



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:06 PM GMT

PDB ID : 4KI3  
Title : 1.70 Angstrom resolution crystal structure of outer-membrane lipoprotein carrier protein (lolA) from Yersinia pestis CO92  
Authors : Halavaty, A.S.; Wawrzak, Z.; Kudritska, M.; Savchenko, A.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)  
Deposited on : 2013-05-01  
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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

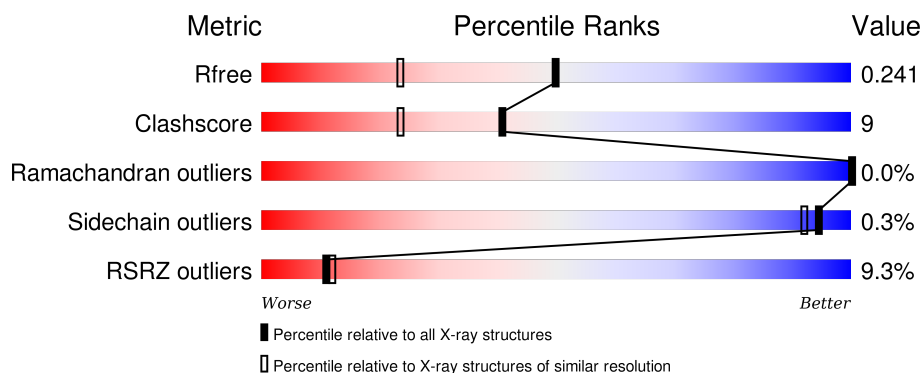
# 1 Overall quality at a glance

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))
$R_{free}$	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (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.

Mol	Chain	Length	Quality of chain
1	A	184	<div> <div>9%</div> <div> <div></div> <div>80%</div> <div>16%</div> <div>.</div> </div> </div>
1	B	184	<div> <div>5%</div> <div> <div></div> <div>76%</div> <div>16%</div> <div>8%</div> </div> </div>
1	C	184	<div> <div>13%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>.</div> </div> </div>
1	D	184	<div> <div>8%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>..</div> </div> </div>
1	E	184	<div> <div>7%</div> <div> <div></div> <div>78%</div> <div>14%</div> <div>8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	184	
1	G	184	
1	H	184	
1	I	184	
1	J	184	
1	K	184	
1	L	184	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	H	301	-	-	X	-
3	PEG	A	302	-	-	-	X
3	PEG	D	302[A]	-	-	-	X
3	PEG	D	302[B]	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19260 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 Outer-membrane lipoprotein carrier protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	12	0
			1490	933	251	304	2			
1	B	169	Total	C	N	O	S	0	14	0
			1453	913	248	289	3			
1	C	177	Total	C	N	O	S	0	12	0
			1491	936	253	299	3			
1	D	179	Total	C	N	O	S	0	14	0
			1524	950	260	312	2			
1	E	169	Total	C	N	O	S	0	9	0
			1409	887	237	283	2			
1	F	177	Total	C	N	O	S	0	11	0
			1482	928	250	301	3			
1	G	179	Total	C	N	O	S	0	15	0
			1520	950	253	315	2			
1	H	172	Total	C	N	O	S	0	10	0
			1434	901	241	290	2			
1	I	180	Total	C	N	O	S	0	10	0
			1494	937	252	302	3			
1	J	177	Total	C	N	O	S	0	13	0
			1503	944	252	304	3			
1	K	171	Total	C	N	O	S	0	5	0
			1389	874	232	280	3			
1	L	176	Total	C	N	O	S	0	10	0
			1464	915	248	298	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	SER	-	EXPRESSION TAG	UNP E8P443
A	20	ASN	-	EXPRESSION TAG	UNP E8P443
B	19	SER	-	EXPRESSION TAG	UNP E8P443
B	20	ASN	-	EXPRESSION TAG	UNP E8P443
C	19	SER	-	EXPRESSION TAG	UNP E8P443

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Chain	Residue	Modelled	Actual	Comment	Reference
C	20	ASN	-	EXPRESSION TAG	UNP E8P443
D	19	SER	-	EXPRESSION TAG	UNP E8P443
D	20	ASN	-	EXPRESSION TAG	UNP E8P443
E	19	SER	-	EXPRESSION TAG	UNP E8P443
E	20	ASN	-	EXPRESSION TAG	UNP E8P443
F	19	SER	-	EXPRESSION TAG	UNP E8P443
F	20	ASN	-	EXPRESSION TAG	UNP E8P443
G	19	SER	-	EXPRESSION TAG	UNP E8P443
G	20	ASN	-	EXPRESSION TAG	UNP E8P443
H	19	SER	-	EXPRESSION TAG	UNP E8P443
H	20	ASN	-	EXPRESSION TAG	UNP E8P443
I	19	SER	-	EXPRESSION TAG	UNP E8P443
I	20	ASN	-	EXPRESSION TAG	UNP E8P443
J	19	SER	-	EXPRESSION TAG	UNP E8P443
J	20	ASN	-	EXPRESSION TAG	UNP E8P443
K	19	SER	-	EXPRESSION TAG	UNP E8P443
K	20	ASN	-	EXPRESSION TAG	UNP E8P443
L	19	SER	-	EXPRESSION TAG	UNP E8P443
L	20	ASN	-	EXPRESSION TAG	UNP E8P443

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



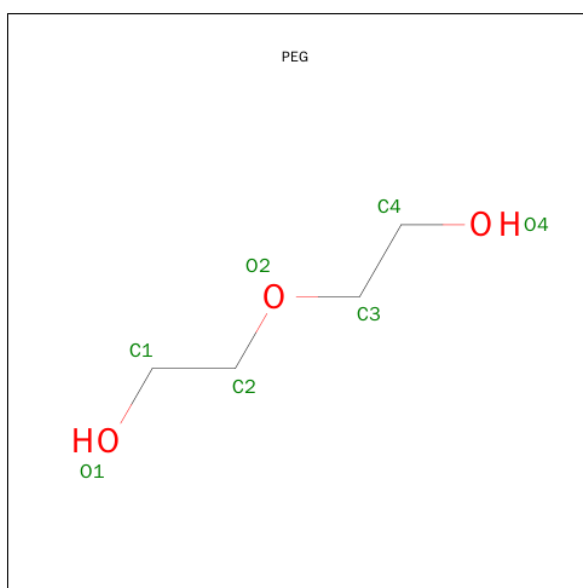
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	C	O	0	0
			4	2	2		
2	F	1	Total	C	O	0	0
			4	2	2		
2	G	1	Total	C	O	0	0
			4	2	2		
2	H	1	Total	C	O	0	0
			4	2	2		
2	I	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	D	1	Total	C	O	0	1
			14	8	6		
3	J	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	143	Total	O	0	3
			144	144		
5	B	137	Total	O	0	5
			141	141		
5	C	122	Total	O	0	7
			128	128		
5	D	146	Total	O	0	8
			153	153		
5	E	100	Total	O	0	2
			102	102		
5	F	116	Total	O	0	8
			119	119		
5	G	133	Total	O	0	8
			139	139		
5	H	146	Total	O	0	5
			149	149		
5	I	137	Total	O	0	3
			138	138		
5	J	104	Total	O	0	4
			108	108		

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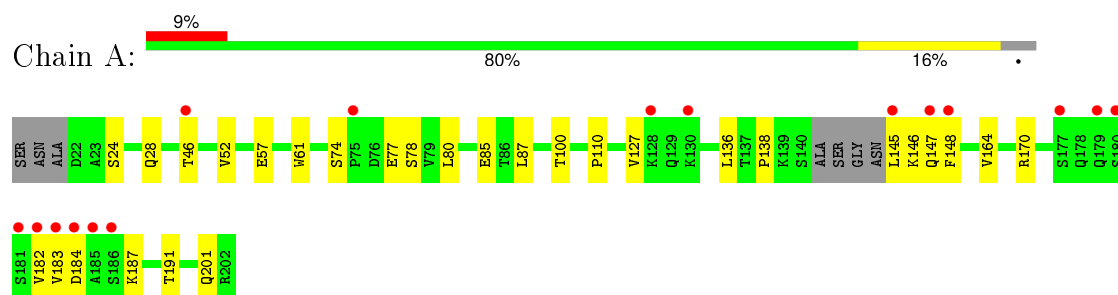
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	K	107	Total 109	O 109	0	3
5	L	106	Total 109	O 109	0	3



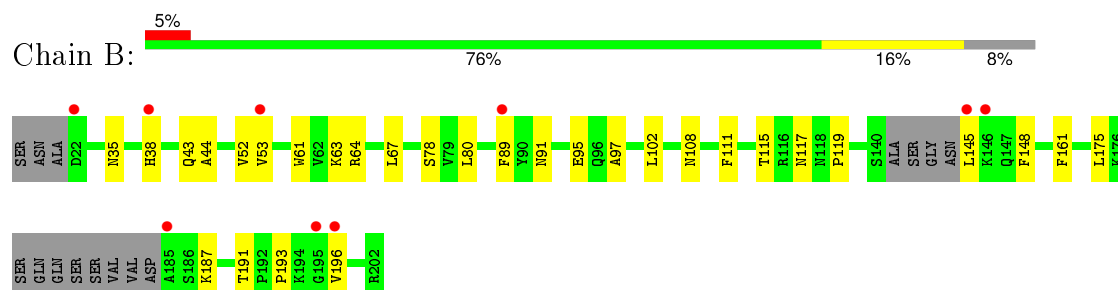
### 3 Residue-property plots [i](#)

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.

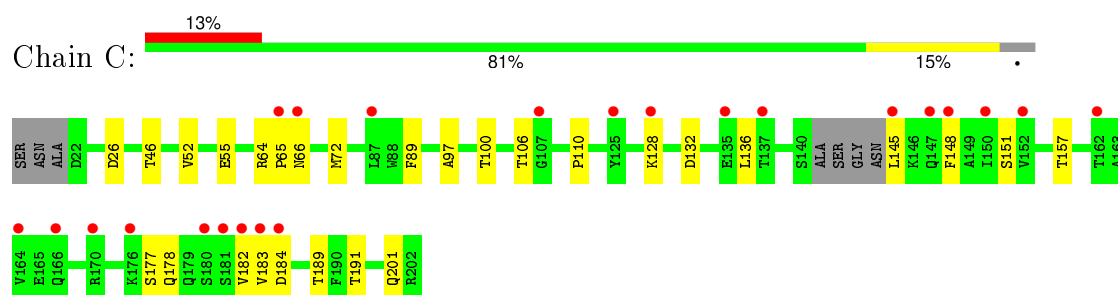
- Molecule 1: Outer-membrane lipoprotein carrier protein



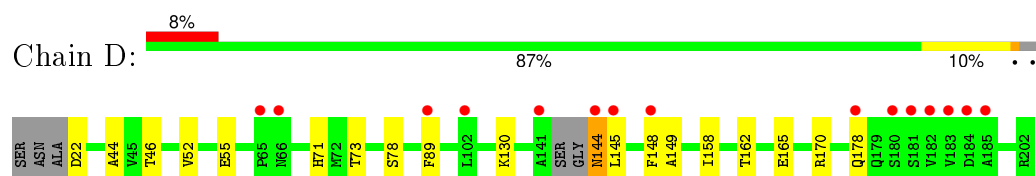
- Molecule 1: Outer-membrane lipoprotein carrier protein



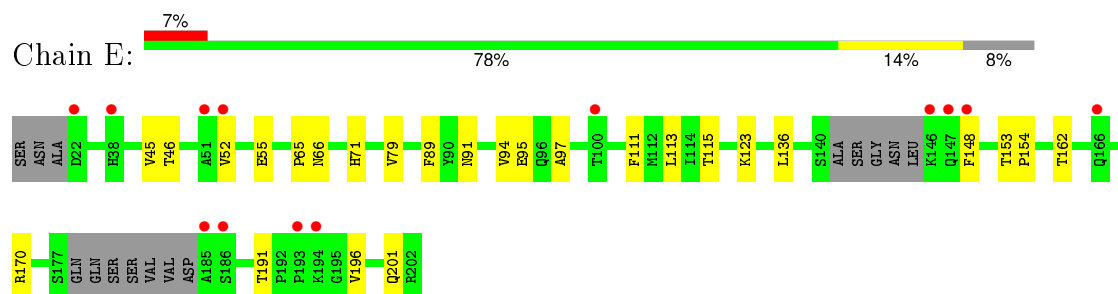
- Molecule 1: Outer-membrane lipoprotein carrier protein



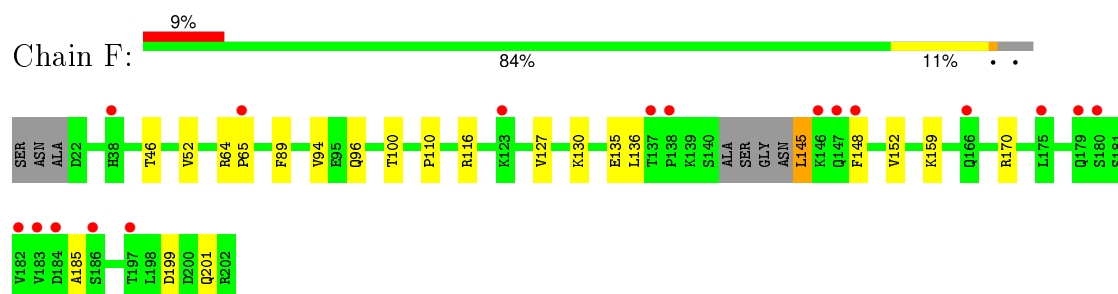
- Molecule 1: Outer-membrane lipoprotein carrier protein



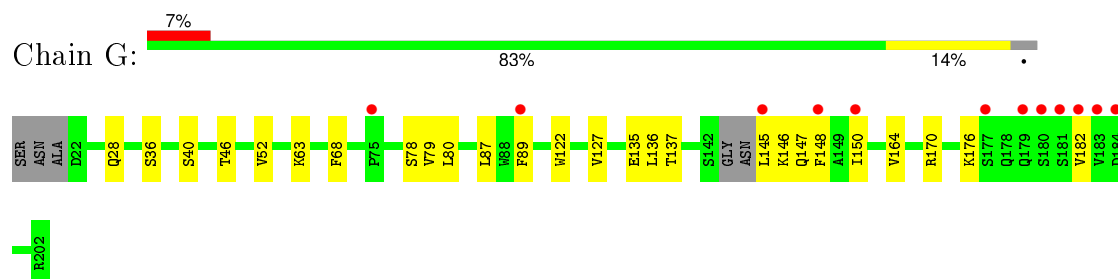
- Molecule 1: Outer-membrane lipoprotein carrier protein



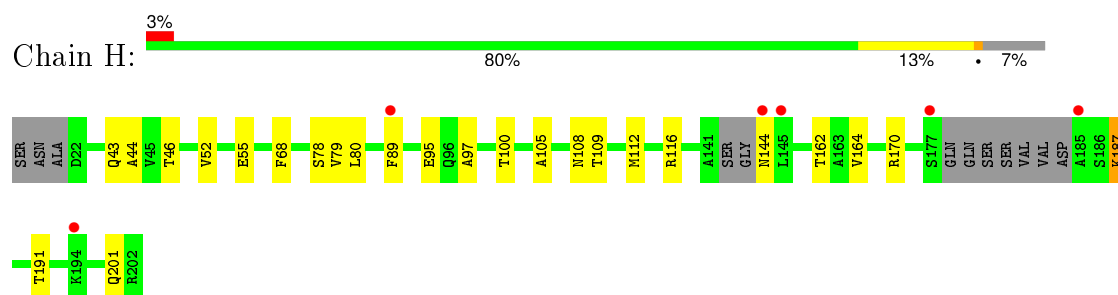
- Molecule 1: Outer-membrane lipoprotein carrier protein



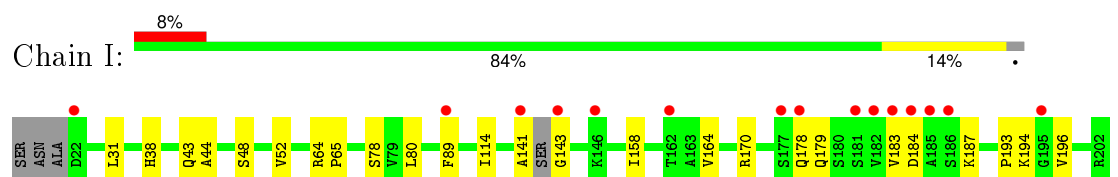
- Molecule 1: Outer-membrane lipoprotein carrier protein



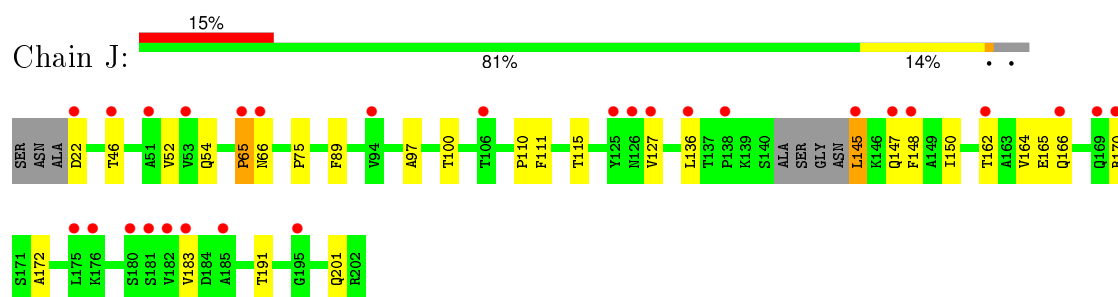
- Molecule 1: Outer-membrane lipoprotein carrier protein



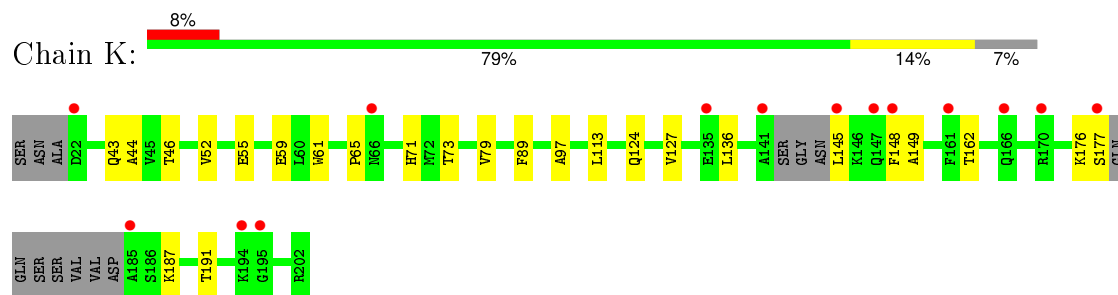
- Molecule 1: Outer-membrane lipoprotein carrier protein



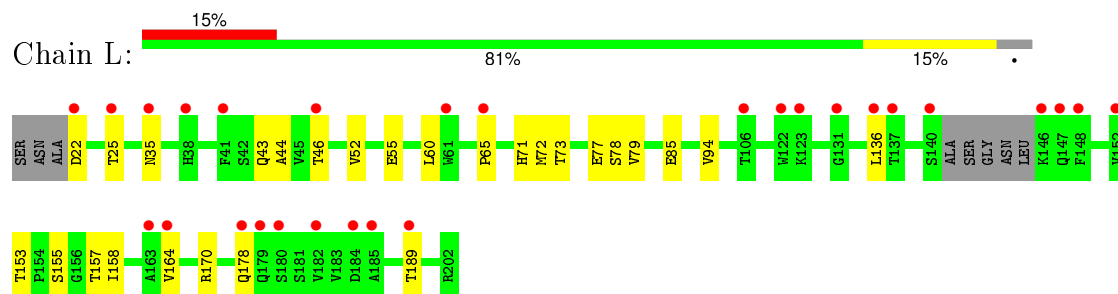
- Molecule 1: Outer-membrane lipoprotein carrier protein



- Molecule 1: Outer-membrane lipoprotein carrier protein



- Molecule 1: Outer-membrane lipoprotein carrier protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.20 Å 67.13 Å 132.56 Å 94.30° 94.01° 120.01°	Depositor
Resolution (Å)	29.09 – 1.70 29.08 – 1.70	Depositor EDS
% Data completeness (in resolution range)	93.8 (29.09-1.70) 89.6 (29.08-1.70)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.49 (at 1.70 Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.204 , 0.240 0.211 , 0.241	Depositor DCC
$R_{free}$ test set	10415 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.5	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 35.7	EDS
Estimated twinning fraction	0.749 for H, K, L 0.251 for -K, -H, -L 0.277 for -k,-h,-l	Xtriage
Reported twinning fraction	0.749 for H, K, L 0.251 for -K, -H, -L	Depositor
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 207034 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	19260	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.48% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 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: GOL, PEG, ACT

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	0.62	0/1524	0.80	0/2071
1	B	0.63	0/1487	0.84	0/2019
1	C	0.55	0/1525	0.82	0/2072
1	D	0.63	0/1558	0.79	0/2112
1	E	0.56	0/1443	0.78	0/1958
1	F	0.58	0/1515	0.81	0/2054
1	G	0.61	0/1554	0.83	0/2113
1	H	0.58	0/1467	0.80	0/1991
1	I	0.60	0/1529	0.79	0/2075
1	J	0.52	0/1538	0.78	0/2089
1	K	0.53	0/1420	0.77	0/1925
1	L	0.55	0/1498	0.78	0/2037
All	All	0.58	0/18058	0.80	0/24516

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	1490	0	1411	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1453	0	1380	28	0
1	C	1491	0	1429	34	0
1	D	1524	0	1435	19	0
1	E	1409	0	1335	20	0
1	F	1482	0	1410	26	0
1	G	1520	0	1431	25	0
1	H	1434	0	1359	32	0
1	I	1494	0	1411	23	0
1	J	1503	0	1425	28	0
1	K	1389	0	1321	25	0
1	L	1464	0	1385	28	0
2	A	4	0	3	0	0
2	B	4	0	3	0	0
2	D	4	0	3	0	0
2	F	4	0	3	1	0
2	G	4	0	3	0	0
2	H	4	0	3	2	0
2	I	4	0	3	0	0
3	A	7	0	10	0	0
3	D	14	0	20	0	0
3	J	7	0	10	0	0
4	A	6	0	8	0	0
4	H	6	0	8	0	0
5	A	144	0	0	5	0
5	B	141	0	0	7	0
5	C	128	0	0	10	0
5	D	153	0	0	6	0
5	E	102	0	0	0	0
5	F	119	0	0	8	0
5	G	139	0	0	6	0
5	H	149	0	0	14	0
5	I	138	0	0	4	0
5	J	108	0	0	4	0
5	K	109	0	0	4	0
5	L	109	0	0	12	0
All	All	19260	0	16809	298	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 9.

The worst 5 of 298 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:J:46[A]:THR:HG22	1:J:52:VAL:HG22	1.62	0.81
1:C:65[B]:PRO:HB3	5:C:409:HOH:O	1.79	0.81
1:L:153[B]:THR:HG22	1:L:157:THR:H	1.47	0.78
1:G:80[B]:LEU:HD21	1:G:87:LEU:HD11	1.67	0.77
1:F:145:LEU:HD21	1:F:148:PHE:CZ	2.20	0.77

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	184/184 (100%)	180 (98%)	4 (2%)	0	100	100
1	B	177/184 (96%)	174 (98%)	3 (2%)	0	100	100
1	C	185/184 (100%)	179 (97%)	6 (3%)	0	100	100
1	D	189/184 (103%)	185 (98%)	4 (2%)	0	100	100
1	E	172/184 (94%)	166 (96%)	6 (4%)	0	100	100
1	F	184/184 (100%)	176 (96%)	8 (4%)	0	100	100
1	G	190/184 (103%)	185 (97%)	5 (3%)	0	100	100
1	H	176/184 (96%)	173 (98%)	3 (2%)	0	100	100
1	I	186/184 (101%)	181 (97%)	5 (3%)	0	100	100
1	J	186/184 (101%)	182 (98%)	2 (1%)	2 (1%)	17	4
1	K	169/184 (92%)	165 (98%)	4 (2%)	0	100	100
1	L	182/184 (99%)	180 (99%)	2 (1%)	0	100	100
All	All	2180/2208 (99%)	2126 (98%)	52 (2%)	2 (0%)	100	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	65[A]	PRO
1	J	65[B]	PRO

### 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	169/161 (105%)	169 (100%)	0	100	100
1	B	163/161 (101%)	162 (99%)	1 (1%)	90	85
1	C	169/161 (105%)	169 (100%)	0	100	100
1	D	172/161 (107%)	171 (99%)	1 (1%)	90	85
1	E	158/161 (98%)	158 (100%)	0	100	100
1	F	168/161 (104%)	167 (99%)	1 (1%)	90	85
1	G	173/161 (108%)	173 (100%)	0	100	100
1	H	161/161 (100%)	160 (99%)	1 (1%)	90	85
1	I	168/161 (104%)	168 (100%)	0	100	100
1	J	170/161 (106%)	169 (99%)	1 (1%)	90	85
1	K	155/161 (96%)	155 (100%)	0	100	100
1	L	166/161 (103%)	166 (100%)	0	100	100
All	All	1992/1932 (103%)	1987 (100%)	5 (0%)	94	92

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	119	PRO
1	D	144	ASN
1	F	145	LEU
1	H	187	LYS
1	J	145	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:



Mol	Chain	Res	Type
1	E	38	HIS

### 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](#)

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	ACT	A	301	-	1,3,3	1.28	0	0,3,3	0.00	-
3	PEG	A	302	-	6,6,6	0.44	0	5,5,5	0.24	0
4	GOL	A	303	-	5,5,5	0.40	0	5,5,5	0.13	0
2	ACT	B	301	-	1,3,3	1.43	0	0,3,3	0.00	-
2	ACT	D	301	-	1,3,3	1.50	0	0,3,3	0.00	-
3	PEG	D	302[A]	-	6,6,6	0.45	0	5,5,5	0.27	0
3	PEG	D	302[B]	-	6,6,6	0.41	0	5,5,5	0.37	0
2	ACT	F	301	-	1,3,3	0.69	0	0,3,3	0.00	-
2	ACT	G	301	-	1,3,3	0.68	0	0,3,3	0.00	-
2	ACT	H	301	-	1,3,3	1.06	0	0,3,3	0.00	-
4	GOL	H	302	-	5,5,5	0.31	0	5,5,5	0.29	0
2	ACT	I	301	-	1,3,3	1.41	0	0,3,3	0.00	-
3	PEG	J	301	-	6,6,6	0.41	0	5,5,5	0.34	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACT	A	301	-	-	0/0/0/0	0/0/0/0
3	PEG	A	302	-	-	0/4/4/4	0/0/0/0
4	GOL	A	303	-	-	0/4/4/4	0/0/0/0
2	ACT	B	301	-	-	0/0/0/0	0/0/0/0
2	ACT	D	301	-	-	0/0/0/0	0/0/0/0
3	PEG	D	302[A]	-	-	0/4/4/4	0/0/0/0
3	PEG	D	302[B]	-	-	0/4/4/4	0/0/0/0
2	ACT	F	301	-	-	0/0/0/0	0/0/0/0
2	ACT	G	301	-	-	0/0/0/0	0/0/0/0
2	ACT	H	301	-	-	0/0/0/0	0/0/0/0
4	GOL	H	302	-	-	0/4/4/4	0/0/0/0
2	ACT	I	301	-	-	0/0/0/0	0/0/0/0
3	PEG	J	301	-	-	0/4/4/4	0/0/0/0

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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	301	ACT	1	0
2	H	301	ACT	2	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	177/184 (96%)	0.62	16 (9%) 12 13	18, 24, 38, 51	0
1	B	169/184 (91%)	0.61	9 (5%) 30 32	18, 24, 33, 40	0
1	C	177/184 (96%)	0.93	23 (12%) 5 5	19, 28, 44, 48	0
1	D	179/184 (97%)	0.58	15 (8%) 14 15	18, 24, 39, 47	0
1	E	169/184 (91%)	0.76	13 (7%) 16 18	19, 28, 40, 48	0
1	F	177/184 (96%)	0.82	17 (9%) 10 11	20, 27, 42, 46	0
1	G	179/184 (97%)	0.71	12 (6%) 21 23	18, 25, 41, 52	0
1	H	172/184 (93%)	0.57	6 (3%) 48 52	19, 25, 36, 42	0
1	I	180/184 (97%)	0.64	15 (8%) 14 16	18, 25, 41, 48	0
1	J	177/184 (96%)	1.06	28 (15%) 3 3	20, 29, 45, 50	0
1	K	171/184 (92%)	0.84	14 (8%) 14 16	21, 30, 43, 52	0
1	L	176/184 (95%)	0.92	28 (15%) 3 3	22, 29, 44, 49	0
All	All	2103/2208 (95%)	0.76	196 (9%) 11 12	18, 27, 42, 52	0

The worst 5 of 196 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	182	VAL	8.0
1	A	182	VAL	6.7
1	G	182	VAL	6.6
1	C	182	VAL	6.2
1	I	143	GLY	6.1

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	PEG	D	302[A]	7/7	0.74	0.20	3.79	31,38,39,40	7
3	PEG	D	302[B]	7/7	0.74	0.20	3.74	40,43,44,44	7
3	PEG	A	302	7/7	0.84	0.18	2.25	32,40,44,44	0
4	GOL	A	303	6/6	0.88	0.14	1.73	31,36,37,39	0
2	ACT	I	301	4/4	0.76	0.20	1.48	38,38,38,38	0
2	ACT	H	301	4/4	0.72	0.18	1.47	37,37,38,39	0
2	ACT	D	301	4/4	0.80	0.20	1.35	44,45,45,45	0
2	ACT	G	301	4/4	0.88	0.16	1.01	42,42,43,43	0
2	ACT	B	301	4/4	0.84	0.14	1.00	38,38,38,39	0
2	ACT	A	301	4/4	0.49	0.22	0.90	36,37,37,38	0
3	PEG	J	301	7/7	0.87	0.18	0.58	42,43,43,44	0
2	ACT	F	301	4/4	0.85	0.12	-	39,39,40,41	0
4	GOL	H	302	6/6	0.76	0.13	-	47,48,48,48	0

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

There are no such residues in this entry.