



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:09 PM UTC

PDB ID : 6RCP / pdb_00006rcp
Title : Crystal structure of the OmpK36 clinical isolate ST258 from Klebsiella pneumonia
Authors : Beis, K.; Romano, M.; Kwong, J.
Deposited on : 2019-04-11
Resolution : 3.23 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 ⓘ 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:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

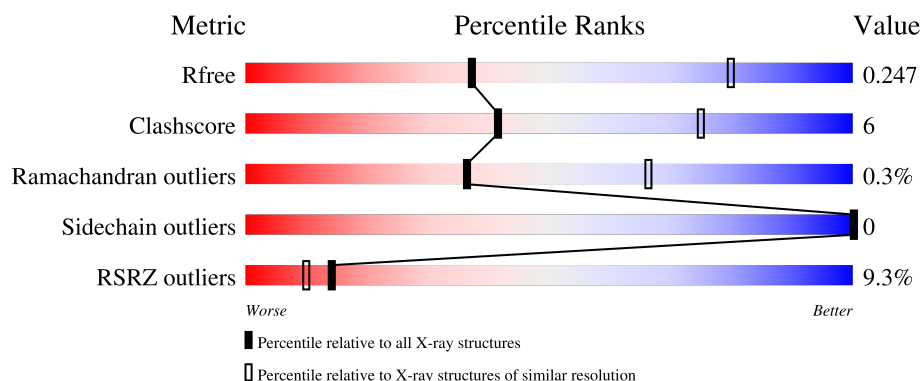
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.23 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))
R_{free}	180053	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

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 $\leq 5\%$. 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.

Mol	Chain	Length	Quality of chain
1	A	349	3% 84% 16%
1	B	349	13% 86% 14%
1	C	349	10% 82% 18%
1	D	349	13% 83% 17%
1	E	349	3% 85% 15%

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Mol	Chain	Length	Quality of chain
1	F	349	
1	G	349	
1	H	349	
1	I	349	
1	J	349	
1	K	349	
1	L	349	
1	M	349	
1	N	349	
1	O	349	
1	P	349	
1	Q	349	
1	R	349	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 48852 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 OmpK36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	B	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	E	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	G	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	H	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	I	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	K	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	L	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	N	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	O	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	P	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	Q	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	R	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	F	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	D	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	J	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	M	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			
1	C	349	Total	C	N	O	S	0	1	0
			2714	1700	450	562	2			

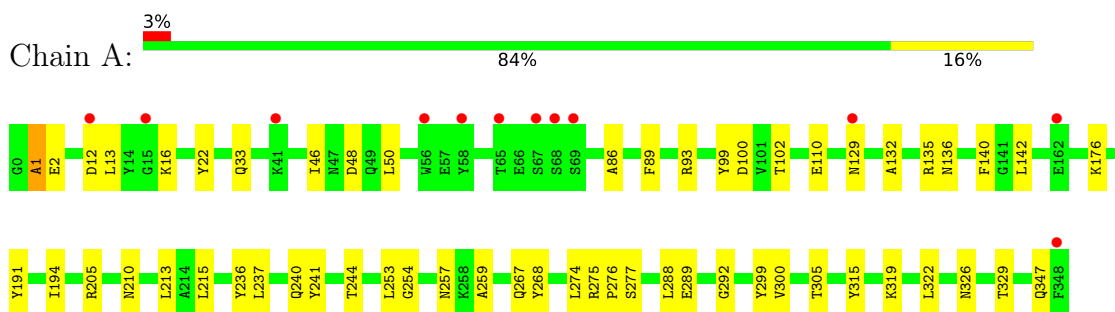
There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP E5G6G2
B	0	GLY	-	expression tag	UNP E5G6G2
E	0	GLY	-	expression tag	UNP E5G6G2
G	0	GLY	-	expression tag	UNP E5G6G2
H	0	GLY	-	expression tag	UNP E5G6G2
I	0	GLY	-	expression tag	UNP E5G6G2
K	0	GLY	-	expression tag	UNP E5G6G2
L	0	GLY	-	expression tag	UNP E5G6G2
N	0	GLY	-	expression tag	UNP E5G6G2
O	0	GLY	-	expression tag	UNP E5G6G2
P	0	GLY	-	expression tag	UNP E5G6G2
Q	0	GLY	-	expression tag	UNP E5G6G2
R	0	GLY	-	expression tag	UNP E5G6G2
F	0	GLY	-	expression tag	UNP E5G6G2
D	0	GLY	-	expression tag	UNP E5G6G2
J	0	GLY	-	expression tag	UNP E5G6G2
M	0	GLY	-	expression tag	UNP E5G6G2
C	0	GLY	-	expression tag	UNP E5G6G2

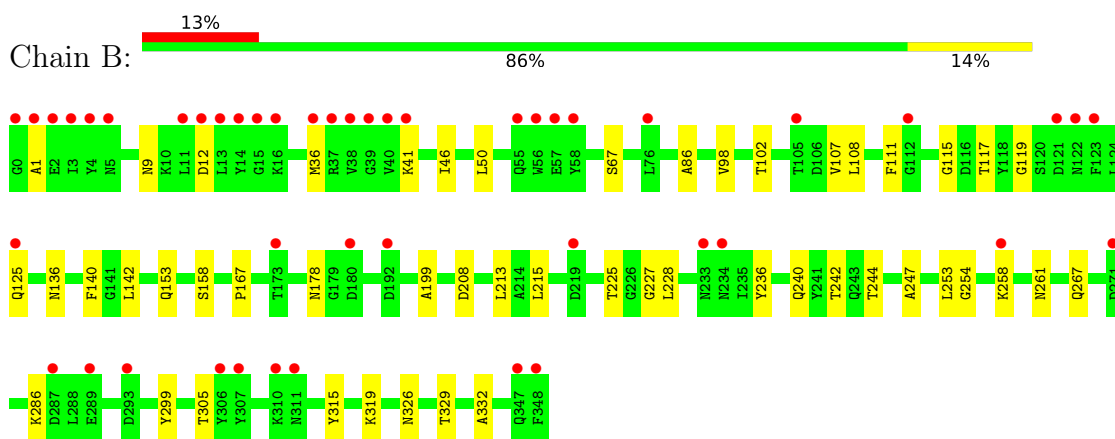
3 Residue-property plots [i](#)

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 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.

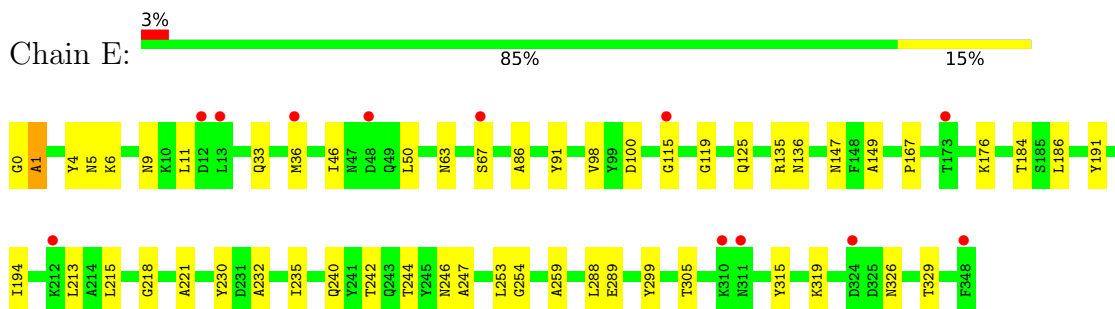
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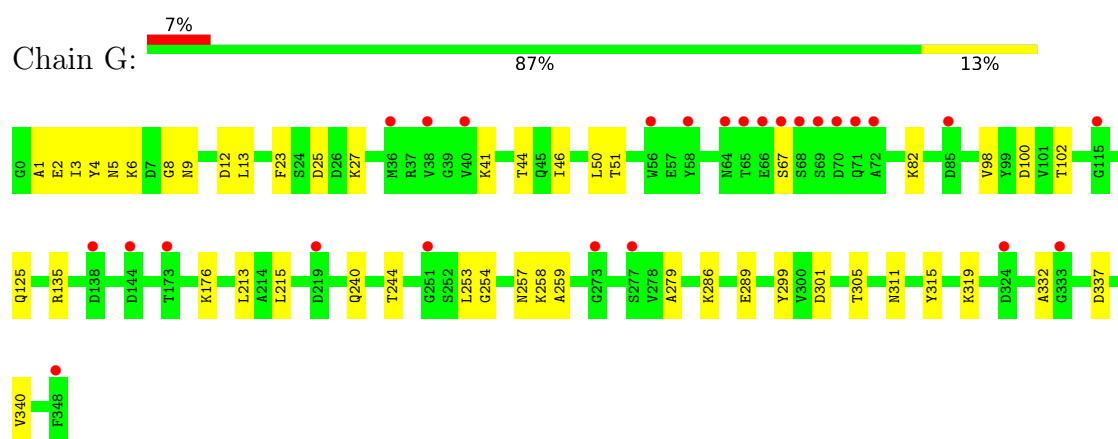
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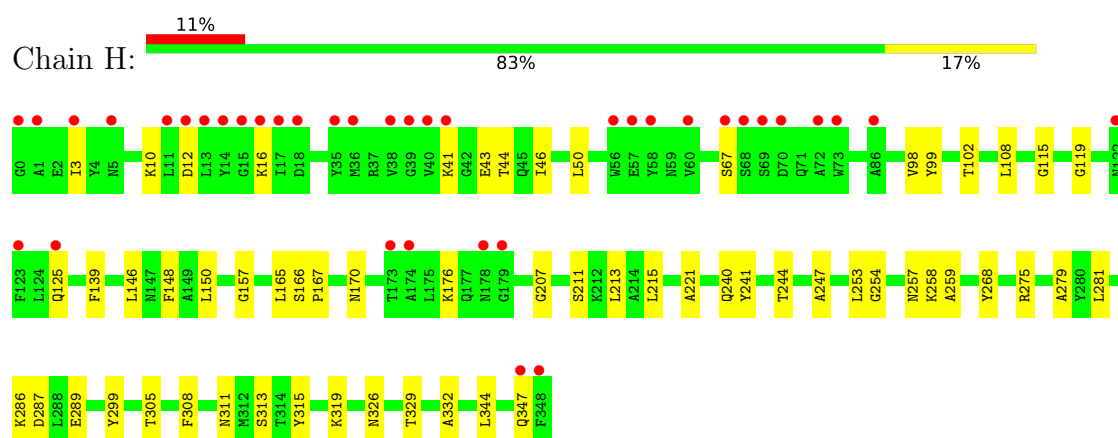
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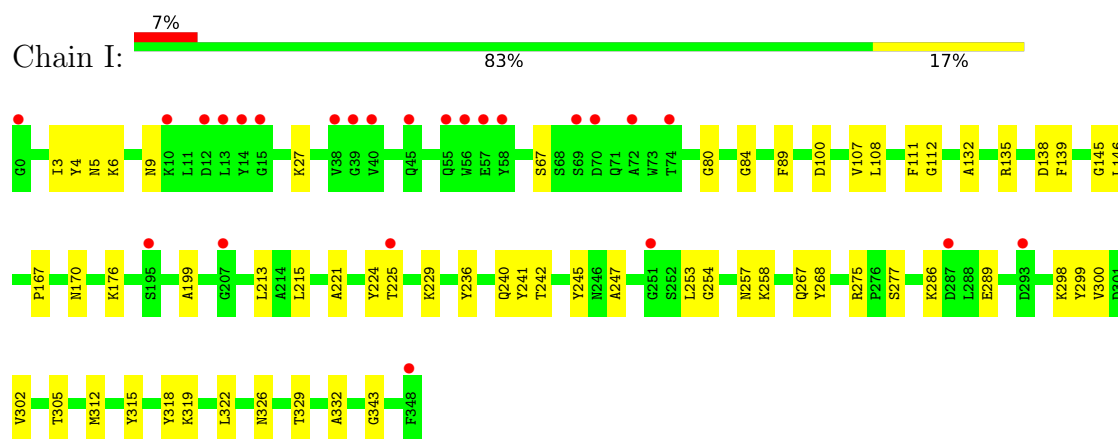
- Molecule 1: OmpK36



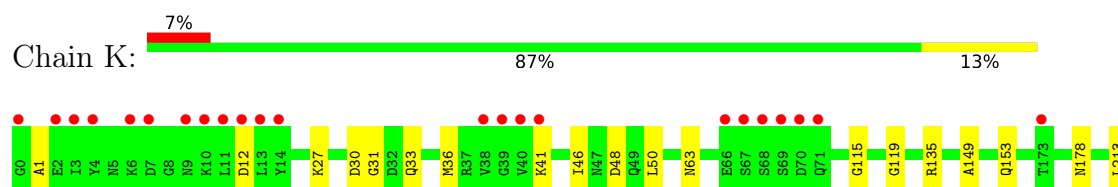
• Molecule 1: OmpK36



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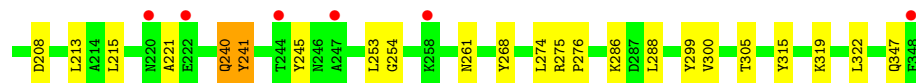
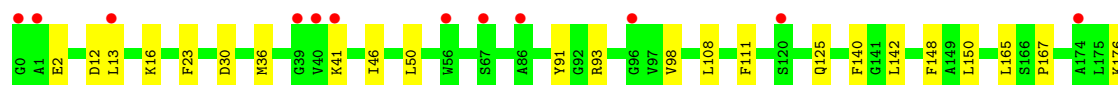
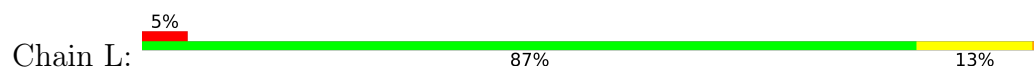


• Molecule 1: OmpK36

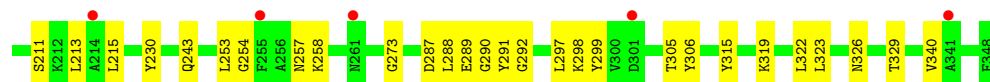
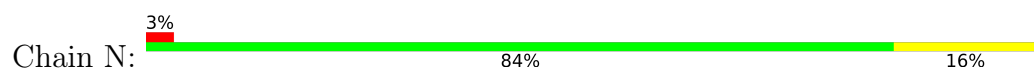




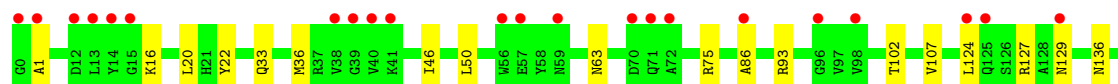
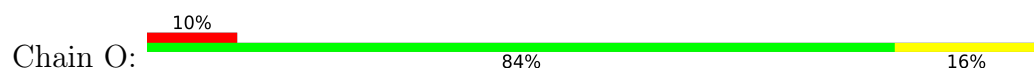
• Molecule 1: OmpK36



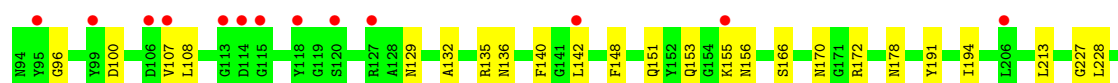
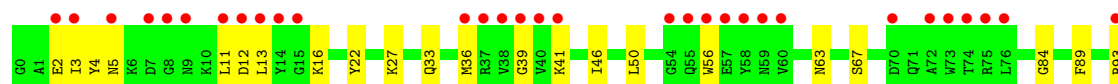
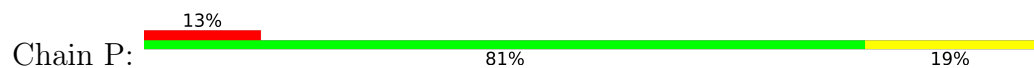
• Molecule 1: OmpK36



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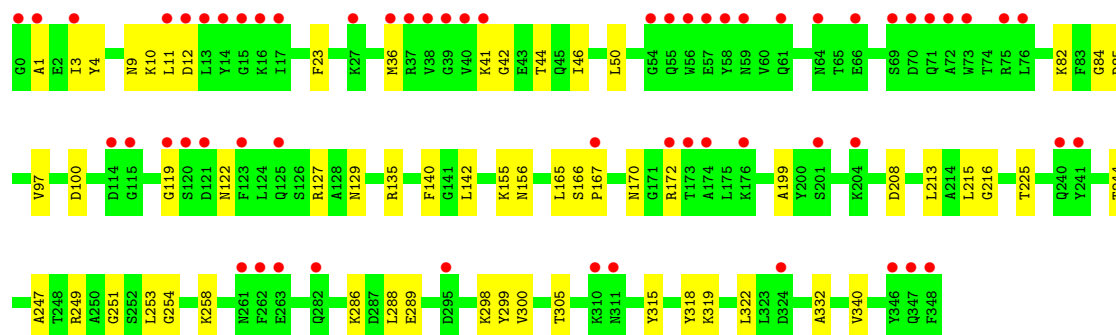
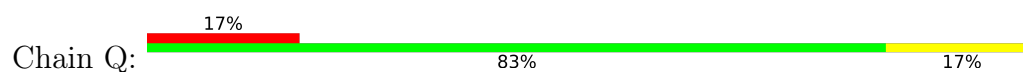


• Molecule 1: OmpK36

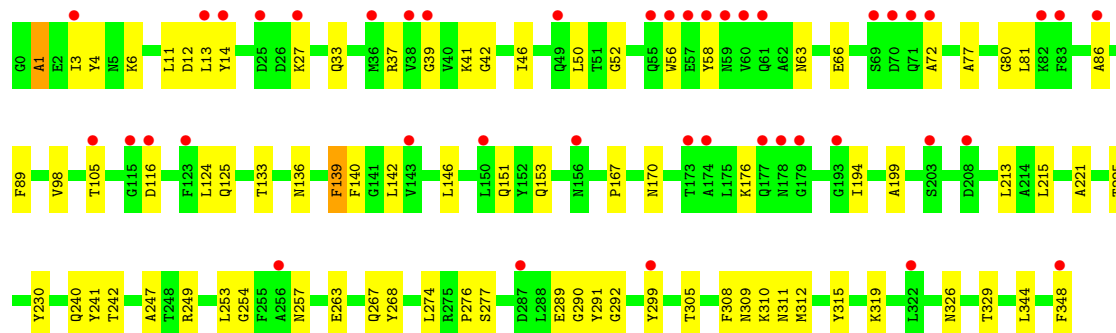
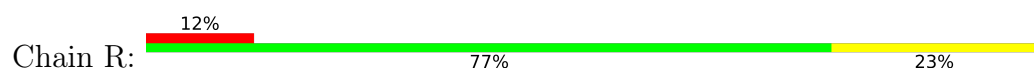




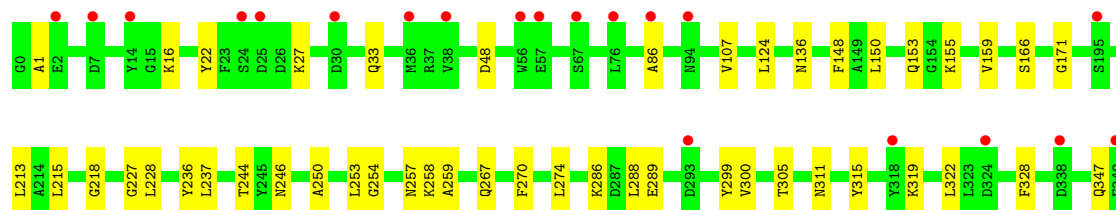
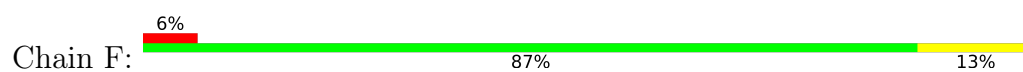
• Molecule 1: OmpK36



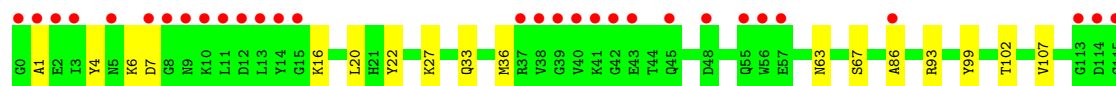
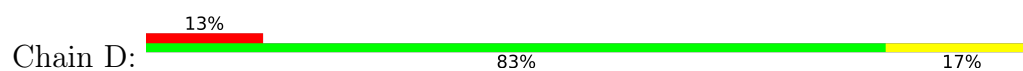
• Molecule 1: OmpK36

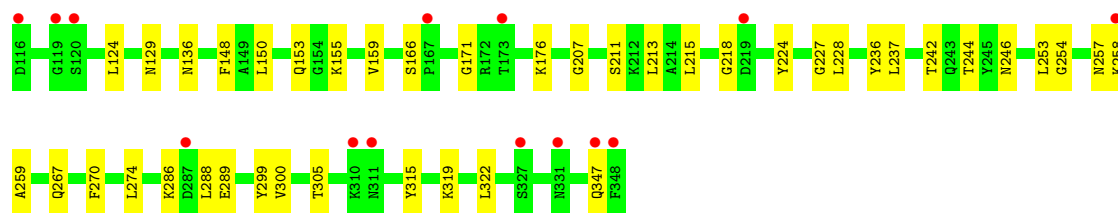


• Molecule 1: OmpK36

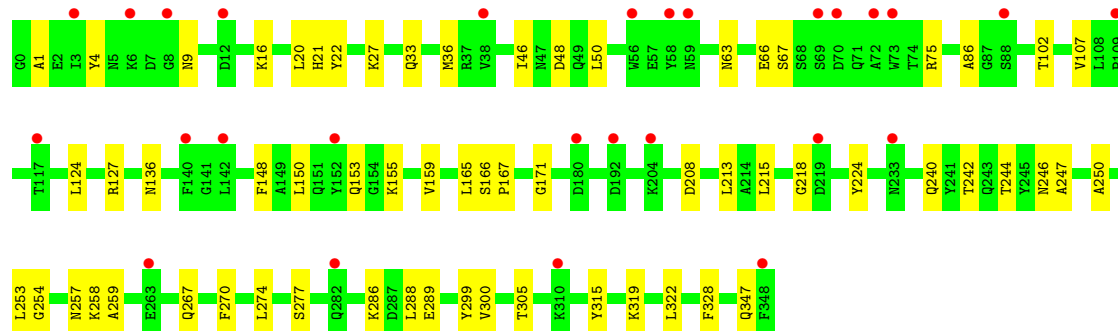
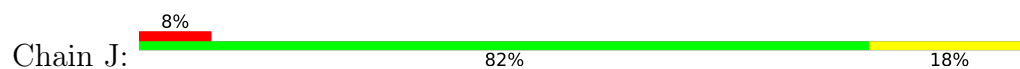


• Molecule 1: OmpK36

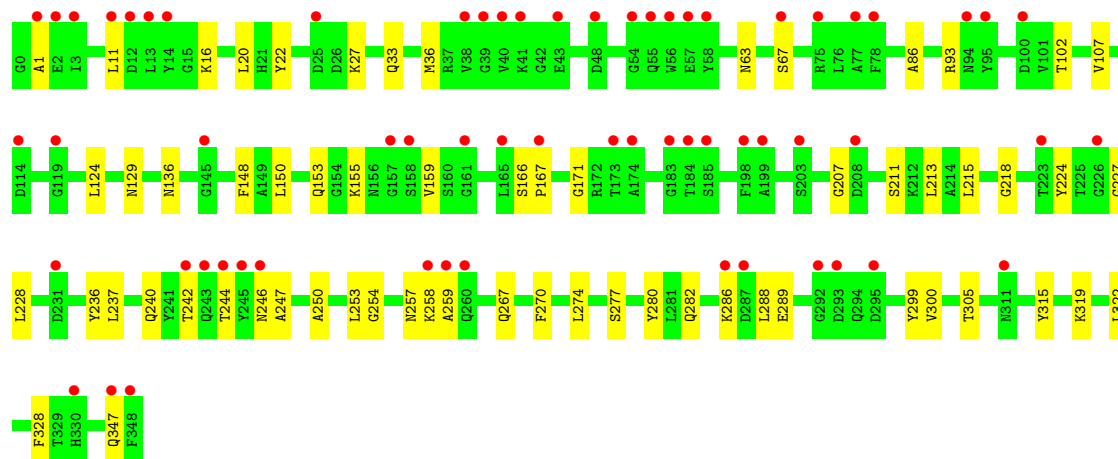
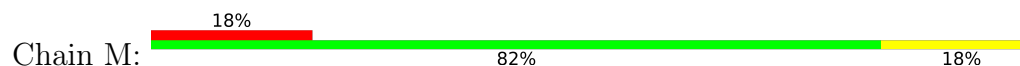




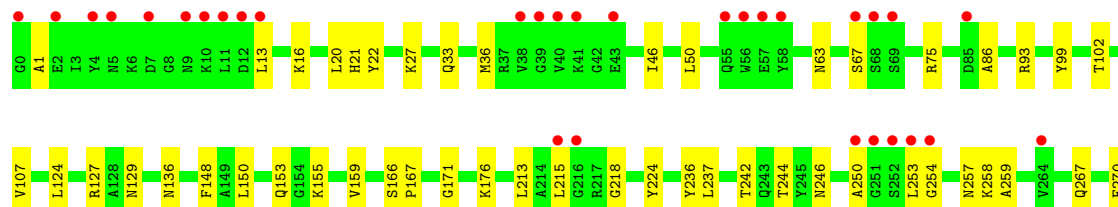
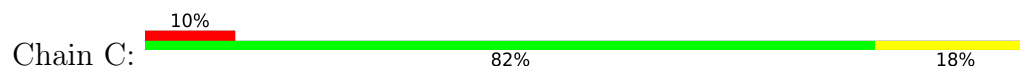
● Molecule 1: OmpK36

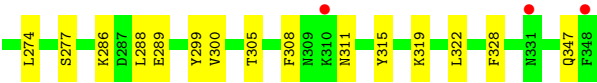


● Molecule 1: OmpK36



● Molecule 1: OmpK36





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	286.04Å 326.11Å 164.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.51 – 3.23 91.51 – 3.23	Depositor EDS
% Data completeness (in resolution range)	51.9 (91.51-3.23) 51.9 (91.51-3.23)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.26Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.218 , 0.250 0.218 , 0.247	Depositor DCC
R_{free} test set	6394 reflections (2.60%)	wwPDB-VP
Wilson B-factor (Å ²)	69.1	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 58.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	48852	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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	0.14	0/2774	0.41	0/3756
1	B	0.15	0/2774	0.43	0/3756
1	C	0.15	0/2774	0.41	0/3756
1	D	0.14	0/2774	0.40	0/3756
1	E	0.17	0/2774	0.44	0/3756
1	F	0.14	0/2774	0.39	0/3756
1	G	0.15	0/2774	0.44	0/3756
1	H	0.15	0/2774	0.42	0/3756
1	I	0.14	0/2774	0.42	0/3756
1	J	0.14	0/2774	0.40	0/3756
1	K	0.14	0/2774	0.43	0/3756
1	L	0.17	1/2774 (0.0%)	0.41	0/3756
1	M	0.14	0/2774	0.40	0/3756
1	N	0.13	0/2774	0.40	0/3756
1	O	0.13	0/2774	0.39	0/3756
1	P	0.15	0/2774	0.42	0/3756
1	Q	0.16	0/2774	0.46	0/3756
1	R	0.16	0/2774	0.44	0/3756
All	All	0.15	1/49932 (0.0%)	0.42	0/67608

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	240	GLN	CA-C	5.14	1.54	1.52

There are no bond angle outliers.

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	2714	0	2506	35	0
1	B	2714	0	2506	29	0
1	C	2714	0	2506	39	0
1	D	2714	0	2506	34	0
1	E	2714	0	2506	35	0
1	F	2714	0	2506	26	0
1	G	2714	0	2506	29	0
1	H	2714	0	2506	39	0
1	I	2714	0	2506	42	0
1	J	2714	0	2506	38	0
1	K	2714	0	2506	28	0
1	L	2714	0	2506	30	0
1	M	2714	0	2506	37	0
1	N	2714	0	2506	34	0
1	O	2714	0	2506	31	0
1	P	2714	0	2506	44	0
1	Q	2714	0	2506	42	0
1	R	2714	0	2506	56	0
All	All	48852	0	45108	601	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 6.

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:K:311:ASN:ND2	1:K:347:GLN:O	1.97	0.98
1:N:100:ASP:OD2	1:N:135:ARG:NH2	2.14	0.80
1:H:305:THR:HG23	1:H:315:TYR:HB3	1.65	0.78
1:G:100:ASP:OD2	1:G:135:ARG:NH2	2.17	0.77
1:H:258:LYS:HB3	1:H:286:LYS:HB2	1.69	0.74

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	348/349 (100%)	312 (90%)	35 (10%)	1 (0%)	36	66
1	B	348/349 (100%)	314 (90%)	33 (10%)	1 (0%)	36	66
1	C	348/349 (100%)	312 (90%)	36 (10%)	0	100	100
1	D	348/349 (100%)	310 (89%)	37 (11%)	1 (0%)	36	66
1	E	348/349 (100%)	314 (90%)	33 (10%)	1 (0%)	36	66
1	F	348/349 (100%)	310 (89%)	37 (11%)	1 (0%)	36	66
1	G	348/349 (100%)	315 (90%)	33 (10%)	0	100	100
1	H	348/349 (100%)	314 (90%)	34 (10%)	0	100	100
1	I	348/349 (100%)	312 (90%)	35 (10%)	1 (0%)	36	66
1	J	348/349 (100%)	312 (90%)	35 (10%)	1 (0%)	36	66
1	K	348/349 (100%)	314 (90%)	34 (10%)	0	100	100
1	L	348/349 (100%)	310 (89%)	37 (11%)	1 (0%)	36	66
1	M	348/349 (100%)	311 (89%)	36 (10%)	1 (0%)	36	66
1	N	348/349 (100%)	313 (90%)	34 (10%)	1 (0%)	36	66
1	O	348/349 (100%)	312 (90%)	35 (10%)	1 (0%)	36	66
1	P	348/349 (100%)	312 (90%)	34 (10%)	2 (1%)	21	53
1	Q	348/349 (100%)	314 (90%)	33 (10%)	1 (0%)	36	66
1	R	348/349 (100%)	313 (90%)	32 (9%)	3 (1%)	14	44
All	All	6264/6282 (100%)	5624 (90%)	623 (10%)	17 (0%)	36	66

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	R	1	ALA
1	F	1	ALA
1	A	1	ALA
1	E	1	ALA

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Mol	Chain	Res	Type
1	N	291	TYR

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	256/278 (92%)	256 (100%)	0	100	100
1	B	277/278 (100%)	277 (100%)	0	100	100
1	C	279/278 (100%)	279 (100%)	0	100	100
1	D	279/278 (100%)	279 (100%)	0	100	100
1	E	260/278 (94%)	260 (100%)	0	100	100
1	F	279/278 (100%)	279 (100%)	0	100	100
1	G	279/278 (100%)	279 (100%)	0	100	100
1	H	266/278 (96%)	266 (100%)	0	100	100
1	I	182/278 (66%)	182 (100%)	0	100	100
1	J	279/278 (100%)	279 (100%)	0	100	100
1	M	279/278 (100%)	279 (100%)	0	100	100
1	N	18/278 (6%)	18 (100%)	0	100	100
1	O	279/278 (100%)	279 (100%)	0	100	100
1	P	279/278 (100%)	279 (100%)	0	100	100
1	Q	279/278 (100%)	279 (100%)	0	100	100
1	R	279/278 (100%)	279 (100%)	0	100	100
All	All	4049/4448 (91%)	4049 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	147	ASN

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Mol	Chain	Res	Type
1	M	59	ASN
1	D	220	ASN
1	J	147	ASN
1	M	220	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 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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	349/349 (100%)	-0.22	12 (3%)	48	30	28, 55, 82, 109	1 (0%)
1	B	349/349 (100%)	0.50	46 (13%)	7	6	31, 56, 90, 115	1 (0%)
1	C	349/349 (100%)	0.57	34 (9%)	13	9	42, 64, 100, 147	1 (0%)
1	D	349/349 (100%)	0.52	44 (12%)	8	6	29, 60, 95, 140	1 (0%)
1	E	349/349 (100%)	0.00	12 (3%)	48	30	31, 55, 79, 106	1 (0%)
1	F	349/349 (100%)	0.36	20 (5%)	29	19	37, 59, 85, 138	1 (0%)
1	G	349/349 (100%)	0.19	26 (7%)	20	14	26, 58, 88, 114	1 (0%)
1	H	349/349 (100%)	0.33	38 (10%)	10	8	30, 58, 88, 116	1 (0%)
1	I	349/349 (100%)	0.36	25 (7%)	21	14	33, 76, 100, 123	1 (0%)
1	J	349/349 (100%)	0.47	27 (7%)	19	13	39, 72, 98, 128	1 (0%)
1	K	349/349 (100%)	0.10	24 (6%)	23	15	33, 56, 82, 112	1 (0%)
1	L	349/349 (100%)	0.17	18 (5%)	33	21	37, 69, 94, 121	1 (0%)
1	M	349/349 (100%)	0.99	63 (18%)	3	3	59, 93, 117, 143	1 (0%)
1	N	349/349 (100%)	0.29	11 (3%)	50	32	53, 86, 113, 144	1 (0%)
1	O	349/349 (100%)	0.50	36 (10%)	12	8	48, 70, 101, 133	1 (0%)
1	P	349/349 (100%)	0.69	46 (13%)	7	6	72, 96, 129, 162	1 (0%)
1	Q	349/349 (100%)	1.03	60 (17%)	4	3	73, 111, 137, 161	1 (0%)
1	R	349/349 (100%)	0.81	43 (12%)	8	6	66, 105, 140, 157	1 (0%)
All	All	6282/6282 (100%)	0.43	585 (9%)	14	10	26, 70, 117, 162	18 (0%)

The worst 5 of 585 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	0	GLY	13.3
1	Q	348	PHE	13.2
1	D	0	GLY	11.4

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Mol	Chain	Res	Type	RSRZ
1	D	12[A]	ASP	10.6
1	P	58	TYR	9.6

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.