wwPDB X-ray Structure Validation Summary Report (i)

Feb 19, 2024 – 11:15 AM EST

PDB ID	:	4KSL
Title	:	Gumby/Fam105B in complex with linear di-ubiquitin
Authors	:	Juang, Y.-C.; Ceccarelli, D.F.; Sicheri, F.
Deposited on	:	2013-05-17
Resolution	:	2.83 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

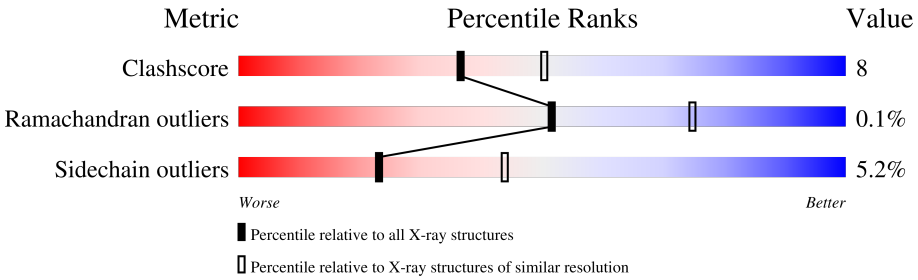
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.83 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	1078 (2.86-2.82)
Ramachandran outliers	138981	1050 (2.86-2.82)
Sidechain outliers	138945	1051 (2.86-2.82)

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 of 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 failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	276	77% 18% 5%
1	B	276	74% 21% 5%
1	E	276	72% 21% • 5%
1	G	276	75% 19% • 5%
1	I	276	80% 14% • 5%
1	K	276	79% 17% • •
1	M	276	70% 22% • 6%
1	O	276	76% 21% • •

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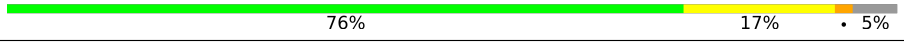
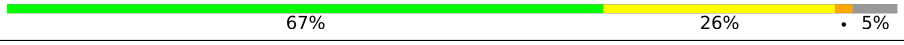
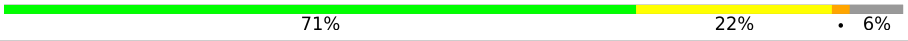
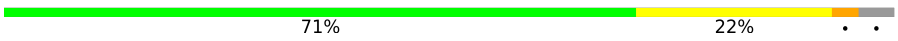
Mol	Chain	Length	Quality of chain
1	Q	276	
1	S	276	
1	U	276	
1	W	276	
2	C	156	
2	D	156	
2	F	156	
2	H	156	
2	J	156	
2	L	156	
2	N	156	
2	P	156	
2	R	156	
2	T	156	
2	V	156	
2	X	156	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 40089 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 Protein FAM105B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			2157	1379	367	398	13			
1	B	263	Total	C	N	O	S	0	0	0
			2157	1379	367	398	13			
1	E	262	Total	C	N	O	S	0	0	0
			2149	1375	365	396	13			
1	G	261	Total	C	N	O	S	0	0	0
			2140	1370	364	393	13			
1	I	262	Total	C	N	O	S	0	0	0
			2149	1375	365	396	13			
1	K	270	Total	C	N	O	S	0	0	0
			2210	1414	376	407	13			
1	M	260	Total	C	N	O	S	0	0	0
			2128	1362	363	390	13			
1	O	270	Total	C	N	O	S	0	0	0
			2210	1414	376	407	13			
1	Q	261	Total	C	N	O	S	0	0	0
			2140	1370	364	393	13			
1	S	263	Total	C	N	O	S	0	0	0
			2153	1377	366	397	13			
1	U	261	Total	C	N	O	S	0	0	0
			2140	1370	364	393	13			
1	W	260	Total	C	N	O	S	0	0	0
			2132	1366	363	390	13			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	GLY	-	expression tag	UNP Q96BN8
A	78	SER	-	expression tag	UNP Q96BN8
A	129	ALA	CYS	engineered mutation	UNP Q96BN8
B	77	GLY	-	expression tag	UNP Q96BN8
B	78	SER	-	expression tag	UNP Q96BN8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	129	ALA	CYS	engineered mutation	UNP Q96BN8
E	77	GLY	-	expression tag	UNP Q96BN8
E	78	SER	-	expression tag	UNP Q96BN8
E	129	ALA	CYS	engineered mutation	UNP Q96BN8
G	77	GLY	-	expression tag	UNP Q96BN8
G	78	SER	-	expression tag	UNP Q96BN8
G	129	ALA	CYS	engineered mutation	UNP Q96BN8
I	77	GLY	-	expression tag	UNP Q96BN8
I	78	SER	-	expression tag	UNP Q96BN8
I	129	ALA	CYS	engineered mutation	UNP Q96BN8
K	77	GLY	-	expression tag	UNP Q96BN8
K	78	SER	-	expression tag	UNP Q96BN8
K	129	ALA	CYS	engineered mutation	UNP Q96BN8
M	77	GLY	-	expression tag	UNP Q96BN8
M	78	SER	-	expression tag	UNP Q96BN8
M	129	ALA	CYS	engineered mutation	UNP Q96BN8
O	77	GLY	-	expression tag	UNP Q96BN8
O	78	SER	-	expression tag	UNP Q96BN8
O	129	ALA	CYS	engineered mutation	UNP Q96BN8
Q	77	GLY	-	expression tag	UNP Q96BN8
Q	78	SER	-	expression tag	UNP Q96BN8
Q	129	ALA	CYS	engineered mutation	UNP Q96BN8
S	77	GLY	-	expression tag	UNP Q96BN8
S	78	SER	-	expression tag	UNP Q96BN8
S	129	ALA	CYS	engineered mutation	UNP Q96BN8
U	77	GLY	-	expression tag	UNP Q96BN8
U	78	SER	-	expression tag	UNP Q96BN8
U	129	ALA	CYS	engineered mutation	UNP Q96BN8
W	77	GLY	-	expression tag	UNP Q96BN8
W	78	SER	-	expression tag	UNP Q96BN8
W	129	ALA	CYS	engineered mutation	UNP Q96BN8

- Molecule 2 is a protein called Polyubiquitin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	149	Total	C	N	O	S	0	0	0
			1183	746	204	231	2			
2	C	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	F	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	H	149	Total	C	N	O	S	0	0	0
			1183	746	204	231	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	L	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	N	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	P	149	Total	C	N	O	S	0	0	0
			1183	746	204	231	2			
2	R	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	T	149	Total	C	N	O	S	0	0	0
			1183	746	204	231	2			
2	V	150	Total	C	N	O	S	0	0	0
			1187	748	205	232	2			
2	X	149	Total	C	N	O	S	0	0	0
			1183	746	204	231	2			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	GLY	-	expression tag	UNP P0CG48
D	-2	ALA	-	expression tag	UNP P0CG48
D	-1	MET	-	expression tag	UNP P0CG48
C	-3	GLY	-	expression tag	UNP P0CG48
C	-2	ALA	-	expression tag	UNP P0CG48
C	-1	MET	-	expression tag	UNP P0CG48
F	-3	GLY	-	expression tag	UNP P0CG48
F	-2	ALA	-	expression tag	UNP P0CG48
F	-1	MET	-	expression tag	UNP P0CG48
H	-3	GLY	-	expression tag	UNP P0CG48
H	-2	ALA	-	expression tag	UNP P0CG48
H	-1	MET	-	expression tag	UNP P0CG48
J	-3	GLY	-	expression tag	UNP P0CG48
J	-2	ALA	-	expression tag	UNP P0CG48
J	-1	MET	-	expression tag	UNP P0CG48
L	-3	GLY	-	expression tag	UNP P0CG48
L	-2	ALA	-	expression tag	UNP P0CG48
L	-1	MET	-	expression tag	UNP P0CG48
N	-3	GLY	-	expression tag	UNP P0CG48
N	-2	ALA	-	expression tag	UNP P0CG48
N	-1	MET	-	expression tag	UNP P0CG48
P	-3	GLY	-	expression tag	UNP P0CG48
P	-2	ALA	-	expression tag	UNP P0CG48

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-1	MET	-	expression tag	UNP P0CG48
R	-3	GLY	-	expression tag	UNP P0CG48
R	-2	ALA	-	expression tag	UNP P0CG48
R	-1	MET	-	expression tag	UNP P0CG48
T	-3	GLY	-	expression tag	UNP P0CG48
T	-2	ALA	-	expression tag	UNP P0CG48
T	-1	MET	-	expression tag	UNP P0CG48
V	-3	GLY	-	expression tag	UNP P0CG48
V	-2	ALA	-	expression tag	UNP P0CG48
V	-1	MET	-	expression tag	UNP P0CG48
X	-3	GLY	-	expression tag	UNP P0CG48
X	-2	ALA	-	expression tag	UNP P0CG48
X	-1	MET	-	expression tag	UNP P0CG48

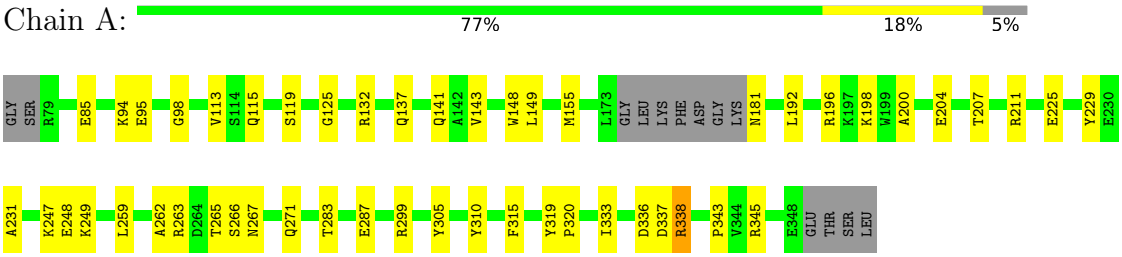
3 Residue-property plots (i)

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.

Note EDS failed to run properly.

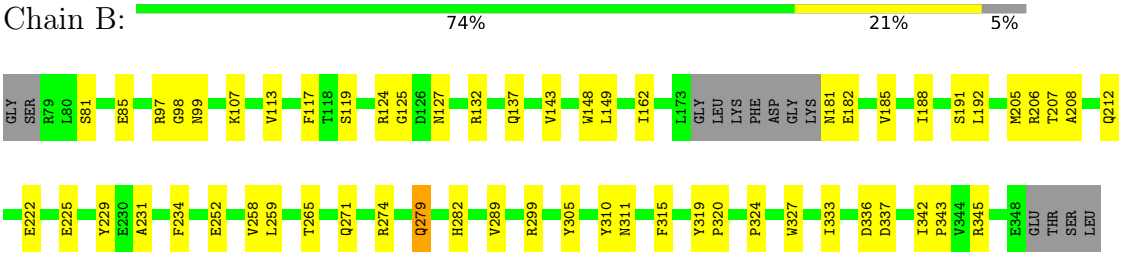
• Molecule 1: Protein FAM105B

Chain A:



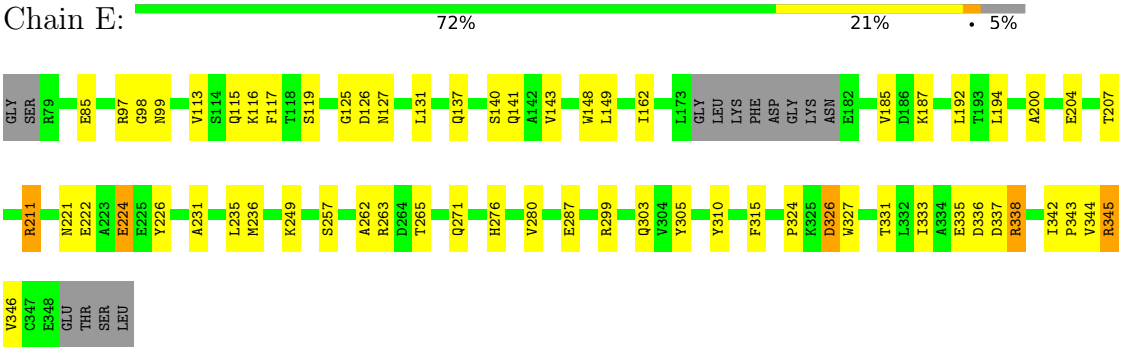
• Molecule 1: Protein FAM105B

Chain B:



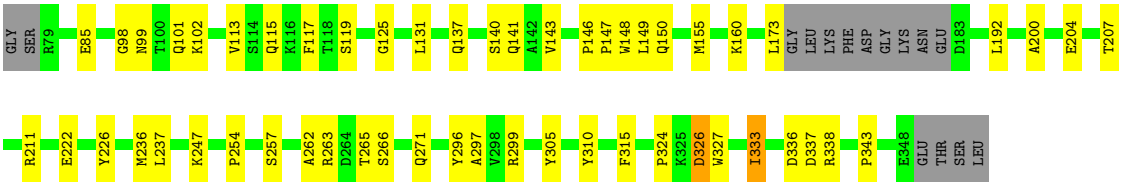
• Molecule 1: Protein FAM105B

Chain E:



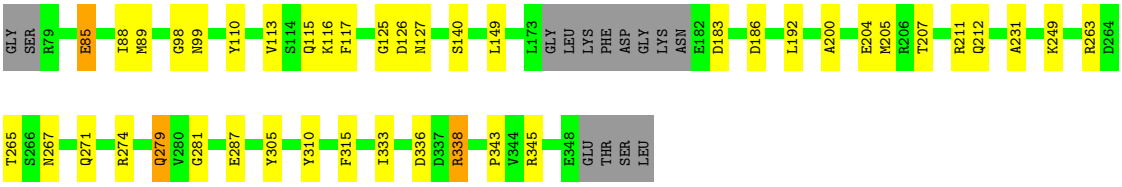
• Molecule 1: Protein FAM105B

Chain G:



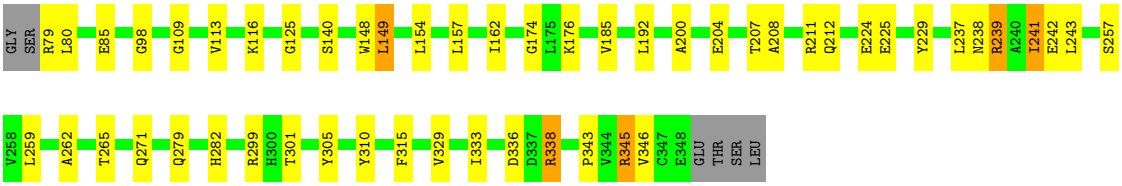
• Molecule 1: Protein FAM105B

Chain I:



• Molecule 1: Protein FAM105B

Chain K:

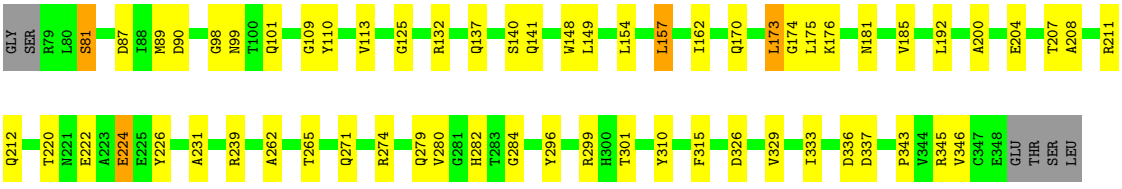


• Molecule 1: Protein FAM105B

Chain M:

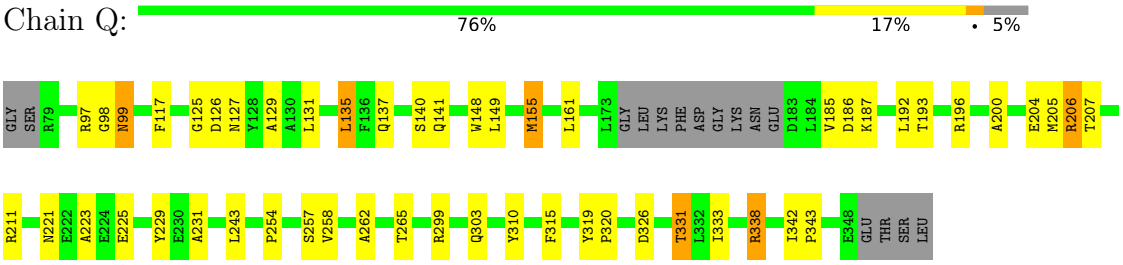
• Molecule 1: Protein FAM105B

Chain O:



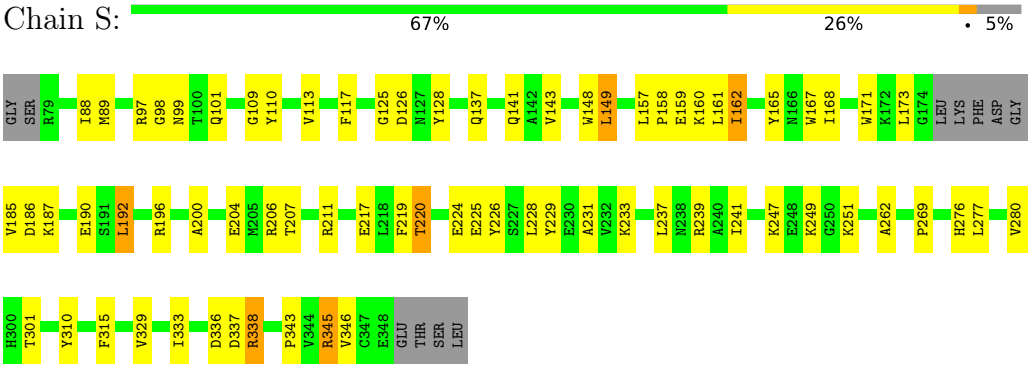
• Molecule 1: Protein FAM105B

Chain Q:



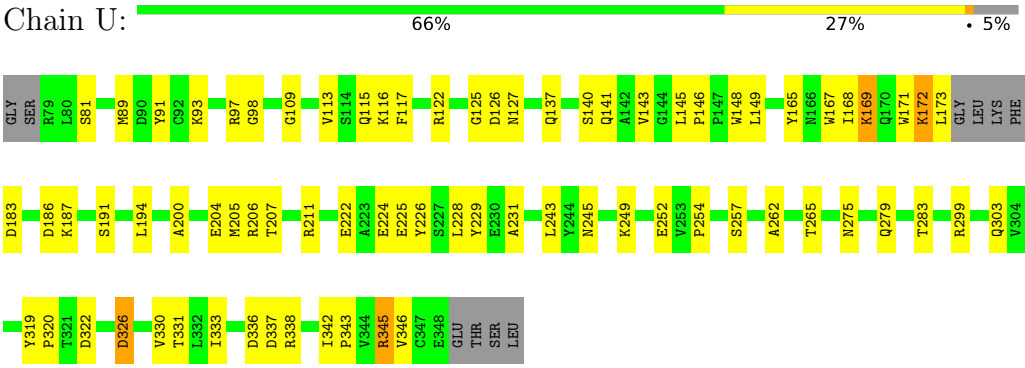
• Molecule 1: Protein FAM105B

Chain S:



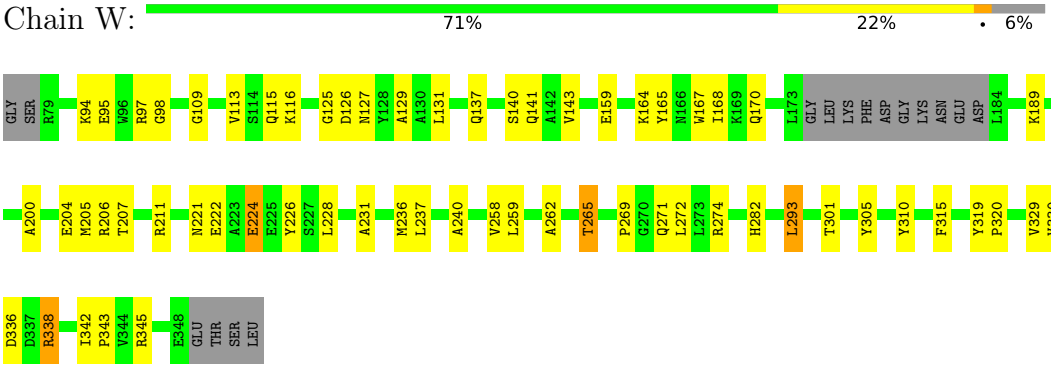
• Molecule 1: Protein FAM105B

Chain U:



• Molecule 1: Protein FAM105B

Chain W:

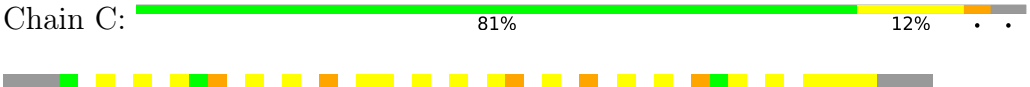


• Molecule 2: Polyubiquitin-C

Chain D:

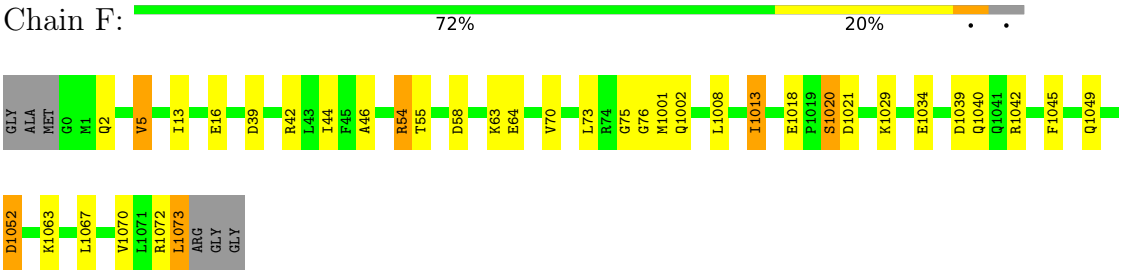
• Molecule 2: Polyubiquitin-C

Chain C:



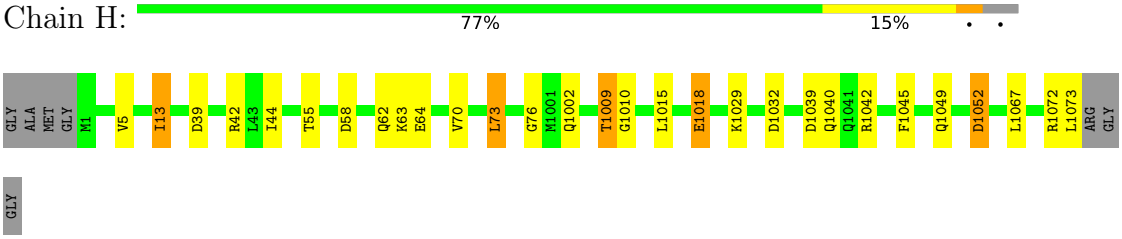
• Molecule 2: Polyubiquitin-C

Chain F:



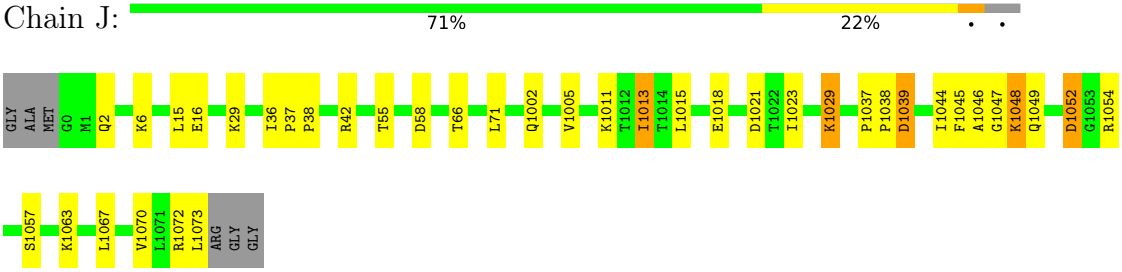
• Molecule 2: Polyubiquitin-C

Chain H:



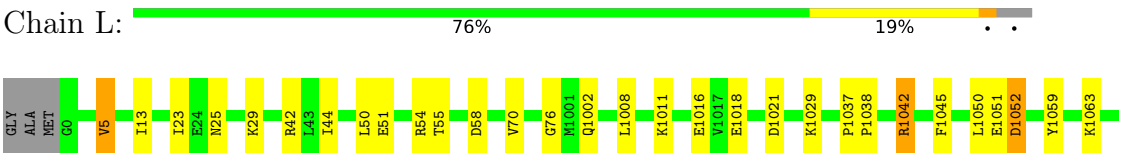
• Molecule 2: Polyubiquitin-C

Chain J:



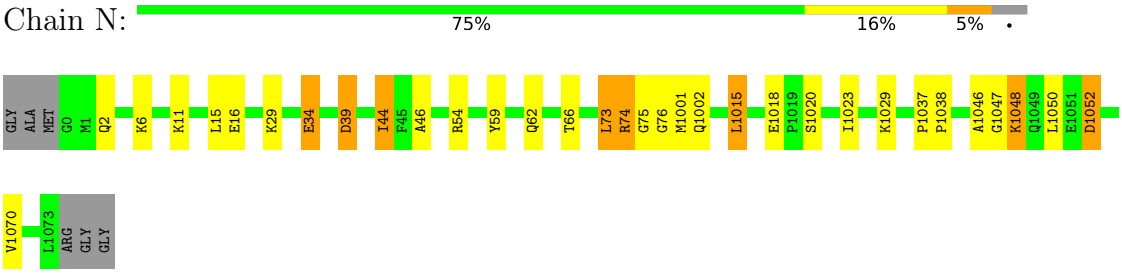
• Molecule 2: Polyubiquitin-C

Chain L:



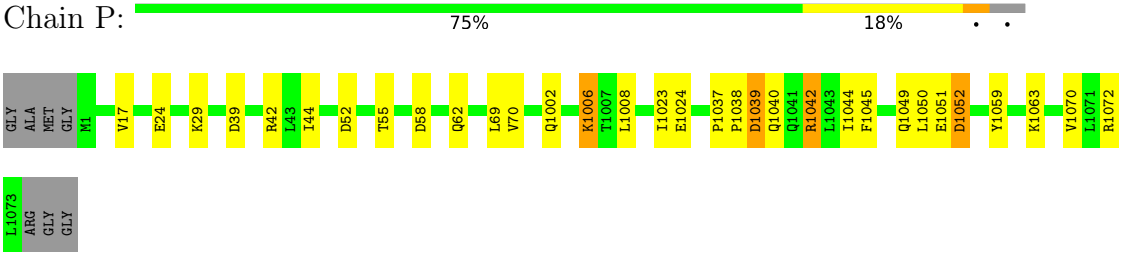
• Molecule 2: Polyubiquitin-C

Chain N:



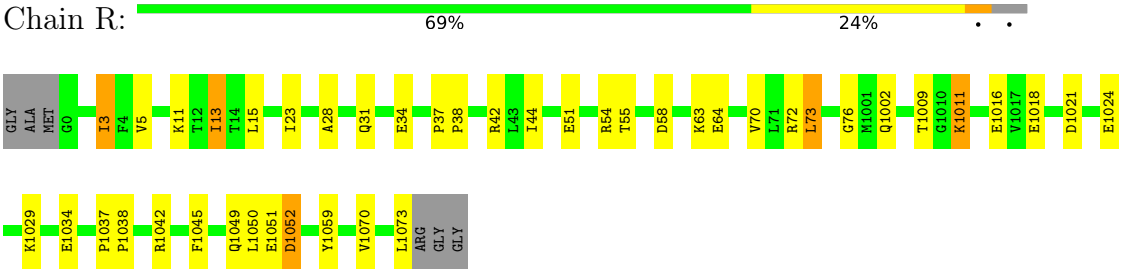
• Molecule 2: Polyubiquitin-C

Chain P:



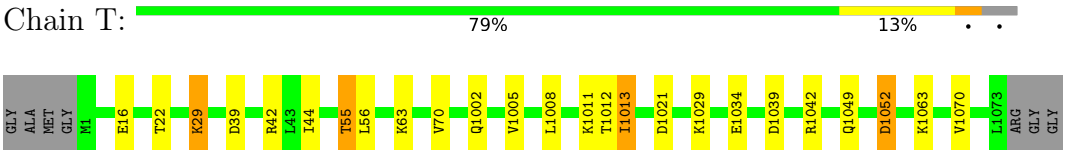
• Molecule 2: Polyubiquitin-C

Chain R:



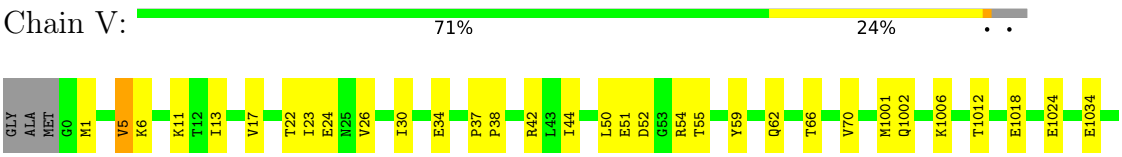
• Molecule 2: Polyubiquitin-C

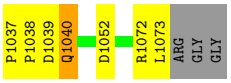
Chain T:



• Molecule 2: Polyubiquitin-C

Chain V:





• Molecule 2: Polyubiquitin-C

Chain X:

4 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	183.62Å 186.09Å 219.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.83	Depositor
% Data completeness (in resolution range)	96.7 (50.00-2.83)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.64 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.224 , 0.254	Depositor
Wilson B-factor (Å^2)	62.5	Xtriage
Anisotropy	0.336	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.000 for k,h,-l	Xtriage
Total number of atoms	40089	wwPDB-VP
Average B, all atoms (Å^2)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.83 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9919e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.28	0/2204	0.51	0/2981
1	B	0.27	0/2204	0.50	0/2981
1	E	0.28	0/2196	0.50	0/2970
1	G	0.28	0/2187	0.52	0/2958
1	I	0.27	0/2196	0.49	0/2970
1	K	0.28	0/2259	0.51	0/3054
1	M	0.28	0/2175	0.52	0/2941
1	O	0.28	0/2259	0.51	0/3054
1	Q	0.29	0/2187	0.51	0/2958
1	S	0.29	0/2200	0.51	0/2975
1	U	0.28	0/2187	0.51	0/2958
1	W	0.28	0/2179	0.51	0/2947
2	C	0.26	0/1200	0.52	0/1616
2	D	0.25	0/1196	0.51	0/1611
2	F	0.25	0/1200	0.52	0/1616
2	H	0.26	0/1196	0.53	0/1611
2	J	0.26	0/1200	0.53	0/1616
2	L	0.27	0/1200	0.52	0/1616
2	N	0.28	0/1200	0.53	0/1616
2	P	0.27	0/1196	0.52	0/1611
2	R	0.27	0/1200	0.52	0/1616
2	T	0.25	0/1196	0.51	0/1611
2	V	0.26	0/1200	0.56	0/1616
2	X	0.26	0/1196	0.53	0/1611
All	All	0.27	0/40813	0.51	0/55114

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2157	0	2152	34	0
1	B	2157	0	2152	36	0
1	E	2149	0	2146	46	0
1	G	2140	0	2140	33	0
1	I	2149	0	2146	32	0
1	K	2210	0	2209	35	0
1	M	2128	0	2128	49	0
1	O	2210	0	2209	46	0
1	Q	2140	0	2140	34	0
1	S	2153	0	2149	59	0
1	U	2140	0	2140	50	0
1	W	2132	0	2136	48	0
2	C	1187	0	1240	14	0
2	D	1183	0	1237	23	0
2	F	1187	0	1240	21	0
2	H	1183	0	1237	18	0
2	J	1187	0	1240	26	0
2	L	1187	0	1240	18	0
2	N	1187	0	1240	22	0
2	P	1183	0	1237	23	0
2	R	1187	0	1240	27	0
2	T	1183	0	1237	14	0
2	V	1187	0	1240	24	0
2	X	1183	0	1237	24	0
All	All	40089	0	40712	641	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 8.

The worst 5 of 641 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)
2:V:1039:ASP:O	2:V:1072:ARG:NH1	1.96	0.98
1:A:98:GLY:HA2	1:K:207:THR:HA	1.47	0.97
1:G:207:THR:HA	1:I:98:GLY:HA2	1.47	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:GLY:HA2	1:U:207:THR:HA	1.45	0.97
1:I:207:THR:HA	1:W:98:GLY:HA2	1.48	0.95

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	259/276 (94%)	253 (98%)	6 (2%)	0	100	100
1	B	259/276 (94%)	253 (98%)	6 (2%)	0	100	100
1	E	258/276 (94%)	247 (96%)	9 (4%)	2 (1%)	19	38
1	G	257/276 (93%)	248 (96%)	9 (4%)	0	100	100
1	I	258/276 (94%)	253 (98%)	5 (2%)	0	100	100
1	K	268/276 (97%)	261 (97%)	7 (3%)	0	100	100
1	M	256/276 (93%)	247 (96%)	9 (4%)	0	100	100
1	O	268/276 (97%)	259 (97%)	9 (3%)	0	100	100
1	Q	257/276 (93%)	250 (97%)	7 (3%)	0	100	100
1	S	259/276 (94%)	250 (96%)	9 (4%)	0	100	100
1	U	257/276 (93%)	246 (96%)	11 (4%)	0	100	100
1	W	256/276 (93%)	249 (97%)	7 (3%)	0	100	100
2	C	148/156 (95%)	144 (97%)	4 (3%)	0	100	100
2	D	147/156 (94%)	143 (97%)	4 (3%)	0	100	100
2	F	148/156 (95%)	145 (98%)	2 (1%)	1 (1%)	22	42
2	H	147/156 (94%)	143 (97%)	3 (2%)	1 (1%)	22	42
2	J	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
2	L	148/156 (95%)	145 (98%)	2 (1%)	1 (1%)	22	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	N	148/156 (95%)	144 (97%)	2 (1%)	2 (1%)	11 24
2	P	147/156 (94%)	143 (97%)	4 (3%)	0	100 100
2	R	148/156 (95%)	145 (98%)	3 (2%)	0	100 100
2	T	147/156 (94%)	144 (98%)	3 (2%)	0	100 100
2	V	148/156 (95%)	144 (97%)	4 (3%)	0	100 100
2	X	147/156 (94%)	143 (97%)	4 (3%)	0	100 100
All	All	4883/5184 (94%)	4744 (97%)	132 (3%)	7 (0%)	51 75

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	337	ASP
2	N	75	GLY
2	L	76	GLY
1	E	335	GLU
2	N	76	GLY

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	234/244 (96%)	228 (97%)	6 (3%)	46 70
1	B	234/244 (96%)	226 (97%)	8 (3%)	37 62
1	E	233/244 (96%)	222 (95%)	11 (5%)	26 50
1	G	232/244 (95%)	221 (95%)	11 (5%)	26 50
1	I	233/244 (96%)	226 (97%)	7 (3%)	41 65
1	K	239/244 (98%)	228 (95%)	11 (5%)	27 51
1	M	230/244 (94%)	219 (95%)	11 (5%)	25 49
1	O	239/244 (98%)	230 (96%)	9 (4%)	33 59
1	Q	232/244 (95%)	217 (94%)	15 (6%)	17 33
1	S	233/244 (96%)	224 (96%)	9 (4%)	32 58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	U	232/244 (95%)	221 (95%)	11 (5%)	26 50
1	W	231/244 (95%)	219 (95%)	12 (5%)	23 44
2	C	135/137 (98%)	126 (93%)	9 (7%)	16 32
2	D	135/137 (98%)	126 (93%)	9 (7%)	16 32
2	F	135/137 (98%)	122 (90%)	13 (10%)	8 17
2	H	135/137 (98%)	128 (95%)	7 (5%)	23 44
2	J	135/137 (98%)	126 (93%)	9 (7%)	16 32
2	L	135/137 (98%)	127 (94%)	8 (6%)	19 37
2	N	135/137 (98%)	123 (91%)	12 (9%)	9 20
2	P	135/137 (98%)	127 (94%)	8 (6%)	19 37
2	R	135/137 (98%)	128 (95%)	7 (5%)	23 44
2	T	135/137 (98%)	124 (92%)	11 (8%)	11 24
2	V	135/137 (98%)	130 (96%)	5 (4%)	34 59
2	X	135/137 (98%)	126 (93%)	9 (7%)	16 32
All	All	4422/4572 (97%)	4194 (95%)	228 (5%)	23 44

5 of 228 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	279	GLN
2	X	73	LEU
2	P	1006	LYS
2	X	26	VAL
1	U	326	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	W	288	GLN
1	W	115	GLN
1	M	115	GLN
1	E	221	ASN
1	Q	137	GLN

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 monosaccharides 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 failed to run properly - this section is therefore empty.

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

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.