



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 23, 2026 – 01:40 PM UTC

PDB ID : 4D9J / pdb_00004d9j
Title : Structure of a 16 nm protein cage designed by fusing symmetric oligomeric domains
Authors : Lai, Y.-T.; Cascio, D.; Yeates, T.O.
Deposited on : 2012-01-11
Resolution : 3.92 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

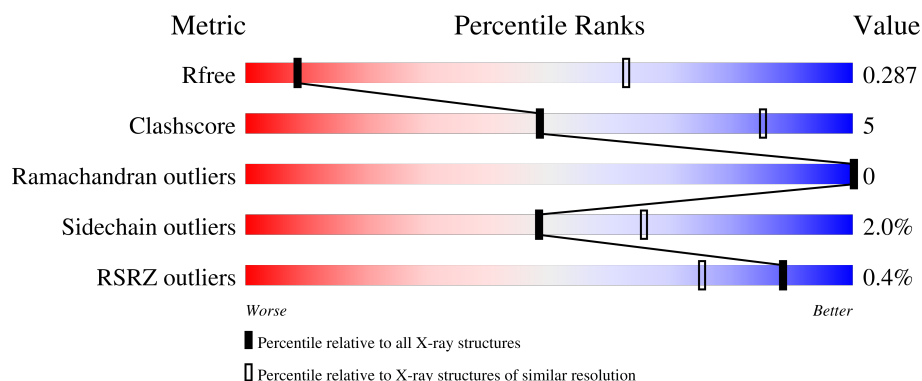
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.92 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	1033 (4.10-3.74)
Clashscore	190562	1070 (4.10-3.74)
Ramachandran outliers	187476	1017 (4.10-3.74)
Sidechain outliers	187428	1010 (4.10-3.74)
RSRZ outliers	180081	1033 (4.10-3.74)

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	456	 80% 15% . .
1	B	456	 79% 16% .
1	C	456	 80% 15% . .
1	D	456	 82% 13% . .
1	E	456	 80% 15% . .

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Mol	Chain	Length	Quality of chain
1	F	456	 82% 13% . .
1	G	456	 79% 16% . .
1	H	456	 81% 14% . .
1	I	456	 84% 11% . .
1	J	456	 79% 16% .
1	K	456	 83% 12% . .
1	L	456	 81% 14% . .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 40596 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 Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	B	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	C	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	D	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	E	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	F	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	G	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	H	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	I	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	J	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	K	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			
1	L	438	Total	C	N	O	S	0	0	0
			3383	2161	569	645	8			

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	VAL	GLN	conflict	UNP P29715
A	118	ALA	LYS	conflict	UNP P29715
A	278	ALA	-	linker	UNP P29715
A	279	LEU	-	linker	UNP P29715

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Chain	Residue	Modelled	Actual	Comment	Reference
A	280	GLU	-	linker	UNP P29715
A	281	ALA	-	linker	UNP P29715
A	282	GLN	-	linker	UNP P29715
A	283	LYS	-	linker	UNP P29715
A	284	GLN	-	linker	UNP P29715
A	285	LYS	-	linker	UNP P29715
A	448	LEU	-	expression tag	UNP P03485
A	449	GLU	-	expression tag	UNP P03485
A	450	HIS	-	expression tag	UNP P03485
A	451	HIS	-	expression tag	UNP P03485
A	452	HIS	-	expression tag	UNP P03485
A	453	HIS	-	expression tag	UNP P03485
A	454	HIS	-	expression tag	UNP P03485
A	455	HIS	-	expression tag	UNP P03485
B	24	VAL	GLN	conflict	UNP P29715
B	118	ALA	LYS	conflict	UNP P29715
B	278	ALA	-	linker	UNP P29715
B	279	LEU	-	linker	UNP P29715
B	280	GLU	-	linker	UNP P29715
B	281	ALA	-	linker	UNP P29715
B	282	GLN	-	linker	UNP P29715
B	283	LYS	-	linker	UNP P29715
B	284	GLN	-	linker	UNP P29715
B	285	LYS	-	linker	UNP P29715
B	448	LEU	-	expression tag	UNP P03485
B	449	GLU	-	expression tag	UNP P03485
B	450	HIS	-	expression tag	UNP P03485
B	451	HIS	-	expression tag	UNP P03485
B	452	HIS	-	expression tag	UNP P03485
B	453	HIS	-	expression tag	UNP P03485
B	454	HIS	-	expression tag	UNP P03485
B	455	HIS	-	expression tag	UNP P03485
C	24	VAL	GLN	conflict	UNP P29715
C	118	ALA	LYS	conflict	UNP P29715
C	278	ALA	-	linker	UNP P29715
C	279	LEU	-	linker	UNP P29715
C	280	GLU	-	linker	UNP P29715
C	281	ALA	-	linker	UNP P29715
C	282	GLN	-	linker	UNP P29715
C	283	LYS	-	linker	UNP P29715
C	284	GLN	-	linker	UNP P29715
C	285	LYS	-	linker	UNP P29715

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Chain	Residue	Modelled	Actual	Comment	Reference
C	448	LEU	-	expression tag	UNP P03485
C	449	GLU	-	expression tag	UNP P03485
C	450	HIS	-	expression tag	UNP P03485
C	451	HIS	-	expression tag	UNP P03485
C	452	HIS	-	expression tag	UNP P03485
C	453	HIS	-	expression tag	UNP P03485
C	454	HIS	-	expression tag	UNP P03485
C	455	HIS	-	expression tag	UNP P03485
D	24	VAL	GLN	conflict	UNP P29715
D	118	ALA	LYS	conflict	UNP P29715
D	278	ALA	-	linker	UNP P29715
D	279	LEU	-	linker	UNP P29715
D	280	GLU	-	linker	UNP P29715
D	281	ALA	-	linker	UNP P29715
D	282	GLN	-	linker	UNP P29715
D	283	LYS	-	linker	UNP P29715
D	284	GLN	-	linker	UNP P29715
D	285	LYS	-	linker	UNP P29715
D	448	LEU	-	expression tag	UNP P03485
D	449	GLU	-	expression tag	UNP P03485
D	450	HIS	-	expression tag	UNP P03485
D	451	HIS	-	expression tag	UNP P03485
D	452	HIS	-	expression tag	UNP P03485
D	453	HIS	-	expression tag	UNP P03485
D	454	HIS	-	expression tag	UNP P03485
D	455	HIS	-	expression tag	UNP P03485
E	24	VAL	GLN	conflict	UNP P29715
E	118	ALA	LYS	conflict	UNP P29715
E	278	ALA	-	linker	UNP P29715
E	279	LEU	-	linker	UNP P29715
E	280	GLU	-	linker	UNP P29715
E	281	ALA	-	linker	UNP P29715
E	282	GLN	-	linker	UNP P29715
E	283	LYS	-	linker	UNP P29715
E	284	GLN	-	linker	UNP P29715
E	285	LYS	-	linker	UNP P29715
E	448	LEU	-	expression tag	UNP P03485
E	449	GLU	-	expression tag	UNP P03485
E	450	HIS	-	expression tag	UNP P03485
E	451	HIS	-	expression tag	UNP P03485
E	452	HIS	-	expression tag	UNP P03485
E	453	HIS	-	expression tag	UNP P03485

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Chain	Residue	Modelled	Actual	Comment	Reference
E	454	HIS	-	expression tag	UNP P03485
E	455	HIS	-	expression tag	UNP P03485
F	24	VAL	GLN	conflict	UNP P29715
F	118	ALA	LYS	conflict	UNP P29715
F	278	ALA	-	linker	UNP P29715
F	279	LEU	-	linker	UNP P29715
F	280	GLU	-	linker	UNP P29715
F	281	ALA	-	linker	UNP P29715
F	282	GLN	-	linker	UNP P29715
F	283	LYS	-	linker	UNP P29715
F	284	GLN	-	linker	UNP P29715
F	285	LYS	-	linker	UNP P29715
F	448	LEU	-	expression tag	UNP P03485
F	449	GLU	-	expression tag	UNP P03485
F	450	HIS	-	expression tag	UNP P03485
F	451	HIS	-	expression tag	UNP P03485
F	452	HIS	-	expression tag	UNP P03485
F	453	HIS	-	expression tag	UNP P03485
F	454	HIS	-	expression tag	UNP P03485
F	455	HIS	-	expression tag	UNP P03485
G	24	VAL	GLN	conflict	UNP P29715
G	118	ALA	LYS	conflict	UNP P29715
G	278	ALA	-	linker	UNP P29715
G	279	LEU	-	linker	UNP P29715
G	280	GLU	-	linker	UNP P29715
G	281	ALA	-	linker	UNP P29715
G	282	GLN	-	linker	UNP P29715
G	283	LYS	-	linker	UNP P29715
G	284	GLN	-	linker	UNP P29715
G	285	LYS	-	linker	UNP P29715
G	448	LEU	-	expression tag	UNP P03485
G	449	GLU	-	expression tag	UNP P03485
G	450	HIS	-	expression tag	UNP P03485
G	451	HIS	-	expression tag	UNP P03485
G	452	HIS	-	expression tag	UNP P03485
G	453	HIS	-	expression tag	UNP P03485
G	454	HIS	-	expression tag	UNP P03485
G	455	HIS	-	expression tag	UNP P03485
H	24	VAL	GLN	conflict	UNP P29715
H	118	ALA	LYS	conflict	UNP P29715
H	278	ALA	-	linker	UNP P29715
H	279	LEU	-	linker	UNP P29715

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Chain	Residue	Modelled	Actual	Comment	Reference
H	280	GLU	-	linker	UNP P29715
H	281	ALA	-	linker	UNP P29715
H	282	GLN	-	linker	UNP P29715
H	283	LYS	-	linker	UNP P29715
H	284	GLN	-	linker	UNP P29715
H	285	LYS	-	linker	UNP P29715
H	448	LEU	-	expression tag	UNP P03485
H	449	GLU	-	expression tag	UNP P03485
H	450	HIS	-	expression tag	UNP P03485
H	451	HIS	-	expression tag	UNP P03485
H	452	HIS	-	expression tag	UNP P03485
H	453	HIS	-	expression tag	UNP P03485
H	454	HIS	-	expression tag	UNP P03485
H	455	HIS	-	expression tag	UNP P03485
I	24	VAL	GLN	conflict	UNP P29715
I	118	ALA	LYS	conflict	UNP P29715
I	278	ALA	-	linker	UNP P29715
I	279	LEU	-	linker	UNP P29715
I	280	GLU	-	linker	UNP P29715
I	281	ALA	-	linker	UNP P29715
I	282	GLN	-	linker	UNP P29715
I	283	LYS	-	linker	UNP P29715
I	284	GLN	-	linker	UNP P29715
I	285	LYS	-	linker	UNP P29715
I	448	LEU	-	expression tag	UNP P03485
I	449	GLU	-	expression tag	UNP P03485
I	450	HIS	-	expression tag	UNP P03485
I	451	HIS	-	expression tag	UNP P03485
I	452	HIS	-	expression tag	UNP P03485
I	453	HIS	-	expression tag	UNP P03485
I	454	HIS	-	expression tag	UNP P03485
I	455	HIS	-	expression tag	UNP P03485
J	24	VAL	GLN	conflict	UNP P29715
J	118	ALA	LYS	conflict	UNP P29715
J	278	ALA	-	linker	UNP P29715
J	279	LEU	-	linker	UNP P29715
J	280	GLU	-	linker	UNP P29715
J	281	ALA	-	linker	UNP P29715
J	282	GLN	-	linker	UNP P29715
J	283	LYS	-	linker	UNP P29715
J	284	GLN	-	linker	UNP P29715
J	285	LYS	-	linker	UNP P29715

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Chain	Residue	Modelled	Actual	Comment	Reference
J	448	LEU	-	expression tag	UNP P03485
J	449	GLU	-	expression tag	UNP P03485
J	450	HIS	-	expression tag	UNP P03485
J	451	HIS	-	expression tag	UNP P03485
J	452	HIS	-	expression tag	UNP P03485
J	453	HIS	-	expression tag	UNP P03485
J	454	HIS	-	expression tag	UNP P03485
J	455	HIS	-	expression tag	UNP P03485
K	24	VAL	GLN	conflict	UNP P29715
K	118	ALA	LYS	conflict	UNP P29715
K	278	ALA	-	linker	UNP P29715
K	279	LEU	-	linker	UNP P29715
K	280	GLU	-	linker	UNP P29715
K	281	ALA	-	linker	UNP P29715
K	282	GLN	-	linker	UNP P29715
K	283	LYS	-	linker	UNP P29715
K	284	GLN	-	linker	UNP P29715
K	285	LYS	-	linker	UNP P29715
K	448	LEU	-	expression tag	UNP P03485
K	449	GLU	-	expression tag	UNP P03485
K	450	HIS	-	expression tag	UNP P03485
K	451	HIS	-	expression tag	UNP P03485
K	452	HIS	-	expression tag	UNP P03485
K	453	HIS	-	expression tag	UNP P03485
K	454	HIS	-	expression tag	UNP P03485
K	455	HIS	-	expression tag	UNP P03485
L	24	VAL	GLN	conflict	UNP P29715
L	118	ALA	LYS	conflict	UNP P29715
L	278	ALA	-	linker	UNP P29715
L	279	LEU	-	linker	UNP P29715
L	280	GLU	-	linker	UNP P29715
L	281	ALA	-	linker	UNP P29715
L	282	GLN	-	linker	UNP P29715
L	283	LYS	-	linker	UNP P29715
L	284	GLN	-	linker	UNP P29715
L	285	LYS	-	linker	UNP P29715
L	448	LEU	-	expression tag	UNP P03485
L	449	GLU	-	expression tag	UNP P03485
L	450	HIS	-	expression tag	UNP P03485
L	451	HIS	-	expression tag	UNP P03485
L	452	HIS	-	expression tag	UNP P03485
L	453	HIS	-	expression tag	UNP P03485

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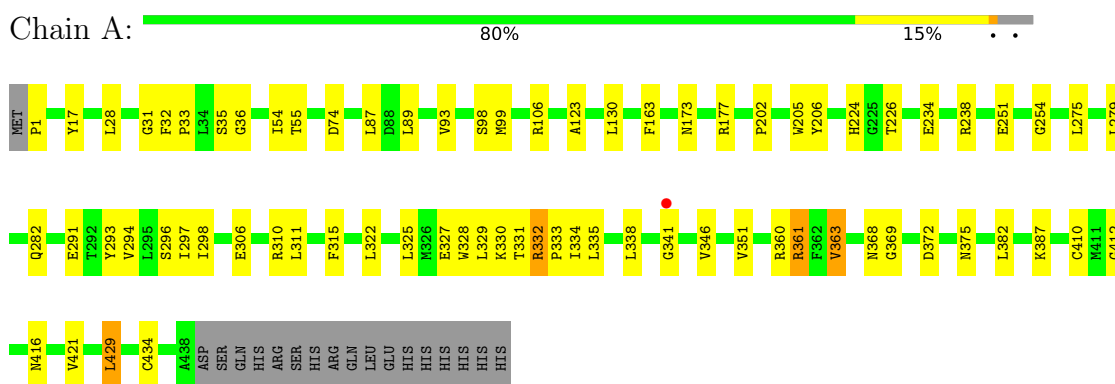
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Chain	Residue	Modelled	Actual	Comment	Reference
L	454	HIS	-	expression tag	UNP P03485
L	455	HIS	-	expression tag	UNP P03485

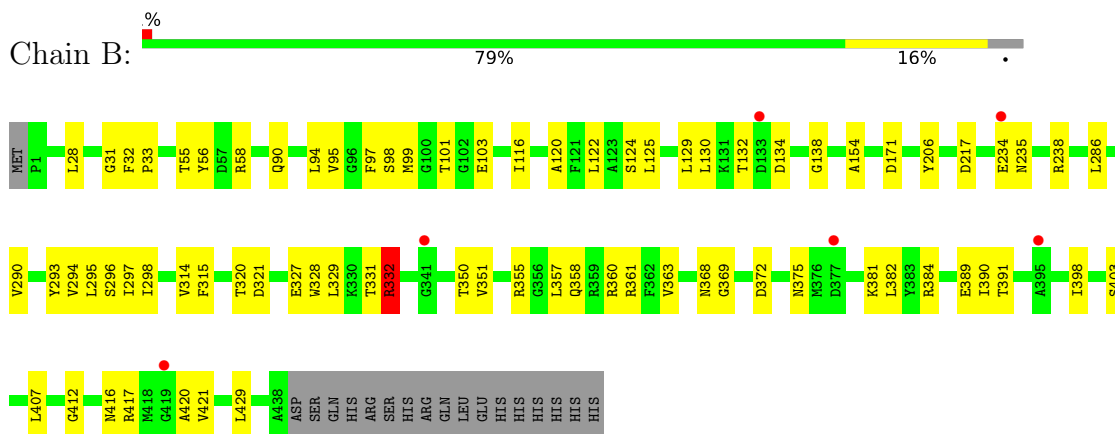
3 Residue-property plots

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.

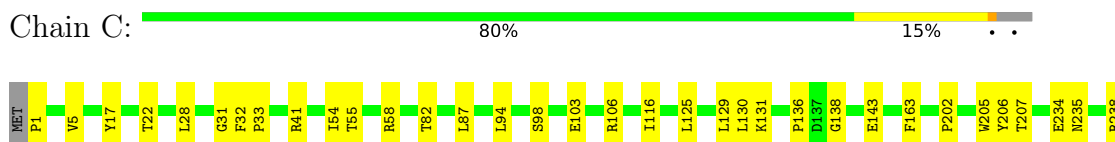
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

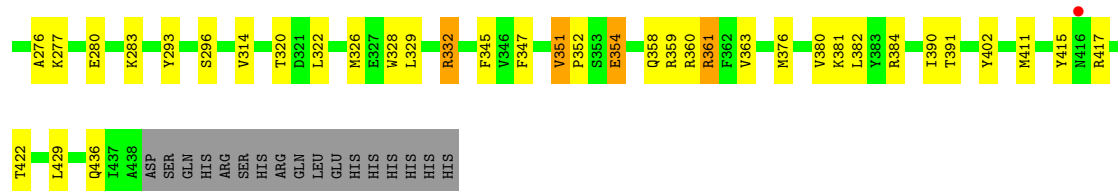


- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1



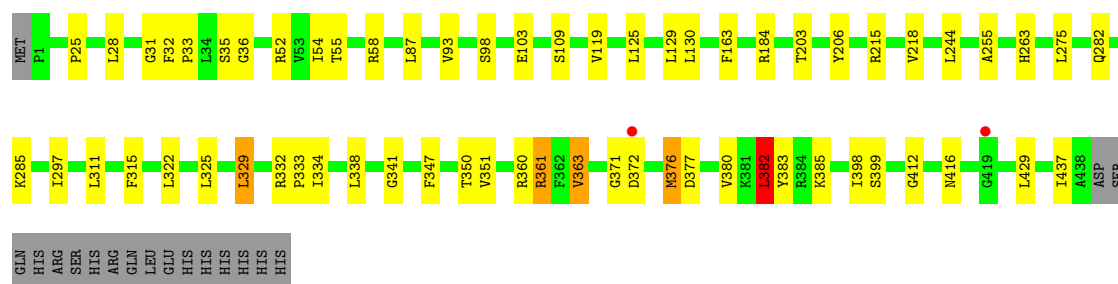
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1





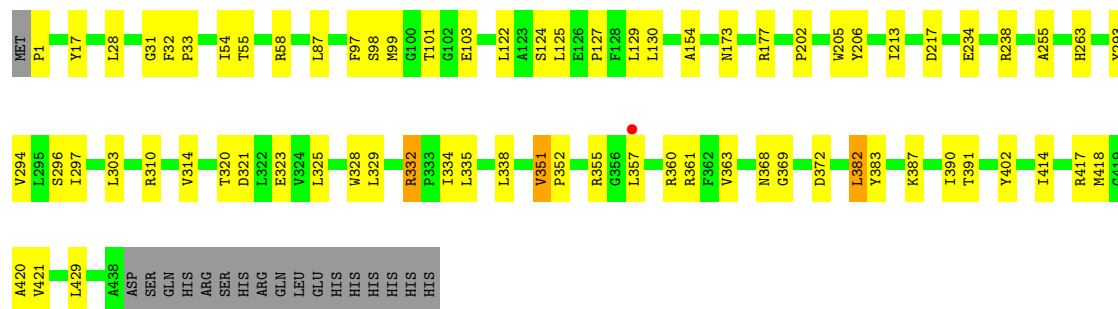
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain D: 82% 13% ..



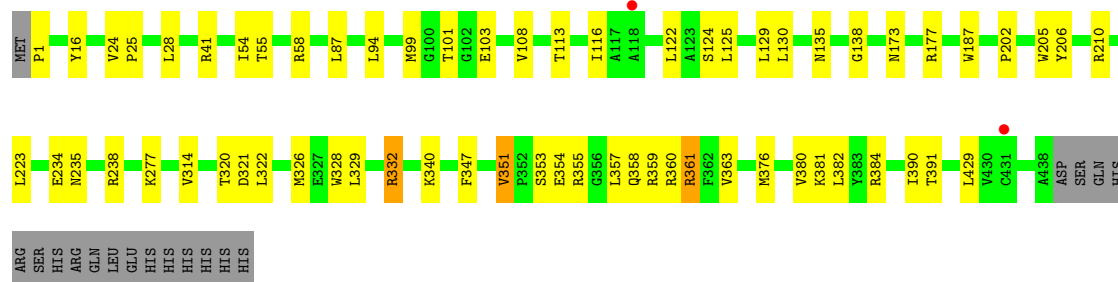
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain E: 80% 15% ..

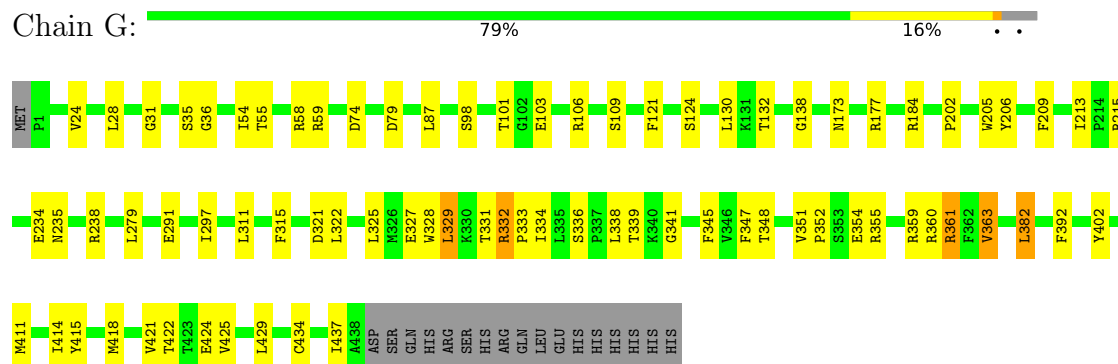


- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

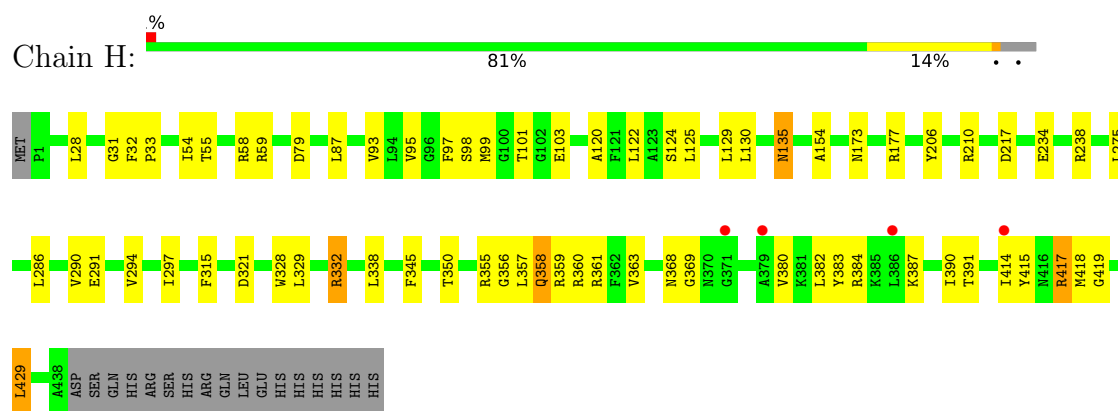
Chain F: 82% 13% ..



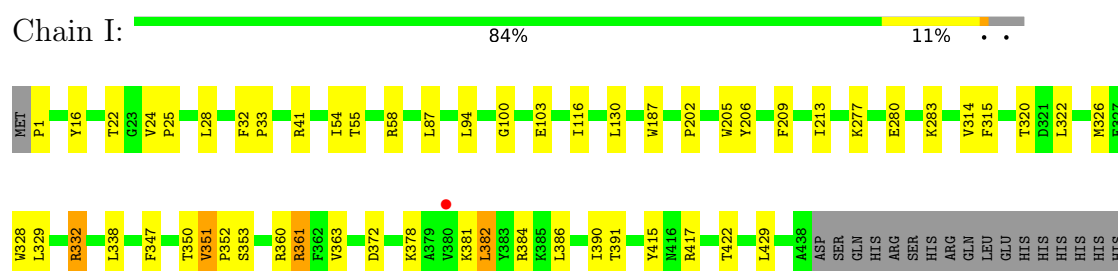
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1



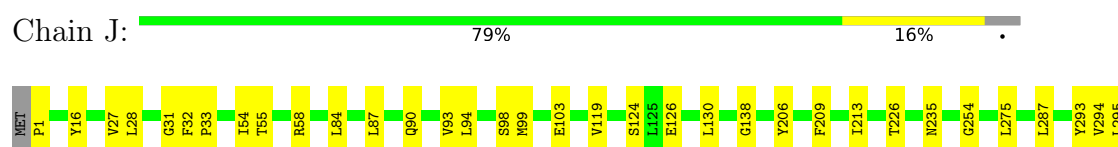
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

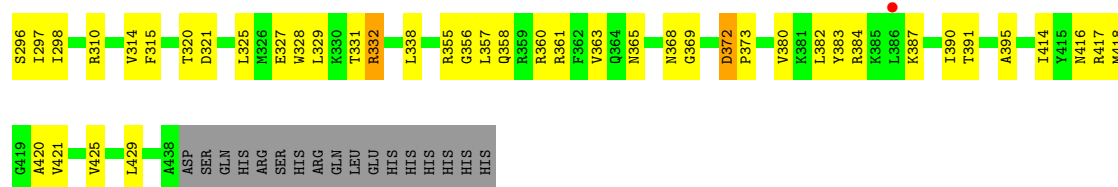


- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1



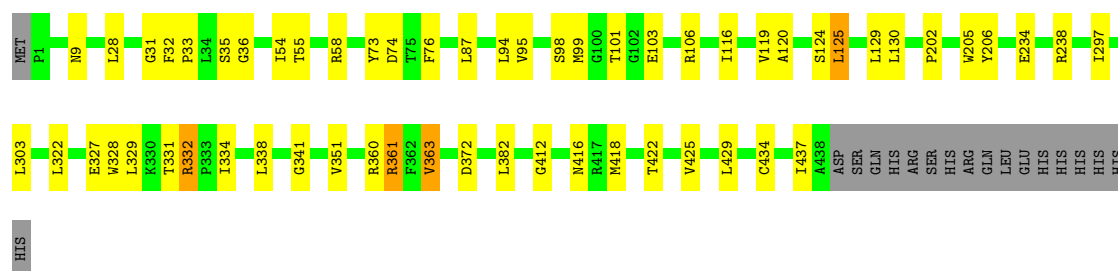
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1





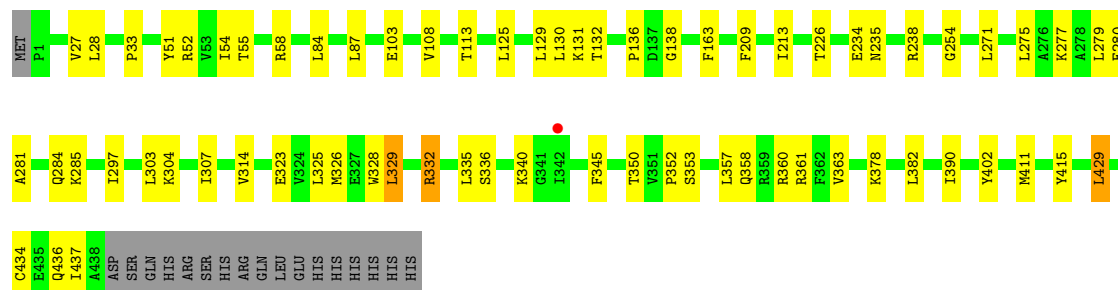
- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain K: 83% 12% . .



- Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain L: 81% 14% . .



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	122.70Å 187.41Å 283.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 3.92 19.89 – 3.92	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.89-3.92) 98.3 (19.89-3.92)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.99 (at 3.94Å)	Xtriage
Refinement program	PHENIX 1.7.3 _928	Depositor
R, R_{free}	0.282 , 0.294 0.277 , 0.287	Depositor DCC
R_{free} test set	2924 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	121.6	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 5.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	40596	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.41% 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	0.30	0/3460	0.77	0/4709
1	B	0.29	0/3460	0.78	5/4709 (0.1%)
1	C	0.29	0/3460	0.75	3/4709 (0.1%)
1	D	0.30	0/3460	0.82	5/4709 (0.1%)
1	E	0.29	0/3460	0.77	5/4709 (0.1%)
1	F	0.29	0/3460	0.77	2/4709 (0.0%)
1	G	0.29	0/3460	0.76	1/4709 (0.0%)
1	H	0.29	0/3460	0.76	5/4709 (0.1%)
1	I	0.29	0/3460	0.74	4/4709 (0.1%)
1	J	0.29	0/3460	0.77	2/4709 (0.0%)
1	K	0.28	0/3460	0.76	5/4709 (0.1%)
1	L	0.34	0/3460	0.86	8/4709 (0.2%)
All	All	0.30	0/41520	0.78	45/56508 (0.1%)

There are no bond length outliers.

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	323	GLU	N-CA-C	8.35	120.38	111.28
1	L	358	GLN	N-CA-C	8.19	120.35	110.19
1	F	351	VAL	CA-C-N	7.92	127.56	119.56
1	F	351	VAL	C-N-CA	7.92	127.56	119.56
1	C	351	VAL	CA-C-N	7.30	126.93	119.56

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	3383	0	3322	44	0
1	B	3383	0	3322	39	0
1	C	3383	0	3322	40	0
1	D	3383	0	3322	34	0
1	E	3383	0	3322	39	0
1	F	3383	0	3322	36	0
1	G	3383	0	3322	41	0
1	H	3383	0	3322	41	0
1	I	3383	0	3322	32	0
1	J	3383	0	3322	43	0
1	K	3383	0	3322	27	0
1	L	3383	0	3322	38	0
All	All	40596	0	39864	439	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 5.

The worst 5 of 439 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:L:303:LEU:HD22	1:L:328:TRP:CH2	2.16	0.80
1:A:291:GLU:HB2	1:A:315:PHE:HE2	1.49	0.77
1:F:130:LEU:HB2	1:F:206:TYR:HB2	1.70	0.73
1:A:322:LEU:HD11	1:A:351:VAL:HG21	1.71	0.70
1:G:74:ASP:OD1	1:G:106:ARG:NH1	2.23	0.70

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	436/456 (96%)	411 (94%)	25 (6%)	0	100	100
1	B	436/456 (96%)	410 (94%)	26 (6%)	0	100	100
1	C	436/456 (96%)	410 (94%)	26 (6%)	0	100	100
1	D	436/456 (96%)	410 (94%)	26 (6%)	0	100	100
1	E	436/456 (96%)	412 (94%)	24 (6%)	0	100	100
1	F	436/456 (96%)	411 (94%)	25 (6%)	0	100	100
1	G	436/456 (96%)	410 (94%)	26 (6%)	0	100	100
1	H	436/456 (96%)	411 (94%)	25 (6%)	0	100	100
1	I	436/456 (96%)	411 (94%)	25 (6%)	0	100	100
1	J	436/456 (96%)	410 (94%)	26 (6%)	0	100	100
1	K	436/456 (96%)	410 (94%)	26 (6%)	0	100	100
1	L	436/456 (96%)	412 (94%)	24 (6%)	0	100	100
All	All	5232/5472 (96%)	4928 (94%)	304 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	B	352/370 (95%)	346 (98%)	6 (2%)	53	68
1	C	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	D	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	E	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	F	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	G	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	H	352/370 (95%)	345 (98%)	7 (2%)	48	65
1	I	352/370 (95%)	344 (98%)	8 (2%)	44	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	J	352/370 (95%)	345 (98%)	7 (2%)	48 65
1	K	352/370 (95%)	345 (98%)	7 (2%)	48 65
1	L	352/370 (95%)	346 (98%)	6 (2%)	53 68
All	All	4224/4440 (95%)	4141 (98%)	83 (2%)	48 65

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	332	ARG
1	K	332	ARG
1	I	361	ARG
1	J	338	LEU
1	K	382	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	135	ASN
1	K	63	GLN
1	H	165	ASN
1	J	135	ASN
1	L	63	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no 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	438/456 (96%)	-0.07	1 (0%) 91 81	24, 43, 76, 127	0
1	B	438/456 (96%)	-0.12	6 (1%) 73 53	25, 48, 96, 136	0
1	C	438/456 (96%)	-0.26	1 (0%) 91 81	29, 53, 98, 143	0
1	D	438/456 (96%)	-0.22	2 (0%) 87 72	24, 43, 76, 127	0
1	E	438/456 (96%)	-0.35	1 (0%) 91 81	25, 48, 96, 136	0
1	F	438/456 (96%)	-0.18	2 (0%) 87 72	29, 53, 98, 143	0
1	G	438/456 (96%)	-0.35	0 100 100	24, 43, 76, 127	0
1	H	438/456 (96%)	-0.12	4 (0%) 81 62	25, 48, 96, 136	0
1	I	438/456 (96%)	-0.06	1 (0%) 91 81	29, 53, 98, 143	0
1	J	438/456 (96%)	-0.27	1 (0%) 91 81	25, 48, 96, 136	0
1	K	438/456 (96%)	-0.44	0 100 100	24, 43, 76, 127	0
1	L	438/456 (96%)	-0.20	1 (0%) 91 81	29, 53, 98, 143	0
All	All	5256/5472 (96%)	-0.22	20 (0%) 88 75	24, 47, 95, 143	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	341	GLY	3.7
1	A	341	GLY	3.7
1	D	372	ASP	3.3
1	H	386	LEU	3.2
1	H	379	ALA	3.1

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 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.