



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:55 AM GMT

PDB ID : 2OOY
Title : Crystal structure of the adenylate sensor from AMP-activated protein kinase complexed with ATP
Authors : Townley, R.; Shapiro, L.
Deposited on : 2007-01-26
Resolution : 2.88 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

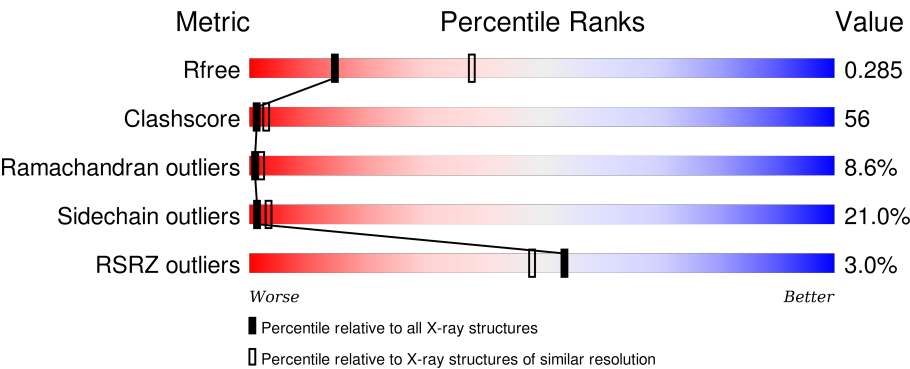
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.88 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	1945 (2.90-2.86)
Clashscore	102246	2202 (2.90-2.86)
Ramachandran outliers	100387	2149 (2.90-2.86)
Sidechain outliers	100360	2152 (2.90-2.86)
RSRZ outliers	91569	1950 (2.90-2.86)

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>10%</div><div>25%50%17%6%</div></div>
1	C	137	<div><div>%</div><div>23%44%14%16%</div></div>
2	B	97	<div><div>3%</div><div>26%41%21%7%5%</div></div>
2	D	97	<div><div>4%</div><div>36%36%15%6%6%</div></div>
3	E	333	<div><div>2%</div><div>28%53%18%</div></div>

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Mol	Chain	Length	Quality of chain
3	G	333	 <div>31% 49% 15% . .</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	ATP	E	401	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9010 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	129	Total	C	N	O	S	0	0	0
			1020	652	178	180	10			
1	C	115	Total	C	N	O	S	0	0	0
			915	594	150	162	9			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	92	Total	C	N	O	S	0	1	0
			714	455	125	132	2			
2	D	91	Total	C	N	O	S	0	0	0
			708	453	122	131	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

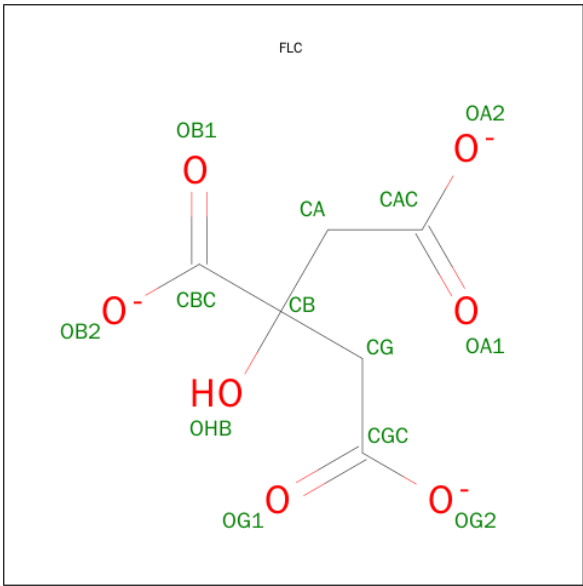
- Molecule 3 is a protein called Hypothetical protein C1556.08c in chromosome I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	324	Total	C	N	O	S	0	1	0
			2544	1627	421	481	15			
3	E	333	Total	C	N	O	S	0	0	0
			2606	1663	432	496	15			

There are 2 discrepancies between the modelled and reference sequences:

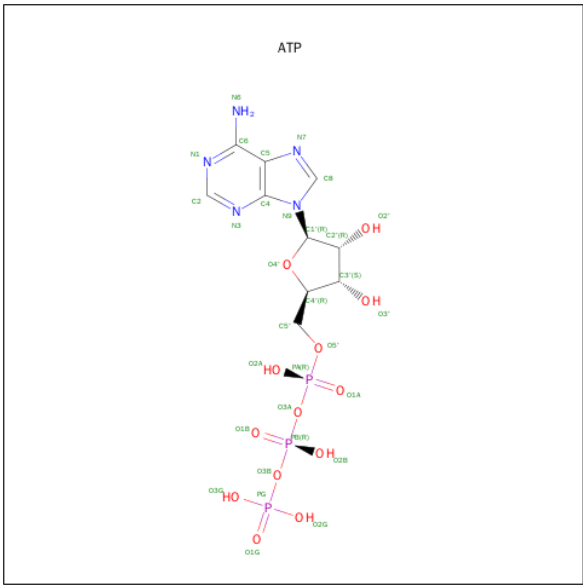
Chain	Residue	Modelled	Actual	Comment	Reference
E	2	MET	-	CLONING ARTIFACT	UNP Q10343
G	2	MET	-	CLONING ARTIFACT	UNP Q10343

- Molecule 4 is CITRATE ANION (three-letter code: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

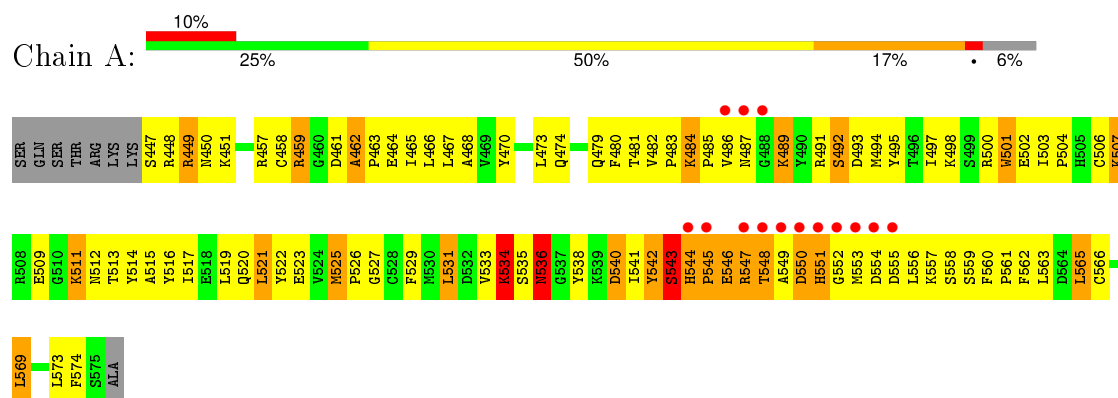
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	50	Total	O	0	0
			50	50		
6	B	41	Total	O	0	0
			41	41		
6	C	50	Total	O	0	0
			50	50		
6	D	36	Total	O	0	0
			36	36		
6	E	125	Total	O	0	0
			125	125		
6	G	126	Total	O	0	0
			126	126		

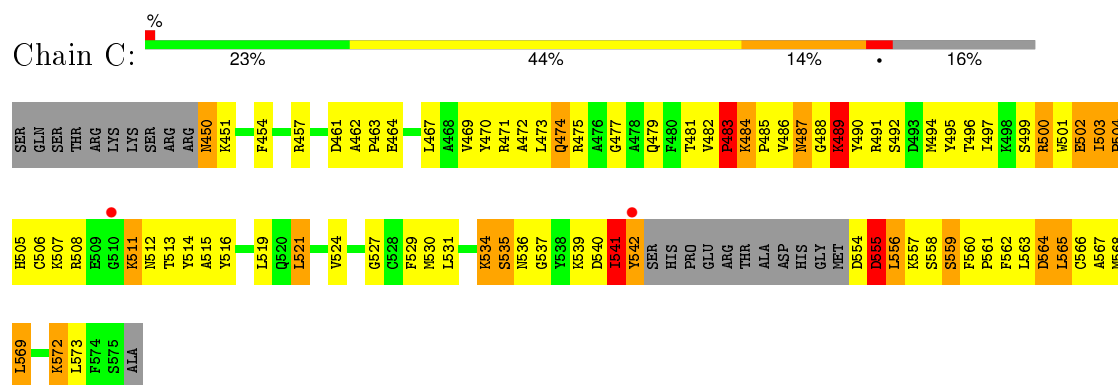
3 Residue-property plots [i](#)

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.

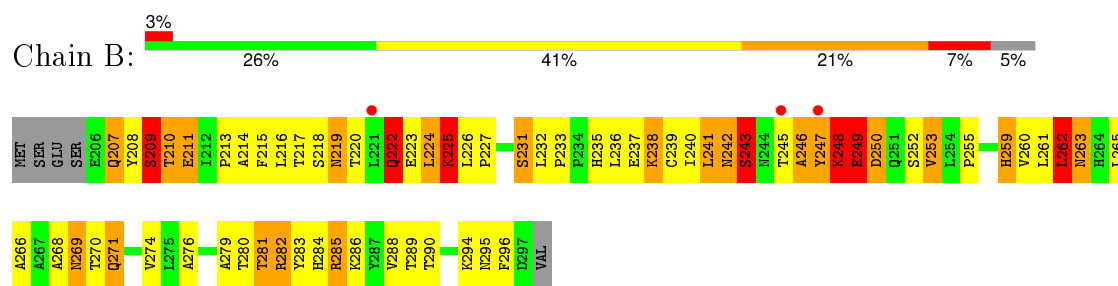
- Molecule 1: SNF1-like protein kinase ssp2



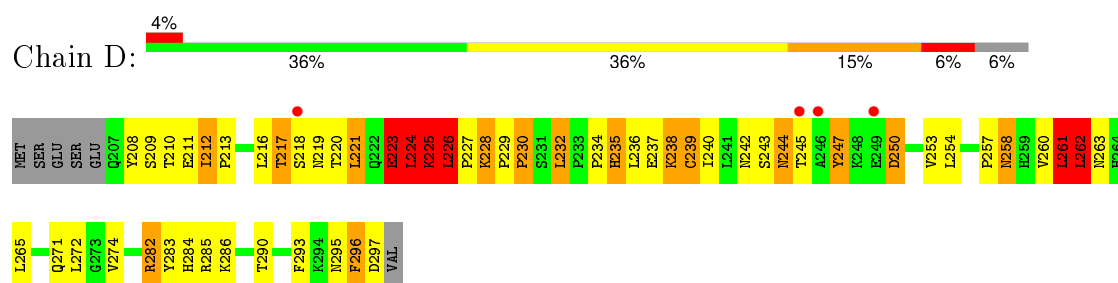
- Molecule 1: SNF1-like protein kinase ssp2



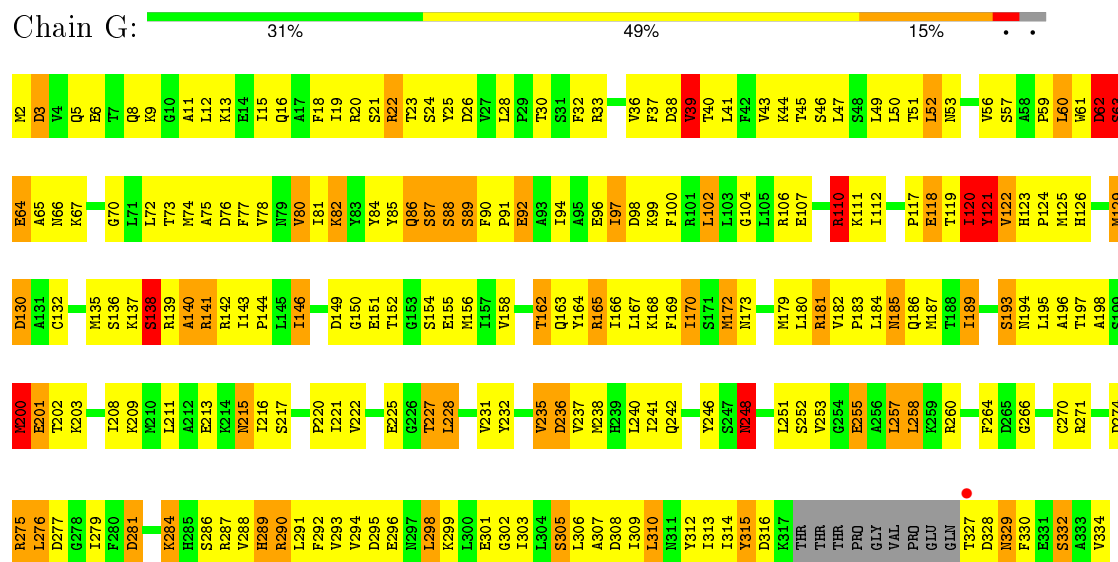
- Molecule 2: SPCC1919.03c protein



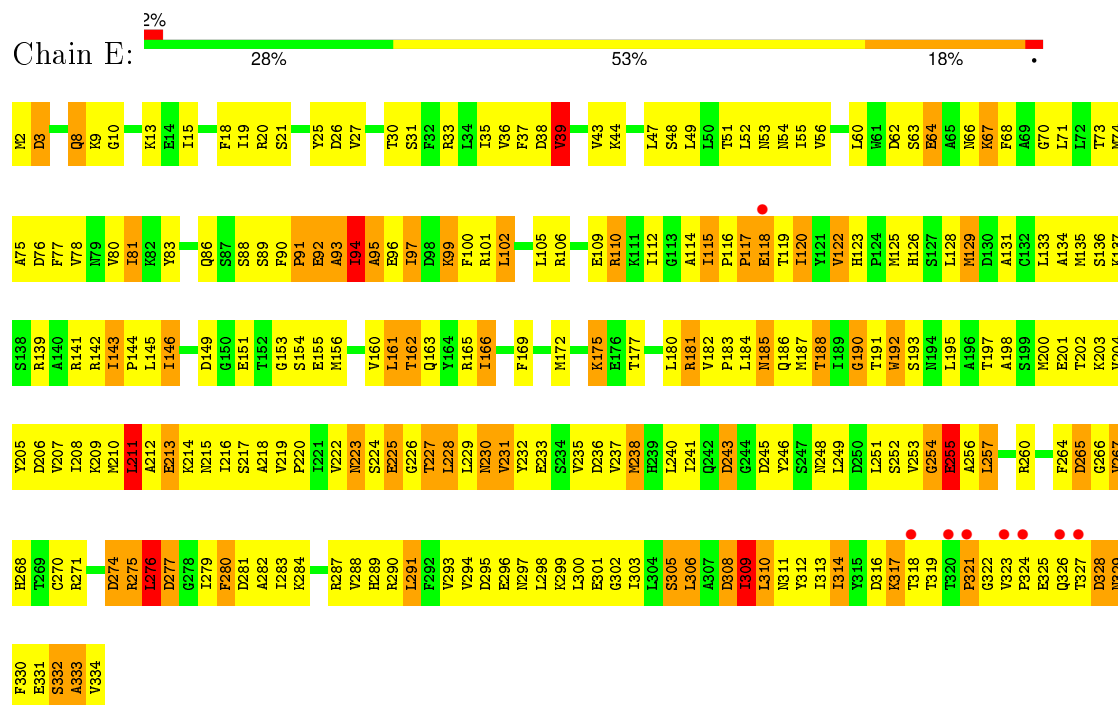
- Molecule 2: SPCC1919.03c protein



• Molecule 3: 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	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.90Å 77.67Å 107.58Å 90.00° 123.99° 90.00°	Depositor
Resolution (Å)	50.00 – 2.88 19.83 – 2.88	Depositor EDS
% Data completeness (in resolution range)	96.3 (50.00-2.88) 96.5 (19.83-2.88)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.88Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.298 0.187 , 0.285	Depositor DCC
R_{free} test set	1265 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	68.2	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 62.6	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 24970 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9010	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: FLC, ATP

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	1.05	1/1047 (0.1%)	1.10	2/1415 (0.1%)
1	C	1.04	0/939	1.10	2/1269 (0.2%)
2	B	0.93	2/735 (0.3%)	1.10	2/1006 (0.2%)
2	D	1.02	2/726 (0.3%)	1.14	5/994 (0.5%)
3	E	1.04	6/2651 (0.2%)	1.13	6/3596 (0.2%)
3	G	1.09	2/2590 (0.1%)	1.12	10/3509 (0.3%)
All	All	1.05	13/8688 (0.1%)	1.12	27/11789 (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	5
1	C	0	1
2	B	0	6
2	D	0	2
3	E	0	3
3	G	0	4
All	All	0	21

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	286	LYS	C-N	-9.06	1.13	1.34
2	D	239	CYS	CB-SG	-8.04	1.68	1.82
2	B	231	SER	CB-OG	6.08	1.50	1.42
3	E	267	VAL	CB-CG2	-5.92	1.40	1.52
3	E	118	GLU	CB-CG	5.84	1.63	1.52

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	286	LYS	O-C-N	-7.90	110.06	122.70
3	E	94	ILE	N-CA-C	-7.39	91.04	111.00
2	B	209	SER	N-CA-C	7.15	130.32	111.00
3	G	257	LEU	CB-CG-CD2	-7.00	99.09	111.00
2	D	286	LYS	CA-C-N	6.84	132.25	117.20

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	449	ARG	Peptide
1	A	485	PRO	Peptide
1	A	536	ASN	Peptide
1	A	549	ALA	Peptide
1	A	550	ASP	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	1020	0	983	126	0
1	C	915	0	886	116	0
2	B	714	0	709	77	0
2	D	708	0	703	92	0
3	E	2606	0	2642	315	0
3	G	2544	0	2568	282	0
4	E	13	0	5	2	0
5	E	31	0	12	12	0
5	G	31	0	12	4	0
6	A	50	0	0	20	0
6	B	41	0	0	2	0
6	C	50	0	0	26	0
6	D	36	0	0	12	0
6	E	125	0	0	65	0
6	G	126	0	0	48	0
All	All	9010	0	8520	960	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 56.

The worst 5 of 960 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:99:LYS:HE3	6:G:478:HOH:O	1.19	1.28
6:G:415:HOH:O	2:D:271:GLN:HG2	1.29	1.27
3:G:162:THR:HG21	6:G:516:HOH:O	1.29	1.27
2:D:210:THR:HB	6:D:322:HOH:O	1.26	1.25
3:E:290:ARG:HA	6:E:520:HOH:O	1.37	1.24

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	127/137 (93%)	90 (71%)	20 (16%)	17 (13%)	0	0
1	C	111/137 (81%)	84 (76%)	18 (16%)	9 (8%)	1	2
2	B	91/97 (94%)	60 (66%)	17 (19%)	14 (15%)	0	0
2	D	89/97 (92%)	71 (80%)	11 (12%)	7 (8%)	1	2
3	E	331/333 (99%)	256 (77%)	49 (15%)	26 (8%)	1	2
3	G	321/333 (96%)	265 (83%)	36 (11%)	20 (6%)	2	5
All	All	1070/1134 (94%)	826 (77%)	151 (14%)	93 (9%)	1	2

5 of 93 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	LYS
1	A	542	TYR
1	A	543	SER

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Mol	Chain	Res	Type
1	A	545	PRO
1	A	548	THR

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	106/120 (88%)	85 (80%)	21 (20%)	1	4
1	C	96/120 (80%)	73 (76%)	23 (24%)	1	2
2	B	80/88 (91%)	59 (74%)	21 (26%)	0	1
2	D	79/88 (90%)	58 (73%)	21 (27%)	0	1
3	E	293/296 (99%)	238 (81%)	55 (19%)	2	5
3	G	283/296 (96%)	228 (81%)	55 (19%)	2	4
All	All	937/1008 (93%)	741 (79%)	196 (21%)	1	3

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	287	ARG
1	C	539	LYS
3	E	260	ARG
3	G	298	LEU
1	C	484	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
3	G	185	ASN
1	C	505	HIS
3	E	242	GLN
3	G	248	ASN
3	G	329	ASN

5.3.3 RNA ⓘ

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 ⓘ

3 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	ATP	E	401	-	24,33,33	1.06	1 (4%)	31,52,52	2.01	4 (12%)
4	FLC	E	402	-	3,12,12	1.19	0	3,17,17	2.89	2 (66%)
5	ATP	G	401	-	24,33,33	1.33	3 (12%)	31,52,52	2.13	8 (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
5	ATP	E	401	-	-	0/18/38/38	0/3/3/3
4	FLC	E	402	-	-	0/6/16/16	0/0/0/0
5	ATP	G	401	-	-	0/18/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	401	ATP	C2-N3	2.16	1.36	1.32
5	G	401	ATP	O4'-C1'	2.57	1.44	1.41
5	E	401	ATP	C5-C4	3.11	1.47	1.40
5	G	401	ATP	C5-C4	4.02	1.49	1.40

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	401	ATP	PA-O3A-PB	-6.73	113.84	132.73
5	E	401	ATP	N3-C2-N1	-6.59	123.85	128.89
5	E	401	ATP	PA-O3A-PB	-5.62	116.96	132.73
5	G	401	ATP	N3-C2-N1	-4.26	125.63	128.89
5	G	401	ATP	C4-C5-N7	-3.96	105.84	109.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	401	ATP	12	0
4	E	402	FLC	2	0
5	G	401	ATP	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	129/137 (94%)	0.02	14 (10%) 7 4	30, 54, 113, 128	0
1	C	115/137 (83%)	-0.37	2 (1%) 73 71	38, 55, 88, 102	0
2	B	92/97 (94%)	-0.22	3 (3%) 50 43	23, 64, 94, 100	0
2	D	91/97 (93%)	-0.09	4 (4%) 38 32	23, 63, 100, 103	0
3	E	333/333 (100%)	-0.52	8 (2%) 62 58	25, 49, 84, 128	0
3	G	324/333 (97%)	-0.61	1 (0%) 94 94	26, 44, 69, 80	0
All	All	1084/1134 (95%)	-0.41	32 (2%) 54 48	23, 50, 91, 128	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	320	THR	6.9
1	A	552	GLY	5.3
1	A	544	HIS	4.7
2	D	246	ALA	4.6
3	E	327	THR	4.3

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
4	FLC	E	402	13/13	0.92	0.23	0.46	99,101,102,102	0
5	ATP	E	401	31/31	0.93	0.16	0.28	55,60,90,92	0
5	ATP	G	401	31/31	0.94	0.15	0.11	50,54,98,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.