



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 08:17 PM GMT

PDB ID : 4RER  
Title : Crystal structure of the phosphorylated human alpha1 beta2 gamma1 holo-AMPK complex bound to AMP and cyclodextrin  
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Deposited on : 2014-09-23  
Resolution : 4.05 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

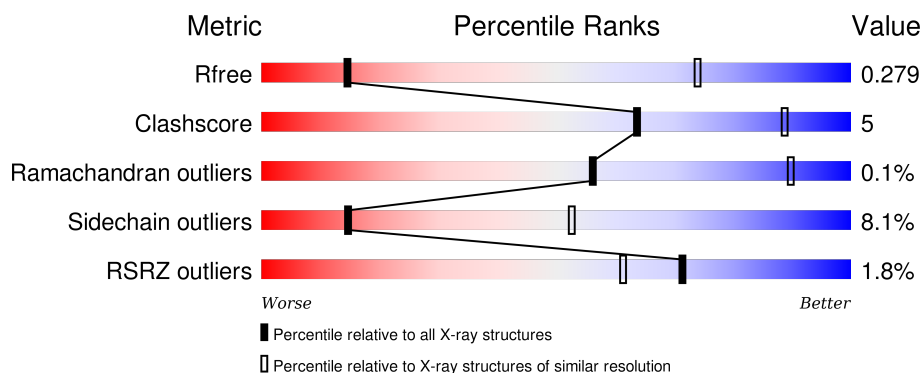
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 4.05 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	1022 (4.50-3.58)
Clashscore	102246	1059 (4.48-3.60)
Ramachandran outliers	100387	1011 (4.48-3.60)
Sidechain outliers	100360	1054 (4.50-3.58)
RSRZ outliers	91569	1025 (4.50-3.58)

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	540	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 10%, orange 15%, yellow 15%, green 68%, grey 15%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>10%</span> <span>68%</span> <span>15%</span> <span>•</span> <span>15%</span> </div> </div>
2	B	197	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 5%, orange 19%, yellow 8%, green 73%, grey 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>5%</span> <span>73%</span> <span>19%</span> <span>•</span> <span>8%</span> </div> </div>
3	G	304	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 81%, yellow 16%, grey 3%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>81%</span> <span>16%</span> <span>••</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
5	EPE	A	602	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7798 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 5'-AMP-activated protein kinase catalytic subunit alpha-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	P	S	0	0	0
			3725	2376	649	677	1	22			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	SER	ARG	CONFLICT	UNP Q13131
A	260	SER	THR	CONFLICT	UNP Q13131
A	471	GLY	GLU	ENGINEERED MUTATION	UNP Q13131
A	474	ALA	GLU	ENGINEERED MUTATION	UNP Q13131
A	476	ALA	LYS	ENGINEERED MUTATION	UNP Q13131

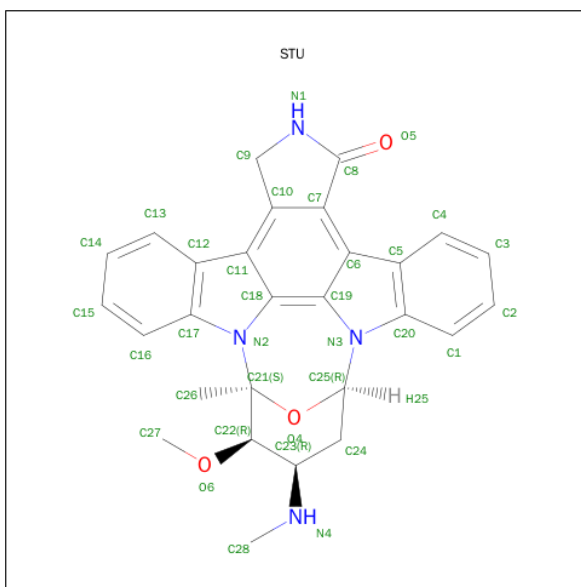
- Molecule 2 is a protein called 5'-AMP-activated protein kinase subunit beta-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	181	Total	C	N	O	P	S	0	0	0
			1458	945	240	268	1	4			

- Molecule 3 is a protein called 5'-AMP-activated protein kinase subunit gamma-1.

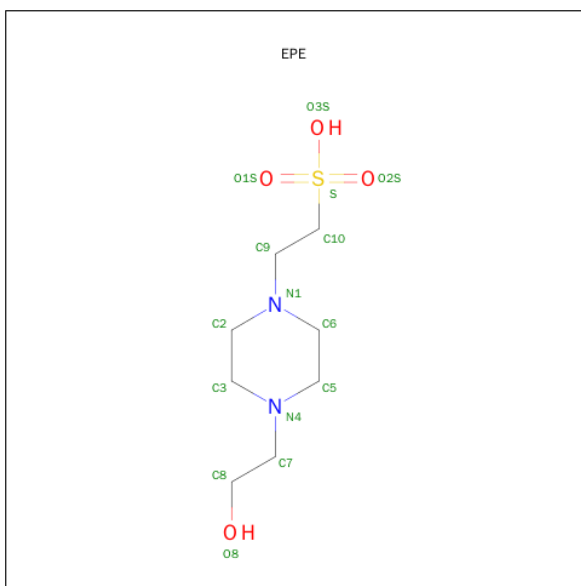
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	300	Total	C	N	O	S	0	0	0
			2419	1571	403	438	7			

- Molecule 4 is STAUROSPORINE (three-letter code: STU) (formula: C<sub>28</sub>H<sub>26</sub>N<sub>4</sub>O<sub>3</sub>).



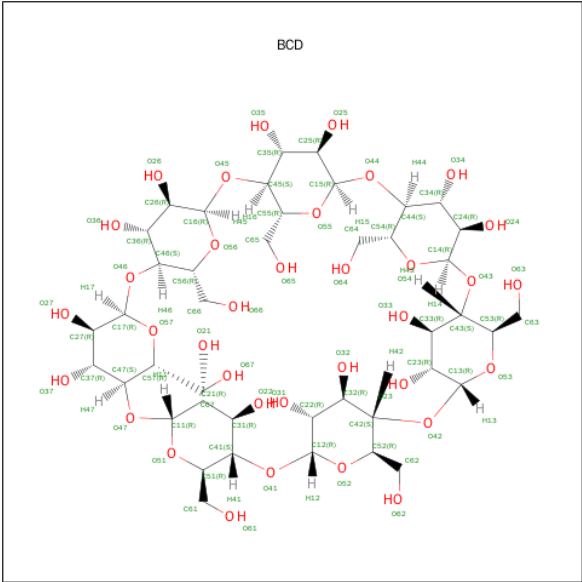
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			35	28	4	3		

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula:  $C_8H_{18}N_2O_4S$ ).



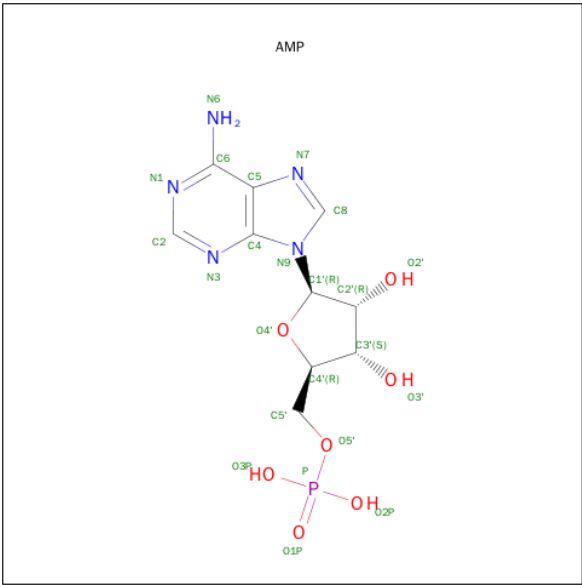
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 6 is SUGAR (BETA-CYCLODEXTRIN) (three-letter code: BCD) (formula:  $C_{42}H_{70}O_{35}$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			77	42	35		

- Molecule 7 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	G	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
7	G	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
7	G	1	Total	C	N	O	P	0	0
			23	10	5	7	1		



R243	F244	D245	V246	I247	R253	R269	S270	H271	V272	F273	C279	V280	L281	L292	H298	R299	L300	V301	V302	K310	G311	I312	L315	L324	THR	GLY	GLY
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.57Å 132.57Å 195.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.66 – 4.05 39.66 – 4.05	Depositor EDS
% Data completeness (in resolution range)	99.0 (39.66-4.05) 99.1 (39.66-4.05)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 4.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.224 , 0.260 0.257 , 0.279	Depositor DCC
$R_{free}$ test set	1213 reflections (7.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	122.7	Xtriage
Anisotropy	0.500	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 118.7	EDS
Estimated twinning fraction	0.036 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 16574 reflections	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	7798	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	168.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% 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: STU, TPO, SEP, BCD, AMP, EPE

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	0.30	0/3800	0.48	1/5132 (0.0%)
2	B	0.31	0/1491	0.54	1/2027 (0.0%)
3	G	0.28	0/2470	0.46	0/3353
All	All	0.30	0/7761	0.49	2/10512 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	187	GLY	C-N-CD	5.84	140.66	128.40
1	A	291	ASP	CB-CG-OD2	5.20	122.98	118.30

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	3725	0	3716	41	0
2	B	1458	0	1446	16	0
3	G	2419	0	2483	26	0
4	A	35	0	26	3	0
5	A	15	0	17	1	0
6	B	77	0	68	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	69	0	36	1	0
All	All	7798	0	7792	81	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 5.

The worst 5 of 81 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:424:TYR:CD2	1:A:438:ARG:HB3	2.12	0.85
1:A:32:VAL:HG12	1:A:47:LYS:HA	1.76	0.68
3:G:101:SER:HB3	3:G:104:VAL:HG22	1.75	0.66
3:G:301:VAL:HG12	3:G:312:ILE:HG12	1.80	0.64
3:G:173:LEU:HD12	3:G:315:LEU:HD22	1.80	0.64

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	448/540 (83%)	426 (95%)	22 (5%)	0	100	100
2	B	176/197 (89%)	165 (94%)	11 (6%)	0	100	100
3	G	298/304 (98%)	285 (96%)	12 (4%)	1 (0%)	46	82
All	All	922/1041 (89%)	876 (95%)	45 (5%)	1 (0%)	56	90

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	106	ILE

### 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	414/484 (86%)	379 (92%)	35 (8%)	13	51
2	B	166/181 (92%)	150 (90%)	16 (10%)	10	44
3	G	275/278 (99%)	257 (94%)	18 (6%)	21	61
All	All	855/943 (91%)	786 (92%)	69 (8%)	15	52

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	438	ARG
2	B	117	ASP
3	G	181	THR
1	A	443	THR
2	B	85	GLU

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	174	1	8,10,11	1.06	0	7,14,16	1.32	1 (14%)
2	SEP	B	108	2	8,9,10	1.51	1 (12%)	8,12,14	1.10	1 (12%)

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	174	1	-	0/8/11/13	0/0/0/0
2	SEP	B	108	2	-	0/6/8/10	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	108	SEP	P-O1P	3.08	1.61	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	TPO	CG2-CB-CA	-2.28	108.53	113.17
2	B	108	SEP	O-C-CA	-2.16	119.87	125.49

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](#)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link

column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	STU	A	601	-	27,42,42	0.88	1 (3%)	23,68,68	1.32	1 (4%)
5	EPE	A	602	-	14,15,15	0.44	0	18,20,20	1.56	4 (22%)
6	BCD	B	301	-	84,84,84	1.27	10 (11%)	126,126,126	1.24	15 (11%)
7	AMP	G	401	-	20,25,25	1.48	3 (15%)	22,38,38	1.98	3 (13%)
7	AMP	G	402	-	20,25,25	1.44	3 (15%)	22,38,38	2.05	3 (13%)
7	AMP	G	403	-	20,25,25	1.45	3 (15%)	22,38,38	1.72	3 (13%)

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	STU	A	601	-	-	0/4/42/42	0/0/8/8
5	EPE	A	602	-	-	0/9/19/19	0/1/1/1
6	BCD	B	301	-	-	0/42/182/182	0/0/8/8
7	AMP	G	401	-	-	0/6/26/26	0/3/3/3
7	AMP	G	402	-	-	0/6/26/26	0/3/3/3
7	AMP	G	403	-	-	0/6/26/26	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	301	BCD	C31-C41	-3.41	1.42	1.52
6	B	301	BCD	O25-C25	-3.13	1.35	1.43
6	B	301	BCD	C33-C43	-3.11	1.43	1.52
7	G	401	AMP	P-O3P	-3.10	1.43	1.54
7	G	402	AMP	P-O3P	-3.03	1.43	1.54

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	402	AMP	N3-C2-N1	-8.28	122.55	128.89
7	G	401	AMP	N3-C2-N1	-7.94	122.82	128.89
7	G	403	AMP	N3-C2-N1	-6.75	123.72	128.89
4	A	601	STU	C27-O6-C22	-3.78	107.17	114.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	402	AMP	C4-C5-N7	-2.64	107.05	109.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	STU	3	0
5	A	602	EPE	1	0
7	G	402	AMP	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	458/540 (84%)	-0.33	8 (1%) 73 63	108, 154, 287, 409	0
2	B	180/197 (91%)	0.10	9 (5%) 32 24	120, 220, 314, 361	0
3	G	300/304 (98%)	-0.52	0 100 100	98, 132, 212, 332	0
All	All	938/1041 (90%)	-0.31	17 (1%) 71 61	98, 151, 281, 409	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	285	TYR	4.0
2	B	93	SER	3.9
1	A	318	HIS	3.8
2	B	142	VAL	3.4
1	A	286	SER	3.3

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

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	174	11/12	0.96	0.17	-	123,136,138,138	0
2	SEP	B	108	10/11	0.73	0.23	-	222,225,311,311	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.



## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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
5	EPE	A	602	15/15	0.74	0.56	2.14	160,165,172,173	0
7	AMP	G	401	23/23	0.89	0.30	1.57	117,127,154,156	0
4	STU	A	601	35/35	0.95	0.24	0.06	121,124,127,127	0
7	AMP	G	403	23/23	0.87	0.25	0.02	111,122,131,133	0
7	AMP	G	402	23/23	0.93	0.24	-0.28	99,101,128,129	0
6	BCD	B	301	77/77	0.78	0.30	-0.47	233,247,260,265	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.