



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:14 PM GMT

PDB ID : 4R7O  
Title : Crystal Structure of Putative Glycerophosphoryl Diester Phosphodiesterase from *Bacillus anthracis*  
Authors : Kim, Y.; Zhou, M.; Shatsman, S.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2014-08-28  
Resolution : 2.53 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

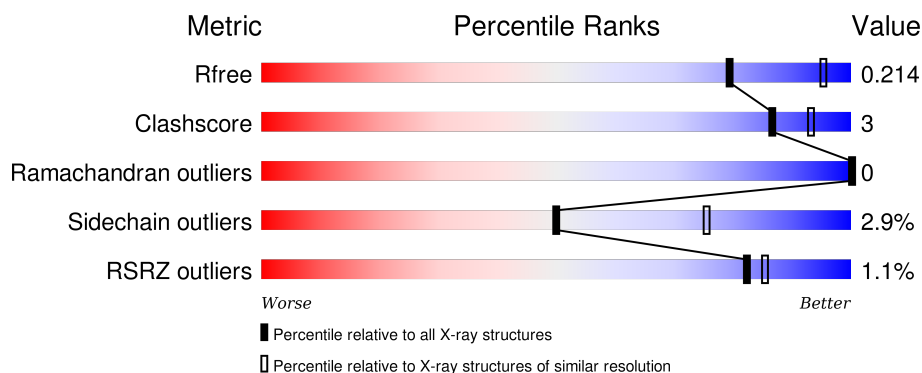
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.53 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))
$R_{free}$	91344	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)

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.

Mol	Chain	Length	Quality of chain
1	A	292	<div> <div>2%</div> <div>88%</div> <div>7%</div> <div>• •</div> </div>
1	B	292	<div> <div>%</div> <div>89%</div> <div>6%</div> <div>• •</div> </div>
1	C	292	<div> <div>85%</div> <div>11%</div> <div>• •</div> </div>
1	D	292	<div> <div>%</div> <div>85%</div> <div>10%</div> <div>• •</div> </div>
1	E	292	<div> <div>%</div> <div>87%</div> <div>7%</div> <div>• 6%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	292	
1	G	292	

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
2	MG	B	401	-	-	-	X
2	MG	E	401	-	-	-	X
4	EDO	A	404	-	-	-	X
5	GOL	E	403	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 16503 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 Glycerophosphoryl diester phosphodiesterase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	279	Total	C	N	O	S	0	0	0
			2260	1437	386	426	11			
1	B	279	Total	C	N	O	S	0	1	0
			2268	1442	387	427	12			
1	C	280	Total	C	N	O	S	0	2	0
			2286	1452	391	432	11			
1	D	279	Total	C	N	O	S	0	2	0
			2280	1449	392	428	11			
1	E	275	Total	C	N	O	S	0	0	0
			2231	1421	381	419	10			
1	F	270	Total	C	N	O	S	0	1	0
			2205	1407	374	414	10			
1	G	272	Total	C	N	O	S	0	0	0
			2213	1412	377	414	10			

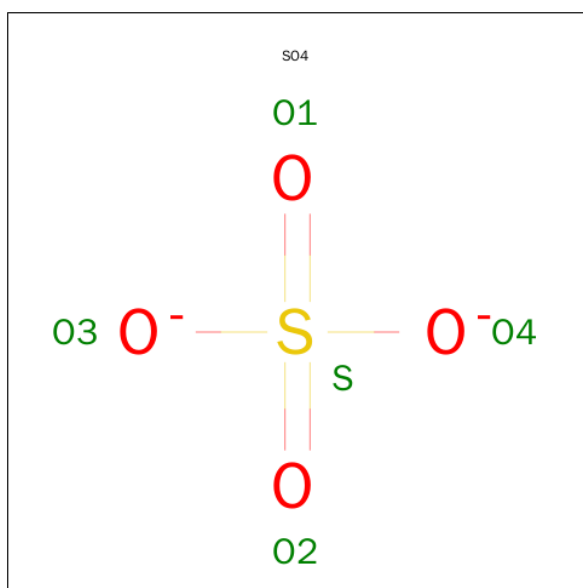
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	SER	-	EXPRESSION TAG	UNP Q81YI6
A	24	ASN	-	EXPRESSION TAG	UNP Q81YI6
B	23	SER	-	EXPRESSION TAG	UNP Q81YI6
B	24	ASN	-	EXPRESSION TAG	UNP Q81YI6
C	23	SER	-	EXPRESSION TAG	UNP Q81YI6
C	24	ASN	-	EXPRESSION TAG	UNP Q81YI6
D	23	SER	-	EXPRESSION TAG	UNP Q81YI6
D	24	ASN	-	EXPRESSION TAG	UNP Q81YI6
E	23	SER	-	EXPRESSION TAG	UNP Q81YI6
E	24	ASN	-	EXPRESSION TAG	UNP Q81YI6
F	23	SER	-	EXPRESSION TAG	UNP Q81YI6
F	24	ASN	-	EXPRESSION TAG	UNP Q81YI6
G	23	SER	-	EXPRESSION TAG	UNP Q81YI6
G	24	ASN	-	EXPRESSION TAG	UNP Q81YI6

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Mg	0	0
			1	1		
2	D	1	Total	Mg	0	0
			1	1		
2	E	2	Total	Mg	0	0
			2	2		
2	B	1	Total	Mg	0	0
			1	1		
2	C	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		
2	F	1	Total	Mg	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		

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



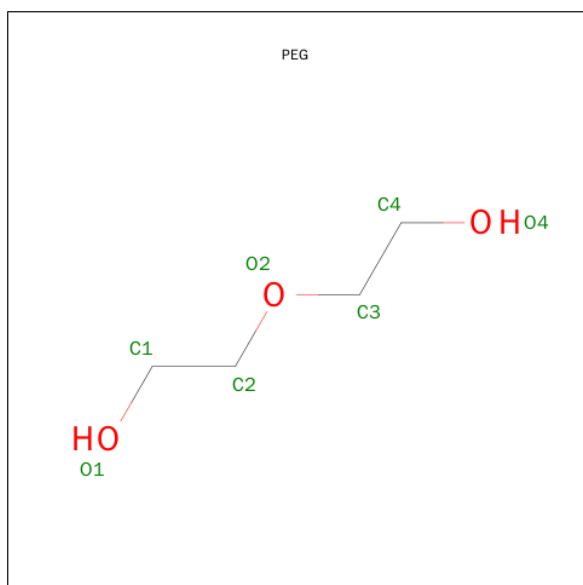
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C O 7 4 3	0	0
6	E	1	Total C O 7 4 3	0	0

- Molecule 7 is water.

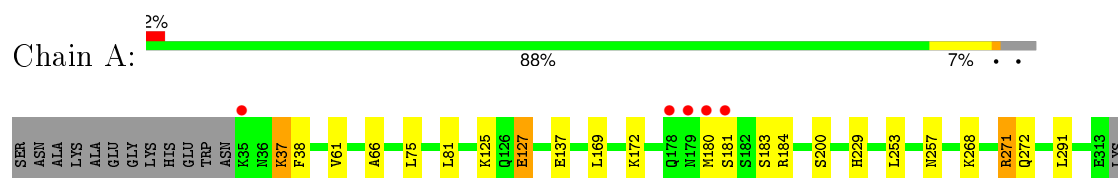
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	108	Total O 108 108	0	0
7	B	102	Total O 102 102	0	0
7	C	124	Total O 124 124	0	0
7	D	92	Total O 92 92	0	0
7	E	116	Total O 116 116	0	0
7	F	85	Total O 85 85	0	0
7	G	23	Total O 23 23	0	0



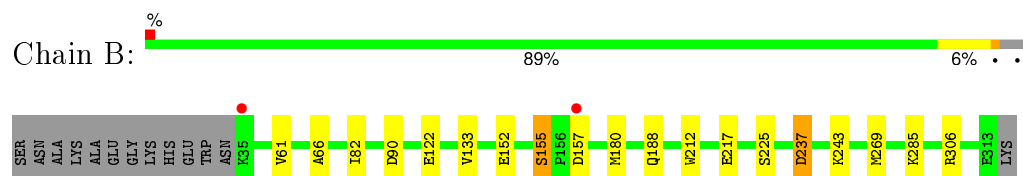
### 3 Residue-property plots [i](#)

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.

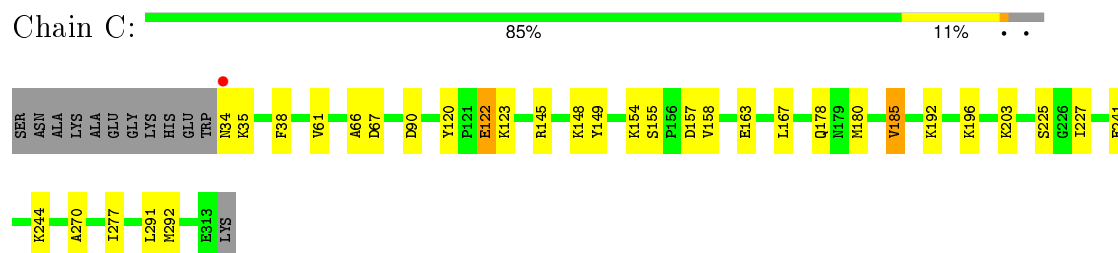
- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



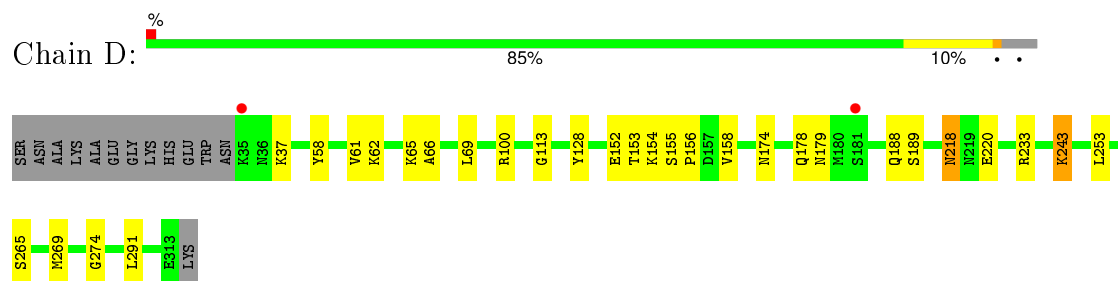
- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



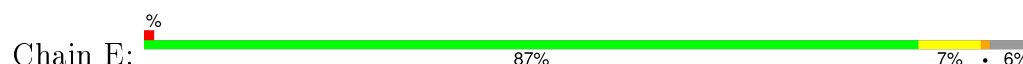
- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative

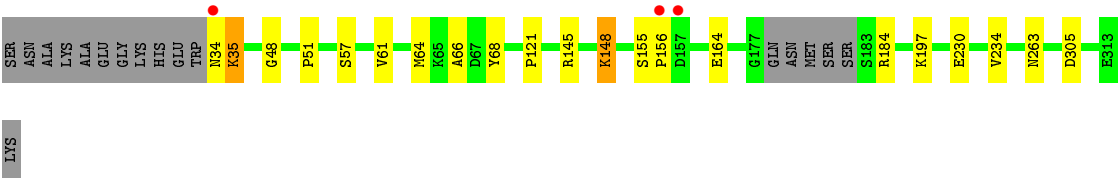


- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative

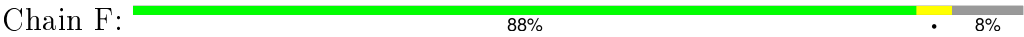


- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative

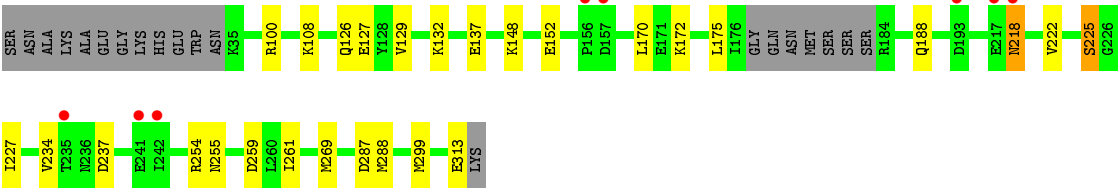
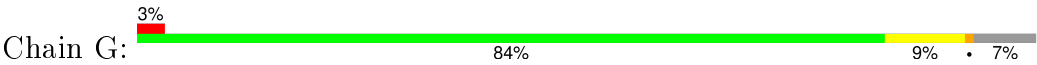




● Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



● Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	209.64Å 85.89Å 191.54Å 90.00° 121.33° 90.00°	Depositor
Resolution (Å)	37.70 – 2.53 49.02 – 2.53	Depositor EDS
% Data completeness (in resolution range)	96.9 (37.70-2.53) 96.5 (49.02-2.53)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.93 (at 2.54Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1745)	Depositor
R, $R_{free}$	0.154 , 0.204 0.166 , 0.214	Depositor DCC
$R_{free}$ test set	2000 reflections (2.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.3	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 42.0	EDS
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 95660 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	16503	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MG, PEG, EDO, SO4

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	0.42	0/2309	0.55	0/3114
1	B	0.42	0/2317	0.56	0/3124
1	C	0.41	0/2335	0.56	0/3148
1	D	0.40	0/2329	0.53	0/3139
1	E	0.41	0/2279	0.53	0/3073
1	F	0.38	0/2253	0.52	0/3040
1	G	0.32	0/2261	0.48	0/3049
All	All	0.39	0/16083	0.53	0/21687

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2260	0	2257	12	0
1	B	2268	0	2265	9	0
1	C	2286	0	2280	15	0
1	D	2280	0	2281	15	0
1	E	2231	0	2229	13	0
1	F	2205	0	2202	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	2213	0	2215	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	2	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
3	A	20	0	0	0	0
3	B	10	0	0	0	0
3	C	10	0	0	0	0
3	D	10	0	0	1	0
3	E	5	0	0	0	0
3	G	5	0	0	1	0
4	A	4	0	6	0	0
5	A	6	0	7	0	0
5	B	6	0	8	0	0
5	D	6	0	8	0	0
5	E	6	0	8	1	0
6	C	7	0	10	0	0
6	E	7	0	10	0	0
7	A	108	0	0	1	0
7	B	102	0	0	1	0
7	C	124	0	0	0	0
7	D	92	0	0	0	0
7	E	116	0	0	1	0
7	F	85	0	0	1	0
7	G	23	0	0	1	0
All	All	16503	0	15786	86	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 3.

All (86) 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:G:288:MET:HG2	1:G:299:MET:HE1	1.60	0.81
1:A:229:HIS:HD2	1:E:121:PRO:HG3	1.53	0.74
1:D:233[A]:ARG:NH2	3:D:404:SO4:O3	2.21	0.73
1:G:137:GLU:OE2	1:G:172:LYS:NZ	2.27	0.68
1:F:230[B]:GLU:OE1	1:F:233:ARG:NH1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:254:ARG:NH1	1:G:287:ASP:OD2	2.30	0.65
1:A:61:VAL:HG13	1:A:66:ALA:HB3	1.79	0.65
1:C:154[B]:LYS:HE2	1:C:158:VAL:HG21	1.79	0.63
1:F:225:SER:HB2	1:F:227:ILE:HG13	1.81	0.61
1:A:271:ARG:HD3	7:A:606:HOH:O	2.00	0.61
1:E:48:GLY:HA2	5:E:403:GOL:H32	1.83	0.61
1:E:61:VAL:HG13	1:E:66:ALA:HB3	1.84	0.60
1:F:61:VAL:HG13	1:F:66:ALA:HB3	1.84	0.59
1:B:237:ASP:N	1:B:237:ASP:OD1	2.36	0.59
1:C:61:VAL:HG13	1:C:66:ALA:HB3	1.86	0.58
1:A:37:LYS:HD3	1:A:38:PHE:H	1.68	0.57
1:A:229:HIS:CD2	1:E:121:PRO:HG3	2.39	0.56
1:F:253:LEU:HD13	1:F:291:LEU:HD21	1.87	0.55
1:B:61:VAL:HG13	1:B:66:ALA:HB3	1.89	0.55
1:D:153:THR:HG22	1:D:189:SER:HB2	1.88	0.54
1:G:234:VAL:HG13	1:G:269:MET:HE2	1.90	0.53
1:F:100:ARG:NH2	1:F:158:VAL:O	2.42	0.52
1:A:75:LEU:HD13	1:A:81:LEU:HD23	1.91	0.52
1:C:225:SER:HB2	1:C:227:ILE:HG13	1.92	0.51
1:D:179:ASN:OD1	1:D:179:ASN:N	2.38	0.51
1:C:122[B]:GLU:HG2	1:C:123:LYS:HG3	1.93	0.50
1:D:58:TYR:CD1	1:D:69:LEU:HD11	2.46	0.50
1:C:38:PHE:CZ	1:C:292:MET:HE1	2.46	0.50
1:D:253:LEU:HD13	1:D:291:LEU:HD21	1.94	0.50
1:D:154[A]:LYS:HG3	1:D:155:SER:N	2.27	0.49
1:E:148:LYS:HG3	1:E:184:ARG:HA	1.95	0.49
1:G:127:GLU:HG3	7:G:523:HOH:O	2.11	0.49
1:D:154[A]:LYS:HE2	1:D:158:VAL:HG11	1.95	0.49
1:B:285:LYS:HE3	1:B:306:ARG:HG2	1.95	0.49
1:G:152:GLU:HB2	1:G:188:GLN:NE2	2.27	0.49
1:G:108:LYS:O	1:G:132:LYS:HE2	2.12	0.48
1:G:255:ASN:HB3	1:G:261:ILE:HD12	1.94	0.48
1:C:67:ASP:O	1:C:148:LYS:HE3	2.13	0.48
1:F:215:PRO:HG3	7:F:576:HOH:O	2.13	0.48
1:D:218:ASN:HB2	1:D:220:GLU:HG2	1.96	0.47
1:C:270:ALA:HB3	1:C:277:ILE:HD11	1.96	0.47
1:D:152:GLU:HA	1:D:188:GLN:HG3	1.96	0.47
1:A:253:LEU:HD13	1:A:291:LEU:HD21	1.96	0.47
1:D:218:ASN:N	1:D:218:ASN:OD1	2.48	0.46
1:A:37:LYS:HD3	1:A:38:PHE:N	2.30	0.46
1:A:125:LYS:HB3	1:A:127:GLU:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:192:LYS:HG2	1:C:196:LYS:HE2	1.99	0.44
1:C:34:ASN:HB3	1:C:35:LYS:H	1.53	0.44
1:G:225:SER:HB2	1:G:227:ILE:HG13	1.98	0.44
1:G:152:GLU:HA	1:G:188:GLN:HG3	1.98	0.44
1:F:111:ASP:OD2	1:F:114:SER:OG	2.22	0.44
1:E:68:TYR:CE2	1:E:148:LYS:HB3	2.52	0.44
1:E:64:MET:HG2	1:E:305:ASP:HB3	1.99	0.44
1:G:126:GLN:O	1:G:129:VAL:HG22	2.17	0.43
1:D:61:VAL:HG21	1:D:69:LEU:HD13	2.00	0.43
1:D:61:VAL:HG13	1:D:66:ALA:HB3	2.00	0.43
1:D:155:SER:HA	1:D:156:PRO:HD3	1.84	0.43
1:E:156:PRO:HB3	1:E:197:LYS:HE3	2.00	0.43
1:G:170:LEU:HD23	1:G:175:LEU:HD12	2.00	0.43
1:G:237:ASP:N	3:G:402:SO4:O4	2.48	0.43
1:G:218:ASN:H	1:G:218:ASN:HD22	1.67	0.43
1:E:51:PRO:O	1:E:57:SER:HB2	2.19	0.42
1:C:241:GLU:OE2	1:C:244:LYS:NZ	2.39	0.42
1:B:122:GLU:H	1:B:122:GLU:CD	2.21	0.42
1:B:212:TRP:NE1	7:B:594:HOH:O	2.36	0.42
1:E:164:GLU:N	1:E:164:GLU:OE1	2.51	0.42
1:C:149:TYR:HB2	1:C:185:VAL:HG22	2.00	0.42
1:A:137:GLU:OE2	1:A:172:LYS:NZ	2.49	0.42
1:E:263:ASN:HB2	7:E:615:HOH:O	2.19	0.42
1:B:155:SER:HB3	1:B:157:ASP:OD1	2.20	0.42
1:G:218:ASN:H	1:G:218:ASN:ND2	2.18	0.41
1:A:169:LEU:HA	1:A:169:LEU:HD12	1.90	0.41
1:D:243:LYS:NZ	1:D:274:GLY:O	2.53	0.41
1:B:217:GLU:CD	1:B:217:GLU:H	2.22	0.41
1:E:68:TYR:CD2	1:E:148:LYS:HB3	2.56	0.41
1:C:120:TYR:HB3	1:C:123:LYS:HD2	2.02	0.41
1:C:163:GLU:O	1:C:167:LEU:HG	2.21	0.41
1:D:113:GLY:HA3	1:D:128:TYR:O	2.21	0.41
1:G:234:VAL:O	1:G:269:MET:HE1	2.20	0.41
1:C:157:ASP:OD1	1:C:158:VAL:N	2.54	0.40
1:G:108:LYS:HD3	1:G:108:LYS:HA	1.94	0.40
1:B:82:ILE:HD12	1:B:133:VAL:HG11	2.03	0.40
1:E:34:ASN:HB3	1:E:35:LYS:H	1.62	0.40
1:B:152:GLU:HB2	1:B:188:GLN:NE2	2.37	0.40
1:A:268:LYS:HE2	1:A:268:LYS:HB2	1.83	0.40
1:C:291:LEU:HD23	1:C:291:LEU:HA	1.84	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	277/292 (95%)	273 (99%)	4 (1%)	0	100	100
1	B	278/292 (95%)	270 (97%)	8 (3%)	0	100	100
1	C	280/292 (96%)	277 (99%)	3 (1%)	0	100	100
1	D	279/292 (96%)	271 (97%)	8 (3%)	0	100	100
1	E	271/292 (93%)	266 (98%)	5 (2%)	0	100	100
1	F	267/292 (91%)	259 (97%)	8 (3%)	0	100	100
1	G	268/292 (92%)	264 (98%)	4 (2%)	0	100	100
All	All	1920/2044 (94%)	1880 (98%)	40 (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	248/258 (96%)	238 (96%)	10 (4%)	38	62
1	B	249/258 (96%)	241 (97%)	8 (3%)	46	72
1	C	251/258 (97%)	242 (96%)	9 (4%)	42	67
1	D	250/258 (97%)	240 (96%)	10 (4%)	38	62
1	E	244/258 (95%)	238 (98%)	6 (2%)	55	80
1	F	241/258 (93%)	239 (99%)	2 (1%)	86	96
1	G	242/258 (94%)	235 (97%)	7 (3%)	50	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1725/1806 (96%)	1673 (97%)	52 (3%)	50 74

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LYS
1	A	127	GLU
1	A	180	MET
1	A	181	SER
1	A	183	SER
1	A	184	ARG
1	A	200	SER
1	A	257	ASN
1	A	271	ARG
1	A	272	GLN
1	B	90	ASP
1	B	155	SER
1	B	180	MET
1	B	225	SER
1	B	237	ASP
1	B	243	LYS
1	B	269[A]	MET
1	B	269[B]	MET
1	C	90	ASP
1	C	122[A]	GLU
1	C	122[B]	GLU
1	C	145	ARG
1	C	155	SER
1	C	178	GLN
1	C	180	MET
1	C	185	VAL
1	C	203	LYS
1	D	37	LYS
1	D	62	LYS
1	D	65	LYS
1	D	100	ARG
1	D	174	ASN
1	D	178	GLN
1	D	218	ASN
1	D	243	LYS
1	D	265	SER
1	D	269	MET

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Mol	Chain	Res	Type
1	E	35	LYS
1	E	145	ARG
1	E	148	LYS
1	E	155	SER
1	E	230	GLU
1	E	234	VAL
1	F	193	ASP
1	F	225	SER
1	G	100	ARG
1	G	148	LYS
1	G	218	ASN
1	G	222	VAL
1	G	225	SER
1	G	259	ASP
1	G	313	GLU

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

Mol	Chain	Res	Type
1	A	36	ASN
1	C	199	HIS
1	C	302	ASN
1	D	36	ASN
1	F	219	ASN
1	G	218	ASN

### 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 27 ligands modelled in this entry, 8 are monoatomic - leaving 19 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	SO4	A	402	-	4,4,4	0.12	0	6,6,6	0.12	0
3	SO4	A	403	-	4,4,4	0.19	0	6,6,6	0.12	0
4	EDO	A	404	-	3,3,3	0.50	0	2,2,2	0.33	0
5	GOL	A	405	2	5,5,5	0.32	0	5,5,5	0.47	0
3	SO4	A	406	-	4,4,4	0.24	0	6,6,6	0.22	0
3	SO4	A	407	-	4,4,4	0.11	0	6,6,6	0.21	0
5	GOL	B	402	-	5,5,5	0.32	0	5,5,5	0.40	0
3	SO4	B	403	-	4,4,4	0.17	0	6,6,6	0.08	0
3	SO4	B	404	-	4,4,4	0.13	0	6,6,6	0.13	0
6	PEG	C	402	-	6,6,6	0.61	0	5,5,5	1.44	0
3	SO4	C	403	-	4,4,4	0.15	0	6,6,6	0.35	0
3	SO4	C	404	-	4,4,4	0.15	0	6,6,6	0.10	0
5	GOL	D	402	-	5,5,5	0.40	0	5,5,5	0.52	0
3	SO4	D	403	-	4,4,4	0.20	0	6,6,6	0.20	0
3	SO4	D	404	-	4,4,4	0.20	0	6,6,6	0.08	0
5	GOL	E	403	-	5,5,5	0.25	0	5,5,5	1.00	0
6	PEG	E	404	-	6,6,6	0.60	0	5,5,5	1.32	0
3	SO4	E	405	-	4,4,4	0.22	0	6,6,6	0.14	0
3	SO4	G	402	-	4,4,4	0.17	0	6,6,6	0.14	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	402	-	-	0/0/0/0	0/0/0/0
3	SO4	A	403	-	-	0/0/0/0	0/0/0/0
4	EDO	A	404	-	-	0/1/1/1	0/0/0/0
5	GOL	A	405	2	-	0/4/4/4	0/0/0/0
3	SO4	A	406	-	-	0/0/0/0	0/0/0/0
3	SO4	A	407	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	B	402	-	-	0/4/4/4	0/0/0/0
3	SO4	B	403	-	-	0/0/0/0	0/0/0/0
3	SO4	B	404	-	-	0/0/0/0	0/0/0/0
6	PEG	C	402	-	-	0/4/4/4	0/0/0/0
3	SO4	C	403	-	-	0/0/0/0	0/0/0/0
3	SO4	C	404	-	-	0/0/0/0	0/0/0/0
5	GOL	D	402	-	-	0/4/4/4	0/0/0/0
3	SO4	D	403	-	-	0/0/0/0	0/0/0/0
3	SO4	D	404	-	-	0/0/0/0	0/0/0/0
5	GOL	E	403	-	-	0/4/4/4	0/0/0/0
6	PEG	E	404	-	-	0/4/4/4	0/0/0/0
3	SO4	E	405	-	-	0/0/0/0	0/0/0/0
3	SO4	G	402	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	404	SO4	1	0
5	E	403	GOL	1	0
3	G	402	SO4	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 ⓘ

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	279/292 (95%)	-0.50	5 (1%) 71 76	18, 32, 61, 127	0
1	B	279/292 (95%)	-0.62	2 (0%) 89 91	18, 33, 62, 105	0
1	C	280/292 (95%)	-0.56	1 (0%) 93 94	19, 32, 57, 94	0
1	D	279/292 (95%)	-0.36	2 (0%) 89 91	19, 36, 75, 129	0
1	E	275/292 (94%)	-0.49	3 (1%) 82 85	19, 32, 59, 105	0
1	F	270/292 (92%)	-0.48	1 (0%) 93 94	22, 36, 61, 98	0
1	G	272/292 (93%)	-0.11	8 (2%) 55 61	34, 65, 94, 149	0
All	All	1934/2044 (94%)	-0.45	22 (1%) 82 85	18, 36, 80, 149	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	157	ASP	4.4
1	A	181	SER	3.7
1	D	35	LYS	3.7
1	A	35	LYS	3.6
1	B	35	LYS	3.4
1	A	180	MET	3.3
1	A	178	GLN	3.1
1	G	217	GLU	2.8
1	G	242	ILE	2.7
1	G	235	THR	2.6
1	G	193	ASP	2.5
1	G	156	PRO	2.5
1	E	157	ASP	2.5
1	B	157	ASP	2.4
1	E	34	ASN	2.4
1	G	218	ASN	2.4
1	F	217	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	156	PRO	2.1
1	A	179	ASN	2.1
1	D	181	SER	2.1
1	G	241	GLU	2.1
1	C	34	ASN	2.0

## 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 carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	GOL	E	403	6/6	0.87	0.29	6.69	45,46,48,49	0
4	EDO	A	404	4/4	0.92	0.17	2.42	57,64,65,66	0
2	MG	B	401	1/1	0.98	0.16	2.32	28,28,28,28	0
2	MG	E	401	1/1	0.95	0.12	2.31	29,29,29,29	0
3	SO4	B	403	5/5	0.93	0.16	1.86	105,108,110,111	0
5	GOL	A	405	6/6	0.97	0.13	1.46	51,53,55,57	0
3	SO4	A	406	5/5	0.98	0.15	1.03	62,70,76,78	0
2	MG	E	402	1/1	0.98	0.12	-0.43	51,51,51,51	0
3	SO4	C	403	5/5	0.99	0.11	-1.27	32,38,44,46	0
3	SO4	D	404	5/5	0.94	0.13	-1.46	90,94,94,96	0
2	MG	A	401	1/1	1.00	0.08	-1.68	18,18,18,18	0
2	MG	F	401	1/1	0.98	0.08	-1.73	36,36,36,36	0
2	MG	C	401	1/1	0.99	0.10	-1.74	28,28,28,28	0
2	MG	D	401	1/1	0.97	0.10	-1.82	34,34,34,34	0
2	MG	G	401	1/1	0.98	0.07	-2.08	44,44,44,44	0
3	SO4	A	403	5/5	0.95	0.20	-	104,107,107,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	GOL	B	402	6/6	0.92	0.14	-	49,50,52,54	0
6	PEG	E	404	7/7	0.90	0.15	-	50,50,63,69	0
5	GOL	D	402	6/6	0.81	0.15	-	44,53,56,57	0
3	SO4	E	405	5/5	0.98	0.18	-	85,86,90,91	0
6	PEG	C	402	7/7	0.91	0.14	-	53,58,63,63	0
3	SO4	A	402	5/5	0.92	0.22	-	93,93,98,101	0
3	SO4	B	404	5/5	0.89	0.21	-	116,119,120,122	0
3	SO4	G	402	5/5	0.80	0.40	-	133,136,137,139	0
3	SO4	D	403	5/5	0.92	0.14	-	93,94,97,99	0
3	SO4	C	404	5/5	0.84	0.18	-	107,107,109,113	0
3	SO4	A	407	5/5	0.89	0.17	-	127,127,128,129	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.