



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:21 AM UTC

PDB ID : 3VDX / pdb_00003vdx
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 : 2012-01-06
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

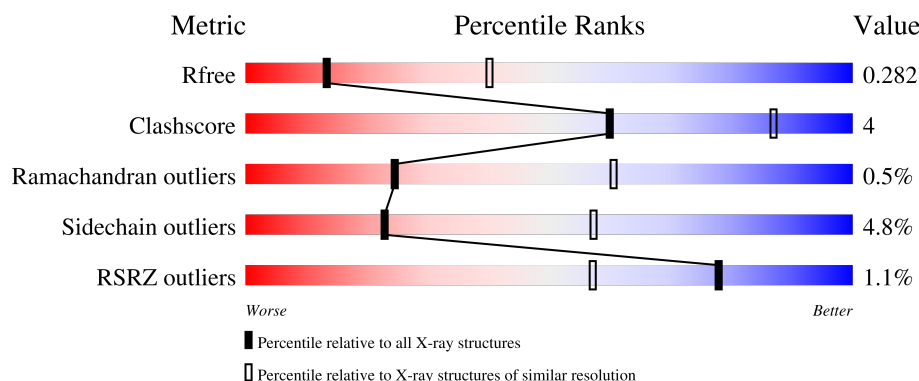
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	456	2% 80% 14% • •
1	B	456	• 82% 12% • •
1	C	456	• 85% 11% • •

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 10149 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			

There are 54 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
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

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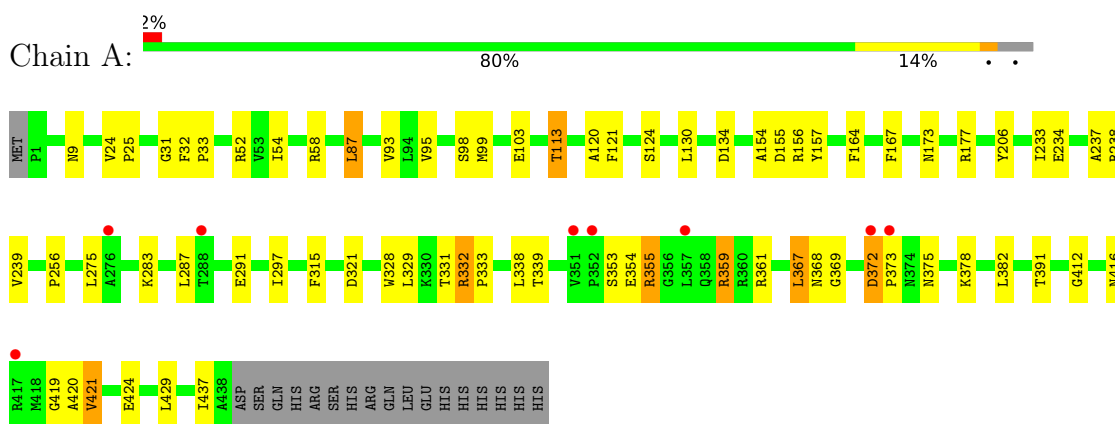
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Chain	Residue	Modelled	Actual	Comment	Reference
B	280	GLU	-	linker	UNP P29715
B	281	ALA	-	linker	UNP P29715
B	282	GLN	-	linker	UNP P29715
B	283	LYS	-	linker	UNP P29715
B	284	GLN	-	linker	UNP P29715
B	285	LYS	-	linker	UNP P29715
B	448	LEU	-	expression 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
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

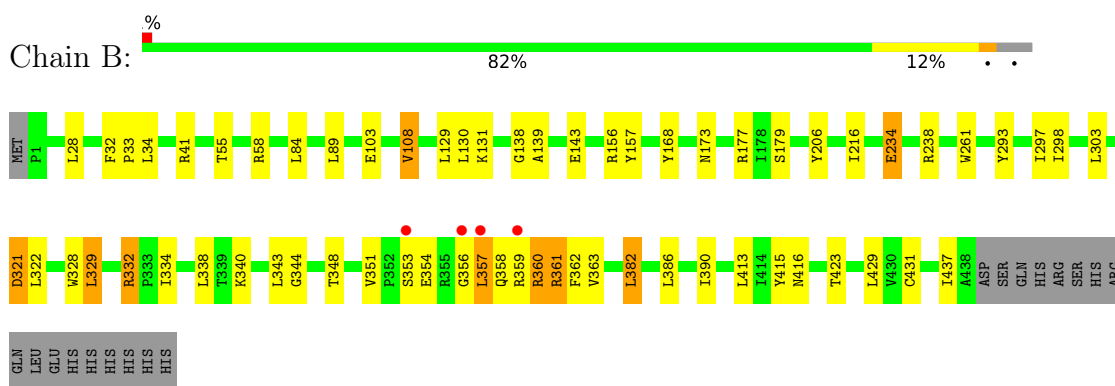
3 Residue-property plots

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





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	122.59Å 127.71Å 204.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.73 – 3.00 19.73 – 3.00	Depositor EDS
% Data completeness (in resolution range)	68.6 (19.73-3.00) 68.3 (19.73-3.00)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.98Å)	Xtriage
Refinement program	PHENIX 1.7.3_928	Depositor
R, R_{free}	0.229 , 0.281 0.225 , 0.282	Depositor DCC
R_{free} test set	1133 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	41.4	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 17.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.029 for k,h,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	10149	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 3.39% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.28	0/3460	0.70	1/4709 (0.0%)
1	B	0.28	0/3460	0.70	1/4709 (0.0%)
1	C	0.28	0/3460	0.69	0/4709
All	All	0.28	0/10380	0.70	2/14127 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	357	LEU	N-CA-C	5.43	115.56	108.07
1	A	9	ASN	CB-CA-C	-5.18	110.19	117.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3383	0	3322	35	0
1	B	3383	0	3322	33	0
1	C	3383	0	3322	20	0
All	All	10149	0	9966	86	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 4.

All (86) 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:B:354:GLU:HG3	1:B:356:GLY:H	1.57	0.68
1:B:328:TRP:O	1:B:332:ARG:NH1	2.29	0.65
1:B:322:LEU:HD13	1:B:351:VAL:HG11	1.79	0.65
1:C:130:LEU:HB2	1:C:206:TYR:HB2	1.80	0.63
1:A:297:ILE:HD11	1:A:437:ILE:HB	1.80	0.62
1:C:168:TYR:O	1:C:173:ASN:ND2	2.31	0.61
1:C:342:ILE:HG12	1:C:411:MET:HE1	1.83	0.59
1:A:130:LEU:HB2	1:A:206:TYR:HB2	1.84	0.59
1:A:353:SER:O	1:A:355:ARG:NH2	2.30	0.59
1:C:332:ARG:HG2	1:C:335:LEU:HD12	1.84	0.58
1:A:354:GLU:OE1	1:A:359:ARG:NH2	2.37	0.58
1:A:173:ASN:HB3	1:A:177:ARG:HB2	1.86	0.57
1:A:328:TRP:O	1:A:332:ARG:NH1	2.37	0.56
1:B:344:GLY:O	1:B:348:THR:OG1	2.22	0.56
1:B:297:ILE:HD12	1:B:437:ILE:HD12	1.87	0.55
1:B:329:LEU:HD11	1:B:343:LEU:HD12	1.88	0.55
1:C:138:GLY:O	1:C:235:ASN:ND2	2.39	0.55
1:B:130:LEU:HB2	1:B:206:TYR:HB2	1.88	0.54
1:B:321:ASP:OD1	1:B:321:ASP:N	2.41	0.54
1:A:372:ASP:HB3	1:A:375:ASN:HB3	1.90	0.53
1:A:412:GLY:O	1:A:416:ASN:ND2	2.35	0.53
1:B:303:LEU:HD12	1:B:334:ILE:HD12	1.90	0.53
1:B:293:TYR:HD2	1:B:431:CYS:HB3	1.74	0.53
1:A:291:GLU:HB2	1:A:315:PHE:HE2	1.75	0.52
1:C:327:GLU:OE1	1:C:360:ARG:NH2	2.43	0.52
1:C:293:TYR:OH	1:C:396:LYS:NZ	2.36	0.51
1:B:359:ARG:NH2	1:B:415:TYR:O	2.44	0.51
1:A:121:PHE:HB3	1:A:124:SER:HB3	1.93	0.50
1:C:54:ILE:HD13	1:C:87:LEU:HD23	1.94	0.49
1:B:168:TYR:O	1:B:173:ASN:ND2	2.45	0.49
1:A:419:GLY:HA2	1:A:420:ALA:HB3	1.94	0.48
1:C:315:PHE:CE1	1:C:350:THR:HG21	2.48	0.48
1:A:233:ILE:HG13	1:A:237:ALA:HB3	1.96	0.47
1:A:367:LEU:HD23	1:A:412:GLY:HA2	1.95	0.47
1:A:372:ASP:CB	1:A:375:ASN:HB3	2.45	0.47
1:B:41:ARG:NH1	1:B:261:TRP:O	2.48	0.47
1:B:298:ILE:HD11	1:B:343:LEU:HD11	1.96	0.47
1:A:154:ALA:O	1:B:41:ARG:NH2	2.34	0.47
1:B:108:VAL:HG11	1:B:216:ILE:HG12	1.97	0.47
1:A:93:VAL:HG11	1:A:275:LEU:HD21	1.97	0.46
1:A:283:LYS:NZ	1:A:424:GLU:OE1	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:ILE:HG12	1:C:238:ARG:HG2	1.97	0.46
1:B:173:ASN:HB3	1:B:177:ARG:HB2	1.98	0.46
1:C:32:PHE:HA	1:C:33:PRO:HA	1.75	0.46
1:B:234:GLU:HA	1:B:238:ARG:HG3	1.97	0.46
1:A:32:PHE:HB2	1:A:99:MET:SD	2.56	0.46
1:C:364:GLN:NE2	1:C:416:ASN:OD1	2.42	0.45
1:A:58:ARG:NE	1:A:103:GLU:OE2	2.41	0.45
1:B:382:LEU:HD22	1:B:386:LEU:HG	1.98	0.45
1:C:173:ASN:HB3	1:C:177:ARG:HB2	1.99	0.45
1:B:354:GLU:C	1:B:356:GLY:H	2.24	0.45
1:A:368:ASN:OD1	1:A:368:ASN:N	2.49	0.45
1:B:156:ARG:NH2	1:B:157:TYR:OH	2.50	0.45
1:B:361:ARG:HD2	1:B:362:PHE:N	2.32	0.45
1:A:25:PRO:HA	1:A:52:ARG:HB3	1.99	0.44
1:A:95:VAL:HG22	1:A:120:ALA:HB3	1.99	0.44
1:A:32:PHE:HA	1:A:33:PRO:HA	1.76	0.44
1:B:351:VAL:HG22	1:B:353:SER:H	1.81	0.44
1:B:84:LEU:HD23	1:B:89:LEU:HD12	1.98	0.44
1:B:58:ARG:NE	1:B:103:GLU:OE2	2.45	0.44
1:B:332:ARG:HB3	1:B:340:LYS:NZ	2.33	0.43
1:A:155:ASP:OD2	1:B:179:SER:OG	2.34	0.43
1:B:129:LEU:O	1:B:139:ALA:N	2.43	0.43
1:C:28:LEU:HB2	1:C:55:THR:HG22	2.00	0.43
1:A:372:ASP:OD1	1:A:373:PRO:HD2	2.19	0.43
1:A:54:ILE:HD13	1:A:87:LEU:HD23	2.01	0.42
1:B:357:LEU:HD23	1:B:357:LEU:HA	1.87	0.42
1:C:166:ASP:HA	1:C:229:ARG:HD2	2.02	0.42
1:C:106:ARG:NE	1:C:212:ASP:OD2	2.52	0.42
1:C:321:ASP:HB2	1:C:355:ARG:NH2	2.34	0.42
1:B:131:LYS:NZ	1:B:138:GLY:O	2.43	0.42
1:B:32:PHE:HA	1:B:33:PRO:HA	1.75	0.42
1:A:420:ALA:HA	1:A:421:VAL:HA	1.70	0.42
1:B:28:LEU:HB2	1:B:55:THR:HG22	2.02	0.41
1:A:156:ARG:NH2	1:A:157:TYR:OH	2.53	0.41
1:A:164:PHE:HA	1:A:167:PHE:HB3	2.02	0.41
1:A:332:ARG:HG3	1:A:333:PRO:HD2	2.01	0.41
1:A:321:ASP:OD1	1:A:321:ASP:N	2.54	0.41
1:C:297:ILE:HD12	1:C:437:ILE:HB	2.02	0.41
1:A:31:GLY:HA3	1:A:98:SER:HB3	2.03	0.41
1:A:113:THR:O	1:A:113:THR:OG1	2.27	0.41
1:A:234:GLU:HA	1:A:238:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:VAL:HA	1:A:25:PRO:HD3	1.93	0.40
1:C:315:PHE:HE1	1:C:350:THR:HG21	1.84	0.40
1:C:234:GLU:HA	1:C:238:ARG:HG3	2.02	0.40
1:B:143:GLU:OE1	1:B:143:GLU:N	2.49	0.40

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%)	412 (94%)	22 (5%)	2 (0%)	24	60
1	B	436/456 (96%)	396 (91%)	37 (8%)	3 (1%)	18	53
1	C	436/456 (96%)	411 (94%)	23 (5%)	2 (0%)	24	60
All	All	1308/1368 (96%)	1219 (93%)	82 (6%)	7 (0%)	24	60

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	GLY
1	B	416	ASN
1	A	256	PRO
1	B	34	LEU
1	B	360	ARG
1	C	256	PRO
1	C	33	PRO

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%)	332 (94%)	20 (6%)	18	52
1	B	352/370 (95%)	337 (96%)	15 (4%)	26	60
1	C	352/370 (95%)	336 (96%)	16 (4%)	24	59
All	All	1056/1110 (95%)	1005 (95%)	51 (5%)	23	57

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	LEU
1	A	113	THR
1	A	134	ASP
1	A	239	VAL
1	A	287	LEU
1	A	329	LEU
1	A	331	THR
1	A	332	ARG
1	A	338	LEU
1	A	339	THR
1	A	355	ARG
1	A	359	ARG
1	A	361	ARG
1	A	367	LEU
1	A	372	ASP
1	A	378	LYS
1	A	382	LEU
1	A	391	THR
1	A	421	VAL
1	A	429	LEU
1	B	108	VAL
1	B	234	GLU
1	B	321	ASP
1	B	329	LEU
1	B	332	ARG
1	B	338	LEU
1	B	358	GLN
1	B	360	ARG
1	B	361	ARG
1	B	363	VAL

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Mol	Chain	Res	Type
1	B	382	LEU
1	B	390	ILE
1	B	413	LEU
1	B	423	THR
1	B	429	LEU
1	C	129	LEU
1	C	223	LEU
1	C	234	GLU
1	C	312	GLU
1	C	325	LEU
1	C	329	LEU
1	C	331	THR
1	C	332	ARG
1	C	334	ILE
1	C	338	LEU
1	C	354	GLU
1	C	361	ARG
1	C	363	VAL
1	C	382	LEU
1	C	388	ARG
1	C	429	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	ASN
1	B	142	GLN
1	B	364	GLN
1	B	436	GLN
1	C	135	ASN
1	C	185	ASN
1	C	263	HIS

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 [i](#)

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 [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	438/456 (96%)	-0.04	8 (1%) 67 44	25, 48, 96, 136	0
1	B	438/456 (96%)	0.06	4 (0%) 81 61	29, 53, 98, 143	0
1	C	438/456 (96%)	-0.19	3 (0%) 84 66	24, 43, 76, 127	0
All	All	1314/1368 (96%)	-0.05	15 (1%) 78 57	24, 47, 95, 143	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	357	LEU	4.1
1	A	352	PRO	3.5
1	A	357	LEU	3.5
1	B	353	SER	2.8
1	B	359	ARG	2.8
1	B	356	GLY	2.8
1	A	276	ALA	2.3
1	A	372	ASP	2.3
1	A	288	THR	2.3
1	A	373	PRO	2.3
1	C	356	GLY	2.2
1	A	417	ARG	2.2
1	C	368	ASN	2.1
1	A	351	VAL	2.0
1	C	334	ILE	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.