



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 10:15 pm GMT

PDB ID : 1I0B  
Title : HIGH RESOLUTION STRUCTURE OF THE MANGANESE-CONTAINING PHOSPHOTRIESTERASE FROM PSEUDOMONAS DIMINUTA  
Authors : Holden, H.M.; Benning, M.M.; Raushel, F.M.; Shim, H.  
Deposited on : 2001-01-29  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

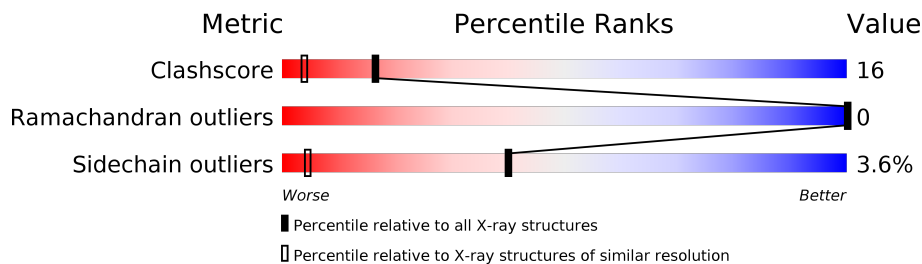
# 1 Overall quality at a glance

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	112137	1185 (1.32-1.28)
Ramachandran outliers	110173	1138 (1.32-1.28)
Sidechain outliers	110143	1138 (1.32-1.28)

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. 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.

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	A	417	-	-	X	-
4	EDO	A	419	-	-	X	-
4	EDO	A	420	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	EDO	A	432	-	-	X	-
4	EDO	B	414	-	-	X	-
4	EDO	B	416	-	-	X	-
4	EDO	B	418	-	-	X	-
4	EDO	B	421	-	-	X	-
4	EDO	B	422	-	-	X	-
4	EDO	B	426	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5917 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	8	0
			2549	1610	453	479	7			
1	B	331	Total	C	N	O	S	0	7	0
			2538	1603	455	473	7			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



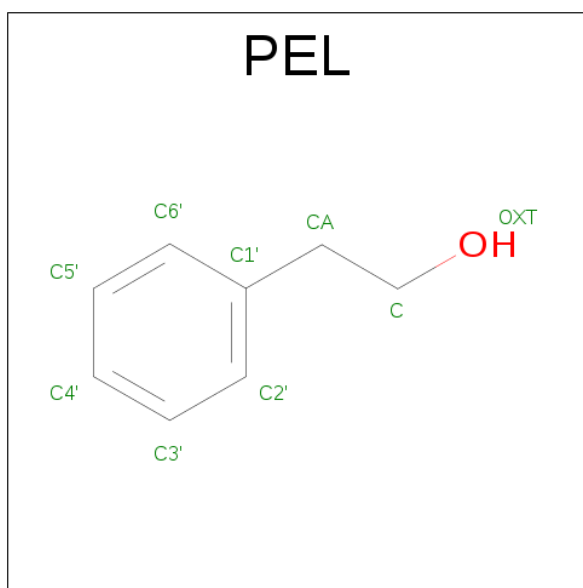
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	1
			4	2	2		
4	A	1	Total	C	O	0	1
			5	2	3		
4	B	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

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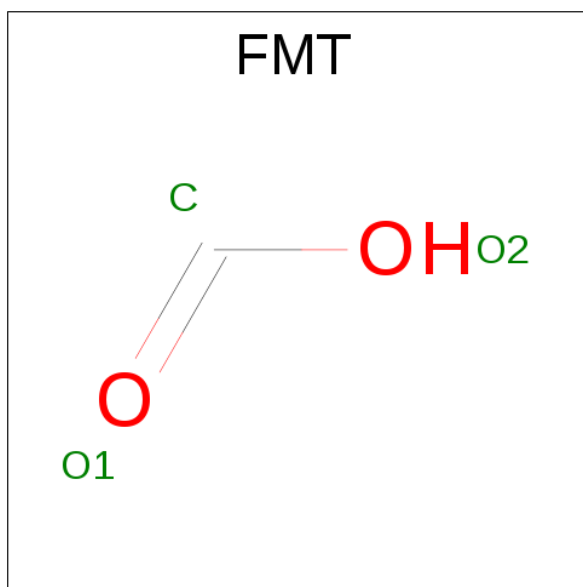
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0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

- Molecule 5 is 2-PHENYL-ETHANOL (three-letter code: PEL) (formula: C<sub>8</sub>H<sub>10</sub>O).



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

- Molecule 6 is FORMIC ACID (three-letter code: FMT) (formula: CH<sub>2</sub>O<sub>2</sub>).



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	333	Total	O	0	0
			333	333		
7	B	362	Total	O	0	0
			362	362		

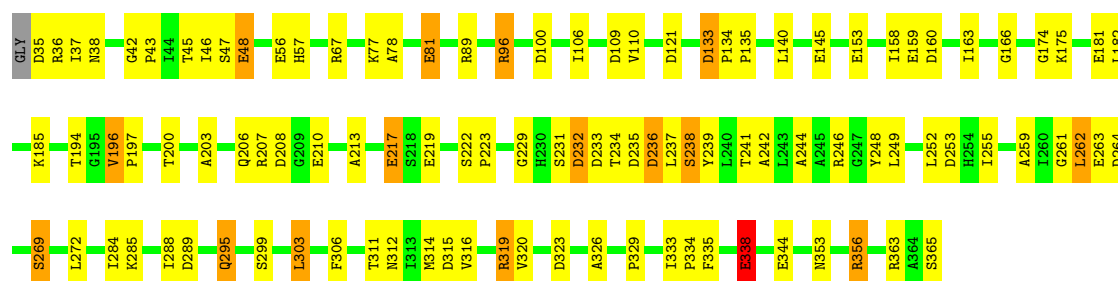
### 3 Residue-property plots

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.


Note EDS was not executed.

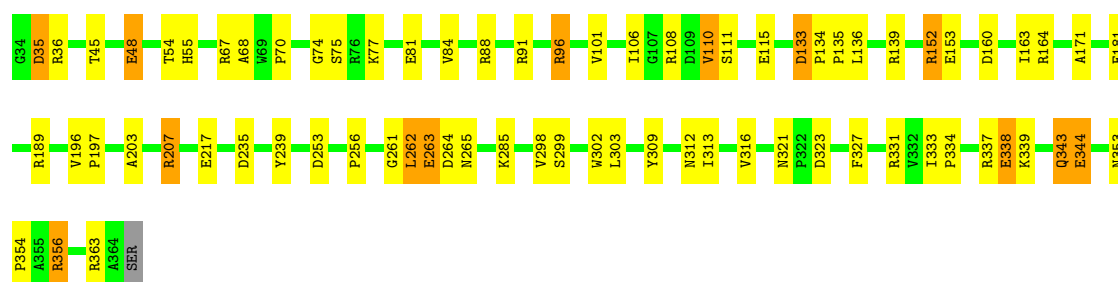
#### • Molecule 1: PHOSPHOTRIESTERASE

Chain A: 



#### • Molecule 1: PHOSPHOTRIESTERASE

Chain B: 



## 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, $\alpha$ , $\beta$ , $\gamma$	128.44Å 90.03Å 68.39Å 90.00° 91.72° 90.00°	Depositor
Resolution (Å)	30.00 – 1.30	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-1.30)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	TNT V. 5-E	Depositor
R, $R_{free}$	0.222 , 0.267	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5917	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	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, NA, FMT, MN, 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	2.25	13/2640 (0.5%)	1.33	31/3587 (0.9%)
1	B	0.88	8/2626 (0.3%)	1.30	25/3566 (0.7%)
All	All	1.71	21/5266 (0.4%)	1.32	56/7153 (0.8%)

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	365	SER	C-OXT	106.28	3.25	1.23
1	A	153	GLU	CD-OE2	6.84	1.33	1.25
1	A	56	GLU	CD-OE2	6.70	1.33	1.25
1	B	263	GLU	CD-OE2	6.10	1.32	1.25
1	B	48	GLU	CD-OE2	6.09	1.32	1.25
1	A	145	GLU	CD-OE2	6.09	1.32	1.25
1	B	153	GLU	CD-OE2	6.09	1.32	1.25
1	A	81	GLU	CD-OE2	6.08	1.32	1.25
1	B	338	GLU	CD-OE2	6.02	1.32	1.25
1	A	210	GLU	CD-OE2	6.01	1.32	1.25
1	A	344	GLU	CD-OE2	5.90	1.32	1.25
1	A	219	GLU	CD-OE2	5.82	1.32	1.25
1	B	344	GLU	CD-OE2	5.81	1.32	1.25
1	A	338	GLU	CD-OE2	5.78	1.32	1.25
1	A	48	GLU	CD-OE2	5.77	1.31	1.25
1	A	181	GLU	CD-OE2	5.58	1.31	1.25
1	A	263	GLU	CD-OE2	5.38	1.31	1.25
1	B	217	GLU	CD-OE2	5.38	1.31	1.25
1	A	217	GLU	CD-OE2	5.34	1.31	1.25
1	B	81	GLU	CD-OE2	5.10	1.31	1.25
1	B	181	GLU	CD-OE2	5.09	1.31	1.25

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	ARG	NE-CZ-NH2	-8.47	116.07	120.30
1	B	253	ASP	CB-CG-OD1	8.04	125.53	118.30
1	B	331	ARG	NE-CZ-NH1	7.76	124.18	120.30
1	A	253	ASP	CB-CG-OD1	7.56	125.11	118.30
1	A	133	ASP	CB-CG-OD2	-7.53	111.53	118.30
1	B	189	ARG	NE-CZ-NH2	-7.39	116.61	120.30
1	A	109	ASP	CB-CG-OD1	7.35	124.92	118.30
1	A	236	ASP	CB-CG-OD1	7.31	124.88	118.30
1	A	356	ARG	NE-CZ-NH1	7.17	123.89	120.30
1	B	323	ASP	CB-CG-OD2	-6.98	112.01	118.30
1	B	171	ALA	CB-CA-C	-6.94	99.70	110.10
1	B	253	ASP	CB-CG-OD2	-6.91	112.08	118.30
1	A	233	ASP	CB-CG-OD1	6.77	124.39	118.30
1	A	35	ASP	CB-CG-OD2	-6.75	112.23	118.30
1	B	35	ASP	CB-CG-OD2	-6.67	112.29	118.30
1	B	133	ASP	CB-CG-OD2	-6.60	112.36	118.30
1	A	36	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	A	109	ASP	CB-CG-OD2	-6.56	112.40	118.30
1	B	164	ARG	NE-CZ-NH2	-6.49	117.05	120.30
1	A	36	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	B	160	ASP	CB-CG-OD1	6.35	124.02	118.30
1	A	264	ASP	CB-CG-OD2	-6.35	112.59	118.30
1	A	235	ASP	CB-CG-OD1	6.32	123.99	118.30
1	B	323	ASP	CB-CG-OD1	6.28	123.96	118.30
1	A	35	ASP	CB-CG-OD1	6.16	123.84	118.30
1	B	262	LEU	CB-CA-C	-6.16	98.50	110.20
1	A	89	ARG	NE-CZ-NH1	6.12	123.36	120.30
1	B	356	ARG	NE-CZ-NH1	6.11	123.35	120.30
1	B	207	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	A	121	ASP	CB-CG-OD2	-6.04	112.86	118.30
1	A	233	ASP	CB-CG-OD2	-6.01	112.89	118.30
1	A	67	ARG	NE-CZ-NH2	-6.00	117.30	120.30
1	B	96	ARG	NE-CZ-NH1	5.83	123.22	120.30
1	A	264	ASP	CB-CG-OD1	5.80	123.52	118.30
1	B	91	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	B	203	ALA	N-CA-C	-5.73	95.52	111.00
1	B	235	ASP	CB-CG-OD2	-5.67	113.20	118.30
1	B	152	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	96	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	A	315	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	A	203	ALA	N-CA-C	-5.45	96.29	111.00
1	B	108	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	A	232	ASP	CB-CG-OD1	5.41	123.16	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	189	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	A	315	ASP	CB-CG-OD1	5.39	123.15	118.30
1	B	35	ASP	CB-CG-OD1	5.33	123.09	118.30
1	A	208	ASP	CB-CG-OD2	-5.32	113.52	118.30
1	A	100	ASP	CB-CG-OD1	5.30	123.07	118.30
1	B	207	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	A	232	ASP	CB-CG-OD2	-5.24	113.59	118.30
1	A	323	ASP	CB-CG-OD1	5.22	123.00	118.30
1	A	235	ASP	CB-CG-OD2	-5.17	113.65	118.30
1	A	160	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	236	ASP	CB-CG-OD2	-5.08	113.73	118.30
1	B	133	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	331	ARG	NE-CZ-NH2	-5.04	117.78	120.30

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	2549	0	2578	90	1
1	B	2538	0	2560	72	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	49	0	72	33	0
4	B	56	0	81	42	0
5	A	9	0	10	1	0
5	B	9	0	10	0	0
6	A	3	0	0	0	0
6	B	3	0	0	0	0
7	A	333	0	0	8	0
7	B	362	0	0	14	0
All	All	5917	0	5311	168	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 16.

All (168) 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:96:ARG:HH11	4:B:418:EDO:H21	1.19	1.04
1:B:337:ARG:HH12	1:B:343:GLN:HG3	1.24	1.00
1:B:68:ALA:HB2	4:B:426:EDO:C2	1.97	0.94
1:B:96:ARG:NH1	4:B:418:EDO:H21	1.84	0.92
1:B:135:PRO:HA	4:B:416:EDO:H21	1.51	0.92
1:B:337:ARG:NH1	1:B:343:GLN:HG3	1.84	0.91
1:A:135:PRO:HA	4:B:416:EDO:H12	1.51	0.90
1:A:96:ARG:CG	4:A:417:EDO:H21	2.05	0.86
1:B:135:PRO:CA	4:B:416:EDO:H21	2.08	0.83
1:A:135:PRO:CA	4:B:416:EDO:H12	2.09	0.81
1:A:96:ARG:HG3	4:A:417:EDO:H21	1.63	0.80
1:A:237:LEU:O	1:A:241[B]:THR:HG22	1.82	0.80
4:A:430:EDO:H21	7:A:934:HOH:O	1.81	0.79
1:A:262:LEU:HD12	1:A:262:LEU:N	2.01	0.76
1:A:159:GLU:CD	4:B:426:EDO:H11	2.06	0.75
1:B:96:ARG:HD2	4:B:418:EDO:H12	1.68	0.74
1:A:246:ARG:HD2	4:A:432:EDO:H21	1.70	0.74
1:B:68:ALA:HB2	4:B:426:EDO:H22	1.70	0.73
1:B:337:ARG:HH12	1:B:343:GLN:CG	1.99	0.72
1:B:337:ARG:HH22	1:B:343:GLN:HG3	1.52	0.72
1:A:159:GLU:OE2	4:B:426:EDO:H11	1.90	0.72
1:B:68:ALA:HB2	4:B:426:EDO:H21	1.71	0.72
1:A:335:PHE:O	1:A:338:GLU:HG3	1.90	0.71
1:A:222[A]:SER:HB2	1:A:363:ARG:HH21	1.55	0.71
1:B:337:ARG:NH2	1:B:343:GLN:HG3	2.04	0.70
1:A:306:PHE:N	4:A:420:EDO:O2	2.23	0.70
4:A:420:EDO:H12	7:A:489:HOH:O	1.91	0.70
1:A:96:ARG:HH11	4:A:417:EDO:H12	1.57	0.69
1:B:207:ARG:NH1	7:B:828:HOH:O	2.25	0.69
1:A:246:ARG:CD	4:A:432:EDO:H21	2.22	0.69
1:A:38:ASN:ND2	7:A:1030:HOH:O	2.26	0.69
1:B:337:ARG:CZ	1:B:343:GLN:HG3	2.23	0.68
1:B:77:LYS:HA	4:B:414:EDO:H21	1.75	0.68
1:B:110[B]:VAL:HG13	1:B:163:ILE:CD1	2.24	0.68
1:A:185:LYS:HE2	7:A:816:HOH:O	1.94	0.67
1:B:74:GLY:HA3	4:B:429:EDO:H21	1.74	0.67
1:B:334:PRO:HB3	4:B:423:EDO:H12	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110[B]:VAL:CG1	1:B:163:ILE:HD12	2.25	0.66
1:B:265:ASN:HD21	4:B:422:EDO:C2	2.07	0.66
1:B:339:LYS:O	4:B:428:EDO:H22	1.96	0.66
1:A:43:PRO:HD2	4:A:419:EDO:C2	2.26	0.65
1:B:67:ARG:NH2	1:B:111[A]:SER:OG	2.29	0.65
1:A:159:GLU:CG	4:B:426:EDO:H11	2.26	0.65
1:A:43:PRO:HD2	4:A:419:EDO:H21	1.78	0.64
1:B:152:ARG:NH2	7:B:797:HOH:O	2.31	0.64
1:A:135:PRO:HG3	7:B:474:HOH:O	1.98	0.63
1:A:306:PHE:H	4:A:420:EDO:C2	2.10	0.63
1:A:246:ARG:NH1	4:A:432:EDO:O2	2.32	0.63
1:B:96:ARG:HH11	4:B:418:EDO:C2	2.05	0.62
4:A:411:EDO:H12	7:A:796:HOH:O	1.99	0.62
1:A:242:ALA:HB1	4:A:432:EDO:H22	1.81	0.61
1:B:115:GLU:OE1	4:B:414:EDO:H11	2.01	0.61
1:B:356:ARG:NH1	7:B:1008:HOH:O	2.33	0.60
1:A:196[B]:VAL:HG13	1:A:197:PRO:HD2	1.83	0.60
1:B:316:VAL:HG21	4:B:422:EDO:H22	1.84	0.59
1:A:159:GLU:HG2	4:B:426:EDO:C1	2.33	0.59
1:A:200:THR:O	1:A:229:GLY:HA3	2.01	0.59
1:A:316:VAL:HG22	1:A:319:ARG:NH2	2.18	0.59
1:A:96:ARG:HD2	4:A:417:EDO:H21	1.83	0.59
1:B:337:ARG:HH22	1:B:343:GLN:CG	2.17	0.58
4:A:410:EDO:H21	7:A:558:HOH:O	2.02	0.58
1:B:136:LEU:HG	1:B:139:ARG:NH2	2.19	0.58
1:A:96:ARG:CD	4:A:417:EDO:H21	2.33	0.58
1:B:285[A]:LYS:NZ	4:B:428:EDO:O2	2.28	0.57
1:B:110[B]:VAL:HG13	1:B:163:ILE:HD12	1.85	0.57
1:A:213:ALA:O	1:A:217:GLU:HG3	2.04	0.56
1:B:265:ASN:HD21	4:B:422:EDO:H22	1.70	0.56
1:A:242:ALA:HB1	4:A:432:EDO:H11	1.88	0.56
1:A:356:ARG:HD2	4:A:427:EDO:H11	1.88	0.56
1:B:261:GLY:O	1:B:262:LEU:HD23	2.06	0.55
1:B:312:ASN:HB2	4:B:422:EDO:O1	2.06	0.55
1:A:236:ASP:OD1	1:A:238[B]:SER:HB2	2.06	0.54
1:A:45:THR:HG23	1:A:48:GLU:OE1	2.07	0.54
1:B:110[B]:VAL:HG13	1:B:163:ILE:HD13	1.87	0.54
1:A:314:MET:HB2	4:A:420:EDO:O2	2.07	0.54
1:A:194:THR:OG1	1:A:196[A]:VAL:HG13	2.08	0.53
1:A:182:LEU:HD21	4:A:410:EDO:H11	1.91	0.52
1:A:159:GLU:HG2	4:B:426:EDO:H11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ARG:NH2	1:A:238[A]:SER:OG	2.43	0.52
1:B:106:ILE:O	1:B:106:ILE:HG22	2.09	0.52
1:A:262:LEU:CD1	1:A:262:LEU:N	2.72	0.51
1:A:43:PRO:HD2	4:A:419:EDO:O2	2.11	0.51
1:A:78:ALA:CB	4:A:430:EDO:H12	2.40	0.51
1:B:68:ALA:CB	4:B:426:EDO:H21	2.40	0.51
1:A:232:ASP:HB3	1:A:252:LEU:HD22	1.93	0.51
1:A:244:ALA:O	1:A:295[C]:GLN:NE2	2.43	0.51
1:A:207:ARG:NH2	1:A:236:ASP:OD2	2.34	0.51
1:B:338:GLU:HB2	7:B:1111:HOH:O	2.10	0.51
1:A:42:GLY:HA3	4:A:419:EDO:H21	1.92	0.50
1:A:284:ILE:O	1:A:288:ILE:HG13	2.12	0.50
1:A:96:ARG:CB	4:A:417:EDO:H21	2.41	0.50
1:B:338:GLU:HG3	7:B:1026:HOH:O	2.12	0.50
1:B:75:SER:HB2	4:B:421:EDO:H12	1.94	0.49
1:B:54:THR:HG23	7:B:763:HOH:O	2.12	0.49
1:B:333:ILE:HB	1:B:334:PRO:HD3	1.93	0.49
1:B:353:ASN:OD1	1:B:356:ARG:NH2	2.42	0.49
1:B:70:PRO:HB2	4:B:421:EDO:H22	1.94	0.49
1:B:136:LEU:HD21	1:B:139:ARG:HH21	1.78	0.49
1:A:96:ARG:NH1	4:A:417:EDO:H12	2.27	0.48
1:B:353:ASN:HB2	1:B:354:PRO:HD3	1.95	0.48
1:A:196[B]:VAL:CG1	1:A:197:PRO:HD2	2.43	0.48
1:A:77:LYS:HE2	1:A:81:GLU:OE1	2.13	0.48
1:B:74:GLY:CA	4:B:429:EDO:H21	2.41	0.48
1:B:70:PRO:HG2	4:B:421:EDO:H22	1.95	0.48
1:A:333:ILE:HB	1:A:334:PRO:HD3	1.95	0.48
1:A:223:PRO:HB3	1:A:248:TYR:CE1	2.49	0.48
1:B:298[A]:VAL:HG22	7:B:639:HOH:O	2.14	0.47
1:A:259:ALA:CB	1:A:269:SER:HA	2.45	0.47
1:B:68:ALA:N	4:B:426:EDO:H12	2.29	0.47
1:A:174:GLY:O	1:A:175:LYS:C	2.54	0.47
1:B:96:ARG:HB3	4:B:418:EDO:H11	1.97	0.47
1:B:74:GLY:HA3	4:B:429:EDO:C2	2.42	0.46
1:B:133:ASP:N	1:B:134:PRO:CD	2.78	0.46
1:B:265:ASN:HD21	4:B:422:EDO:H21	1.79	0.46
1:A:246:ARG:HD3	4:A:432:EDO:H21	1.95	0.46
1:A:234:THR:O	1:A:234:THR:HG23	2.15	0.45
1:A:106:ILE:O	1:A:106:ILE:HG22	2.16	0.45
1:A:259:ALA:C	1:A:262:LEU:HD13	2.36	0.45
1:A:57:HIS:HB2	1:A:303:LEU:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110[B]:VAL:CG2	1:A:163:ILE:HG21	2.47	0.45
1:A:140:LEU:CD1	1:B:309:TYR:HA	2.47	0.45
1:A:159:GLU:HG2	4:B:426:EDO:H12	1.99	0.44
1:B:55:HIS:CE1	1:B:101:VAL:HG21	2.52	0.44
1:A:242:ALA:HB1	4:A:432:EDO:C1	2.46	0.44
1:A:207:ARG:HA	1:A:239:TYR:CE2	2.53	0.44
1:A:320:VAL:HG13	7:A:581:HOH:O	2.18	0.44
1:B:207:ARG:HG2	1:B:239:TYR:CD2	2.52	0.44
1:A:242:ALA:HB1	4:A:432:EDO:C2	2.45	0.44
1:B:313:ILE:HG13	1:B:313:ILE:O	2.17	0.43
1:B:298[A]:VAL:HG23	7:B:640:HOH:O	2.17	0.43
1:B:363:ARG:N	7:B:711:HOH:O	2.21	0.43
1:A:242:ALA:CB	4:A:432:EDO:H22	2.46	0.43
1:B:77:LYS:HA	4:B:414:EDO:C2	2.46	0.43
1:B:135:PRO:N	4:B:416:EDO:H21	2.33	0.43
4:B:421:EDO:H12	7:B:655:HOH:O	2.19	0.43
1:A:353:ASN:OD1	5:A:434:PEL:H3	2.19	0.42
1:A:206:GLN:O	1:A:207:ARG:HB2	2.17	0.42
1:A:159:GLU:CG	4:B:426:EDO:C1	2.92	0.42
1:A:236:ASP:OD1	1:A:238[A]:SER:HB3	2.20	0.42
1:A:133:ASP:N	1:A:134:PRO:CD	2.82	0.42
1:A:207:ARG:HA	1:A:239:TYR:CZ	2.54	0.42
1:A:285:LYS:NZ	1:A:289:ASP:OD1	2.32	0.42
1:A:231:SER:O	1:A:234:THR:HG22	2.20	0.41
1:A:311:THR:O	1:A:312:ASN:HB2	2.20	0.41
1:A:353:ASN:OD1	1:A:356:ARG:NH2	2.51	0.41
1:B:196:VAL:HB	1:B:197:PRO:HD2	2.02	0.41
1:B:339:LYS:HG2	7:B:1111:HOH:O	2.20	0.41
1:A:255:ILE:HG12	1:A:255:ILE:H	1.62	0.41
1:A:326:ALA:O	1:A:329:PRO:HD2	2.20	0.41
1:A:37:ILE:HG13	1:A:46:ILE:HD13	2.02	0.41
1:B:77:LYS:CA	4:B:414:EDO:H21	2.47	0.41
1:B:263:GLU:HA	7:B:833:HOH:O	2.20	0.41
1:A:110[A]:VAL:HG21	1:A:158:ILE:CG2	2.51	0.41
1:A:110[B]:VAL:HG21	1:A:163:ILE:HG21	2.03	0.41
1:B:302:TRP:CH2	1:B:321:ASN:HB3	2.56	0.41
1:B:256:PRO:HB3	1:B:327:PHE:CD2	2.56	0.41
1:A:223:PRO:HB3	1:A:248:TYR:CD1	2.56	0.41
1:A:259:ALA:HB2	1:A:272:LEU:HB2	2.03	0.41
4:A:424:EDO:H11	7:A:457:HOH:O	2.20	0.41
1:B:136:LEU:CD2	1:B:139:ARG:NH2	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:416:EDO:H22	7:B:836:HOH:O	2.21	0.41
1:A:261:GLY:C	1:A:262:LEU:HD12	2.39	0.40
1:A:96:ARG:HB3	4:A:417:EDO:C2	2.51	0.40
1:B:45:THR:OG1	1:B:48:GLU:HG3	2.21	0.40
1:B:84:VAL:O	1:B:88:ARG:HG3	2.21	0.40
1:A:166:GLY:O	1:A:196[B]:VAL:HG13	2.21	0.40
1:A:246:ARG:HH11	4:A:432:EDO:C2	2.35	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)
1:A:236:ASP:OD1	1:A:236:ASP:OD1[2_656]	2.19	0.01

## 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	338/332 (102%)	323 (96%)	15 (4%)	0	100	100
1	B	336/332 (101%)	326 (97%)	10 (3%)	0	100	100
All	All	674/664 (102%)	649 (96%)	25 (4%)	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	275/266 (103%)	260 (94%)	15 (6%)	25	2
1	B	272/266 (102%)	263 (97%)	9 (3%)	43	6
All	All	547/532 (103%)	523 (96%)	24 (4%)	40	2

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	SER
1	A	196[A]	VAL
1	A	196[B]	VAL
1	A	238[A]	SER
1	A	238[B]	SER
1	A	249	LEU
1	A	262	LEU
1	A	269	SER
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	319	ARG
1	A	338	GLU
1	B	35	ASP
1	B	36	ARG
1	B	110[A]	VAL
1	B	110[B]	VAL
1	B	264	ASP
1	B	299	SER
1	B	303	LEU
1	B	343	GLN
1	B	344	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	212	GLN
1	B	38	ASN
1	B	212	GLN
1	B	343	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 37 ligands modelled in this entry, 6 are monoatomic - leaving 31 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	FMT	A	369	1,2	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	A	408[A]	-	3,3,3	0.49	0	2,2,2	0.43	0
4	EDO	A	408[B]	-	3,3,3	0.50	0	2,2,2	0.42	0
4	EDO	A	410	-	3,3,3	0.56	0	2,2,2	0.17	0
4	EDO	A	411	-	3,3,3	0.40	0	2,2,2	0.53	0
4	EDO	A	412	-	3,3,3	0.45	0	2,2,2	0.54	0
4	EDO	A	413	-	3,3,3	0.45	0	2,2,2	0.38	0
4	EDO	A	417	-	3,3,3	0.41	0	2,2,2	0.34	0
4	EDO	A	419	-	3,3,3	0.42	0	2,2,2	0.43	0
4	EDO	A	420	-	3,3,3	0.40	0	2,2,2	0.22	0
4	EDO	A	424	-	3,3,3	0.44	0	2,2,2	0.47	0
4	EDO	A	427	-	3,3,3	0.48	0	2,2,2	0.30	0
4	EDO	A	430	-	3,3,3	0.37	0	2,2,2	0.45	0
4	EDO	A	432	-	3,3,3	0.52	0	2,2,2	0.42	0
5	PEL	A	434	-	9,9,9	1.04	0	10,10,10	0.66	0
6	FMT	B	369	1,2	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	B	407[B]	-	3,3,3	0.45	0	2,2,2	0.39	0
4	EDO	B	409	-	3,3,3	0.34	0	2,2,2	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	EDO	B	414	-	3,3,3	0.47	0	2,2,2	0.27	0
4	EDO	B	415	-	3,3,3	0.36	0	2,2,2	0.91	0
4	EDO	B	416	-	3,3,3	0.39	0	2,2,2	0.40	0
4	EDO	B	418	-	3,3,3	0.41	0	2,2,2	0.37	0
4	EDO	B	421	-	3,3,3	0.35	0	2,2,2	0.34	0
4	EDO	B	422	-	3,3,3	0.43	0	2,2,2	0.44	0
4	EDO	B	423	-	3,3,3	0.44	0	2,2,2	0.32	0
4	EDO	B	425	-	3,3,3	0.47	0	2,2,2	0.39	0
4	EDO	B	426	-	3,3,3	0.37	0	2,2,2	0.32	0
4	EDO	B	428	-	3,3,3	0.42	0	2,2,2	0.39	0
4	EDO	B	429	-	3,3,3	0.43	0	2,2,2	0.44	0
4	EDO	B	431	-	3,3,3	0.40	0	2,2,2	0.43	0
5	PEL	B	433	-	9,9,9	1.00	0	10,10,10	0.80	1 (10%)

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	FMT	A	369	1,2	-	0/0/0/0	0/0/0/0
4	EDO	A	408[A]	-	-	0/1/1/1	0/0/0/0
4	EDO	A	408[B]	-	-	0/1/1/1	0/0/0/0
4	EDO	A	410	-	-	0/1/1/1	0/0/0/0
4	EDO	A	411	-	-	0/1/1/1	0/0/0/0
4	EDO	A	412	-	-	0/1/1/1	0/0/0/0
4	EDO	A	413	-	-	0/1/1/1	0/0/0/0
4	EDO	A	417	-	-	0/1/1/1	0/0/0/0
4	EDO	A	419	-	-	0/1/1/1	0/0/0/0
4	EDO	A	420	-	-	0/1/1/1	0/0/0/0
4	EDO	A	424	-	-	0/1/1/1	0/0/0/0
4	EDO	A	427	-	-	0/1/1/1	0/0/0/0
4	EDO	A	430	-	-	0/1/1/1	0/0/0/0
4	EDO	A	432	-	-	0/1/1/1	0/0/0/0
5	PEL	A	434	-	-	0/3/3/3	0/1/1/1
6	FMT	B	369	1,2	-	0/0/0/0	0/0/0/0
4	EDO	B	407[B]	-	-	0/1/1/1	0/0/0/0
4	EDO	B	409	-	-	0/1/1/1	0/0/0/0
4	EDO	B	414	-	-	0/1/1/1	0/0/0/0
4	EDO	B	415	-	-	0/1/1/1	0/0/0/0
4	EDO	B	416	-	-	0/1/1/1	0/0/0/0
4	EDO	B	418	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	421	-	-	0/1/1/1	0/0/0/0
4	EDO	B	422	-	-	0/1/1/1	0/0/0/0
4	EDO	B	423	-	-	0/1/1/1	0/0/0/0
4	EDO	B	425	-	-	0/1/1/1	0/0/0/0
4	EDO	B	426	-	-	0/1/1/1	0/0/0/0
4	EDO	B	428	-	-	0/1/1/1	0/0/0/0
4	EDO	B	429	-	-	0/1/1/1	0/0/0/0
4	EDO	B	431	-	-	0/1/1/1	0/0/0/0
5	PEL	B	433	-	-	0/3/3/3	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	433	PEL	C4'-C5'-C6'	-2.13	117.28	120.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

19 monomers are involved in 76 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	410	EDO	2	0
4	A	411	EDO	1	0
4	A	417	EDO	8	0
4	A	419	EDO	4	0
4	A	420	EDO	4	0
4	A	424	EDO	1	0
4	A	427	EDO	1	0
4	A	430	EDO	2	0
4	A	432	EDO	10	0
5	A	434	PEL	1	0
4	B	414	EDO	4	0
4	B	416	EDO	6	0
4	B	418	EDO	5	0
4	B	421	EDO	4	0
4	B	422	EDO	5	0
4	B	423	EDO	1	0
4	B	426	EDO	12	0
4	B	428	EDO	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	429	EDO	3	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.