



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 07:18 AM EDT

PDB ID : 6QWP
Title : Crystal structure of T7 bacteriophage portal protein, 13mer, closed valve
Authors : Fabrega-Ferrer, M.; Cuervo, A.; Machon, C.; Fernandez, F.J.; Perez-Luque, R.; Pous, J.; Vega, M.C.; Carrascosa, J.L.; Coll, M.
Deposited on : 2019-03-06
Resolution : 3.40 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 : 4.02b-467
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

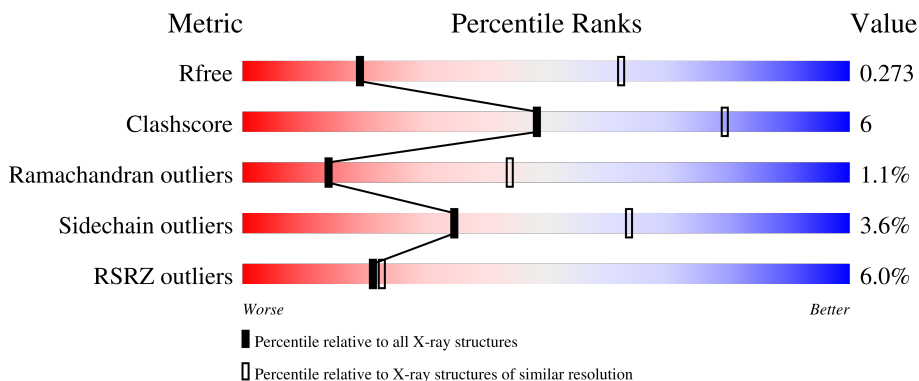
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	547	 4% 74% 14% • 11%
1	B	547	 4% 73% 16% • 11%
1	C	547	 3% 74% 15% • 11%
1	D	547	 5% 75% 13% • 11%
1	E	547	 6% 72% 17% • 11%

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Mol	Chain	Length	Quality of chain
1	F	547	<p>6% 73% 15% • 11%</p>
1	G	547	<p>6% 72% 15% • 11%</p>
1	H	547	<p>8% 73% 15% • 11%</p>
1	I	547	<p>6% 75% 13% • 11%</p>
1	J	547	<p>4% 75% 13% • 11%</p>
1	K	547	<p>6% 71% 17% • 11%</p>
1	L	547	<p>7% 75% 13% • 11%</p>
1	M	547	<p>5% 71% 17% • 11%</p>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 49530 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 Portal protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	486	3810	2397	646	749	18	0	0	0
1	B	486	3810	2397	646	749	18	0	0	0
1	C	486	3810	2397	646	749	18	0	0	0
1	D	486	3810	2397	646	749	18	0	0	0
1	E	486	3810	2397	646	749	18	0	0	0
1	F	486	3810	2397	646	749	18	0	0	0
1	G	486	3810	2397	646	749	18	0	0	0
1	H	486	3810	2397	646	749	18	0	0	0
1	I	486	3810	2397	646	749	18	0	0	0
1	J	486	3810	2397	646	749	18	0	0	0
1	K	486	3810	2397	646	749	18	0	0	0
1	L	486	3810	2397	646	749	18	0	0	0
1	M	486	3810	2397	646	749	18	0	0	0

There are 143 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	ALA	-	expression tag	UNP P03728
A	538	ALA	-	expression tag	UNP P03728
A	539	ALA	-	expression tag	UNP P03728

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Chain	Residue	Modelled	Actual	Comment	Reference
A	540	LEU	-	expression tag	UNP P03728
A	541	GLU	-	expression tag	UNP P03728
A	542	HIS	-	expression tag	UNP P03728
A	543	HIS	-	expression tag	UNP P03728
A	544	HIS	-	expression tag	UNP P03728
A	545	HIS	-	expression tag	UNP P03728
A	546	HIS	-	expression tag	UNP P03728
A	547	HIS	-	expression tag	UNP P03728
B	537	ALA	-	expression tag	UNP P03728
B	538	ALA	-	expression tag	UNP P03728
B	539	ALA	-	expression tag	UNP P03728
B	540	LEU	-	expression tag	UNP P03728
B	541	GLU	-	expression tag	UNP P03728
B	542	HIS	-	expression tag	UNP P03728
B	543	HIS	-	expression tag	UNP P03728
B	544	HIS	-	expression tag	UNP P03728
B	545	HIS	-	expression tag	UNP P03728
B	546	HIS	-	expression tag	UNP P03728
B	547	HIS	-	expression tag	UNP P03728
C	537	ALA	-	expression tag	UNP P03728
C	538	ALA	-	expression tag	UNP P03728
C	539	ALA	-	expression tag	UNP P03728
C	540	LEU	-	expression tag	UNP P03728
C	541	GLU	-	expression tag	UNP P03728
C	542	HIS	-	expression tag	UNP P03728
C	543	HIS	-	expression tag	UNP P03728
C	544	HIS	-	expression tag	UNP P03728
C	545	HIS	-	expression tag	UNP P03728
C	546	HIS	-	expression tag	UNP P03728
C	547	HIS	-	expression tag	UNP P03728
D	537	ALA	-	expression tag	UNP P03728
D	538	ALA	-	expression tag	UNP P03728
D	539	ALA	-	expression tag	UNP P03728
D	540	LEU	-	expression tag	UNP P03728
D	541	GLU	-	expression tag	UNP P03728
D	542	HIS	-	expression tag	UNP P03728
D	543	HIS	-	expression tag	UNP P03728
D	544	HIS	-	expression tag	UNP P03728
D	545	HIS	-	expression tag	UNP P03728
D	546	HIS	-	expression tag	UNP P03728
D	547	HIS	-	expression tag	UNP P03728
E	537	ALA	-	expression tag	UNP P03728

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Chain	Residue	Modelled	Actual	Comment	Reference
E	538	ALA	-	expression tag	UNP P03728
E	539	ALA	-	expression tag	UNP P03728
E	540	LEU	-	expression tag	UNP P03728
E	541	GLU	-	expression tag	UNP P03728
E	542	HIS	-	expression tag	UNP P03728
E	543	HIS	-	expression tag	UNP P03728
E	544	HIS	-	expression tag	UNP P03728
E	545	HIS	-	expression tag	UNP P03728
E	546	HIS	-	expression tag	UNP P03728
E	547	HIS	-	expression tag	UNP P03728
F	537	ALA	-	expression tag	UNP P03728
F	538	ALA	-	expression tag	UNP P03728
F	539	ALA	-	expression tag	UNP P03728
F	540	LEU	-	expression tag	UNP P03728
F	541	GLU	-	expression tag	UNP P03728
F	542	HIS	-	expression tag	UNP P03728
F	543	HIS	-	expression tag	UNP P03728
F	544	HIS	-	expression tag	UNP P03728
F	545	HIS	-	expression tag	UNP P03728
F	546	HIS	-	expression tag	UNP P03728
F	547	HIS	-	expression tag	UNP P03728
G	537	ALA	-	expression tag	UNP P03728
G	538	ALA	-	expression tag	UNP P03728
G	539	ALA	-	expression tag	UNP P03728
G	540	LEU	-	expression tag	UNP P03728
G	541	GLU	-	expression tag	UNP P03728
G	542	HIS	-	expression tag	UNP P03728
G	543	HIS	-	expression tag	UNP P03728
G	544	HIS	-	expression tag	UNP P03728
G	545	HIS	-	expression tag	UNP P03728
G	546	HIS	-	expression tag	UNP P03728
G	547	HIS	-	expression tag	UNP P03728
H	537	ALA	-	expression tag	UNP P03728
H	538	ALA	-	expression tag	UNP P03728
H	539	ALA	-	expression tag	UNP P03728
H	540	LEU	-	expression tag	UNP P03728
H	541	GLU	-	expression tag	UNP P03728
H	542	HIS	-	expression tag	UNP P03728
H	543	HIS	-	expression tag	UNP P03728
H	544	HIS	-	expression tag	UNP P03728
H	545	HIS	-	expression tag	UNP P03728
H	546	HIS	-	expression tag	UNP P03728

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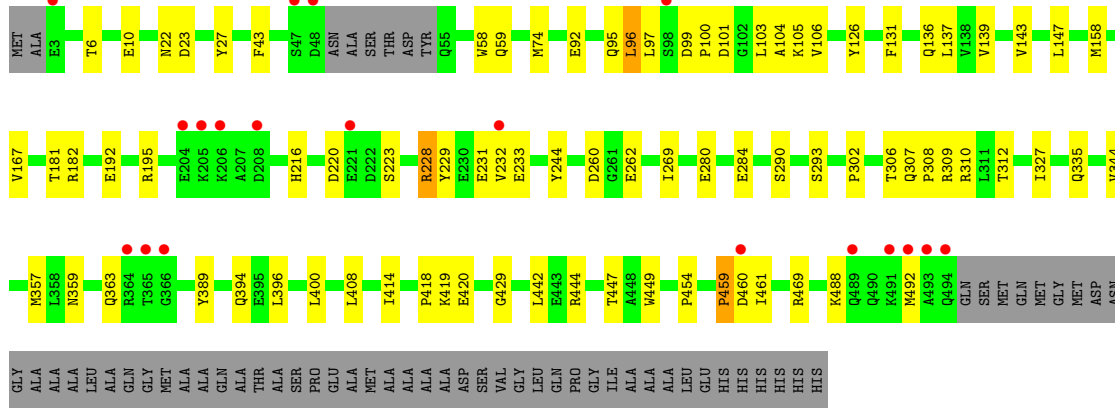
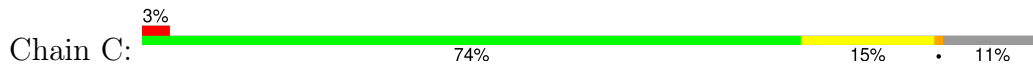
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Chain	Residue	Modelled	Actual	Comment	Reference
H	547	HIS	-	expression tag	UNP P03728
I	537	ALA	-	expression tag	UNP P03728
I	538	ALA	-	expression tag	UNP P03728
I	539	ALA	-	expression tag	UNP P03728
I	540	LEU	-	expression tag	UNP P03728
I	541	GLU	-	expression tag	UNP P03728
I	542	HIS	-	expression tag	UNP P03728
I	543	HIS	-	expression tag	UNP P03728
I	544	HIS	-	expression tag	UNP P03728
I	545	HIS	-	expression tag	UNP P03728
I	546	HIS	-	expression tag	UNP P03728
I	547	HIS	-	expression tag	UNP P03728
J	537	ALA	-	expression tag	UNP P03728
J	538	ALA	-	expression tag	UNP P03728
J	539	ALA	-	expression tag	UNP P03728
J	540	LEU	-	expression tag	UNP P03728
J	541	GLU	-	expression tag	UNP P03728
J	542	HIS	-	expression tag	UNP P03728
J	543	HIS	-	expression tag	UNP P03728
J	544	HIS	-	expression tag	UNP P03728
J	545	HIS	-	expression tag	UNP P03728
J	546	HIS	-	expression tag	UNP P03728
J	547	HIS	-	expression tag	UNP P03728
K	537	ALA	-	expression tag	UNP P03728
K	538	ALA	-	expression tag	UNP P03728
K	539	ALA	-	expression tag	UNP P03728
K	540	LEU	-	expression tag	UNP P03728
K	541	GLU	-	expression tag	UNP P03728
K	542	HIS	-	expression tag	UNP P03728
K	543	HIS	-	expression tag	UNP P03728
K	544	HIS	-	expression tag	UNP P03728
K	545	HIS	-	expression tag	UNP P03728
K	546	HIS	-	expression tag	UNP P03728
K	547	HIS	-	expression tag	UNP P03728
L	537	ALA	-	expression tag	UNP P03728
L	538	ALA	-	expression tag	UNP P03728
L	539	ALA	-	expression tag	UNP P03728
L	540	LEU	-	expression tag	UNP P03728
L	541	GLU	-	expression tag	UNP P03728
L	542	HIS	-	expression tag	UNP P03728
L	543	HIS	-	expression tag	UNP P03728
L	544	HIS	-	expression tag	UNP P03728

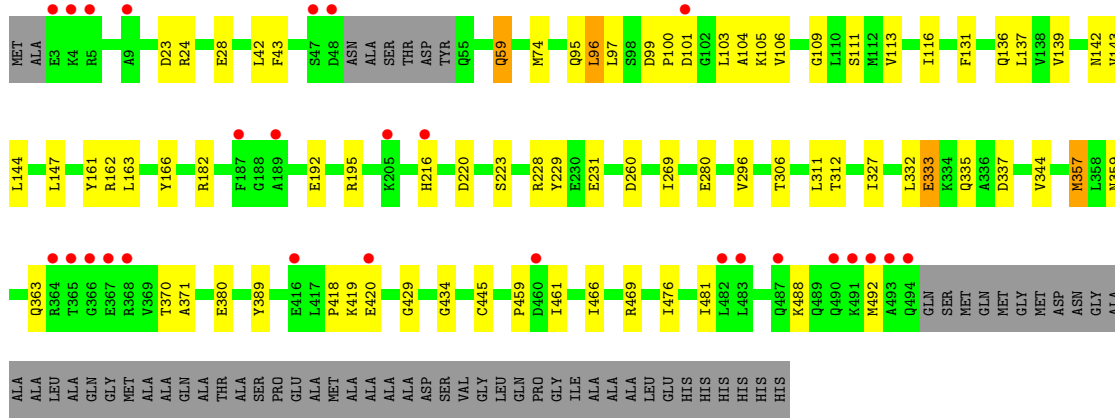
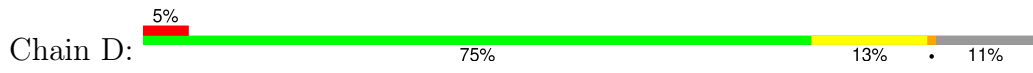
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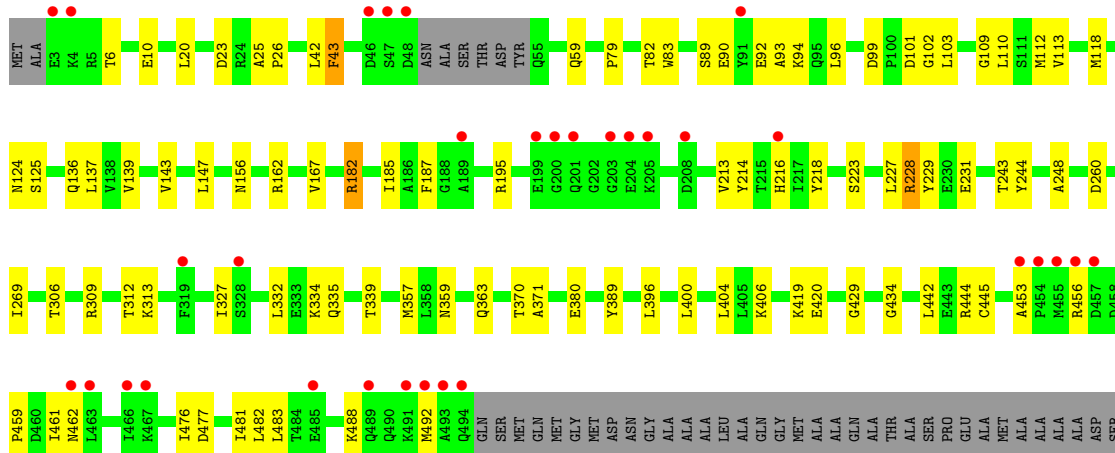
Chain	Residue	Modelled	Actual	Comment	Reference
L	545	HIS	-	expression tag	UNP P03728
L	546	HIS	-	expression tag	UNP P03728
L	547	HIS	-	expression tag	UNP P03728
M	537	ALA	-	expression tag	UNP P03728
M	538	ALA	-	expression tag	UNP P03728
M	539	ALA	-	expression tag	UNP P03728
M	540	LEU	-	expression tag	UNP P03728
M	541	GLU	-	expression tag	UNP P03728
M	542	HIS	-	expression tag	UNP P03728
M	543	HIS	-	expression tag	UNP P03728
M	544	HIS	-	expression tag	UNP P03728
M	545	HIS	-	expression tag	UNP P03728
M	546	HIS	-	expression tag	UNP P03728
M	547	HIS	-	expression tag	UNP P03728



• Molecule 1: Portal protein



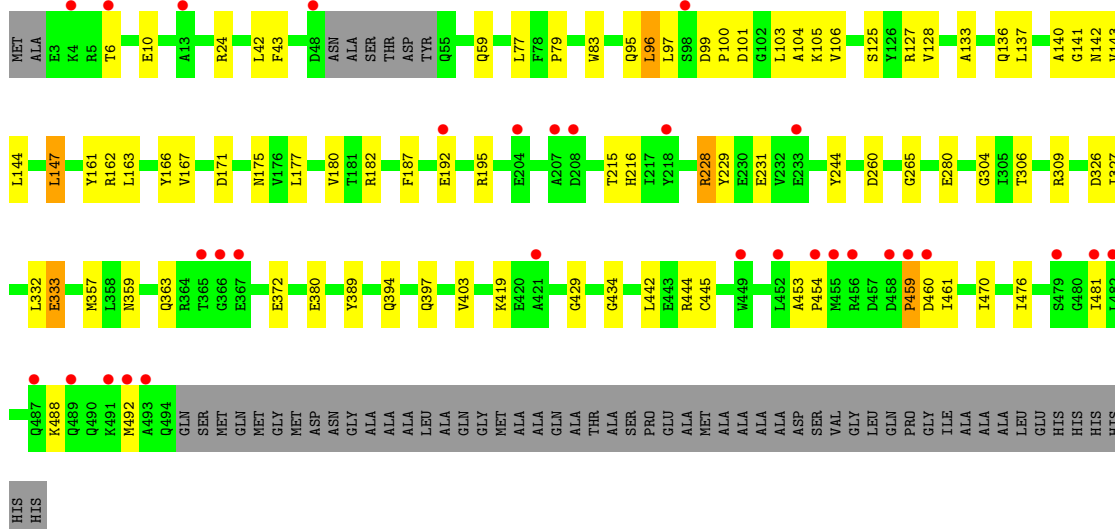
• Molecule 1: Portal protein



VAL
GLY
LEU
GLN
PRO
GLY
ILE
ALA
ALA
LEU
LEU
GLU
HIS
HIS
HIS
HIS
HIS

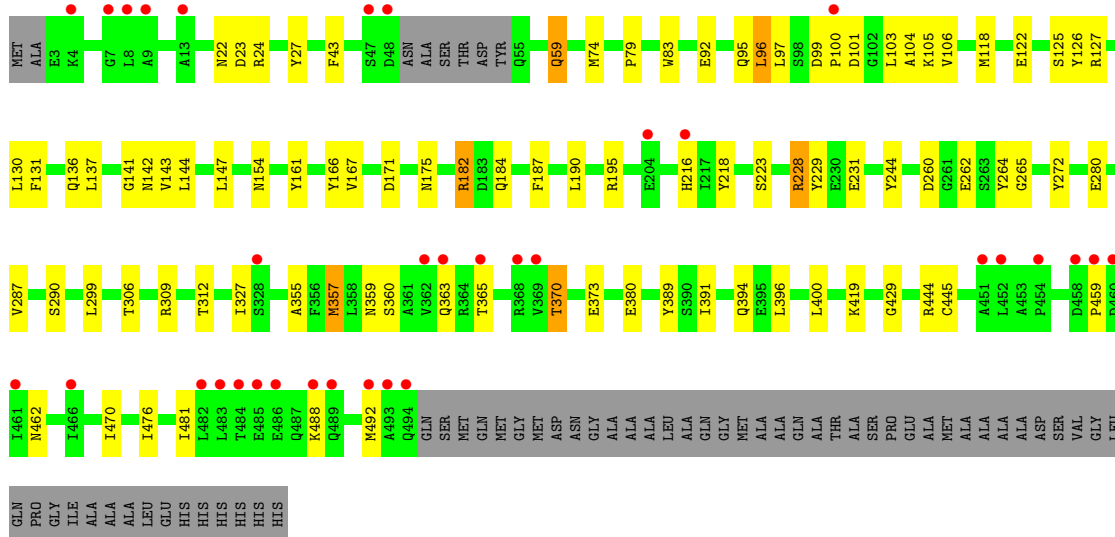
• Molecule 1: Portal protein

Chain F: 6% 73% 15% 11%



• Molecule 1: Portal protein

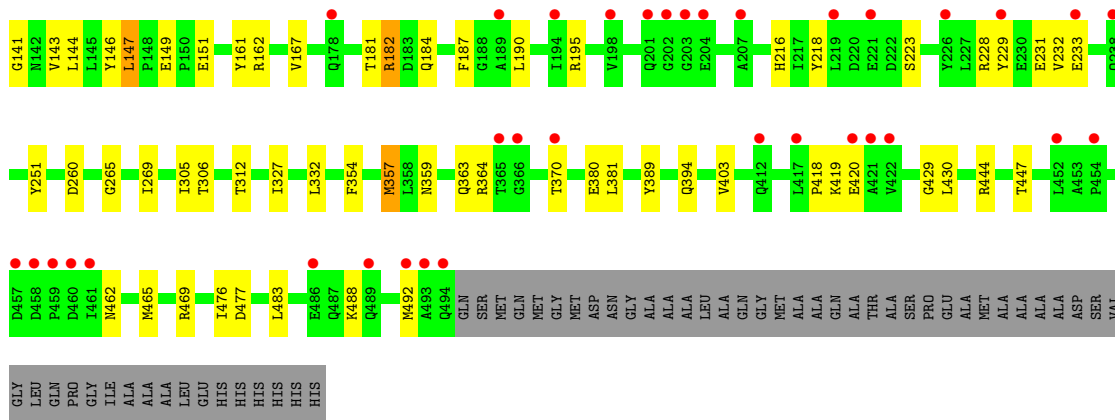
Chain G: 6% 72% 15% 11%



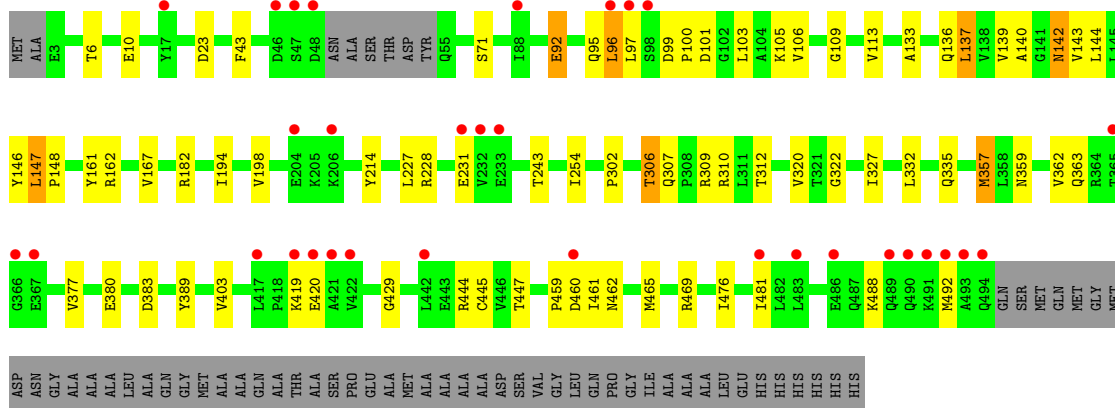
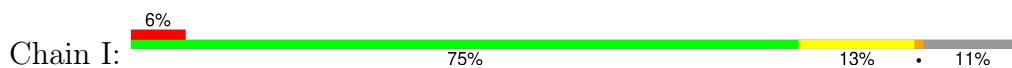
• Molecule 1: Portal protein

Chain H: 8% 73% 15% 11%

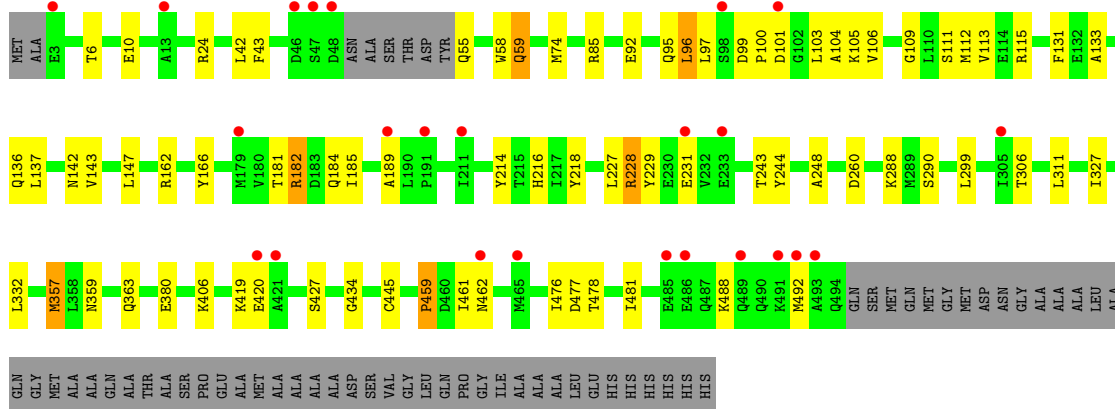
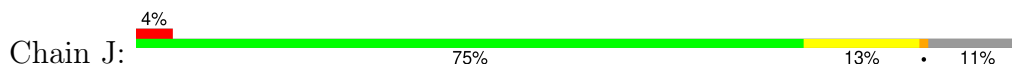




• Molecule 1: Portal protein



• Molecule 1: Portal protein



• Molecule 1: Portal protein



4 Data and refinement statistics i

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	261.57Å 261.57Å 256.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.56 – 3.40 58.49 – 3.40	Depositor EDS
% Data completeness (in resolution range)	95.7 (58.56-3.40) 95.8 (58.49-3.40)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.230 , 0.275 0.229 , 0.273	Depositor DCC
R_{free} test set	5822 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	77.4	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 54.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.025 for -h,-l,-k 0.007 for l,-k,h	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	49530	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.80% 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	0.39	0/3868	0.61	0/5232
1	B	0.40	0/3868	0.63	0/5232
1	C	0.40	0/3868	0.62	0/5232
1	D	0.40	0/3868	0.62	0/5232
1	E	0.40	0/3868	0.62	0/5232
1	F	0.40	0/3868	0.61	0/5232
1	G	0.39	0/3868	0.62	0/5232
1	H	0.40	0/3868	0.62	0/5232
1	I	0.40	0/3868	0.63	0/5232
1	J	0.40	0/3868	0.63	0/5232
1	K	0.39	0/3868	0.61	0/5232
1	L	0.38	0/3868	0.61	0/5232
1	M	0.39	0/3868	0.61	0/5232
All	All	0.40	0/50284	0.62	0/68016

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	M	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	228	ARG	Sidechain

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	3810	0	3823	58	0
1	B	3810	0	3823	49	0
1	C	3810	0	3823	49	0
1	D	3810	0	3823	41	0
1	E	3810	0	3823	57	0
1	F	3810	0	3823	53	0
1	G	3810	0	3823	54	0
1	H	3810	0	3823	52	0
1	I	3810	0	3823	45	0
1	J	3810	0	3823	47	0
1	K	3810	0	3823	57	0
1	L	3810	0	3823	44	0
1	M	3810	0	3823	61	0
All	All	49530	0	49699	596	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 596 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:137:LEU:HD13	1:A:143:VAL:HG23	1.29	1.11
1:J:137:LEU:HD13	1:J:143:VAL:HG23	1.53	0.91
1:A:137:LEU:HD13	1:A:143:VAL:CG2	2.02	0.89
1:M:137:LEU:HD13	1:M:143:VAL:HG23	1.60	0.84
1:E:92:GLU:HG2	1:E:420:GLU:HA	1.63	0.80

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	482/547 (88%)	438 (91%)	38 (8%)	6 (1%)	13	41
1	B	482/547 (88%)	444 (92%)	31 (6%)	7 (2%)	10	36
1	C	482/547 (88%)	437 (91%)	39 (8%)	6 (1%)	13	41
1	D	482/547 (88%)	445 (92%)	31 (6%)	6 (1%)	13	41
1	E	482/547 (88%)	448 (93%)	32 (7%)	2 (0%)	34	67
1	F	482/547 (88%)	444 (92%)	32 (7%)	6 (1%)	13	41
1	G	482/547 (88%)	444 (92%)	32 (7%)	6 (1%)	13	41
1	H	482/547 (88%)	438 (91%)	38 (8%)	6 (1%)	13	41
1	I	482/547 (88%)	442 (92%)	36 (8%)	4 (1%)	19	51
1	J	482/547 (88%)	438 (91%)	38 (8%)	6 (1%)	13	41
1	K	482/547 (88%)	439 (91%)	38 (8%)	5 (1%)	15	46
1	L	482/547 (88%)	439 (91%)	39 (8%)	4 (1%)	19	51
1	M	482/547 (88%)	444 (92%)	32 (7%)	6 (1%)	13	41
All	All	6266/7111 (88%)	5740 (92%)	456 (7%)	70 (1%)	14	44

5 of 70 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	363	GLN
1	D	419	LYS
1	E	363	GLN
1	E	419	LYS
1	H	363	GLN

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	412/450 (92%)	390 (95%)	22 (5%)	22	52
1	B	412/450 (92%)	396 (96%)	16 (4%)	32	61
1	C	412/450 (92%)	398 (97%)	14 (3%)	37	65
1	D	412/450 (92%)	399 (97%)	13 (3%)	39	67
1	E	412/450 (92%)	397 (96%)	15 (4%)	35	63
1	F	412/450 (92%)	402 (98%)	10 (2%)	49	74
1	G	412/450 (92%)	392 (95%)	20 (5%)	25	55
1	H	412/450 (92%)	396 (96%)	16 (4%)	32	61
1	I	412/450 (92%)	394 (96%)	18 (4%)	28	58
1	J	412/450 (92%)	401 (97%)	11 (3%)	44	70
1	K	412/450 (92%)	399 (97%)	13 (3%)	39	67
1	L	412/450 (92%)	399 (97%)	13 (3%)	39	67
1	M	412/450 (92%)	398 (97%)	14 (3%)	37	65
All	All	5356/5850 (92%)	5161 (96%)	195 (4%)	35	63

5 of 195 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	167	VAL
1	I	383	ASP
1	H	228	ARG
1	I	137	LEU
1	J	228	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	156	ASN
1	L	307	GLN
1	H	487	GLN
1	K	184	GLN
1	H	307	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 monosaccharides 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 [i](#)

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

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	486/547 (88%)	0.32	24 (4%) 29 29	33, 70, 152, 199	1 (0%)
1	B	486/547 (88%)	0.22	21 (4%) 35 35	31, 71, 141, 194	1 (0%)
1	C	486/547 (88%)	0.21	19 (3%) 39 38	30, 73, 139, 198	1 (0%)
1	D	486/547 (88%)	0.33	27 (5%) 24 25	35, 75, 146, 183	1 (0%)
1	E	486/547 (88%)	0.36	32 (6%) 18 20	36, 75, 132, 208	1 (0%)
1	F	486/547 (88%)	0.40	31 (6%) 19 20	37, 80, 143, 192	1 (0%)
1	G	486/547 (88%)	0.32	34 (6%) 16 18	37, 79, 144, 225	1 (0%)
1	H	486/547 (88%)	0.43	43 (8%) 10 11	38, 79, 149, 224	1 (0%)
1	I	486/547 (88%)	0.39	32 (6%) 18 20	38, 80, 155, 215	1 (0%)
1	J	486/547 (88%)	0.39	24 (4%) 29 29	39, 89, 150, 215	1 (0%)
1	K	486/547 (88%)	0.33	31 (6%) 19 20	38, 88, 156, 203	1 (0%)
1	L	486/547 (88%)	0.43	37 (7%) 13 15	37, 84, 151, 197	1 (0%)
1	M	486/547 (88%)	0.34	27 (5%) 24 25	37, 80, 150, 195	1 (0%)
All	All	6318/7111 (88%)	0.34	382 (6%) 21 23	30, 79, 148, 225	13 (0%)

The worst 5 of 382 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	48	ASP	10.0
1	M	47	SER	7.4
1	J	3	GLU	7.3
1	I	48	ASP	6.4
1	A	98	SER	6.3

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 monosaccharides 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.