



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:59 PM GMT

PDB ID : 4UKD  
Title : UMP/CMP KINASE FROM SLIME MOLD COMPLEXED WITH ADP,  
UDP, BERYLLIUM FLUORIDE  
Authors : Schlichting, I.; Reinstein, J.  
Deposited on : 1997-05-20  
Resolution : 2.00 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.

---

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

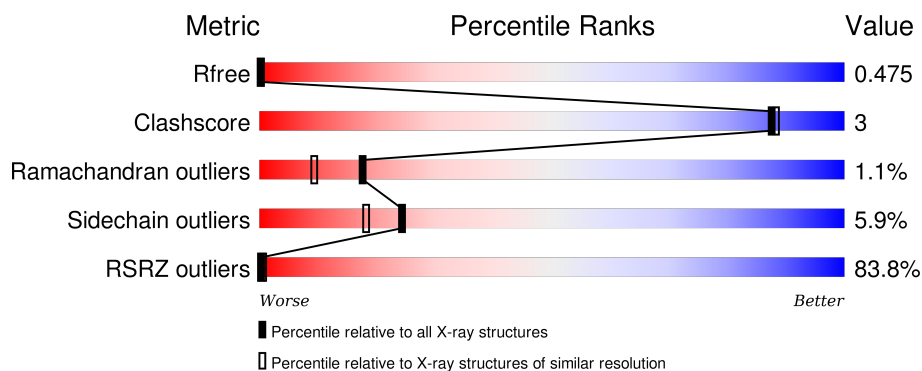
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	194	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 1679 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 URIDYLMONOPHOSPHATE/CYTIDYLMONOPHOSPHATE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	191	Total	C	N	O	S	0	0	0
			1516	952	264	293	7			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

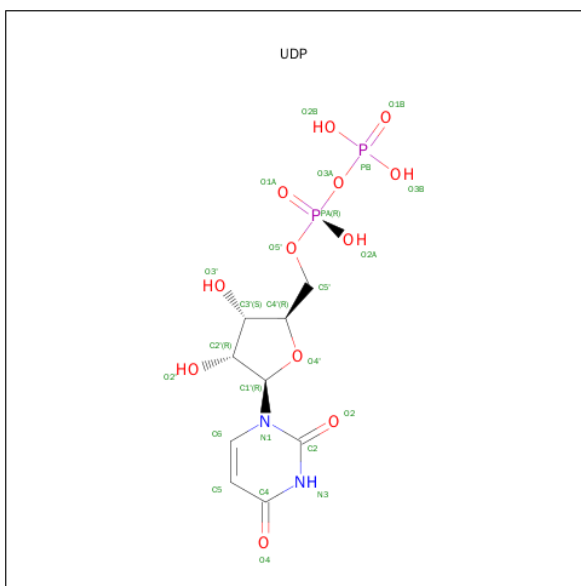
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- 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>).



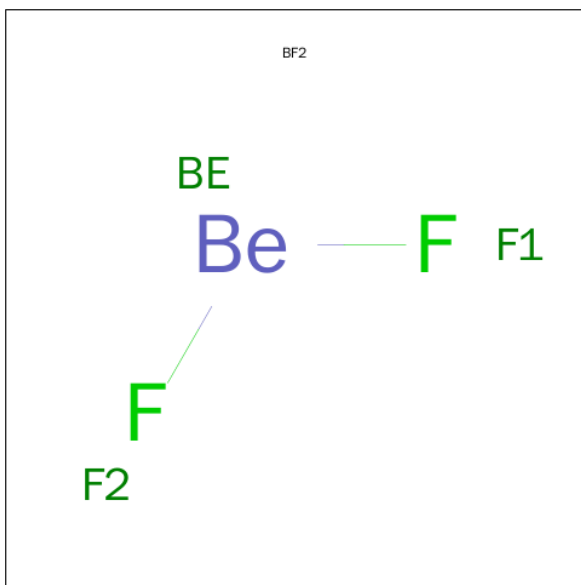
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 5 is BERYLLIUM DIFLUORIDE (three-letter code: BF2) (formula:  $BeF_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	Be	F	0	0
			3	1	2		

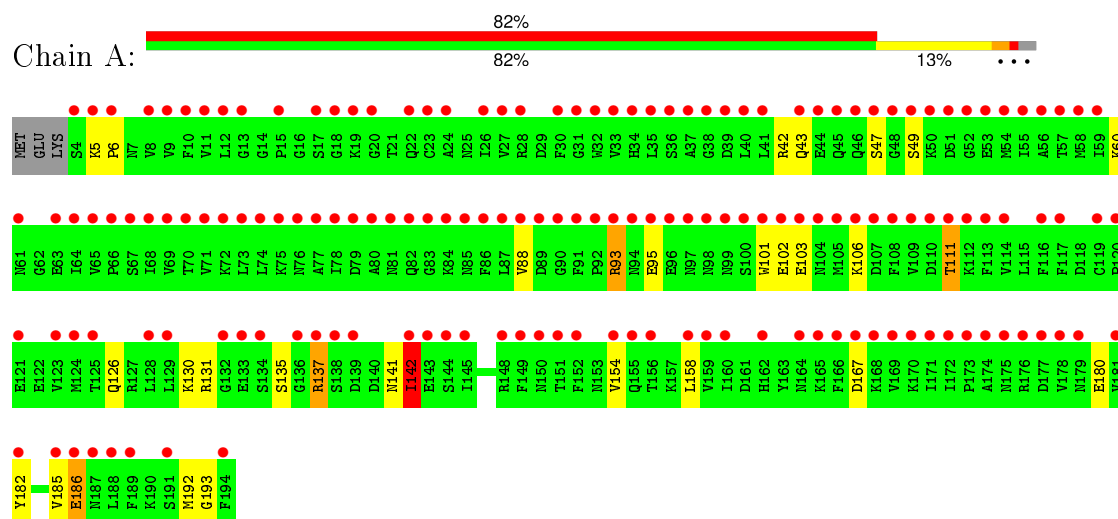
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	107	Total 107	O 107	0	0

### 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: URIDYLMONOPHOSPHATE/CYTIDYLMONOPHOSPHATE KINASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.10Å 78.10Å 101.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.00 – 2.00 39.05 – 1.98	Depositor EDS
% Data completeness (in resolution range)	95.0 (39.00-2.00) 84.4 (39.05-1.98)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 1.98Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.194 , 0.212 0.470 , 0.475	Depositor DCC
$R_{free}$ test set	900 reflections (4.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.2	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 49.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 19164 reflections	Xtriage
$F_o, F_c$ correlation	0.67	EDS
Total number of atoms	1679	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: BF2, MG, UDP, 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	0.65	1/1542 (0.1%)	0.74	5/2073 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	141	ASN	C-N	11.57	1.60	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	ARG	NE-CZ-NH2	7.97	124.29	120.30
1	A	42	ARG	NE-CZ-NH2	7.10	123.85	120.30
1	A	142	ILE	O-C-N	-6.16	112.84	122.70
1	A	93	ARG	NE-CZ-NH2	6.10	123.35	120.30
1	A	141	ASN	C-N-CA	-5.86	107.06	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	142	ILE	Mainchain



## 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	1516	0	1493	8	6
2	A	1	0	0	0	0
3	A	27	0	12	0	0
4	A	25	0	11	0	0
5	A	3	0	0	0	0
6	A	107	0	0	1	3
All	All	1679	0	1516	8	6

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 (8) 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:182:TYR:O	1:A:185:VAL:O	2.25	0.55
1:A:101:TRP:HE1	1:A:111:THR:HG21	1.76	0.50
1:A:131:ARG:HG2	1:A:135:SER:HB3	1.95	0.48
1:A:185:VAL:O	1:A:186:GLU:CB	2.62	0.48
1:A:102:GLU:O	1:A:106:LYS:HB2	2.16	0.46
1:A:182:TYR:O	1:A:182:TYR:CG	2.71	0.44
1:A:5:LYS:HA	1:A:6:PRO:HD3	1.90	0.42
1:A:93:ARG:HG3	6:A:199:HOH:O	2.20	0.42

All (6) 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:47:SER:OG	1:A:95:GLU:OE1[3_655]	1.82	0.38
1:A:193:GLY:O	6:A:532:HOH:O[6_564]	1.89	0.31
1:A:154:VAL:CG1	6:A:207:HOH:O[4_464]	1.95	0.25
1:A:47:SER:CB	1:A:95:GLU:OE1[3_655]	1.97	0.23
1:A:126:GLN:NE2	1:A:192:MET:O[6_464]	2.02	0.18
1:A:43:GLN:NE2	6:A:577:HOH:O[3_655]	2.10	0.10

## 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	189/194 (97%)	182 (96%)	5 (3%)	2 (1%)	17 9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	SER
1	A	186	GLU

### 5.3.2 Protein sidechains [i](#)

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	170/173 (98%)	160 (94%)	10 (6%)	24 18

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LYS
1	A	88	VAL
1	A	103	GLU
1	A	111	THR
1	A	130	LYS
1	A	137	ARG
1	A	142	ILE
1	A	158	LEU
1	A	167	ASP

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	180	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	99	ASN
1	A	164	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	195	2,5	22,29,29	1.47	5 (22%)	27,45,45	0.91	0
4	UDP	A	196	5	18,26,26	2.46	6 (33%)	26,40,40	2.26	8 (30%)
5	BF2	A	501	3,2,4	0,2,2	0.00	-	0,1,1	0.00	-

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	195	2,5	-	0/12/32/32	0/3/3/3
4	UDP	A	196	5	-	0/12/32/32	0/2/2/2
5	BF2	A	501	3,2,4	-	0/0/0/0	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	196	UDP	PB-O2B	-3.02	1.43	1.54
3	A	195	ADP	PA-O2A	-2.98	1.42	1.54
3	A	195	ADP	PB-O2B	-2.79	1.44	1.54
3	A	195	ADP	C8-N7	-2.56	1.29	1.34
4	A	196	UDP	PA-O2A	-2.40	1.44	1.54
4	A	196	UDP	PB-O1B	-2.34	1.43	1.51
4	A	196	UDP	O4'-C4'	-2.24	1.39	1.45
3	A	195	ADP	O2'-C2'	-2.24	1.37	1.43
3	A	195	ADP	PB-O1B	-2.21	1.43	1.51
4	A	196	UDP	O4-C4	4.18	1.34	1.24
4	A	196	UDP	C6-N1	7.46	1.46	1.35

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	196	UDP	C6-N1-C2	-6.64	110.52	121.28
4	A	196	UDP	C5-C4-N3	-2.66	116.29	123.12
4	A	196	UDP	O4'-C4'-C3'	-2.37	100.37	105.15
4	A	196	UDP	O3B-PB-O1B	-2.00	104.13	110.58
4	A	196	UDP	PA-O3A-PB	2.06	139.58	132.67
4	A	196	UDP	O2B-PB-O1B	2.07	117.24	110.58
4	A	196	UDP	C6-C5-C4	4.28	125.28	117.28
4	A	196	UDP	C4-N3-C2	5.98	120.07	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	191/194 (98%)	3.56	160 (83%) 0 0	15, 26, 48, 54	0

All (160) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	48	GLY	11.1
1	A	27	VAL	8.5
1	A	50	LYS	8.1
1	A	136	GLY	7.8
1	A	5	LYS	7.6
1	A	178	VAL	6.9
1	A	117	PHE	6.7
1	A	128	LEU	6.5
1	A	108	PHE	6.3
1	A	104	ASN	6.3
1	A	35	LEU	6.2
1	A	33	VAL	6.2
1	A	91	PHE	6.2
1	A	40	LEU	6.2
1	A	49	SER	6.1
1	A	174	ALA	6.0
1	A	97	ASN	5.9
1	A	20	GLY	5.9
1	A	64	ILE	5.8
1	A	47	SER	5.8
1	A	83	GLY	5.8
1	A	113	PHE	5.7
1	A	4	SER	5.6
1	A	134	SER	5.6
1	A	55	ILE	5.5
1	A	166	PHE	5.5
1	A	80	ALA	5.5

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	37	ALA	5.5
1	A	32	TRP	5.4
1	A	103	GLU	5.4
1	A	11	VAL	5.4
1	A	71	VAL	5.4
1	A	132	GLY	5.3
1	A	159	VAL	5.2
1	A	186	GLU	5.1
1	A	116	PHE	5.0
1	A	52	GLY	5.0
1	A	156	THR	4.9
1	A	54	MET	4.8
1	A	12	LEU	4.8
1	A	99	ASN	4.8
1	A	149	PHE	4.8
1	A	57	THR	4.7
1	A	181	VAL	4.7
1	A	189	PHE	4.7
1	A	109	VAL	4.6
1	A	82	GLN	4.5
1	A	65	VAL	4.5
1	A	30	PHE	4.5
1	A	194	PHE	4.4
1	A	15	PRO	4.4
1	A	75	LYS	4.4
1	A	73	LEU	4.3
1	A	23	CYS	4.3
1	A	31	GLY	4.2
1	A	87	LEU	4.2
1	A	151	THR	4.1
1	A	26	ILE	4.1
1	A	58	MET	4.1
1	A	10	PHE	4.1
1	A	79	ASP	4.1
1	A	51	ASP	4.1
1	A	110	ASP	4.0
1	A	45	GLN	4.0
1	A	152	PHE	4.0
1	A	158	LEU	4.0
1	A	111	THR	4.0
1	A	68	ILE	4.0
1	A	6	PRO	3.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	119	CYS	3.9
1	A	24	ALA	3.9
1	A	123	VAL	3.9
1	A	8	VAL	3.8
1	A	154	VAL	3.7
1	A	168	LYS	3.7
1	A	72	LYS	3.7
1	A	165	LYS	3.7
1	A	185	VAL	3.7
1	A	138	SER	3.7
1	A	145	ILE	3.7
1	A	41	LEU	3.7
1	A	9	VAL	3.7
1	A	170	LYS	3.6
1	A	81	ASN	3.6
1	A	155	GLN	3.5
1	A	121	GLU	3.5
1	A	125	THR	3.5
1	A	139	ASP	3.4
1	A	70	THR	3.4
1	A	34	HIS	3.4
1	A	88	VAL	3.4
1	A	179	ASN	3.4
1	A	69	VAL	3.4
1	A	17	SER	3.4
1	A	182	TYR	3.4
1	A	93	ARG	3.3
1	A	107	ASP	3.3
1	A	46	GLN	3.3
1	A	78	ILE	3.3
1	A	74	LEU	3.2
1	A	169	VAL	3.2
1	A	114	VAL	3.2
1	A	171	ILE	3.1
1	A	133	GLU	3.1
1	A	89	ASP	3.1
1	A	101	TRP	3.1
1	A	95	GLU	3.1
1	A	177	ASP	3.0
1	A	143	GLU	3.0
1	A	43	GLN	3.0
1	A	86	PHE	3.0

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	112	LYS	2.9
1	A	167	ASP	2.9
1	A	92	PRO	2.8
1	A	13	GLY	2.8
1	A	100	SER	2.8
1	A	105	MET	2.7
1	A	90	GLY	2.7
1	A	137	ARG	2.7
1	A	63	GLU	2.7
1	A	188	LEU	2.7
1	A	162	HIS	2.7
1	A	76	ASN	2.7
1	A	164	ASN	2.7
1	A	173	PRO	2.7
1	A	77	ALA	2.6
1	A	38	GLY	2.6
1	A	44	GLU	2.6
1	A	191	SER	2.6
1	A	94	ASN	2.6
1	A	106	LYS	2.6
1	A	59	ILE	2.6
1	A	160	ILE	2.6
1	A	172	ILE	2.6
1	A	18	GLY	2.5
1	A	144	SER	2.5
1	A	36	SER	2.5
1	A	129	LEU	2.5
1	A	22	GLN	2.5
1	A	148	ARG	2.5
1	A	39	ASP	2.4
1	A	28	ARG	2.4
1	A	67	SER	2.4
1	A	66	PRO	2.3
1	A	61	ASN	2.3
1	A	175	ASN	2.3
1	A	176	ARG	2.3
1	A	142	ILE	2.3
1	A	53	GLU	2.3
1	A	96	GLU	2.3
1	A	19	LYS	2.2
1	A	85	ASN	2.2
1	A	150	ASN	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	102	GLU	2.1
1	A	124	MET	2.1
1	A	187	ASN	2.0
1	A	56	ALA	2.0
1	A	84	LYS	2.0
1	A	98	ASN	2.0
1	A	120	PRO	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 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(Å <sup>2</sup> )	Q<0.9
4	UDP	A	196	25/25	0.70	0.28	-0.49	18,20,21,22	0
5	BF2	A	501	3/3	0.62	0.21	-1.12	15,15,19,19	0
3	ADP	A	195	27/27	0.75	0.22	-1.12	17,19,21,24	0
2	MG	A	500	1/1	0.84	0.14	-2.33	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.