



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 02:23 PM GMT

PDB ID : 2W3X  
Title : CRYSTAL STRUCTURE OF A BIFUNCTIONAL HOTDOG FOLD  
THIOESTERASE IN ENEDIYNE BIOSYNTHESIS, CALE7  
Authors : Kotaka, M.; Kong, R.; Qureshi, I.; Ho, Q.S.; Sun, H.; Liew, C.W.; Goh, L.P.;  
Cheung, P.; Mu, Y.; Lescar, J.; Liang, Z.X.  
Deposited on : 2008-11-17  
Resolution : 1.75 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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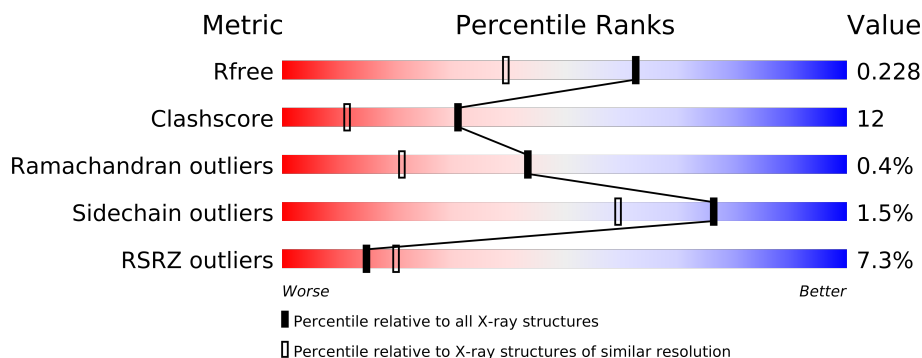
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.75 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))
$R_{free}$	66092	1134 (1.76-1.76)
Clashscore	79885	1304 (1.76-1.76)
Ramachandran outliers	78287	1288 (1.76-1.76)
Sidechain outliers	78261	1288 (1.76-1.76)
RSRZ outliers	66119	1135 (1.76-1.76)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	147	
1	B	147	
1	C	147	
1	D	147	
1	E	147	
1	F	147	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	PO4	A	1146	-	X
2	PO4	B	1146	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	JEF	A	1147	-	X
5	GOL	C	1145	-	X

## 2 Entry composition

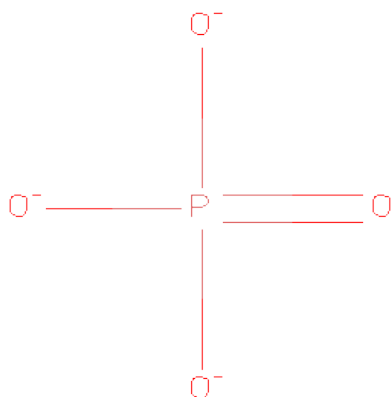
There are 6 unique types of molecules in this entry. The entry contains 7599 atoms, of which 0 are hydrogen and 0 are deuterium.

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 CALE7.

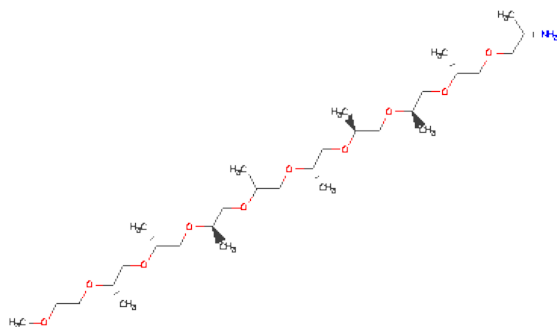
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	142	Total	C	N	O	S	0	0	1
			1163	743	211	202	7			
1	B	145	Total	C	N	O	S	0	0	1
			1185	756	214	206	9			
1	C	144	Total	C	N	O	S	0	0	1
			1178	752	213	204	9			
1	D	138	Total	C	N	O	S	0	0	1
			1138	728	207	196	7			
1	E	144	Total	C	N	O	S	0	0	0
			1183	755	214	207	7			
1	F	142	Total	C	N	O	S	0	0	1
			1164	744	211	201	8			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



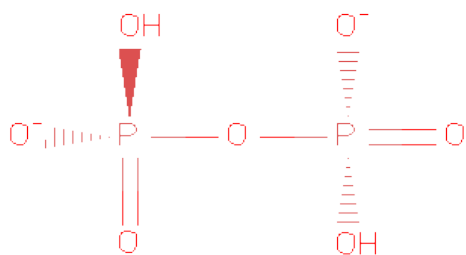
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is O-(O-(2-AMINOPROPYL)-O'-(2-METHOXYETHYL)POLYPROPYLEN EGLYCOL 500) (three-letter code: JEF) (formula: C<sub>30</sub>H<sub>63</sub>NO<sub>10</sub>).



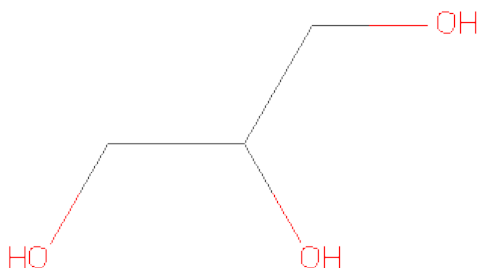
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			22	16	1	5		

- Molecule 4 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: H<sub>2</sub>O<sub>7</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			9	7	2		
4	D	1	Total	O	P	0	0
			9	7	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is water.

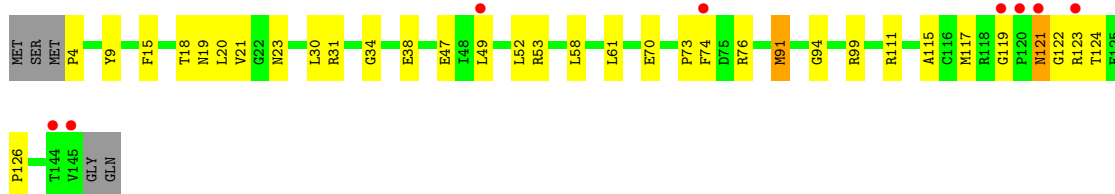
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	106	Total 106	O 106	0	0
6	B	79	Total 79	O 79	0	0
6	C	88	Total 88	O 88	0	0
6	D	85	Total 85	O 85	0	0
6	E	83	Total 83	O 83	0	0
6	F	85	Total 85	O 85	0	0

### 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 errors 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.

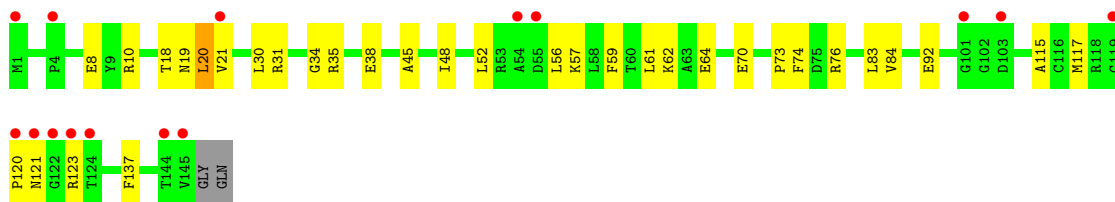
#### • Molecule 1: CALE7

Chain A: 



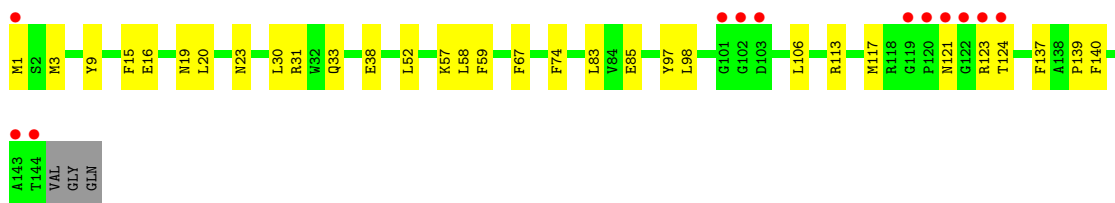
#### • Molecule 1: CALE7

Chain B: 



#### • Molecule 1: CALE7

Chain C: 



#### • Molecule 1: CALE7

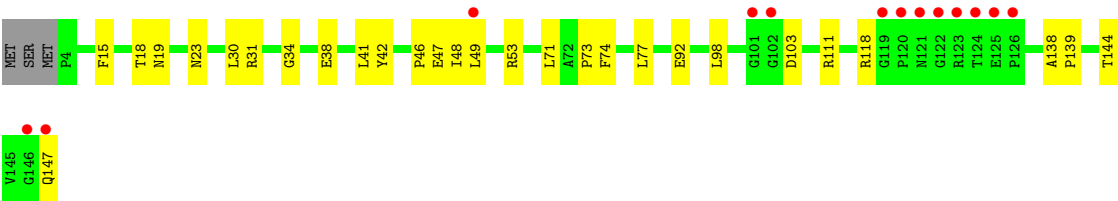
Chain D: 





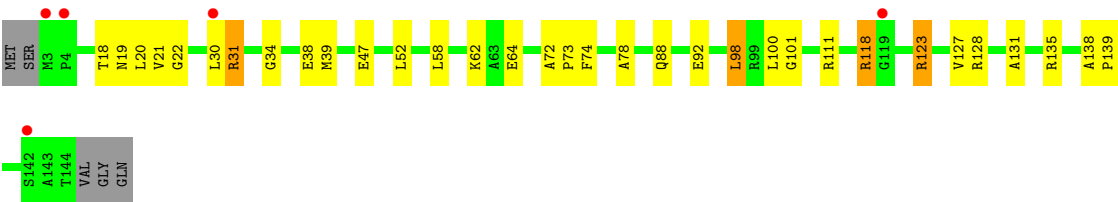
● Molecule 1: CALE7

Chain E: 



● Molecule 1: CALE7

Chain F: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	101.95Å 73.32Å 124.41Å 90.00° 98.69° 90.00°	Depositor
Resolution (Å)	29.68 – 1.75 29.68 – 1.75	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.68-1.75) 99.2 (29.68-1.75)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.50 (at 1.75Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.196 , 0.235 0.192 , 0.228	Depositor DCC
$R_{free}$ test set	4559 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.5	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 54.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 90876 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7599	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.20% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4, JEF, POP

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	0.36	0/1190	0.63	0/1607
1	B	0.34	0/1212	0.62	0/1636
1	C	0.35	0/1205	0.63	0/1626
1	D	0.35	0/1164	0.61	0/1571
1	E	0.31	0/1210	0.58	0/1632
1	F	0.34	0/1191	0.59	0/1608
All	All	0.34	0/7172	0.61	0/9680

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1163	0	1151	29	0
1	B	1185	0	1176	28	0
1	C	1178	0	1169	29	0
1	D	1138	0	1126	32	0
1	E	1183	0	1171	31	0
1	F	1164	0	1152	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	5	0	0	1	1
2	B	5	0	0	1	1
3	A	22	0	32	1	0
4	C	9	0	0	1	0
4	D	9	0	0	0	0
5	C	12	0	16	1	0
6	A	106	0	0	3	0
6	B	79	0	0	3	0
6	C	88	0	0	1	0
6	D	85	0	0	6	0
6	E	83	0	0	3	0
6	F	85	0	0	1	0
All	All	7599	0	6993	164	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (164) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:123:ARG:HH11	1:F:123:ARG:HG3	0.92	1.08
1:A:18:THR:HG21	1:A:73:PRO:HG3	1.39	1.04
1:B:18:THR:HG21	1:B:73:PRO:HG3	1.37	1.02
1:F:123:ARG:NH1	1:F:123:ARG:HG3	1.71	0.97
1:C:1:MET:HG3	1:C:3:MET:H	1.33	0.93
1:E:49:LEU:HD13	6:E:2040:HOH:O	1.69	0.92
1:D:5:ARG:HG2	1:D:6:TYR:H	1.35	0.91
1:E:46:PRO:HA	1:E:49:LEU:CD1	2.03	0.87
1:E:49:LEU:O	1:E:53:ARG:HG3	1.80	0.82
1:A:19:ASN:OD1	1:A:21:VAL:HG22	1.81	0.81
1:A:49:LEU:HG	1:A:53:ARG:HD2	1.63	0.81
1:D:10:ARG:HH11	1:D:10:ARG:HG3	1.46	0.78
1:C:1:MET:SD	1:C:3:MET:HB2	2.26	0.76
1:B:120:PRO:HB2	1:B:123:ARG:HB2	1.67	0.76
1:E:41:LEU:HB3	1:E:49:LEU:CD2	2.16	0.75
1:E:30:LEU:HD13	1:F:30:LEU:HG	1.68	0.74
1:E:41:LEU:HB3	1:E:49:LEU:HD21	1.71	0.72
1:A:30:LEU:HD13	1:B:30:LEU:HD22	1.74	0.70
1:D:5:ARG:HG2	1:D:6:TYR:N	2.05	0.69
1:F:123:ARG:HH11	1:F:123:ARG:CG	1.85	0.68
1:A:4:PRO:HD3	6:A:2001:HOH:O	1.94	0.68
1:E:49:LEU:HD22	6:E:2040:HOH:O	1.93	0.68
1:D:5:ARG:N	1:D:5:ARG:NE	2.43	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:52:LEU:HD21	1:F:58:LEU:HG	1.77	0.67
1:E:31:ARG:HH22	1:F:31:ARG:HH12	1.43	0.66
1:D:5:ARG:N	1:D:5:ARG:HE	1.93	0.66
1:E:92:GLU:OE2	1:E:111:ARG:NH1	2.29	0.65
1:D:61:LEU:HD11	1:D:115:ALA:HB2	1.78	0.65
1:B:56:LEU:O	1:B:57:LYS:HD2	1.98	0.64
1:D:77:LEU:HD12	1:D:98:LEU:O	1.97	0.64
1:E:46:PRO:HA	1:E:49:LEU:HG	1.79	0.64
1:F:19:ASN:OD1	1:F:21:VAL:HG22	1.97	0.64
1:C:30:LEU:HG	1:D:30:LEU:HG	1.80	0.64
1:B:56:LEU:C	1:B:57:LYS:HD2	2.19	0.63
1:B:20:LEU:HD12	1:B:21:VAL:N	2.14	0.63
1:A:18:THR:CG2	1:A:73:PRO:HG3	2.24	0.62
1:A:61:LEU:HD11	1:A:115:ALA:HB2	1.82	0.61
1:F:31:ARG:HD2	6:F:2025:HOH:O	1.99	0.61
1:D:20:LEU:HD21	1:E:18:THR:HG21	1.83	0.61
1:E:46:PRO:HA	1:E:49:LEU:CG	2.31	0.61
1:C:57:LYS:HD2	1:C:124:THR:HG21	1.83	0.61
1:D:101:GLY:O	1:D:102:GLY:C	2.37	0.61
1:C:57:LYS:NZ	1:C:121:ASN:HA	2.15	0.61
1:D:10:ARG:NH1	1:D:10:ARG:HG3	2.13	0.61
1:C:83:LEU:HD22	1:C:137:PHE:HB3	1.83	0.60
1:B:61:LEU:HD11	1:B:115:ALA:HB2	1.84	0.60
1:A:34:GLY:O	1:A:38:GLU:HG2	2.01	0.60
1:C:117:MET:HE1	5:C:1146:GOL:H31	1.84	0.58
1:A:31:ARG:HD3	6:B:2016:HOH:O	2.03	0.58
1:C:98:LEU:HD13	1:C:106:LEU:HA	1.86	0.58
1:E:138:ALA:HB3	1:E:139:PRO:HD3	1.86	0.57
1:A:121:ASN:HD22	1:A:122:GLY:N	2.03	0.56
1:F:92:GLU:OE2	1:F:111:ARG:HD3	2.05	0.56
1:E:46:PRO:HA	1:E:49:LEU:HD11	1.85	0.56
1:E:71:LEU:HD11	1:E:77:LEU:HD13	1.87	0.56
1:E:144:THR:O	1:E:147:GLN:HB2	2.06	0.56
1:C:31:ARG:NH2	6:C:2030:HOH:O	2.38	0.56
1:F:131:ALA:HB1	1:F:135:ARG:HH12	1.72	0.55
1:D:5:ARG:HA	6:D:2001:HOH:O	2.06	0.55
1:F:19:ASN:ND2	1:F:20:LEU:HD23	2.22	0.55
1:A:121:ASN:ND2	1:B:70:GLU:OE1	2.39	0.55
1:B:83:LEU:HD22	1:B:137:PHE:HB3	1.88	0.55
1:F:47:GLU:H	1:F:47:GLU:CD	2.10	0.55
1:A:61:LEU:HD21	3:A:1147:JEF:H141	1.88	0.55
1:C:1:MET:SD	1:C:3:MET:CB	2.93	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:123:ARG:HH11	1:C:123:ARG:HG2	1.72	0.55
1:C:38:GLU:OE1	1:E:15:PHE:HB2	2.07	0.54
1:E:46:PRO:HA	1:E:49:LEU:HD12	1.89	0.54
1:F:72:ALA:HB1	1:F:73:PRO:HD2	1.90	0.53
1:A:49:LEU:CG	1:A:53:ARG:HD2	2.37	0.53
1:E:34:GLY:O	1:E:38:GLU:HG2	2.09	0.53
1:F:118:ARG:HB2	1:F:127:VAL:HG11	1.91	0.53
1:A:20:LEU:HD12	1:A:21:VAL:N	2.23	0.53
1:B:19:ASN:OD1	1:B:21:VAL:HB	2.09	0.52
1:A:30:LEU:CD1	1:B:30:LEU:HD22	2.39	0.52
1:C:57:LYS:HZ1	1:C:121:ASN:N	2.08	0.52
1:C:15:PHE:CZ	1:C:74:PHE:HE1	2.28	0.52
1:D:16:GLU:HB3	6:D:2012:HOH:O	2.10	0.52
1:C:16:GLU:OE2	1:E:31:ARG:NH1	2.43	0.52
1:B:31:ARG:NH2	6:B:2016:HOH:O	2.43	0.51
1:D:16:GLU:OE2	1:F:31:ARG:HD3	2.10	0.51
1:B:8:GLU:OE1	1:B:10:ARG:NH1	2.41	0.51
1:F:62:LYS:HE2	1:F:64:GLU:OE1	2.10	0.51
1:B:84:VAL:HG22	1:B:92:GLU:O	2.11	0.50
1:C:19:ASN:ND2	1:C:23:ASN:OD1	2.43	0.50
1:D:122:GLY:C	1:D:123:ARG:HD2	2.32	0.50
1:A:52:LEU:HD21	1:A:58:LEU:HG	1.93	0.50
1:D:20:LEU:HD11	1:E:73:PRO:HG2	1.94	0.50
1:A:47:GLU:HG2	1:F:101:GLY:HA2	1.93	0.49
1:F:88:GLN:OE1	1:F:128:ARG:NH1	2.46	0.49
1:D:117:MET:CE	1:D:126:PRO:HG3	2.43	0.49
1:A:94:GLY:HA2	1:A:111:ARG:HD3	1.95	0.49
1:C:57:LYS:HZ1	1:C:121:ASN:CA	2.26	0.48
1:C:20:LEU:CD1	1:F:22:GLY:HA2	2.43	0.48
1:B:45:ALA:O	1:B:48:ILE:HG12	2.13	0.48
1:E:73:PRO:O	1:E:74:PHE:HB2	2.12	0.48
1:E:30:LEU:HD13	1:F:30:LEU:CG	2.41	0.48
1:B:76:ARG:HD2	6:B:2040:HOH:O	2.12	0.48
1:B:120:PRO:O	1:B:123:ARG:N	2.33	0.47
1:B:62:LYS:HE2	1:B:64:GLU:OE1	2.13	0.47
1:A:49:LEU:O	1:A:53:ARG:N	2.47	0.47
1:C:33:GLN:HG3	1:C:97:TYR:OH	2.15	0.47
1:A:123:ARG:O	1:A:123:ARG:HG3	2.14	0.47
1:A:20:LEU:C	1:A:20:LEU:HD12	2.35	0.47
1:A:99:ARG:NE	6:A:2079:HOH:O	2.47	0.47
1:D:138:ALA:HB3	1:D:139:PRO:HD3	1.97	0.47
1:B:120:PRO:HD2	1:B:123:ARG:O	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:58:LEU:HD21	6:D:2043:HOH:O	2.13	0.46
1:C:20:LEU:HD13	1:F:22:GLY:HA2	1.97	0.46
1:E:46:PRO:CA	1:E:49:LEU:HG	2.44	0.46
1:F:18:THR:HG21	1:F:73:PRO:HD3	1.98	0.46
1:B:48:ILE:O	1:B:52:LEU:HG	2.16	0.46
6:D:2085:HOH:O	1:F:39:MET:HE2	2.16	0.46
1:D:23:ASN:CG	1:D:70:GLU:OE1	2.54	0.45
1:C:57:LYS:NZ	1:C:121:ASN:CA	2.79	0.45
1:D:99:ARG:O	1:D:104:ASP:HA	2.16	0.45
1:B:35:ARG:HG2	2:B:1146:PO4:O1	2.15	0.45
1:D:98:LEU:HD23	1:D:106:LEU:HA	1.99	0.44
1:F:34:GLY:O	1:F:38:GLU:HG2	2.17	0.44
1:B:18:THR:CG2	1:B:73:PRO:HG3	2.25	0.44
1:B:73:PRO:O	1:B:74:PHE:HB2	2.17	0.44
1:E:41:LEU:C	1:E:49:LEU:HD21	2.38	0.44
1:D:123:ARG:N	1:D:123:ARG:HD2	2.33	0.44
1:E:118:ARG:HD2	6:E:2075:HOH:O	2.18	0.43
1:E:98:LEU:HD12	1:E:98:LEU:N	2.32	0.43
1:E:42:TYR:HA	1:E:49:LEU:HD11	2.00	0.43
1:A:117:MET:HE3	1:A:126:PRO:N	2.34	0.43
1:E:47:GLU:HG2	1:E:48:ILE:N	2.34	0.43
1:A:119:GLY:O	1:A:124:THR:HG22	2.18	0.43
1:C:9:TYR:OH	4:C:1144:POP:O5	2.20	0.43
1:C:67:PHE:N	1:C:67:PHE:CD2	2.87	0.43
1:B:59:PHE:HB2	1:B:117:MET:HE2	2.01	0.43
1:E:18:THR:HG22	1:E:19:ASN:N	2.34	0.43
1:F:73:PRO:O	1:F:74:PHE:HB2	2.18	0.43
1:C:52:LEU:HD21	1:C:58:LEU:HG	2.01	0.43
1:B:59:PHE:HB2	1:B:117:MET:CE	2.49	0.42
1:D:58:LEU:CD2	6:D:2043:HOH:O	2.67	0.42
1:D:72:ALA:HB1	1:D:73:PRO:HD2	1.99	0.42
1:A:76:ARG:HD2	6:A:2064:HOH:O	2.19	0.42
1:D:88:GLN:HG3	6:D:2064:HOH:O	2.18	0.42
1:B:34:GLY:O	1:B:38:GLU:HG2	2.18	0.42
1:C:85:GLU:CD	1:C:113:ARG:HH12	2.22	0.42
1:A:23:ASN:ND2	1:A:70:GLU:OE2	2.52	0.42
1:A:91:MET:HE2	1:A:91:MET:HB2	1.94	0.42
1:C:123:ARG:HG2	1:C:123:ARG:NH1	2.33	0.42
1:F:138:ALA:N	1:F:139:PRO:HD2	2.35	0.42
1:F:78:ALA:HB2	1:F:100:LEU:HD11	2.02	0.41
1:D:119:GLY:O	1:D:124:THR:HG22	2.20	0.41
1:D:116:CYS:C	1:D:117:MET:HG2	2.40	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:98:LEU:N	1:F:98:LEU:HD22	2.35	0.41
1:C:59:PHE:HE2	1:D:70:GLU:HG2	1.85	0.41
1:B:20:LEU:HD12	1:B:21:VAL:HG23	2.03	0.41
1:D:123:ARG:HG2	1:D:123:ARG:HH11	1.86	0.41
1:F:30:LEU:N	1:F:30:LEU:HD22	2.36	0.41
1:A:9:TYR:CE1	2:A:1146:PO4:O1	2.74	0.41
1:D:21:VAL:HG12	1:D:21:VAL:O	2.21	0.41
1:F:19:ASN:HD22	1:F:20:LEU:HD23	1.86	0.41
1:F:131:ALA:HB1	1:F:135:ARG:NH1	2.36	0.40
1:D:18:THR:HA	1:D:23:ASN:O	2.21	0.40
1:A:15:PHE:CE1	1:A:74:PHE:CE1	3.09	0.40
1:E:18:THR:HG23	1:E:23:ASN:O	2.21	0.40
1:B:20:LEU:HD12	1:B:21:VAL:H	1.82	0.40
1:C:139:PRO:HG2	1:C:140:PHE:CD1	2.57	0.40
1:C:57:LYS:HZ2	1:C:121:ASN:HA	1.86	0.40

All (2) 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	Distance(Å)	Clash(Å)
2:A:1146:PO4:O4	2:A:1146:PO4:O4[2_556]	1.85	0.35
2:B:1146:PO4:O2	2:B:1146:PO4:O2[2_556]	1.87	0.33

## 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	140/147 (95%)	137 (98%)	3 (2%)	0	100	100
1	B	143/147 (97%)	136 (95%)	6 (4%)	1 (1%)	30	11
1	C	142/147 (97%)	134 (94%)	8 (6%)	0	100	100
1	D	136/147 (92%)	130 (96%)	4 (3%)	2 (2%)	15	2
1	E	142/147 (97%)	136 (96%)	6 (4%)	0	100	100
1	F	140/147 (95%)	135 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	843/882 (96%)	808 (96%)	32 (4%)	3 (0%)	43	21

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	121	ASN
1	D	102	GLY
1	D	141	ARG

### 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	119/124 (96%)	117 (98%)	2 (2%)	73	52
1	B	122/124 (98%)	121 (99%)	1 (1%)	89	80
1	C	121/124 (98%)	121 (100%)	0	100	100
1	D	116/124 (94%)	113 (97%)	3 (3%)	59	31
1	E	121/124 (98%)	120 (99%)	1 (1%)	89	80
1	F	119/124 (96%)	115 (97%)	4 (3%)	49	21
All	All	718/744 (96%)	707 (98%)	11 (2%)	76	59

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	MET
1	A	121	ASN
1	B	20	LEU
1	D	5	ARG
1	D	117	MET
1	D	123	ARG
1	E	103	ASP
1	F	31	ARG
1	F	98	LEU
1	F	118	ARG
1	F	123	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	121	ASN
1	E	121	ASN
1	F	44	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

7 ligands are modelled in this entry.

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	$\# Z  > 2$
2	PO4	A	1146	-	4,4,4	0.97	0	6,6,6	0.31	0
3	JEF	A	1147	-	20,21,40	0.75	1 (5%)	24,25,48	1.08	2 (8%)
2	PO4	B	1146	-	4,4,4	1.02	0	6,6,6	0.31	0
4	POP	C	1144	-	8,8,8	1.68	1 (12%)	13,13,13	1.66	3 (23%)
5	GOL	C	1145	-	5,5,5	0.19	0	5,5,5	0.27	0
5	GOL	C	1146	-	5,5,5	0.30	0	5,5,5	0.43	0
4	POP	D	1143	-	8,8,8	2.27	3 (37%)	13,13,13	1.89	3 (23%)

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
2	PO4	A	1146	-	-	0/0/0/0	0/0/0/0
3	JEF	A	1147	-	-	0/23/23/46	0/0/0/0
2	PO4	B	1146	-	-	0/0/0/0	0/0/0/0
4	POP	C	1144	-	-	0/6/6/6	0/0/0/0
5	GOL	C	1145	-	-	0/4/4/4	0/0/0/0
5	GOL	C	1146	-	-	0/4/4/4	0/0/0/0
4	POP	D	1143	-	-	0/6/6/6	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1143	POP	P1-O	4.14	1.70	1.60
4	D	1143	POP	P1-O1	2.88	1.59	1.50
3	A	1147	JEF	O2-C5	-2.27	1.44	1.46
4	D	1143	POP	P2-O4	2.08	1.57	1.50
4	C	1144	POP	P2-O4	2.07	1.57	1.50

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1143	POP	P2-O-P1	-4.87	117.09	131.74
4	C	1144	POP	P2-O-P1	-3.96	119.83	131.74
4	D	1143	POP	O3-P1-O	3.22	116.59	106.65
4	C	1144	POP	O3-P1-O	2.88	115.53	106.65
3	A	1147	JEF	C4-O3-C7	-2.70	110.44	115.00
4	C	1144	POP	O-P2-O4	2.33	114.50	107.57
4	D	1143	POP	O-P2-O4	2.23	114.20	107.57
3	A	1147	JEF	O2-C5-C4	2.00	110.32	105.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	142/147 (96%)	0.26	8 (5%) 24 30	20, 31, 60, 102	0
1	B	145/147 (98%)	0.38	15 (10%) 7 10	21, 34, 73, 133	0
1	C	144/147 (97%)	0.41	12 (8%) 11 16	21, 34, 74, 110	0
1	D	138/147 (93%)	0.16	10 (7%) 15 21	24, 33, 75, 99	0
1	E	144/147 (97%)	0.39	13 (9%) 10 12	24, 39, 81, 137	0
1	F	142/147 (96%)	0.08	5 (3%) 42 50	24, 34, 58, 87	0
All	All	855/882 (96%)	0.28	63 (7%) 15 20	20, 34, 75, 137	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	145	VAL	13.0
1	C	144	THR	8.0
1	B	145	VAL	7.2
1	C	119	GLY	6.5
1	B	123	ARG	6.4
1	A	123	ARG	6.3
1	B	120	PRO	6.1
1	B	121	ASN	5.7
1	D	102	GLY	5.1
1	C	123	ARG	4.9
1	A	144	THR	4.9
1	C	122	GLY	4.7
1	B	1	MET	4.7
1	A	120	PRO	4.7
1	D	142	SER	4.7
1	A	49	LEU	4.7
1	E	124	THR	4.6
1	C	120	PRO	4.6
1	E	120	PRO	4.2

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Mol	Chain	Res	Type	RSRZ
1	E	121	ASN	4.2
1	C	1	MET	4.1
1	F	3	MET	4.1
1	E	123	ARG	4.1
1	E	49	LEU	4.0
1	C	102	GLY	4.0
1	D	101	GLY	3.9
1	D	5	ARG	3.9
1	C	121	ASN	3.9
1	D	123	ARG	3.6
1	B	119	GLY	3.4
1	A	121	ASN	3.3
1	B	144	THR	3.1
1	E	125	GLU	3.1
1	E	146	GLY	3.0
1	C	103	ASP	2.9
1	C	143	ALA	2.9
1	E	122	GLY	2.9
1	D	140	PHE	2.9
1	E	102	GLY	2.9
1	D	103	ASP	2.8
1	B	124	THR	2.7
1	C	124	THR	2.7
1	B	54	ALA	2.7
1	B	4	PRO	2.7
1	B	103	ASP	2.6
1	A	119	GLY	2.5
1	E	119	GLY	2.5
1	F	142	SER	2.5
1	D	119	GLY	2.5
1	D	120	PRO	2.4
1	F	119	GLY	2.4
1	A	74	PHE	2.4
1	B	21	VAL	2.3
1	B	55	ASP	2.2
1	D	122	GLY	2.2
1	E	147	GLN	2.2
1	C	101	GLY	2.2
1	B	101	GLY	2.1
1	E	101	GLY	2.1
1	E	126	PRO	2.1
1	B	122	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	30	LEU	2.0
1	F	4	PRO	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	JEF	A	1147	22/41	0.24	5.52	55,69,74,78	0
2	PO4	A	1146	5/5	0.13	3.75	44,49,57,61	0
5	GOL	C	1145	6/6	0.16	3.17	52,57,63,64	0
2	PO4	B	1146	5/5	0.17	2.64	58,63,65,72	0
5	GOL	C	1146	6/6	0.16	1.72	66,68,70,75	0
4	POP	D	1143	9/9	0.12	0.83	51,57,65,67	0
4	POP	C	1144	9/9	0.10	-0.37	44,48,53,55	0

## 6.5 Other polymers

There are no such residues in this entry.