



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:07 PM GMT

PDB ID : 4NST  
Title : Crystal structure of human Cdk12/Cyclin K in complex with ADP-aluminum fluoride  
Authors : Boesken, C.A.; Farnung, L.; Anand, K.; Geyer, M.  
Deposited on : 2013-11-29  
Resolution : 2.20 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

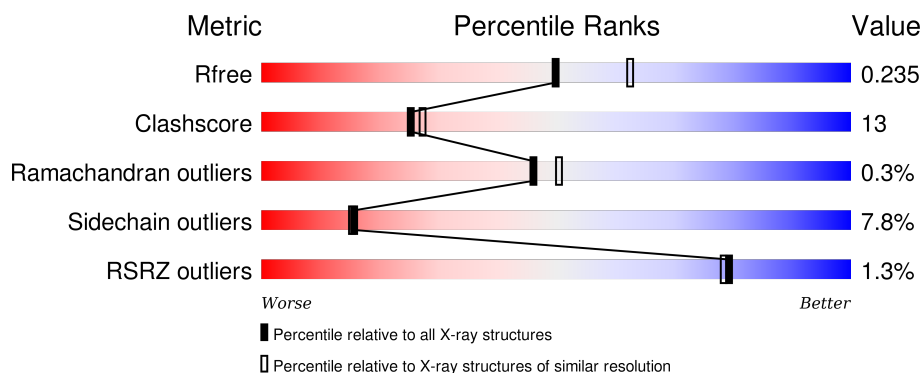
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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  $\geq 3$ , 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	351	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 25%, green 64%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>1%</span> <span>64%</span> <span>25%</span> <span>8%</span> </div> </div>
1	C	351	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 1%, yellow 24%, green 64%, grey 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>64%</span> <span>24%</span> <span>9%</span> </div> </div>
2	B	268	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 77%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>1%</span> <span>77%</span> <span>12%</span> <span>8%</span> </div> </div>
2	D	268	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 15%, green 73%, grey 10%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>73%</span> <span>15%</span> <span>10%</span> </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
4	AF3	C	1102	-	-	-	X
5	MG	A	1105	-	-	-	X
5	MG	D	301	-	-	-	X
6	EDO	A	1106	-	-	-	X
6	EDO	C	1105	-	-	X	X
6	EDO	D	303	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9618 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 12.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	P	S	0	0	0
			2588	1660	438	472	1	17			
1	C	318	Total	C	N	O	P	S	0	0	0
			2541	1631	426	466	1	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	713	GLY	-	EXPRESSION TAG	UNP Q9NYV4
C	713	GLY	-	EXPRESSION TAG	UNP Q9NYV4

- Molecule 2 is a protein called Cyclin-K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	246	Total	C	N	O	S	0	0	0
			2023	1313	337	361	12			
2	D	241	Total	C	N	O	S	0	0	0
			1988	1293	330	353	12			

There are 2 discrepancies between the modelled and reference sequences:

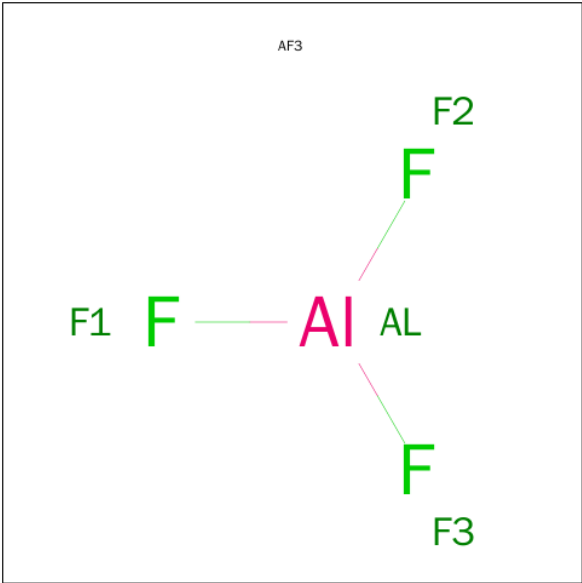
Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	EXPRESSION TAG	UNP O75909
D	0	GLY	-	EXPRESSION TAG	UNP O75909

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



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 ALUMINUM FLUORIDE (three-letter code: AF3) (formula: AlF<sub>3</sub>).

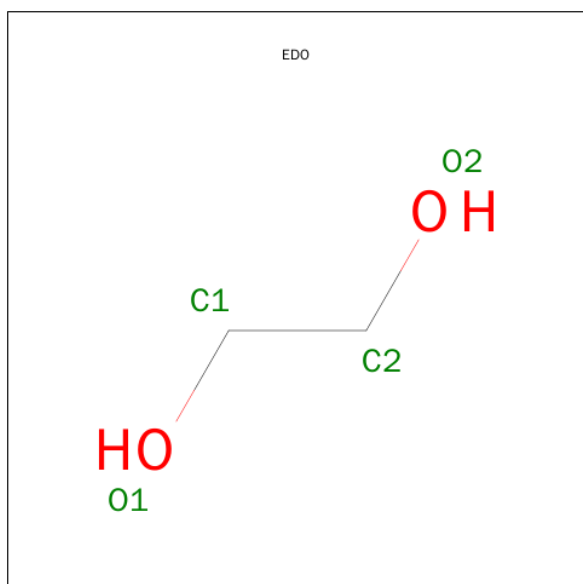


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Al	F	0	0
			4	1	3		
4	C	1	Total	Al	F	0	0
			4	1	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Mg	0	0
			3	3		
5	D	2	Total	Mg	0	0
			2	2		
5	C	2	Total	Mg	0	0
			2	2		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	107	Total	O	0	0
			107	107		
7	B	92	Total	O	0	0
			92	92		

*Continued on next page...*

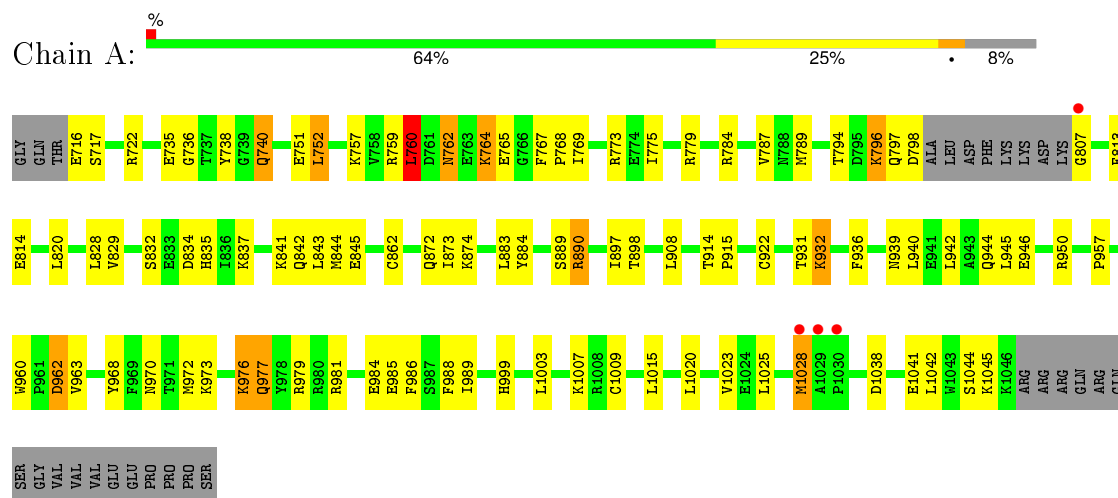
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	C	96	Total 96	O 96	0	0
7	D	98	Total 98	O 98	0	0

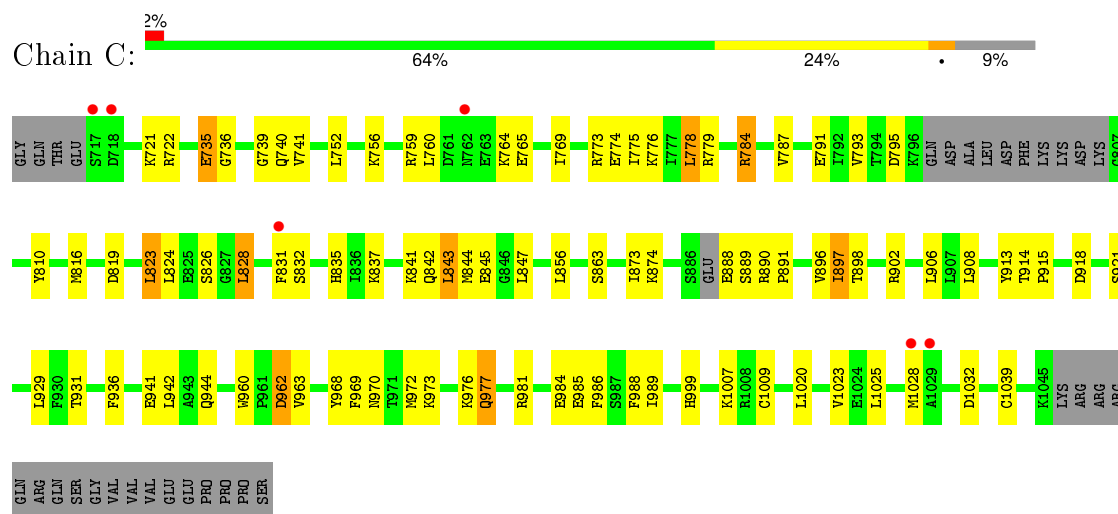
### 3 Residue-property plots

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.

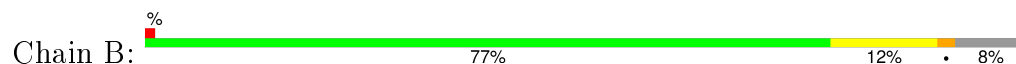
#### • Molecule 1: Cyclin-dependent kinase 12



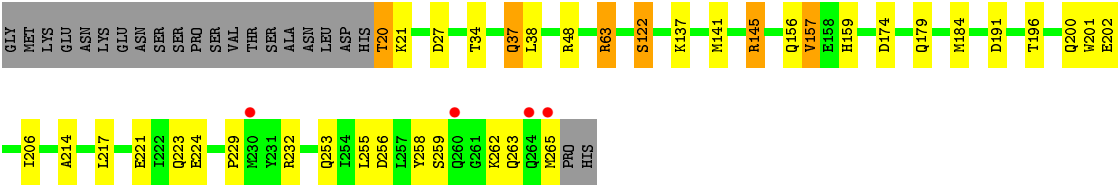
#### • Molecule 1: Cyclin-dependent kinase 12



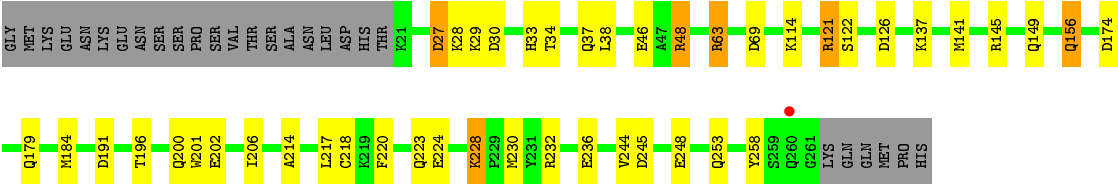
#### • Molecule 2: Cyclin-K







• Molecule 2: Cyclin-K



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.72Å 78.85Å 91.49Å 104.04° 85.76° 101.46°	Depositor
Resolution (Å)	48.71 – 2.20 48.71 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (48.71-2.20) 90.2 (48.71-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.195 , 0.240 0.197 , 0.235	Depositor DCC
$R_{free}$ test set	3264 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.6	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 48.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 65263 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9618	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.26% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, MG, EDO, ADP, AF3

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	1.08	0/2636	0.84	4/3562 (0.1%)
1	C	1.00	0/2588	0.83	2/3502 (0.1%)
2	B	0.92	1/2078 (0.0%)	0.74	1/2818 (0.0%)
2	D	0.92	0/2043	0.72	0/2770
All	All	0.99	1/9345 (0.0%)	0.79	7/12652 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	157	VAL	CB-CG1	-5.42	1.41	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	976	LYS	CB-CA-C	-8.37	93.67	110.40
1	C	891	PRO	O-C-N	6.36	132.88	122.70
1	A	760	LEU	CA-CB-CG	6.34	129.89	115.30
1	A	1038	ASP	CB-CG-OD1	5.60	123.34	118.30
1	C	856	LEU	CA-CB-CG	5.38	127.66	115.30

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	2588	0	2555	76	1
1	C	2541	0	2492	90	0
2	B	2023	0	1972	39	0
2	D	1988	0	1945	39	0
3	A	27	0	12	1	0
3	C	27	0	9	2	0
4	A	4	0	0	0	0
4	C	4	0	0	0	0
5	A	3	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	4	0	6	2	0
6	B	4	0	6	0	0
6	C	4	0	6	7	0
6	D	4	0	6	0	0
7	A	107	0	0	8	0
7	B	92	0	0	4	0
7	C	96	0	0	6	0
7	D	98	0	0	4	0
All	All	9618	0	9009	230	1

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 13.

The worst 5 of 230 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:C:739:GLY:HA2	1:C:759:ARG:NH1	1.46	1.30
1:A:939:ASN:ND2	1:A:940:LEU:HD12	1.55	1.22
1:A:796:LYS:HD3	1:A:796:LYS:N	1.48	1.21
1:A:740:GLN:OE1	1:A:759:ARG:NH2	1.74	1.19
1:C:888:GLU:HG3	1:C:890:ARG:NH1	1.58	1.18

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:ASN:ND2	1:A:1015:LEU:O[1_455]	1.37	0.83

## 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	318/351 (91%)	313 (98%)	4 (1%)	1 (0%)	46	50
1	C	311/351 (89%)	304 (98%)	5 (2%)	2 (1%)	30	29
2	B	244/268 (91%)	244 (100%)	0	0	100	100
2	D	239/268 (89%)	239 (100%)	0	0	100	100
All	All	1112/1238 (90%)	1100 (99%)	9 (1%)	3 (0%)	46	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	897	ILE
1	C	897	ILE
1	C	764	LYS

### 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	279/316 (88%)	249 (89%)	30 (11%)	8	7
1	C	274/316 (87%)	252 (92%)	22 (8%)	15	15
2	B	215/241 (89%)	204 (95%)	11 (5%)	29	34
2	D	212/241 (88%)	199 (94%)	13 (6%)	23	26
All	All	980/1114 (88%)	904 (92%)	76 (8%)	16	15

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	145	ARG
1	C	735	GLU
2	D	156	GLN
2	B	156	GLN
2	B	224	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	253	GLN
1	C	835	HIS
2	D	33	HIS
2	B	179	GLN
2	D	67	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	893	1	8,10,11	1.38	1 (12%)	7,14,16	1.51	1 (14%)
1	TPO	C	893	1	8,10,11	0.92	0	7,14,16	2.23	1 (14%)

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	893	1	-	0/8/11/13	0/0/0/0
1	TPO	C	893	1	-	0/8/11/13	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	893	TPO	CB-CA	2.18	1.58	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	893	TPO	CG2-CB-CA	-4.87	103.26	113.17
1	A	893	TPO	CG2-CB-CA	-3.40	106.24	113.17

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 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 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	1101	5	22,29,29	1.12	2 (9%)	27,45,45	2.19	6 (22%)
4	AF3	A	1102	-	0,3,3	0.00	-	0,3,3	0.00	-
6	EDO	A	1106	-	3,3,3	0.34	0	2,2,2	1.13	0
6	EDO	B	301	-	3,3,3	0.62	0	2,2,2	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	ADP	C	1101	5	22,29,29	1.66	7 (31%)	27,45,45	3.59	9 (33%)
4	AF3	C	1102	-	0,3,3	0.00	-	0,3,3	0.00	-
6	EDO	C	1105	-	3,3,3	0.63	0	2,2,2	0.72	0
6	EDO	D	303	-	3,3,3	0.31	0	2,2,2	1.12	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	1101	5	-	0/12/32/32	0/3/3/3
4	AF3	A	1102	-	-	0/0/0/0	0/0/0/0
6	EDO	A	1106	-	-	0/1/1/1	0/0/0/0
6	EDO	B	301	-	-	0/1/1/1	0/0/0/0
3	ADP	C	1101	5	-	0/12/32/32	0/3/3/3
4	AF3	C	1102	-	-	0/0/0/0	0/0/0/0
6	EDO	C	1105	-	-	0/1/1/1	0/0/0/0
6	EDO	D	303	-	-	0/1/1/1	0/0/0/0

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1101	ADP	C5-C4	-3.44	1.32	1.40
3	C	1101	ADP	O2'-C2'	-2.54	1.36	1.43
3	C	1101	ADP	O3'-C3'	-2.32	1.37	1.43
3	C	1101	ADP	O4'-C1'	-2.03	1.38	1.41
3	C	1101	ADP	O4'-C4'	2.10	1.49	1.45

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1101	ADP	N3-C2-N1	-10.45	120.89	128.89
3	A	1101	ADP	N3-C2-N1	-7.55	123.11	128.89
3	C	1101	ADP	C4'-O4'-C1'	-5.76	103.39	109.72
3	A	1101	ADP	C2'-C1'-N9	-4.89	106.83	114.29
3	A	1101	ADP	O5'-PA-O1A	-3.53	95.92	109.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.



4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1101	ADP	1	0
6	A	1106	EDO	2	0
3	C	1101	ADP	2	0
6	C	1105	EDO	7	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	322/351 (91%)	0.05	4 (1%) 81 80	23, 41, 74, 98	0
1	C	317/351 (90%)	0.04	6 (1%) 70 68	24, 42, 74, 99	0
2	B	246/268 (91%)	-0.01	4 (1%) 74 73	19, 36, 72, 88	0
2	D	241/268 (89%)	-0.05	1 (0%) 93 93	21, 37, 65, 87	0
All	All	1126/1238 (90%)	0.02	15 (1%) 79 78	19, 40, 72, 99	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1029	ALA	5.3
2	B	264	GLN	5.0
1	A	1028	MET	4.0
2	B	230	MET	3.2
1	C	762	ASN	3.1

### 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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	TPO	A	893	11/12	0.93	0.15	-	24,35,43,44	0
1	TPO	C	893	11/12	0.96	0.11	-	27,34,41,48	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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, 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
6	EDO	C	1105	4/4	0.81	0.24	12.53	39,43,45,52	0
5	MG	A	1105	1/1	0.81	0.29	10.44	70,70,70,70	0
6	EDO	A	1106	4/4	0.67	0.27	9.06	48,53,59,65	0
6	EDO	D	303	4/4	0.84	0.20	3.88	44,46,57,60	0
4	AF3	C	1102	4/4	0.88	0.13	2.90	45,69,86,132	0
5	MG	D	301	1/1	0.93	0.25	2.51	49,49,49,49	0
3	ADP	A	1101	27/27	0.92	0.17	1.75	26,56,63,65	0
3	ADP	C	1101	27/27	0.97	0.12	-0.13	23,32,40,42	0
4	AF3	A	1102	4/4	0.95	0.11	-1.19	41,68,89,97	0
5	MG	C	1104	1/1	0.97	0.07	-	56,56,56,56	0
5	MG	A	1104	1/1	0.92	0.07	-	51,51,51,51	0
6	EDO	B	301	4/4	0.77	0.27	-	64,71,73,77	0
5	MG	C	1103	1/1	0.89	0.13	-	32,32,32,32	0
5	MG	D	302	1/1	0.87	0.25	-	74,74,74,74	0
5	MG	A	1103	1/1	0.96	0.08	-	27,27,27,27	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.