



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:44 PM UTC

PDB ID : 7O49 / pdb_00007o49
Title : Crystal structure of Penicillin-Binding Protein 1 (PBP1) from *Staphylococcus aureus*
Authors : Martinez Caballero, S.; Hermoso, J.A.
Deposited on : 2021-04-05
Resolution : 3.03 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:

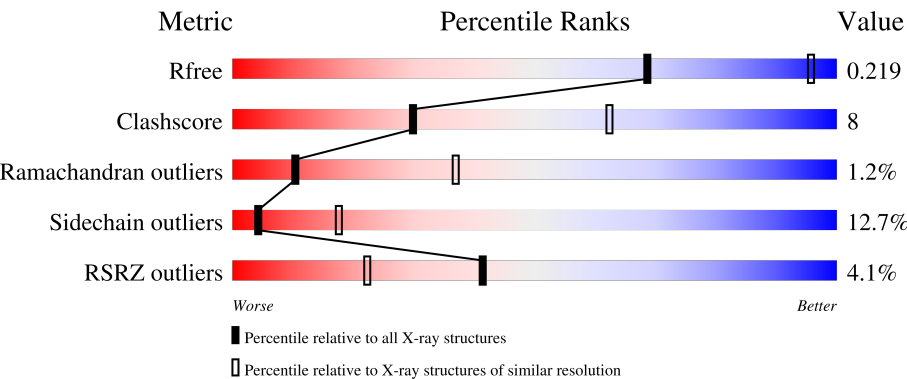
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 3.03 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	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

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	650	3% 60% 18% • 20%
1	B	650	3% 59% 19% • 19%
1	C	650	2% 61% 16% • 20%
1	D	650	5% 58% 16% • 23%
1	E	650	2% 58% 18% • 20%

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Mol	Chain	Length	Quality of chain
1	F	650	
1	G	650	
1	H	650	
1	I	650	
1	J	650	
1	K	650	
1	L	650	

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
4	CL	C	802	-	-	X	-
4	CL	E	802	-	-	X	-
4	CL	K	801	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 48707 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 Penicillin-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	521	Total	C	N	O	S	0	0	0
			4105	2609	706	774	16			
1	B	527	Total	C	N	O	S	0	0	0
			4156	2639	716	785	16			
1	C	520	Total	C	N	O	S	0	0	0
			4098	2604	705	773	16			
1	D	502	Total	C	N	O	S	0	0	0
			3958	2514	677	751	16			
1	E	523	Total	C	N	O	S	0	0	0
			4120	2617	709	778	16			
1	F	528	Total	C	N	O	S	0	0	0
			4165	2645	718	786	16			
1	G	520	Total	C	N	O	S	0	0	0
			4098	2604	705	773	16			
1	H	471	Total	C	N	O	S	0	0	0
			3703	2355	631	702	15			
1	I	518	Total	C	N	O	S	0	0	0
			4083	2595	702	770	16			
1	J	518	Total	C	N	O	S	0	0	0
			4080	2592	701	771	16			
1	K	511	Total	C	N	O	S	0	0	0
			4029	2562	690	761	16			
1	L	494	Total	C	N	O	S	0	0	0
			3894	2479	662	737	16			

There are 12 discrepancies between the modelled and reference sequences:

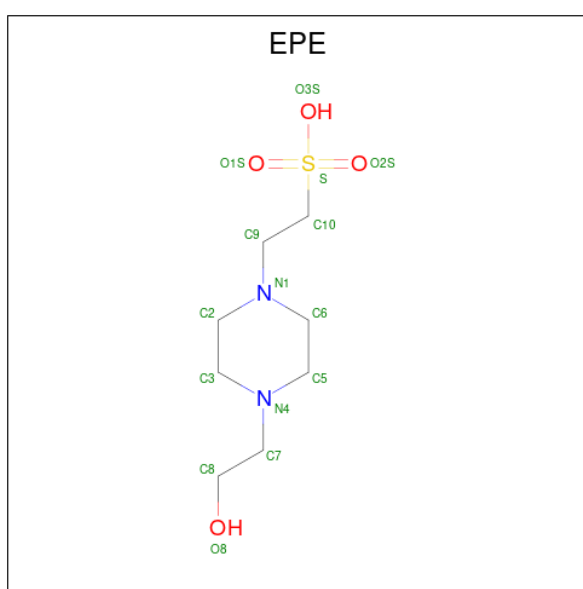
Chain	Residue	Modelled	Actual	Comment	Reference
A	64	MET	-	initiating methionine	UNP A0A0H2WVW5
B	64	MET	-	initiating methionine	UNP A0A0H2WVW5
C	64	MET	-	initiating methionine	UNP A0A0H2WVW5
D	64	MET	-	initiating methionine	UNP A0A0H2WVW5
E	64	MET	-	initiating methionine	UNP A0A0H2WVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	64	MET	-	initiating methionine	UNP A0A0H2WVW5
G	64	MET	-	initiating methionine	UNP A0A0H2WVW5
H	64	MET	-	initiating methionine	UNP A0A0H2WVW5
I	64	MET	-	initiating methionine	UNP A0A0H2WVW5
J	64	MET	-	initiating methionine	UNP A0A0H2WVW5
K	64	MET	-	initiating methionine	UNP A0A0H2WVW5
L	64	MET	-	initiating methionine	UNP A0A0H2WVW5

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	E	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	F	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	G	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	I	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	J	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is CADMIUM ION (CCD ID: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cd	0	0
			1	1		
3	B	1	Total	Cd	0	0
			1	1		
3	C	1	Total	Cd	0	0
			1	1		
3	D	1	Total	Cd	0	0
			1	1		
3	E	1	Total	Cd	0	0
			1	1		
3	F	1	Total	Cd	0	0
			1	1		
3	G	1	Total	Cd	0	0
			1	1		
3	H	1	Total	Cd	0	0
			1	1		
3	I	1	Total	Cd	0	0
			1	1		
3	J	1	Total	Cd	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		
4	E	1	Total	Cl	0	0
			1	1		
4	F	1	Total	Cl	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total 1	Cl 1	0	0
4	J	1	Total 1	Cl 1	0	0
4	K	1	Total 1	Cl 1	0	0
4	L	1	Total 1	Cl 1	0	0

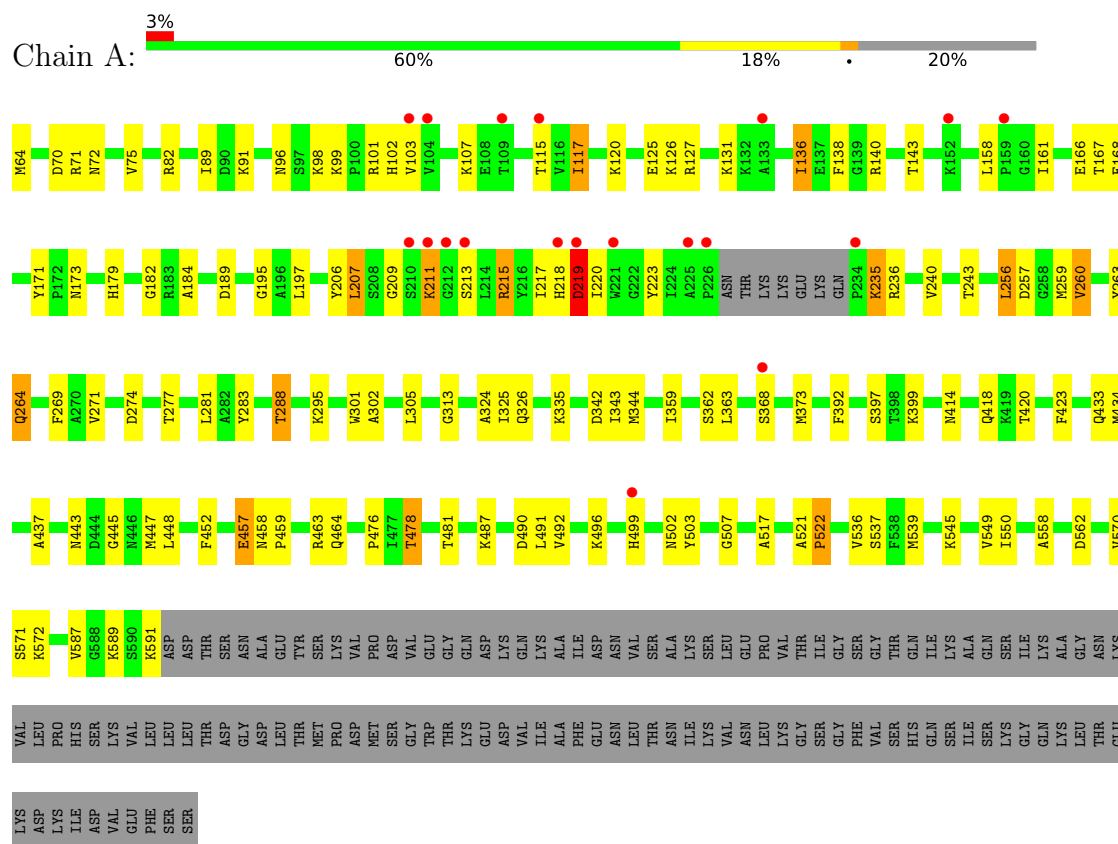
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	O 3	0	0
5	B	3	Total 3	O 3	0	0
5	C	6	Total 6	O 6	0	0
5	D	3	Total 3	O 3	0	0
5	E	7	Total 7	O 7	0	0
5	F	8	Total 8	O 8	0	0
5	G	5	Total 5	O 5	0	0
5	H	3	Total 3	O 3	0	0
5	I	4	Total 4	O 4	0	0
5	J	4	Total 4	O 4	0	0
5	K	3	Total 3	O 3	0	0
5	L	1	Total 1	O 1	0	0

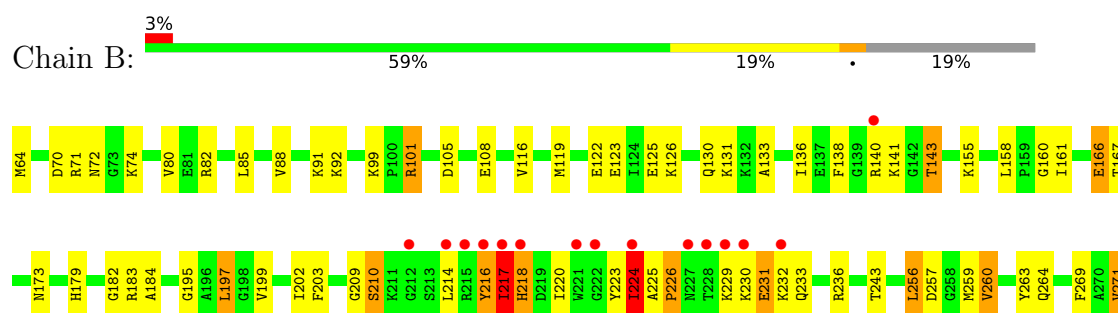
3 Residue-property plots

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

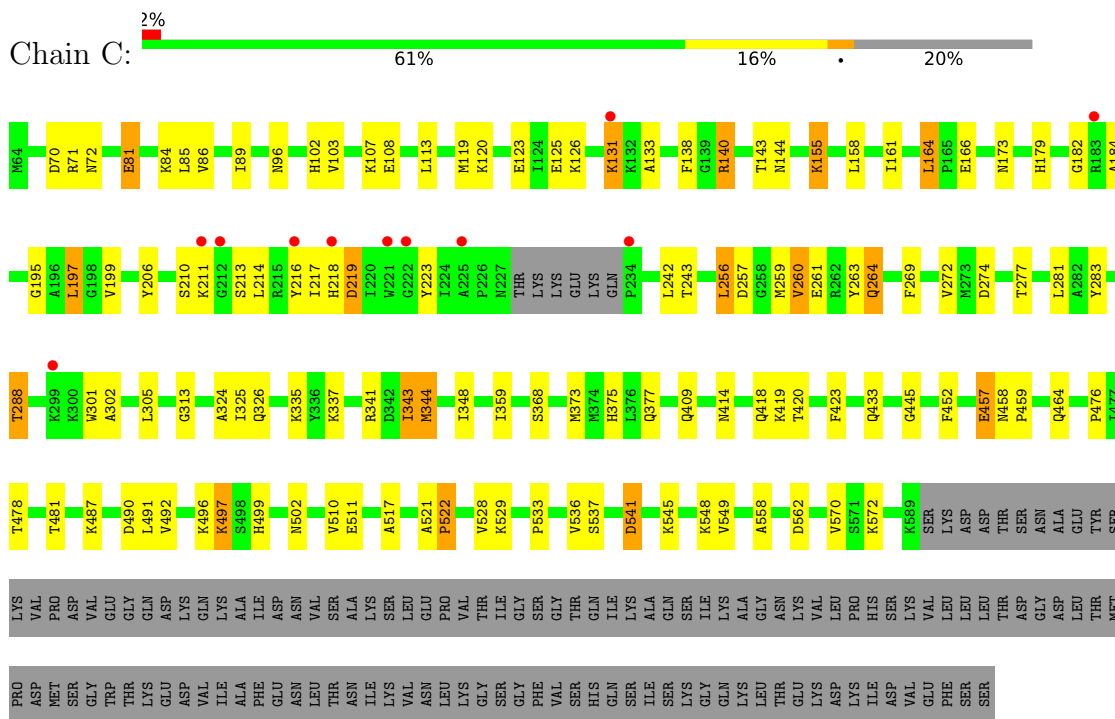
• Molecule 1: Penicillin-binding protein 1



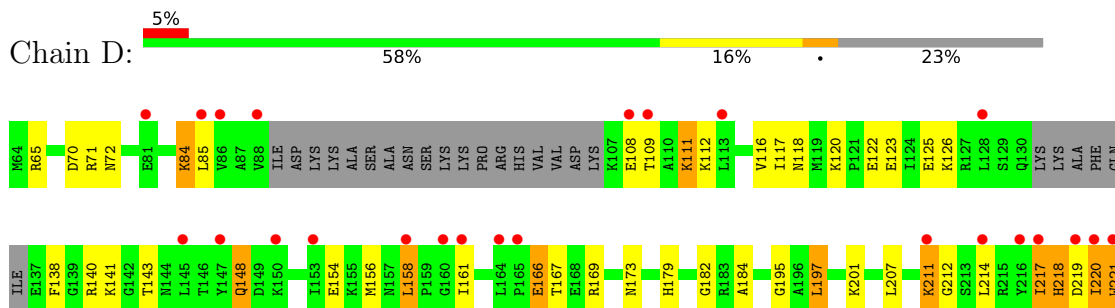
• Molecule 1: Penicillin-binding protein 1

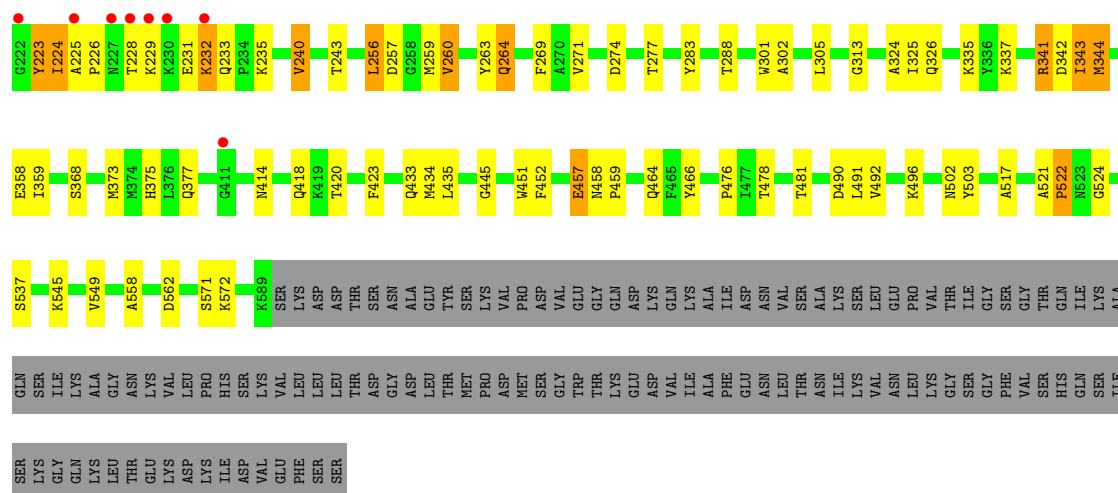


- Molecule 1: Penicillin-binding protein 1

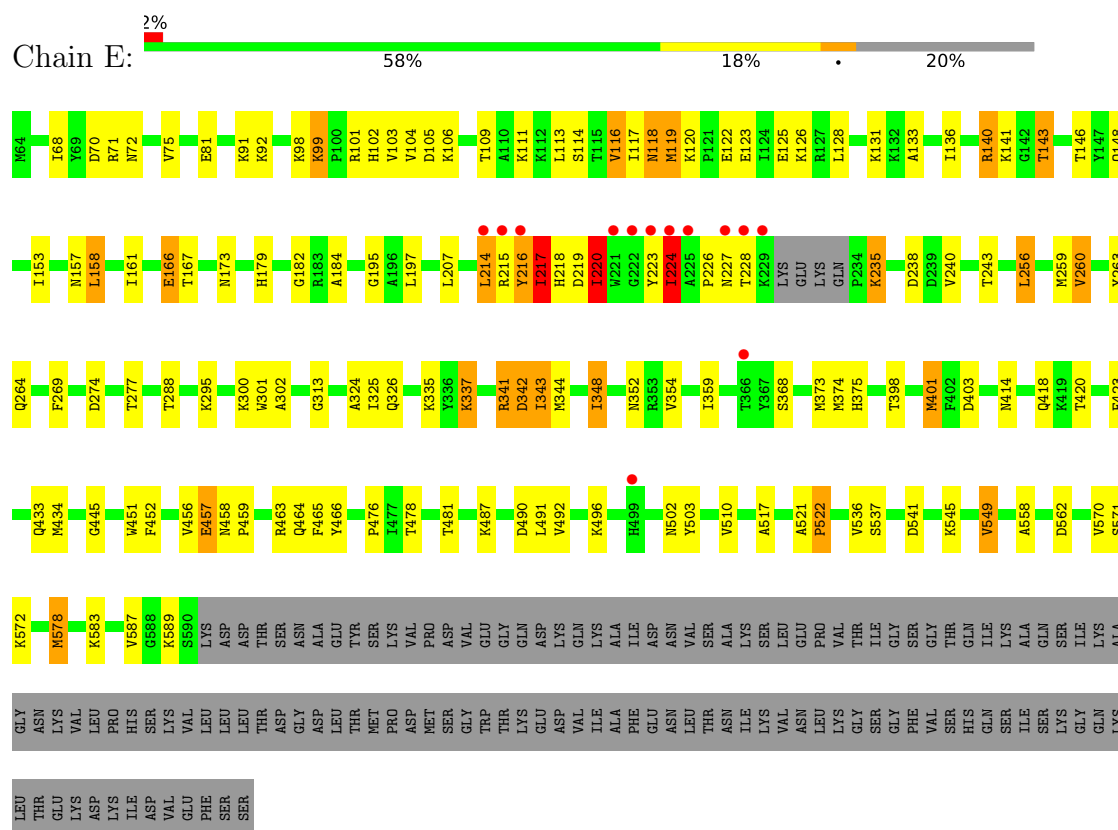


- Molecule 1: Penicillin-binding protein 1

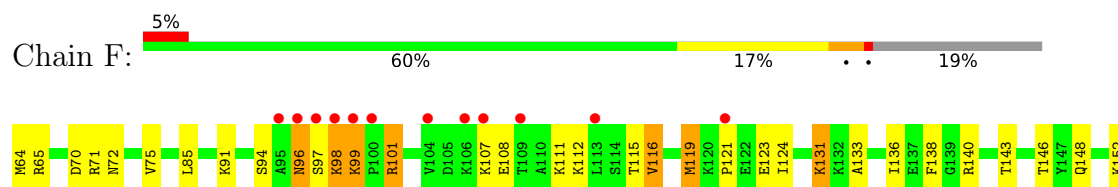


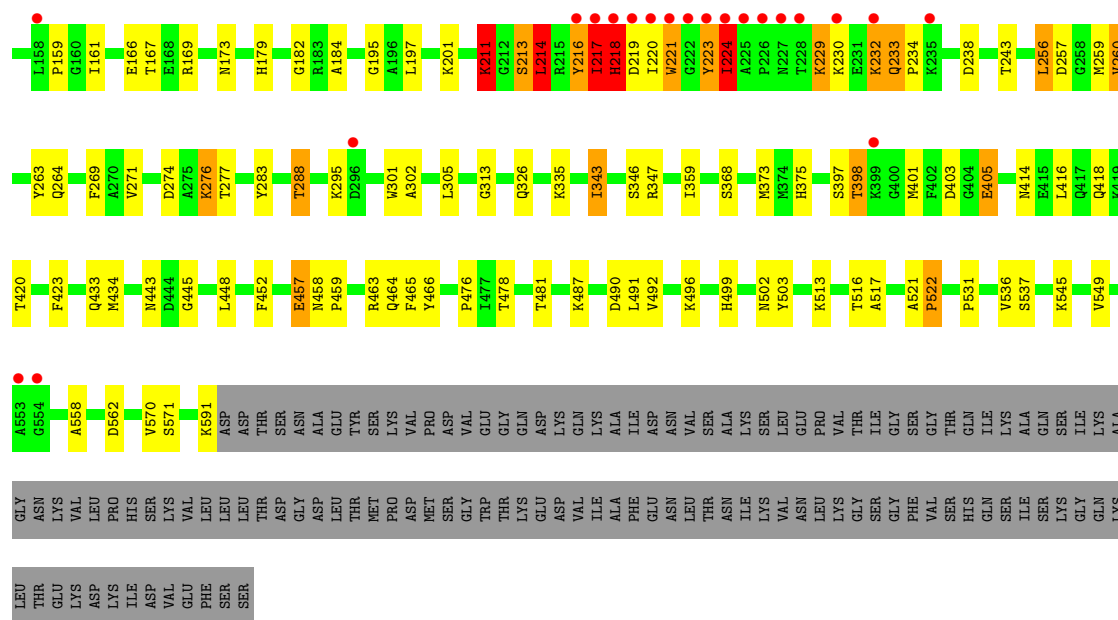


• Molecule 1: Penicillin-binding protein 1

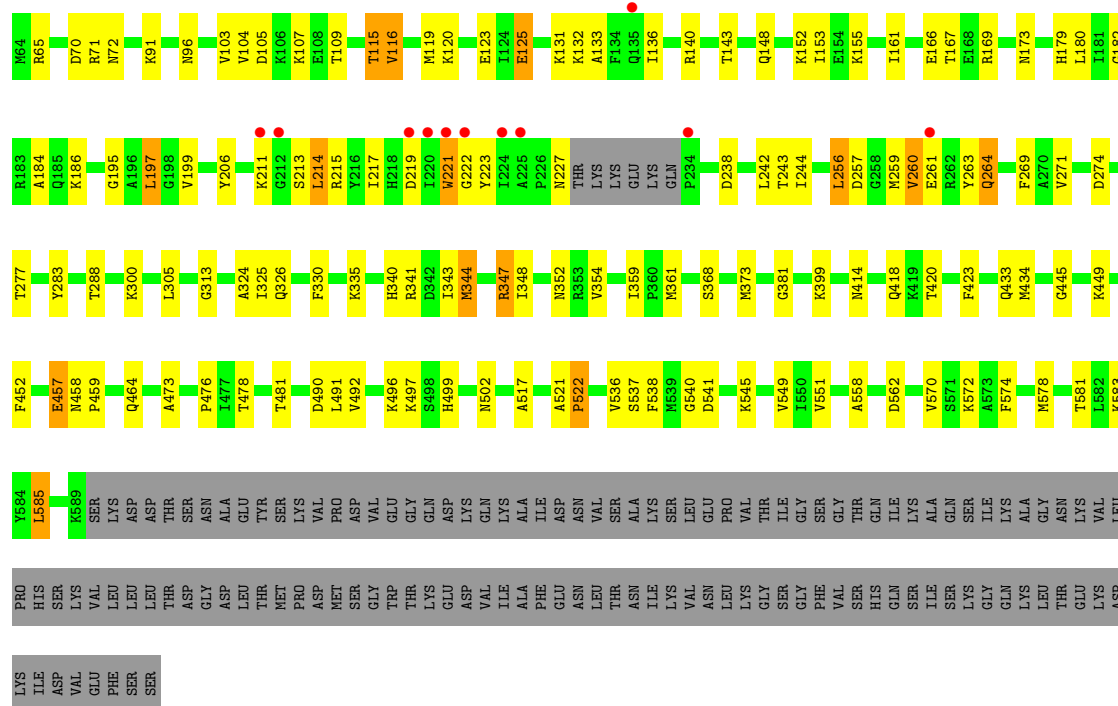


• Molecule 1: Penicillin-binding protein 1

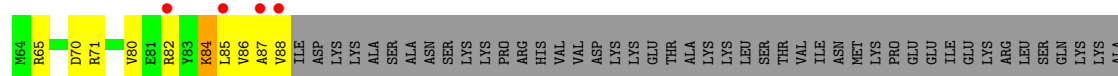




• Molecule 1: Penicillin-binding protein 1

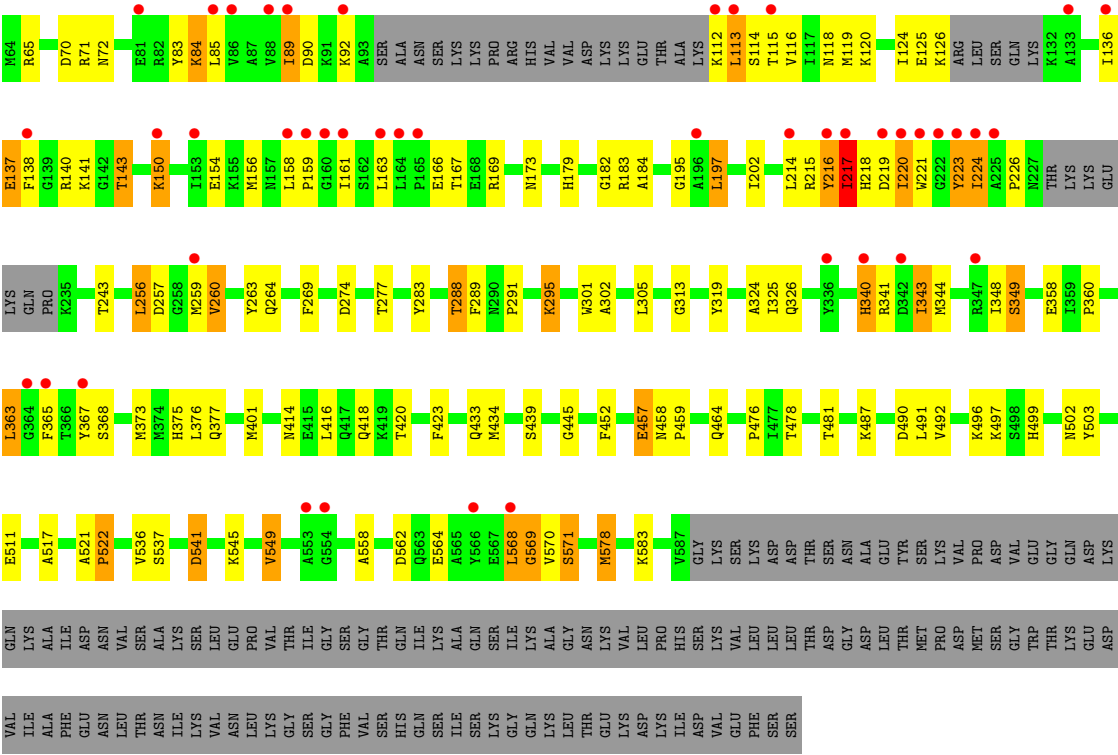


• Molecule 1: Penicillin-binding protein 1









4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	311.86Å 197.15Å 221.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.00 – 3.03 49.00 – 3.03	Depositor EDS
% Data completeness (in resolution range)	55.2 (49.00-3.03) 55.2 (49.00-3.03)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.77 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.211 , 0.246 (Not available) , 0.219	Depositor DCC
R_{free} test set	7237 reflections (2.75%)	wwPDB-VP
Wilson B-factor (Å ²)	81.7	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 97.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	48707	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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

Bond lengths and bond angles in the following residue types are not validated in this section: CL, EPE, CD

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	1.02	1/4195 (0.0%)	1.44	11/5641 (0.2%)
1	B	1.04	4/4247 (0.1%)	1.45	8/5712 (0.1%)
1	C	1.02	1/4188 (0.0%)	1.45	4/5633 (0.1%)
1	D	1.02	1/4044 (0.0%)	1.44	5/5440 (0.1%)
1	E	1.03	2/4210 (0.0%)	1.43	2/5662 (0.0%)
1	F	1.04	2/4256 (0.0%)	1.45	9/5723 (0.2%)
1	G	1.01	1/4188 (0.0%)	1.42	2/5633 (0.0%)
1	H	1.04	2/3787 (0.1%)	1.43	9/5099 (0.2%)
1	I	1.02	3/4172 (0.1%)	1.43	4/5611 (0.1%)
1	J	1.03	1/4169 (0.0%)	1.44	11/5608 (0.2%)
1	K	1.06	3/4117 (0.1%)	1.43	7/5537 (0.1%)
1	L	1.08	4/3979 (0.1%)	1.45	8/5354 (0.1%)
All	All	1.03	25/49552 (0.1%)	1.44	80/66653 (0.1%)

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	218	HIS	CE1-NE2	11.29	1.43	1.32
1	L	340	HIS	CE1-NE2	8.34	1.40	1.32
1	I	340	HIS	CE1-NE2	8.33	1.40	1.32
1	K	89	ILE	C-O	7.49	1.31	1.23
1	B	218	HIS	CE1-NE2	6.85	1.39	1.32

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	342	ASP	CA-CB-CG	9.05	121.65	112.60
1	B	342	ASP	CA-CB-CG	8.57	121.17	112.60
1	L	568	LEU	CA-C-O	-8.15	112.91	122.13
1	F	405	GLU	CB-CG-CD	7.92	126.06	112.60
1	A	131	LYS	CB-CA-C	-7.84	105.36	116.34

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	4105	0	4096	73	0
1	B	4156	0	4149	80	0
1	C	4098	0	4084	65	0
1	D	3958	0	3928	67	0
1	E	4120	0	4109	85	0
1	F	4165	0	4162	79	0
1	G	4098	0	4084	75	0
1	H	3703	0	3646	67	0
1	I	4083	0	4070	61	0
1	J	4080	0	4062	67	0
1	K	4029	0	4013	80	0
1	L	3894	0	3855	65	0
2	A	15	0	18	0	0
2	B	15	0	18	0	0
2	C	15	0	17	0	0
2	D	15	0	17	0	0
2	E	15	0	17	0	0
2	F	15	0	17	1	0
2	G	15	0	17	0	0
2	H	15	0	18	1	0
2	I	15	0	18	1	0
2	J	15	0	18	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
4	C	1	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	1	0
4	E	1	0	0	2	0
4	F	1	0	0	1	0
4	H	1	0	0	1	0
4	J	1	0	0	1	0
4	K	1	0	0	2	0
4	L	1	0	0	1	0
5	A	3	0	0	1	0
5	B	3	0	0	0	0
5	C	6	0	0	0	0
5	D	3	0	0	1	0
5	E	7	0	0	0	0
5	F	8	0	0	1	0
5	G	5	0	0	0	0
5	H	3	0	0	0	0
5	I	4	0	0	1	0
5	J	4	0	0	1	0
5	K	3	0	0	1	0
5	L	1	0	0	0	0
All	All	48707	0	48433	824	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 824 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:E:343:ILE:HG21	1:E:348:ILE:HD11	1.16	1.15
1:J:117:ILE:HD11	1:J:141:LYS:O	1.51	1.11
1:H:85:LEU:HD12	1:H:163:LEU:HD21	1.40	1.02
1:F:223:TYR:O	1:F:224:ILE:HG12	1.58	1.01
1:A:437:ALA:HA	1:A:447:MET:HE2	1.42	1.01

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	517/650 (80%)	454 (88%)	59 (11%)	4 (1%)	16	46
1	B	525/650 (81%)	455 (87%)	63 (12%)	7 (1%)	9	35
1	C	516/650 (79%)	452 (88%)	59 (11%)	5 (1%)	12	41
1	D	496/650 (76%)	429 (86%)	59 (12%)	8 (2%)	7	30
1	E	519/650 (80%)	456 (88%)	56 (11%)	7 (1%)	9	35
1	F	526/650 (81%)	456 (87%)	61 (12%)	9 (2%)	7	29
1	G	516/650 (79%)	453 (88%)	59 (11%)	4 (1%)	16	46
1	H	465/650 (72%)	403 (87%)	57 (12%)	5 (1%)	11	39
1	I	514/650 (79%)	449 (87%)	59 (12%)	6 (1%)	10	37
1	J	514/650 (79%)	449 (87%)	61 (12%)	4 (1%)	16	46
1	K	507/650 (78%)	438 (86%)	63 (12%)	6 (1%)	10	37
1	L	486/650 (75%)	424 (87%)	53 (11%)	9 (2%)	6	27
All	All	6101/7800 (78%)	5318 (87%)	709 (12%)	74 (1%)	10	37

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	213	SER
1	D	232	LYS
1	F	97	SER
1	F	214	LEU
1	F	233	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	438/552 (79%)	381 (87%)	57 (13%)	4	17
1	B	444/552 (80%)	383 (86%)	61 (14%)	3	15
1	C	437/552 (79%)	388 (89%)	49 (11%)	6	22
1	D	422/552 (76%)	371 (88%)	51 (12%)	5	19
1	E	440/552 (80%)	375 (85%)	65 (15%)	3	13
1	F	445/552 (81%)	388 (87%)	57 (13%)	4	17
1	G	437/552 (79%)	386 (88%)	51 (12%)	5	20
1	H	392/552 (71%)	346 (88%)	46 (12%)	5	20
1	I	435/552 (79%)	389 (89%)	46 (11%)	6	24
1	J	435/552 (79%)	379 (87%)	56 (13%)	4	17
1	K	429/552 (78%)	372 (87%)	57 (13%)	4	16
1	L	414/552 (75%)	352 (85%)	62 (15%)	3	12
All	All	5168/6624 (78%)	4510 (87%)	658 (13%)	4	17

5 of 658 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	295	LYS
1	K	256	LEU
1	I	541	ASP
1	I	288	THR
1	J	337	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 116 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	532	ASN
1	L	443	ASN
1	I	72	ASN
1	L	433	GLN
1	K	436	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 18 are monoatomic - leaving 10 for Mogul analysis.

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	EPE	D	801	-	15,15,15	1.14	1 (6%)	19,20,20	1.26	1 (5%)
2	EPE	B	801	-	15,15,15	0.64	1 (6%)	19,20,20	0.81	0
2	EPE	E	801	-	15,15,15	0.99	1 (6%)	19,20,20	0.89	2 (10%)
2	EPE	G	801	-	15,15,15	1.03	1 (6%)	19,20,20	1.03	2 (10%)
2	EPE	H	801	-	15,15,15	0.63	1 (6%)	19,20,20	0.65	0
2	EPE	I	801	-	15,15,15	0.79	1 (6%)	19,20,20	0.88	0
2	EPE	A	801	-	15,15,15	0.68	1 (6%)	19,20,20	0.72	0
2	EPE	C	801	-	15,15,15	1.05	1 (6%)	19,20,20	1.13	1 (5%)
2	EPE	J	801	-	15,15,15	0.70	1 (6%)	19,20,20	0.92	0
2	EPE	F	801	-	15,15,15	1.03	1 (6%)	19,20,20	0.95	2 (10%)

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	EPE	D	801	-	-	4/9/19/19	0/1/1/1
2	EPE	B	801	-	-	7/9/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EPE	E	801	-	-	6/9/19/19	0/1/1/1
2	EPE	G	801	-	-	3/9/19/19	0/1/1/1
2	EPE	H	801	-	-	6/9/19/19	0/1/1/1
2	EPE	I	801	-	-	5/9/19/19	0/1/1/1
2	EPE	A	801	-	-	5/9/19/19	0/1/1/1
2	EPE	C	801	-	-	6/9/19/19	0/1/1/1
2	EPE	J	801	-	-	5/9/19/19	0/1/1/1
2	EPE	F	801	-	-	5/9/19/19	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	EPE	O1S-S	3.76	1.55	1.45
2	G	801	EPE	O1S-S	3.66	1.55	1.45
2	F	801	EPE	O2S-S	3.65	1.55	1.45
2	E	801	EPE	O2S-S	3.59	1.55	1.45
2	D	801	EPE	O1S-S	3.58	1.55	1.45

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	801	EPE	O3S-S-O2S	3.13	119.22	111.40
2	F	801	EPE	O3S-S-O1S	2.72	118.20	111.40
2	E	801	EPE	O3S-S-O1S	2.66	118.06	111.40
2	G	801	EPE	O3S-S-O2S	2.54	117.76	111.40
2	D	801	EPE	O3S-S-O2S	2.37	117.33	111.40

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	EPE	C10-C9-N1-C2
2	A	801	EPE	C10-C9-N1-C6
2	B	801	EPE	S-C10-C9-N1
2	B	801	EPE	C9-C10-S-O1S
2	D	801	EPE	C10-C9-N1-C6

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	801	EPE	1	0
2	I	801	EPE	1	0
2	F	801	EPE	1	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 [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	521/650 (80%)	0.10	19 (3%)	46	25	42, 79, 150, 203	0
1	B	527/650 (81%)	-0.02	18 (3%)	48	27	44, 82, 132, 200	1 (0%)
1	C	520/650 (80%)	0.06	11 (2%)	63	39	44, 86, 162, 191	0
1	D	502/650 (77%)	0.16	32 (6%)	25	13	41, 83, 199, 280	0
1	E	523/650 (80%)	0.06	13 (2%)	58	34	43, 90, 135, 185	1 (0%)
1	F	528/650 (81%)	0.21	33 (6%)	26	13	46, 93, 164, 196	1 (0%)
1	G	520/650 (80%)	0.03	11 (2%)	63	39	50, 84, 136, 198	0
1	H	471/650 (72%)	0.14	22 (4%)	36	19	46, 85, 166, 213	0
1	I	518/650 (79%)	0.02	14 (2%)	56	32	42, 88, 134, 186	0
1	J	518/650 (79%)	0.11	10 (1%)	66	42	40, 93, 174, 230	0
1	K	511/650 (78%)	0.47	28 (5%)	30	15	49, 110, 192, 273	0
1	L	494/650 (76%)	0.58	44 (8%)	15	8	64, 122, 194, 253	0
All	All	6153/7800 (78%)	0.16	255 (4%)	41	22	40, 90, 166, 280	3 (0%)

The worst 5 of 255 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	225	ALA	6.3
1	C	221	TRP	6.1
1	E	221	TRP	6.1
1	D	216	TYR	5.7
1	F	100	PRO	5.7

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](#)

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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
2	EPE	F	801	15/15	0.76	0.24	144,157,176,177	0
2	EPE	J	801	15/15	0.79	0.20	83,113,191,192	0
2	EPE	E	801	15/15	0.82	0.21	85,140,193,198	0
3	CD	H	803	1/1	0.82	0.16	37,37,37,37	0
2	EPE	C	801	15/15	0.84	0.19	86,113,196,197	0
2	EPE	G	801	15/15	0.84	0.19	86,121,204,211	0
2	EPE	D	801	15/15	0.85	0.18	79,123,194,197	0
2	EPE	H	801	15/15	0.85	0.21	96,123,197,213	0
2	EPE	A	801	15/15	0.86	0.20	100,111,190,196	0
3	CD	G	802	1/1	0.86	0.10	108,108,108,108	0
2	EPE	I	801	15/15	0.86	0.18	73,111,167,179	0
2	EPE	B	801	15/15	0.88	0.17	89,134,175,176	0
4	CL	H	802	1/1	0.91	0.07	76,76,76,76	0
4	CL	K	801	1/1	0.92	0.06	93,93,93,93	0
4	CL	L	801	1/1	0.93	0.05	87,87,87,87	0
4	CL	F	802	1/1	0.94	0.05	88,88,88,88	0
4	CL	J	802	1/1	0.94	0.07	70,70,70,70	0
4	CL	C	802	1/1	0.95	0.09	72,72,72,72	0
4	CL	D	802	1/1	0.96	0.07	82,82,82,82	0
3	CD	I	802	1/1	0.96	0.05	101,101,101,101	0
3	CD	A	802	1/1	0.97	0.05	98,98,98,98	0
3	CD	B	802	1/1	0.97	0.05	131,131,131,131	0
4	CL	E	802	1/1	0.97	0.05	102,102,102,102	0
3	CD	C	803	1/1	0.97	0.07	94,94,94,94	0
3	CD	D	803	1/1	0.99	0.05	97,97,97,97	0
3	CD	E	803	1/1	0.99	0.02	110,110,110,110	0
3	CD	F	803	1/1	0.99	0.02	131,131,131,131	0
3	CD	J	803	1/1	0.99	0.05	102,102,102,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.