1:B:107:ARG:HB2	1:B:113:LEU:HA	1.67	0.74
1:A:245:GLU:O	1:A:246:ARG:HB3	1.87	0.73
1:B:108:SER:CB	1:B:198:PHE:HE2	2.02	0.73
1:C:211:LYS:HG3	1:C:212:TRP:CD1	2.24	0.72
1:A:182:HIS:CE1	1:A:215:ASP:HB3	2.21	0.72
1:A:80:GLU:OE2	1:A:194[A]:ARG:NH2	2.23	0.72
1:B:58:ILE:HG22	1:B:59:ILE:HD12	1.72	0.72
1:A:138:PRO:HB2	1:A:141:TYR:CD2	2.24	0.71
1:A:72:ALA:HB3	1:A:204:GLN:H	1.55	0.71
1:C:245:GLU:HB3	1:C:246:ARG:HA	1.72	0.71
1:A:192:LYS:HG3	1:A:202:THR:HG23	1.73	0.71
1:B:2:ASP:HB2	1:B:5:VAL:HB	1.71	0.71
1:C:72:ALA:HB3	1:C:204:GLN:H	1.57	0.70
1:B:158:THR:HG22	1:B:159:THR:N	2.07	0.69
1:B:198:PHE:HA	1:B:246:ARG:HG2	1.72	0.69
1:B:26:THR:HG22	1:B:28:ALA:H	1.56	0.69
1:A:164:TYR:HE1	3:A:301:DTD:HO3	1.41	0.69
1:B:245:GLU:O	1:B:246:ARG:HB2	1.92	0.69
1:A:33:GLY:HA3	4:A:302:3PH:H2A2	1.74	0.69
1:C:185:ARG:HH22	1:C:204:GLN:NE2	1.91	0.68
1:A:97:HIS:HB3	1:A:159:THR:OG1	1.93	0.68
1:A:107:ARG:CZ	1:A:113:LEU:HD21	2.23	0.68
1:B:246:ARG:NH2	1:B:246:ARG:HG2	2.07	0.68
1:B:246:ARG:HG2	1:B:246:ARG:HH21	1.55	0.68
1:B:89:LEU:HB2	1:B:158:THR:OG1	1.93	0.67
1:C:149:ASP:CB	1:C:153:ASN:CB	2.71	0.67
1:B:79:LEU:HB2	1:B:143:ARG:NH1	2.10	0.67
1:B:190:HIS:CD2	1:B:204:GLN:HB3	2.24	0.67
1:A:175:LEU:O	1:A:175:LEU:HD12	1.94	0.67
1:C:185:ARG:HD2	1:C:218:CYS:SG	2.34	0.67
1:B:108:SER:CB	1:B:198:PHE:CE2	2.78	0.67
1:A:100:LEU:HD11	1:A:238[B]:MET:HE2	1.76	0.66
1:C:185:ARG:HH22	1:C:204:GLN:HE22	1.40	0.66
1:C:149:ASP:O	1:C:152:GLY:N	2.30	0.65
1:B:148:THR:HB	1:B:152:GLY:HA2	1.78	0.65
1:A:182:HIS:CD2	1:A:217:CYS:HB3	2.32	0.64
1:A:80:GLU:OE2	1:A:194[B]:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:TRP:O	1:A:190:HIS:HB2	1.96	0.64
1:A:77:TYR:CD1	1:A:133:ILE:HD13	2.32	0.64
1:B:50:LEU:HG	4:B:302:3PH:H3F2	1.80	0.64
1:A:69:SER:HB3	1:A:243:VAL:H	1.63	0.64
1:B:196:ASP:OD1	1:B:197:GLY:N	2.30	0.64
1:A:227:THR:HG21	1:A:238[A]:MET:CE	2.28	0.63
1:C:97:HIS:HE1	1:C:142:TYR:OH	1.80	0.63
1:A:182:HIS:CD2	1:A:184:TRP:H	2.17	0.63
1:A:78:PHE:HB2	1:A:122:TRP:CZ2	2.34	0.63
1:A:86:GLU:HB2	1:A:87:GLY:HA2	1.81	0.63
1:B:107:ARG:CB	1:B:113:LEU:HA	2.29	0.63
1:A:99:PRO:HB2	1:A:235:VAL:HG13	1.82	0.62
1:B:190:HIS:HD2	1:B:204:GLN:CB	2.10	0.62
1:C:122:TRP:O	1:C:190:HIS:HB2	1.99	0.62
1:B:37:LEU:HD11	4:B:302:3PH:H2G1	1.81	0.62
1:B:50:LEU:CD2	4:B:302:3PH:H3F2	2.29	0.62
1:B:163:PRO:HD3	1:B:187:ALA:HB2	1.83	0.61
1:A:86:GLU:N	1:A:87:GLY:HA3	2.15	0.60
1:A:164:TYR:HE1	3:A:301:DTD:O3	1.84	0.60
1:C:149:ASP:O	1:C:152:GLY:CA	2.49	0.60
1:A:108:SER:HB3	1:A:112:GLU:HG2	1.84	0.59
1:B:55:ASN:HD21	1:B:73:ILE:HB	1.67	0.59
4:A:302:3PH:H32	4:A:302:3PH:P	2.42	0.59
1:A:227:THR:HG21	1:A:238[A]:MET:HE2	1.84	0.58
1:B:198:PHE:HA	1:B:246:ARG:CB	2.34	0.58
1:A:125:THR:HG22	1:A:129:LEU:O	2.03	0.58
1:C:48:LEU:O	1:C:52:VAL:HG13	2.03	0.58
1:B:55:ASN:ND2	1:B:73:ILE:HB	2.19	0.58
1:B:182:HIS:HE1	1:B:215:ASP:CG	2.05	0.58
1:B:185:ARG:HD2	1:B:218:CYS:SG	2.44	0.58
1:B:154:TYR:HE2	1:B:242:PHE:HE2	1.52	0.58
1:B:26:THR:HB	1:B:29:GLU:H	1.69	0.58
1:C:97:HIS:CE1	1:C:142:TYR:OH	2.57	0.57
1:B:130:TYR:H	1:B:134:HIS:CE1	2.22	0.57
1:B:198:PHE:CB	1:B:246:ARG:HB3	2.31	0.57
1:A:126:PRO:O	1:A:162:VAL:HG21	2.04	0.57
1:B:125:THR:HG23	1:B:129:LEU:O	2.03	0.57
1:C:151:GLN:CB	1:C:153:ASN:CB	2.82	0.57
1:C:211:LYS:HE2	1:C:212:TRP:CE2	2.39	0.57
1:C:45:GLU:OE1	1:C:172:THR:HG23	2.05	0.57
1:B:138:PRO:HG2	1:B:141:TYR:CD2	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:ILE:HB	1:A:146:LEU:HB2	1.88	0.56
1:B:79:LEU:HB2	1:B:143:ARG:HH12	1.70	0.56
1:A:245:GLU:O	1:A:246:ARG:CB	2.52	0.56
1:A:185:ARG:HH12	1:A:204:GLN:HE22	1.54	0.56
1:A:48:LEU:CD2	1:A:167:PRO:HD2	2.36	0.56
1:B:164:TYR:CE2	1:B:188:HIS:CE1	2.94	0.55
1:A:194[B]:ARG:HG2	1:A:194[B]:ARG:HH11	1.72	0.55
1:C:45:GLU:OE2	1:C:170:GLY:HA3	2.06	0.55
1:B:131:SER:CB	1:B:141:TYR:O	2.54	0.55
1:C:168:TYR:HB3	1:C:183:THR:HG21	1.88	0.55
1:C:186:PRO:HG2	1:C:206:TYR:CE1	2.42	0.55
1:B:50:LEU:HD23	4:B:302:3PH:H3F1	1.85	0.55
1:B:148:THR:HG22	1:B:154:TYR:HB3	1.89	0.55
1:B:36:TYR:CD2	4:B:302:3PH:H351	2.42	0.55
1:A:39:GLU:O	1:A:43:THR:HG23	2.06	0.55
1:B:92:TYR:HB3	1:B:94:THR:HG23	1.89	0.54
1:B:148:THR:CG2	1:B:154:TYR:HB3	2.37	0.54
1:A:99:PRO:HB3	1:A:157:ARG:NH2	2.23	0.54
1:B:50:LEU:CG	4:B:302:3PH:H3F2	2.38	0.54
1:C:163:PRO:HD3	1:C:187:ALA:HB2	1.90	0.53
1:A:132:GLY:HA3	1:A:139:VAL:HG22	1.90	0.53
1:C:204:GLN:NE2	1:C:206:TYR:OH	2.39	0.53
1:C:149:ASP:C	1:C:152:GLY:H	2.12	0.53
1:C:74:GLN:HG2	1:C:75:GLY:O	2.09	0.53
1:B:197:GLY:O	1:B:198:PHE:CD1	2.61	0.53
1:B:196:ASP:O	1:B:198:PHE:CE1	2.61	0.53
1:B:33:GLY:HA3	4:B:302:3PH:C2C	2.39	0.53
1:C:152:GLY:H	1:C:153:ASN:CB	2.18	0.53
1:B:50:LEU:HD23	4:B:302:3PH:C3F	2.36	0.52
1:B:70:ALA:HB1	1:B:225:LEU:HD21	1.91	0.52
1:B:76:PRO:HG2	1:B:77:TYR:CD2	2.45	0.52
1:A:106:VAL:HG23	1:A:119:ILE:HD11	1.91	0.52
1:A:47:ALA:HA	1:A:50:LEU:HD12	1.92	0.52
1:A:77:TYR:O	1:A:143:ARG:NH2	2.31	0.52
1:B:158:THR:CG2	1:B:159:THR:N	2.73	0.52
1:B:161:PRO:HG3	1:B:189:VAL:HG22	1.92	0.52
4:B:302:3PH:O21	4:B:302:3PH:C24	2.42	0.51
1:B:103:ARG:O	1:B:239:THR:HA	2.09	0.51
1:B:77:TYR:CG	1:B:130:TYR:CD2	2.98	0.51
1:B:76:PRO:HG2	1:B:77:TYR:CE2	2.45	0.51
1:C:182:HIS:HD2	1:C:184:TRP:H	1.59	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:190:HIS:CE1	1:C:204:GLN:OE1	2.64	0.51
1:A:210:GLY:O	1:A:213:VAL:HG23	2.10	0.51
1:A:125:THR:OG1	1:A:126:PRO:HD2	2.11	0.51
1:B:131:SER:O	1:B:143:ARG:NH2	2.44	0.50
1:A:97:HIS:HD2	1:A:159:THR:HG21	1.77	0.50
1:A:164:TYR:CE1	3:A:301:DTD:O3	2.64	0.50
1:A:182:HIS:HD2	1:A:217:CYS:HB3	1.73	0.50
1:C:29:GLU:O	1:C:32:ALA:HB3	2.10	0.50
1:B:227:THR:OG1	1:B:227:THR:O	2.28	0.50
1:B:97:HIS:CD2	1:B:159:THR:HG21	2.47	0.50
1:A:113:LEU:HD13	1:A:151:GLN:O	2.10	0.50
1:A:106:VAL:HB	1:A:148:THR:HG21	1.93	0.50
1:B:58:ILE:HG22	1:B:59:ILE:CD1	2.39	0.50
1:C:211:LYS:HE2	1:C:212:TRP:NE1	2.26	0.50
1:A:194[B]:ARG:NH1	1:A:194[B]:ARG:HG2	2.26	0.50
1:B:164:TYR:CE2	1:B:188:HIS:HE1	2.30	0.50
1:B:182:HIS:CD2	1:B:184:TRP:H	2.22	0.49
1:A:164:TYR:CZ	1:A:188:HIS:HE1	2.30	0.49
1:B:4:ARG:NH1	1:B:7:GLU:OE2	2.44	0.49
1:B:232:GLU:N	1:B:235:VAL:O	2.45	0.49
1:B:33:GLY:HA3	4:B:302:3PH:H2C2	1.93	0.49
1:A:206:TYR:CD1	1:A:221:VAL:HG23	2.48	0.49
1:A:194[A]:ARG:NH1	8:A:266:HOH:O	2.45	0.49
1:A:48:LEU:HD22	1:A:167:PRO:HD2	1.94	0.49
1:C:166:ILE:O	1:C:167:PRO:C	2.50	0.49
1:A:161:PRO:HG3	1:A:189:VAL:HG23	1.94	0.49
1:C:188:HIS:CD2	1:C:190:HIS:NE2	2.81	0.49
1:B:191:PHE:CE2	1:B:205:TYR:HD2	2.31	0.48
1:C:72:ALA:HB3	1:C:204:GLN:N	2.26	0.48
1:B:164:TYR:HE2	1:B:188:HIS:CE1	2.30	0.48
1:A:13:VAL:O	1:A:17:ARG:HG3	2.13	0.48
1:B:96:ASP:C	1:B:96:ASP:OD1	2.51	0.48
1:C:152:GLY:CA	1:C:153:ASN:CB	2.90	0.48
1:B:222:THR:OG1	1:B:225:LEU:HG	2.13	0.48
1:C:185:ARG:NH2	1:C:204:GLN:HE22	2.10	0.48
4:A:302:3PH:C3	4:A:302:3PH:P	3.02	0.48
1:B:99:PRO:HA	1:B:159:THR:HA	1.96	0.48
1:B:76:PRO:CD	3:B:301:DTD:H12	2.44	0.48
1:B:92:TYR:HD2	1:B:142:TYR:HH	1.60	0.48
1:A:198:PHE:N	1:A:198:PHE:CD1	2.82	0.48
4:B:302:3PH:H3B2	4:B:302:3PH:H3E2	1.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:TYR:O	1:B:227:THR:HG23	2.14	0.48
1:C:36:TYR:O	1:C:40:VAL:HG23	2.13	0.48
1:C:69:SER:O	1:C:71:PRO:HD3	2.13	0.48
1:C:182:HIS:HD2	1:C:184:TRP:N	2.12	0.47
1:C:122:TRP:CH2	1:C:190:HIS:HB3	2.50	0.47
1:A:206:TYR:CE1	1:A:221:VAL:HA	2.49	0.47
4:B:302:3PH:H32	4:B:302:3PH:P	2.55	0.47
1:C:211:LYS:O	1:C:212:TRP:HB2	2.15	0.47
1:A:151:GLN:HB3	1:A:153:ASN:OD1	2.14	0.47
1:A:182:HIS:HD2	1:A:184:TRP:H	1.60	0.47
1:C:192:LYS:CB	1:C:202:THR:HG22	2.44	0.47
1:B:154:TYR:C	1:B:154:TYR:CD1	2.87	0.47
1:C:151:GLN:C	1:C:153:ASN:CB	2.82	0.47
1:B:245:GLU:O	1:B:246:ARG:CB	2.61	0.46
4:A:302:3PH:O13	4:A:302:3PH:H32	2.15	0.46
1:A:50:LEU:HD23	4:A:302:3PH:H3C2	1.98	0.46
1:A:125:THR:HG22	1:A:129:LEU:H	1.81	0.46
1:B:117:ALA:O	1:B:147:VAL:HA	2.14	0.46
1:C:119:ILE:O	1:C:119:ILE:CG1	2.64	0.46
1:B:158:THR:HG22	1:B:159:THR:H	1.81	0.46
1:B:231:ILE:HA	1:B:235:VAL:O	2.15	0.46
4:B:302:3PH:C3	4:B:302:3PH:P	3.04	0.46
1:C:168:TYR:CB	1:C:183:THR:HG21	2.46	0.46
1:A:130:TYR:CE2	1:A:164:TYR:CE2	3.04	0.46
1:A:227:THR:HG21	1:A:238[A]:MET:HE3	1.96	0.46
1:B:185:ARG:HE	1:B:218:CYS:HB2	1.81	0.46
1:C:115:ALA:HB1	1:C:150:SER:HA	1.98	0.46
1:C:117:ALA:O	1:C:148:THR:N	2.39	0.46
1:A:195:LYS:HG2	1:A:198:PHE:CE1	2.51	0.45
1:A:227:THR:HG21	1:A:238[B]:MET:HG2	1.98	0.45
1:B:148:THR:HG22	1:B:154:TYR:N	2.31	0.45
1:B:69:SER:O	1:B:201:LEU:HD11	2.17	0.45
1:A:164:TYR:OH	1:A:188:HIS:CE1	2.69	0.45
1:A:195:LYS:HG2	1:A:198:PHE:CD1	2.51	0.45
1:B:196:ASP:O	1:B:198:PHE:CD1	2.70	0.45
1:A:130:TYR:HE2	1:A:164:TYR:CE2	2.33	0.45
1:B:45:GLU:OE2	1:B:170:GLY:HA3	2.16	0.45
1:C:121:VAL:N	1:C:144:GLY:O	2.38	0.45
1:B:122:TRP:O	1:B:190:HIS:HB2	2.17	0.45
1:B:139:VAL:O	1:B:140:ASP:CB	2.64	0.45
1:B:186:PRO:HB3	1:B:212:TRP:C	2.37	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:SER:O	1:C:111:GLY:N	2.50	0.44
1:C:176:LEU:HA	1:C:176:LEU:HD23	1.70	0.44
1:A:67:ARG:O	1:A:245:GLU:HB3	2.18	0.44
1:B:131:SER:O	1:B:143:ARG:CZ	2.66	0.44
1:B:164:TYR:CZ	1:B:188:HIS:HE1	2.36	0.44
1:B:62:LYS:O	1:B:66:SER:CB	2.66	0.44
1:B:154:TYR:CZ	1:B:242:PHE:HE2	2.35	0.44
1:B:182:HIS:HD2	1:B:184:TRP:N	2.07	0.43
1:C:49:LEU:HG	1:C:172:THR:HG22	1.98	0.43
1:A:100:LEU:HD11	1:A:238[A]:MET:HG3	1.99	0.43
1:B:106:VAL:HG22	1:B:106:VAL:O	2.18	0.43
1:A:121:VAL:HA	1:A:190:HIS:O	2.18	0.43
1:A:90:LYS:HD3	1:A:141:TYR:CZ	2.52	0.43
1:A:120:ASP:OD2	1:A:145:LYS:HE2	2.19	0.43
1:C:149:ASP:CB	1:C:152:GLY:H	2.32	0.43
1:C:179:LEU:HA	1:C:179:LEU:HD23	1.69	0.43
1:B:162:VAL:HB	1:B:163:PRO:HD2	2.01	0.43
1:B:62:LYS:O	1:B:66:SER:N	2.43	0.43
1:B:70:ALA:N	1:B:71:PRO:HD3	2.33	0.43
1:A:122:TRP:CE2	1:A:190:HIS:HB3	2.54	0.42
1:B:176:LEU:HD13	1:B:182:HIS:O	2.19	0.42
1:A:101:ILE:HG13	1:A:235:VAL:CG1	2.49	0.42
1:A:142:TYR:HE1	1:A:159:THR:HG21	1.84	0.42
1:A:105:THR:OG1	1:A:241:ASP:OD1	2.34	0.42
1:B:211:LYS:HG2	1:B:212:TRP:CD1	2.53	0.42
1:C:49:LEU:O	1:C:52:VAL:HG22	2.19	0.42
1:B:72:ALA:HB3	1:B:203:THR:HA	2.01	0.42
1:C:149:ASP:C	1:C:152:GLY:N	2.72	0.42
1:C:54:LEU:O	1:C:57:THR:N	2.51	0.42
1:A:74:GLN:O	1:A:190:HIS:CE1	2.72	0.42
1:B:197:GLY:O	1:B:246:ARG:NH2	2.53	0.42
1:B:48:LEU:HD21	1:B:172:THR:HG21	2.02	0.42
1:A:198:PHE:HA	1:A:246:ARG:HG2	2.00	0.42
1:A:20:LEU:HA	1:A:20:LEU:HD23	1.74	0.42
1:A:103:ARG:NH1	1:A:232:GLU:OE1	2.53	0.42
1:A:72:ALA:HB3	1:A:204:GLN:N	2.30	0.42
1:B:138:PRO:CG	1:B:141:TYR:CD2	3.02	0.42
1:C:182:HIS:CD2	1:C:184:TRP:H	2.38	0.42
1:A:137:ILE:HA	1:A:138:PRO:HD3	1.93	0.42
1:B:164:TYR:OH	1:B:188:HIS:HE1	2.01	0.41
1:C:140:ASP:OD1	1:C:140:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:HIS:CE1	1:A:212:TRP:CZ3	3.08	0.41
1:A:211:LYS:O	1:A:212:TRP:HB2	2.21	0.41
1:B:132:GLY:H	1:B:137:ILE:CB	2.34	0.41
1:B:199:GLU:H	1:B:246:ARG:HB2	1.84	0.41
1:A:114:LEU:HD21	1:A:198:PHE:CZ	2.55	0.41
1:B:21:LEU:HA	1:B:21:LEU:HD23	1.78	0.41
1:C:199:GLU:HA	1:C:200:PRO:HD3	1.92	0.41
1:C:188:HIS:CD2	1:C:204:GLN:OE1	2.73	0.41
1:A:238[A]:MET:HE2	1:A:238[A]:MET:HB3	1.90	0.41
1:B:148:THR:HG22	1:B:154:TYR:H	1.86	0.41
1:B:182:HIS:HE1	1:B:215:ASP:OD1	2.03	0.41
1:B:198:PHE:HA	1:B:246:ARG:HG3	1.97	0.41
4:B:302:3PH:H372	4:B:302:3PH:H342	1.75	0.41
1:C:83:PRO:O	1:C:144:GLY:HA2	2.20	0.41
1:C:204:GLN:O	1:C:225:LEU:HD22	2.21	0.41
1:A:127:ASP:HB2	1:A:129:LEU:HG	2.02	0.41
1:B:7:GLU:HG3	1:B:8:VAL:N	2.34	0.41
1:B:207:PHE:O	1:B:213:VAL:HG21	2.21	0.41
1:A:131:SER:C	1:A:133:ILE:H	2.24	0.40
1:A:33:GLY:O	1:A:36:TYR:HB3	2.22	0.40
1:B:118:VAL:HA	1:B:147:VAL:HG22	2.04	0.40
1:C:38:THR:O	1:C:41:ALA:HB3	2.21	0.40
1:C:51:ASP:O	1:C:55:ASN:HB3	2.21	0.40
1:A:148:THR:HB	1:A:152:GLY:HA2	2.03	0.40
1:B:188:HIS:CD2	1:B:190:HIS:NE2	2.89	0.40
1:B:33:GLY:HA3	4:B:302:3PH:H2C1	2.04	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	246/260 (95%)	243 (99%)	3 (1%)	0	100	100
1	B	238/260 (92%)	234 (98%)	4 (2%)	0	100	100
1	C	228/260 (88%)	223 (98%)	5 (2%)	0	100	100
All	All	712/780 (91%)	700 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	202/220 (92%)	189 (94%)	13 (6%)	17	47
1	B	153/220 (70%)	137 (90%)	16 (10%)	7	25
1	C	127/220 (58%)	116 (91%)	11 (9%)	10	34
All	All	482/660 (73%)	442 (92%)	40 (8%)	11	36

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	THR
1	A	46	THR
1	A	58	ILE
1	A	59	ILE
1	A	95	ASP
1	A	112	GLU
1	A	120	ASP
1	A	121	VAL
1	A	150	SER
1	A	151	GLN
1	A	174	ARG
1	A	183	THR
1	A	202	THR
1	B	22	ASP
1	B	24	ARG

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Mol	Chain	Res	Type
1	B	44	ARG
1	B	46[A]	THR
1	B	46[B]	THR
1	B	48	LEU
1	B	57	THR
1	B	58	ILE
1	B	91	THR
1	B	106	VAL
1	B	109	ASP
1	B	179	LEU
1	B	198	PHE
1	B	201	LEU
1	B	227	THR
1	B	246	ARG
1	C	38	THR
1	C	46	THR
1	C	49	LEU
1	C	58	ILE
1	C	78	PHE
1	C	80	GLU
1	C	127	ASP
1	C	150	SER
1	C	198	PHE
1	C	201	LEU
1	C	213	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	A	178	HIS
1	A	182	HIS
1	A	188	HIS
1	A	204	GLN
1	B	55	ASN
1	B	182	HIS
1	C	97	HIS
1	C	165	GLN
1	C	182	HIS
1	C	204	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 13 ligands modelled in this entry, 5 are monoatomic - leaving 8 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	$\# Z  > 2$
3	DTD	B	301	-	6,8,8	0.48	0	6,10,10	0.47	0
4	3PH	B	302	-	47,47,47	0.81	1 (2%)	51,52,52	1.10	3 (5%)
6	ACT	A	305	-	1,3,3	1.72	0	0,3,3	0.00	-
4	3PH	A	302	-	47,47,47	0.81	1 (2%)	51,52,52	1.09	3 (5%)
7	GOL	B	306[B]	-	5,5,5	0.39	0	5,5,5	0.25	0
3	DTD	A	301	-	6,8,8	0.49	0	6,10,10	0.48	0
7	GOL	B	306[A]	-	5,5,5	0.38	0	5,5,5	0.22	0
7	GOL	B	303	-	5,5,5	0.42	0	5,5,5	0.35	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
3	DTD	B	301	-	-	-	0/0/1/1
4	3PH	B	302	-	-	33/49/49/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	3PH	A	302	-	-	27/49/49/49	-
7	GOL	B	306[B]	-	-	3/4/4/4	-
3	DTD	A	301	-	-	-	0/0/1/1
7	GOL	B	306[A]	-	-	4/4/4/4	-
7	GOL	B	303	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	302	3PH	P-O12	3.63	1.62	1.50
4	A	302	3PH	P-O12	3.62	1.62	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	302	3PH	C2-O21-C21	-3.37	109.48	117.79
4	A	302	3PH	C2-O21-C21	-3.35	109.54	117.79
4	B	302	3PH	O13-P-O11	2.47	113.30	106.73
4	A	302	3PH	O13-P-O11	2.45	113.25	106.73
4	B	302	3PH	C3-O31-C31	-2.05	109.52	117.12
4	A	302	3PH	C3-O31-C31	-2.04	109.55	117.12

There are no chirality outliers.

All (69) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	302	3PH	C1-O11-P-O13
4	B	302	3PH	C1-O11-P-O14
4	B	302	3PH	C1-O11-P-O12
4	B	302	3PH	C22-C21-O21-C2
4	A	302	3PH	C1-O11-P-O13
4	A	302	3PH	C1-O11-P-O14
4	A	302	3PH	C1-O11-P-O12
4	A	302	3PH	C22-C21-O21-C2
7	B	306[B]	GOL	O1-C1-C2-C3
7	B	306[A]	GOL	O1-C1-C2-C3
4	B	302	3PH	O22-C21-O21-C2
4	A	302	3PH	O22-C21-O21-C2
4	B	302	3PH	C34-C35-C36-C37
4	A	302	3PH	C3A-C3B-C3C-C3D

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Mol	Chain	Res	Type	Atoms
4	B	302	3PH	C3B-C3C-C3D-C3E
4	B	302	3PH	C32-C33-C34-C35
7	B	306[B]	GOL	O1-C1-C2-O2
4	B	302	3PH	C3A-C3B-C3C-C3D
4	B	302	3PH	C3D-C3E-C3F-C3G
4	B	302	3PH	C3E-C3F-C3G-C3H
7	B	306[A]	GOL	C1-C2-C3-O3
4	B	302	3PH	C27-C28-C29-C2A
4	B	302	3PH	C2B-C2C-C2D-C2E
4	A	302	3PH	C35-C36-C37-C38
4	A	302	3PH	C23-C24-C25-C26
4	A	302	3PH	C2D-C2E-C2F-C2G
7	B	306[A]	GOL	O1-C1-C2-O2
4	B	302	3PH	C2E-C2F-C2G-C2H
4	B	302	3PH	C28-C29-C2A-C2B
4	B	302	3PH	C2C-C2D-C2E-C2F
4	A	302	3PH	C34-C35-C36-C37
4	A	302	3PH	C28-C29-C2A-C2B
4	A	302	3PH	C3B-C3C-C3D-C3E
7	B	306[B]	GOL	C1-C2-C3-O3
4	A	302	3PH	C37-C38-C39-C3A
4	B	302	3PH	C2F-C2G-C2H-C2I
4	A	302	3PH	O11-C1-C2-C3
4	A	302	3PH	C21-C22-C23-C24
4	B	302	3PH	C32-C31-O31-C3
4	B	302	3PH	C25-C26-C27-C28
7	B	306[A]	GOL	O2-C2-C3-O3
4	A	302	3PH	C2C-C2D-C2E-C2F
4	A	302	3PH	C3D-C3E-C3F-C3G
4	A	302	3PH	C24-C25-C26-C27
4	B	302	3PH	C2-C1-O11-P
4	A	302	3PH	C2-C1-O11-P
4	A	302	3PH	C38-C39-C3A-C3B
4	B	302	3PH	O11-C1-C2-C3
4	B	302	3PH	C1-C2-O21-C21
4	B	302	3PH	O32-C31-O31-C3
4	A	302	3PH	C36-C37-C38-C39
4	B	302	3PH	O11-C1-C2-O21
4	A	302	3PH	O11-C1-C2-O21
4	A	302	3PH	C22-C23-C24-C25
4	B	302	3PH	C38-C39-C3A-C3B
4	A	302	3PH	C25-C26-C27-C28

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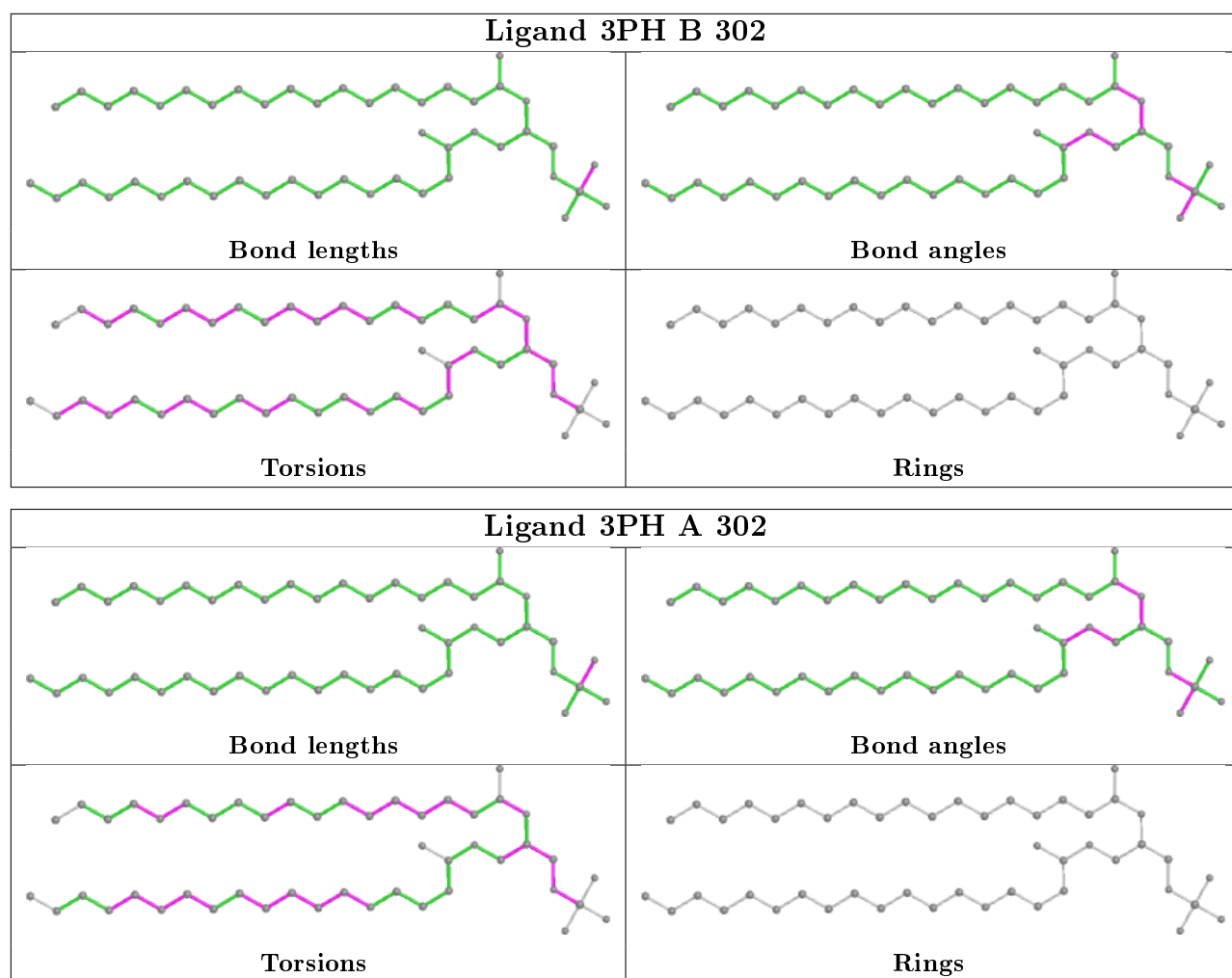
Mol	Chain	Res	Type	Atoms
4	A	302	3PH	C3C-C3D-C3E-C3F
4	A	302	3PH	O21-C2-C3-O31
4	B	302	3PH	C26-C27-C28-C29
4	A	302	3PH	C1-C2-C3-O31
7	B	303	GOL	O1-C1-C2-C3
7	B	303	GOL	O1-C1-C2-O2
4	B	302	3PH	O21-C21-C22-C23
4	B	302	3PH	C37-C38-C39-C3A
4	B	302	3PH	C23-C24-C25-C26
4	B	302	3PH	O31-C31-C32-C33
4	B	302	3PH	C2A-C2B-C2C-C2D
4	B	302	3PH	C3F-C3G-C3H-C3I
4	B	302	3PH	O32-C31-C32-C33

There are no ring outliers.

4 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	DTD	1	0
4	B	302	3PH	22	0
4	A	302	3PH	10	0
3	A	301	DTD	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	246/260 (94%)	-0.26	0	100	100	25, 39, 60, 88	0
1	B	243/260 (93%)	0.09	7 (2%)	51	50	30, 78, 118, 137	7 (2%)
1	C	238/260 (91%)	0.18	11 (4%)	32	32	42, 89, 126, 143	1 (0%)
All	All	727/780 (93%)	0.00	18 (2%)	57	55	25, 63, 119, 143	8 (1%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	144	GLY	4.3
1	C	117	ALA	4.0
1	C	142	TYR	3.2
1	C	191	PHE	2.8
1	B	121	VAL	2.6
1	B	234	GLY	2.6
1	C	146	LEU	2.6
1	C	140	ASP	2.6
1	B	153	ASN	2.5
1	C	118	VAL	2.5
1	C	116	GLY	2.4
1	C	123	HIS	2.4
1	B	146	LEU	2.3
1	B	123	HIS	2.2
1	C	82	ALA	2.1
1	C	144	GLY	2.1
1	C	132	GLY	2.1
1	B	159	THR	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 ⓘ

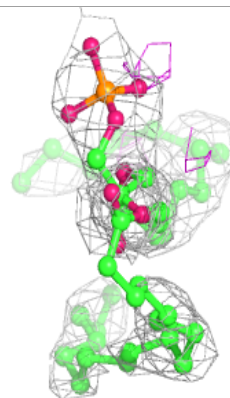
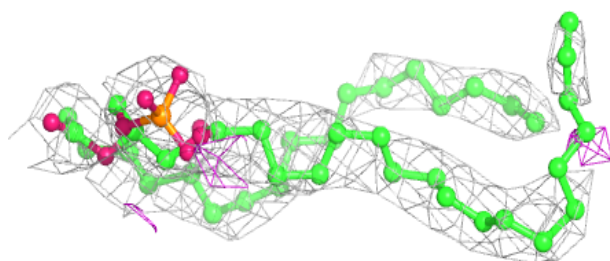
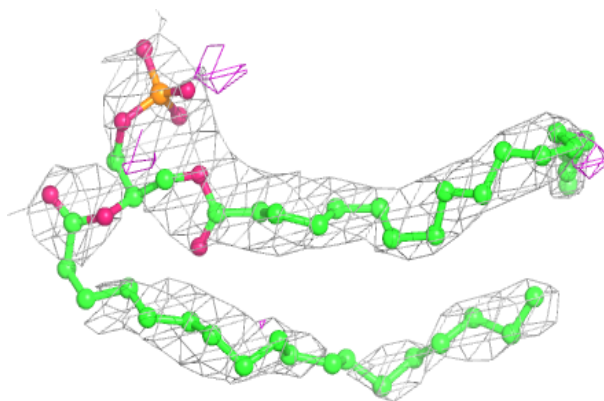
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	ACT	A	305	4/4	0.75	0.37	50,53,53,57	0
3	DTD	A	301	8/8	0.79	0.53	73,74,78,107	0
7	GOL	B	306[B]	6/6	0.85	0.31	27,29,30,30	6
7	GOL	B	306[A]	6/6	0.85	0.31	30,31,31,32	6
5	MG	A	304	1/1	0.87	0.12	29,29,29,29	0
4	3PH	B	302	48/48	0.91	0.44	24,45,76,141	1
4	3PH	A	302	48/48	0.92	0.42	19,39,64,85	23
7	GOL	B	303	6/6	0.92	0.36	58,63,64,64	0
3	DTD	B	301	8/8	0.94	0.33	70,74,96,188	0
5	MG	A	303	1/1	0.94	0.19	24,24,24,24	0
2	FE	C	300	1/1	0.97	0.07	91,91,91,91	0
2	FE	B	300	1/1	0.98	0.12	61,61,61,61	0
2	FE	A	300	1/1	0.98	0.16	35,35,35,35	0

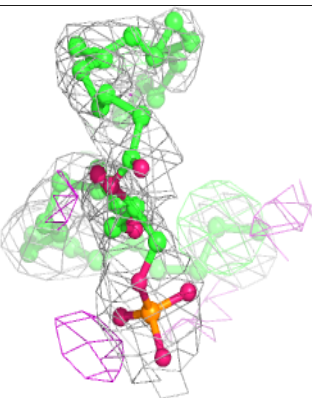
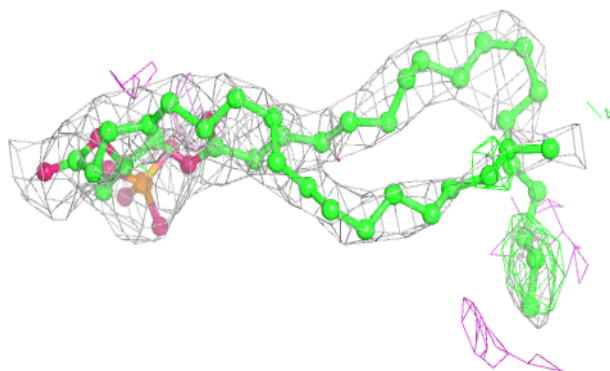
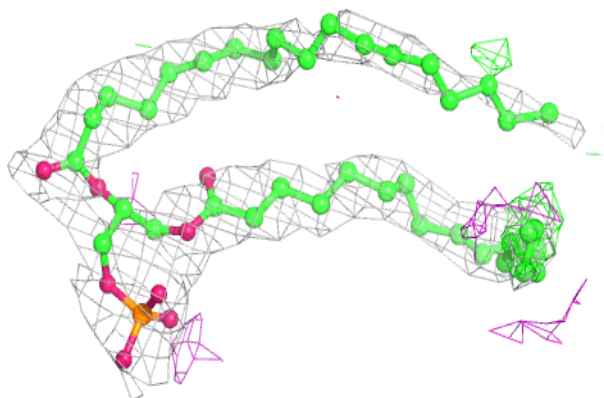
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around 3PH B 302:**

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

**Electron density around 3PH A 302:**

$2mF_o-DF_c$  (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.