



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:14 PM UTC

PDB ID : 3GP3 / pdb\_00003gp3  
Title : Crystal structure of phosphoglyceromutase from Burkholderia pseudomallei with 2-phosphoserine  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2009-03-20  
Resolution : 1.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

<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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

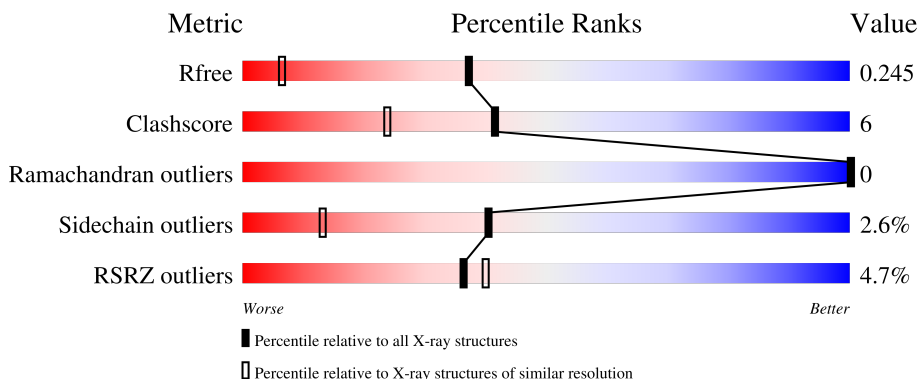
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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))
$R_{free}$	180053	4037 (1.50-1.50)
Clashscore	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)
RSRZ outliers	180081	4039 (1.50-1.50)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	257	 4% 75% 13% • 11%
1	B	257	 4% 78% 9% • 11%
1	C	257	 5% 70% 19% • 11%
1	D	257	 4% 78% 11% 11%

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	PO3	A	251	-	-	X	-
3	PO3	B	251	-	-	X	-
3	PO3	C	252	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8274 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 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	229	Total 1858	C 1188	N 328	O 338	S 4	0	5	0
1	B	229	Total 1850	C 1180	N 329	O 337	S 4	0	4	0
1	C	230	Total 1875	C 1193	N 334	O 344	S 4	0	5	0
1	D	230	Total 1841	C 1173	N 326	O 338	S 4	0	1	0

There are 32 discrepancies between the modelled and reference sequences:

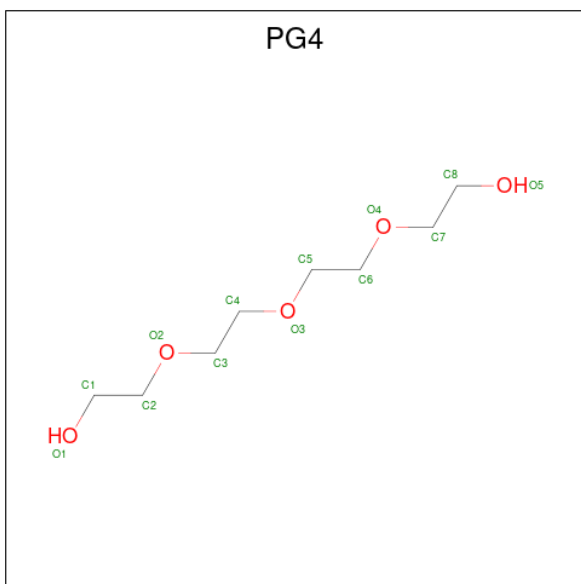
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP Q63XU7
A	-6	ALA	-	expression tag	UNP Q63XU7
A	-5	HIS	-	expression tag	UNP Q63XU7
A	-4	HIS	-	expression tag	UNP Q63XU7
A	-3	HIS	-	expression tag	UNP Q63XU7
A	-2	HIS	-	expression tag	UNP Q63XU7
A	-1	HIS	-	expression tag	UNP Q63XU7
A	0	HIS	-	expression tag	UNP Q63XU7
B	-7	MET	-	expression tag	UNP Q63XU7
B	-6	ALA	-	expression tag	UNP Q63XU7
B	-5	HIS	-	expression tag	UNP Q63XU7
B	-4	HIS	-	expression tag	UNP Q63XU7
B	-3	HIS	-	expression tag	UNP Q63XU7
B	-2	HIS	-	expression tag	UNP Q63XU7
B	-1	HIS	-	expression tag	UNP Q63XU7
B	0	HIS	-	expression tag	UNP Q63XU7
C	-7	MET	-	expression tag	UNP Q63XU7
C	-6	ALA	-	expression tag	UNP Q63XU7
C	-5	HIS	-	expression tag	UNP Q63XU7
C	-4	HIS	-	expression tag	UNP Q63XU7
C	-3	HIS	-	expression tag	UNP Q63XU7

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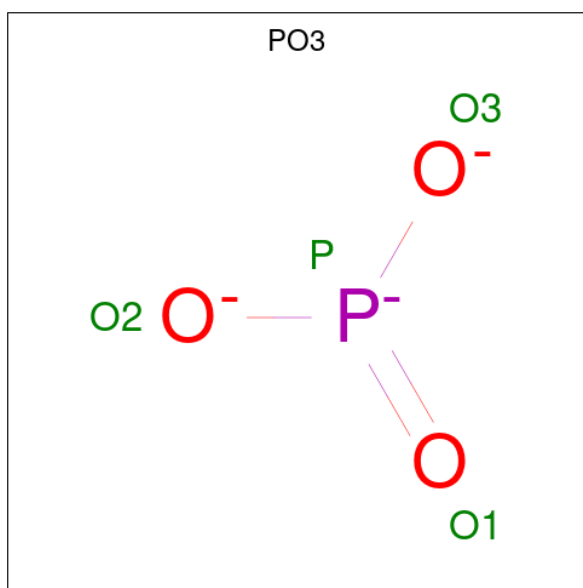
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP Q63XU7
C	-1	HIS	-	expression tag	UNP Q63XU7
C	0	HIS	-	expression tag	UNP Q63XU7
D	-7	MET	-	expression tag	UNP Q63XU7
D	-6	ALA	-	expression tag	UNP Q63XU7
D	-5	HIS	-	expression tag	UNP Q63XU7
D	-4	HIS	-	expression tag	UNP Q63XU7
D	-3	HIS	-	expression tag	UNP Q63XU7
D	-2	HIS	-	expression tag	UNP Q63XU7
D	-1	HIS	-	expression tag	UNP Q63XU7
D	0	HIS	-	expression tag	UNP Q63XU7

- Molecule 2 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula:  $C_8H_{18}O_5$ ).



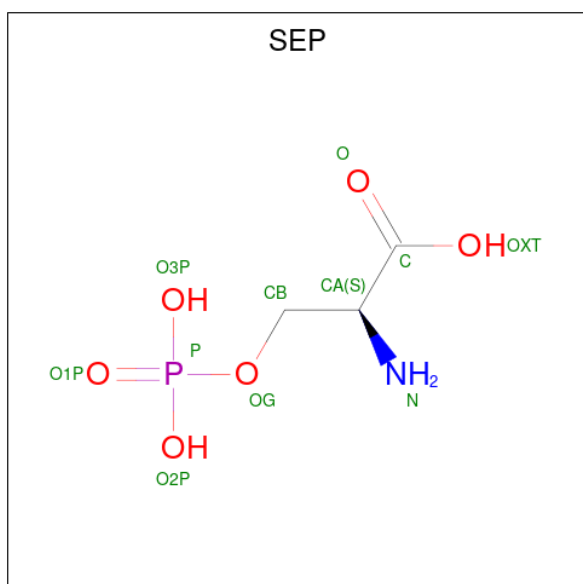
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 13 8 5	0	0
2	B	1	Total C O 13 8 5	0	0
2	C	1	Total C O 13 8 5	0	0
2	C	1	Total C O 13 8 5	0	0
2	D	1	Total C O 13 8 5	0	0
2	D	1	Total C O 13 8 5	0	0

- Molecule 3 is PHOSPHITE ION (CCD ID: PO3) (formula:  $O_3P$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 4 3 1	0	0
3	B	1	Total O P 4 3 1	0	0
3	C	1	Total O P 4 3 1	0	0
3	D	1	Total O P 4 3 1	0	0

- Molecule 4 is PHOSPHOSERINE (CCD ID: SEP) (formula:  $C_3H_8NO_6P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			11	3	1	6	1		
4	B	1	Total	C	N	O	P	0	0
			11	3	1	6	1		
4	C	1	Total	C	N	O	P	0	0
			11	3	1	6	1		
4	D	1	Total	C	N	O	P	0	0
			11	3	1	6	1		

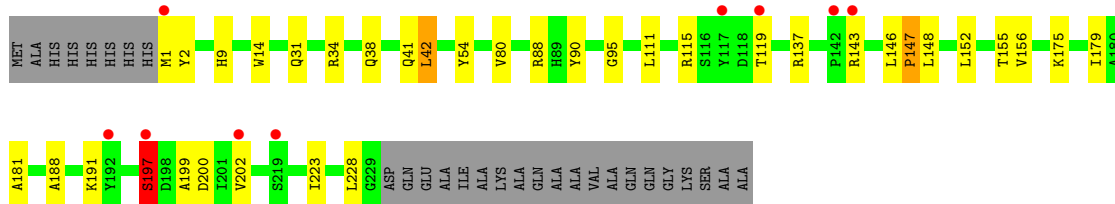
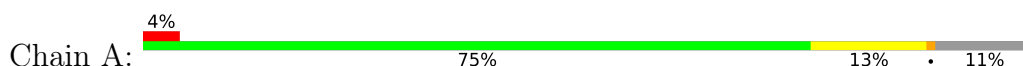
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	192	Total	O	0	0
			192	192		
5	B	174	Total	O	0	0
			174	174		
5	C	171	Total	O	0	0
			171	171		
5	D	175	Total	O	0	0
			175	175		

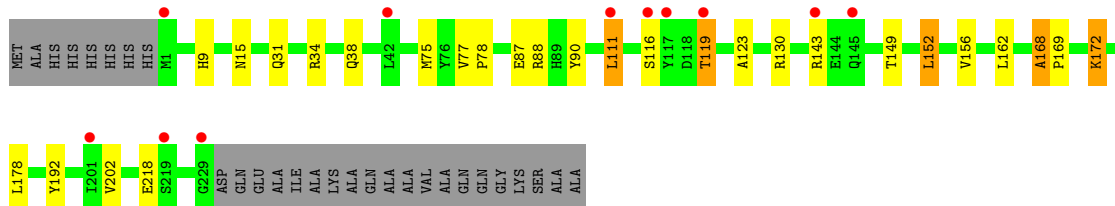
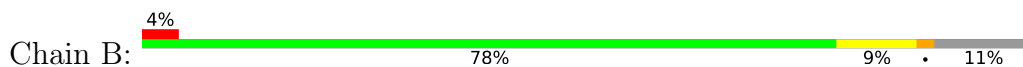
### 3 Residue-property plots [i](#)

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.

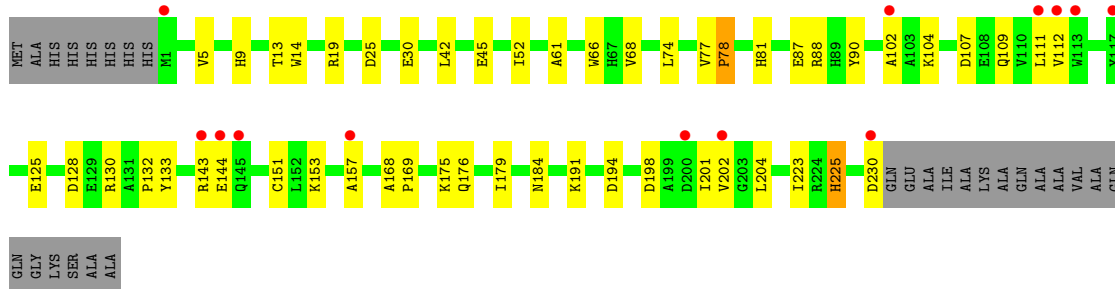
- Molecule 1: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase



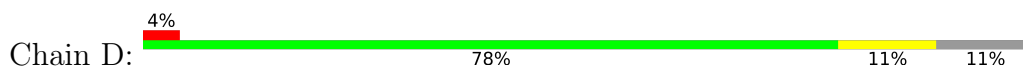
- Molecule 1: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase

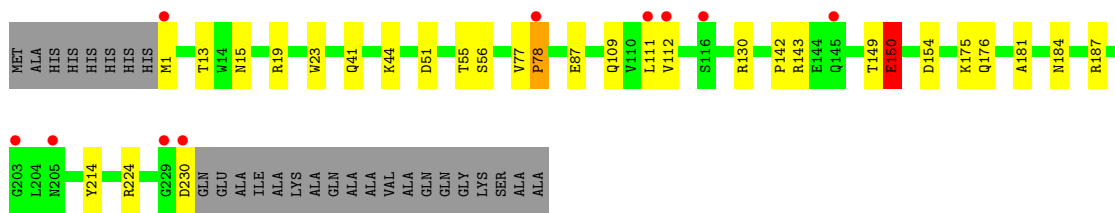


- Molecule 1: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase



- Molecule 1: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.26Å 72.05Å 78.04Å 107.96° 93.00° 104.20°	Depositor
Resolution (Å)	50.00 – 1.50 50.00 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.8 (50.00-1.50) 94.9 (50.00-1.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.11 (at 1.50Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.237 , 0.268 (Not available) , 0.245	Depositor DCC
$R_{free}$ test set	7460 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.6	Xtrriage
Anisotropy	0.039	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 47.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.36$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8274	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 90.11 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6291e-08. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.333 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: SEP, PO3, PG4

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	1.50	10/1904 (0.5%)	1.27	8/2598 (0.3%)
1	B	1.49	7/1896 (0.4%)	1.27	7/2585 (0.3%)
1	C	1.52	16/1921 (0.8%)	1.27	10/2619 (0.4%)
1	D	1.58	11/1887 (0.6%)	1.26	4/2573 (0.2%)
All	All	1.52	44/7608 (0.6%)	1.27	29/10375 (0.3%)

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	150	GLU	CA-CB	8.62	1.72	1.54
1	C	81	HIS	C-O	7.74	1.33	1.24
1	D	56	SER	CA-C	-6.67	1.44	1.53
1	A	179	ILE	CA-CB	-6.64	1.46	1.54
1	C	61	ALA	N-CA	6.55	1.54	1.46

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	223	ILE	N-CA-C	-9.13	103.96	111.81
1	D	150	GLU	N-CA-CB	7.39	125.28	111.53
1	C	68	VAL	N-CA-C	-6.80	104.14	110.53
1	D	15	ASN	N-CA-C	-6.42	104.20	111.07
1	C	77	VAL	CA-C-N	-6.25	113.34	119.78

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	1858	0	1846	27	0
1	B	1850	0	1834	16	0
1	C	1875	0	1854	37	0
1	D	1841	0	1820	16	0
2	A	13	0	18	4	0
2	B	13	0	18	0	0
2	C	26	0	36	4	0
2	D	26	0	36	1	0
3	A	4	0	0	2	0
3	B	4	0	0	2	0
3	C	4	0	0	2	0
3	D	4	0	0	0	0
4	A	11	0	5	0	0
4	B	11	0	5	0	0
4	C	11	0	5	0	0
4	D	11	0	5	0	0
5	A	192	0	0	1	0
5	B	174	0	0	2	0
5	C	171	0	0	20	0
5	D	175	0	0	10	0
All	All	8274	0	7482	96	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 6.

The worst 5 of 96 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:9:HIS:NE2	3:B:251:PO3:P	2.00	1.34
1:A:9:HIS:NE2	3:A:251:PO3:P	2.01	1.33
1:C:9:HIS:NE2	3:C:252:PO3:P	2.00	1.32
1:A:31[B]:GLN:NE2	5:A:602:HOH:O	1.78	1.13
1:D:150:GLU:HA	5:D:691:HOH:O	1.49	1.09

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	232/257 (90%)	226 (97%)	6 (3%)	0	100	100
1	B	231/257 (90%)	225 (97%)	6 (3%)	0	100	100
1	C	233/257 (91%)	230 (99%)	3 (1%)	0	100	100
1	D	229/257 (89%)	223 (97%)	6 (3%)	0	100	100
All	All	925/1028 (90%)	904 (98%)	21 (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	194/211 (92%)	188 (97%)	6 (3%)	35	9
1	B	193/211 (92%)	188 (97%)	5 (3%)	40	13
1	C	196/211 (93%)	189 (96%)	7 (4%)	31	6
1	D	192/211 (91%)	187 (97%)	5 (3%)	40	13
All	All	775/844 (92%)	752 (97%)	23 (3%)	40	9

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	143[A]	ARG
1	C	230	ASP
1	C	153	LYS

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Mol	Chain	Res	Type
1	D	1	MET
1	B	90	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	18	ASN
1	D	41	GLN
1	D	71	GLN
1	B	71	GLN
1	A	205	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

14 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	PG4	C	251	-	12,12,12	0.56	0	11,11,11	0.99	1 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PG4	D	250	-	12,12,12	0.56	0	11,11,11	0.38	0
2	PG4	A	250	-	12,12,12	0.61	0	11,11,11	0.73	0
2	PG4	B	250	-	12,12,12	0.56	0	11,11,11	0.45	0
4	SEP	D	253	-	9,10,10	1.69	3 (33%)	9,14,14	1.65	2 (22%)
4	SEP	A	252	-	9,10,10	1.70	2 (22%)	9,14,14	2.19	2 (22%)
4	SEP	B	252	-	9,10,10	1.73	3 (33%)	9,14,14	3.28	3 (33%)
3	PO3	C	252	-	0,3,3	-	-	0,3,3	-	-
4	SEP	C	253	-	9,10,10	1.43	2 (22%)	9,14,14	1.55	2 (22%)
2	PG4	C	250	-	12,12,12	0.44	0	11,11,11	0.61	0
3	PO3	D	252	-	0,3,3	-	-	0,3,3	-	-
3	PO3	A	251	-	0,3,3	-	-	0,3,3	-	-
3	PO3	B	251	-	0,3,3	-	-	0,3,3	-	-
2	PG4	D	251	-	12,12,12	0.44	0	11,11,11	0.56	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
2	PG4	C	251	-	-	6/10/10/10	-
2	PG4	D	250	-	-	6/10/10/10	-
2	PG4	A	250	-	-	6/10/10/10	-
2	PG4	B	250	-	-	3/10/10/10	-
4	SEP	D	253	-	-	5/10/10/10	-
4	SEP	A	252	-	-	5/10/10/10	-
4	SEP	B	252	-	-	5/10/10/10	-
4	SEP	C	253	-	-	1/10/10/10	-
2	PG4	C	250	-	-	2/10/10/10	-
2	PG4	D	251	-	-	2/10/10/10	-

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	252	SEP	P-O1P	3.91	1.62	1.50
4	D	253	SEP	P-O1P	3.74	1.62	1.50
4	B	252	SEP	OXT-C	-3.19	1.20	1.30
4	C	253	SEP	P-O1P	2.70	1.58	1.50
4	A	252	SEP	P-OG	2.64	1.68	1.60

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	252	SEP	OG-CB-CA	8.16	115.18	108.06
4	A	252	SEP	OG-CB-CA	5.42	112.79	108.06
4	B	252	SEP	OG-P-O1P	3.66	116.32	106.44
4	D	253	SEP	O2P-P-OG	-3.25	98.20	106.67
4	C	253	SEP	O2P-P-OG	-2.89	99.13	106.67

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	252	SEP	N-CA-CB-OG
4	A	252	SEP	C-CA-CB-OG
4	A	252	SEP	CB-OG-P-O2P
4	A	252	SEP	CB-OG-P-O3P
4	B	252	SEP	N-CA-CB-OG

There are no ring outliers.

6 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	251	PG4	4	0
2	D	250	PG4	1	0
2	A	250	PG4	4	0
3	C	252	PO3	2	0
3	A	251	PO3	2	0
3	B	251	PO3	2	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, 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	229/257 (89%)	0.33	9 (3%) 43 47	6, 16, 30, 35	5 (2%)
1	B	229/257 (89%)	0.32	11 (4%) 35 39	5, 16, 29, 34	4 (1%)
1	C	230/257 (89%)	0.31	13 (5%) 29 32	6, 16, 31, 42	5 (2%)
1	D	230/257 (89%)	0.36	10 (4%) 40 44	8, 16, 31, 42	1 (0%)
All	All	918/1028 (89%)	0.33	43 (4%) 36 40	5, 16, 30, 42	15 (1%)

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	219	SER	3.4
1	A	143	ARG	3.4
1	B	143[A]	ARG	3.4
1	B	117	TYR	3.2
1	C	111	LEU	3.0

### 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 oligosaccharides 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, 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PG4	A	250	13/13	0.69	0.18	39,45,54,57	0
2	PG4	D	250	13/13	0.70	0.21	40,45,55,58	0
2	PG4	C	250	13/13	0.71	0.19	38,44,50,54	0
2	PG4	C	251	13/13	0.83	0.17	38,40,46,46	0
2	PG4	B	250	13/13	0.83	0.12	35,40,45,46	0
2	PG4	D	251	13/13	0.88	0.12	28,33,43,47	0
4	SEP	A	252	11/11	0.94	0.09	18,25,28,31	0
4	SEP	C	253	11/11	0.94	0.09	23,26,30,30	0
4	SEP	D	253	11/11	0.95	0.08	20,24,27,28	0
4	SEP	B	252	11/11	0.96	0.08	17,24,28,31	0
3	PO3	B	251	4/4	0.97	0.08	14,16,16,17	0
3	PO3	C	252	4/4	0.98	0.07	16,17,17,17	0
3	PO3	D	252	4/4	0.98	0.07	15,16,16,19	0
3	PO3	A	251	4/4	0.98	0.08	16,16,16,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.