



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:35 PM GMT

PDB ID : 1KY4
Title : S-Adenosylhomocysteine hydrolase refined with noncrystallographic restraints
Authors : Takata, Y.; Takusagawa, F.
Deposited on : 2002-02-03
Resolution : 2.80 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

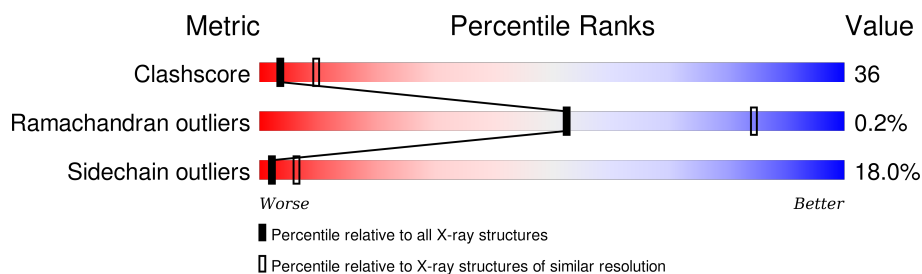
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.



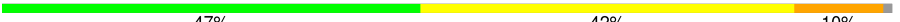
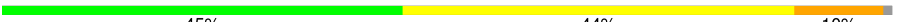
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	431	 48% 42% 10% .
1	B	431	 46% 44% 9% .
1	C	431	 47% 42% 10% .
1	D	431	 45% 44% 10% .

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13650 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 S-adenosylhomocysteine hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3302	2098	568	611	25			
1	B	428	Total	C	N	O	S	0	0	0
			3302	2098	568	611	25			
1	C	428	Total	C	N	O	S	0	0	0
			3302	2098	568	611	25			
1	D	428	Total	C	N	O	S	0	0	0
			3302	2098	568	611	25			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

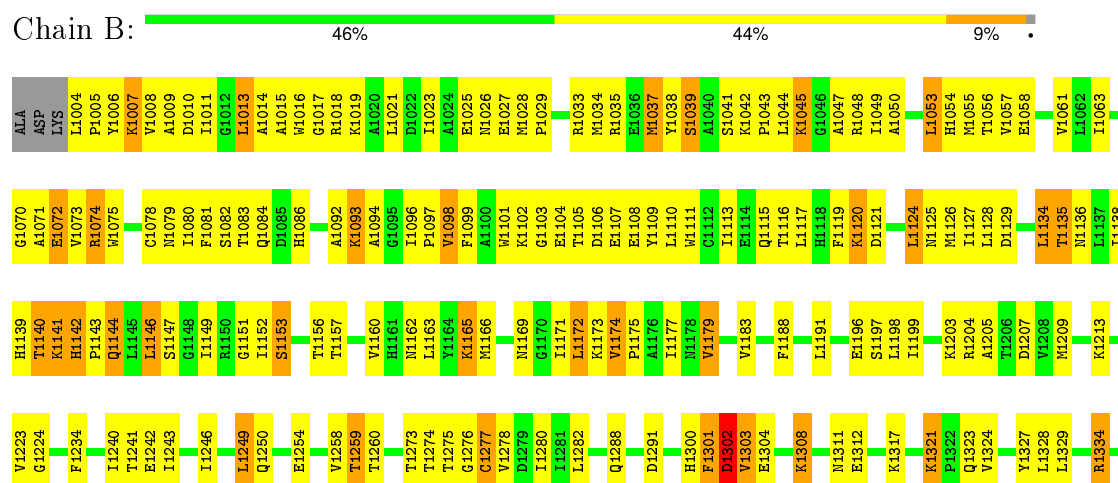
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is water.

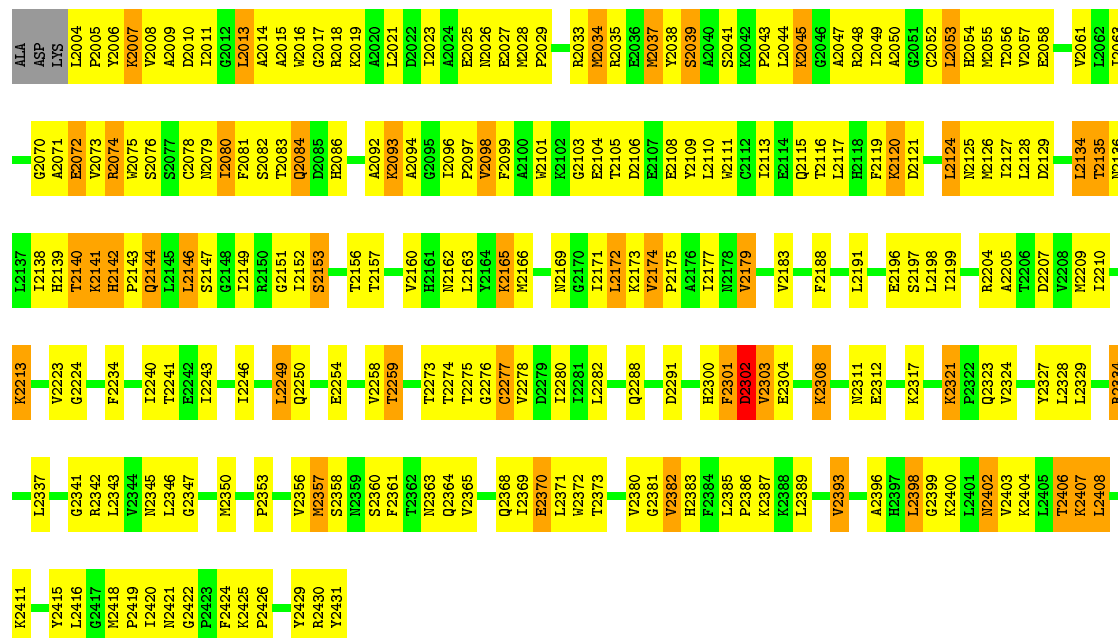
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	68	Total	O	0	0
			68	68		
3	B	75	Total	O	0	0
			75	75		
3	C	60	Total	O	0	0
			60	60		
3	D	63	Total	O	0	0
			63	63		





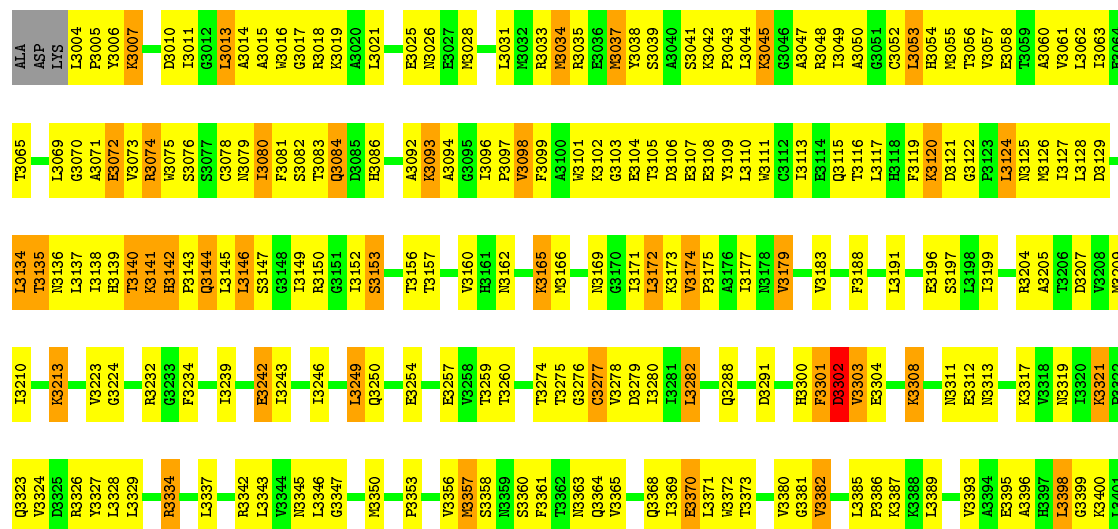
• Molecule 1: S-adenosylhomocysteine hydrolase

Chain C: 47% 42% 10%



• Molecule 1: S-adenosylhomocysteine hydrolase

Chain D: 45% 44% 10%



N3402	Q3412	Y3429
V3403	Y3415	R3430
K3404	L3416	Y3431
L3405	G3417	
T3406	M3418	
K3407	P3419	
L3408	I3420	
T3409	N3421	
	G3422	
	F3423	
	F3424	
	K3425	
	P3426	

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	94.76 Å 134.48 Å 102.26 Å 90.00° 114.35° 90.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.228 , 0.278	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	13650	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

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: NAD

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	0.37	0/3367	0.63	1/4557 (0.0%)
1	B	0.37	0/3367	0.62	1/4557 (0.0%)
1	C	0.37	0/3367	0.62	1/4557 (0.0%)
1	D	0.37	0/3367	0.62	1/4557 (0.0%)
All	All	0.37	0/13468	0.62	4/18228 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	3302	ASP	N-CA-C	5.47	125.76	111.00
1	A	302	ASP	N-CA-C	5.31	125.33	111.00
1	C	2302	ASP	N-CA-C	5.06	124.67	111.00
1	B	1302	ASP	N-CA-C	5.01	124.53	111.00

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	3302	0	3324	253	0
1	B	3302	0	3324	268	0
1	C	3302	0	3324	259	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3302	0	3324	266	0
2	A	44	0	26	1	0
2	B	44	0	26	0	0
2	C	44	0	26	1	0
2	D	44	0	26	0	0
3	A	68	0	0	2	0
3	B	75	0	0	8	0
3	C	60	0	0	2	0
3	D	63	0	0	10	0
All	All	13650	0	13400	968	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 36.

The worst 5 of 968 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:C:2430:ARG:HB3	1:D:3430:ARG:HB3	1.25	1.15
1:A:430:ARG:HB3	1:B:1430:ARG:HB3	1.29	1.15
1:D:3370:GLU:HG3	1:D:3389:LEU:HD11	1.41	1.03
1:A:370:GLU:HG3	1:A:389:LEU:HD11	1.41	1.03
1:C:2370:GLU:HG3	1:C:2389:LEU:HD11	1.39	1.01

There are no symmetry-related clashes.

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	426/431 (99%)	409 (96%)	16 (4%)	1 (0%)	52 84
1	B	426/431 (99%)	407 (96%)	18 (4%)	1 (0%)	52 84

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	426/431 (99%)	410 (96%)	15 (4%)	1 (0%)	52	84
1	D	426/431 (99%)	408 (96%)	17 (4%)	1 (0%)	52	84
All	All	1704/1724 (99%)	1634 (96%)	66 (4%)	4 (0%)	52	84

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	302	ASP
1	B	1302	ASP
1	C	2302	ASP
1	D	3302	ASP

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	351/353 (99%)	288 (82%)	63 (18%)	2	6
1	B	351/353 (99%)	288 (82%)	63 (18%)	2	6
1	C	351/353 (99%)	287 (82%)	64 (18%)	2	6
1	D	351/353 (99%)	288 (82%)	63 (18%)	2	6
All	All	1404/1412 (99%)	1151 (82%)	253 (18%)	2	6

5 of 253 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1370	GLU
1	C	2098	VAL
1	D	3301	PHE
1	B	1393	VAL
1	C	2026	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1169	ASN
1	C	2084	GLN
1	D	3169	ASN
1	B	1300	HIS
1	C	2115	GLN

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](#)

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	$\# Z > 2$
2	NAD	A	432	-	38,48,48	1.99	7 (18%)	47,73,73	2.50	12 (25%)
2	NAD	B	1432	-	38,48,48	2.08	7 (18%)	47,73,73	2.53	12 (25%)
2	NAD	C	2432	-	38,48,48	2.08	7 (18%)	47,73,73	2.46	11 (23%)
2	NAD	D	3432	-	38,48,48	2.08	6 (15%)	47,73,73	2.46	11 (23%)

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	NAD	A	432	-	-	0/22/62/62	0/5/5/5
2	NAD	B	1432	-	-	0/22/62/62	0/5/5/5
2	NAD	C	2432	-	-	0/22/62/62	0/5/5/5
2	NAD	D	3432	-	-	0/22/62/62	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	432	NAD	O4B-C1B	-4.78	1.35	1.41
2	D	3432	NAD	O4B-C1B	-4.67	1.35	1.41
2	C	2432	NAD	O4B-C1B	-4.52	1.35	1.41
2	B	1432	NAD	O4B-C1B	-3.91	1.36	1.41
2	A	432	NAD	C6N-C5N	-2.20	1.33	1.38

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1432	NAD	O3-PN-O5D	-9.40	77.99	102.94
2	A	432	NAD	O3-PN-O5D	-9.26	78.36	102.94
2	D	3432	NAD	O3-PN-O5D	-9.19	78.56	102.94
2	C	2432	NAD	O3-PN-O5D	-8.97	79.13	102.94
2	A	432	NAD	O5D-PN-O1N	-7.07	82.16	109.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	432	NAD	1	0
2	C	2432	NAD	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.