



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:04 AM UTC

PDB ID : 1HZY / pdb_00001hzy
Title : HIGH RESOLUTION STRUCTURE OF THE ZINC-CONTAINING PHOSPHOTRIESTERASE FROM PSEUDOMONAS DIMINUTA
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Deposited on : 2001-01-26
Resolution : 1.30 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

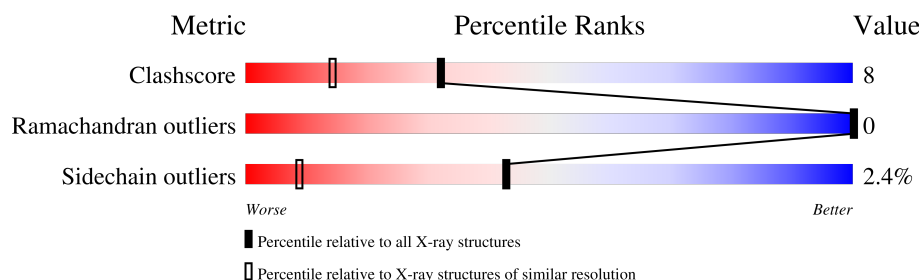
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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))
Clashscore	190562	1595 (1.30-1.30)
Ramachandran outliers	187476	1551 (1.30-1.30)
Sidechain outliers	187428	1551 (1.30-1.30)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	332	
1	B	332	

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
4	EDO	B	424	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5974 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 PHOSPHOTRIESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	9	0
			2554	1613	453	481	7			
1	B	331	Total	C	N	O	S	0	8	0
			2546	1609	455	475	7			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	B	1	Total	Na	0	0
			1	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



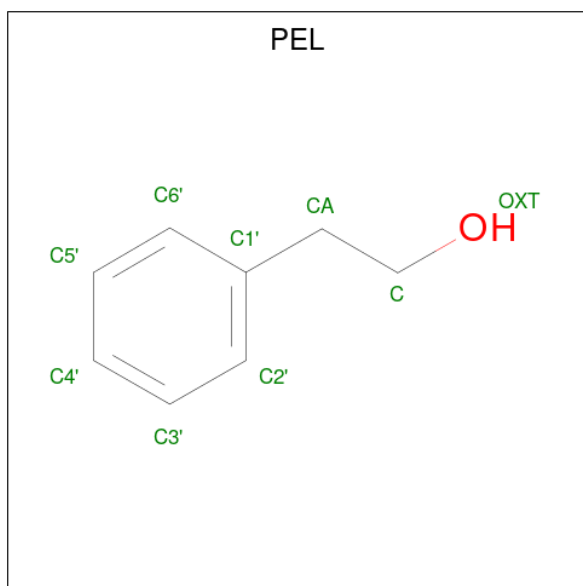
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total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

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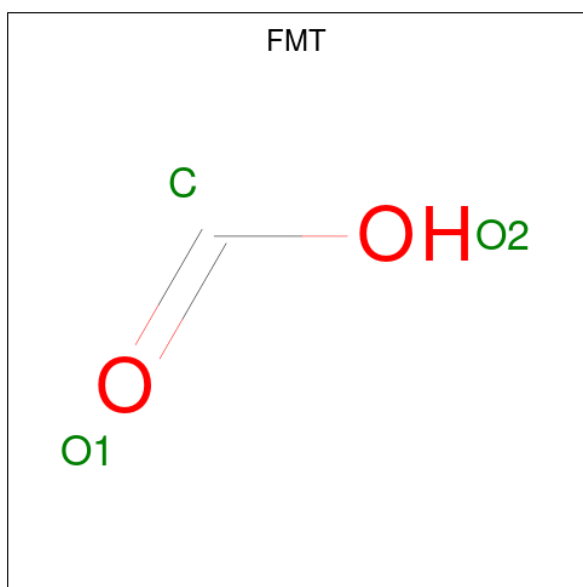
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 2-PHENYL-ETHANOL (CCD ID: PEL) (formula: $C_8H_{10}O$).



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

- Molecule 6 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			3	1	2		
6	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	389	Total	O	0	0
			389	389		
7	B	375	Total	O	0	0
			375	375		

3 Residue-property plots

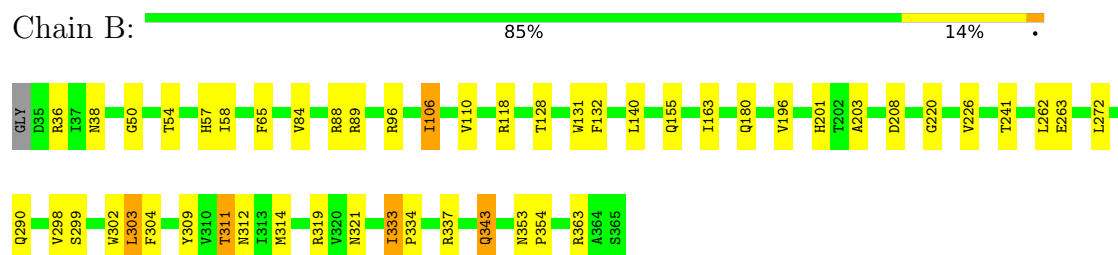
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: PHOSPHOTRIESTERASE



• Molecule 1: PHOSPHOTRIESTERASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	128.40Å 90.03Å 68.40Å 90.00° 91.70° 90.00°	Depositor
Resolution (Å)	30.00 – 1.30	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-1.30)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.196 , 0.228	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5974	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

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: PEL, FMT, ZN, NA, EDO

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	2.24	1/2649 (0.0%)	1.42	20/3599 (0.6%)
1	B	1.03	1/2636 (0.0%)	1.36	15/3580 (0.4%)
All	All	1.74	2/5285 (0.0%)	1.39	35/7179 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	365	SER	C-OXT	102.09	3.27	1.23
1	B	89	ARG	NE-CZ	5.45	1.39	1.33

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	106	ILE	N-CA-C	-7.88	103.74	112.80
1	B	203	ALA	N-CA-C	-7.66	94.38	108.24
1	B	311	THR	CA-C-N	-7.66	114.84	126.86
1	B	311	THR	C-N-CA	-7.66	114.84	126.86
1	B	58	ILE	N-CA-C	-7.55	102.77	111.00
1	A	311	THR	CA-C-N	-7.50	115.09	126.86
1	A	311	THR	C-N-CA	-7.50	115.09	126.86
1	A	236	ASP	N-CA-CB	7.49	123.14	110.49
1	A	203	ALA	N-CA-C	-7.33	92.61	107.41
1	A	226	VAL	N-CA-C	6.94	117.83	108.11
1	A	106	ILE	N-CA-C	-6.85	104.93	112.80
1	A	54	THR	N-CA-C	6.78	121.40	113.20
1	A	58	ILE	N-CA-C	-6.74	103.66	111.00
1	A	352	THR	N-CA-C	6.27	117.77	111.07
1	B	208	ASP	CA-CB-CG	6.20	118.80	112.60
1	A	312	ASN	CB-CA-C	6.18	115.95	109.83
1	B	54	THR	N-CA-C	6.08	120.54	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	332	VAL	N-CA-C	6.05	116.22	110.53
1	B	304	PHE	CA-CB-CG	-5.96	107.84	113.80
1	B	226	VAL	N-CA-C	5.91	116.63	108.12
1	A	201	HIS	N-CA-C	-5.90	100.08	109.76
1	B	65	PHE	N-CA-C	5.89	117.37	111.07
1	A	304	PHE	CA-CB-CG	-5.78	108.02	113.80
1	A	272	LEU	N-CA-C	5.67	120.33	112.90
1	A	295[A]	GLN	CB-CA-C	-5.64	101.95	111.02
1	A	295[B]	GLN	CB-CA-C	-5.64	101.95	111.02
1	A	295[C]	GLN	CB-CA-C	-5.64	101.95	111.02
1	B	262	LEU	CB-CA-C	-5.61	102.43	111.18
1	B	155	GLN	N-CA-C	5.47	118.42	111.69
1	B	272	LEU	N-CA-C	5.27	119.76	113.23
1	B	333	ILE	CA-C-O	5.21	122.18	118.69
1	B	128	THR	N-CA-C	-5.10	101.69	109.65
1	A	241[A]	THR	N-CA-C	5.07	116.81	111.28
1	A	241[B]	THR	N-CA-C	5.07	116.81	111.28
1	A	67	ARG	CA-CB-CG	-5.04	104.02	114.10

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	2554	0	2580	43	0
1	B	2546	0	2567	41	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	44	0	66	8	0
4	B	36	0	54	10	0
5	A	9	0	10	0	0
5	B	9	0	10	0	0
6	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	3	0	0	1	0
7	A	389	0	0	13	0
7	B	375	0	0	7	0
All	All	5974	0	5287	84	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 8.

All (84) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:263:GLU:HA	7:B:954:HOH:O	1.82	0.80
1:A:335:PHE:O	1:A:338:GLU:HG3	1.82	0.78
1:A:207:ARG:NH2	1:A:236:ASP:OD2	2.17	0.78
1:B:96:ARG:HH11	4:B:424:EDO:C1	1.97	0.78
1:A:36:ARG:HD2	1:A:43:PRO:HB2	1.65	0.77
1:A:77:LYS:HE3	7:A:498:HOH:O	1.83	0.77
1:B:241:THR:HG21	1:B:290:GLN:HE21	1.53	0.73
1:B:96:ARG:HG3	4:B:424:EDO:H11	1.71	0.72
1:B:96:ARG:HH11	4:B:424:EDO:H12	1.55	0.72
1:A:222[A]:SER:HB2	1:A:363:ARG:HH21	1.51	0.71
1:B:319:ARG:NH2	7:B:782:HOH:O	2.30	0.64
1:A:38:ASN:ND2	7:A:837:HOH:O	2.31	0.64
1:A:237:LEU:O	1:A:241[B]:THR:HG22	2.00	0.62
1:B:314:MET:HB3	4:B:414:EDO:H22	1.81	0.62
1:A:269:SER:HB2	4:A:418:EDO:H11	1.81	0.61
1:B:96:ARG:HH11	4:B:424:EDO:H11	1.67	0.59
1:B:337:ARG:HD2	7:B:1076:HOH:O	2.01	0.59
1:A:262:LEU:HD12	1:A:262:LEU:N	2.19	0.58
1:A:309:TYR:HA	1:B:140:LEU:HD12	1.85	0.58
4:A:410:EDO:H22	7:A:838:HOH:O	2.03	0.58
1:B:50:GLY:HA3	4:B:424:EDO:H22	1.86	0.58
1:B:110[B]:VAL:CG1	1:B:163:ILE:HD12	2.34	0.58
1:B:110[B]:VAL:CG1	1:B:163:ILE:CD1	2.84	0.56
1:B:110[B]:VAL:HG12	1:B:163:ILE:HD12	1.88	0.55
1:A:266:ALA:C	4:A:418:EDO:HO2	2.13	0.54
1:B:110[B]:VAL:HG13	1:B:163:ILE:HD13	1.90	0.54
1:B:96:ARG:CG	4:B:424:EDO:H11	2.38	0.53
1:A:362:LEU:HA	7:A:1181:HOH:O	2.09	0.52
1:A:309:TYR:CA	1:B:140:LEU:HD12	2.39	0.51
1:A:236:ASP:OD1	1:A:238[A]:SER:OG	2.21	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:263:GLU:H	1:B:263:GLU:CD	2.19	0.51
1:B:220:GLY:O	1:B:363:ARG:NH1	2.44	0.51
1:A:309:TYR:HA	1:B:140:LEU:CD1	2.41	0.50
1:A:335:PHE:HA	1:A:338:GLU:CG	2.42	0.50
1:B:110[A]:VAL:CG2	1:B:163:ILE:HG21	2.42	0.50
1:B:333:ILE:HB	1:B:334:PRO:HD3	1.92	0.50
1:B:38:ASN:ND2	7:B:634:HOH:O	2.46	0.49
1:A:109:ASP:OD1	1:A:111[A]:SER:OG	2.27	0.49
1:A:236:ASP:CG	1:A:239:TYR:H	2.20	0.49
1:B:96:ARG:NH1	4:B:424:EDO:H12	2.26	0.49
1:A:363:ARG:HB3	7:A:855:HOH:O	2.12	0.48
1:B:57:HIS:O	1:B:303:LEU:HA	2.12	0.48
4:A:410:EDO:H11	7:A:541:HOH:O	2.12	0.48
1:A:266:ALA:HB1	4:A:418:EDO:O2	2.12	0.48
1:A:200:THR:O	1:A:229:GLY:HA3	2.13	0.48
1:A:131:TRP:CG	1:A:132:PHE:H	2.33	0.47
1:A:292:TYR:HB3	1:A:295[A]:GLN:HG3	1.95	0.47
4:A:416:EDO:C1	7:A:537:HOH:O	2.63	0.47
1:A:106:ILE:HG22	1:A:106:ILE:O	2.15	0.46
1:A:242:ALA:HB3	7:A:907:HOH:O	2.15	0.46
1:A:302:TRP:CH2	1:A:321:ASN:HB3	2.51	0.46
1:A:57:HIS:O	1:A:303:LEU:HA	2.16	0.46
1:A:38:ASN:ND2	7:A:437:HOH:O	2.49	0.46
1:A:279:THR:OG1	4:A:419:EDO:H12	2.16	0.46
1:A:312:ASN:HA	7:A:610:HOH:O	2.15	0.46
1:B:311:THR:O	1:B:312:ASN:HB2	2.15	0.46
1:B:298[A]:VAL:HG23	7:B:651:HOH:O	2.15	0.45
1:B:302:TRP:CH2	1:B:321:ASN:HB3	2.51	0.45
1:A:202:THR:HB	1:A:208:ASP:HB2	1.98	0.45
1:B:353:ASN:HB2	1:B:354:PRO:HD3	1.99	0.45
1:B:311:THR:O	1:B:312:ASN:CB	2.65	0.43
1:A:334:PRO:O	1:A:338:GLU:HG2	2.19	0.43
1:B:180:GLN:NE2	4:B:421:EDO:H12	2.34	0.43
1:B:337:ARG:HH12	1:B:343:GLN:HB2	1.83	0.43
1:B:131:TRP:CG	1:B:132:PHE:H	2.37	0.43
1:A:222[B]:SER:OG	1:A:363:ARG:NH2	2.30	0.42
1:A:236:ASP:CB	7:A:1154:HOH:O	2.66	0.42
4:A:416:EDO:H12	7:A:537:HOH:O	2.18	0.42
1:A:236:ASP:CG	1:A:238[A]:SER:HG	2.24	0.42
1:B:84:VAL:O	1:B:88:ARG:HG3	2.19	0.42
1:B:180:GLN:HE21	4:B:421:EDO:H12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:ASN:HB2	1:A:354:PRO:HD3	2.02	0.42
1:B:201:HIS:HB2	6:B:369:FMT:O2	2.19	0.42
1:B:263:GLU:HG3	7:B:954:HOH:O	2.19	0.42
1:B:118[A]:ARG:NH1	7:B:1165:HOH:O	2.23	0.42
1:A:236:ASP:OD1	1:A:236:ASP:C	2.63	0.41
1:A:207:ARG:HH11	1:A:207:ARG:HD3	1.76	0.41
1:A:260:ILE:O	1:A:262:LEU:HD12	2.21	0.41
1:B:110[A]:VAL:HG21	1:B:163:ILE:HG21	2.02	0.40
1:A:43:PRO:HB3	7:A:837:HOH:O	2.22	0.40
1:B:106:ILE:HG22	1:B:106:ILE:O	2.21	0.40
1:A:140:LEU:HD12	1:B:309:TYR:HA	2.03	0.40
1:A:262:LEU:C	1:A:264:ASP:N	2.79	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	339/332 (102%)	326 (96%)	13 (4%)	0	100	100
1	B	337/332 (102%)	329 (98%)	8 (2%)	0	100	100
All	All	676/664 (102%)	655 (97%)	21 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	276/266 (104%)	265 (96%)	11 (4%)	28 2
1	B	274/266 (103%)	268 (98%)	6 (2%)	45 10
All	All	550/532 (103%)	533 (97%)	17 (3%)	43 5

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196[A]	VAL
1	A	196[B]	VAL
1	A	262	LEU
1	A	295[A]	GLN
1	A	295[B]	GLN
1	A	295[C]	GLN
1	A	299	SER
1	A	303	LEU
1	A	338	GLU
1	A	339	LYS
1	A	363	ARG
1	B	36	ARG
1	B	196[A]	VAL
1	B	196[B]	VAL
1	B	299	SER
1	B	303	LEU
1	B	343	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	212	GLN
1	A	312	ASN
1	B	38	ASN
1	B	212	GLN
1	B	290	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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 30 ligands modelled in this entry, 6 are monoatomic - leaving 24 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	EDO	B	409	-	3,3,3	0.31	0	2,2,2	0.41	0
4	EDO	A	408	-	3,3,3	0.35	0	2,2,2	0.48	0
4	EDO	B	413	-	3,3,3	0.39	0	2,2,2	0.59	0
5	PEL	A	428	-	9,9,9	1.30	0	10,10,10	0.95	1 (10%)
6	FMT	A	369	2,1	2,2,2	0.43	0	1,1,1	0.07	0
4	EDO	A	416	-	3,3,3	0.65	0	2,2,2	0.11	0
4	EDO	A	410	-	3,3,3	0.52	0	2,2,2	0.14	0
4	EDO	A	420	-	3,3,3	0.46	0	2,2,2	0.40	0
4	EDO	A	411	-	3,3,3	0.48	0	2,2,2	0.93	0
4	EDO	B	424	-	3,3,3	0.43	0	2,2,2	0.25	0
4	EDO	B	423	-	3,3,3	0.20	0	2,2,2	0.86	0
4	EDO	A	417	-	3,3,3	0.34	0	2,2,2	0.64	0
5	PEL	B	427	-	9,9,9	1.45	2 (22%)	10,10,10	1.02	1 (10%)
4	EDO	B	407	-	3,3,3	0.26	0	2,2,2	1.07	0
4	EDO	A	418	-	3,3,3	0.44	0	2,2,2	0.44	0
4	EDO	B	415	-	3,3,3	0.45	0	2,2,2	0.74	0
4	EDO	B	422	-	3,3,3	0.29	0	2,2,2	0.53	0
4	EDO	B	414	-	3,3,3	0.36	0	2,2,2	0.53	0
4	EDO	A	426	-	3,3,3	0.38	0	2,2,2	0.42	0
4	EDO	B	421	-	3,3,3	0.40	0	2,2,2	0.04	0
6	FMT	B	369	2,1	2,2,2	0.24	0	1,1,1	0.07	0
4	EDO	A	412	-	3,3,3	0.36	0	2,2,2	0.42	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	425	-	3,3,3	0.38	0	2,2,2	0.42	0
4	EDO	A	419	-	3,3,3	0.41	0	2,2,2	0.34	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
4	EDO	B	409	-	-	0/1/1/1	-
4	EDO	A	408	-	-	0/1/1/1	-
4	EDO	B	413	-	-	1/1/1/1	-
5	PEL	A	428	-	-	1/3/3/3	0/1/1/1
4	EDO	A	416	-	-	1/1/1/1	-
4	EDO	A	410	-	-	0/1/1/1	-
4	EDO	A	420	-	-	0/1/1/1	-
4	EDO	A	411	-	-	1/1/1/1	-
4	EDO	B	424	-	-	1/1/1/1	-
4	EDO	B	423	-	-	1/1/1/1	-
4	EDO	A	417	-	-	1/1/1/1	-
5	PEL	B	427	-	-	1/3/3/3	0/1/1/1
4	EDO	B	407	-	-	0/1/1/1	-
4	EDO	A	418	-	-	0/1/1/1	-
4	EDO	B	415	-	-	1/1/1/1	-
4	EDO	B	422	-	-	0/1/1/1	-
4	EDO	B	414	-	-	0/1/1/1	-
4	EDO	A	426	-	-	1/1/1/1	-
4	EDO	B	421	-	-	0/1/1/1	-
4	EDO	A	412	-	-	1/1/1/1	-
4	EDO	A	425	-	-	0/1/1/1	-
4	EDO	A	419	-	-	0/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	427	PEL	C2'-C1'	2.10	1.43	1.38
5	B	427	PEL	C4'-C3'	2.03	1.42	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	427	PEL	C4'-C3'-C2'	-2.43	117.24	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	428	PEL	C4'-C5'-C6'	-2.08	117.68	120.24

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	428	PEL	OXT-C-CA-C1'
5	B	427	PEL	OXT-C-CA-C1'
4	A	412	EDO	O1-C1-C2-O2
4	A	426	EDO	O1-C1-C2-O2
4	B	424	EDO	O1-C1-C2-O2
4	A	416	EDO	O1-C1-C2-O2
4	B	413	EDO	O1-C1-C2-O2
4	B	423	EDO	O1-C1-C2-O2
4	A	417	EDO	O1-C1-C2-O2
4	B	415	EDO	O1-C1-C2-O2
4	A	411	EDO	O1-C1-C2-O2

There are no ring outliers.

8 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	416	EDO	2	0
4	A	410	EDO	2	0
4	B	424	EDO	7	0
4	A	418	EDO	3	0
4	B	414	EDO	1	0
4	B	421	EDO	2	0
6	B	369	FMT	1	0
4	A	419	EDO	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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.