



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:40 PM GMT

PDB ID : 1LDK  
Title : Structure of the Cul1-Rbx1-Skp1-F boxSkp2 SCF Ubiquitin Ligase Complex  
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Deposited on : 2002-04-08  
Resolution : 3.10 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

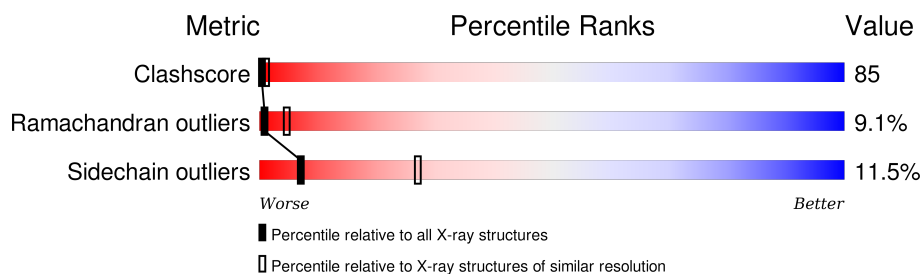
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)

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	396	
2	B	366	
3	C	90	
4	D	133	
5	E	41	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7922 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 CULLIN HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	0	0
			2950	1870	508	558	14			

- Molecule 2 is a protein called CULLIN HOMOLOG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	366	Total	C	N	O	S	0	0	0
			2981	1894	503	569	15			

- Molecule 3 is a protein called ring-box protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	88	Total	C	N	O	S	574	0	0
			731	464	133	125	9			

- Molecule 4 is a protein called CYCLIN A/CDK2-ASSOCIATED PROTEIN P19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	118	Total	C	N	O	S	0	0	0
			926	594	149	178	5			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	ASP	DELETION	UNP P63208
D	?	-	ASP	DELETION	UNP P63208
D	?	-	GLU	DELETION	UNP P63208
D	?	-	GLY	DELETION	UNP P63208
D	?	-	ASP	DELETION	UNP P63208
D	?	-	ASP	DELETION	UNP P63208

- Molecule 5 is a protein called SKP2-like protein type gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	41	Total	C	N	O	S	0	0	0
			331	218	52	58	3			

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

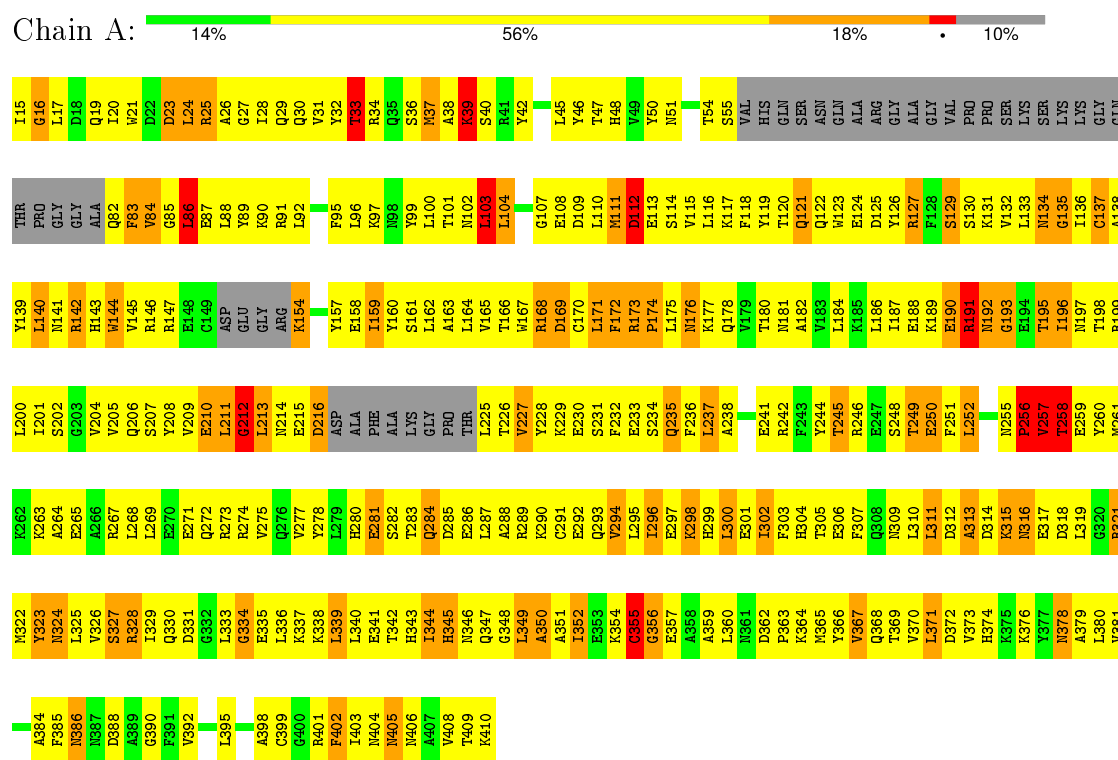
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	3	Total	Zn	0	0
			3	3		

### 3 Residue-property plots

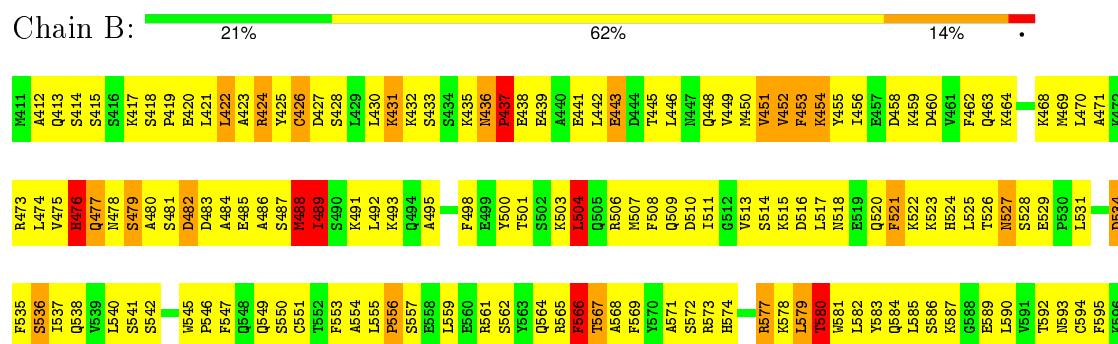
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

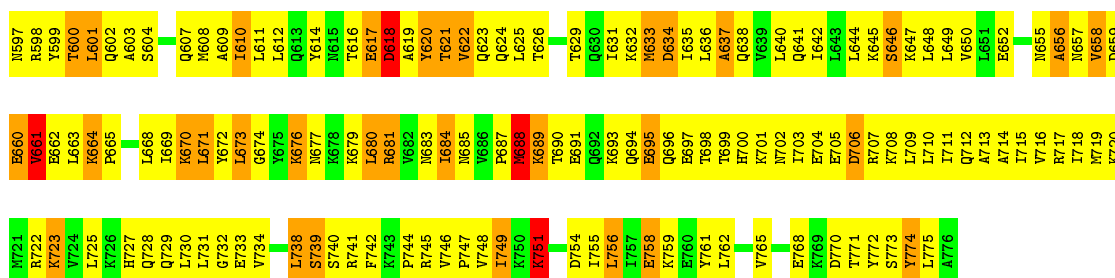
Note EDS was not executed.

#### • Molecule 1: CULLIN HOMOLOG



#### • Molecule 2: CULLIN HOMOLOG





## 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 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	219.38 Å   50.53 Å   158.61 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	20.00 – 3.10	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-3.10)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.289 , 0.331	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7922	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	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: ZN

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	0.78	7/2999 (0.2%)	1.22	32/4039 (0.8%)
2	B	0.75	8/3027 (0.3%)	1.12	28/4069 (0.7%)
3	C	0.32	0/752	0.64	1/1020 (0.1%)
4	D	0.84	3/940 (0.3%)	1.07	7/1271 (0.6%)
5	E	0.76	1/340 (0.3%)	1.14	4/461 (0.9%)
All	All	0.74	19/8058 (0.2%)	1.12	72/10860 (0.7%)

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	5
2	B	0	3
4	D	0	1
All	All	0	9

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	2102	GLU	N-CA	18.23	1.82	1.46
1	A	135	GLY	N-CA	10.90	1.62	1.46
2	B	453	PHE	N-CA	9.67	1.65	1.46
2	B	489	ILE	N-CA	9.53	1.65	1.46
1	A	210	GLU	N-CA	8.53	1.63	1.46

The worst 5 of 72 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	112	ASP	O-C-N	-16.77	95.86	122.70
1	A	213	LEU	CA-C-N	-14.28	85.80	117.20
3	C	1023	GLU	N-CA-CB	-12.15	88.73	110.60
5	E	3146	GLU	N-CA-C	-11.82	79.08	111.00
1	A	212	GLY	C-N-CA	-11.81	92.19	121.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	111	MET	Mainchain
1	A	112	ASP	Mainchain,Peptide
1	A	113	GLU	Mainchain
1	A	323	TYR	Sidechain
2	B	443	GLU	Mainchain

## 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	2950	0	2915	537	1
2	B	2981	0	3049	548	3
3	C	731	0	689	28	1
4	D	926	0	944	170	0
5	E	331	0	331	43	0
6	C	3	0	0	0	0
All	All	7922	0	7928	1256	4

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 85.

The worst 5 of 1256 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:409:THR:CG2	2:B:415:SER:HA	1.32	1.58
2:B:555:LEU:CD2	2:B:559:LEU:HD22	1.11	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ILE:CG1	1:A:296:ILE:CD1	1.85	1.55
2:B:553:PHE:CD1	2:B:631:ILE:HG12	1.37	1.53
4:D:2038:PRO:O	4:D:2040:PRO:CD	1.63	1.47

All (4) 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:A:199:ARG:NH2	1:A:305:THR:OG1[3_546]	1.76	0.44
2:B:597:ASN:OD1	2:B:659:ASP:OD2[3_547]	2.00	0.20
2:B:572:SER:O	3:C:1061:ALA:CB[1_545]	2.04	0.16
2:B:660:GLU:OE1	2:B:676:LYS:CB[3_557]	2.04	0.16

## 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	350/396 (88%)	236 (67%)	92 (26%)	22 (6%)	2	10
2	B	364/366 (100%)	261 (72%)	75 (21%)	28 (8%)	1	6
3	C	86/90 (96%)	44 (51%)	24 (28%)	18 (21%)	0	0
4	D	114/133 (86%)	68 (60%)	31 (27%)	15 (13%)	0	1
5	E	39/41 (95%)	26 (67%)	9 (23%)	4 (10%)	1	4
All	All	953/1026 (93%)	635 (67%)	231 (24%)	87 (9%)	1	5

5 of 87 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	83	PHE
1	A	174	PRO
1	A	176	ASN

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Mol	Chain	Res	Type
1	A	192	ASN
1	A	193	GLY

### 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	321/347 (92%)	272 (85%)	49 (15%)	3	14
2	B	338/338 (100%)	301 (89%)	37 (11%)	8	30
3	C	78/79 (99%)	70 (90%)	8 (10%)	9	32
4	D	105/122 (86%)	101 (96%)	4 (4%)	40	76
5	E	37/38 (97%)	34 (92%)	3 (8%)	15	47
All	All	879/924 (95%)	778 (88%)	101 (12%)	7	27

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	371	LEU
2	B	488	MET
3	C	1100	GLU
1	A	386	ASN
2	B	437	PRO

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	A	386	ASN
2	B	509	GLN
4	D	2090	GLN
2	B	476	HIS
1	A	214	ASN

### 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](#)

Of 3 ligands modelled in this entry, 3 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 [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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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

### 6.5 Other polymers [i](#)

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