wwPDB X-ray Structure Validation Summary Report (i)

Jan 31, 2016 – 08:30 PM GMT

PDB ID	:	1KK4
Title	:	Crystal Structure of Vat(D) in Complex with Acetyl-CoA
Authors	:	Sugantino, M.; Roderick, S.L.
Deposited on	:	2001-12-06
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 (i) symbol.

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

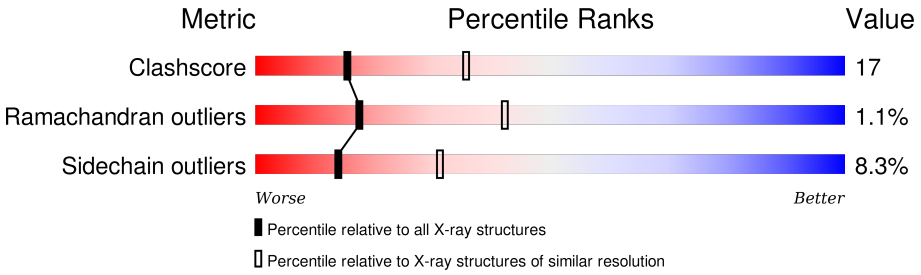
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (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 <=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	209	59% 34% 5% •
1	B	209	67% 27% • •
1	C	209	63% 33% • •
1	D	209	64% 31% • •
1	E	209	67% 29% • •
1	F	209	65% 30% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10155 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 STREPTOGRAMIN A ACETYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1621	1044	267	301	9			
1	B	205	Total	C	N	O	S	0	0	0
			1614	1040	266	299	9			
1	C	205	Total	C	N	O	S	0	0	0
			1617	1041	266	301	9			
1	D	206	Total	C	N	O	S	0	0	0
			1625	1047	267	302	9			
1	E	206	Total	C	N	O	S	0	0	0
			1613	1037	265	302	9			
1	F	206	Total	C	N	O	S	0	0	0
			1624	1045	268	302	9			

- Molecule 2 is ACETYL COENZYME *A (three-letter code: ACO) (formula: $C_{23}H_{38}N_7O_{17}P_3S$).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	20	Total	O	0	0
			20	20		
3	B	25	Total	O	0	0
			25	25		
3	C	21	Total	O	0	0
			21	21		
3	D	24	Total	O	0	0
			24	24		
3	E	21	Total	O	0	0
			21	21		
3	F	24	Total	O	0	0
			24	24		

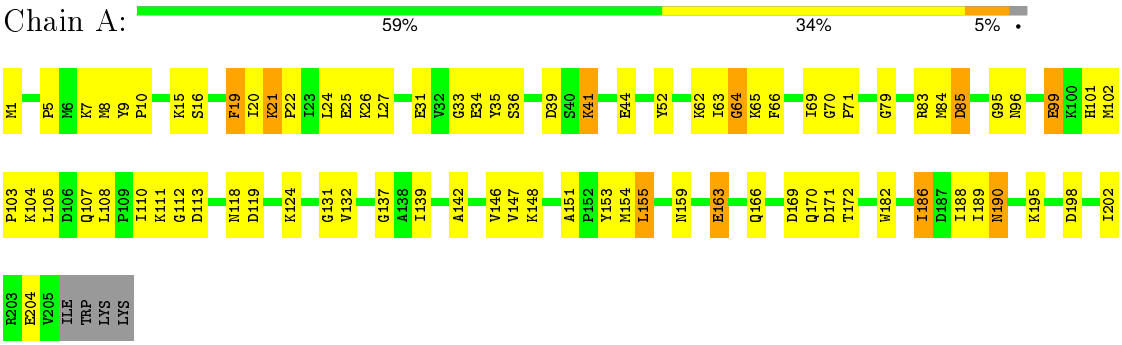
3 Residue-property plots (i)

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.

Note EDS was not executed.

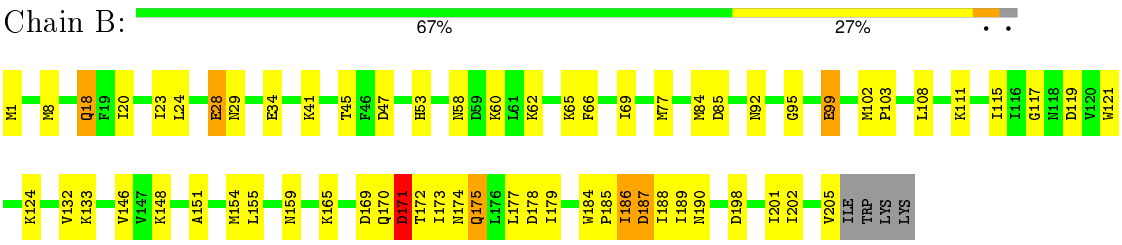
• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

Chain A:



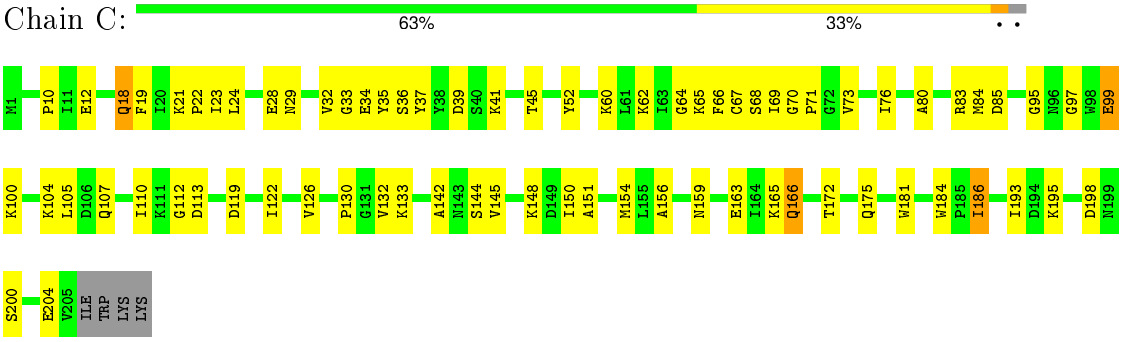
• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

Chain B:



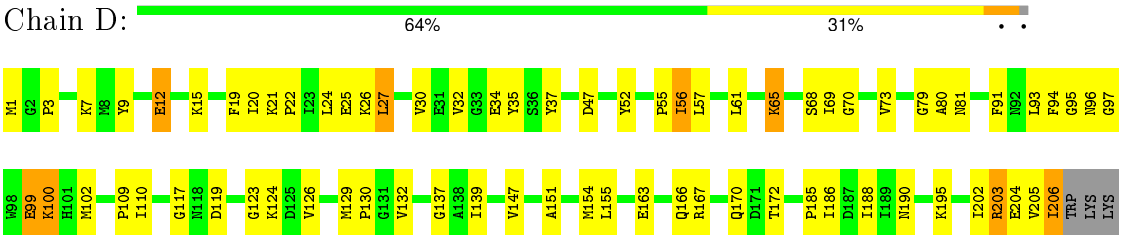
• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

Chain C:



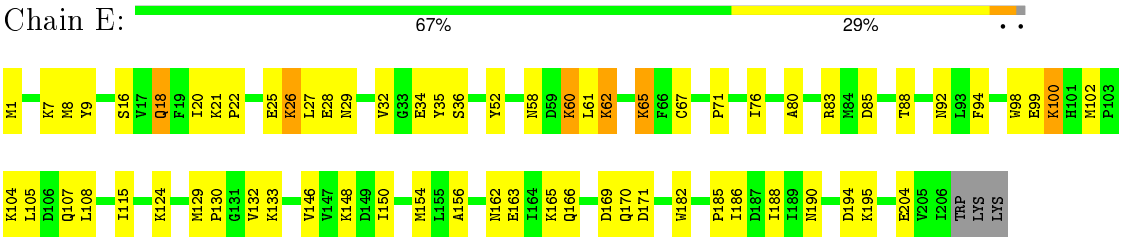
• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

Chain D:



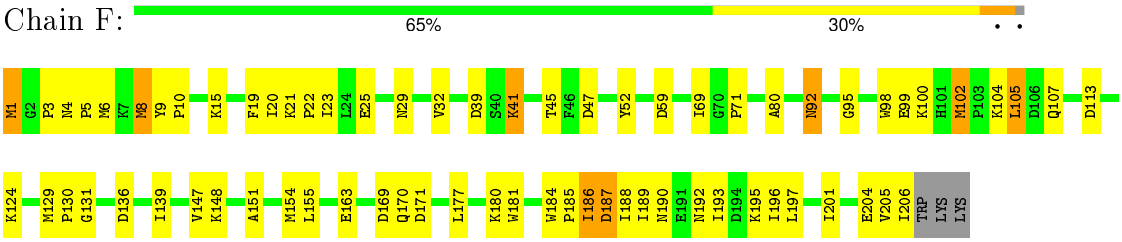
• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

Chain E:



• Molecule 1: STREPTOGRAMIN A ACETYLTRANSFERASE

Chain F:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	186.30Å 186.30Å 186.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 2.70	Depositor
% Data completeness (in resolution range)	94.0 (99.00-2.70)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.188 , 0.246	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10155	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.47	0/1660	0.70	0/2251
1	B	0.47	1/1653 (0.1%)	0.74	3/2243 (0.1%)
1	C	0.41	0/1656	0.66	0/2247
1	D	0.43	0/1664	0.68	1/2258 (0.0%)
1	E	0.43	0/1652	0.67	0/2245
1	F	0.44	0/1663	0.66	0/2255
All	All	0.44	1/9948 (0.0%)	0.69	4/13499 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	205	VAL	CA-CB	-5.95	1.42	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	205	VAL	N-CA-C	10.39	139.05	111.00
1	D	206	ILE	N-CA-C	6.96	129.80	111.00
1	B	205	VAL	CB-CA-C	-6.26	99.50	111.40
1	B	205	VAL	CA-C-O	5.67	132.00	120.10

There are no chirality outliers.

There are no planarity outliers.

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	1621	0	1611	75	0
1	B	1614	0	1601	50	0
1	C	1617	0	1600	44	0
1	D	1625	0	1614	67	0
1	E	1613	0	1575	53	0
1	F	1624	0	1609	64	0
2	A	51	0	27	5	0
2	B	51	0	27	3	0
2	C	51	0	27	6	0
2	D	51	0	27	1	0
2	E	51	0	27	0	0
2	F	51	0	27	1	0
3	A	20	0	0	2	0
3	B	25	0	0	3	0
3	C	21	0	0	0	0
3	D	24	0	0	8	0
3	E	21	0	0	9	0
3	F	24	0	0	4	0
All	All	10155	0	9772	340	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 17.

The worst 5 of 340 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:E:26:LYS:O	1:E:27:LEU:HD23	1.53	1.05
1:B:60:LYS:HE3	3:B:3512:HOH:O	1.58	1.01
1:F:195:LYS:NZ	1:F:204:GLU:HG3	1.77	0.99
1:B:186:ILE:HG23	1:B:187:ASP:H	1.30	0.93
1:A:195:LYS:HZ1	1:A:204:GLU:CD	1.70	0.93

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	203/209 (97%)	185 (91%)	16 (8%)	2 (1%)	19 45
1	B	203/209 (97%)	187 (92%)	12 (6%)	4 (2%)	9 24
1	C	203/209 (97%)	188 (93%)	15 (7%)	0	100 100
1	D	204/209 (98%)	186 (91%)	15 (7%)	3 (2%)	13 32
1	E	204/209 (98%)	187 (92%)	15 (7%)	2 (1%)	19 45
1	F	204/209 (98%)	188 (92%)	14 (7%)	2 (1%)	19 45
All	All	1221/1254 (97%)	1121 (92%)	87 (7%)	13 (1%)	17 42

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	186	ILE
1	B	187	ASP
1	A	64	GLY
1	D	56	ILE
1	E	170	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	176/183 (96%)	159 (90%)	17 (10%)	10 23
1	B	175/183 (96%)	160 (91%)	15 (9%)	13 29
1	C	175/183 (96%)	161 (92%)	14 (8%)	15 33
1	D	177/183 (97%)	163 (92%)	14 (8%)	15 34
1	E	172/183 (94%)	158 (92%)	14 (8%)	15 33
1	F	176/183 (96%)	163 (93%)	13 (7%)	17 39
All	All	1051/1098 (96%)	964 (92%)	87 (8%)	14 31

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	105	LEU
1	D	12	GLU
1	F	100	LYS
1	C	132	VAL
1	C	186	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	190	ASN
1	C	92	ASN
1	E	166	GLN
1	B	174	ASN
1	E	170	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)

6 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	ACO	A	301	-	43,53,53	11.51	15 (34%)	55,79,79	14.46	20 (36%)
2	ACO	B	302	-	43,53,53	11.49	17 (39%)	55,79,79	14.46	21 (38%)
2	ACO	C	303	-	43,53,53	11.45	16 (37%)	55,79,79	14.44	21 (38%)
2	ACO	D	304	-	43,53,53	11.46	17 (39%)	55,79,79	14.45	21 (38%)
2	ACO	E	305	-	43,53,53	11.49	15 (34%)	55,79,79	14.46	21 (38%)
2	ACO	F	306	-	43,53,53	11.51	15 (34%)	55,79,79	14.44	20 (36%)

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	ACO	A	301	-	-	0/47/67/67	0/3/3/3
2	ACO	B	302	-	-	0/47/67/67	0/3/3/3
2	ACO	C	303	-	-	0/47/67/67	0/3/3/3
2	ACO	D	304	-	-	0/47/67/67	0/3/3/3
2	ACO	E	305	-	-	0/47/67/67	0/3/3/3
2	ACO	F	306	-	-	0/47/67/67	0/3/3/3

The worst 5 of 95 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	304	ACO	P3B-O9A	-2.91	1.44	1.54
2	F	306	ACO	P3B-O9A	-2.69	1.45	1.54
2	B	302	ACO	P3B-O9A	-2.54	1.45	1.54
2	E	305	ACO	P3B-O9A	-2.46	1.45	1.54
2	F	306	ACO	P2A-O5A	-2.45	1.44	1.54

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	301	ACO	CDP-CBP-CCP	-58.35	32.86	108.50
2	B	302	ACO	CDP-CBP-CCP	-58.32	32.90	108.50
2	F	306	ACO	CDP-CBP-CCP	-58.26	32.97	108.50
2	E	305	ACO	CDP-CBP-CCP	-58.24	33.00	108.50
2	D	304	ACO	CDP-CBP-CCP	-58.22	33.04	108.50

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	ACO	5	0
2	B	302	ACO	3	0
2	C	303	ACO	6	0
2	D	304	ACO	1	0
2	F	306	ACO	1	0

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

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.