wwPDB X-ray Structure Validation Summary Report (i)

May 14, 2020 – 05:13 pm BST

PDB ID	:	1L1L
Title	:	CRYSTAL STRUCTURE OF B-12 DEPENDENT (CLASS II) RIBONUCLEOTIDE REDUCTASE
Authors	:	Sintchak, M.D.; Arjara, G.; Kellogg, B.A.; Stubbe, J.; Drennan, C.L.
Deposited on	:	2002-02-18
Resolution	:	1.75 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

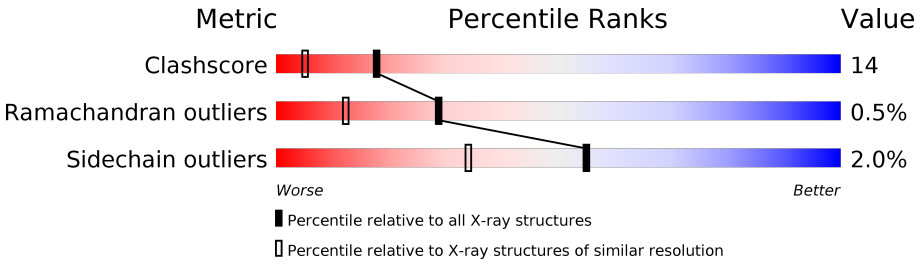
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.75 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	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)

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 respectively. 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	739	70% 26%
1	B	739	80% 17%
1	C	739	75% 21%
1	D	739	68% 28%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 25227 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 RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	717	Total	C	N	O	S	0	0	0
			5588	3526	956	1089	17			
1	B	717	Total	C	N	O	S	0	0	0
			5588	3526	956	1089	17			
1	C	717	Total	C	N	O	S	0	0	0
			5588	3526	956	1089	17			
1	D	717	Total	C	N	O	S	0	0	0
			5588	3526	956	1089	17			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	152	PHE	CYS	SEE REMARK 999	UNP Q59490
B	152	PHE	CYS	SEE REMARK 999	UNP Q59490
C	152	PHE	CYS	SEE REMARK 999	UNP Q59490
D	152	PHE	CYS	SEE REMARK 999	UNP Q59490

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	652	Total	O	0	0
			652	652		
2	B	960	Total	O	0	0
			960	960		
2	C	684	Total	O	0	0
			684	684		
2	D	579	Total	O	0	0
			579	579		

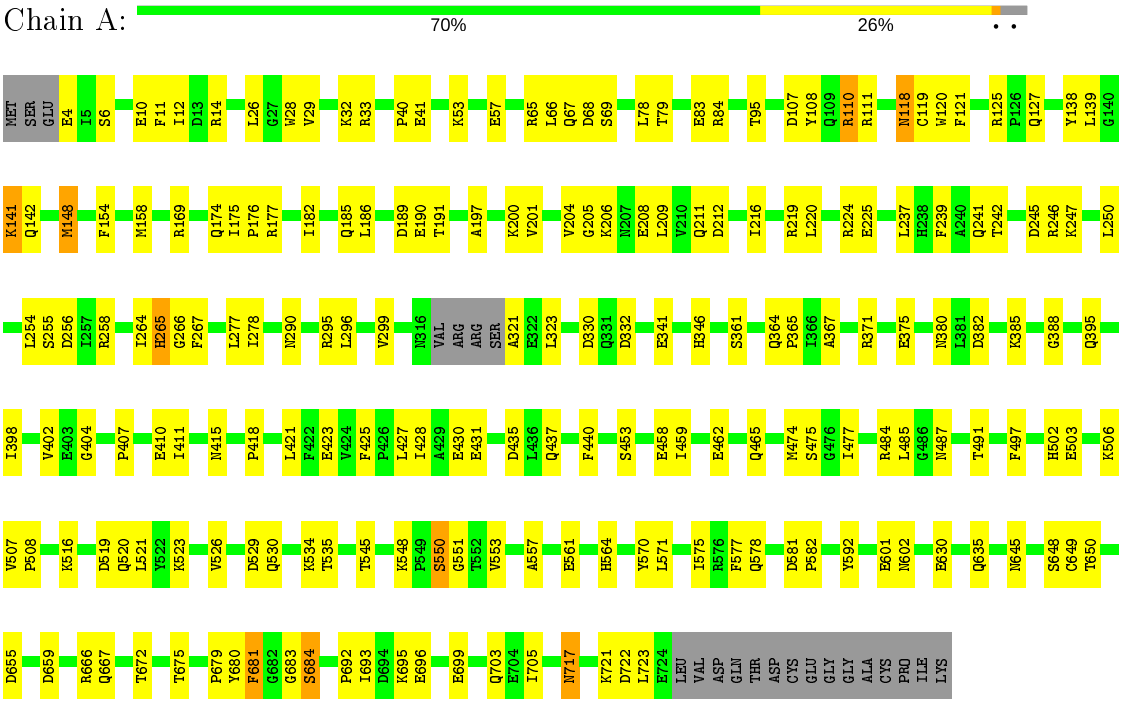
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

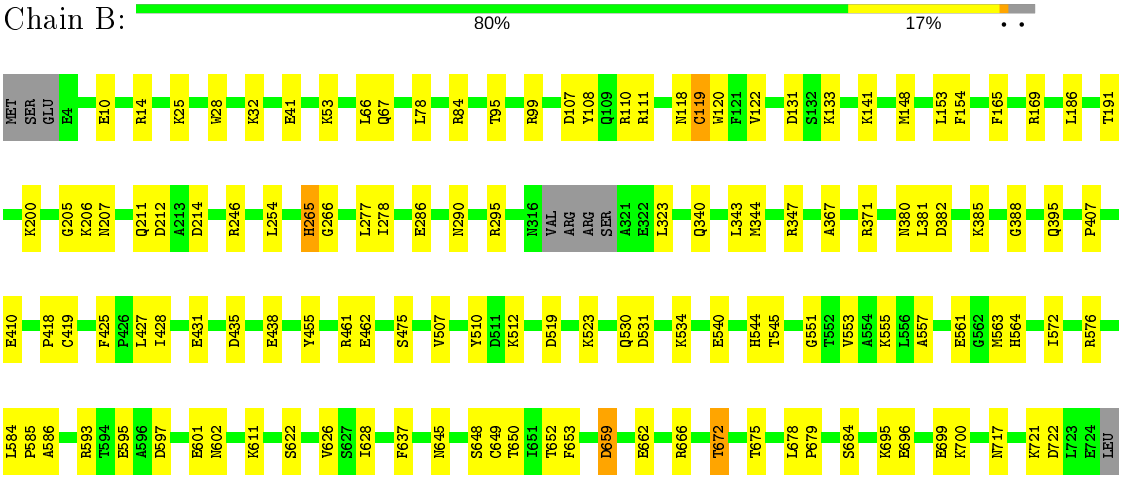
- Molecule 1: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE

Chain A:



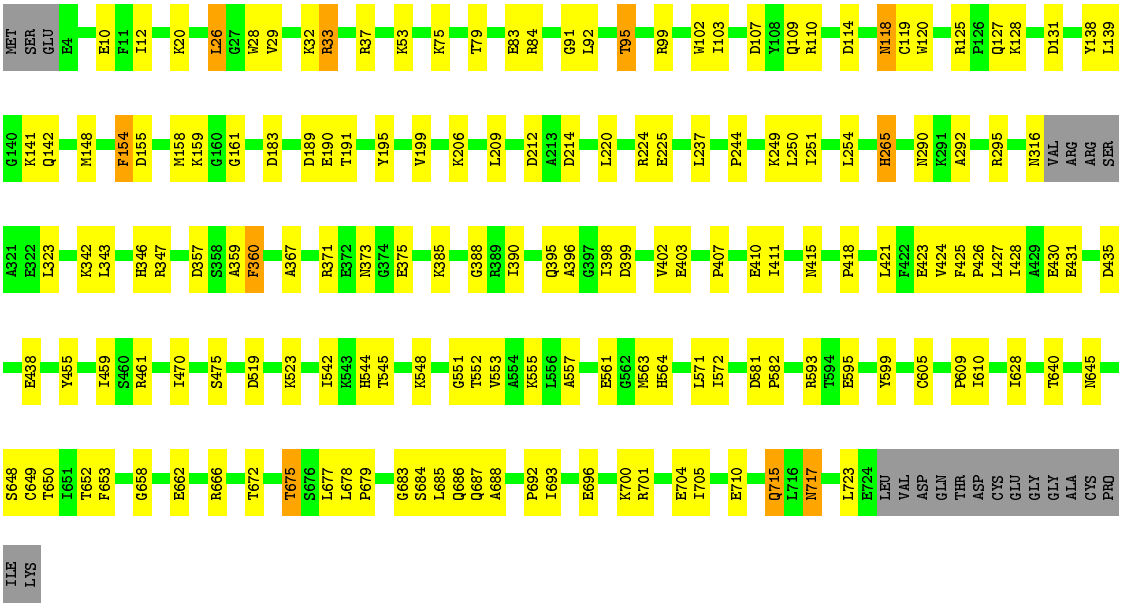
- Molecule 1: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE

Chain B:



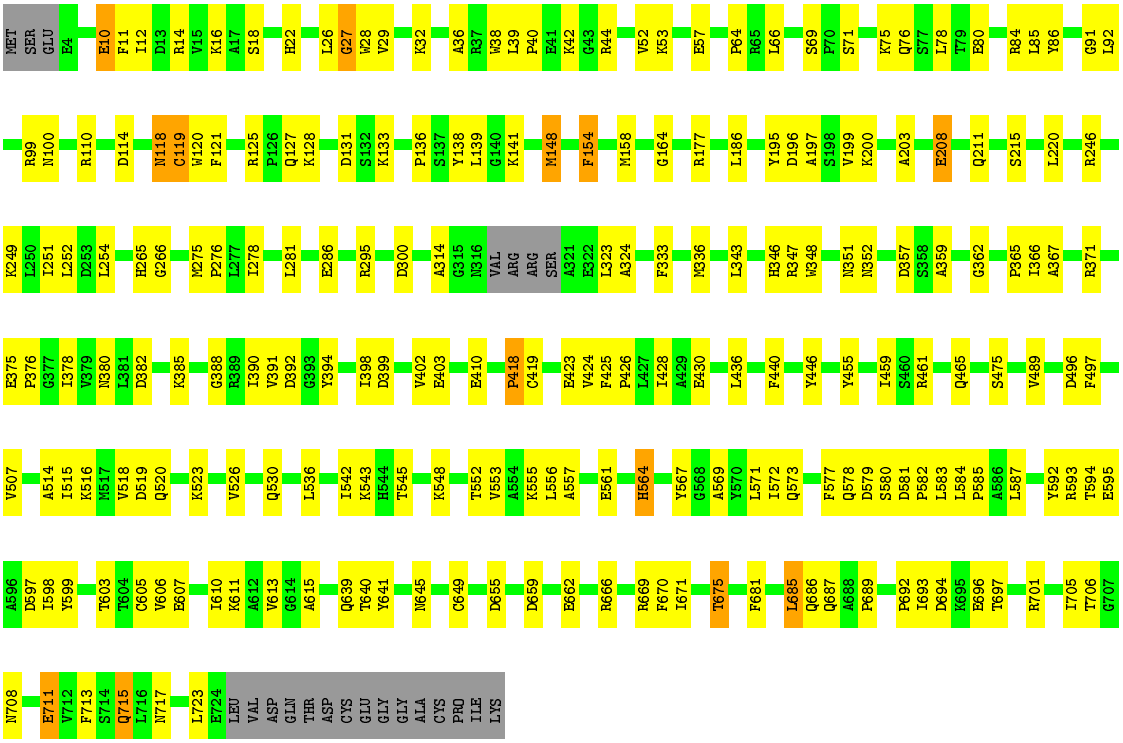
• Molecule 1: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE

Chain C:



• Molecule 1: RIBONUCLEOSIDE TRIPHOSPHATE REDUCTASE

Chain D:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	120.50Å 114.70Å 121.30Å 90.00° 110.20° 90.00°	Depositor
Resolution (Å)	30.00 – 1.75	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-1.75)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.223 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	25227	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.35	0/5702	0.60	1/7731 (0.0%)
1	B	0.46	0/5702	0.68	3/7731 (0.0%)
1	C	0.35	0/5702	0.61	2/7731 (0.0%)
1	D	0.34	0/5702	0.60	1/7731 (0.0%)
All	All	0.38	0/22808	0.63	7/30924 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	388	GLY	N-CA-C	-7.18	95.15	113.10
1	B	388	GLY	N-CA-C	-7.03	95.52	113.10
1	C	388	GLY	N-CA-C	-6.42	97.06	113.10
1	D	388	GLY	N-CA-C	-6.33	97.29	113.10
1	C	435	ASP	N-CA-C	-5.31	96.67	111.00

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	5588	0	5456	186	0
1	B	5588	0	5456	111	0
1	C	5588	0	5456	127	0
1	D	5588	0	5456	180	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	652	0	0	64	0
2	B	960	0	0	54	1
2	C	684	0	0	45	1
2	D	579	0	0	72	0
All	All	25227	0	21824	601	2

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 14.

The worst 5 of 601 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:D:706:THR:HG22	2:D:1110:HOH:O	1.26	1.33
1:C:190:GLU:HG2	2:C:1386:HOH:O	1.29	1.30
1:D:158:MET:HE1	2:D:1285:HOH:O	1.28	1.30
1:B:534:LYS:HE3	2:B:1454:HOH:O	1.15	1.26
1:C:563:MET:HE2	2:C:1422:HOH:O	1.34	1.25

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	Interatomic distance (Å)	Clash overlap (Å)
1:D:715:GLN:CG	2:B:1694:HOH:O[2_545]	1.97	0.23
2:C:907:HOH:O	2:C:1175:HOH:O[2_756]	2.15	0.05

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	713/739 (96%)	672 (94%)	36 (5%)	5 (1%)	22 8
1	B	713/739 (96%)	688 (96%)	24 (3%)	1 (0%)	51 33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	713/739 (96%)	674 (94%)	36 (5%)	3 (0%)	34 17
1	D	713/739 (96%)	670 (94%)	38 (5%)	5 (1%)	22 8
All	All	2852/2956 (96%)	2704 (95%)	134 (5%)	14 (0%)	29 12

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	684	SER
1	B	684	SER
1	A	550	SER
1	C	360	PHE
1	D	579	ASP

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	598/623 (96%)	585 (98%)	13 (2%)	52 29
1	B	598/623 (96%)	588 (98%)	10 (2%)	60 42
1	C	598/623 (96%)	586 (98%)	12 (2%)	55 34
1	D	598/623 (96%)	584 (98%)	14 (2%)	50 28
All	All	2392/2492 (96%)	2343 (98%)	49 (2%)	55 34

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	717	ASN
1	C	119	CYS
1	D	685	LEU
1	C	33	ARG
1	C	148	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	602	ASN
1	C	248	GLN
1	D	578	GLN
1	B	717	ASN
1	A	564	HIS

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

There are no ligands in this entry.

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.