wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 03:45 PM GMT

PDB ID	:	4D9J
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

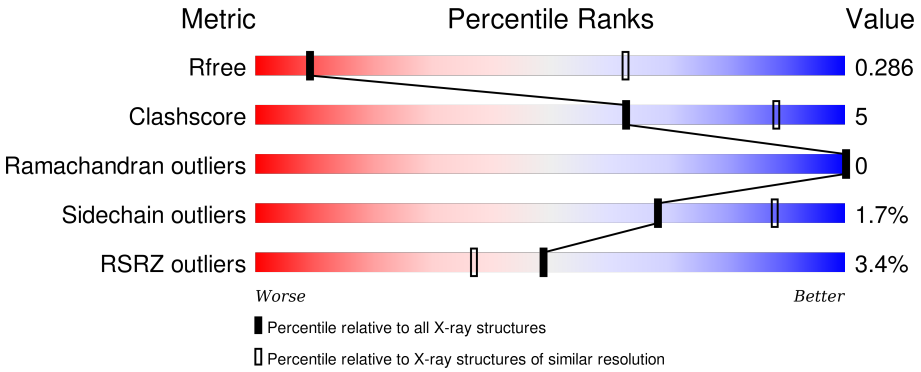
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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}	91344	1047 (4.32-3.52)
Clashscore	102246	1008 (4.26-3.58)
Ramachandran outliers	100387	1044 (4.30-3.54)
Sidechain outliers	100360	1035 (4.30-3.54)
RSRZ outliers	91569	1002 (4.30-3.54)

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 >=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 <=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	7% 80% 15%
1	B	456	4% 81% 15%
1	C	456	% 82% 13%
1	D	456	7% 83% 13%
1	E	456	3% 81% 15%

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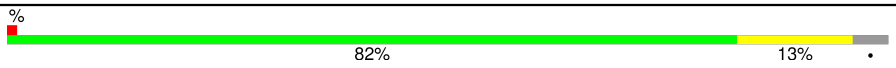
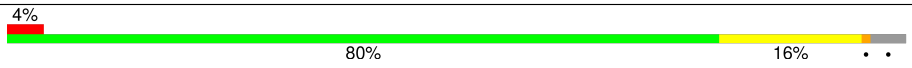
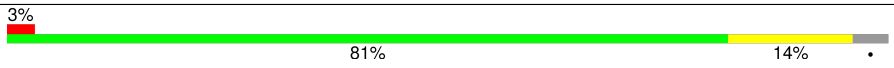
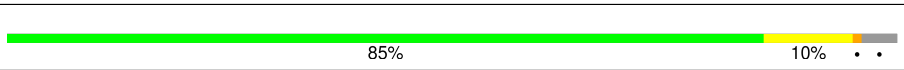
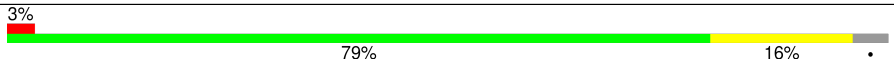
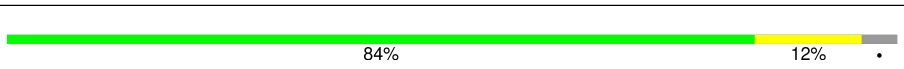
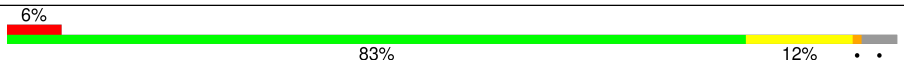
Mol	Chain	Length	Quality of chain
1	F	456	
1	G	456	
1	H	456	
1	I	456	
1	J	456	
1	K	456	
1	L	456	

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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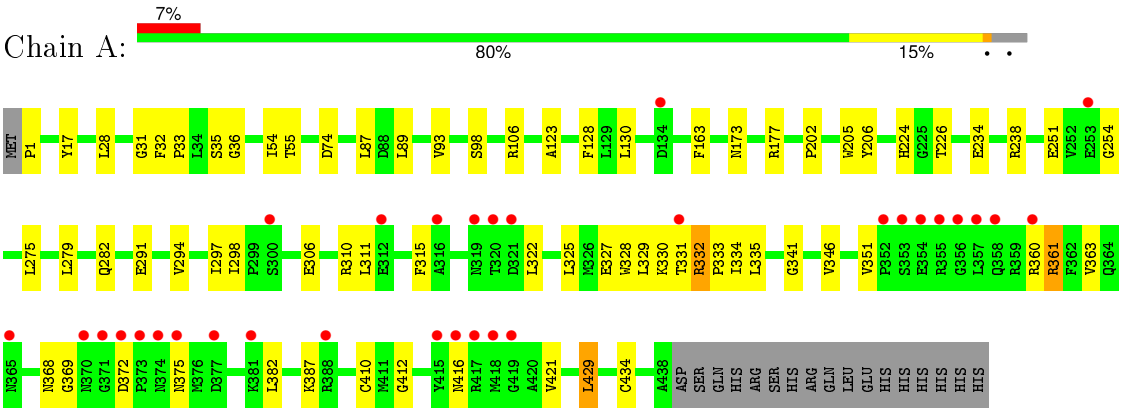
Chain	Residue	Modelled	Actual	Comment	Reference
L	454	HIS	-	EXPRESSION TAG	UNP P03485
L	455	HIS	-	EXPRESSION TAG	UNP P03485

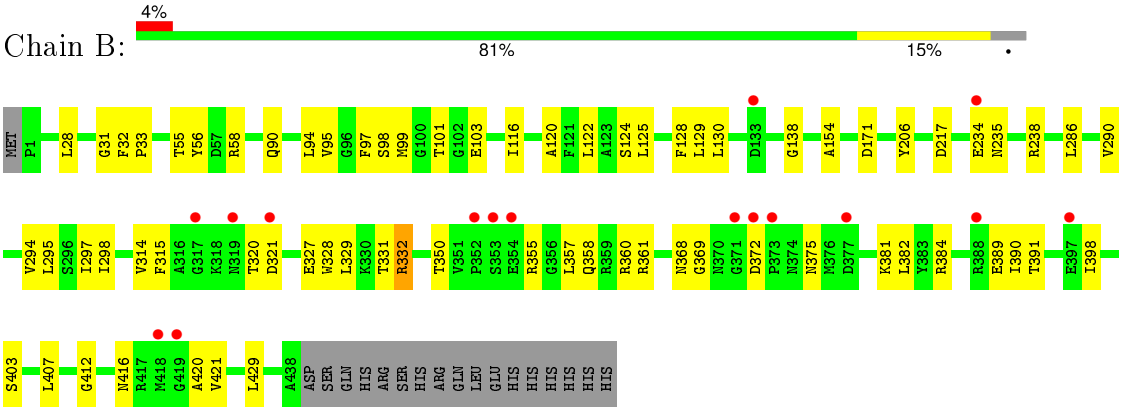
3 Residue-property plots (i)

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.

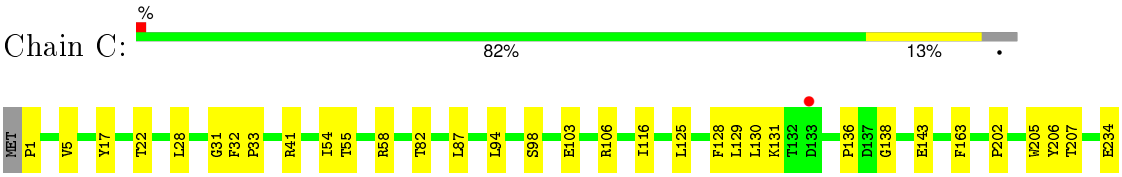
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

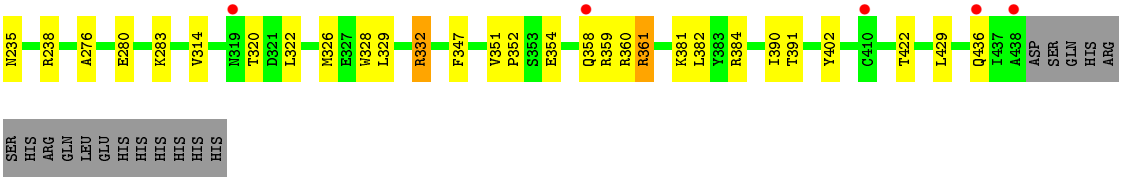


• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1



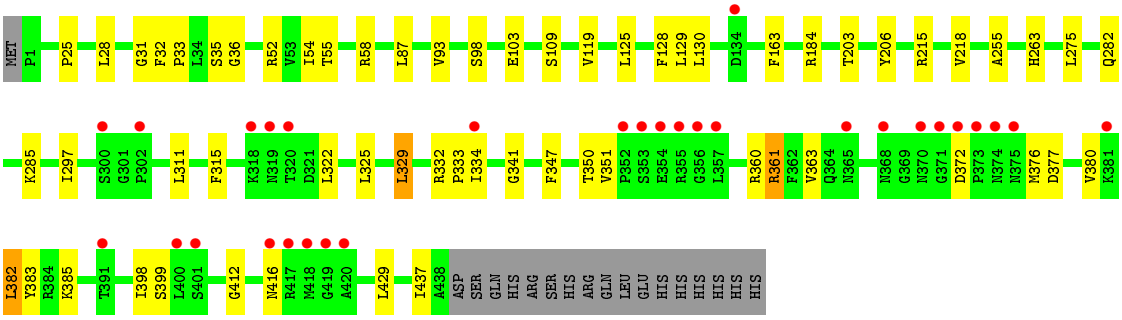
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1





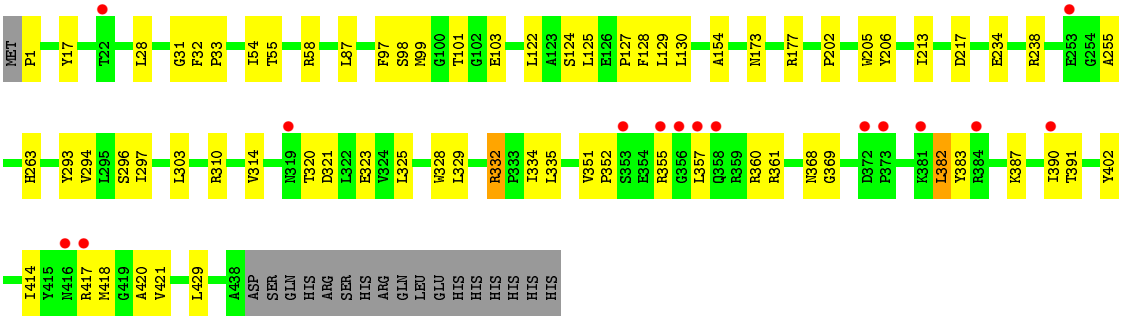
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain D:



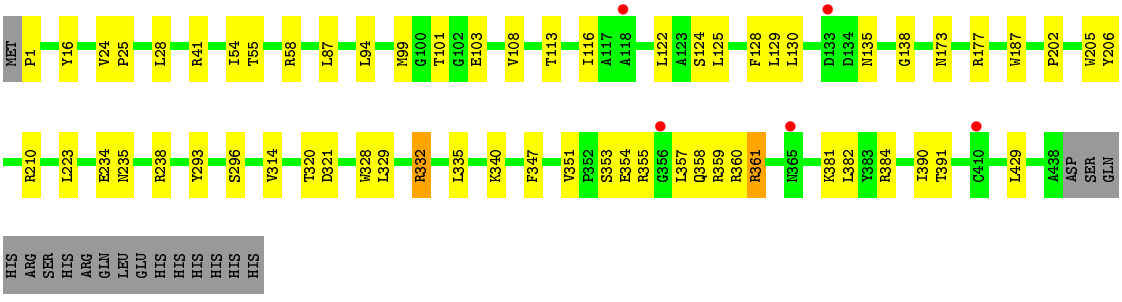
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain E:



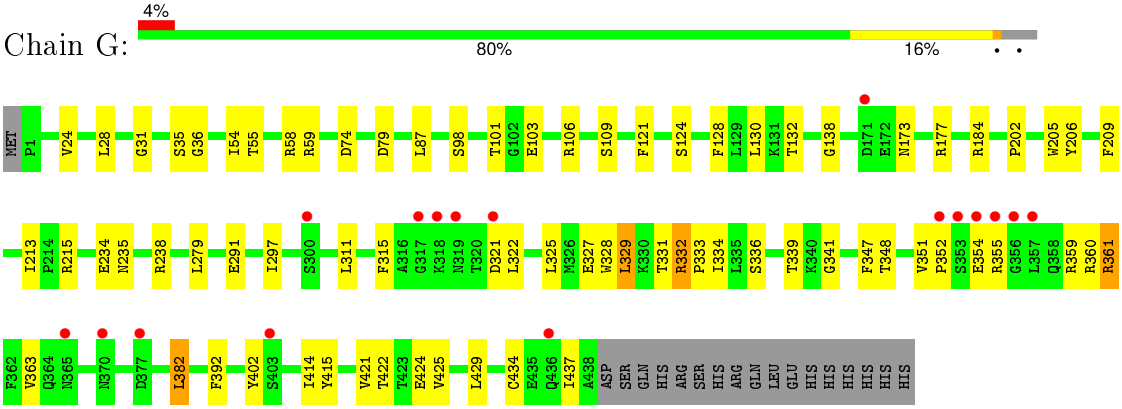
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain F:



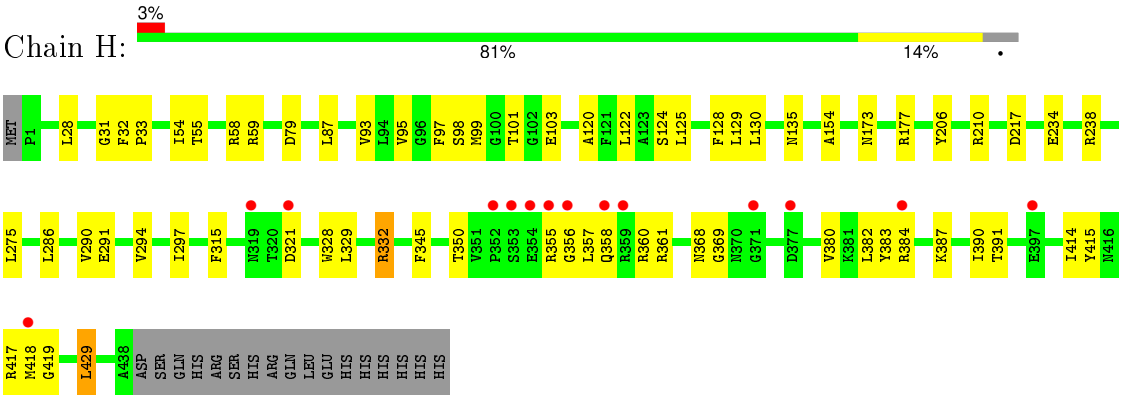
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain G:



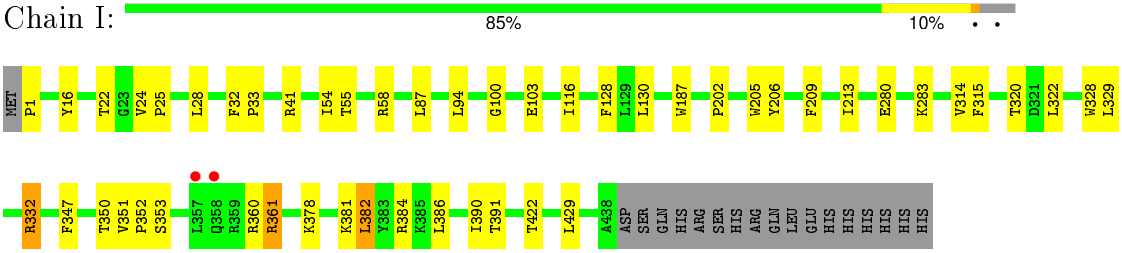
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain H:



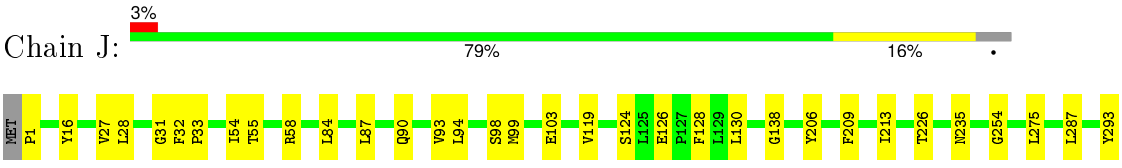
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

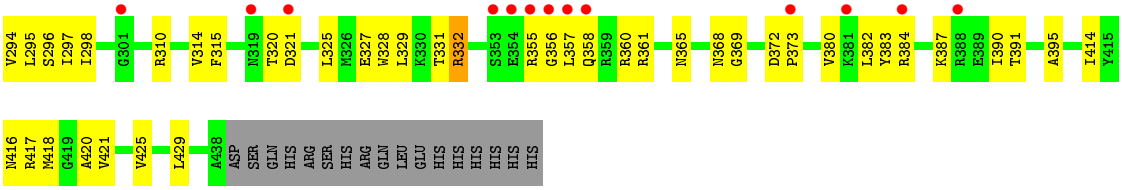
Chain I:



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

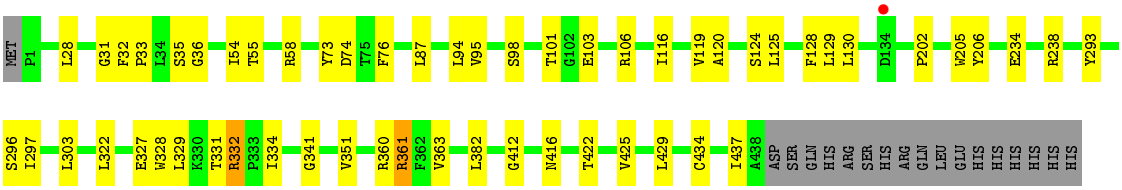
Chain J:





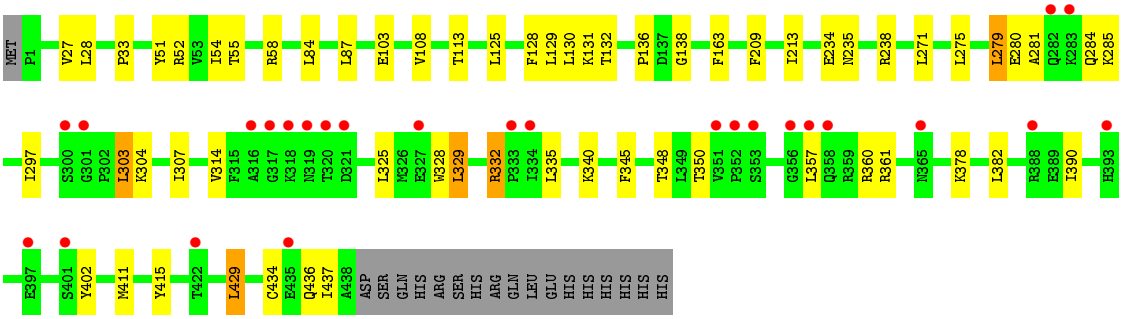
• Molecule 1: Designed 16nm tetrahedral protein cage containing Non-haem bromoperoxidase BPO-A2 and Matrix protein 1

Chain K:



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

Chain L:



4 Data and refinement statistics (i)

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) 99.1 (19.89-3.92)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.99 (at 3.94Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.282 , 0.294 0.272 , 0.286	Depositor DCC
R_{free} test set	2923 reflections (5.00%)	DCC
Wilson B-factor (Å^2)	121.6	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 1.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Outliers	0 of 58471 reflections	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.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.22	0/3460	0.43	0/4709
1	B	0.23	0/3460	0.43	0/4709
1	C	0.22	0/3460	0.41	0/4709
1	D	0.22	0/3460	0.45	0/4709
1	E	0.22	0/3460	0.42	0/4709
1	F	0.22	0/3460	0.41	0/4709
1	G	0.22	0/3460	0.42	0/4709
1	H	0.22	0/3460	0.42	0/4709
1	I	0.22	0/3460	0.40	0/4709
1	J	0.22	0/3460	0.42	0/4709
1	K	0.22	0/3460	0.40	0/4709
1	L	0.26	0/3460	0.49	2/4709 (0.0%)
All	All	0.22	0/41520	0.42	2/56508 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	L	303	LEU	CB-CG-CD2	5.24	119.92	111.00
1	L	279	LEU	CA-CB-CG	5.19	127.25	115.30

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	43	0
1	B	3383	0	3322	36	0
1	C	3383	0	3322	34	0
1	D	3383	0	3322	34	0
1	E	3383	0	3322	39	0
1	F	3383	0	3322	35	0
1	G	3383	0	3322	40	0
1	H	3383	0	3322	41	0
1	I	3383	0	3322	30	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	427	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 427 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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 (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	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	B	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	C	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	D	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	E	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	F	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	G	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	H	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	I	352/370 (95%)	346 (98%)	6 (2%)	68	88
1	J	352/370 (95%)	346 (98%)	6 (2%)	68	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	K	352/370 (95%)	346 (98%)	6 (2%)	68 88
1	L	352/370 (95%)	346 (98%)	6 (2%)	68 88
All	All	4224/4440 (95%)	4152 (98%)	72 (2%)	68 88

5 of 72 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	332	ARG
1	G	382	LEU
1	L	128	PHE
1	F	361	ARG
1	G	128	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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^{th} 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%)	0.21	32 (7%)	18	12	24, 43, 76, 127	0
1	B	438/456 (96%)	-0.04	16 (3%)	45	34	25, 48, 96, 136	0
1	C	438/456 (96%)	-0.16	6 (1%)	78	68	29, 53, 98, 143	0
1	D	438/456 (96%)	0.21	30 (6%)	20	13	24, 43, 76, 127	0
1	E	438/456 (96%)	-0.04	15 (3%)	49	37	25, 48, 96, 136	0
1	F	438/456 (96%)	-0.07	5 (1%)	82	75	29, 53, 98, 143	0
1	G	438/456 (96%)	-0.07	17 (3%)	43	32	24, 43, 76, 127	0
1	H	438/456 (96%)	-0.06	14 (3%)	51	38	25, 48, 96, 136	0
1	I	438/456 (96%)	-0.14	2 (0%)	91	88	29, 53, 98, 143	0
1	J	438/456 (96%)	-0.07	13 (2%)	54	40	25, 48, 96, 136	0
1	K	438/456 (96%)	-0.28	1 (0%)	95	94	24, 43, 76, 127	0
1	L	438/456 (96%)	0.11	26 (5%)	26	17	29, 53, 98, 143	0
All	All	5256/5472 (96%)	-0.03	177 (3%)	49	37	24, 47, 95, 143	0

The worst 5 of 177 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	353	SER	8.2
1	L	319	ASN	6.5
1	G	356	GLY	6.3
1	A	373	PRO	6.0
1	H	353	SER	5.9

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)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.