



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2023 – 12:18 PM EDT

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

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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

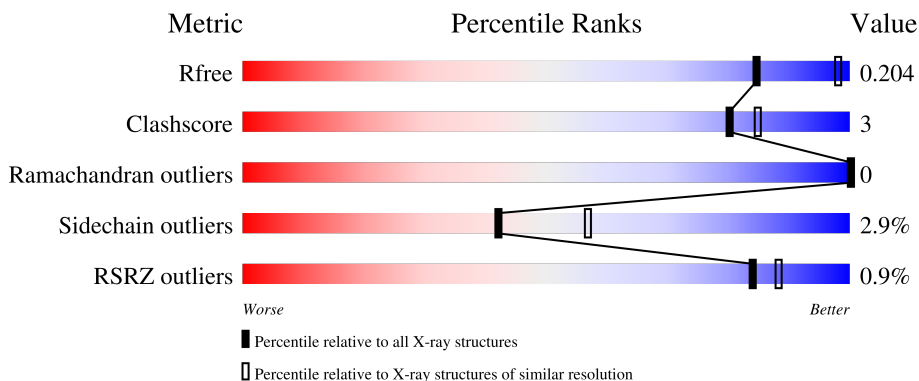
1 Overall quality at a glance i

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}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	292	 88% 7% . .
1	B	292	 89% 6% . .
1	C	292	 85% 11% . .
1	D	292	 85% 10% . .
1	E	292	 87% 7% . 6%

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Mol	Chain	Length	Quality of chain
1	F	292	 88% 8%
1	G	292	 84% 9% 7%

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
3	SO4	G	402	-	-	-	X

2 Entry composition i

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

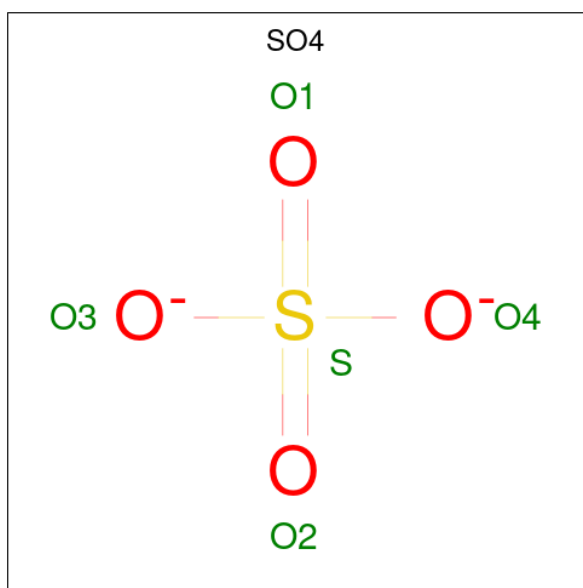
There are 14 discrepancies between the modelled and reference sequences:

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	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	E	2	Total Mg 2 2	0	0
2	F	1	Total Mg 1 1	0	0
2	G	1	Total Mg 1 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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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: C₂H₆O₂).



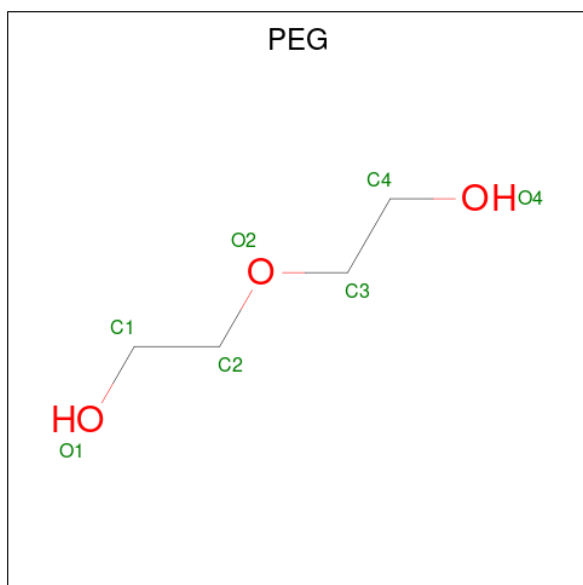
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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	0	0
			7	4	3		
6	E	1	Total	C	O	0	0
			7	4	3		

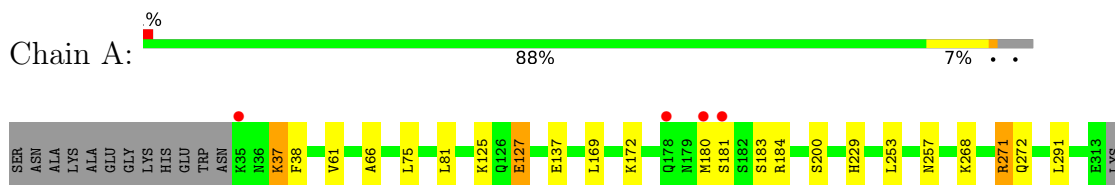
- Molecule 7 is water.

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

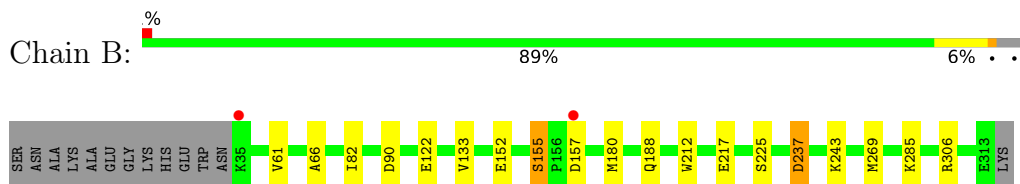
3 Residue-property plots [i](#)

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

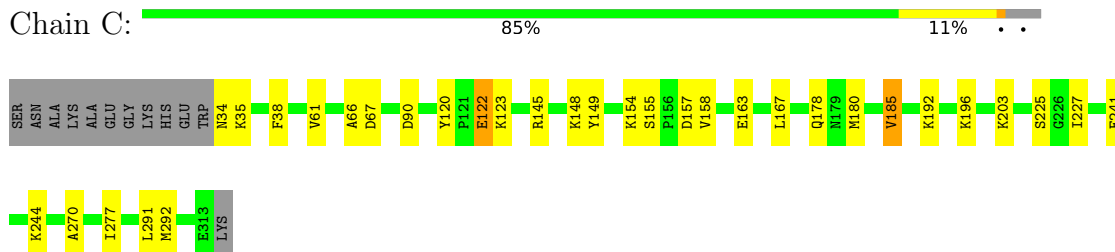
- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



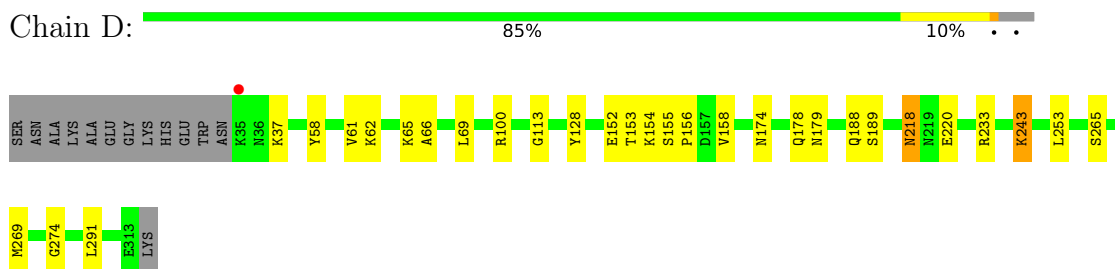
- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



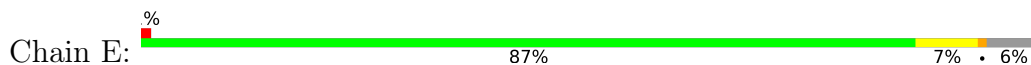
- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative

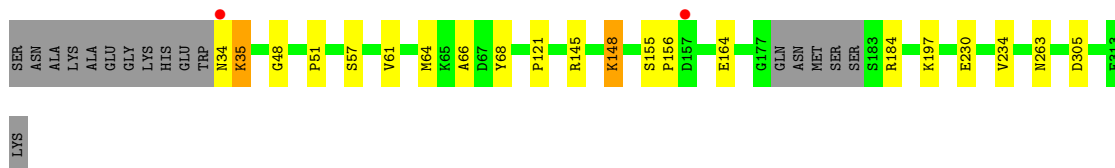


- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative

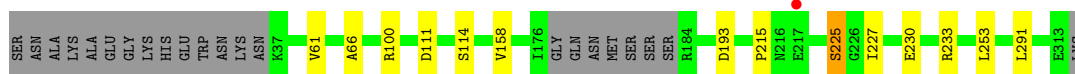
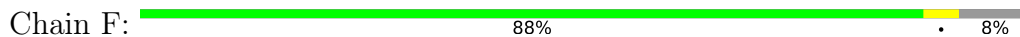


- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative

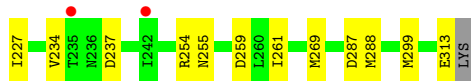
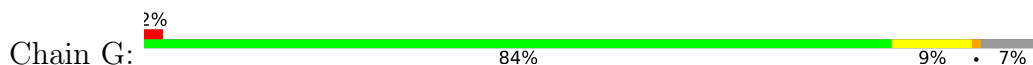




- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



- Molecule 1: Glycerophosphoryl diester phosphodiesterase, putative



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.54Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: dev_1745)	Depositor
R, R_{free}	0.154 , 0.204 0.156 , 0.204	Depositor DCC
R_{free} test set	2000 reflections (2.09%)	wwPDB-VP
Wilson B-factor (Å ²)	33.3	Xtrriage
Anisotropy	0.167	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16503	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage'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.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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:B:237:ASP:OD1	1:B:237:ASP:N	2.36	0.59
1:F:61:VAL:HG13	1:F:66:ALA:HB3	1.84	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:A:75:LEU:HD13	1:A:81:LEU:HD23	1.91	0.52
1:F:100:ARG:NH2	1:F:158:VAL:O	2.42	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:C:67:ASP:O	1:C:148:LYS:HE3	2.13	0.48
1:G:255:ASN:HB3	1:G:261:ILE:HD12	1.94	0.48
1:F:215:PRO:HG3	7:F:576:HOH:O	2.13	0.48
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:D:218:ASN:HB2	1:D:220:GLU:HG2	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:34:ASN:HB3	1:C:35:LYS:H	1.53	0.44
1:C:192:LYS:HG2	1:C:196:LYS:HE2	1.99	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:C:241:GLU:OE2	1:C:244:LYS:NZ	2.39	0.42
1:E:51:PRO:O	1:E:57:SER:HB2	2.19	0.42
1:B:122:GLU:CD	1:B:122:GLU:H	2.21	0.42
1:B:212:TRP:NE1	7:B:594:HOH:O	2.36	0.42
1:E:164:GLU:OE1	1:E:164:GLU:N	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:B:155:SER:HB3	1:B:157:ASP:OD1	2.20	0.42
1:E:263:ASN:HB2	7:E:615:HOH:O	2.19	0.42
1:A:169:LEU:HD12	1:A:169:LEU:HA	1.90	0.41
1:G:218:ASN:H	1:G:218:ASN:ND2	2.18	0.41
1:D:243:LYS:NZ	1:D:274:GLY:O	2.53	0.41
1:B:217:GLU:H	1:B:217:GLU:CD	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:B:82:ILE:HD12	1:B:133:VAL:HG11	2.03	0.40
1:B:152:GLU:HB2	1:B:188:GLN:NE2	2.37	0.40
1:C:157:ASP:OD1	1:C:158:VAL:N	2.54	0.40
1:E:34:ASN:HB3	1:E:35:LYS:H	1.62	0.40
1:G:108:LYS:HD3	1:G:108:LYS:HA	1.94	0.40
1:A:268:LYS:HE2	1:A:268:LYS:HB2	1.83	0.40
1:C:291:LEU:HA	1:C:291:LEU:HD23	1.84	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	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 [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	248/258 (96%)	238 (96%)	10 (4%)	31	43
1	B	249/258 (96%)	241 (97%)	8 (3%)	39	53
1	C	251/258 (97%)	242 (96%)	9 (4%)	35	47
1	D	250/258 (97%)	240 (96%)	10 (4%)	31	43
1	E	244/258 (95%)	238 (98%)	6 (2%)	47	62
1	F	241/258 (93%)	239 (99%)	2 (1%)	81	88
1	G	242/258 (94%)	235 (97%)	7 (3%)	42	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1725/1806 (96%)	1673 (97%)	52 (3%)	42 55

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

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	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 [i](#)

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 monosaccharides 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	406	-	4,4,4	0.13	0	6,6,6	0.21	0
3	SO4	E	405	-	4,4,4	0.16	0	6,6,6	0.08	0
5	GOL	A	405	2	5,5,5	0.33	0	5,5,5	0.49	0
3	SO4	A	407	-	4,4,4	0.15	0	6,6,6	0.14	0
5	GOL	E	403	-	5,5,5	0.27	0	5,5,5	1.04	0
3	SO4	D	404	-	4,4,4	0.16	0	6,6,6	0.12	0
3	SO4	C	404	-	4,4,4	0.14	0	6,6,6	0.14	0
3	SO4	A	402	-	4,4,4	0.16	0	6,6,6	0.12	0
3	SO4	A	403	-	4,4,4	0.18	0	6,6,6	0.12	0
4	EDO	A	404	-	3,3,3	0.49	0	2,2,2	0.24	0
3	SO4	G	402	-	4,4,4	0.17	0	6,6,6	0.17	0
3	SO4	C	403	-	4,4,4	0.14	0	6,6,6	0.38	0
3	SO4	D	403	-	4,4,4	0.13	0	6,6,6	0.21	0
5	GOL	D	402	-	5,5,5	0.44	0	5,5,5	0.52	0
3	SO4	B	403	-	4,4,4	0.14	0	6,6,6	0.13	0
6	PEG	E	404	-	6,6,6	0.60	0	5,5,5	1.42	0
6	PEG	C	402	-	6,6,6	0.62	0	5,5,5	1.54	0
3	SO4	B	404	-	4,4,4	0.15	0	6,6,6	0.16	0
5	GOL	B	402	-	5,5,5	0.36	0	5,5,5	0.45	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
5	GOL	A	405	2	-	2/4/4/4	-
5	GOL	D	402	-	-	2/4/4/4	-
4	EDO	A	404	-	-	0/1/1/1	-
6	PEG	E	404	-	-	3/4/4/4	-
6	PEG	C	402	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	E	403	-	-	2/4/4/4	-
5	GOL	B	402	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	405	GOL	O1-C1-C2-C3
5	B	402	GOL	O1-C1-C2-O2
5	E	403	GOL	O1-C1-C2-C3
6	E	404	PEG	C1-C2-O2-C3
6	C	402	PEG	C1-C2-O2-C3
6	E	404	PEG	O1-C1-C2-O2
5	B	402	GOL	O1-C1-C2-C3
5	D	402	GOL	O1-C1-C2-C3
5	A	405	GOL	O1-C1-C2-O2
5	E	403	GOL	O1-C1-C2-O2
6	E	404	PEG	O2-C3-C4-O4
5	D	402	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	403	GOL	1	0
3	D	404	SO4	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	279/292 (95%)	-0.54	4 (1%) 75 81	18, 32, 61, 127	0
1	B	279/292 (95%)	-0.65	2 (0%) 87 90	18, 33, 62, 105	0
1	C	280/292 (95%)	-0.60	0 100 100	19, 32, 57, 94	0
1	D	279/292 (95%)	-0.40	1 (0%) 92 96	19, 36, 75, 129	0
1	E	275/292 (94%)	-0.53	2 (0%) 87 90	19, 32, 59, 105	0
1	F	270/292 (92%)	-0.51	1 (0%) 92 96	22, 36, 61, 98	0
1	G	272/292 (93%)	-0.16	7 (2%) 56 62	34, 65, 94, 149	0
All	All	1934/2044 (94%)	-0.49	17 (0%) 84 88	18, 36, 80, 149	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	157	ASP	4.2
1	A	181	SER	3.5
1	D	35	LYS	3.5
1	A	35	LYS	3.4
1	B	35	LYS	3.3
1	A	180	MET	3.1
1	A	178	GLN	3.0
1	G	217	GLU	2.7
1	G	242	ILE	2.6
1	G	235	THR	2.4
1	G	193	ASP	2.4
1	G	156	PRO	2.4
1	E	157	ASP	2.3
1	G	218	ASN	2.3
1	E	34	ASN	2.3
1	B	157	ASP	2.3
1	F	217	GLU	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	G	402	5/5	0.80	0.40	133,136,137,139	0
5	GOL	D	402	6/6	0.81	0.15	44,53,56,57	0
3	SO4	C	404	5/5	0.84	0.18	107,107,109,113	0
5	GOL	E	403	6/6	0.87	0.29	45,46,48,49	0
3	SO4	A	407	5/5	0.89	0.17	127,127,128,129	0
3	SO4	B	404	5/5	0.89	0.21	116,119,120,122	0
6	PEG	E	404	7/7	0.90	0.15	50,50,63,69	0
6	PEG	C	402	7/7	0.91	0.14	53,58,63,63	0
3	SO4	D	403	5/5	0.92	0.14	93,94,97,99	0
3	SO4	A	402	5/5	0.92	0.22	93,93,98,101	0
4	EDO	A	404	4/4	0.92	0.17	57,64,65,66	0
5	GOL	B	402	6/6	0.92	0.14	49,50,52,54	0
3	SO4	B	403	5/5	0.93	0.16	105,108,110,111	0
3	SO4	D	404	5/5	0.94	0.14	90,94,94,96	0
3	SO4	A	403	5/5	0.95	0.20	104,107,107,109	0
2	MG	E	401	1/1	0.95	0.12	29,29,29,29	0
2	MG	D	401	1/1	0.97	0.10	34,34,34,34	0
2	MG	F	401	1/1	0.97	0.08	36,36,36,36	0
5	GOL	A	405	6/6	0.97	0.13	51,53,55,57	0
3	SO4	E	405	5/5	0.97	0.18	85,86,90,91	0
3	SO4	A	406	5/5	0.98	0.15	62,70,76,78	0
2	MG	G	401	1/1	0.98	0.07	44,44,44,44	0
2	MG	E	402	1/1	0.98	0.12	51,51,51,51	0
2	MG	B	401	1/1	0.98	0.16	28,28,28,28	0
2	MG	C	401	1/1	0.99	0.10	28,28,28,28	0
3	SO4	C	403	5/5	0.99	0.11	32,38,44,46	0
2	MG	A	401	1/1	1.00	0.08	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.