



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:27 AM UTC

PDB ID : 3DHH / pdb_00003dhh
Title : Crystal Structure of Resting State Toluene 4-Monooxygenase Hydroxylase Complexed with Effector Protein
Authors : Bailey, L.J.; Mccoy, J.G.; Phillips Jr., G.N.; Fox, B.G.
Deposited on : 2008-06-17
Resolution : 1.94 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

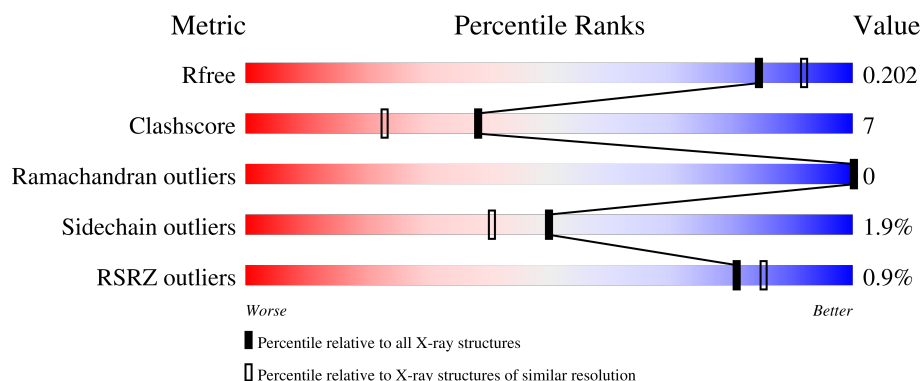
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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}	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	500	
2	B	327	
3	C	84	
4	E	103	

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
6	BML	A	503	-	-	X	-
6	BML	A	507	-	-	X	-
6	BML	B	508	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 8972 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 4-monooxygenase hydroxylase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	6	14	0
			4091	2630	683	754	24			

- Molecule 2 is a protein called toluene 4-monooxygenase hydroxylase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	305	Total	C	N	O	S	0	9	0
			2564	1625	441	482	16			

- Molecule 3 is a protein called toluene 4-monooxygenase hydroxylase gamma subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	83	Total	C	N	O	S	5	2	0
			669	420	118	127	4			

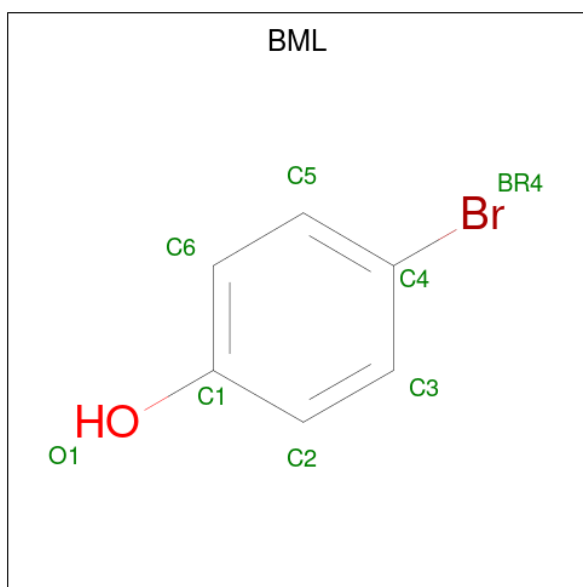
- Molecule 4 is a protein called Toluene-4-monooxygenase system effector protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	102	Total	C	N	O	S	0	2	0
			817	513	140	162	2			

- Molecule 5 is FE (III) ION (CCD ID: FE) (formula: Fe).

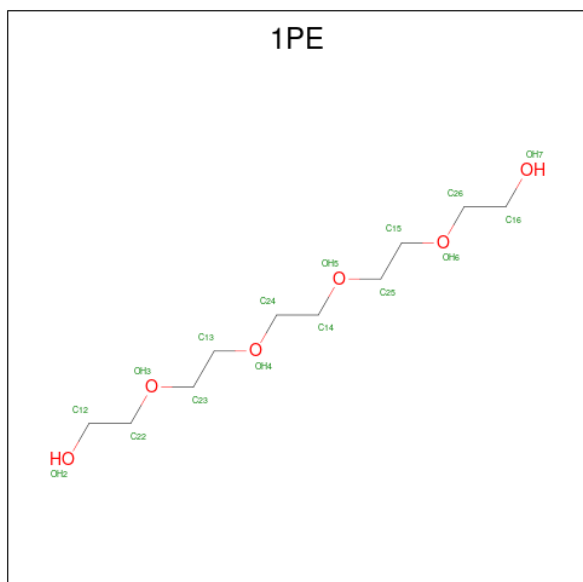
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Fe	0	0
			2	2		

- Molecule 6 is 4-BROMOPHENOL (CCD ID: BML) (formula: C₆H₅BrO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	Br	C	O	0	0
			8	1	6	1		
6	A	1	Total	Br	C	O	0	0
			8	1	6	1		
6	A	1	Total	Br	C	O	0	0
			8	1	6	1		
6	B	1	Total	Br	C	O	0	0
			8	1	6	1		
6	E	1	Total	Br	C	O	0	0
			8	1	6	1		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).

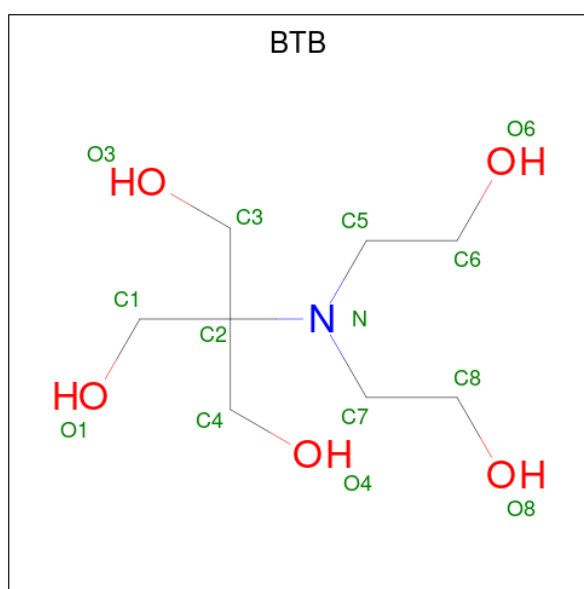


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			8	5	3		

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Cl	0	0
			1	1		

- Molecule 9 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			14	8	1	5		

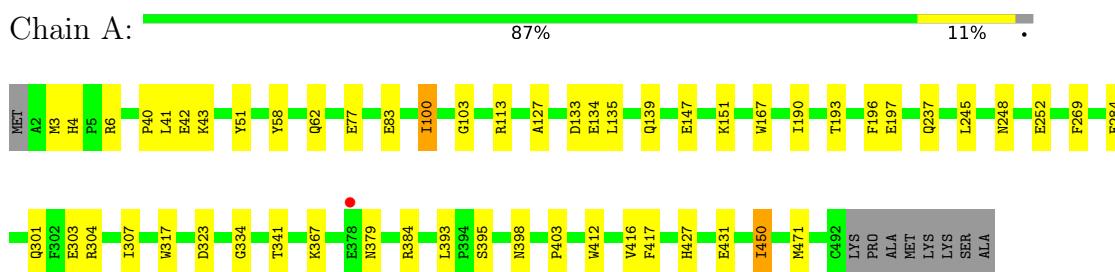
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	385	Total	O	0	0
			385	385		
10	B	228	Total	O	0	0
			228	228		
10	C	49	Total	O	0	0
			49	49		
10	E	104	Total	O	0	0
			104	104		

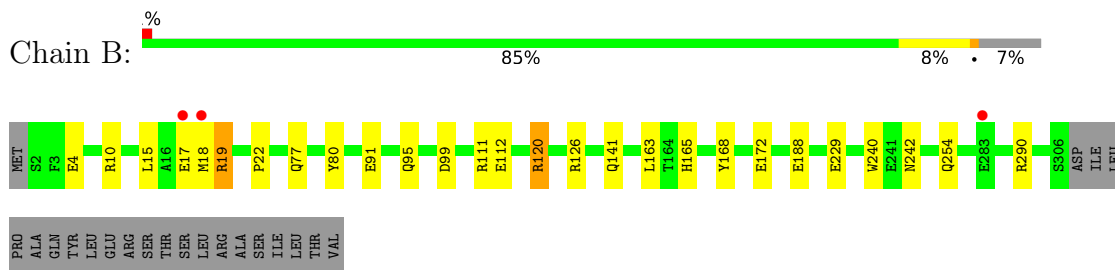
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

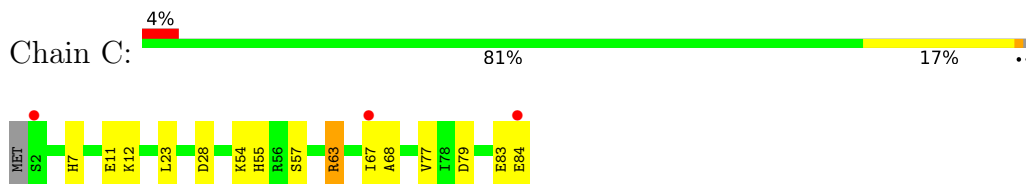
- Molecule 1: toluene 4-monooxygenase hydroxylase alpha subunit



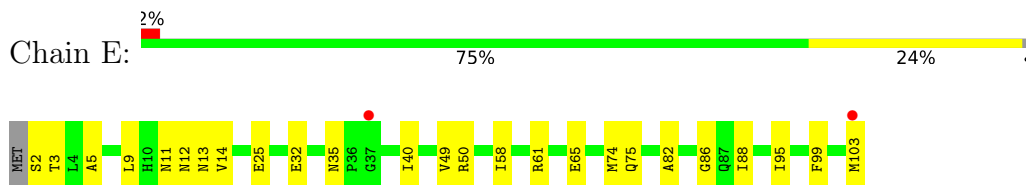
- Molecule 2: toluene 4-monooxygenase hydroxylase beta subunit



- Molecule 3: toluene 4-monooxygenase hydroxylase gamma subunit



- Molecule 4: Toluene-4-monooxygenase system effector protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	100.42Å 115.61Å 182.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.29 – 1.94 91.20 – 1.94	Depositor EDS
% Data completeness (in resolution range)	99.4 (91.29-1.94) 99.4 (91.20-1.94)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.70 (at 1.94Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.157 , 0.202 0.158 , 0.202	Depositor DCC
R_{free} test set	3889 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8972	wwPDB-VP
Average B, all atoms (Å ²)	25.0	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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BML, CL, 1PE, BTB, FE

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	0.93	4/4256 (0.1%)	0.86	2/5780 (0.0%)
2	B	0.82	0/2655	0.88	1/3606 (0.0%)
3	C	0.78	0/684	0.86	0/925
4	E	1.02	3/833 (0.4%)	0.86	0/1127
All	All	0.89	7/8428 (0.1%)	0.87	3/11438 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	134	GLU	C-O	-7.12	1.14	1.24
1	A	133	ASP	C-O	-6.61	1.16	1.24
1	A	135	LEU	C-O	-6.29	1.16	1.24
4	E	49	VAL	C-O	-5.92	1.18	1.24
1	A	40	PRO	C-O	-5.85	1.17	1.23
4	E	14	VAL	C-O	-5.54	1.18	1.24
4	E	82	ALA	CA-CB	-5.22	1.45	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100[A]	ILE	N-CA-C	6.96	117.55	111.56
1	A	100[B]	ILE	N-CA-C	6.96	117.55	111.56
2	B	229	GLU	CB-CA-C	-5.01	102.33	110.85

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4091	0	3879	60	0
2	B	2564	0	2446	38	0
3	C	669	0	659	14	0
4	E	817	0	816	21	0
5	A	2	0	0	0	0
6	A	24	0	13	12	0
6	B	8	0	4	5	0
6	E	8	0	4	2	0
7	A	8	0	8	2	0
8	A	1	0	0	0	0
9	A	14	0	19	1	0
10	A	385	0	0	4	1
10	B	228	0	0	3	0
10	C	49	0	0	0	0
10	E	104	0	0	0	0
All	All	8972	0	7848	111	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (111) 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:B:15:LEU:HB3	2:B:18:MET:HE2	1.44	0.99
1:A:3:MET:SD	6:B:508:BML:BR4	2.76	0.99
1:A:450:ILE:HG21	6:A:507:BML:H5	1.49	0.94
2:B:18:MET:HE1	2:B:22:PRO:HG3	1.49	0.92
4:E:12:ASN:HD21	4:E:103:MET:H	1.11	0.91
4:E:88:ILE:HD11	4:E:95[A]:ILE:HD11	1.56	0.88
4:E:35:ASN:HD21	4:E:58:ILE:H	1.22	0.88
2:B:18:MET:CE	2:B:22:PRO:HG3	2.04	0.87
1:A:303[A]:GLU:HG3	1:A:317:TRP:CH2	2.11	0.86
2:B:120:ARG:HG3	2:B:120:ARG:HH11	1.40	0.85
4:E:11:ASN:HD22	4:E:13:ASN:H	1.24	0.85
1:A:416:VAL:H	3:C:55:HIS:HE1	1.24	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:MET:HE1	2:B:95:GLN:O	1.76	0.84
1:A:450:ILE:CG2	6:A:507:BML:H5	2.10	0.81
1:A:450:ILE:HG21	6:A:507:BML:C5	2.13	0.79
1:A:416:VAL:H	3:C:55:HIS:CE1	2.00	0.78
1:A:139:GLN:HE22	2:B:80:TYR:H	1.33	0.77
1:A:113:ARG:HH11	2:B:141:GLN:HE21	1.30	0.76
1:A:403:PRO:HG2	6:A:503:BML:C5	2.17	0.75
1:A:379:ASN:HD22	1:A:384:ARG:HH11	1.36	0.73
1:A:301:GLN:HE21	4:E:50:ARG:HH12	1.36	0.71
2:B:165:HIS:HD2	2:B:254:GLN:HE21	1.40	0.69
2:B:95:GLN:HB3	6:B:508:BML:H3	1.73	0.68
4:E:74:MET:HE2	4:E:95[B]:ILE:HD12	1.76	0.68
2:B:19:ARG:HH11	2:B:19:ARG:HB3	1.59	0.68
1:A:3:MET:HE3	2:B:95:GLN:OE1	1.94	0.67
1:A:3:MET:CE	2:B:95:GLN:OE1	2.42	0.67
1:A:3:MET:HE2	2:B:99:ASP:HB2	1.75	0.67
1:A:303[A]:GLU:HG3	1:A:317:TRP:HH2	1.59	0.67
2:B:18:MET:HE1	2:B:22:PRO:CG	2.25	0.67
1:A:304:ARG:HH11	4:E:12:ASN:HD22	1.43	0.66
1:A:398:ASN:HD22	1:A:427:HIS:H	1.41	0.66
1:A:100[A]:ILE:HD12	7:A:505:1PE:H152	1.78	0.66
2:B:168:TYR:CD1	6:B:508:BML:H5	2.30	0.65
3:C:28:ASP:OD1	3:C:63:ARG:HD2	1.98	0.64
2:B:120:ARG:HG3	2:B:120:ARG:NH1	2.12	0.63
1:A:43:LYS:HD2	1:A:248:ASN:HD21	1.64	0.62
4:E:32:GLU:HA	4:E:40[A]:ILE:HD13	1.81	0.61
2:B:15:LEU:HB3	2:B:18:MET:CE	2.26	0.61
3:C:23:LEU:HA	3:C:67[A]:ILE:HD11	1.83	0.61
1:A:403:PRO:HG2	6:A:503:BML:C4	2.31	0.61
3:C:55:HIS:HD2	3:C:79:ASP:OD1	1.83	0.60
1:A:252[A]:GLU:OE2	10:A:836:HOH:O	2.17	0.59
1:A:334:GLY:HA3	6:A:503:BML:BR4	2.57	0.59
1:A:301:GLN:NE2	4:E:50:ARG:HH12	2.01	0.58
2:B:168:TYR:CE1	6:B:508:BML:H5	2.37	0.58
1:A:393[A]:LEU:HD23	6:A:504:BML:BR4	2.59	0.58
1:A:190:ILE:HD11	1:A:245:LEU:CD1	2.34	0.58
1:A:379:ASN:ND2	1:A:384:ARG:HH11	2.01	0.58
1:A:196:PHE:HE1	1:A:269:PHE:HE1	1.52	0.57
1:A:139:GLN:NE2	2:B:80:TYR:H	2.02	0.57
1:A:196:PHE:CE1	1:A:269:PHE:HE1	2.23	0.57
1:A:3:MET:CE	2:B:99:ASP:HB2	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:165:HIS:CD2	2:B:254:GLN:HE21	2.22	0.57
2:B:95:GLN:CB	6:B:508:BML:H3	2.36	0.56
4:E:12:ASN:HD21	4:E:103:MET:N	1.94	0.56
2:B:126:ARG:HB2	2:B:163:LEU:CD1	2.36	0.55
1:A:367:LYS:HD3	10:A:759:HOH:O	2.07	0.55
1:A:190:ILE:HD11	1:A:245:LEU:HD12	1.89	0.54
2:B:17[C]:GLU:H	2:B:17[C]:GLU:CD	2.15	0.54
1:A:113:ARG:HH11	2:B:141:GLN:NE2	2.04	0.52
4:E:88:ILE:CD1	4:E:95[A]:ILE:HD11	2.34	0.51
1:A:6:ARG:HH12	4:E:75:GLN:NE2	2.07	0.51
4:E:74:MET:HE2	4:E:95[B]:ILE:CD1	2.41	0.50
1:A:113:ARG:NH1	2:B:141:GLN:HE21	2.06	0.50
1:A:341:THR:HG22	1:A:471:MET:HE1	1.93	0.50
2:B:91:GLU:OE1	2:B:165:HIS:HE1	1.95	0.50
10:A:694:HOH:O	4:E:2:SER:HB2	2.13	0.48
1:A:51:TYR:CE2	6:E:507:BML:H3	2.48	0.48
3:C:54:LYS:O	3:C:57:SER:HB2	2.13	0.48
1:A:103:GLY:HA3	7:A:505:1PE:C26	2.44	0.47
1:A:77:GLU:OE2	1:A:147:GLU:OE1	2.33	0.47
1:A:403:PRO:HD3	6:A:507:BML:O1	2.15	0.47
2:B:240:TRP:HA	10:B:726:HOH:O	2.15	0.47
10:A:657:HOH:O	2:B:4:GLU:HG2	2.15	0.46
3:C:23:LEU:HG	3:C:68:ALA:HB2	1.98	0.46
1:A:395:SER:OG	3:C:7:HIS:HD2	1.98	0.46
1:A:4:HIS:HE1	2:B:172:GLU:OE1	1.98	0.46
3:C:11:GLU:HG2	3:C:12:LYS:HG3	1.96	0.46
4:E:35:ASN:ND2	4:E:58:ILE:H	2.03	0.46
1:A:403:PRO:HB2	6:A:503:BML:BR4	2.71	0.46
9:A:509:BTB:O6	9:A:509:BTB:H81	2.15	0.46
1:A:193:THR:HA	1:A:197:GLU:OE1	2.16	0.45
3:C:23:LEU:O	3:C:67[A]:ILE:HG13	2.16	0.45
4:E:86:GLY:HA2	4:E:99:PHE:CE1	2.51	0.45
1:A:412:TRP:CG	3:C:12:LYS:H	2.35	0.45
2:B:77:GLN:NE2	10:B:404:HOH:O	2.47	0.45
4:E:95[B]:ILE:HD11	6:E:507:BML:C5	2.47	0.44
1:A:3:MET:HE1	2:B:95:GLN:C	2.42	0.44
1:A:334:GLY:HA3	6:A:503:BML:C4	2.48	0.44
1:A:307:ILE:HD12	4:E:9:LEU:HD11	2.00	0.44
2:B:111:ARG:HD2	2:B:242:ASN:ND2	2.33	0.44
1:A:83:GLU:OE2	1:A:151:LYS:HE2	2.18	0.44
2:B:18:MET:HE3	2:B:18:MET:HB2	1.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:TRP:CZ2	6:A:503:BML:H2	2.52	0.44
1:A:395:SER:OG	3:C:7:HIS:CD2	2.71	0.43
2:B:77:GLN:HG3	10:B:622:HOH:O	2.17	0.43
3:C:55:HIS:HB2	3:C:77:VAL:HG12	1.99	0.43
4:E:2:SER:HA	4:E:5:ALA:HB3	2.00	0.43
1:A:58:TYR:CZ	1:A:62:GLN:HG3	2.53	0.43
1:A:304:ARG:HH11	4:E:12:ASN:ND2	2.10	0.42
1:A:127:ALA:HB2	1:A:237:GLN:HE22	1.83	0.42
3:C:23:LEU:HD12	3:C:67[A]:ILE:HD11	2.02	0.42
1:A:417:PHE:CE1	1:A:431:GLU:HG2	2.55	0.42
2:B:18:MET:HE1	2:B:22:PRO:CB	2.51	0.41
1:A:303[A]:GLU:CG	1:A:317:TRP:CH2	2.94	0.41
1:A:450:ILE:HG21	6:A:507:BML:C6	2.50	0.41
2:B:19:ARG:HB3	2:B:19:ARG:NH1	2.33	0.40
1:A:341:THR:CG2	1:A:471:MET:HE1	2.51	0.40
4:E:61:ARG:HH12	4:E:65:GLU:CD	2.29	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:817:HOH:O	10:A:817:HOH:O[4_545]	2.16	0.04

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	501/500 (100%)	483 (96%)	18 (4%)	0	100	100
2	B	309/327 (94%)	307 (99%)	2 (1%)	0	100	100
3	C	82/84 (98%)	79 (96%)	3 (4%)	0	100	100
4	E	102/103 (99%)	100 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	994/1014 (98%)	969 (98%)	25 (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	428/423 (101%)	423 (99%)	5 (1%)	63	57
2	B	282/296 (95%)	276 (98%)	6 (2%)	47	37
3	C	75/75 (100%)	72 (96%)	3 (4%)	28	14
4	E	88/87 (101%)	86 (98%)	2 (2%)	44	33
All	All	873/881 (99%)	857 (98%)	16 (2%)	50	43

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LEU
1	A	42	GLU
1	A	284	GLU
1	A	323	ASP
1	A	450	ILE
2	B	10	ARG
2	B	19	ARG
2	B	112	GLU
2	B	120	ARG
2	B	188	GLU
2	B	290	ARG
3	C	63	ARG
3	C	83	GLU
3	C	84	GLU
4	E	3	THR
4	E	25	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	HIS
1	A	123	ASN
1	A	139	GLN
1	A	141	GLN
1	A	204	GLN
1	A	236	GLN
1	A	237	GLN
1	A	248	ASN
1	A	301	GLN
1	A	379	ASN
1	A	382	ASN
1	A	398	ASN
1	A	439	GLN
2	B	14	HIS
2	B	77	GLN
2	B	84	ASN
2	B	102	ASN
2	B	140	GLN
2	B	141	GLN
2	B	150	ASN
2	B	165	HIS
2	B	242	ASN
2	B	254	GLN
3	C	7	HIS
3	C	55	HIS
4	E	11	ASN
4	E	12	ASN
4	E	13	ASN
4	E	35	ASN
4	E	75	GLN
4	E	87	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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	BML	E	507	-	8,8,8	0.63	0	10,10,10	1.01	0
7	1PE	A	505	5	7,7,15	0.49	0	6,6,14	0.64	0
6	BML	B	508	-	8,8,8	1.03	0	10,10,10	1.96	3 (30%)
9	BTB	A	509	-	13,13,13	0.75	0	7,16,16	0.36	0
6	BML	A	507	-	8,8,8	0.74	0	10,10,10	1.08	1 (10%)
6	BML	A	503	-	8,8,8	0.71	0	10,10,10	0.51	0
6	BML	A	504	-	8,8,8	0.48	0	10,10,10	0.66	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
7	1PE	A	505	5	-	5/5/5/13	-
6	BML	E	507	-	-	-	0/1/1/1
6	BML	B	508	-	-	-	0/1/1/1
9	BTB	A	509	-	-	5/21/21/21	-
6	BML	A	507	-	-	-	0/1/1/1
6	BML	A	503	-	-	-	0/1/1/1
6	BML	A	504	-	-	-	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	508	BML	BR4-C4-C3	4.35	125.23	119.30
6	B	508	BML	C6-C5-C4	2.42	122.08	119.18
6	B	508	BML	BR4-C4-C5	-2.19	116.31	119.30
6	A	507	BML	BR4-C4-C3	2.10	122.15	119.30

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	509	BTB	C1-C2-N-C5
9	A	509	BTB	C3-C2-N-C5
9	A	509	BTB	C4-C2-N-C5
9	A	509	BTB	N-C7-C8-O8
7	A	505	1PE	OH6-C15-C25-OH5
7	A	505	1PE	OH5-C14-C24-OH4
7	A	505	1PE	C15-C25-OH5-C14
7	A	505	1PE	C24-C14-OH5-C25
7	A	505	1PE	C25-C15-OH6-C26
9	A	509	BTB	C6-C5-N-C2

There are no ring outliers.

7 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	507	BML	2	0
7	A	505	1PE	2	0
6	B	508	BML	5	0
9	A	509	BTB	1	0
6	A	507	BML	5	0
6	A	503	BML	6	0
6	A	504	BML	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	491/500 (98%)	-0.44	1 (0%) 91 94	10, 21, 31, 45	12 (2%)
2	B	305/327 (93%)	-0.18	3 (0%) 79 84	11, 24, 39, 48	5 (1%)
3	C	83/84 (98%)	0.29	3 (3%) 46 52	17, 33, 46, 60	1 (1%)
4	E	102/103 (99%)	-0.15	2 (1%) 65 72	13, 22, 38, 48	2 (1%)
All	All	981/1014 (96%)	-0.27	9 (0%) 81 85	10, 23, 39, 60	20 (2%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	2	SER	2.5
4	E	103	MET	2.5
3	C	67[A]	ILE	2.4
2	B	283	GLU	2.4
2	B	17[A]	GLU	2.4
3	C	84	GLU	2.2
1	A	378	GLU	2.2
4	E	37	GLY	2.1
2	B	18	MET	2.1

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
6	BML	B	508	8/8	0.78	0.23	59,61,61,62	0
9	BTB	A	509	14/14	0.79	0.14	32,41,44,50	0
7	1PE	A	505	8/16	0.86	0.12	31,35,38,40	0
6	BML	A	504	8/8	0.92	0.17	49,49,50,51	8
6	BML	A	507	8/8	0.94	0.18	36,37,37,39	7
6	BML	A	503	8/8	0.97	0.14	22,23,23,25	8
6	BML	E	507	8/8	0.97	0.11	33,35,37,37	8
8	CL	A	506	1/1	0.99	0.07	26,26,26,26	1
5	FE	A	501	1/1	1.00	0.01	17,17,17,17	0
5	FE	A	502	1/1	1.00	0.02	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.