



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:27 AM GMT

PDB ID : 2QRC
Title : Crystal structure of the adenylate sensor from AMP-activated protein kinase
in complex with ADP and AMP
Authors : Jin, X.; Townley, R.; Shapiro, L.
Deposited on : 2007-07-28
Resolution : 2.70 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 (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

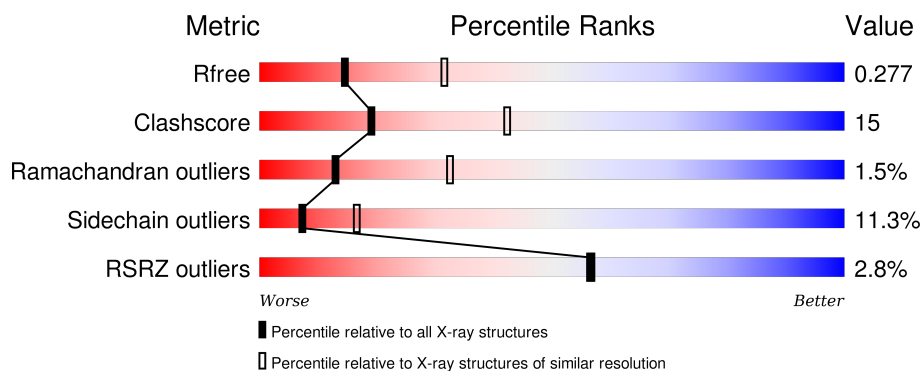
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



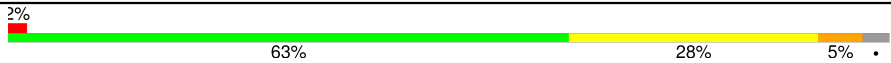
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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>3%</div> <div>58% 22% 15%</div> </div>
1	C	137	<div> <div>%</div> <div>53% 26% 18%</div> </div>
2	B	97	<div> <div>10%</div> <div>58% 24% 12% 6%</div> </div>
2	D	97	<div> <div>4%</div> <div>66% 19% 7% 6%</div> </div>
3	E	334	<div> <div>%</div> <div>68% 24% . .</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	334	 A horizontal bar chart showing the quality of chain G. The bar is divided into four segments: a small red segment at the beginning labeled '2%', followed by a large green segment labeled '63%', then a yellow segment labeled '28%', and a small orange segment at the end labeled '5%'. A small black dot is visible at the far right end of the bar.

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8540 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	116	Total	C	N	O	S	0	0	0
			939	608	159	163	9			
1	C	112	Total	C	N	O	S	0	1	0
			907	587	158	153	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	91	Total	C	N	O	S	0	0	0
			711	453	123	133	2			
2	D	91	Total	C	N	O	S	0	0	0
			714	456	122	134	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	202	MET	-	EXPRESSION TAG	UNP P78789
D	202	MET	-	EXPRESSION TAG	UNP P78789

- Molecule 3 is a protein called Protein C1556.08c.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	324	Total	C	N	O	S	0	0	0
			2543	1624	424	480	15			
3	E	324	Total	C	N	O	S	0	0	0
			2543	1623	424	482	14			

There are 4 discrepancies between the modelled and reference sequences:

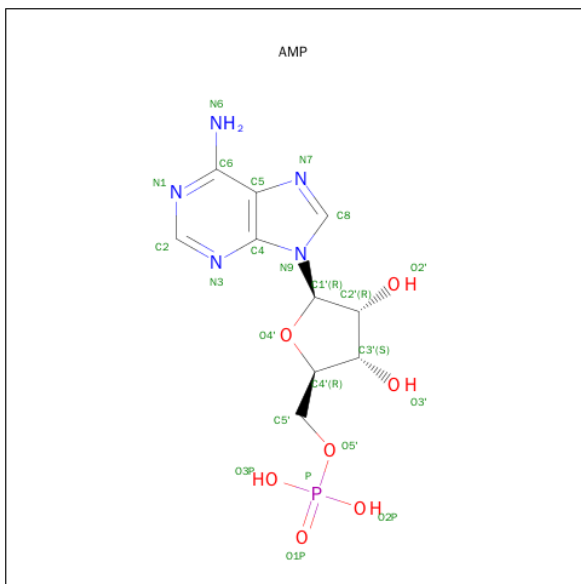
Chain	Residue	Modelled	Actual	Comment	Reference
G	1	ALA	-	EXPRESSION TAG	UNP Q10343
G	2	MET	-	EXPRESSION TAG	UNP Q10343

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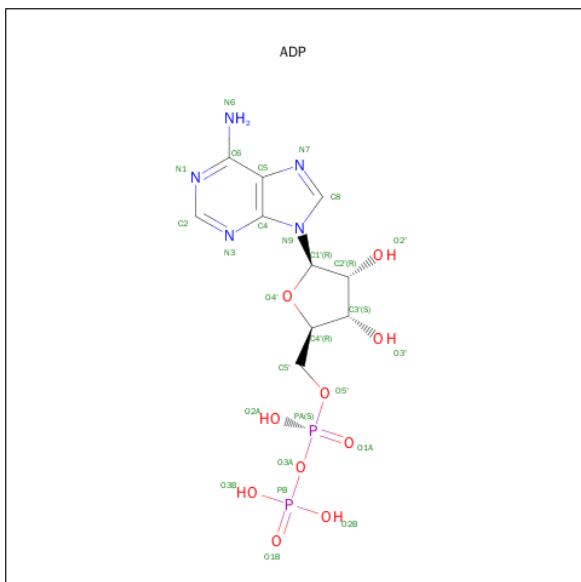
Chain	Residue	Modelled	Actual	Comment	Reference
E	1	ALA	-	EXPRESSION TAG	UNP Q10343
E	2	MET	-	EXPRESSION TAG	UNP Q10343

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



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

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



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

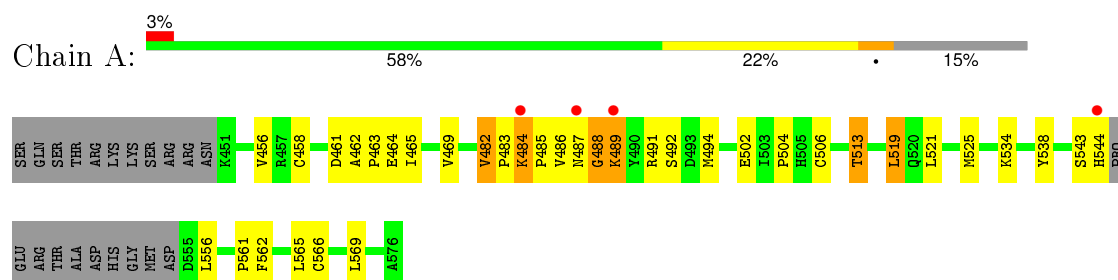
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	8	Total	O	0	0
			8	8		
6	B	10	Total	O	0	0
			10	10		
6	C	11	Total	O	0	0
			11	11		
6	D	11	Total	O	0	0
			11	11		
6	E	20	Total	O	0	0
			20	20		
6	G	19	Total	O	0	0
			19	19		

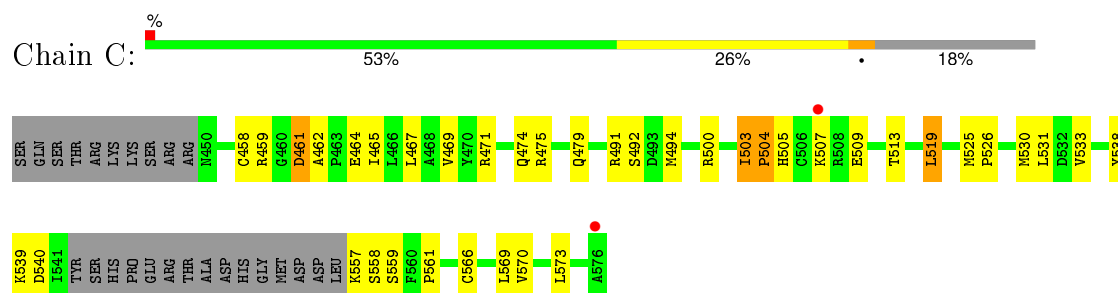
3 Residue-property plots [i](#)

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.

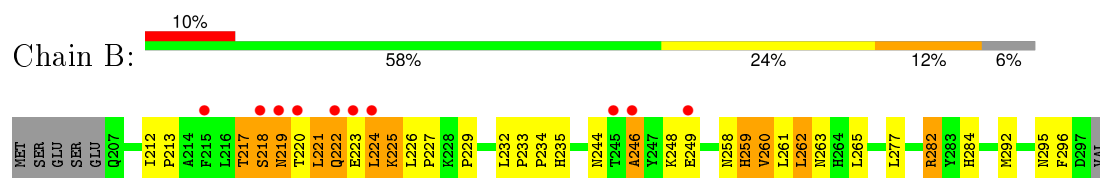
• Molecule 1: SNF1-like protein kinase ssp2



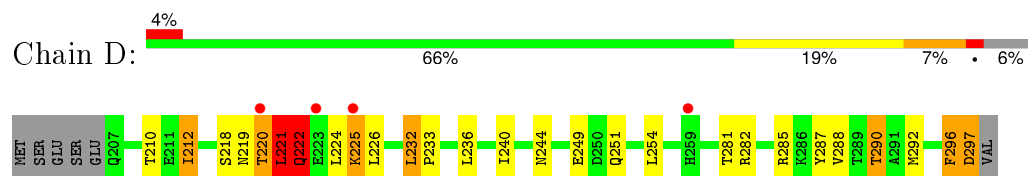
• Molecule 1: SNF1-like protein kinase ssp2



• Molecule 2: SPCC1919.03c protein

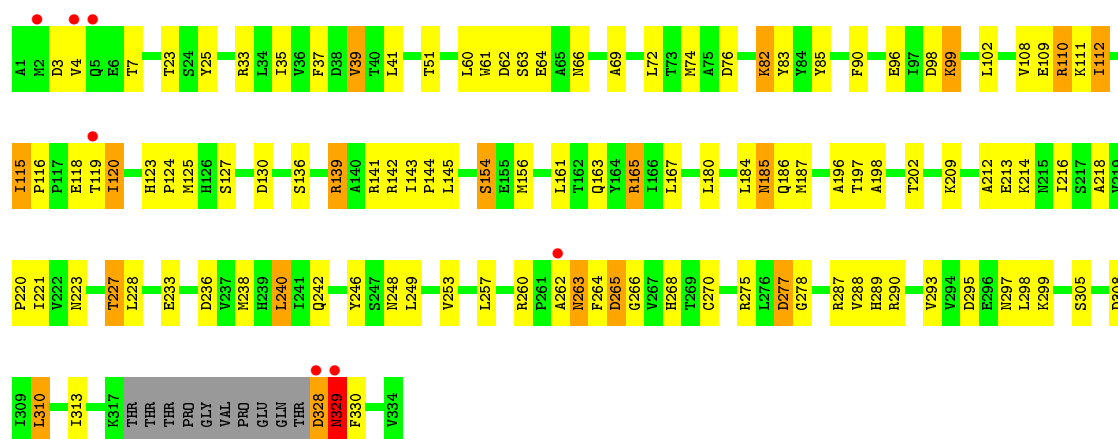


• Molecule 2: SPCC1919.03c protein

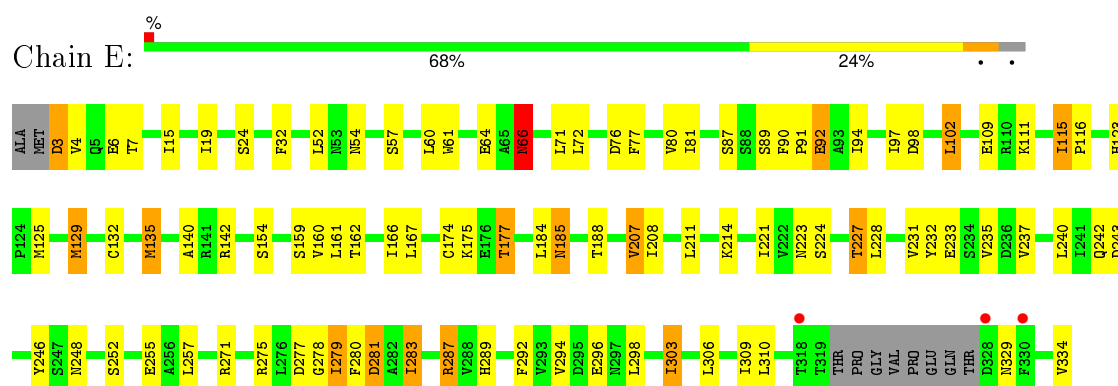


• Molecule 3: Protein C1556.08c





• Molecule 3: Protein C1556.08c



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.29Å 78.09Å 108.55Å 90.00° 124.13° 90.00°	Depositor
Resolution (Å)	48.28 – 2.70 48.28 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.3 (48.28-2.70) 96.3 (48.28-2.70)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.206 , 0.289 0.203 , 0.277	Depositor DCC
R_{free} test set	1558 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	64.9	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 58.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 30916 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8540	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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, 0.375 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: AMP, 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	0/963	0.75	1/1295 (0.1%)
1	C	0.62	0/933	0.73	0/1253
2	B	0.54	0/728	0.96	4/995 (0.4%)
2	D	0.56	0/732	0.79	2/1002 (0.2%)
3	E	0.60	0/2585	0.71	0/3502
3	G	0.62	0/2585	0.75	1/3501 (0.0%)
All	All	0.61	0/8526	0.76	8/11548 (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
2	B	0	4
3	E	0	3
3	G	0	4
All	All	0	11

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	224	LEU	CB-CA-C	14.08	136.95	110.20
2	B	225	LYS	N-CA-CB	11.11	130.60	110.60
3	G	330	PHE	N-CA-CB	9.93	128.48	110.60
2	B	232	LEU	CA-CB-CG	5.68	128.37	115.30
2	D	296	PHE	CB-CA-C	-5.57	99.26	110.40

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	218	SER	Peptide
2	B	221	LEU	Peptide
2	B	222	GLN	Peptide
2	B	296	PHE	Peptide
3	G	262	ALA	Peptide

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	939	0	936	27	0
1	C	907	0	909	24	0
2	B	711	0	717	48	0
2	D	714	0	713	37	0
3	E	2543	0	2572	55	0
3	G	2543	0	2583	78	0
4	G	23	0	12	0	0
5	E	54	0	24	1	0
5	G	27	0	12	4	0
6	A	8	0	0	0	0
6	B	10	0	0	0	0
6	C	11	0	0	1	0
6	D	11	0	0	0	0
6	E	20	0	0	0	0
6	G	19	0	0	3	0
All	All	8540	0	8478	257	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 15.

The worst 5 of 257 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)
2:D:219:ASN:CA	2:D:220:THR:HG22	1.17	1.56
2:D:219:ASN:HA	2:D:220:THR:CG2	1.18	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:SER:CB	1:A:544:HIS:HA	1.51	1.31
1:A:543:SER:HB3	1:A:544:HIS:CA	1.64	1.26
2:D:221:LEU:O	2:D:222:GLN:HB2	1.46	1.08

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	112/137 (82%)	104 (93%)	5 (4%)	3 (3%)	6	16
1	C	109/137 (80%)	104 (95%)	4 (4%)	1 (1%)	21	49
2	B	89/97 (92%)	72 (81%)	15 (17%)	2 (2%)	8	22
2	D	89/97 (92%)	70 (79%)	15 (17%)	4 (4%)	3	6
3	E	320/334 (96%)	302 (94%)	16 (5%)	2 (1%)	30	59
3	G	320/334 (96%)	303 (95%)	13 (4%)	4 (1%)	15	37
All	All	1039/1136 (92%)	955 (92%)	68 (6%)	16 (2%)	13	32

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	LYS
3	G	263	ASN
3	G	265	ASP
2	D	221	LEU
2	D	222	GLN

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	100/120 (83%)	90 (90%)	10 (10%)	9	22
1	C	95/120 (79%)	86 (90%)	9 (10%)	11	24
2	B	81/88 (92%)	73 (90%)	8 (10%)	10	22
2	D	81/88 (92%)	70 (86%)	11 (14%)	5	11
3	E	284/296 (96%)	250 (88%)	34 (12%)	6	14
3	G	284/296 (96%)	252 (89%)	32 (11%)	7	16
All	All	925/1008 (92%)	821 (89%)	104 (11%)	7	17

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	310	LEU
1	C	569	LEU
3	E	257	LEU
3	G	313	ILE
1	C	503	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
3	G	242	GLN
3	G	329	ASN
3	E	126	HIS
3	G	268	HIS
3	G	289	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 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$
5	ADP	E	1002	-	22,29,29	1.01	2 (9%)	27,45,45	1.76	5 (18%)
5	ADP	E	1004	-	22,29,29	1.05	1 (4%)	27,45,45	1.96	4 (14%)
4	AMP	G	1001	-	20,25,25	1.25	2 (10%)	22,38,38	2.34	7 (31%)
5	ADP	G	1003	-	22,29,29	1.07	1 (4%)	27,45,45	1.90	6 (22%)

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
5	ADP	E	1002	-	-	0/12/32/32	0/3/3/3
5	ADP	E	1004	-	-	0/12/32/32	0/3/3/3
4	AMP	G	1001	-	-	0/6/26/26	0/3/3/3
5	ADP	G	1003	-	-	0/12/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1002	ADP	C2-N3	2.07	1.35	1.32
4	G	1001	AMP	C5-C4	2.97	1.47	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1002	ADP	C5-C4	3.00	1.47	1.40
5	E	1004	ADP	C5-C4	3.20	1.47	1.40
4	G	1001	AMP	O4'-C1'	3.44	1.45	1.41

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	1003	ADP	N3-C2-N1	-7.34	123.27	128.89
4	G	1001	AMP	N3-C2-N1	-7.26	123.33	128.89
5	E	1004	ADP	N3-C2-N1	-7.01	123.53	128.89
5	E	1002	ADP	N3-C2-N1	-5.34	124.80	128.89
4	G	1001	AMP	C4-C5-N7	-3.68	106.09	109.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1004	ADP	1	0
5	G	1003	ADP	4	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, 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	116/137 (84%)	0.28	4 (3%)	49	49	40, 52, 59, 63	0
1	C	112/137 (81%)	0.20	2 (1%)	71	72	45, 52, 57, 62	0
2	B	91/97 (93%)	0.66	10 (10%)	7	5	47, 52, 61, 65	0
2	D	91/97 (93%)	0.60	4 (4%)	38	37	45, 52, 60, 63	0
3	E	324/334 (97%)	0.13	3 (0%)	85	86	41, 52, 64, 76	0
3	G	324/334 (97%)	0.09	7 (2%)	65	66	27, 52, 61, 74	1 (0%)
All	All	1058/1136 (93%)	0.23	30 (2%)	56	57	27, 52, 61, 76	1 (0%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	220	THR	5.9
3	G	328	ASP	5.0
2	B	224	LEU	4.9
2	B	223	GLU	4.4
1	A	489	LYS	4.1

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

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

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, 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
5	ADP	G	1003	27/27	0.93	0.22	1.06	61,65,74,75	0
5	ADP	E	1004	27/27	0.94	0.21	0.89	70,72,80,81	0
4	AMP	G	1001	23/23	0.96	0.16	-0.16	41,47,48,49	0
5	ADP	E	1002	27/27	0.94	0.16	-0.51	43,45,63,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.