



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:02 AM GMT

PDB ID : 2LTN  
Title : DESIGN, EXPRESSION, AND CRYSTALLIZATION OF RECOMBINANT  
LECTIN FROM THE GARDEN PEA (PISUM SATIVUM)  
Authors : Suddath, F.L.; Phillips, S.R.; Einspahr, H.  
Deposited on : 1990-06-26  
Resolution : 1.70 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](mailto: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.

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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

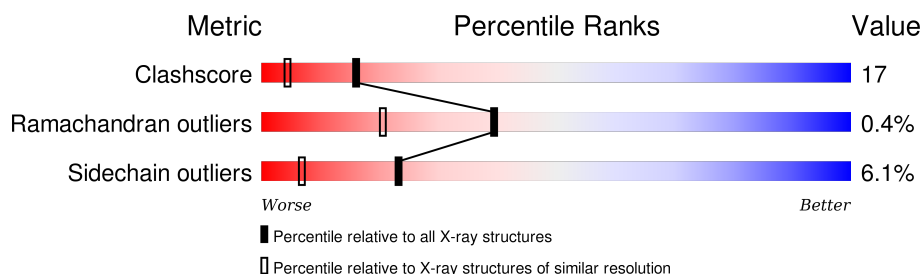
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)

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  $\geq 3$ , 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	181	 60% 30% 8% .
1	C	181	 59% 33% 8% .
2	B	52	 60% 29% . 8%
2	D	52	 62% 27% . 8%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3866 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 PEA LECTIN, ALPHA CHAIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	0	0	0
			1417	903	233	281			
1	C	181	Total	C	N	O	0	0	0
			1417	903	233	281			

- Molecule 2 is a protein called PEA LECTIN, BETA CHAIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	48	Total	C	N	O	0	0	1
			367	236	58	73			
2	D	48	Total	C	N	O	0	0	1
			367	236	58	73			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mn	0	0
			1	1		
3	C	1	Total	Mn	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

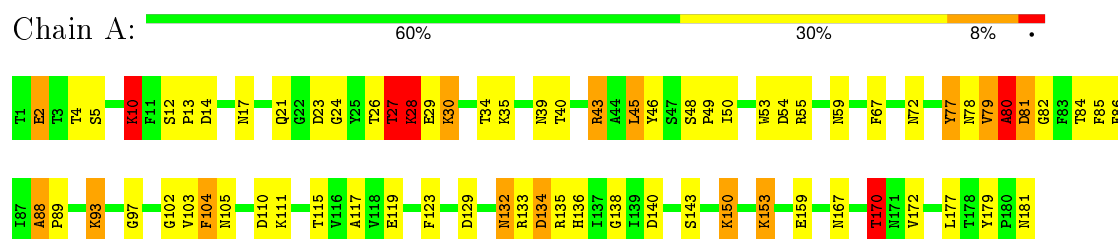
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	120	Total 120	O 120	0	0
5	B	27	Total 27	O 27	0	0
5	C	125	Total 125	O 125	0	0
5	D	22	Total 22	O 22	0	0

### 3 Residue-property plots

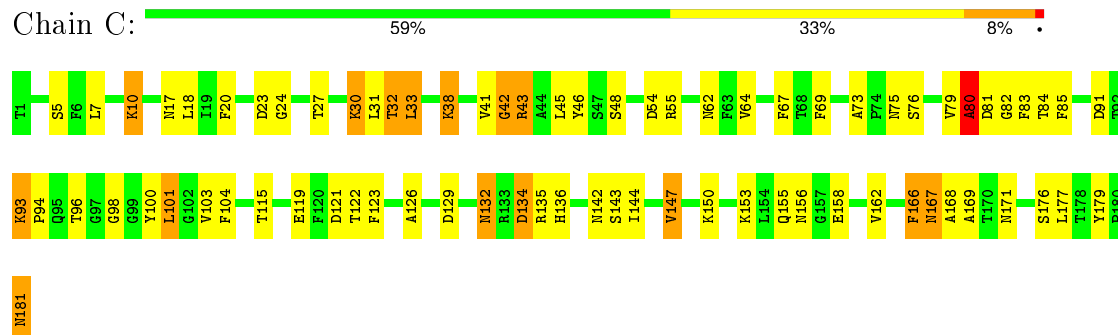
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

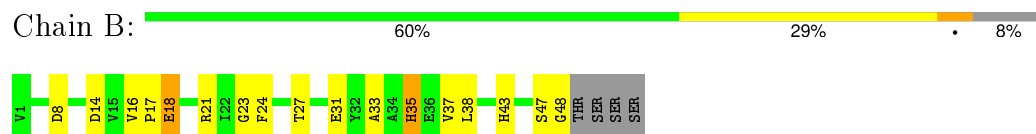
#### • Molecule 1: PEA LECTIN, ALPHA CHAIN



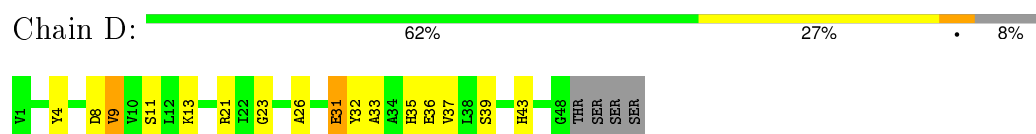
#### • Molecule 1: PEA LECTIN, ALPHA CHAIN



#### • Molecule 2: PEA LECTIN, BETA CHAIN



#### • Molecule 2: PEA LECTIN, BETA CHAIN



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	50.73Å 61.16Å 136.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.70)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.177 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3866	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	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: CA, MN

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	1.52	9/1451 (0.6%)	2.27	70/1981 (3.5%)
1	C	1.47	11/1451 (0.8%)	2.25	63/1981 (3.2%)
2	B	1.57	2/377 (0.5%)	2.16	17/517 (3.3%)
2	D	1.44	1/377 (0.3%)	2.00	15/517 (2.9%)
All	All	1.49	23/3656 (0.6%)	2.22	165/4996 (3.3%)

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	1	2
1	C	1	3
All	All	2	5

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	80	ALA	N-CA	-10.05	1.26	1.46
1	A	80	ALA	N-CA	-8.79	1.28	1.46
1	C	80	ALA	CA-CB	8.54	1.70	1.52
1	C	119	GLU	CD-OE2	-7.99	1.16	1.25
2	D	39	SER	CA-CB	7.22	1.63	1.52

The worst 5 of 165 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	79	VAL	O-C-N	23.56	160.40	122.70
1	C	80	ALA	N-CA-C	18.54	161.06	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	43	ARG	NE-CZ-NH1	17.10	128.85	120.30
1	C	79	VAL	O-C-N	16.46	149.04	122.70
1	A	79	VAL	CA-C-N	-14.62	85.04	117.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	27	THR	CA
1	C	80	ALA	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	80	ALA	Mainchain,Peptide
1	C	43	ARG	Sidechain
1	C	80	ALA	Mainchain,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	1417	0	1364	70	0
1	C	1417	0	1366	47	0
2	B	367	0	349	10	0
2	D	367	0	349	9	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	A	120	0	0	5	0
5	B	27	0	0	0	0
5	C	125	0	0	0	0
5	D	22	0	0	0	0
All	All	3866	0	3428	118	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 118 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:A:153:LYS:CB	1:A:153:LYS:HZ3	1.33	1.32
1:A:153:LYS:HB2	1:A:153:LYS:NZ	1.18	1.25
1:A:27:THR:HG23	1:A:29:GLU:N	1.62	1.11
1:A:28:LYS:HE3	1:A:30:LYS:HE2	1.33	1.09
1:A:27:THR:CG2	1:A:29:GLU:H	1.74	1.01

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	179/181 (99%)	172 (96%)	5 (3%)	2 (1%)	17	4
1	C	179/181 (99%)	176 (98%)	3 (2%)	0	100	100
2	B	46/52 (88%)	46 (100%)	0	0	100	100
2	D	46/52 (88%)	46 (100%)	0	0	100	100
All	All	450/466 (97%)	440 (98%)	8 (2%)	2 (0%)	39	20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	LYS
1	A	27	THR

### 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	156/156 (100%)	145 (93%)	11 (7%)	18	4
1	C	156/156 (100%)	144 (92%)	12 (8%)	16	3
2	B	41/45 (91%)	41 (100%)	0	100	100
2	D	41/45 (91%)	40 (98%)	1 (2%)	57	36
All	All	394/402 (98%)	370 (94%)	24 (6%)	23	7

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	THR
1	C	32	THR
1	C	167	ASN
1	C	10	LYS
1	C	30	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	35	HIS
1	C	39	ASN
1	C	156	ASN
1	A	171	ASN
1	C	167	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

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.