



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 06:36 AM GMT

PDB ID : 2FSH
Title : Complex SecA:AMP-PNP from Escherichia coli
Authors : Papanikolau, Y.; Petratos, K.; Economou, A.
Deposited on : 2006-01-23
Resolution : 2.00 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

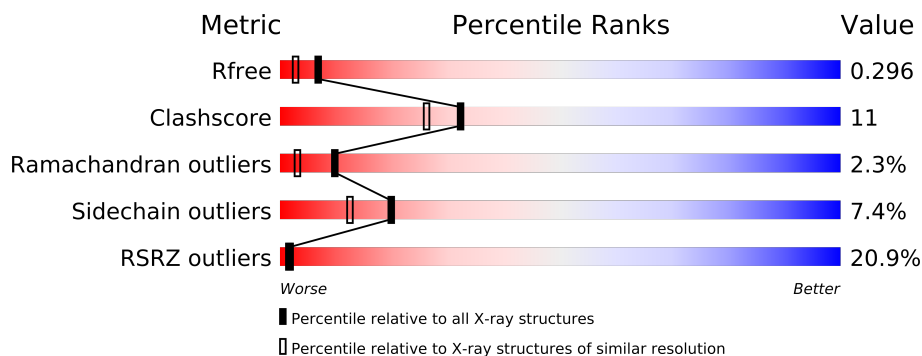
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance



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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	853	
1	B	853	

2 Entry composition i

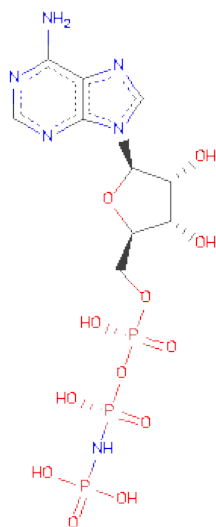
There are 3 unique types of molecules in this entry. The entry contains 11728 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Preprotein translocase secA subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	691	Total	C	N	O	S	0	0	0
			5500	3445	971	1058	26			
1	B	722	Total	C	N	O	S	0	0	0
			5735	3596	1008	1102	29			

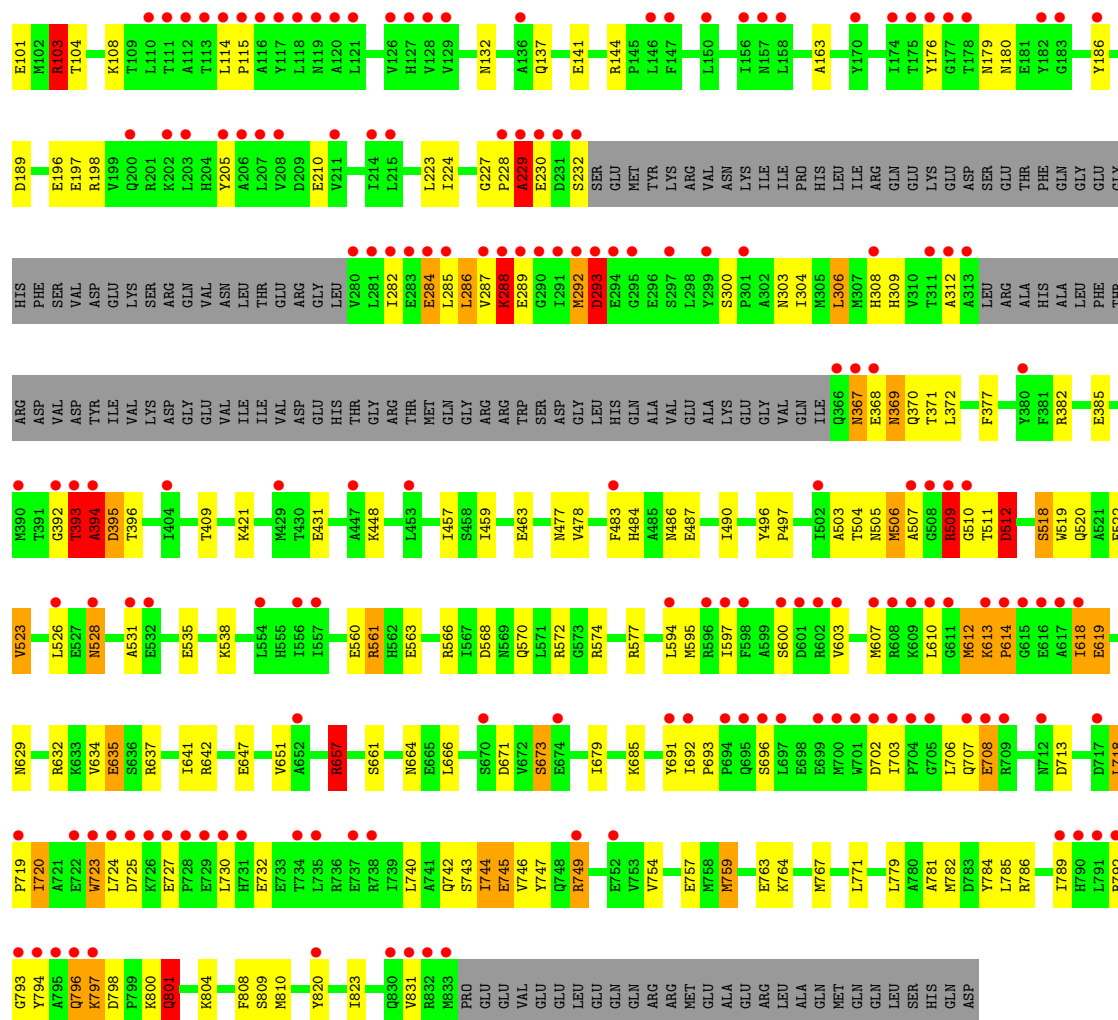
- Molecule 2 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	189	Total 189	O 189	0	0
3	B	242	Total 242	O 242	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.02Å 90.01Å 163.02Å 90.00° 100.52° 90.00°	Depositor
Resolution (Å)	19.97 – 2.00 19.97 – 2.00	Depositor EDS
% Data completeness (in resolution range)	90.5 (19.97-2.00) 90.5 (19.97-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.204 , 0.255 0.255 , 0.296	Depositor DCC
R_{free} test set	6535 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 56.8	EDS
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 130193 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11728	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 3.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: ANP

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	1.19	15/5590 (0.3%)	1.00	15/7542 (0.2%)
1	B	1.29	33/5827 (0.6%)	1.07	17/7861 (0.2%)
All	All	1.25	48/11417 (0.4%)	1.04	32/15403 (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	3
1	B	0	4
All	All	0	7

The worst 5 of 48 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	698	GLU	C-O	17.67	1.56	1.23
1	A	699	GLU	CD-OE2	14.21	1.41	1.25
1	A	98	CYS	CB-SG	-11.81	1.62	1.82
1	B	23	LYS	CE-NZ	10.56	1.75	1.49
1	A	696	SER	CB-OG	10.43	1.55	1.42

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	657	ARG	NE-CZ-NH2	11.13	125.87	120.30
1	A	72	ARG	NE-CZ-NH2	8.82	124.71	120.30
1	B	23	LYS	CD-CE-NZ	8.12	130.37	111.70
1	A	805	ARG	NE-CZ-NH2	-7.96	116.32	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	72	ARG	NE-CZ-NH1	-7.21	116.70	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	366	GLN	Peptide
1	A	393	THR	Peptide
1	A	800	LYS	Peptide
1	B	229	ALA	Peptide
1	B	393	THR	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5500	0	5481	107	0
1	B	5735	0	5724	152	0
2	A	31	0	13	1	0
2	B	31	0	13	7	0
3	A	189	0	0	18	1
3	B	242	0	0	25	1
All	All	11728	0	11231	256	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

The worst 5 of 256 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:23:LYS:CE	1:B:23:LYS:NZ	1.75	1.49
1:B:369:ASN:C	1:B:369:ASN:HD22	1.39	1.24
1:B:757:GLU:HG3	3:B:1056:HOH:O	1.51	1.08
1:A:731:HIS:CE1	1:A:733:GLU:HB3	1.94	1.01
1:B:369:ASN:C	1:B:369:ASN:ND2	2.18	0.96

All (2) 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	Distance(Å)	Clash(Å)
3:A:972:HOH:O	3:A:999:HOH:O[1_455]	2.05	0.15
3:B:1057:HOH:O	3:B:1069:HOH:O[1_655]	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	687/853 (80%)	640 (93%)	32 (5%)	15 (2%)	10	3
1	B	716/853 (84%)	661 (92%)	38 (5%)	17 (2%)	9	3
All	All	1403/1706 (82%)	1301 (93%)	70 (5%)	32 (2%)	10	3

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	GLU
1	A	368	GLU
1	A	394	ALA
1	A	532	GLU
1	A	599	ALA

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	586/728 (80%)	549 (94%)	37 (6%)	25	18
1	B	612/728 (84%)	560 (92%)	52 (8%)	15	9
All	All	1198/1456 (82%)	1109 (93%)	89 (7%)	20	12

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	103	ARG
1	B	306	LEU
1	B	754	VAL
1	B	196	GLU
1	B	286	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	303	ASN
1	B	484	HIS
1	B	761	HIS
1	B	369	ASN
1	B	520	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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
2	ANP	A	900	-	33,33,33	4.85	7 (21%)	51,52,52	2.44	19 (37%)
2	ANP	B	901	-	33,33,33	6.69	15 (45%)	51,52,52	3.48	21 (41%)

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
2	ANP	A	900	-	-	0/18/38/38	0/1/3/3
2	ANP	B	901	-	-	0/18/38/38	0/1/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	ANP	PG-N3B	30.60	1.91	1.64
2	A	900	ANP	PG-N3B	19.21	1.81	1.64
2	B	901	ANP	PG-O1G	18.90	1.69	1.46
2	A	900	ANP	PB-N3B	16.65	1.78	1.64
2	A	900	ANP	PG-O1G	6.71	1.54	1.46

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	ANP	PB-N3B-PG	-10.77	111.96	130.07
2	B	901	ANP	O2B-PB-N3B	7.86	127.95	106.61
2	A	900	ANP	N3-C2-N1	-7.69	122.28	128.71
2	A	900	ANP	N3-C4-N9	7.42	138.84	125.43
2	B	901	ANP	O3A-PB-N3B	-6.72	87.95	106.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	691/853 (81%)	0.85	113 (16%) 2 2	36, 50, 81, 93	0
1	B	722/853 (84%)	1.30	182 (25%) 1 1	34, 51, 83, 98	0
All	All	1413/1706 (82%)	1.08	295 (20%) 1 2	34, 50, 82, 98	0

The worst 5 of 295 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	789	ILE	11.7
1	B	728	PRO	10.4
1	B	794	TYR	10.2
1	A	229	ALA	9.3
1	A	791	LEU	9.1

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 ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ANP	A	900	31/31	0.25	1.34	39,57,62,63	0
2	ANP	B	901	31/31	0.20	-0.02	25,47,63,63	0

6.5 Other polymers ⓘ

There are no such residues in this entry.