



Full wwPDB X-ray Structure Validation Report ⓘ

May 4, 2016 – 10:59 AM EDT

PDB ID : 5J1W
Title : Crystal structure of human CLK1 in complex with pyrido[3,4-g]quinazoline derivative ZW31 (compound 14)
Authors : Chaikuad, A.; Esvan, Y.J.; Zeinyeh, W.; Boibessot, T.; Nauton, L.; Thery, V.; Loaec, N.; Meijer, L.; Giraud, F.; Moreau, P.; Anizon, F.; von Delft, F.; Bountra, C.; Arrowsmith, C.H.; Edwards, A.M.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on : 2016-03-29
Resolution : 2.42 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
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027457
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) : rb-20027457

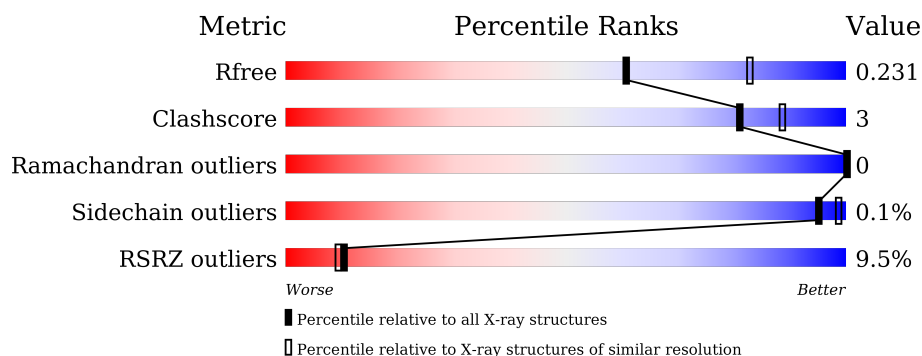
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 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	3386 (2.44-2.40)
Clashscore	102246	3897 (2.44-2.40)
Ramachandran outliers	100387	3837 (2.44-2.40)
Sidechain outliers	100360	3838 (2.44-2.40)
RSRZ outliers	91569	3396 (2.44-2.40)

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. 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	339	<div> <div>6%</div> <div> <div></div> <div>93%</div> <div>6%</div> </div> </div>
1	B	339	<div> <div>10%</div> <div> <div></div> <div>93%</div> <div>7%</div> </div> </div>
1	C	339	<div> <div>12%</div> <div> <div></div> <div>84%</div> <div>9%</div> <div>7%</div> </div> </div>

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	GOL	A	501	-	-	-	X
2	GOL	A	504	-	-	X	-
2	GOL	C	502	-	-	-	X
4	PO4	B	502	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8253 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.

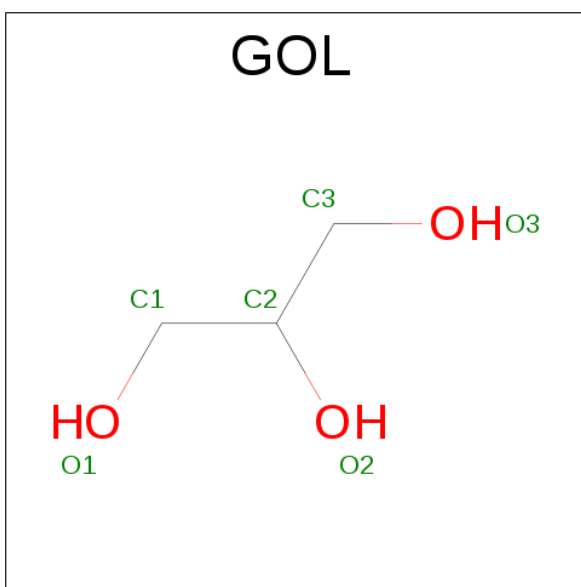
- Molecule 1 is a protein called Dual specificity protein kinase CLK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	1	0
			2752	1758	477	500	17			
1	B	337	Total	C	N	O	S	0	1	0
			2741	1752	473	499	17			
1	C	316	Total	C	N	O	S	0	0	0
			2522	1614	428	463	17			

There are 9 discrepancies between the modelled and reference sequences:

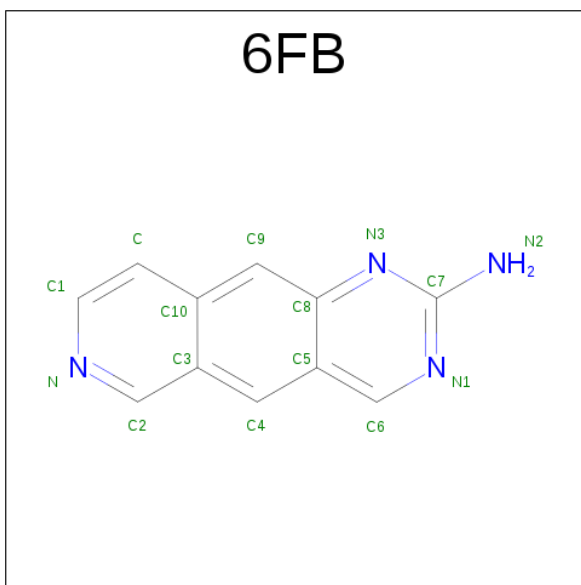
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP P49759
A	0	MET	-	expression tag	UNP P49759
A	432	ALA	ARG	conflict	UNP P49759
B	-1	SER	-	expression tag	UNP P49759
B	0	MET	-	expression tag	UNP P49759
B	432	ALA	ARG	conflict	UNP P49759
C	-1	SER	-	expression tag	UNP P49759
C	0	MET	-	expression tag	UNP P49759
C	432	ALA	ARG	conflict	UNP P49759

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



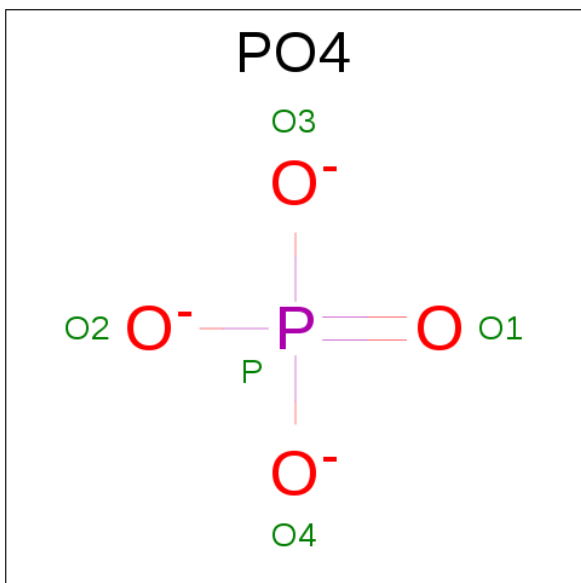
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total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

- Molecule 3 is pyrido[3,4-g]quinazolin-2-amine (three-letter code: 6FB) (formula: C₁₁H₈N₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			15	11	4		
3	B	1	Total	C	N	0	0
			15	11	4		
3	C	1	Total	C	N	0	0
			15	11	4		
3	C	1	Total	C	N	0	0
			15	11	4		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

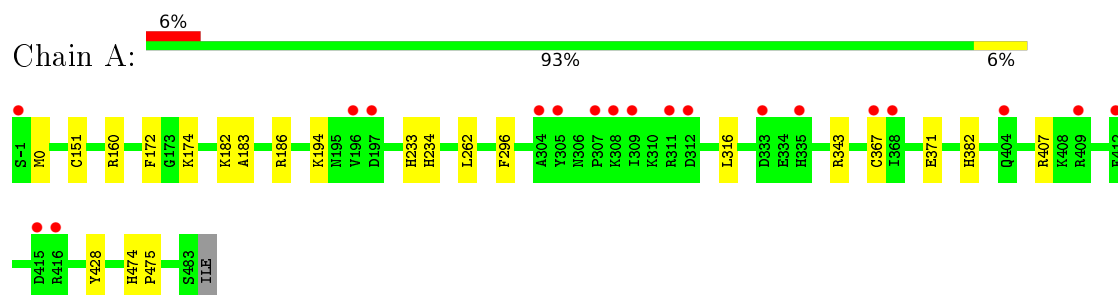
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	46	Total	O	0	0
			46	46		
5	B	32	Total	O	0	0
			32	32		
5	C	36	Total	O	0	0
			36	36		

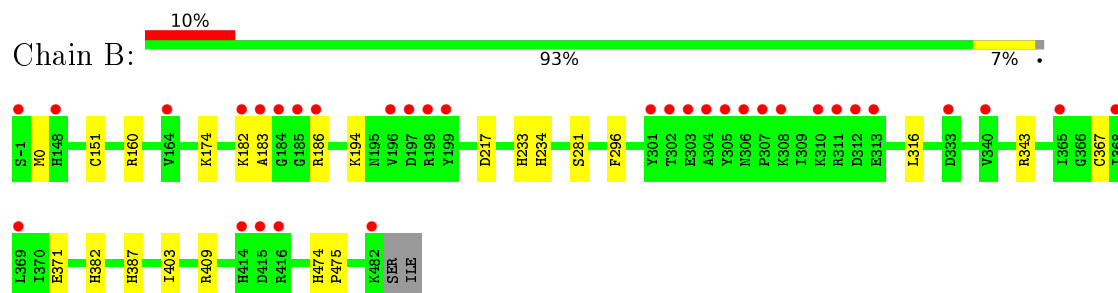
3 Residue-property plots [i](#)

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.

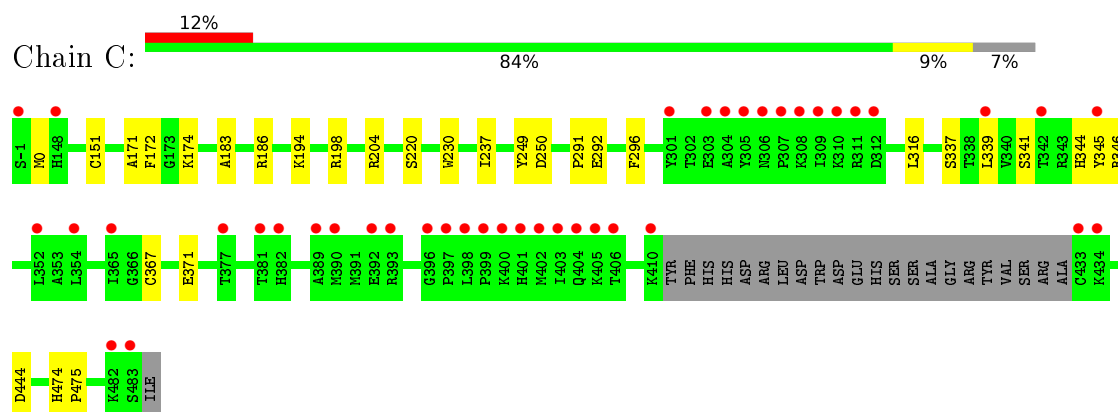
- Molecule 1: Dual specificity protein kinase CLK1



- Molecule 1: Dual specificity protein kinase CLK1



- Molecule 1: Dual specificity protein kinase CLK1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.63 Å 118.04 Å 90.50 Å 90.00° 99.55° 90.00°	Depositor
Resolution (Å)	35.59 – 2.42 35.36 – 2.42	Depositor EDS
% Data completeness (in resolution range)	99.8 (35.59-2.42) 99.8 (35.36-2.42)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.42 Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.189 , 0.228 0.197 , 0.231	Depositor DCC
R_{free} test set	2159 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	50.4	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8253	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.79% 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, 0.375 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, PO4, 6FB

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	0.70	1/2826 (0.0%)	0.66	0/3824
1	B	0.64	0/2815	0.64	0/3810
1	C	0.70	1/2584 (0.0%)	0.66	0/3504
All	All	0.68	2/8225 (0.0%)	0.65	0/11138

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	292	GLU	CG-CD	5.34	1.59	1.51
1	A	428	TYR	CB-CG	5.12	1.59	1.51

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	2752	0	2682	15	0
1	B	2741	0	2669	14	0
1	C	2522	0	2435	22	0
2	A	30	0	40	5	0
2	B	6	0	8	0	0
2	C	18	0	24	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	15	0	0	3	0
3	B	15	0	0	0	0
3	C	30	0	0	1	0
4	B	5	0	0	2	0
4	C	5	0	0	0	0
5	A	46	0	0	1	0
5	B	32	0	0	0	0
5	C	36	0	0	2	0
All	All	8253	0	7858	52	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 (52) 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:151:CYS:SG	1:B:174:LYS:NZ	2.40	0.95
1:A:151:CYS:SG	1:A:174:LYS:NZ	2.41	0.93
1:C:151:CYS:SG	1:C:174:LYS:NZ	2.43	0.91
1:C:444:ASP:OD1	5:C:602:HOH:O	2.15	0.64
2:A:504:GOL:O3	2:A:504:GOL:O1	2.16	0.64
1:B:403:ILE:O	1:B:409:ARG:NH1	2.35	0.60
1:B:296:PHE:CZ	1:B:316:LEU:HD11	2.38	0.59
1:B:281:SER:O	1:C:230:TRP:HZ2	1.85	0.59
2:A:504:GOL:H32	3:A:506:6FB:N3	2.17	0.58
1:A:296:PHE:CZ	1:A:316:LEU:HD11	2.41	0.56
1:A:343:ARG:NH2	5:A:602:HOH:O	2.40	0.55
1:B:343:ARG:NE	1:B:382:HIS:HA	2.23	0.54
1:C:296:PHE:CZ	1:C:316:LEU:HD11	2.43	0.53
1:A:367:CYS:O	1:A:371:GLU:HG3	2.10	0.51
1:B:367:CYS:O	1:B:371:GLU:HG3	2.10	0.51
1:C:250:ASP:OD2	2:C:503:GOL:O1	2.18	0.51
1:A:343:ARG:NE	1:A:382:HIS:HA	2.26	0.50
1:B:0:MET:HE3	1:B:194:LYS:HG3	1.95	0.48
1:C:367:CYS:O	1:C:371:GLU:HG3	2.13	0.48
1:C:183:ALA:HB1	1:C:186:ARG:HD2	1.96	0.48
1:C:237:ILE:HG13	3:C:506:6FB:C2	2.43	0.48
1:C:337:SER:C	1:C:339:LEU:H	2.16	0.48
1:C:341:SER:O	1:C:346:ARG:NH2	2.47	0.48
4:B:502:PO4:O4	1:C:204:ARG:NH1	2.36	0.47
2:A:504:GOL:C3	3:A:506:6FB:N3	2.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:ASP:OD1	4:B:502:PO4:O3	2.33	0.47
1:B:183:ALA:HB1	1:B:186:ARG:HD2	1.98	0.46
1:A:474:HIS:CG	1:A:475:PRO:HD2	2.51	0.46
1:C:474:HIS:CG	1:C:475:PRO:HD2	2.51	0.46
1:A:183:ALA:HB1	1:A:186:ARG:HD2	1.99	0.45
1:B:233:HIS:O	1:B:234:HIS:C	2.55	0.45
1:A:172:PHE:CD1	1:A:172:PHE:C	2.91	0.44
1:C:220:SER:HA	5:C:609:HOH:O	2.15	0.44
1:B:281:SER:O	1:C:230:TRP:CZ2	2.68	0.44
2:A:504:GOL:O2	3:A:506:6FB:N2	2.52	0.43
1:A:262:LEU:H	2:A:501:GOL:H11	1.84	0.43
1:B:160:ARG:HD2	1:B:182:LYS:HG3	2.02	0.42
1:B:151:CYS:SG	1:B:174:LYS:HD3	2.59	0.42
1:A:151:CYS:SG	1:A:174:LYS:HD3	2.60	0.42
1:C:0:MET:HE3	1:C:194:LYS:HG3	2.01	0.42
1:A:160:ARG:HD2	1:A:182:LYS:HG3	2.02	0.42
1:C:172:PHE:C	1:C:172:PHE:CD1	2.93	0.41
1:C:344:HIS:HB2	1:C:345:TYR:CE1	2.55	0.41
1:A:0:MET:HB2	1:A:0:MET:HE3	1.98	0.41
1:C:0:MET:HE3	1:C:0:MET:HB2	1.99	0.41
1:C:151:CYS:SG	1:C:174:LYS:HD3	2.61	0.41
1:A:233:HIS:O	1:A:234:HIS:C	2.58	0.41
1:B:474:HIS:CG	1:B:475:PRO:HD2	2.55	0.41
1:C:171:ALA:O	1:C:194:LYS:NZ	2.39	0.41
1:A:407:ARG:HA	1:C:198:ARG:HD3	2.03	0.41
1:A:0:MET:HE3	1:A:194:LYS:HG3	2.03	0.40
1:C:249:TYR:HB2	1:C:291:PRO:HB2	2.03	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	337/339 (99%)	322 (96%)	15 (4%)	0	100	100
1	B	336/339 (99%)	321 (96%)	15 (4%)	0	100	100
1	C	312/339 (92%)	298 (96%)	14 (4%)	0	100	100
All	All	985/1017 (97%)	941 (96%)	44 (4%)	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	301/308 (98%)	301 (100%)	0	100	100
1	B	300/308 (97%)	299 (100%)	1 (0%)	94	98
1	C	274/308 (89%)	274 (100%)	0	100	100
All	All	875/924 (95%)	874 (100%)	1 (0%)	95	99

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	387	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

15 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	GOL	A	501	-	5,5,5	0.38	0	5,5,5	0.79	0
2	GOL	A	502	-	5,5,5	0.75	0	5,5,5	0.96	0
2	GOL	A	503	-	5,5,5	0.56	0	5,5,5	1.11	0
2	GOL	A	504	-	5,5,5	0.12	0	5,5,5	1.04	0
2	GOL	A	505	-	5,5,5	0.38	0	5,5,5	0.27	0
3	6FB	A	506	-	17,17,17	0.42	0	22,24,24	0.52	0
2	GOL	B	501	-	5,5,5	0.43	0	5,5,5	0.26	0
4	PO4	B	502	-	4,4,4	0.45	0	6,6,6	0.25	0
3	6FB	B	503	-	17,17,17	0.60	0	22,24,24	0.54	0
2	GOL	C	501	-	5,5,5	0.32	0	5,5,5	0.74	0
2	GOL	C	502	-	5,5,5	0.48	0	5,5,5	0.38	0
2	GOL	C	503	-	5,5,5	0.40	0	5,5,5	0.70	0
4	PO4	C	504	-	4,4,4	0.27	0	6,6,6	0.24	0
3	6FB	C	505	-	17,17,17	0.40	0	22,24,24	0.53	0
3	6FB	C	506	-	17,17,17	0.21	0	22,24,24	0.51	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	GOL	A	501	-	-	0/4/4/4	0/0/0/0
2	GOL	A	502	-	-	0/4/4/4	0/0/0/0
2	GOL	A	503	-	-	0/4/4/4	0/0/0/0
2	GOL	A	504	-	-	0/4/4/4	0/0/0/0
2	GOL	A	505	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	6FB	A	506	-	-	0/0/0/0	0/3/3/3
2	GOL	B	501	-	-	0/4/4/4	0/0/0/0
4	PO4	B	502	-	-	0/0/0/0	0/0/0/0
3	6FB	B	503	-	-	0/0/0/0	0/3/3/3
2	GOL	C	501	-	-	0/4/4/4	0/0/0/0
2	GOL	C	502	-	-	0/4/4/4	0/0/0/0
2	GOL	C	503	-	-	0/4/4/4	0/0/0/0
4	PO4	C	504	-	-	0/0/0/0	0/0/0/0
3	6FB	C	505	-	-	0/0/0/0	0/3/3/3
3	6FB	C	506	-	-	0/0/0/0	0/3/3/3

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.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	GOL	1	0
2	A	504	GOL	4	0
3	A	506	6FB	3	0
4	B	502	PO4	2	0
2	C	503	GOL	1	0
3	C	506	6FB	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, 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	338/339 (99%)	0.21	19 (5%)	28 27	30, 55, 104, 134	0
1	B	337/339 (99%)	0.41	33 (9%)	10 8	40, 64, 112, 132	0
1	C	316/339 (93%)	0.65	42 (13%)	4 4	34, 62, 131, 164	0
All	All	991/1017 (97%)	0.42	94 (9%)	10 9	30, 60, 115, 164	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	433	CYS	7.6
1	C	304	ALA	7.4
1	C	305	TYR	7.1
1	A	304	ALA	6.7
1	C	309	ILE	6.7
1	C	404	GLN	6.6
1	C	434	LYS	6.4
1	C	308	LYS	6.3
1	C	382	HIS	6.2
1	C	307	PRO	6.2
1	C	306	ASN	5.6
1	C	403	ILE	5.5
1	B	307	PRO	5.1
1	C	406	THR	5.0
1	A	415	ASP	4.8
1	A	308	LYS	4.5
1	C	483	SER	4.3
1	B	482	LYS	4.0
1	C	311	ARG	4.0
1	B	415	ASP	4.0
1	B	-1	SER	4.0
1	C	482	LYS	4.0
1	C	402	MET	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	304	ALA	3.8
1	C	312	ASP	3.8
1	C	400	LYS	3.7
1	C	301	TYR	3.7
1	B	185	GLY	3.7
1	C	339	LEU	3.6
1	C	354	LEU	3.4
1	B	303	GLU	3.3
1	C	397	PRO	3.3
1	B	301	TYR	3.2
1	B	183	ALA	3.2
1	C	303	GLU	3.2
1	B	186	ARG	3.2
1	B	302	THR	3.1
1	C	148	HIS	3.1
1	C	352	LEU	3.1
1	C	392	GLU	3.0
1	C	396	GLY	3.0
1	C	381	THR	3.0
1	C	405	LYS	3.0
1	C	398	LEU	2.9
1	B	148	HIS	2.9
1	C	401	HIS	2.9
1	A	-1	SER	2.9
1	B	416	ARG	2.8
1	B	310	LYS	2.8
1	B	164	VAL	2.8
1	A	312	ASP	2.8
1	B	340	VAL	2.8
1	A	335	HIS	2.7
1	A	409	ARG	2.7
1	B	305	TYR	2.7
1	A	311	ARG	2.7
1	A	333	ASP	2.7
1	B	368	ILE	2.6
1	C	365	ILE	2.6
1	B	308	LYS	2.6
1	C	345	TYR	2.6
1	C	377	THR	2.6
1	B	414	HIS	2.5
1	C	389	ALA	2.5
1	A	412	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	367	CYS	2.4
1	B	313	GLU	2.4
1	A	305	TYR	2.4
1	A	307	PRO	2.4
1	C	393	ARG	2.4
1	B	182	LYS	2.3
1	A	309	ILE	2.3
1	B	184	GLY	2.3
1	C	310	LYS	2.3
1	C	390	MET	2.3
1	B	306	ASN	2.3
1	B	369	LEU	2.3
1	A	196	VAL	2.2
1	B	311	ARG	2.2
1	B	198	ARG	2.2
1	B	333	ASP	2.2
1	B	197	ASP	2.2
1	C	410	LYS	2.2
1	B	196	VAL	2.2
1	A	416	ARG	2.2
1	B	312	ASP	2.1
1	C	399	PRO	2.1
1	A	404	GLN	2.1
1	A	368	ILE	2.1
1	C	-1	SER	2.1
1	A	197	ASP	2.1
1	B	199	TYR	2.1
1	C	342	THR	2.0
1	B	365	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	GOL	A	501	6/6	0.72	0.33	7.31	59,60,67,79	0
2	GOL	C	502	6/6	0.94	0.23	3.12	71,84,89,106	0
4	PO4	B	502	5/5	0.98	0.21	2.05	60,67,70,82	0
2	GOL	C	501	6/6	0.87	0.17	0.74	78,79,81,82	0
3	6FB	C	505	15/15	0.97	0.17	0.30	25,30,32,35	0
2	GOL	A	505	6/6	0.79	0.17	0.26	67,76,86,87	0
2	GOL	C	503	6/6	0.95	0.18	0.04	47,55,66,72	0
4	PO4	C	504	5/5	0.93	0.23	-0.06	76,79,96,100	0
2	GOL	B	501	6/6	0.91	0.15	-0.07	64,67,70,76	0
3	6FB	A	506	15/15	0.97	0.17	-0.14	26,30,36,40	0
3	6FB	C	506	15/15	0.95	0.14	-0.26	48,51,68,68	0
2	GOL	A	504	6/6	0.96	0.14	-0.44	52,64,65,71	0
3	6FB	B	503	15/15	0.97	0.14	-0.57	27,31,44,44	0
2	GOL	A	502	6/6	0.86	0.14	-0.64	67,75,80,82	0
2	GOL	A	503	6/6	0.80	0.15	-	63,67,70,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.