



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 04:23 pm GMT

PDB ID : 4II5
Title : Structure of PC DK2/CYCLINA bound to ADP and 1 MAGNESIUM ION
Authors : Jacobsen, D.M.; Bao, Z.-Q.; O'Brien, P.J.; Brooks III, C.L.; Young, M.A.
Deposited on : 2012-12-19
Resolution : 2.15 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

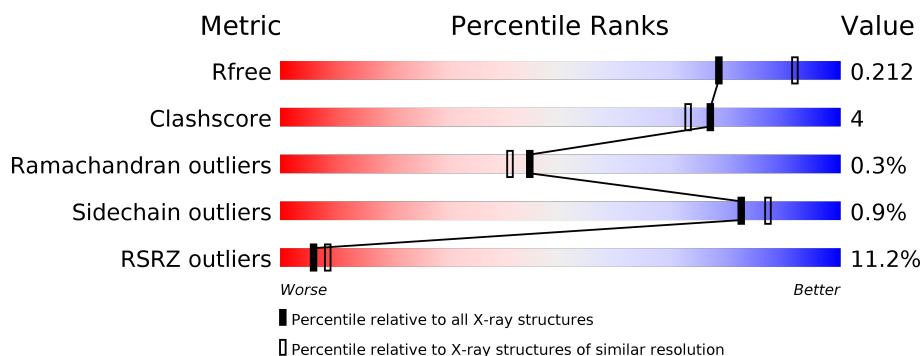
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	100719	1170 (2.16-2.16)
Clashscore	112137	1278 (2.16-2.16)
Ramachandran outliers	110173	1256 (2.16-2.16)
Sidechain outliers	110143	1255 (2.16-2.16)
RSRZ outliers	101464	1175 (2.16-2.16)

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	298	<div> <div>15%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>
1	C	298	<div> <div>13%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>
2	B	258	<div> <div>8%</div> <div>93%</div> <div>6%</div> <div>.</div> </div>
2	D	258	<div> <div>7%</div> <div>93%</div> <div>7%</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 crite-

ria:

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

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9527 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.

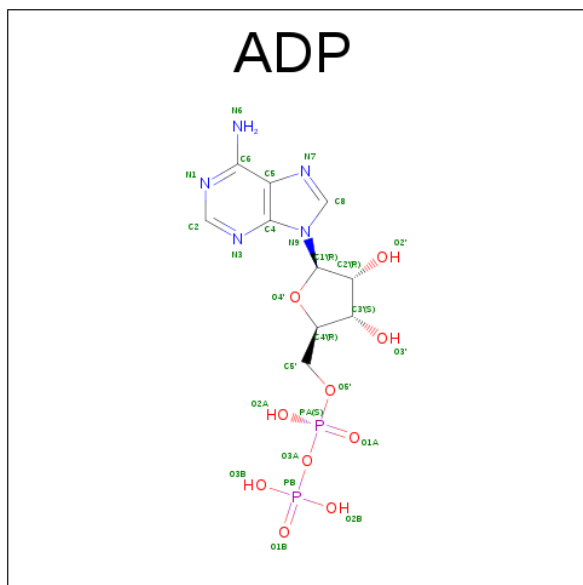
- Molecule 1 is a protein called Cyclin-dependent kinase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	P	S	0	0	0
			2382	1547	403	423	1	8			
1	C	296	Total	C	N	O	P	S	0	0	0
			2382	1547	403	423	1	8			

- Molecule 2 is a protein called Cyclin-A2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	256	Total	C	N	O	S	0	1	0
			2068	1341	335	381	11			
2	D	257	Total	C	N	O	S	0	1	0
			2074	1344	336	383	11			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

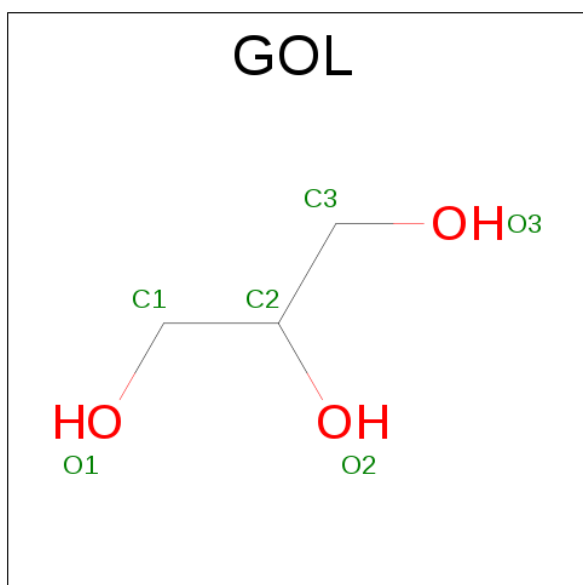


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- 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	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

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

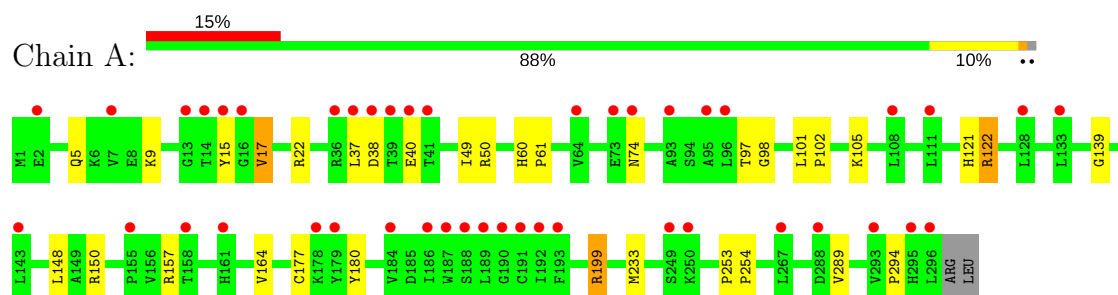
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	145	Total	O	0	0
			145	145		
6	B	100	Total	O	0	0
			100	100		
6	C	137	Total	O	0	0
			137	137		
6	D	135	Total	O	0	0
			135	135		

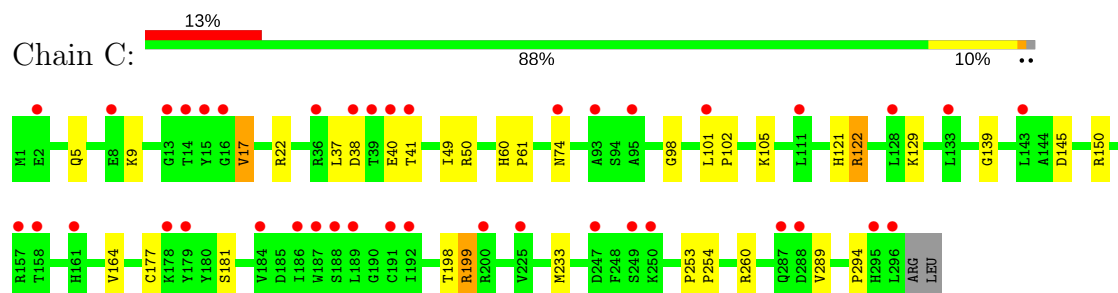
3 Residue-property plots [i](#)

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.

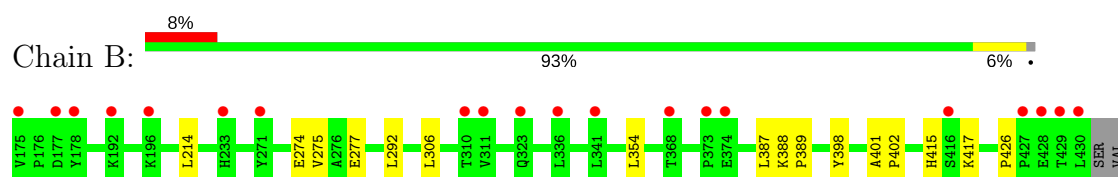
• Molecule 1: Cyclin-dependent kinase 2



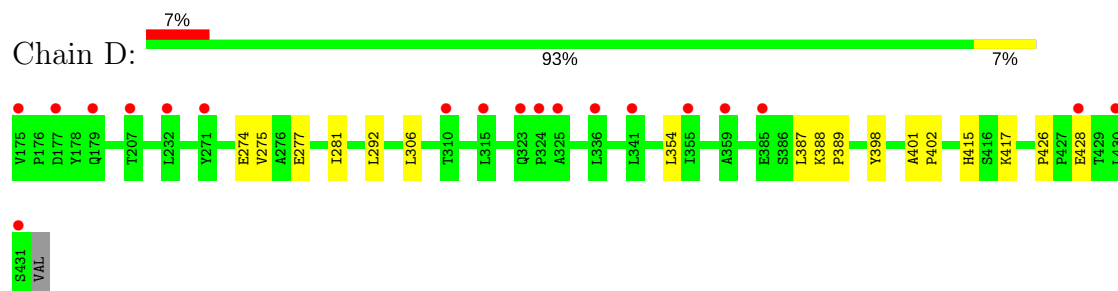
• Molecule 1: Cyclin-dependent kinase 2



• Molecule 2: Cyclin-A2



• Molecule 2: Cyclin-A2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.14Å 164.14Å 73.45Å 90.00° 107.04° 90.00°	Depositor
Resolution (Å)	29.56 – 2.15 29.56 – 2.15	Depositor EDS
% Data completeness (in resolution range)	95.3 (29.56-2.15) 95.3 (29.56-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.16Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.200 , 0.226 0.184 , 0.212	Depositor DCC
R_{free} test set	2010 reflections (2.42%)	DCC
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9527	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.02% 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: TPO, GOL, MG, ADP

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	0.51	0/2432	0.54	0/3300
1	C	0.49	0/2432	0.54	0/3300
2	B	0.41	0/2121	0.53	0/2882
2	D	0.42	0/2127	0.53	0/2890
All	All	0.46	0/9112	0.54	0/12372

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	2382	0	2425	20	0
1	C	2382	0	2425	24	0
2	B	2068	0	2088	11	0
2	D	2074	0	2093	11	0
3	A	27	0	11	0	0
3	C	27	0	12	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	12	0	16	2	0
5	C	12	0	16	0	0
5	D	18	0	24	0	0
6	A	145	0	0	3	0
6	B	100	0	0	0	0
6	C	137	0	0	8	0
6	D	135	0	0	1	0
All	All	9527	0	9118	64	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 (64) 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:15:TYR:HD1	6:A:543:HOH:O	1.52	0.93
1:A:177:CYS:HB2	1:A:233:MET:HE1	1.72	0.70
1:C:177:CYS:HB2	1:C:233:MET:HE1	1.75	0.69
1:A:139:GLY:HA2	1:A:294:PRO:HD3	1.80	0.63
1:C:139:GLY:HA2	1:C:294:PRO:HD3	1.82	0.61
1:A:253:PRO:HB2	1:A:254:PRO:HD3	1.86	0.58
1:C:253:PRO:HB2	1:C:254:PRO:HD3	1.86	0.58
1:C:199:ARG:HD2	6:C:467:HOH:O	2.06	0.55
2:D:428:GLU:HG2	6:D:637:HOH:O	2.06	0.54
2:B:274:GLU:HG2	2:B:277:GLU:HG3	1.90	0.53
2:D:274:GLU:HG2	2:D:277:GLU:HG3	1.92	0.53
1:A:121:HIS:O	1:A:122:ARG:HG3	2.10	0.51
2:B:214:LEU:HA	5:B:502:GOL:C3	2.42	0.49
2:B:214:LEU:HA	5:B:502:GOL:H31	1.95	0.49
2:B:354:LEU:HD12	2:B:387:LEU:HD23	1.96	0.48
1:A:98:GLY:HA2	1:A:199:ARG:HD2	1.95	0.48
1:A:148:LEU:CD1	6:A:544:HOH:O	2.62	0.48
1:A:101:LEU:HB2	1:A:102:PRO:HD3	1.96	0.48
1:C:9:LYS:HE2	1:C:17:VAL:HG11	1.96	0.48
1:A:50:ARG:HD3	6:A:426:HOH:O	2.14	0.47
1:C:260:ARG:HD3	6:C:519:HOH:O	2.14	0.47
1:C:98:GLY:HA2	1:C:199:ARG:HD2	1.95	0.47
1:C:199:ARG:HG3	6:C:467:HOH:O	2.14	0.47
1:C:49:ILE:HG23	2:D:306:LEU:HD12	1.96	0.47
1:C:121:HIS:O	1:C:122:ARG:HG3	2.14	0.47
1:C:101:LEU:HB2	1:C:102:PRO:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:398:TYR:CD2	2:B:426:PRO:HB3	2.51	0.46
2:D:415:HIS:ND1	2:D:417:LYS:HG2	2.31	0.46
1:A:9:LYS:HE2	1:A:17:VAL:HG11	1.96	0.46
1:C:105:LYS:HG2	1:C:289:VAL:HG23	1.96	0.46
2:D:354:LEU:HD12	2:D:387:LEU:HD23	1.97	0.45
1:A:37:LEU:O	1:A:40:GLU:HB2	2.16	0.45
1:C:37:LEU:O	1:C:40:GLU:HB2	2.17	0.45
1:C:41:THR:HA	6:C:514:HOH:O	2.16	0.45
1:C:199:ARG:CD	6:C:467:HOH:O	2.62	0.45
1:C:38:ASP:HB3	1:C:74:ASN:ND2	2.31	0.45
1:A:38:ASP:HB3	1:A:74:ASN:ND2	2.31	0.45
2:D:398:TYR:CD2	2:D:426:PRO:HB3	2.52	0.45
2:B:415:HIS:ND1	2:B:417:LYS:HG2	2.32	0.44
1:A:49:ILE:HG23	2:B:306:LEU:HD12	2.00	0.44
2:D:275:VAL:HG21	2:D:292:LEU:HD21	2.00	0.44
2:B:388:LYS:HB3	2:B:389:PRO:HD3	1.98	0.44
1:A:121:HIS:C	1:A:122:ARG:HG3	2.39	0.43
1:A:60:HIS:CG	1:A:61:PRO:HD2	2.53	0.43
1:C:181:SER:HB3	6:C:484:HOH:O	2.19	0.43
2:D:388:LYS:HB3	2:D:389:PRO:HD3	1.99	0.43
1:A:105:LYS:HG2	1:A:289:VAL:HG23	2.01	0.43
1:A:5:GLN:HG2	1:A:22:ARG:HB3	2.01	0.43
1:C:253:PRO:CB	1:C:254:PRO:HD3	2.48	0.43
1:C:50:ARG:HD3	6:C:476:HOH:O	2.19	0.42
1:C:60:HIS:CG	1:C:61:PRO:HD2	2.54	0.42
2:B:275:VAL:HG21	2:B:292:LEU:HD21	2.01	0.42
1:C:121:HIS:C	1:C:122:ARG:HG3	2.40	0.42
2:B:274:GLU:CG	2:B:277:GLU:HG3	2.50	0.42
2:D:274:GLU:CG	2:D:277:GLU:HG3	2.49	0.42
2:B:401:ALA:N	2:B:402:PRO:CD	2.82	0.42
1:C:5:GLN:HG2	1:C:22:ARG:HB3	2.01	0.41
2:D:281:ILE:HA	2:D:281:ILE:HD12	1.96	0.41
1:A:253:PRO:CB	1:A:254:PRO:HD3	2.49	0.41
1:A:97:THR:HG22	1:A:98:GLY:O	2.21	0.41
1:A:180:TYR:CD1	1:A:180:TYR:C	2.94	0.41
1:C:129:LYS:NZ	6:C:438:HOH:O	2.51	0.41
2:D:401:ALA:N	2:D:402:PRO:CD	2.84	0.41
1:C:198:THR:O	1:C:199:ARG:HB2	2.21	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	293/298 (98%)	287 (98%)	5 (2%)	1 (0%)	44	41
1	C	293/298 (98%)	287 (98%)	4 (1%)	2 (1%)	25	17
2	B	255/258 (99%)	255 (100%)	0	0	100	100
2	D	256/258 (99%)	256 (100%)	0	0	100	100
All	All	1097/1112 (99%)	1085 (99%)	9 (1%)	3 (0%)	44	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	VAL
1	C	164	VAL
1	C	145	ASP

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	260/262 (99%)	255 (98%)	5 (2%)	62	66
1	C	260/262 (99%)	256 (98%)	4 (2%)	70	75
2	B	230/231 (100%)	230 (100%)	0	100	100
2	D	231/231 (100%)	231 (100%)	0	100	100
All	All	981/986 (100%)	972 (99%)	9 (1%)	82	87

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	VAL
1	A	122	ARG
1	A	150	ARG
1	A	157	ARG
1	A	199	ARG
1	C	17	VAL
1	C	122	ARG
1	C	150	ARG
1	C	199	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	71	HIS
1	A	85	GLN
2	B	296	HIS
1	C	5	GLN
1	C	71	HIS
1	C	85	GLN
1	C	295	HIS
2	D	296	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	TPO	A	160	1	9,10,11	0.85	0	10,14,16	1.17	1 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	TPO	C	160	1	9,10,11	0.95	0	10,14,16	1.23	2 (20%)

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	TPO	A	160	1	-	0/8/11/13	0/0/0/0
1	TPO	C	160	1	-	0/8/11/13	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	160	TPO	O-C-CA	-2.18	120.07	125.15
1	C	160	TPO	CG2-CB-CA	-2.17	109.19	113.22
1	A	160	TPO	O-C-CA	-2.13	120.18	125.15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	ADP	A	301	4	25,29,29	0.96	1 (4%)	24,45,45	2.10	7 (29%)
5	GOL	A	303	-	5,5,5	0.32	0	5,5,5	0.18	0
5	GOL	B	501	-	5,5,5	0.40	0	5,5,5	0.34	0
5	GOL	B	502	-	5,5,5	0.36	0	5,5,5	0.28	0
3	ADP	C	301	4	25,29,29	0.99	1 (4%)	24,45,45	1.72	3 (12%)
5	GOL	C	303	-	5,5,5	0.34	0	5,5,5	0.30	0
5	GOL	C	304	-	5,5,5	0.31	0	5,5,5	0.12	0
5	GOL	D	501	-	5,5,5	0.39	0	5,5,5	0.27	0
5	GOL	D	502	-	5,5,5	0.31	0	5,5,5	0.18	0
5	GOL	D	503	-	5,5,5	0.23	0	5,5,5	0.30	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	A	301	4	-	0/12/32/32	0/3/3/3
5	GOL	A	303	-	-	0/4/4/4	0/0/0/0
5	GOL	B	501	-	-	0/4/4/4	0/0/0/0
5	GOL	B	502	-	-	0/4/4/4	0/0/0/0
3	ADP	C	301	4	-	0/12/32/32	0/3/3/3
5	GOL	C	303	-	-	0/4/4/4	0/0/0/0
5	GOL	C	304	-	-	0/4/4/4	0/0/0/0
5	GOL	D	501	-	-	0/4/4/4	0/0/0/0
5	GOL	D	502	-	-	0/4/4/4	0/0/0/0
5	GOL	D	503	-	-	0/4/4/4	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	ADP	C5-C4	3.04	1.47	1.40
3	C	301	ADP	C5-C4	3.04	1.47	1.40

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	ADP	N3-C2-N1	-7.03	122.74	128.86
3	C	301	ADP	N3-C2-N1	-6.83	122.91	128.86
3	C	301	ADP	C4-C5-N7	-2.53	106.96	109.41
3	A	301	ADP	C4'-O4'-C1'	-2.53	107.08	109.77
3	A	301	ADP	C4-C5-N7	-2.10	107.38	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	ADP	C2-N1-C6	2.06	122.37	118.77
3	C	301	ADP	C2-N1-C6	2.09	122.43	118.77
3	A	301	ADP	C5'-C4'-C3'	2.38	124.36	115.29
3	A	301	ADP	O4'-C4'-C5'	3.05	119.70	109.40
3	A	301	ADP	O4'-C4'-C3'	3.61	112.34	105.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	502	GOL	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 ⓘ

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	295/298 (98%)	0.76	44 (14%) 3 4	24, 39, 86, 136	0
1	C	295/298 (98%)	0.64	40 (13%) 3 4	25, 40, 86, 135	0
2	B	256/258 (99%)	0.39	20 (7%) 14 18	23, 39, 63, 96	0
2	D	257/258 (99%)	0.43	19 (7%) 15 19	21, 37, 62, 96	0
All	All	1103/1112 (99%)	0.57	123 (11%) 6 8	21, 39, 78, 136	0

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	38	ASP	9.2
1	C	14	THR	7.4
1	A	39	THR	7.2
2	D	175	VAL	6.7
1	C	38	ASP	6.3
2	B	175	VAL	6.1
1	A	15	TYR	5.9
1	A	178	LYS	5.6
1	A	14	THR	5.6
1	A	13	GLY	5.4
2	B	271	TYR	5.0
1	C	295	HIS	4.9
1	A	36	ARG	4.9
1	A	296	LEU	4.8
1	C	15	TYR	4.7
1	A	295	HIS	4.7
1	A	74	ASN	4.7
1	A	2	GLU	4.5
1	A	189	LEU	4.5
1	C	39	THR	4.4
1	C	128	LEU	4.4

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Mol	Chain	Res	Type	RSRZ
2	D	323	GLN	4.3
1	C	40	GLU	4.1
2	B	428	GLU	4.1
1	A	179	TYR	4.0
2	D	271	TYR	4.0
1	C	178	LYS	3.9
1	C	161	HIS	3.9
1	C	288	ASP	3.8
1	C	13	GLY	3.8
1	C	2	GLU	3.8
1	A	143	LEU	3.7
1	C	36	ARG	3.7
1	A	37	LEU	3.7
1	C	250	LYS	3.7
1	C	16	GLY	3.7
1	C	189	LEU	3.6
1	C	225	VAL	3.6
2	D	336	LEU	3.6
1	A	16	GLY	3.6
1	C	74	ASN	3.5
2	D	428	GLU	3.5
1	A	161	HIS	3.5
2	B	341	LEU	3.5
1	A	96	LEU	3.4
1	A	41	THR	3.4
1	A	111	LEU	3.3
1	A	128	LEU	3.3
2	D	355	ILE	3.3
1	C	179	TYR	3.3
1	A	192	ILE	3.3
1	C	143	LEU	3.3
1	A	133	LEU	3.2
2	D	324	PRO	3.2
1	A	188	SER	3.2
1	C	192	ILE	3.2
1	C	133	LEU	3.1
2	D	315	LEU	3.1
1	A	95	ALA	3.0
2	D	310	THR	3.0
2	B	196	LYS	2.9
2	B	427	PRO	2.9
1	A	249	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	93	ALA	2.9
1	A	193	PHE	2.9
1	C	296	LEU	2.9
1	A	40	GLU	2.8
2	B	429	THR	2.8
2	D	359	ALA	2.8
1	C	188	SER	2.8
1	C	249	SER	2.8
2	D	431	SER	2.8
1	C	95	ALA	2.7
1	A	7	VAL	2.7
1	A	191	CYS	2.7
1	A	293	VAL	2.7
2	D	385	GLU	2.7
2	D	341	LEU	2.7
1	A	158	THR	2.7
2	B	373	PRO	2.6
1	C	8	GLU	2.6
1	C	191	CYS	2.6
1	C	186	ILE	2.6
1	C	200	ARG	2.5
1	A	186	ILE	2.5
2	B	192	LYS	2.5
1	C	287	GLN	2.5
1	C	187	TRP	2.5
1	A	108	LEU	2.5
1	C	93	ALA	2.5
1	A	190	GLY	2.5
1	C	41	THR	2.4
1	A	187	TRP	2.4
1	A	288	ASP	2.4
1	A	73	GLU	2.4
1	C	101	LEU	2.4
1	A	250	LYS	2.4
2	B	177	ASP	2.4
1	A	184	VAL	2.4
1	C	158	THR	2.4
2	D	177	ASP	2.3
2	B	430	LEU	2.3
2	B	311	VAL	2.3
1	C	184	VAL	2.3
2	B	310	THR	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	178	TYR	2.3
2	D	207	THR	2.3
2	D	430	LEU	2.2
1	C	111	LEU	2.2
2	B	416	SER	2.2
1	A	155	PRO	2.2
2	D	232	LEU	2.2
2	B	336	LEU	2.1
1	A	64	VAL	2.1
1	A	267	LEU	2.1
2	D	325	ALA	2.1
2	B	368	THR	2.1
2	B	233	HIS	2.1
2	B	323	GLN	2.1
1	C	247	ASP	2.0
1	C	157	ARG	2.0
2	D	179	GLN	2.0
2	B	374	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	A	160	11/12	0.93	0.22	-	39,53,58,67	0
1	TPO	C	160	11/12	0.95	0.20	-	39,53,58,67	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 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
5	GOL	D	501	6/6	0.77	0.29	18.59	56,63,66,66	0
5	GOL	B	501	6/6	0.61	0.26	7.37	62,64,68,72	0
5	GOL	C	303	6/6	0.90	0.13	1.83	44,51,54,55	0
5	GOL	D	503	6/6	0.91	0.18	1.78	52,54,67,72	0
5	GOL	C	304	6/6	0.86	0.19	1.68	66,69,74,74	0
5	GOL	A	303	6/6	0.95	0.14	1.11	40,50,58,60	0
3	ADP	C	301	27/27	0.92	0.16	-0.23	41,58,64,238	0
3	ADP	A	301	27/27	0.92	0.14	-0.73	32,56,66,280	0
5	GOL	B	502	6/6	0.90	0.14	-	55,58,63,64	0
4	MG	C	302	1/1	0.84	0.05	-	52,52,52,52	0
4	MG	A	302	1/1	0.88	0.08	-	49,49,49,49	0
5	GOL	D	502	6/6	0.76	0.20	-	60,68,77,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.