



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 05:00 pm GMT

PDB ID : 2OOX
Title : Crystal structure of the adenylate sensor from AMP-activated protein kinase complexed with AMP
Authors : Townley, R.; Shapiro, L.
Deposited on : 2007-01-26
Resolution : 2.60 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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

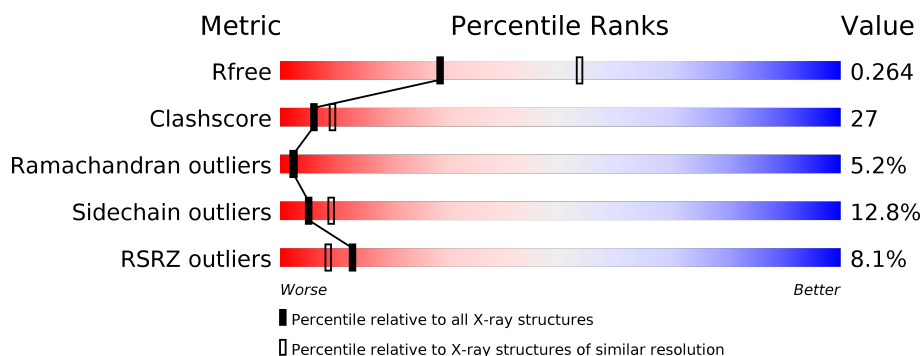
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	137	<div> <div>7%</div> <div> <div>53%</div> <div>31%</div> <div>9%</div> <div>7%</div> </div> </div>
1	C	137	<div> <div>15%</div> <div> <div>49%</div> <div>31%</div> <div>12%</div> <div>7%</div> </div> </div>
2	B	97	<div> <div>14%</div> <div> <div>52%</div> <div>29%</div> <div>12%</div> <div>•</div> </div> </div>
2	D	97	<div> <div>12%</div> <div> <div>45%</div> <div>30%</div> <div>15%</div> <div>5%</div> <div>•</div> </div> </div>
3	E	333	<div> <div>6%</div> <div> <div>63%</div> <div>30%</div> <div>6%</div> <div>•</div> </div> </div>
3	G	333	<div> <div>4%</div> <div> <div>57%</div> <div>30%</div> <div>10%</div> <div>•</div> </div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9329 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 SNF1-like protein kinase ssp2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	0	0	0
			1025	657	178	180	10			
1	C	128	Total	C	N	O	S	0	0	0
			1003	646	173	175	9			

- Molecule 2 is a protein called SPCC1919.03c protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	93	Total	C	N	O	S	0	0	0
			733	467	125	139	2			
2	D	93	Total	C	N	O	S	6	0	0
			733	467	125	139	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	202	MET	-	CLONING ARTIFACT	UNP P78789
D	202	MET	-	CLONING ARTIFACT	UNP P78789

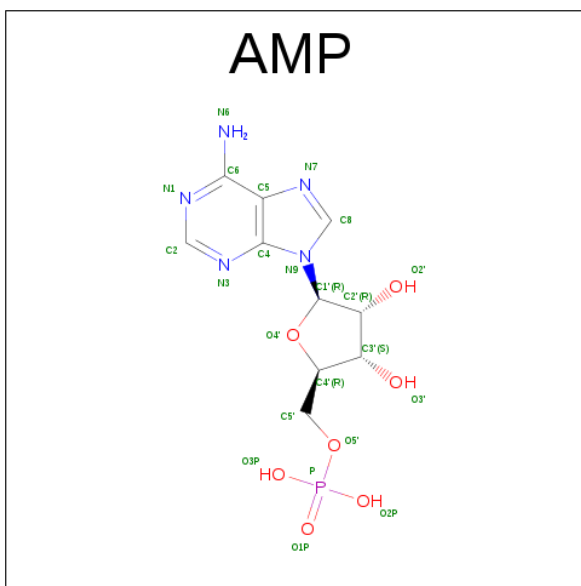
- Molecule 3 is a protein called Hypothetical protein C1556.08c in chromosome I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	324	Total	C	N	O	S	0	1	0
			2548	1629	426	478	15			
3	E	333	Total	C	N	O	S	0	0	0
			2589	1649	433	492	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	2	MET	-	CLONING ARTIFACT	UNP Q10343
G	2	MET	-	CLONING ARTIFACT	UNP Q10343

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



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

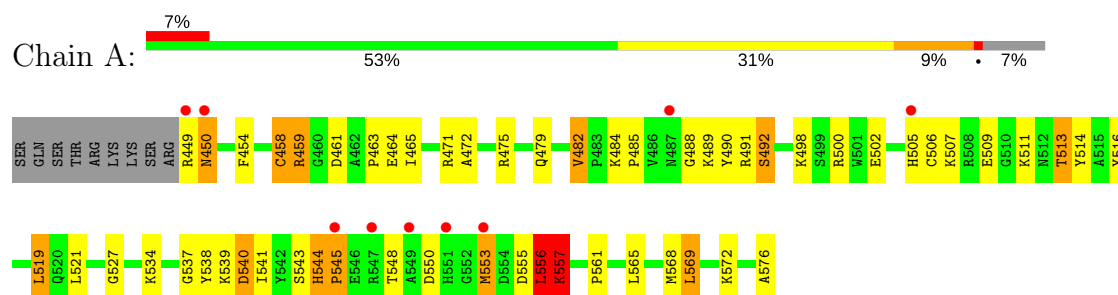
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	94	Total	O	0	0
			94	94		
5	B	78	Total	O	0	0
			78	78		
5	C	66	Total	O	0	0
			66	66		
5	D	51	Total	O	0	0
			51	51		
5	E	146	Total	O	0	0
			146	146		
5	G	217	Total	O	0	0
			217	217		

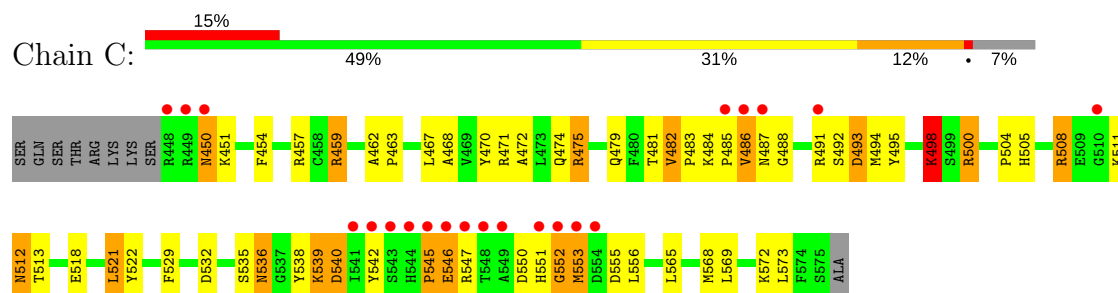
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

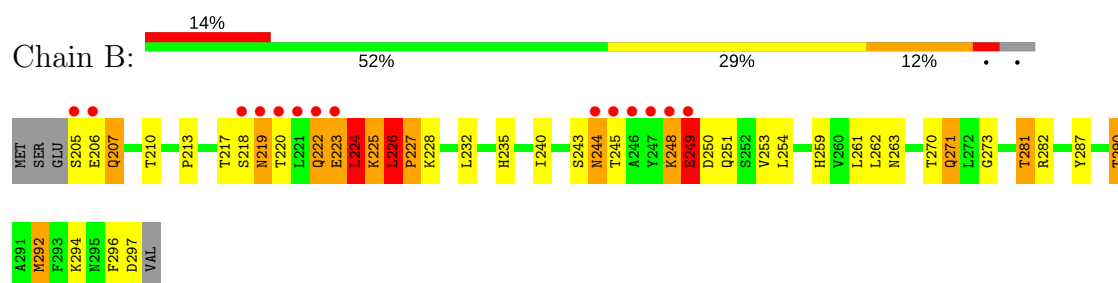
- Molecule 1: SNF1-like protein kinase ssp2



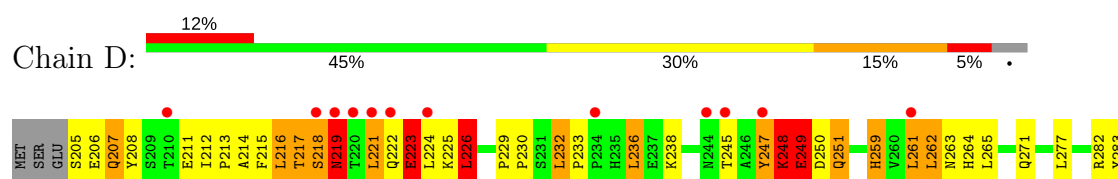
- Molecule 1: SNF1-like protein kinase ssp2

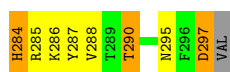


- Molecule 2: SPCC1919.03c protein

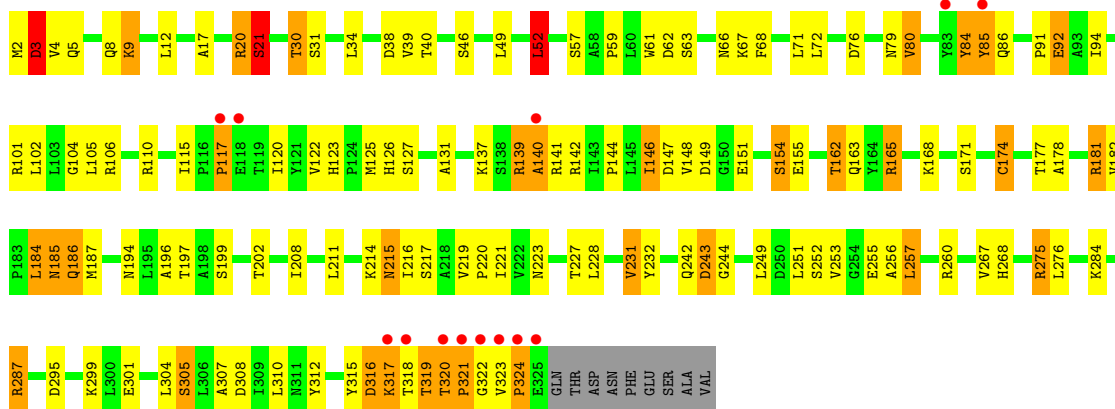


- Molecule 2: SPCC1919.03c protein

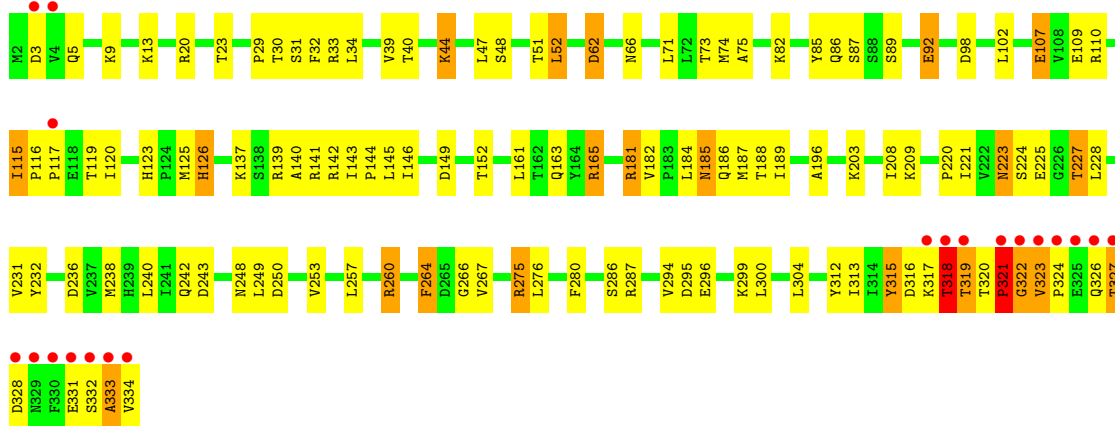




• Molecule 3: Hypothetical protein C1556.08c in chromosome I



• Molecule 3: Hypothetical protein C1556.08c in chromosome I



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.46Å 97.39Å 168.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 29.69 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.60) 99.9 (29.69-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.91 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.273 0.200 , 0.264	Depositor DCC
R_{free} test set	1899 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	37.3	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9329	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AMP

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	0.79	0/1053	0.93	4/1420 (0.3%)
1	C	0.77	2/1030 (0.2%)	0.82	1/1393 (0.1%)
2	B	0.74	0/751	0.89	1/1026 (0.1%)
2	D	1.03	3/751 (0.4%)	0.96	2/1026 (0.2%)
3	E	0.74	0/2631	0.83	3/3565 (0.1%)
3	G	0.76	1/2596 (0.0%)	0.85	2/3521 (0.1%)
All	All	0.78	6/8812 (0.1%)	0.86	13/11951 (0.1%)

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	2
1	C	0	1
2	D	0	2
3	E	0	2
3	G	0	2
All	All	0	9

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	218	SER	CB-OG	16.16	1.63	1.42
2	D	284	HIS	CA-CB	-10.79	1.30	1.53
1	C	481	THR	C-N	-10.41	1.10	1.34
2	D	286	LYS	C-N	-8.59	1.14	1.34
1	C	482	VAL	C-N	6.38	1.46	1.34

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	285	ARG	O-C-N	-8.71	108.77	122.70
3	E	321	PRO	N-CA-CB	7.76	112.61	103.30
1	A	519	LEU	CA-CB-CG	6.15	129.45	115.30
1	A	459	ARG	NE-CZ-NH1	-6.07	117.27	120.30
3	G	52	LEU	CA-CB-CG	6.04	129.19	115.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	545	PRO	Peptide
1	A	553	MET	Peptide
1	C	487	ASN	Peptide
3	G	243	ASP	Peptide
3	G	323	VAL	Peptide

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	1025	0	997	60	0
1	C	1003	0	964	77	0
2	B	733	0	735	66	0
2	D	733	0	733	68	0
3	E	2589	0	2608	109	0
3	G	2548	0	2601	139	1
4	E	23	0	12	2	0
4	G	23	0	12	0	0
5	A	94	0	0	27	0
5	B	78	0	0	20	0
5	C	66	0	0	25	0
5	D	51	0	0	13	0
5	E	146	0	0	28	3
5	G	217	0	0	56	2
All	All	9329	0	8662	476	3

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 27.

The worst 5 of 476 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)
3:G:79:ASN:HB2	5:G:569:HOH:O	1.32	1.24
3:G:46:SER:HB2	5:G:440:HOH:O	1.37	1.22
3:E:30:THR:O	5:E:526:HOH:O	1.53	1.20
5:C:593:HOH:O	3:E:152:THR:HB	1.43	1.16
1:C:474:GLN:HB3	5:C:615:HOH:O	1.47	1.11

All (3) 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)
5:G:434:HOH:O	5:E:408:HOH:O[2_554]	1.79	0.41
3:G:126:HIS:CD2	5:E:545:HOH:O[2_554]	2.10	0.10
5:G:430:HOH:O	5:E:406:HOH:O[2_554]	2.16	0.04

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	126/137 (92%)	112 (89%)	9 (7%)	5 (4%)	3	4
1	C	126/137 (92%)	103 (82%)	12 (10%)	11 (9%)	1	1
2	B	91/97 (94%)	74 (81%)	6 (7%)	11 (12%)	0	0
2	D	91/97 (94%)	65 (71%)	15 (16%)	11 (12%)	0	0
3	E	331/333 (99%)	305 (92%)	16 (5%)	10 (3%)	5	8
3	G	323/333 (97%)	303 (94%)	11 (3%)	9 (3%)	6	9
All	All	1088/1134 (96%)	962 (88%)	69 (6%)	57 (5%)	2	2

5 of 57 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	207	GLN
2	B	224	LEU
2	B	225	LYS
2	B	227	PRO
2	B	244	ASN

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	107/120 (89%)	91 (85%)	16 (15%)	3	6
1	C	102/120 (85%)	87 (85%)	15 (15%)	3	6
2	B	84/88 (96%)	71 (84%)	13 (16%)	3	5
2	D	84/88 (96%)	72 (86%)	12 (14%)	4	6
3	E	286/296 (97%)	259 (91%)	27 (9%)	10	19
3	G	287/296 (97%)	249 (87%)	38 (13%)	5	8
All	All	950/1008 (94%)	829 (87%)	121 (13%)	5	9

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	227	THR
1	C	450	ASN
3	E	227	THR
3	G	231	VAL
3	G	287	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	474	GLN
2	D	207	GLN
3	E	223	ASN
1	C	520	GLN

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Mol	Chain	Res	Type
2	D	219	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](#)

2 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	AMP	E	401	-	22,25,25	1.09	1 (4%)	24,38,38	2.04	6 (25%)
4	AMP	G	401	-	22,25,25	1.22	1 (4%)	24,38,38	1.54	4 (16%)

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	AMP	E	401	-	-	0/6/26/26	0/3/3/3
4	AMP	G	401	-	-	0/6/26/26	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	401	AMP	C5-C4	2.87	1.47	1.40
4	G	401	AMP	C5-C4	3.28	1.47	1.40

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	401	AMP	N3-C2-N1	-6.57	123.13	128.86
4	G	401	AMP	N3-C2-N1	-4.56	124.88	128.86
4	G	401	AMP	C4-C5-N7	-2.22	107.27	109.41
4	E	401	AMP	C4'-O4'-C1'	2.01	111.91	109.77
4	E	401	AMP	N6-C6-N1	2.06	122.84	118.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	401	AMP	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 [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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	128/137 (93%)	-0.03	9 (7%) 17 12	12, 26, 74, 85	2 (1%)
1	C	128/137 (93%)	0.85	21 (16%) 2 1	19, 42, 86, 94	0
2	B	93/97 (95%)	0.27	14 (15%) 3 1	12, 31, 68, 73	0
2	D	93/97 (95%)	0.55	12 (12%) 4 2	18, 51, 81, 89	1 (1%)
3	E	333/333 (100%)	-0.21	20 (6%) 23 17	10, 27, 61, 123	0
3	G	324/333 (97%)	-0.42	13 (4%) 39 31	8, 24, 49, 81	3 (0%)
All	All	1099/1134 (96%)	-0.02	89 (8%) 13 8	8, 28, 72, 123	6 (0%)

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	547	ARG	12.5
3	E	329	ASN	10.1
1	C	548	THR	9.6
1	C	549	ALA	7.9
3	E	332	SER	7.3

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	AMP	G	401	23/23	0.97	0.13	-0.26	19,21,29,31	0
4	AMP	E	401	23/23	0.97	0.12	-0.59	20,22,31,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.