



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:58 AM GMT

PDB ID : 3QHW  
Title : Structure of a pCDK2/CyclinA transition-state mimic  
Authors : Young, M.A.; Jacobsen, D.M.; Bao, Z.Q.  
Deposited on : 2011-01-26  
Resolution : 1.91 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](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

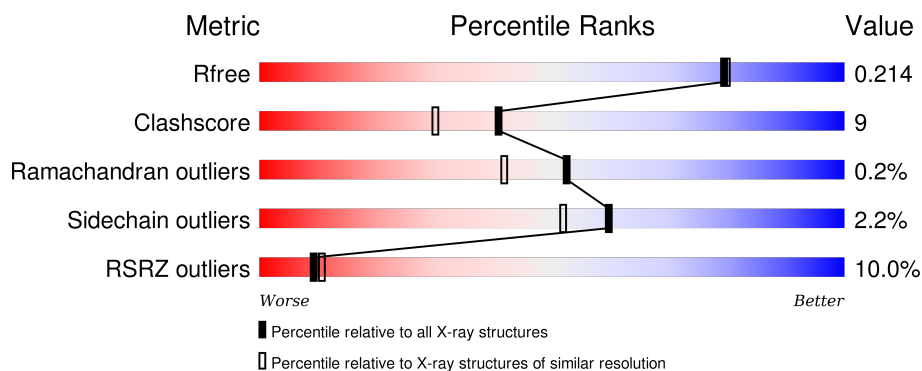
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.91 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	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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	298	<div> <div>11%</div> <div>87%</div> <div>11%</div> </div>
1	C	298	<div> <div>12%</div> <div>85%</div> <div>14%</div> </div>
2	B	261	<div> <div>4%</div> <div>90%</div> <div>8%</div> </div>
2	D	261	<div> <div>7%</div> <div>88%</div> <div>10%</div> </div>
3	J	10	<div> <div>50%</div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
3	K	10	<p>90% 60% 30% 10%</p>
3	L	10	<p>20% 40% 60%</p>
3	M	10	<p>20% 40% 60%</p>

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 10157 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 Cell division protein kinase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	P	S	0	0	0
			2396	1555	407	425	1	8			
1	C	298	Total	C	N	O	P	S	0	10	0
			2466	1600	419	438	1	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P24941
A	0	HIS	-	EXPRESSION TAG	UNP P24941
C	-1	GLY	-	EXPRESSION TAG	UNP P24941
C	0	HIS	-	EXPRESSION TAG	UNP P24941

- Molecule 2 is a protein called Cyclin-A2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	261	Total	C	N	O	S		0	0	0
			2099	1357	341	391	10				
2	D	261	Total	C	N	O	S		0	0	0
			2099	1357	341	391	10				

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	172	SER	-	EXPRESSION TAG	UNP P51943
D	172	SER	-	EXPRESSION TAG	UNP P51943

- Molecule 3 is a protein called CDK2 substrate peptide: PKTPKKAKKL.

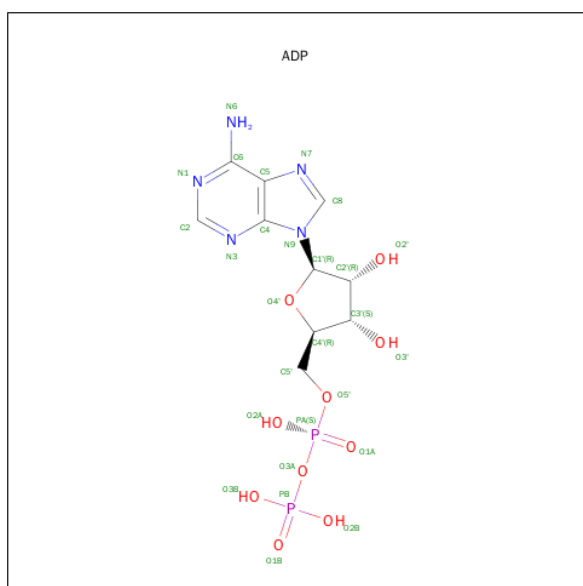
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	J	10	Total	C	N	O	0	0	0
			79	53	15	11			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	K	10	Total	C	N	O	0	0	0
			79	53	15	11			
3	L	4	Total	C	N	O	0	0	0
			31	21	6	4			
3	M	4	Total	C	N	O	0	0	0
			31	21	6	4			

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).

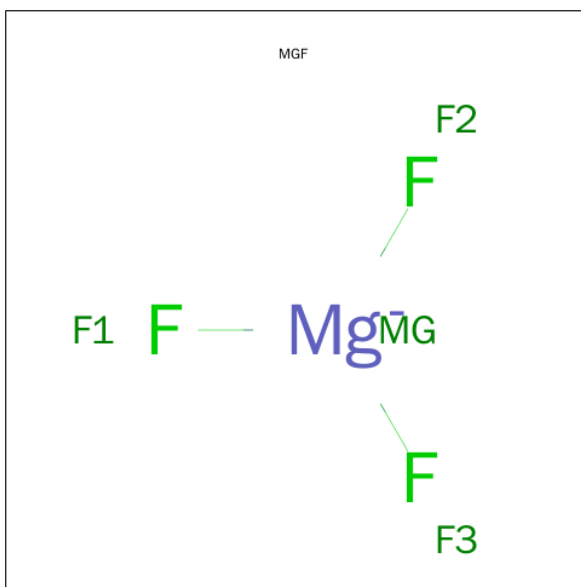


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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

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

- Molecule 6 is TRIFLUOROMAGNESATE (three-letter code: MGF) (formula:  $F_3Mg$ ).

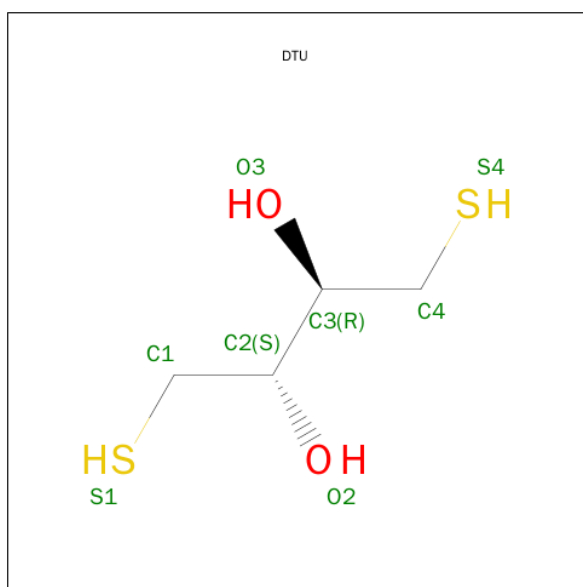


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	F	Mg	0	0
			4	3	1		
6	C	1	Total	F	Mg	0	0
			4	3	1		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		
7	C	1	Total	Cl	0	0
			1	1		

- Molecule 8 is (2R,3S)-1,4-DIMERCAPTOBUTANE-2,3-DIOL (three-letter code: DTU) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>2</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	1	Total	C	O	S	0	0
			8	4	2	2		
8	D	1	Total	C	O	S	0	0
			8	4	2	2		

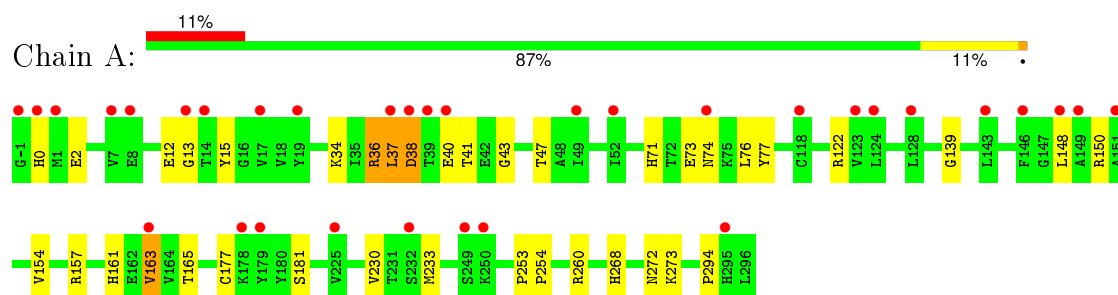
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	194	Total	O	0	0
			194	194		
9	B	216	Total	O	0	0
			216	216		
9	C	192	Total	O	0	0
			192	192		
9	D	180	Total	O	0	0
			180	180		
9	J	6	Total	O	0	0
			6	6		
9	K	2	Total	O	0	0
			2	2		
9	L	2	Total	O	0	0
			2	2		
9	M	1	Total	O	0	0
			1	1		

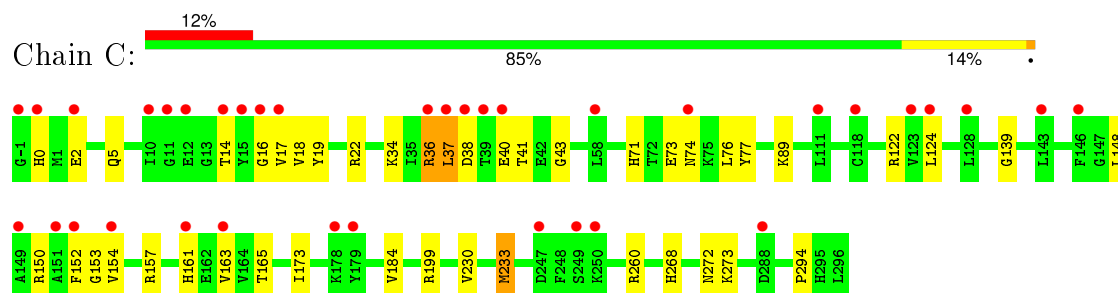
### 3 Residue-property plots

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.

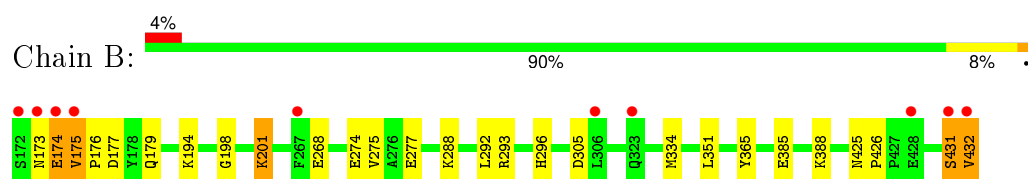
- Molecule 1: Cell division protein kinase 2



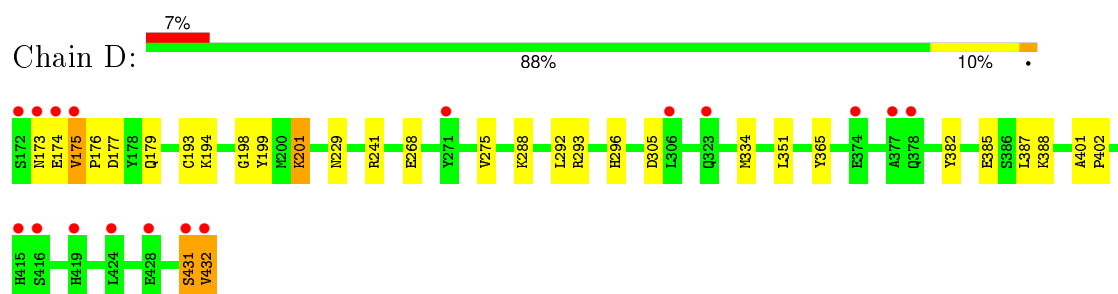
- Molecule 1: Cell division protein kinase 2



- Molecule 2: Cyclin-A2

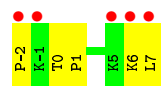


- Molecule 2: Cyclin-A2

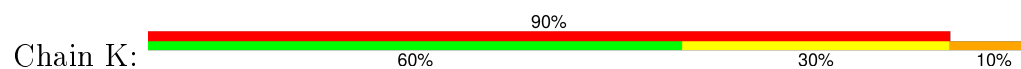




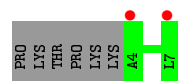
- Molecule 3: CDK2 substrate peptide: PKTPKKAKKL



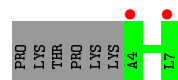
- Molecule 3: CDK2 substrate peptide: PKTPKKAKKL



- Molecule 3: CDK2 substrate peptide: PKTPKKAKKL



- Molecule 3: CDK2 substrate peptide: PKTPKKAKKL



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.03Å 163.45Å 73.39Å 90.00° 107.08° 90.00°	Depositor
Resolution (Å)	39.73 – 1.91 39.72 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.73-1.91) 99.6 (39.72-1.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 1.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, $R_{free}$	0.188 , 0.219 0.184 , 0.214	Depositor DCC
$R_{free}$ test set	2402 reflections (1.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.7	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 54.2	EDS
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 123345 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	10157	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.46	0/2447	0.57	0/3320
1	C	0.45	0/2521	0.60	0/3420
2	B	0.49	0/2149	0.58	0/2921
2	D	0.47	0/2149	0.58	0/2921
3	J	0.38	0/80	0.52	0/103
3	K	0.36	0/80	0.48	0/103
3	L	0.30	0/30	0.43	0/37
3	M	0.32	0/30	0.42	0/37
All	All	0.47	0/9486	0.58	0/12862

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	2396	0	2435	50	0
1	C	2466	0	2507	51	0
2	B	2099	0	2110	42	0
2	D	2099	0	2110	40	0
3	J	79	0	104	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	79	0	104	8	0
3	L	31	0	41	0	0
3	M	31	0	41	0	0
4	A	27	0	12	0	0
4	C	27	0	12	0	0
5	A	2	0	0	0	0
5	C	2	0	0	0	0
6	A	4	0	0	0	0
6	C	4	0	0	1	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
8	B	8	0	10	1	0
8	D	8	0	10	2	0
9	A	194	0	0	10	0
9	B	216	0	0	9	0
9	C	192	0	0	13	0
9	D	180	0	0	3	0
9	J	6	0	0	0	0
9	K	2	0	0	0	0
9	L	2	0	0	0	0
9	M	1	0	0	0	0
All	All	10157	0	9496	160	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 9.

All (160) 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:154:VAL:HG13	2:B:175:VAL:HG11	1.33	1.10
2:B:177:ASP:HB2	9:B:534:HOH:O	1.50	1.09
2:B:334:MET:HG2	9:B:711:HOH:O	1.53	1.05
1:A:40:GLU:HG2	1:A:43:GLY:O	1.56	1.04
2:D:175:VAL:O	2:D:175:VAL:HG22	1.60	1.00
2:B:175:VAL:HG23	9:B:775:HOH:O	1.61	1.00
1:A:34:LYS:HE2	1:A:77:TYR:HE1	1.30	0.97
1:C:41:THR:HG22	2:D:288:LYS:HE2	1.44	0.96
1:C:41:THR:HG22	2:D:288:LYS:CE	1.95	0.95
1:A:47:THR:HG22	9:A:388:HOH:O	1.67	0.94
1:C:272:ASN:OD1	2:D:174:GLU:HB3	1.67	0.94
1:C:5:GLN:HG2	9:C:390:HOH:O	1.66	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:VAL:O	3:J:1:PRO:HG2	1.66	0.94
1:A:41:THR:HG22	2:B:288:LYS:NZ	1.82	0.93
1:C:161:HIS:HD2	9:C:688:HOH:O	1.51	0.92
1:C:41:THR:HG22	2:D:288:LYS:NZ	1.87	0.88
1:C:34:LYS:HE2	1:C:77:TYR:HE1	1.36	0.88
2:B:388:LYS:HE2	2:B:432:VAL:HG13	1.57	0.87
1:A:34:LYS:HE2	1:A:77:TYR:CE1	2.09	0.86
1:C:34:LYS:HE2	1:C:77:TYR:CE1	2.12	0.84
3:K:6:LYS:O	3:K:7:LEU:HB2	1.75	0.83
1:A:177:CYS:SG	9:B:638:HOH:O	2.36	0.83
2:D:334:MET:HG2	9:D:694:HOH:O	1.78	0.82
1:A:41:THR:HG22	2:B:288:LYS:CE	2.10	0.81
1:A:154:VAL:CG1	2:B:175:VAL:HG11	2.10	0.81
2:D:388:LYS:HE2	2:D:432:VAL:HG13	1.63	0.79
2:D:175:VAL:O	2:D:175:VAL:CG2	2.30	0.78
2:B:175:VAL:H	2:B:176:PRO:HD3	1.46	0.78
1:A:163:VAL:O	3:J:1:PRO:CG	2.31	0.77
1:A:41:THR:CG2	2:B:288:LYS:NZ	2.49	0.76
1:A:41:THR:HG22	2:B:288:LYS:HZ1	1.50	0.75
1:C:40:GLU:HG2	1:C:43:GLY:O	1.85	0.75
1:C:165:THR:HG21	3:K:-2:PRO:HB2	1.69	0.75
1:A:181:SER:HB3	9:B:532:HOH:O	1.87	0.75
2:D:175:VAL:N	2:D:176:PRO:HD3	2.03	0.74
2:D:175:VAL:H	2:D:176:PRO:HD3	1.54	0.73
1:A:41:THR:HG22	2:B:288:LYS:HE2	1.69	0.73
1:A:165:THR:HG21	3:J:-2:PRO:HB2	1.70	0.72
1:C:41:THR:CG2	2:D:288:LYS:NZ	2.52	0.72
2:B:201:LYS:HG2	9:B:765:HOH:O	1.89	0.72
1:A:36:ARG:HD3	1:A:36:ARG:H	1.54	0.71
2:D:175:VAL:O	2:D:179:GLN:HB2	1.91	0.71
1:A:273:LYS:HE2	9:A:669:HOH:O	1.93	0.68
1:A:163:VAL:O	3:J:1:PRO:CD	2.42	0.68
1:A:41:THR:HG23	9:A:393:HOH:O	1.93	0.66
2:B:175:VAL:N	2:B:176:PRO:CD	2.60	0.64
2:B:175:VAL:N	2:B:176:PRO:HD3	2.10	0.64
1:C:71:HIS:CE1	2:D:296:HIS:CD2	2.87	0.63
9:A:627:HOH:O	2:B:173:ASN:HB3	1.98	0.63
1:C:157:ARG:NH2	2:D:268:GLU:OE2	2.32	0.63
1:A:41:THR:CG2	2:B:288:LYS:HZ1	2.12	0.62
1:A:71:HIS:CE1	2:B:296:HIS:CD2	2.87	0.62
2:B:175:VAL:HG12	2:B:179:GLN:HB2	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:GLU:H	1:A:2:GLU:CD	2.04	0.61
2:B:175:VAL:HG12	2:B:175:VAL:O	2.00	0.61
1:C:22:ARG:HD3	9:C:390:HOH:O	1.99	0.61
1:C:163:VAL:O	3:K:1:PRO:CG	2.48	0.61
1:C:199:ARG:HG2	9:C:388:HOH:O	2.00	0.60
1:C:36[A]:ARG:H	1:C:36[A]:ARG:HD3	1.66	0.60
1:C:268:HIS:NE2	1:C:273:LYS:HE3	2.17	0.59
2:B:388:LYS:HE2	2:B:432:VAL:CG1	2.30	0.59
2:D:275:VAL:HG21	2:D:292:LEU:HD21	1.86	0.58
1:A:154:VAL:HG13	2:B:175:VAL:CG1	2.22	0.58
1:C:41:THR:HG22	2:D:288:LYS:HZ1	1.67	0.58
1:C:2:GLU:H	1:C:2:GLU:CD	2.06	0.58
1:C:41:THR:CG2	2:D:288:LYS:HE2	2.29	0.57
2:D:305:ASP:HB3	8:D:4:DTU:H3	1.86	0.57
1:C:73:GLU:HG3	1:C:74:ASN:N	2.20	0.56
1:C:230:VAL:O	1:C:233:MET:HG3	2.05	0.56
1:A:230:VAL:O	1:A:233:MET:HG3	2.05	0.56
1:A:73:GLU:HG3	1:A:74:ASN:N	2.21	0.56
1:C:71:HIS:CD2	1:C:76:LEU:HD13	2.41	0.56
1:A:163:VAL:O	3:J:1:PRO:HD2	2.05	0.55
1:A:268:HIS:NE2	1:A:273:LYS:HE3	2.22	0.55
1:C:273:LYS:HE2	9:C:685:HOH:O	2.07	0.55
2:B:275:VAL:HG21	2:B:292:LEU:HD21	1.88	0.55
1:C:154:VAL:HG13	2:D:175:VAL:HG21	1.87	0.54
1:C:14[A]:THR:N	6:C:300:MGF:F2	2.26	0.54
1:A:163:VAL:C	3:J:1:PRO:HG2	2.28	0.54
1:C:260:ARG:HD3	9:C:538:HOH:O	2.08	0.54
1:C:163:VAL:O	3:K:1:PRO:HD2	2.08	0.54
2:B:175:VAL:O	2:B:179:GLN:HB2	2.08	0.54
3:K:6:LYS:O	3:K:7:LEU:CB	2.52	0.54
2:D:175:VAL:N	2:D:176:PRO:CD	2.72	0.53
1:A:71:HIS:CD2	1:A:76:LEU:HD13	2.43	0.53
2:D:385:GLU:O	2:D:388:LYS:HB2	2.10	0.52
1:C:163:VAL:O	3:K:1:PRO:CD	2.57	0.52
2:B:334:MET:HE2	9:B:711:HOH:O	2.10	0.52
1:A:36:ARG:HD3	1:A:36:ARG:N	2.22	0.51
1:C:161:HIS:CD2	9:C:688:HOH:O	2.38	0.51
2:D:388:LYS:HE2	2:D:432:VAL:CG1	2.37	0.50
2:B:175:VAL:CG2	9:B:775:HOH:O	2.36	0.50
2:B:334:MET:HE3	9:B:670:HOH:O	2.12	0.50
9:C:662:HOH:O	2:D:173:ASN:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:41:THR:CG2	2:D:288:LYS:HZ3	2.25	0.49
2:B:198:GLY:O	2:B:201:LYS:HG3	2.11	0.49
1:A:161:HIS:HE1	9:A:341:HOH:O	1.94	0.49
1:C:16[B]:GLY:HA3	1:C:34:LYS:O	2.12	0.49
1:C:17[B]:VAL:HG22	1:C:19:TYR:CE2	2.47	0.49
1:C:71:HIS:HD2	1:C:76:LEU:HD13	1.77	0.49
2:B:305:ASP:HB3	8:B:3:DTU:H3	1.95	0.48
1:C:153:GLY:HA3	9:C:420:HOH:O	2.13	0.48
2:D:334:MET:HE2	9:D:694:HOH:O	2.12	0.48
1:C:0:HIS:HB3	1:C:2:GLU:OE2	2.12	0.48
1:A:71:HIS:HE1	2:B:296:HIS:CD2	2.30	0.48
2:B:175:VAL:H	2:B:176:PRO:CD	2.16	0.48
2:D:193:CYS:O	2:D:241:ARG:HD2	2.14	0.47
1:A:0:HIS:HB3	1:A:2:GLU:OE2	2.14	0.47
1:A:272:ASN:OD1	2:B:174:GLU:HB3	2.13	0.47
1:C:71:HIS:HE1	2:D:296:HIS:CD2	2.32	0.47
1:A:37:LEU:O	1:A:40:GLU:HB3	2.14	0.47
9:C:345:HOH:O	3:K:-2:PRO:HG3	2.15	0.47
1:C:17[B]:VAL:HG21	1:C:19:TYR:CZ	2.50	0.47
1:C:173:ILE:HD11	1:C:184:VAL:HG11	1.97	0.47
3:J:6:LYS:O	3:J:7:LEU:CB	2.63	0.47
1:C:139:GLY:HA2	1:C:294:PRO:HD3	1.97	0.47
1:A:260:ARG:HD3	9:A:787:HOH:O	2.15	0.46
2:B:194:LYS:HD3	2:B:351:LEU:HD23	1.96	0.46
2:D:365:TYR:OH	2:D:431:SER:HB3	2.14	0.46
1:A:41:THR:CG2	2:B:288:LYS:HZ3	2.26	0.46
1:A:12:GLU:HB3	9:A:389:HOH:O	2.15	0.46
1:C:38:ASP:HB3	1:C:74:ASN:OD1	2.15	0.46
2:D:194:LYS:HD3	2:D:351:LEU:HD23	1.98	0.46
1:A:157:ARG:NH2	2:B:268:GLU:OE2	2.48	0.46
1:C:89:LYS:NZ	9:C:546:HOH:O	2.48	0.46
2:B:274:GLU:HG2	2:B:277:GLU:HG3	1.97	0.46
1:C:17[B]:VAL:HG23	1:C:18[B]:VAL:N	2.30	0.45
2:D:175:VAL:HG22	2:D:179:GLN:HB2	1.99	0.45
1:A:15:TYR:CE1	1:A:47:THR:HG21	2.51	0.45
3:K:7:LEU:HD23	3:K:7:LEU:HA	1.83	0.45
3:J:6:LYS:O	3:J:7:LEU:HB3	2.17	0.45
1:C:41:THR:CG2	2:D:288:LYS:HZ1	2.28	0.44
1:C:161:HIS:HE1	9:C:357:HOH:O	2.01	0.44
1:C:41:THR:HG21	2:D:288:LYS:HZ3	1.82	0.44
1:A:13:GLY:N	9:A:389:HOH:O	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:37:LEU:O	1:C:40:GLU:O	2.36	0.43
1:A:139:GLY:HA2	1:A:294:PRO:HD3	2.00	0.43
2:D:382:TYR:HB3	2:D:387:LEU:CD1	2.49	0.43
2:B:365:TYR:OH	2:B:431:SER:HB3	2.17	0.43
2:B:388:LYS:CE	2:B:432:VAL:HG13	2.39	0.42
3:J:0:THR:HA	3:J:1:PRO:HD3	1.91	0.42
2:D:305:ASP:CB	8:D:4:DTU:H3	2.49	0.42
1:A:157:ARG:HB2	9:A:712:HOH:O	2.19	0.42
1:A:71:HIS:HD2	1:A:76:LEU:HD13	1.84	0.42
2:D:198:GLY:O	2:D:201:LYS:HG3	2.20	0.42
2:B:175:VAL:CG1	2:B:175:VAL:O	2.67	0.41
1:A:2:GLU:HG3	2:D:293:ARG:HH22	1.85	0.41
2:B:385:GLU:O	2:B:388:LYS:HB2	2.21	0.41
1:C:268:HIS:CD2	9:C:762:HOH:O	2.72	0.41
1:A:47:THR:HG23	9:A:396:HOH:O	2.20	0.41
2:B:293:ARG:HH22	1:C:2:GLU:HG3	1.85	0.41
1:A:38:ASP:HB3	1:A:74:ASN:OD1	2.20	0.41
1:A:253:PRO:HB2	1:A:254:PRO:HD3	2.01	0.41
1:A:37:LEU:O	1:A:40:GLU:O	2.39	0.41
1:C:124:LEU:HG	1:C:152:PHE:CD2	2.56	0.41
2:D:334:MET:HE3	9:D:679:HOH:O	2.21	0.41
2:D:401:ALA:N	2:D:402:PRO:CD	2.84	0.41
2:D:229:ASN:HD22	2:D:334:MET:CE	2.35	0.40
2:B:425:ASN:HA	2:B:426:PRO:HD3	1.97	0.40
2:D:199:TYR:C	2:D:199:TYR:CD1	2.94	0.40

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	295/298 (99%)	291 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	305/298 (102%)	301 (99%)	4 (1%)	0	100	100
2	B	259/261 (99%)	258 (100%)	0	1 (0%)	39	27
2	D	259/261 (99%)	257 (99%)	1 (0%)	1 (0%)	39	27
3	J	8/10 (80%)	8 (100%)	0	0	100	100
3	K	8/10 (80%)	8 (100%)	0	0	100	100
3	L	2/10 (20%)	2 (100%)	0	0	100	100
3	M	2/10 (20%)	2 (100%)	0	0	100	100
All	All	1138/1158 (98%)	1127 (99%)	9 (1%)	2 (0%)	52	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	175	VAL
2	B	175	VAL

### 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	261/261 (100%)	254 (97%)	7 (3%)	52	42
1	C	268/261 (103%)	261 (97%)	7 (3%)	54	44
2	B	234/234 (100%)	230 (98%)	4 (2%)	68	63
2	D	234/234 (100%)	230 (98%)	4 (2%)	68	63
3	J	9/9 (100%)	9 (100%)	0	100	100
3	K	9/9 (100%)	8 (89%)	1 (11%)	8	2
3	L	3/9 (33%)	3 (100%)	0	100	100
3	M	3/9 (33%)	3 (100%)	0	100	100
All	All	1021/1026 (100%)	998 (98%)	23 (2%)	60	50

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG
1	A	37	LEU
1	A	38	ASP
1	A	122	ARG
1	A	148	LEU
1	A	150	ARG
1	A	163	VAL
2	B	174	GLU
2	B	201	LYS
2	B	431	SER
2	B	432	VAL
1	C	36[A]	ARG
1	C	36[B]	ARG
1	C	37	LEU
1	C	122	ARG
1	C	148	LEU
1	C	150	ARG
1	C	233	MET
2	D	177	ASP
2	D	201	LYS
2	D	431	SER
2	D	432	VAL
3	K	7	LEU

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 ⓘ

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	8,10,11	1.14	0	7,14,16	1.01	0
1	TPO	C	160	1	8,10,11	1.19	0	7,14,16	1.10	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	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 (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	160	TPO	O-C-CA	-2.18	119.67	125.44

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, 6 are monoatomic - leaving 6 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	ADP	A	297	5,6	22,29,29	1.02	1 (4%)	27,45,45	2.11	4 (14%)
6	MGF	A	300	3,4	0,3,3	0.00	-	0,3,3	0.00	-
8	DTU	B	3	2	7,7,7	1.09	0	4,8,8	2.03	1 (25%)
4	ADP	C	297	5,6	22,29,29	1.03	1 (4%)	27,45,45	1.99	5 (18%)
6	MGF	C	300	3,4	0,3,3	0.00	-	0,3,3	0.00	-
8	DTU	D	4	2	7,7,7	0.94	0	4,8,8	2.01	1 (25%)

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	ADP	A	297	5,6	-	0/12/32/32	0/3/3/3
6	MGF	A	300	3,4	-	0/0/0/0	0/0/0/0
8	DTU	B	3	2	-	0/8/8/8	0/0/0/0
4	ADP	C	297	5,6	-	0/12/32/32	0/3/3/3
6	MGF	C	300	3,4	-	0/0/0/0	0/0/0/0
8	DTU	D	4	2	-	0/8/8/8	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	297	ADP	C5-C4	3.05	1.47	1.40
4	C	297	ADP	C5-C4	3.18	1.47	1.40

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	297	ADP	N3-C2-N1	-7.26	123.33	128.89
4	C	297	ADP	N3-C2-N1	-6.90	123.61	128.89
4	A	297	ADP	C2'-C1'-N9	-5.99	105.14	114.29
4	C	297	ADP	C2'-C1'-N9	-5.30	106.20	114.29
8	B	3	DTU	O2-C2-C3	-3.96	101.70	109.79
8	D	4	DTU	O2-C2-C3	-3.20	103.26	109.79
4	C	297	ADP	C4-C5-N7	-2.34	107.33	109.48
4	A	297	ADP	O3A-PA-O5'	-2.29	96.86	102.94
4	A	297	ADP	C4-C5-N7	-2.01	107.63	109.48
4	C	297	ADP	O3B-PB-O2B	2.09	115.35	107.38
4	C	297	ADP	O2A-PA-O3A	2.27	115.41	105.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	3	DTU	1	0
6	C	300	MGF	1	0
8	D	4	DTU	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, 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	297/298 (99%)	0.49	33 (11%) 7 8	23, 36, 88, 136	0
1	C	297/298 (99%)	0.39	36 (12%) 6 6	23, 36, 78, 136	0
2	B	261/261 (100%)	0.17	10 (3%) 44 48	19, 34, 63, 146	0
2	D	261/261 (100%)	0.23	17 (6%) 22 25	21, 36, 64, 146	0
3	J	10/10 (100%)	2.43	5 (50%) 0 0	52, 67, 89, 107	0
3	K	10/10 (100%)	4.00	9 (90%) 0 0	53, 67, 89, 107	0
3	L	4/10 (40%)	2.42	2 (50%) 0 0	49, 67, 69, 73	0
3	M	4/10 (40%)	2.10	2 (50%) 0 0	54, 67, 68, 73	0
All	All	1144/1158 (98%)	0.39	114 (9%) 9 11	19, 36, 80, 146	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	172	SER	14.3
2	D	173	ASN	13.9
2	B	432	VAL	9.7
2	D	175	VAL	9.5
2	B	175	VAL	8.7
2	B	173	ASN	8.7
2	D	174	GLU	8.6
1	A	38	ASP	8.1
1	C	38	ASP	7.9
3	K	-2	PRO	7.6
1	C	0	HIS	7.4
2	D	432	VAL	6.3
2	D	172	SER	6.1
1	A	0	HIS	5.9
2	B	431	SER	5.8
2	B	174	GLU	5.8

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Mol	Chain	Res	Type	RSRZ
1	C	39	THR	5.7
3	J	-2	PRO	5.6
2	D	431	SER	5.5
3	K	7	LEU	5.4
1	A	39	THR	5.2
1	A	13	GLY	4.9
1	C	15[A]	TYR	4.9
3	K	5	LYS	4.8
3	L	4	ALA	4.3
3	K	0	THR	4.0
3	K	2	LYS	4.0
1	C	249	SER	4.0
3	J	7	LEU	3.9
3	K	4	ALA	3.8
3	K	-1	LYS	3.8
1	C	36[A]	ARG	3.6
1	A	-1	GLY	3.6
1	C	163	VAL	3.6
1	A	37	LEU	3.4
1	C	179	TYR	3.4
1	A	52	ILE	3.3
2	B	306	LEU	3.3
1	A	17	VAL	3.3
1	A	74	ASN	3.3
1	A	151	ALA	3.2
1	C	250	LYS	3.2
1	A	178	LYS	3.1
1	A	14	THR	3.1
3	J	-1	LYS	3.1
3	M	4	ALA	3.1
1	C	40	GLU	3.1
1	A	40	GLU	3.0
1	A	143	LEU	3.0
1	C	17[A]	VAL	3.0
1	A	149	ALA	2.9
2	D	306	LEU	2.8
1	C	178	LYS	2.8
1	A	163	VAL	2.8
3	J	6	LYS	2.8
1	C	12[A]	GLU	2.8
2	B	323	GLN	2.8
1	A	249	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	143	LEU	2.7
1	A	146	PHE	2.7
1	C	123	VAL	2.7
2	D	416	SER	2.7
1	C	118	CYS	2.6
2	D	424	LEU	2.6
1	A	295	HIS	2.6
1	A	128	LEU	2.6
3	M	7	LEU	2.6
1	A	49	ILE	2.6
1	A	232	SER	2.6
2	B	267	PHE	2.5
2	D	323	GLN	2.5
2	D	428	GLU	2.5
1	C	37	LEU	2.5
1	A	250	LYS	2.5
2	B	428	GLU	2.4
1	A	124	LEU	2.4
1	C	-1	GLY	2.4
1	C	74	ASN	2.4
1	A	179	TYR	2.4
1	C	128	LEU	2.4
3	K	6	LYS	2.4
1	A	8	GLU	2.3
1	C	151	ALA	2.3
2	D	415	HIS	2.3
1	C	149	ALA	2.3
1	C	2	GLU	2.3
1	C	124	LEU	2.3
1	C	111	LEU	2.3
3	K	1	PRO	2.3
2	D	377	ALA	2.3
3	L	7	LEU	2.2
1	C	154	VAL	2.2
1	C	247	ASP	2.2
1	C	146	PHE	2.2
2	D	378	GLN	2.2
1	C	14[A]	THR	2.2
1	C	58	LEU	2.1
1	C	11[A]	GLY	2.1
1	C	161	HIS	2.1
1	A	148	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
2	D	419	HIS	2.1
1	A	225	VAL	2.1
1	C	152	PHE	2.1
1	A	118	CYS	2.1
2	D	271	TYR	2.1
1	A	7	VAL	2.1
1	A	123	VAL	2.1
1	A	19	TYR	2.0
2	D	374	GLU	2.0
1	C	10[A]	ILE	2.0
3	J	5	LYS	2.0
1	A	1	MET	2.0
1	C	16[A]	GLY	2.0
1	C	288	ASP	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, 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( $\text{\AA}^2$ )	Q<0.9
1	TPO	A	160	11/12	0.95	0.10	-	29,37,47,49	1
1	TPO	C	160	11/12	0.92	0.12	-	28,39,48,56	2

## 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, 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( $\text{\AA}^2$ )	Q<0.9
6	MGF	C	300	4/4	0.90	0.22	0.16	47,63,64,96	0
5	MG	C	298	1/1	0.90	0.14	-0.10	44,44,44,44	0
5	MG	C	299	1/1	0.57	0.17	-0.12	62,62,62,62	1
8	DTU	D	4	8/8	0.91	0.10	-0.27	35,44,48,51	0
6	MGF	A	300	4/4	0.90	0.17	-0.33	47,60,80,89	0
4	ADP	A	297	27/27	0.92	0.11	-0.40	48,53,67,81	0
8	DTU	B	3	8/8	0.94	0.08	-0.53	32,38,42,42	0
4	ADP	C	297	27/27	0.91	0.12	-0.64	52,63,78,89	0
7	CL	C	301	1/1	0.96	0.04	-0.96	47,47,47,47	0
7	CL	A	301	1/1	0.98	0.04	-1.09	49,49,49,49	0
5	MG	A	299	1/1	0.75	0.11	-1.51	65,65,65,65	0
5	MG	A	298	1/1	0.98	0.05	-2.92	34,34,34,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.