



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 09:31 PM UTC

PDB ID : 6R7F / pdb_00006r7f
EMDB ID : EMD-4739
Title : Structural basis of Cullin-2 RING E3 ligase regulation by the COP9 signalosome
Authors : Faull, S.V.; Lau, A.M.C.; Martens, C.; Ahdash, Z.; Yebenes, H.; Schmidt, C.; Beuron, F.; Cronin, N.B.; Morris, E.P.; Politis, A.
Deposited on : 2019-03-28
Resolution : 8.20 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

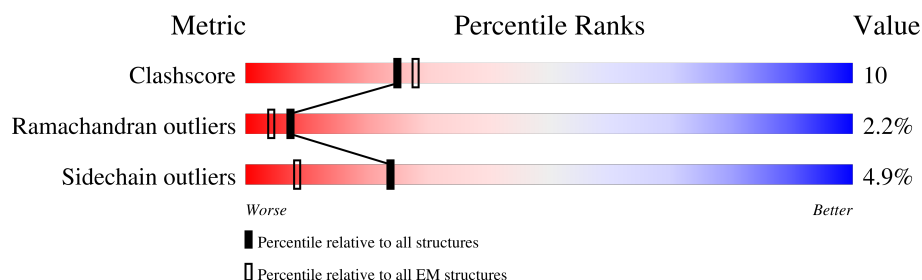
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 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.



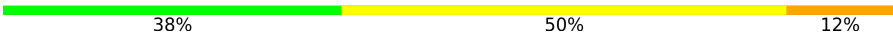
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	433	44% 51% 5%
2	B	443	37% 46% 10% 7%
3	C	403	48% 43% 8% .
4	D	406	47% 48% . .
5	E	311	41% 49% 8% .
6	F	288	42% 48% 9% .
7	H	209	33% 42% 5% 20%
8	G	208	41% 54% . .
9	V	160	32% 62% 6%

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Mol	Chain	Length	Quality of chain
10	P	118	 42%52%5% •
11	Q	112	 54%39%5% •
12	O	745	 39%52%9% •
13	R	90	 38%50%12%
14	N	76	 53%43%•

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 31558 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 COP9 signalosome complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	433	Total	C	N	O	S	0	0
			3450	2174	605	649	22		

- Molecule 2 is a protein called COP9 signalosome complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	414	Total	C	N	O	S	0	0
			3386	2149	579	643	15		

- Molecule 3 is a protein called COP9 signalosome complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	403	Total	C	N	O	S	0	0
			3205	2040	537	601	27		

- Molecule 4 is a protein called COP9 signalosome complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	406	Total	C	N	O	S	0	0
			3251	2047	566	622	16		

- Molecule 5 is a protein called COP9 signalosome complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	311	Total	C	N	O	S	0	0
			2472	1575	412	471	14		

- Molecule 6 is a protein called COP9 signalosome complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	288	Total	C	N	O	S	0	0
			2280	1452	379	434	15		

- Molecule 7 is a protein called COP9 signalosome complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	168	Total	C	N	O	S	0	0
			1340	859	232	245	4		

- Molecule 8 is a protein called COP9 signalosome complex subunit 7b.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	208	Total	C	N	O	S	0	0
			1645	1039	279	321	6		

- Molecule 9 is a protein called von Hippel-Lindau disease tumor suppressor.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	V	160	Total	C	N	O	S	0	0
			1308	824	245	235	4		

- Molecule 10 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	P	118	Total	C	N	O	S	0	0
			921	575	156	185	5		

- Molecule 11 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Q	112	Total	C	N	O	S	0	0
			873	553	139	173	8		

- Molecule 12 is a protein called Cullin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	744	Total	C	N	O	S	0	0
			6090	3869	1029	1146	46		

- Molecule 13 is a protein called E3 ubiquitin-protein ligase RBX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	90	Total	C	N	O	S	0	0
			746	472	137	128	9		

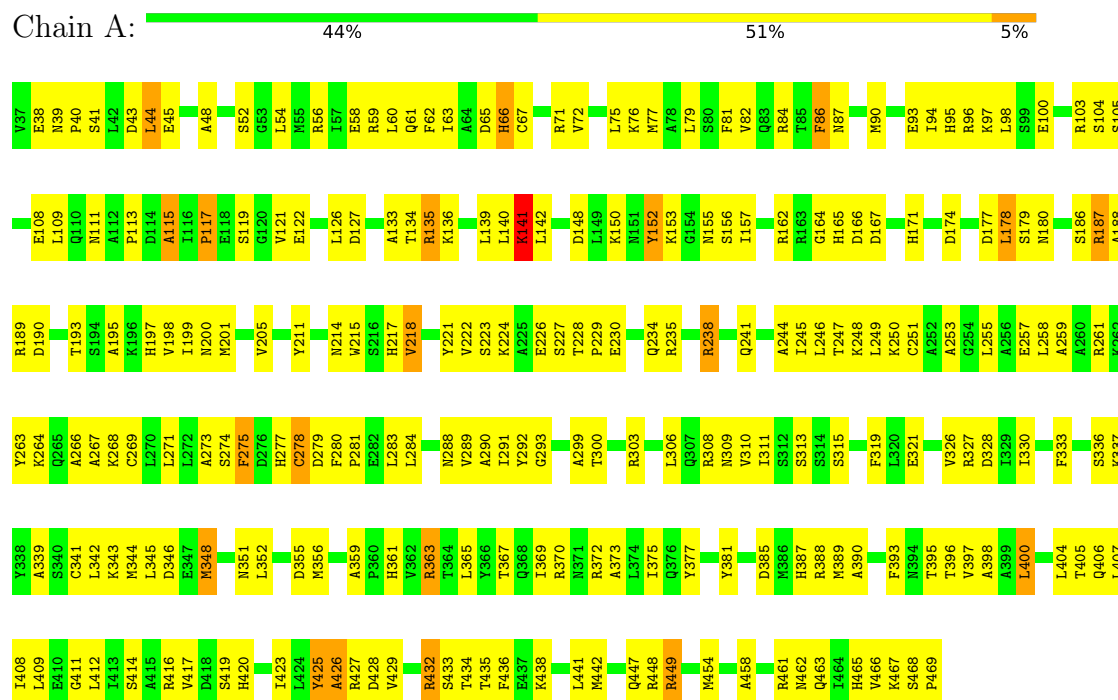
- Molecule 14 is a protein called NEDD8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	76	Total	C	N	O	S	0	0
			591	372	102	115	2		

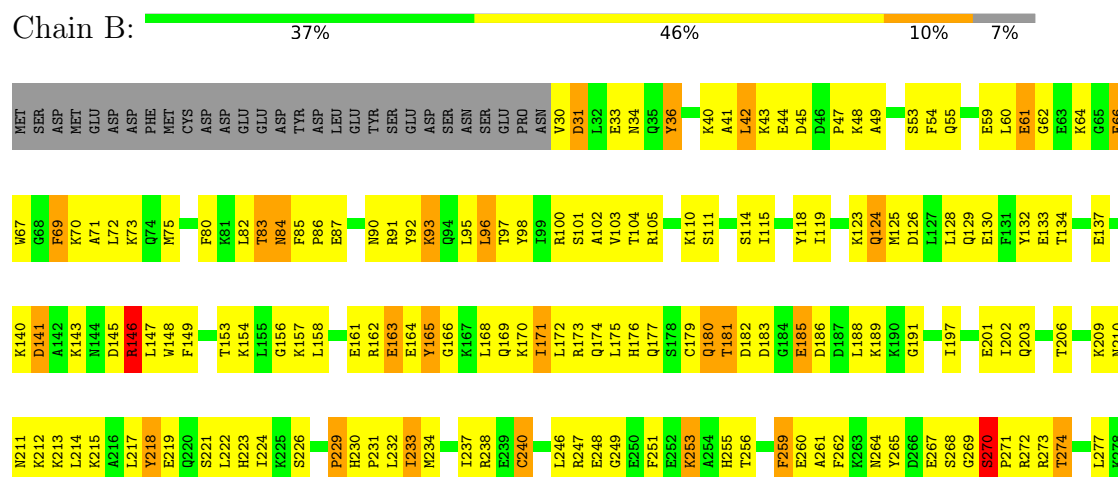
3 Residue-property plots

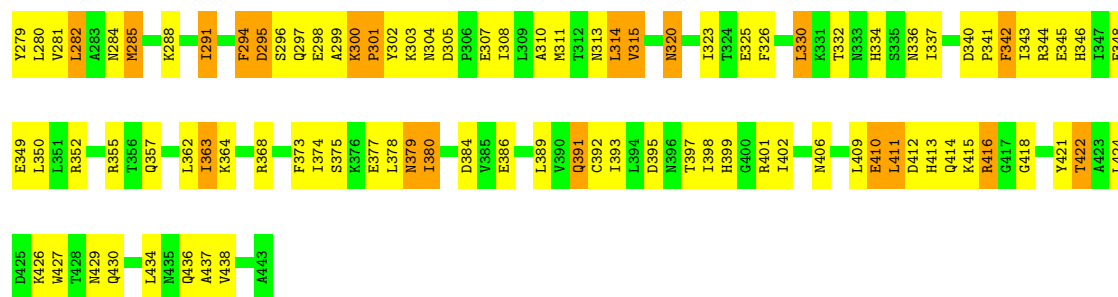
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

• Molecule 1: COP9 signalosome complex subunit 1



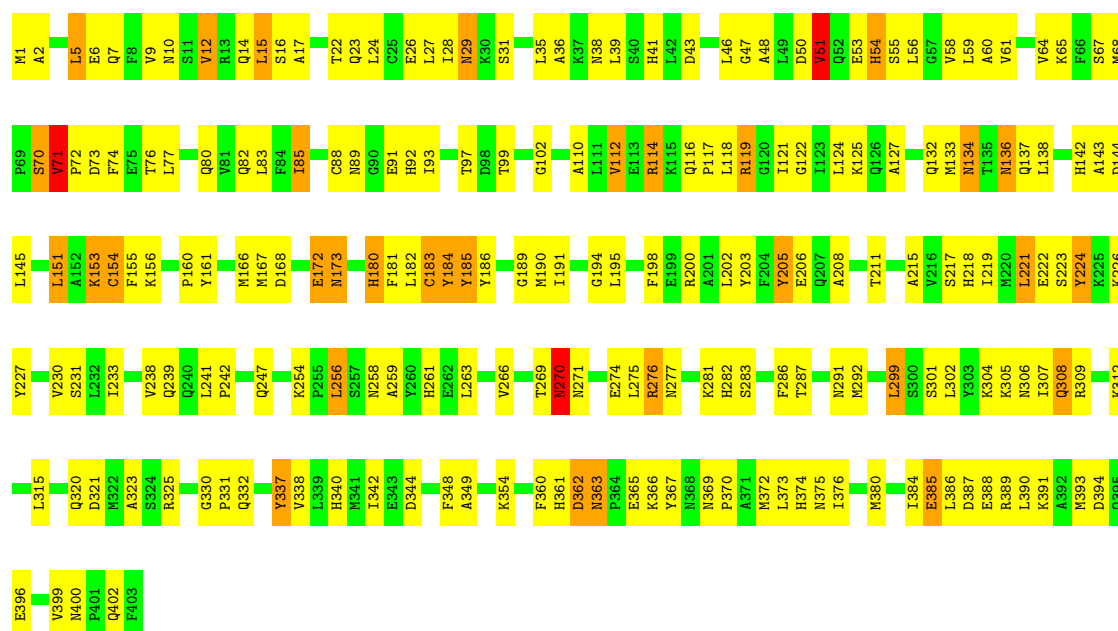
• Molecule 2: COP9 signalosome complex subunit 2





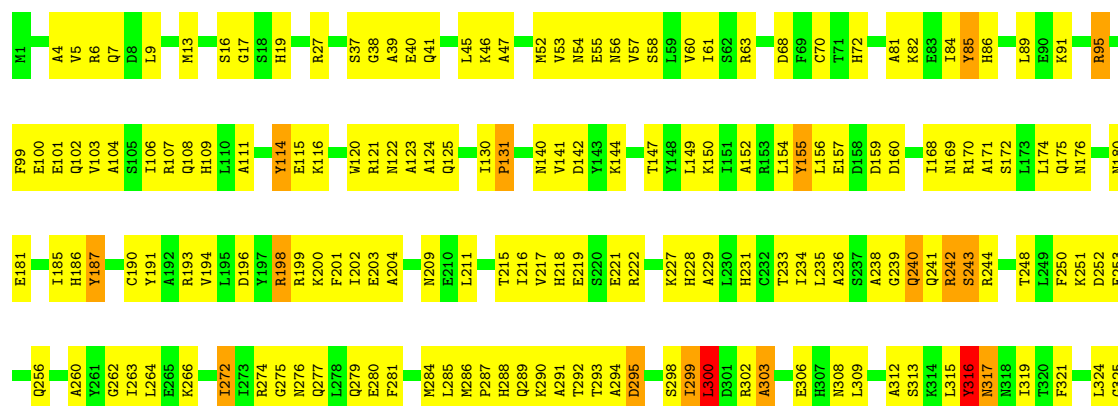
• Molecule 3: COP9 signalosome complex subunit 3

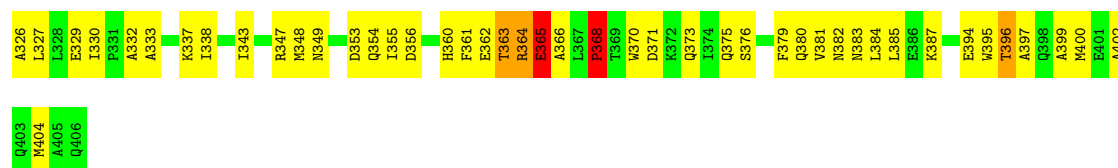
Chain C: 48% 43% 8%



• Molecule 4: COP9 signalosome complex subunit 4

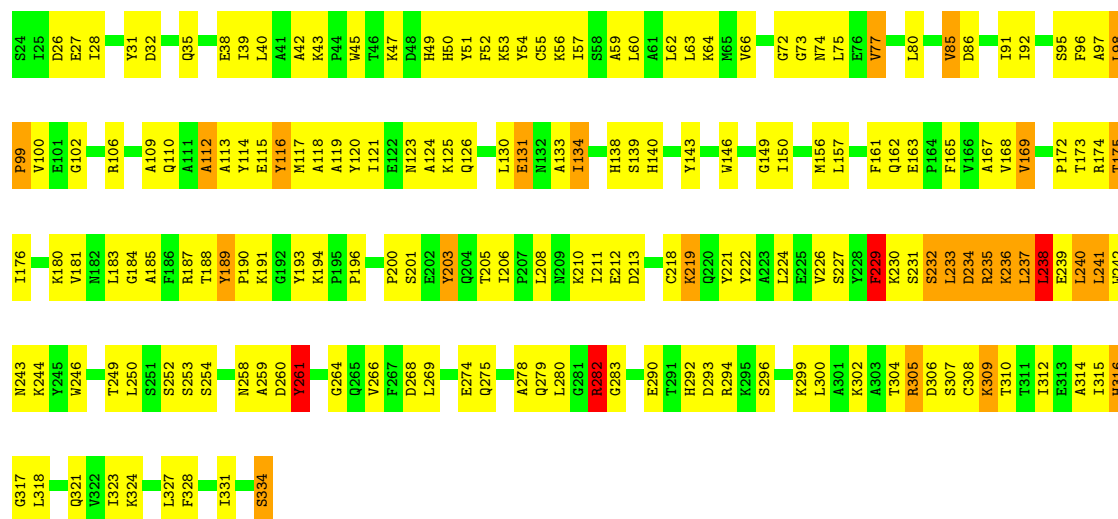
Chain D: 47% 48%





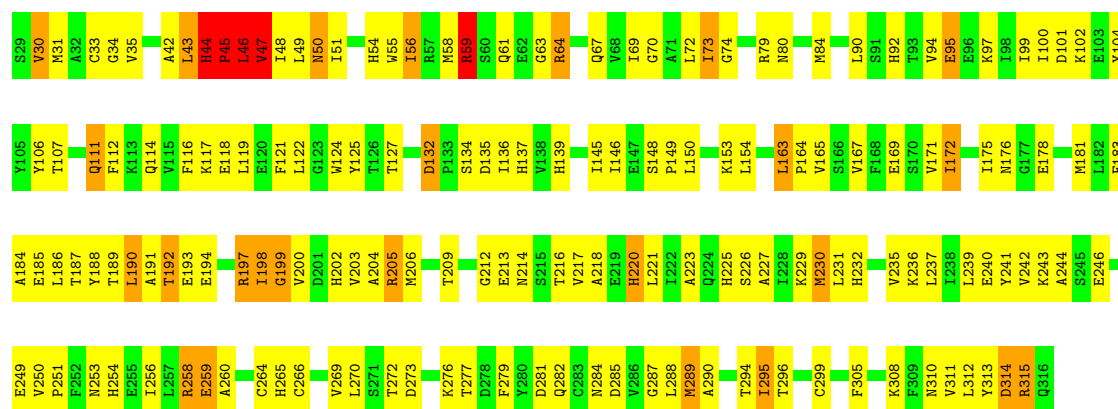
• Molecule 5: COP9 signalosome complex subunit 5

Chain E: 41% 49% 8% .



• Molecule 6: COP9 signalosome complex subunit 6

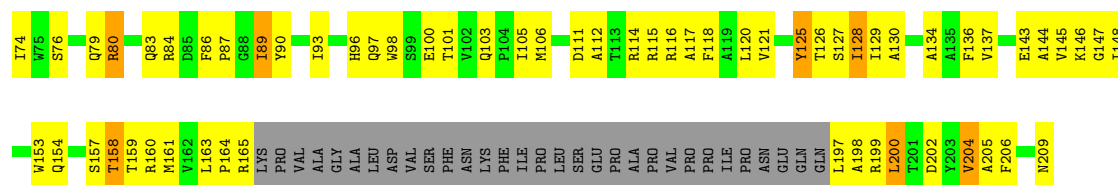
Chain F: 42% 48% 9% .



• Molecule 7: COP9 signalosome complex subunit 8

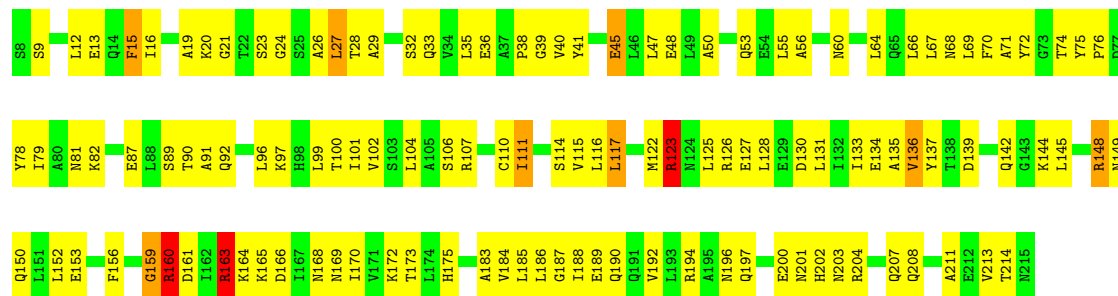
Chain H: 33% 42% 5% 20%





• Molecule 8: COP9 signalosome complex subunit 7b

Chain G: 41% 54%



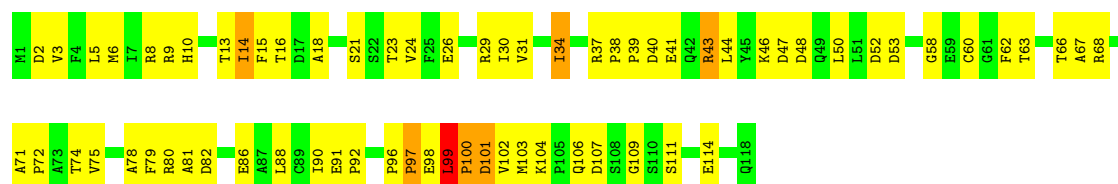
• Molecule 9: von Hippel-Lindau disease tumor suppressor

Chain V: 32% 62% 6%



• Molecule 10: Elongin-B

Chain P: 42% 52% 5%



• Molecule 11: Elongin-C

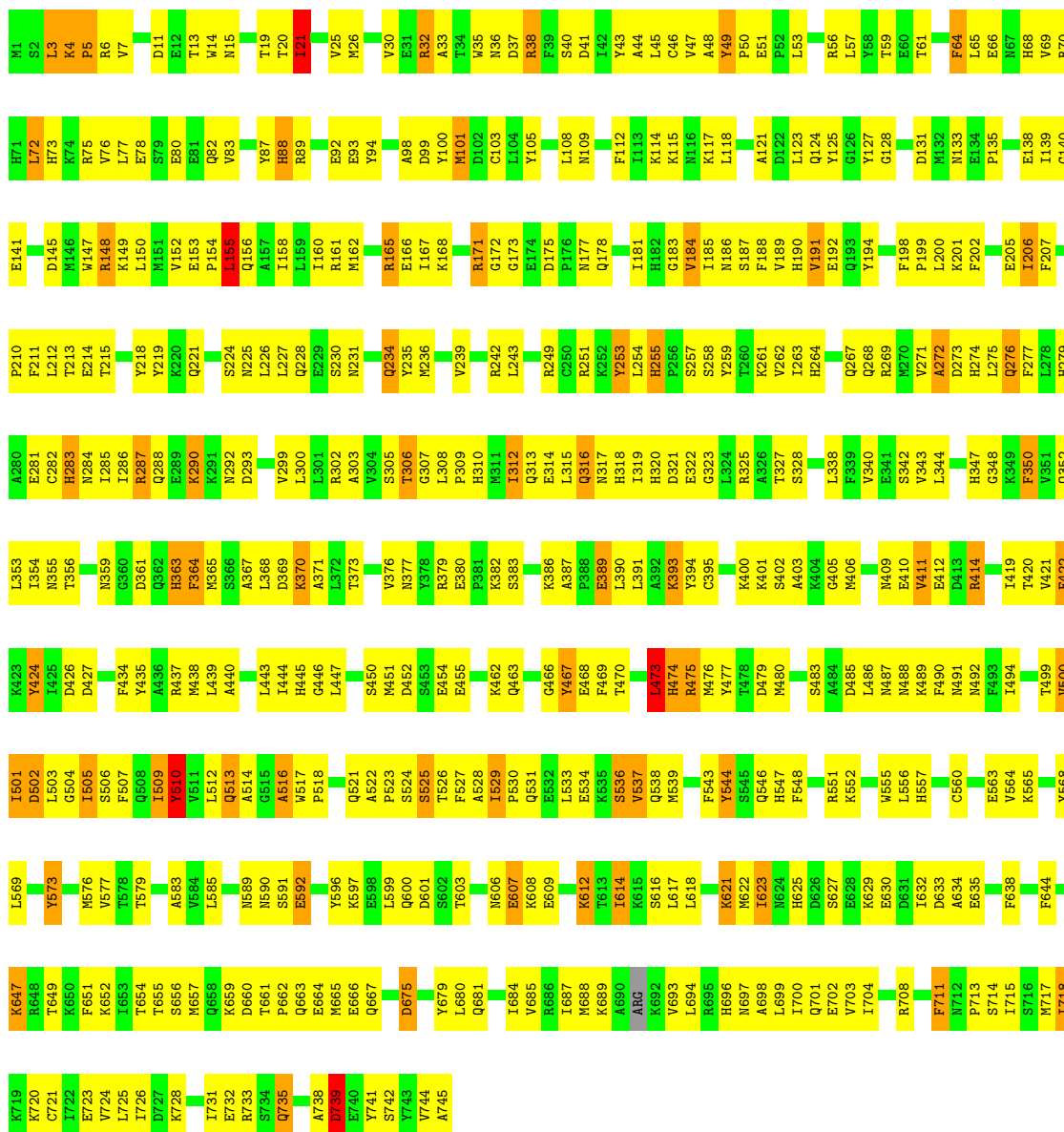
Chain Q: 54% 39% 5%





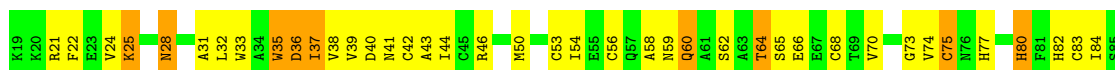
• Molecule 12: Cullin-2

Chain O: 39% 52% 9%



• Molecule 13: E3 ubiquitin-protein ligase RBX1

Chain R: 38% 50% 12%





● Molecule 14: NEDD8



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	20055	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor

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	2.29	139/3509 (4.0%)	2.51	260/4733 (5.5%)
2	B	3.27	125/3444 (3.6%)	2.58	257/4634 (5.5%)
3	C	2.18	102/3264 (3.1%)	2.47	207/4407 (4.7%)
4	D	2.28	127/3303 (3.8%)	2.58	245/4460 (5.5%)
5	E	3.38	91/2526 (3.6%)	2.56	196/3411 (5.7%)
6	F	2.27	84/2327 (3.6%)	2.62	183/3153 (5.8%)
7	H	2.23	46/1372 (3.4%)	2.55	106/1865 (5.7%)
8	G	2.19	47/1665 (2.8%)	2.52	133/2253 (5.9%)
9	V	1.42	0/1341	1.58	10/1824 (0.5%)
10	P	2.36	41/938 (4.4%)	2.39	56/1267 (4.4%)
11	Q	2.21	24/892 (2.7%)	2.38	48/1204 (4.0%)
12	O	2.14	186/6207 (3.0%)	2.44	439/8358 (5.3%)
13	R	2.48	32/768 (4.2%)	2.52	56/1040 (5.4%)
14	N	0.45	0/596	0.87	0/800
All	All	2.42	1044/32152 (3.2%)	2.46	2196/43409 (5.1%)

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	12
2	B	0	15
3	C	0	6
4	D	0	10
5	E	0	10
6	F	0	7
7	H	0	7
8	G	0	9
10	P	0	2
11	Q	0	5
12	O	0	17

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	R	0	2
All	All	0	102

The worst 5 of 1044 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	294	PHE	CA-C	140.04	3.36	1.52
5	E	309	LYS	CA-CB	121.17	3.41	1.53
5	E	203	TYR	CG-CD2	16.34	1.73	1.39
13	R	106	TYR	CG-CD2	16.28	1.73	1.39
10	P	38	PRO	CA-C	16.22	1.60	1.51

The worst 5 of 2196 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	45	PRO	N-CA-C	19.84	153.33	112.47
6	F	44	HIS	CA-CB-CG	19.16	132.96	113.80
5	E	234	ASP	N-CA-C	16.32	129.14	111.36
6	F	44	HIS	O-C-N	-14.65	104.47	121.32
6	F	46	LEU	N-CA-C	13.89	127.69	111.71

There are no chirality outliers.

5 of 102 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	135	ARG	Sidechain
1	A	152	TYR	Sidechain
1	A	187	ARG	Sidechain
1	A	221	TYR	Sidechain
1	A	66	HIS	Sidechain

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	3450	0	3482	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3386	0	3424	38	0
3	C	3205	0	3225	16	0
4	D	3251	0	3253	14	0
5	E	2472	0	2444	78	0
6	F	2280	0	2263	41	0
7	H	1340	0	1324	2	0
8	G	1645	0	1667	4	0
9	V	1308	0	1299	329	0
10	P	921	0	908	92	0
11	Q	873	0	845	91	0
12	O	6090	0	6071	183	0
13	R	746	0	705	29	0
14	N	591	0	616	48	0
All	All	31558	0	31526	660	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 10.

The worst 5 of 660 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)
9:V:178:LEU:CD2	10:P:103:MET:HG3	1.06	1.53
9:V:178:LEU:CD1	10:P:103:MET:HE3	1.32	1.53
9:V:171:LYS:NZ	10:P:106:GLN:CB	1.70	1.52
9:V:178:LEU:CD2	10:P:103:MET:CG	1.75	1.50
9:V:178:LEU:HD21	10:P:103:MET:CG	1.27	1.50

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 PDB entries followed by that with respect to all EM entries.

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	431/433 (100%)	399 (93%)	26 (6%)	6 (1%)	9	40
2	B	412/443 (93%)	364 (88%)	33 (8%)	15 (4%)	2	20
3	C	401/403 (100%)	361 (90%)	26 (6%)	14 (4%)	3	20
4	D	404/406 (100%)	387 (96%)	8 (2%)	9 (2%)	5	29
5	E	309/311 (99%)	290 (94%)	15 (5%)	4 (1%)	9	42
6	F	286/288 (99%)	272 (95%)	8 (3%)	6 (2%)	5	30
7	H	164/209 (78%)	158 (96%)	5 (3%)	1 (1%)	21	59
8	G	206/208 (99%)	189 (92%)	13 (6%)	4 (2%)	6	32
9	V	158/160 (99%)	154 (98%)	1 (1%)	3 (2%)	6	32
10	P	116/118 (98%)	109 (94%)	7 (6%)	0	100	100
11	Q	110/112 (98%)	102 (93%)	8 (7%)	0	100	100
12	O	738/745 (99%)	691 (94%)	29 (4%)	18 (2%)	4	27
13	R	88/90 (98%)	70 (80%)	13 (15%)	5 (6%)	1	14
14	N	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
All	All	3897/4002 (97%)	3617 (93%)	195 (5%)	85 (2%)	7	29

5 of 85 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	115	ALA
1	A	426	ALA
2	B	61	GLU
2	B	141	ASP
2	B	186	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 PDB entries followed by that with respect to all EM entries.

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	377/377 (100%)	361 (96%)	16 (4%)	26	48
2	B	376/405 (93%)	353 (94%)	23 (6%)	17	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	359/359 (100%)	343 (96%)	16 (4%)	24	46
4	D	347/347 (100%)	340 (98%)	7 (2%)	48	66
5	E	267/267 (100%)	248 (93%)	19 (7%)	13	35
6	F	255/255 (100%)	235 (92%)	20 (8%)	11	32
7	H	139/173 (80%)	132 (95%)	7 (5%)	22	43
8	G	181/181 (100%)	172 (95%)	9 (5%)	22	43
9	V	147/147 (100%)	146 (99%)	1 (1%)	76	81
10	P	103/103 (100%)	99 (96%)	4 (4%)	28	49
11	Q	96/96 (100%)	93 (97%)	3 (3%)	35	56
12	O	680/681 (100%)	646 (95%)	34 (5%)	22	43
13	R	79/79 (100%)	73 (92%)	6 (8%)	12	33
14	N	64/66 (97%)	59 (92%)	5 (8%)	11	32
All	All	3470/3536 (98%)	3300 (95%)	170 (5%)	24	43

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	G	136	VAL
12	O	420	THR
10	P	34	ILE
12	O	155	LEU
12	O	565	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	159	GLN
14	N	41	GLN
8	G	169	ASN
14	N	39	GLN
12	O	538	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	O	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	O	654:THR	C	655:THR	N	4.12

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-4739. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections ⓘ

This section was not generated.

6.2 Central slices ⓘ

This section was not generated.

6.3 Largest variance slices ⓘ

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

This section was not generated.

6.5 Orthogonal surface views ⓘ

This section was not generated.

6.6 Mask visualisation ⓘ

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.