



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 04:56 am BST

PDB ID : 6NPZ
Title : Crystal structure of Akt1 (aa 123-480) kinase with a bisubstrate
Authors : Chu, N.; Cole, P.A.; Gabelli, S.B.
Deposited on : 2019-01-18
Resolution : 2.12 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 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 : 2.11
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) : 2.11

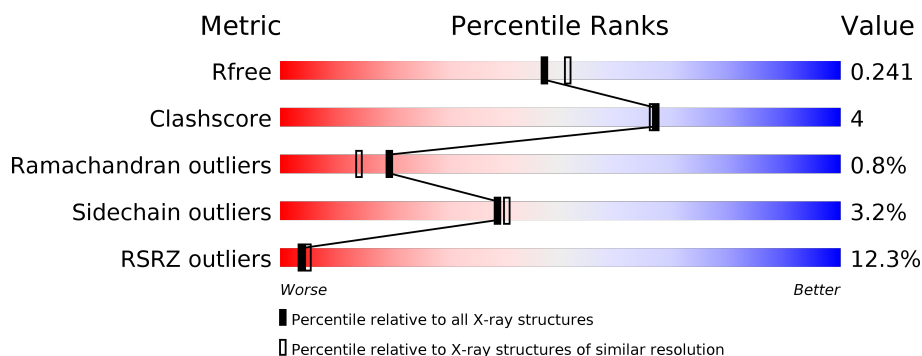
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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 ≥ 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	358	
1	B	358	
2	F	10	
2	G	10	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	B	501	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6057 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 RAC-alpha serine/threonine-protein kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	P	S	0	2	0
			2656	1700	450	488	3	15			
1	B	323	Total	C	N	O	P	S	0	3	0
			2667	1711	450	487	3	16			

- Molecule 2 is a protein called bisubstrate.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	F	10	Total	C	N	O	P	S	0	0	0
			112	59	22	27	3	1			
2	G	10	Total	C	N	O	P	S	0	0	0
			112	59	22	27	3	1			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Mn	0	0
			1	1		
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		
3	F	1	Total	Mn	0	0
			1	1		

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



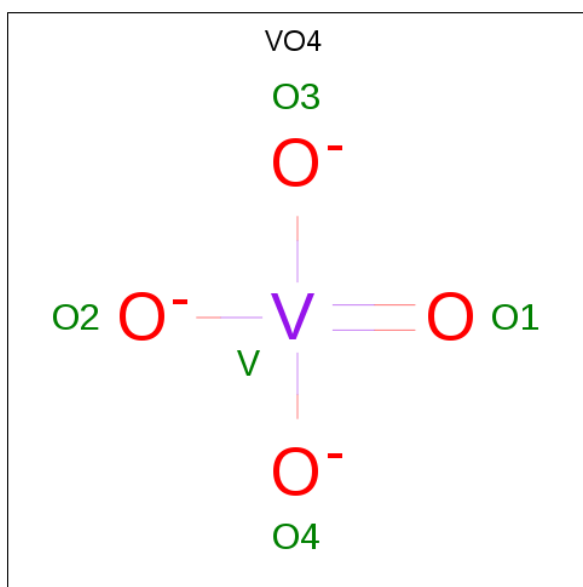
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		

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



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

- Molecule 6 is VANADATE ION (three-letter code: VO4) (formula: O_4V).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	V	0	0
			5	4	1		

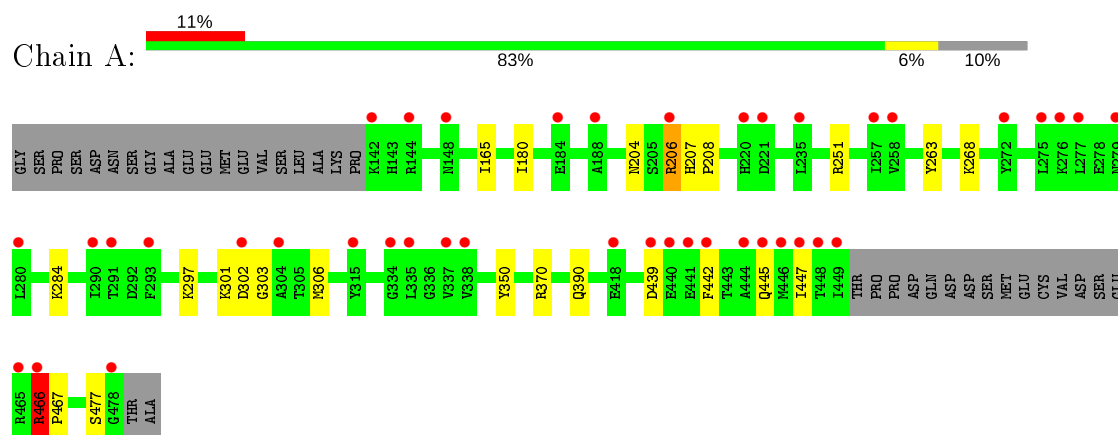
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	216	Total	O	0	0
			216	216		
7	B	226	Total	O	0	0
			226	226		
7	F	15	Total	O	0	0
			15	15		
7	G	18	Total	O	0	0
			18	18		

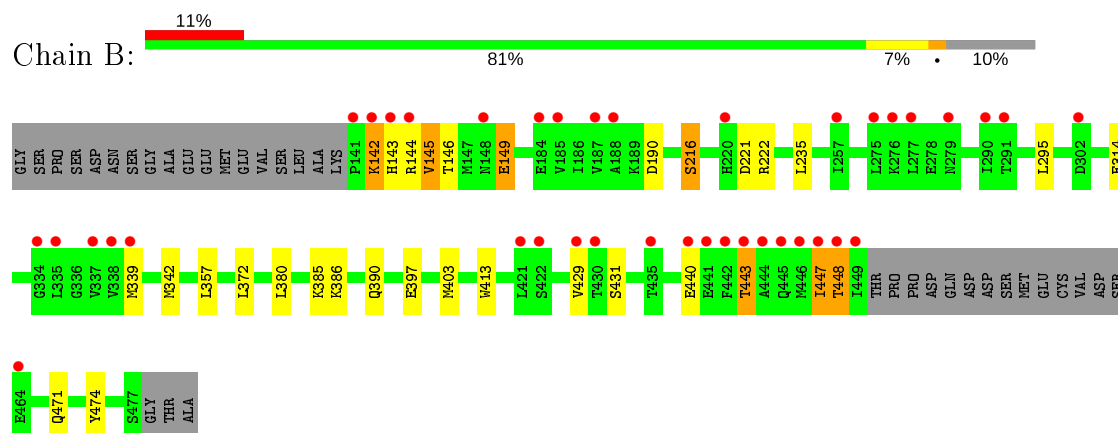
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: RAC-alpha serine/threonine-protein kinase



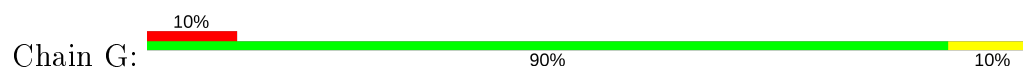
- Molecule 1: RAC-alpha serine/threonine-protein kinase

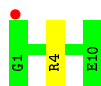


- Molecule 2: bisubstrate



- Molecule 2: bisubstrate





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.32Å 56.09Å 92.02Å 90.00° 104.56° 90.00°	Depositor
Resolution (Å)	29.82 – 2.12 29.82 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.82-2.12) 98.7 (29.82-2.12)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.12Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.241 0.198 , 0.241	Depositor DCC
R_{free} test set	2364 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.171	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6057	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.07 % 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 1.0455e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GOL, PGE, SEP, TPO, MN, VO4, ZXW

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	0.89	0/2688	0.95	0/3609
1	B	0.86	0/2706	0.96	1/3632 (0.0%)
2	F	0.64	0/72	1.18	0/94
2	G	1.00	0/72	1.18	0/94
All	All	0.88	0/5538	0.96	1/7429 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	339	MET	CA-CB-CG	-5.29	104.31	113.30

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	2656	0	2616	20	0
1	B	2667	0	2640	20	0
2	F	112	0	72	1	0
2	G	112	0	72	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1	0	0	0	0
3	G	1	0	0	0	0
4	A	20	0	28	1	0
5	B	6	0	8	4	0
6	B	5	0	0	0	0
7	A	216	0	0	3	0
7	B	226	0	0	4	0
7	F	15	0	0	0	0
7	G	18	0	0	0	0
All	All	6057	0	5436	43	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 4.

All (43) 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:A:442:PHE:HA	1:A:445:GLN:NE2	1.87	0.89
1:A:466:ARG:HB3	1:A:467:PRO:CD	2.10	0.82
1:A:442:PHE:HA	1:A:445:GLN:HE21	1.50	0.75
1:B:440:GLU:HA	1:B:443:THR:HG22	1.72	0.72
1:A:447:ILE:O	1:A:447:ILE:HG22	1.92	0.69
1:A:251[A]:ARG:NH2	7:A:601:HOH:O	2.27	0.66
1:A:466:ARG:HB3	1:A:467:PRO:HD3	1.78	0.65
1:A:206:ARG:NH1	1:A:477:SEP:O2P	2.30	0.63
1:B:385:LYS:HA	5:B:501:GOL:H12	1.80	0.62
1:B:372:LEU:HD21	1:B:380:LEU:HD12	1.84	0.59
1:B:145:VAL:HA	1:B:149:GLU:OE2	2.04	0.57
2:G:4:ARG:HH21	2:G:4:ARG:HG2	1.71	0.56
1:B:146:THR:HB	7:B:735:HOH:O	2.05	0.55
1:A:165:ILE:HD12	1:A:180:ILE:HD12	1.88	0.54
1:B:390:GLN:HG2	7:B:816:HOH:O	2.08	0.53
1:B:314:GLU:HA	1:B:357:LEU:HD21	1.92	0.52
2:G:4:ARG:NH2	2:G:4:ARG:HG2	2.27	0.50
1:B:386:LYS:HB2	5:B:501:GOL:H31	1.92	0.50
1:B:443:THR:HG21	7:B:604:HOH:O	2.11	0.49
1:B:397:GLU:OE2	1:B:397:GLU:HA	2.12	0.49
1:B:142:LYS:O	1:B:142:LYS:CG	2.62	0.48
1:B:386:LYS:H	5:B:501:GOL:C1	2.26	0.48
1:B:386:LYS:H	5:B:501:GOL:H12	1.79	0.48
1:B:144:ARG:HG3	7:B:810:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:TYR:CG	4:A:503:PGE:H5	2.50	0.47
1:B:447:ILE:HA	1:B:448:THR:HB	1.98	0.46
1:B:403:MET:HE2	1:B:413:TRP:CG	2.50	0.46
1:B:216:SER:HB2	1:B:474:TYR:HB3	1.98	0.46
1:A:206:ARG:NE	1:A:477:SEP:O2P	2.49	0.45
1:A:466:ARG:HB3	1:A:467:PRO:HD2	1.93	0.45
1:B:142:LYS:HD2	1:B:142:LYS:HA	1.84	0.44
1:A:442:PHE:HA	1:A:445:GLN:HE22	1.74	0.43
1:A:204:ASN:O	1:A:268:LYS:HD2	2.18	0.43
1:A:390:GLN:HG3	7:A:810:HOH:O	2.19	0.43
1:A:251[B]:ARG:NH2	7:A:608:HOH:O	2.51	0.43
1:A:297:LYS:HG2	1:A:306:MET:HG2	2.01	0.42
1:A:263:TYR:OH	1:A:268:LYS:HE3	2.19	0.42
1:A:447:ILE:O	1:A:447:ILE:CG2	2.63	0.42
2:F:2:ARG:NH1	2:F:5:THR:HG23	2.33	0.42
1:B:142:LYS:O	1:B:143:HIS:HB2	2.19	0.42
1:A:207:HIS:CG	1:A:208:PRO:HD2	2.55	0.42
1:A:301:LYS:O	1:A:303:GLY:N	2.54	0.41
1:B:235:LEU:CD1	1:B:342:MET:HE1	2.51	0.41

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	317/358 (88%)	307 (97%)	8 (2%)	2 (1%)	25	20
1	B	320/358 (89%)	309 (97%)	8 (2%)	3 (1%)	17	12
2	F	7/10 (70%)	7 (100%)	0	0	100	100
2	G	7/10 (70%)	7 (100%)	0	0	100	100
All	All	651/736 (88%)	630 (97%)	16 (2%)	5 (1%)	19	14

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	466	ARG
1	B	447	ILE
1	A	302	ASP
1	B	145	VAL
1	B	448	THR

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	280/310 (90%)	275 (98%)	5 (2%)	59	63
1	B	282/310 (91%)	271 (96%)	11 (4%)	32	32
2	F	7/7 (100%)	5 (71%)	2 (29%)	0	0
2	G	7/7 (100%)	7 (100%)	0	100	100
All	All	576/634 (91%)	558 (97%)	18 (3%)	39	42

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	206	ARG
1	A	284	LYS
1	A	370	ARG
1	A	439	ASP
1	A	466	ARG
1	B	142	LYS
1	B	149	GLU
1	B	190	ASP
1	B	216	SER
1	B	221	ASP
1	B	222	ARG
1	B	295	LEU
1	B	429	VAL
1	B	431	SER
1	B	443	THR

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Mol	Chain	Res	Type
1	B	471	GLN
2	F	6	THR
2	F	10	GLU

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	204	ASN
1	A	445	GLN
1	B	194	HIS
1	B	324	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SEP	A	473	1	8,9,10	0.81	0	8,12,14	1.38	1 (12%)
1	TPO	B	308	1	8,10,11	1.40	1 (12%)	10,14,16	1.05	1 (10%)
1	TPO	A	308	1	8,10,11	1.27	1 (12%)	10,14,16	0.88	1 (10%)
1	SEP	B	477	1	8,9,10	0.99	0	8,12,14	0.95	0
1	SEP	B	473	1	8,9,10	0.84	0	8,12,14	2.01	2 (25%)
1	SEP	A	477	1	8,9,10	0.70	0	8,12,14	0.83	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
1	SEP	A	473	1	-	1/5/8/10	-
1	TPO	B	308	1	-	0/9/11/13	-
1	TPO	A	308	1	-	0/9/11/13	-
1	SEP	B	477	1	-	1/5/8/10	-
1	SEP	B	473	1	-	4/5/8/10	-
1	SEP	A	477	1	-	0/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	308	TPO	P-OG1	3.50	1.65	1.59
1	A	308	TPO	P-OG1	2.87	1.64	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	473	SEP	OG-P-O1P	-3.36	97.06	106.47
1	B	473	SEP	O3P-P-OG	3.29	115.50	106.73
1	B	308	TPO	P-OG1-CB	-2.59	115.38	123.21
1	A	473	SEP	O3P-P-OG	-2.30	100.60	106.73
1	A	308	TPO	P-OG1-CB	-2.05	117.01	123.21

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	473	SEP	CB-OG-P-O3P
1	B	477	SEP	CB-OG-P-O3P
1	B	473	SEP	N-CA-CB-OG
1	B	473	SEP	CB-OG-P-O1P
1	B	473	SEP	CB-OG-P-O2P
1	B	473	SEP	CB-OG-P-O3P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	477	SEP	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z > 2$
4	PGE	A	502	-	9,9,9	0.14	0	8,8,8	0.14	0
4	PGE	A	503	-	9,9,9	0.75	0	8,8,8	0.73	0
6	VO4	B	502	-	1,4,4	2.57	1 (100%)	-		
5	GOL	B	501	-	5,5,5	0.60	0	5,5,5	0.89	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
4	PGE	A	502	-	-	2/7/7/7	-
4	PGE	A	503	-	-	4/7/7/7	-
5	GOL	B	501	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	502	VO4	O1-V	2.57	1.78	1.63

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	501	GOL	O1-C1-C2-C3
5	B	501	GOL	C1-C2-C3-O3
5	B	501	GOL	O1-C1-C2-O2
4	A	503	PGE	O2-C3-C4-O3
4	A	503	PGE	C3-C4-O3-C5
4	A	502	PGE	O1-C1-C2-O2
4	A	503	PGE	C4-C3-O2-C2
4	A	503	PGE	C6-C5-O3-C4
5	B	501	GOL	O2-C2-C3-O3
4	A	502	PGE	O2-C3-C4-O3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	PGE	1	0
5	B	501	GOL	4	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, 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	319/358 (89%)	0.65	41 (12%) 3 4	20, 36, 82, 137	0
1	B	320/358 (89%)	0.60	39 (12%) 4 5	19, 35, 80, 141	0
2	F	9/10 (90%)	0.19	0 100 100	32, 35, 58, 69	0
2	G	9/10 (90%)	0.19	1 (11%) 5 6	35, 36, 61, 62	0
All	All	657/736 (89%)	0.61	81 (12%) 4 5	19, 36, 82, 141	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	449	ILE	10.0
1	A	449	ILE	9.3
1	A	447	ILE	8.3
1	A	444	ALA	8.2
1	A	446	MET	8.0
1	B	446	MET	7.5
1	B	143	HIS	6.6
1	B	141	PRO	6.6
1	B	444	ALA	6.6
1	A	478	GLY	6.5
1	B	448	THR	5.6
1	A	465	ARG	5.3
1	A	441	GLU	4.8
1	A	442	PHE	4.8
1	A	448	THR	4.7
1	A	280	LEU	4.7
1	A	275	LEU	4.5
1	A	440	GLU	4.4
1	A	220	HIS	4.4
1	A	290	ILE	4.3
1	B	440	GLU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	439	ASP	4.1
1	B	441	GLU	4.0
1	A	445	GLN	3.9
1	A	184	GLU	3.8
1	A	338	VAL	3.8
1	B	447	ILE	3.8
1	A	302	ASP	3.8
1	B	445	GLN	3.8
1	A	277	LEU	3.6
1	B	144	ARG	3.5
1	B	187	VAL	3.4
1	A	188	ALA	3.3
1	B	443	THR	3.3
1	B	338	VAL	3.3
1	B	257	ILE	3.2
1	B	275	LEU	3.2
1	A	142	LYS	3.0
1	A	221	ASP	3.0
1	A	337	VAL	3.0
1	B	290	ILE	3.0
1	A	279	ASN	2.9
1	A	315	TYR	2.9
1	B	421	LEU	2.8
1	A	276	LYS	2.8
1	B	302	ASP	2.8
1	B	184	GLU	2.8
1	B	277	LEU	2.7
1	B	276	LYS	2.7
1	A	293	PHE	2.7
1	B	148	ASN	2.7
1	A	335	LEU	2.7
1	B	429	VAL	2.7
1	B	442	PHE	2.7
1	B	188	ALA	2.6
1	A	291	THR	2.6
1	B	291	THR	2.6
1	A	144	ARG	2.6
1	B	335	LEU	2.6
1	B	142	LYS	2.5
1	B	337	VAL	2.4
1	B	422	SER	2.4
2	G	1	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	418	GLU	2.4
1	B	185	VAL	2.4
1	A	257	ILE	2.3
1	B	220	HIS	2.2
1	B	430	THR	2.2
1	A	148	ASN	2.2
1	B	279	ASN	2.2
1	B	435	THR	2.2
1	B	464	GLU	2.2
1	A	206	ARG	2.2
1	A	235	LEU	2.1
1	A	334	GLY	2.1
1	A	304	ALA	2.1
1	A	466	ARG	2.1
1	A	272	TYR	2.1
1	B	334	GLY	2.0
1	B	339	MET	2.0
1	A	258	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	SEP	B	477	10/11	0.74	0.33	56,83,103,107	0
1	SEP	A	477	10/11	0.82	0.34	55,91,102,103	0
1	SEP	B	473	10/11	0.85	0.13	38,49,69,91	0
1	SEP	A	473	10/11	0.92	0.12	35,46,74,79	0
1	TPO	A	308	11/12	0.95	0.09	28,32,40,47	0
1	TPO	B	308	11/12	0.98	0.07	27,31,37,47	0

6.3 Carbohydrates ⓘ

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. 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
4	PGE	A	503	10/10	0.59	0.39	48,69,76,87	0
5	GOL	B	501	6/6	0.64	0.30	39,52,63,68	0
4	PGE	A	502	10/10	0.64	0.25	68,84,93,100	0
3	MN	G	501	1/1	0.89	0.10	86,86,86,86	0
6	VO4	B	502	5/5	0.91	0.56	20,20,20,20	0
3	MN	A	501	1/1	0.94	0.07	48,48,48,48	0
3	MN	B	503	1/1	0.95	0.09	76,76,76,76	0
3	MN	F	101	1/1	0.96	0.05	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.