



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:54 PM UTC

PDB ID : 7DBW / pdb_00007dbw
Title : PnpA1, the oxygenase component of a two-component para-nitrophenol hydroxylase from *Rhodococcus imtechensis* RKJ300
Authors : Guo, Y.; Zheng, J.T.; Zhou, N.Y.
Deposited on : 2020-10-22
Resolution : 2.50 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

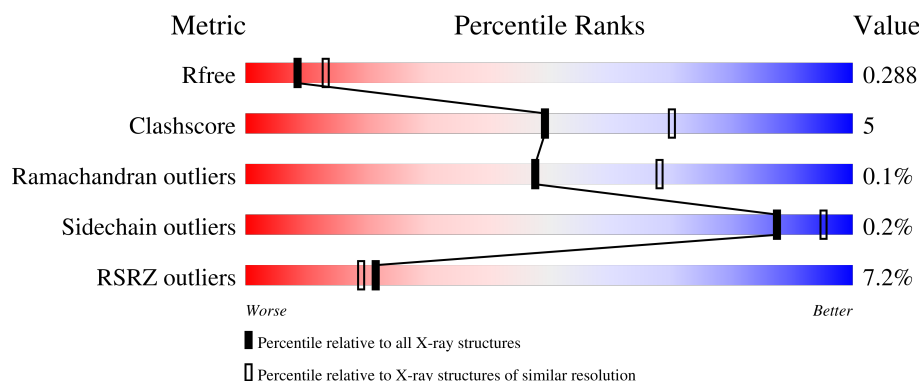
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	528	7% 80% 14% 6%
1	B	528	7% 82% 12% 6%
1	C	528	6% 86% 9% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11969 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 4-hydroxyphenylacetate 3-hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	498	Total	C	N	O	S	0	0	0
			3965	2512	698	741	14			
1	A	498	Total	C	N	O	S	0	0	0
			3965	2512	698	741	14			
1	B	498	Total	C	N	O	S	0	0	0
			3965	2512	698	741	14			

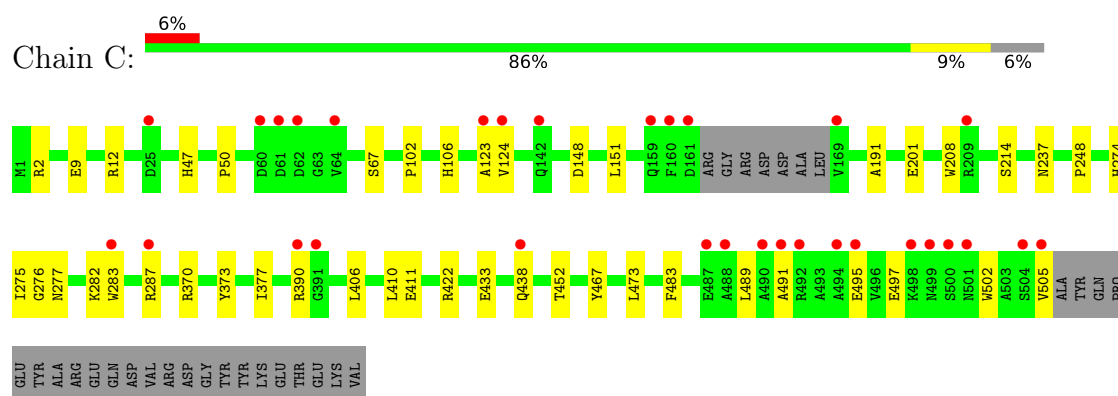
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	52	Total	O	0	0
			52	52		
2	A	12	Total	O	0	0
			12	12		
2	B	10	Total	O	0	0
			10	10		

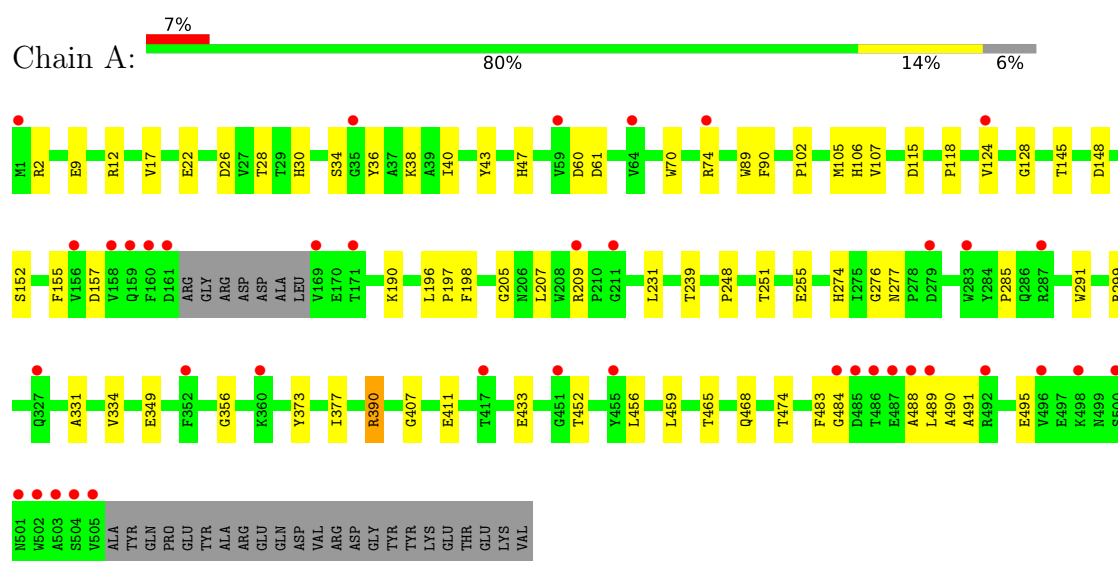
3 Residue-property plots [i](#)

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.

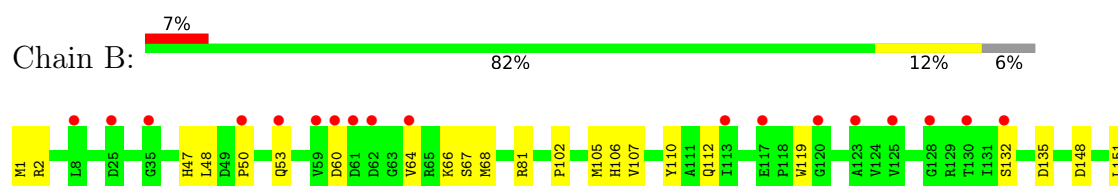
- Molecule 1: 4-hydroxyphenylacetate 3-hydroxylase

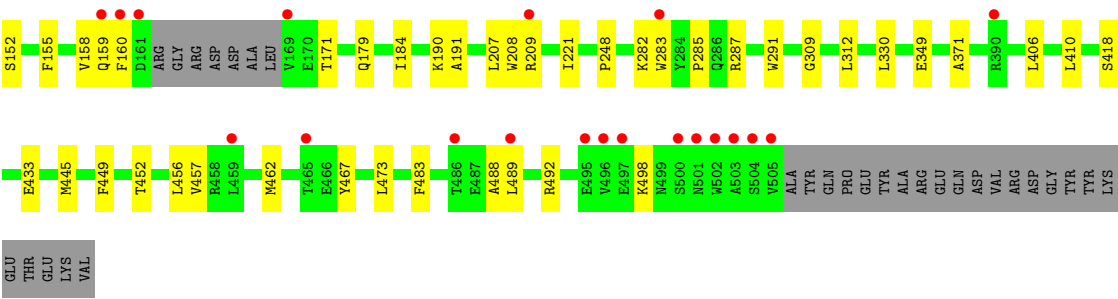


- Molecule 1: 4-hydroxyphenylacetate 3-hydroxylase



- Molecule 1: 4-hydroxyphenylacetate 3-hydroxylase





4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	150.01Å 150.01Å 321.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.78 – 2.50 22.78 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (22.78-2.50) 99.7 (22.78-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.242 , 0.291 0.241 , 0.288	Depositor DCC
R_{free} test set	3237 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 33.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11969	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.49 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.3305e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.37	0/4068	0.55	0/5540
1	B	0.37	0/4068	0.56	1/5540 (0.0%)
1	C	0.45	0/4068	0.65	1/5540 (0.0%)
All	All	0.40	0/12204	0.59	2/16620 (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	C	191	ALA	N-CA-C	10.71	123.03	111.36
1	B	191	ALA	N-CA-C	9.93	122.19	111.36

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	3965	0	3815	50	0
1	B	3965	0	3815	49	0
1	C	3965	0	3815	36	0
2	A	12	0	0	0	0
2	B	10	0	0	0	0
2	C	52	0	0	0	0
All	All	11969	0	11445	126	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.

All (126) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:GLU:HG3	1:B:349:GLU:HG3	1.51	0.92
1:C:406:LEU:O	1:C:410:LEU:HD22	1.72	0.90
1:A:331:ALA:HA	1:B:462:MET:HE3	1.53	0.89
1:B:159:GLN:HA	1:B:209:ARG:HH12	1.37	0.89
1:B:488:ALA:O	1:B:492:ARG:HG3	1.79	0.81
1:B:1:MET:HE2	1:B:48:LEU:HD23	1.62	0.80
1:C:406:LEU:O	1:C:410:LEU:CD2	2.30	0.80
1:B:406:LEU:O	1:B:410:LEU:CD2	2.33	0.76
1:B:60:ASP:OD2	1:B:66:LYS:HE3	1.86	0.76
1:B:467:TYR:HD1	1:B:473:LEU:HD22	1.54	0.73
1:A:17:VAL:HG22	1:A:231:LEU:HD12	1.73	0.70
1:C:124:VAL:HB	1:C:276:GLY:HA3	1.74	0.69
1:B:406:LEU:O	1:B:410:LEU:HD22	1.93	0.69
1:C:9:GLU:OE2	1:C:12:ARG:NH1	2.27	0.68
1:B:406:LEU:O	1:B:410:LEU:HD23	1.95	0.65
1:C:248:PRO:HD2	1:C:433:GLU:HG3	1.79	0.65
1:A:331:ALA:CA	1:B:462:MET:HE3	2.25	0.65
1:A:465:THR:HA	1:A:468:GLN:HG2	1.79	0.64
1:B:2:ARG:HG3	1:B:148:ASP:HB3	1.79	0.63
1:B:207:LEU:CD1	1:B:285:PRO:HB2	2.30	0.62
1:B:207:LEU:HD13	1:B:285:PRO:HB2	1.81	0.62
1:C:283:TRP:CD1	1:C:287:ARG:HD2	2.35	0.61
1:B:179:GLN:HG2	1:B:184:ILE:HG22	1.83	0.61
1:B:452:THR:HG23	1:B:456:LEU:HD23	1.81	0.61
1:C:502:TRP:HB2	1:C:505:VAL:HG12	1.83	0.60
1:A:248:PRO:HD2	1:A:433:GLU:HG3	1.83	0.59
1:C:467:TYR:CD1	1:C:473:LEU:HD22	2.38	0.59
1:A:124:VAL:HB	1:A:276:GLY:HA3	1.85	0.59
1:C:497:GLU:HG3	1:C:502:TRP:HZ3	1.68	0.58
1:B:159:GLN:HA	1:B:209:ARG:NH1	2.15	0.58
1:C:124:VAL:HB	1:C:276:GLY:CA	2.33	0.58
1:B:208:TRP:CG	1:B:282:LYS:HG2	2.40	0.57
1:B:47:HIS:CD2	1:B:67:SER:HB3	2.41	0.55
1:A:197:PRO:HG2	1:A:198:PHE:CE2	2.43	0.53
1:C:283:TRP:HE1	1:C:287:ARG:CZ	2.20	0.53
1:A:390:ARG:HG2	1:A:390:ARG:HH21	1.72	0.53
1:A:274:HIS:HE1	1:A:277:ASN:H	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:248:PRO:HD2	1:C:433:GLU:CG	2.38	0.53
1:C:467:TYR:HD1	1:C:473:LEU:HD22	1.73	0.53
1:C:50:PRO:HG3	1:A:61:ASP:CG	2.33	0.53
1:C:2:ARG:HG3	1:C:148:ASP:HB3	1.89	0.52
1:C:124:VAL:HB	1:C:276:GLY:C	2.34	0.52
1:A:2:ARG:HG3	1:A:148:ASP:HB3	1.90	0.52
1:B:132:SER:HB2	1:B:135:ASP:HB2	1.91	0.52
1:B:371:ALA:HB2	1:B:457:VAL:HG11	1.92	0.52
1:B:283:TRP:HD1	1:B:287:ARG:HH11	1.58	0.52
1:C:373:TYR:CE2	1:C:377:ILE:HD13	2.44	0.52
1:C:274:HIS:HE1	1:C:277:ASN:H	1.58	0.52
1:B:151:LEU:HD22	1:B:221:ILE:HD11	1.91	0.51
1:A:407:GLY:O	1:A:411:GLU:HG3	2.11	0.51
1:C:411:GLU:OE1	1:C:422:ARG:HD2	2.11	0.51
1:C:124:VAL:N	1:C:275:ILE:O	2.41	0.50
1:A:34:SER:O	1:A:38:LYS:HG2	2.10	0.50
1:A:26:ASP:OD1	1:A:28:THR:OG1	2.25	0.50
1:A:70:TRP:CD2	1:A:145:THR:HG22	2.46	0.50
1:B:248:PRO:HD2	1:B:433:GLU:HG3	1.94	0.50
1:A:207:LEU:HD13	1:A:285:PRO:HB2	1.92	0.50
1:B:107:VAL:HB	1:B:291:TRP:HB3	1.93	0.50
1:A:107:VAL:HB	1:A:291:TRP:HB3	1.94	0.49
1:A:274:HIS:CE1	1:A:277:ASN:H	2.31	0.49
1:C:370:ARG:NH1	1:C:452:THR:O	2.37	0.49
1:A:22:GLU:OE2	1:A:30:HIS:NE2	2.38	0.49
1:B:467:TYR:CD1	1:B:473:LEU:HD22	2.41	0.49
1:B:445:MET:HE3	1:B:449:PHE:HE2	1.78	0.49
1:A:331:ALA:HA	1:B:462:MET:CE	2.35	0.49
1:B:160:PHE:CD1	1:B:171:THR:HG22	2.48	0.49
1:C:47:HIS:CD2	1:C:67:SER:HB3	2.48	0.48
1:C:124:VAL:HG23	1:C:277:ASN:HB2	1.93	0.48
1:A:373:TYR:CE2	1:A:377:ILE:HD13	2.48	0.48
1:A:9:GLU:OE2	1:A:12:ARG:NH1	2.46	0.48
1:B:50:PRO:HA	1:B:53:GLN:HG3	1.96	0.48
1:A:155:PHE:HB3	1:A:207:LEU:CD2	2.44	0.47
1:B:107:VAL:HG12	1:B:110:TYR:CE2	2.49	0.47
1:A:483:PHE:CD2	1:A:489:LEU:HD11	2.49	0.47
1:A:452:THR:HG23	1:A:456:LEU:HD23	1.96	0.47
1:C:283:TRP:CD1	1:C:287:ARG:NH1	2.83	0.47
1:A:483:PHE:CD1	1:A:489:LEU:HD21	2.49	0.47
1:A:484:GLY:HA3	1:A:488:ALA:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1:MET:HE3	1:B:47:HIS:HB3	1.96	0.47
1:A:157:ASP:OD1	1:A:190:LYS:NZ	2.47	0.47
1:B:483:PHE:CD2	1:B:489:LEU:HD21	2.49	0.47
1:A:491:ALA:O	1:A:495:GLU:HG2	2.15	0.46
1:B:102:PRO:HB3	1:B:106:HIS:CE1	2.49	0.46
1:C:406:LEU:O	1:C:410:LEU:HD23	2.13	0.46
1:A:190:LYS:HD2	1:A:190:LYS:HA	1.65	0.46
1:A:102:PRO:HB3	1:A:106:HIS:CE1	2.50	0.46
1:A:105:MET:SD	1:A:152:SER:HB2	2.56	0.46
1:A:115:ASP:O	1:A:118:PRO:HD2	2.16	0.45
1:C:123:ALA:HA	1:C:274:HIS:CD2	2.52	0.45
1:C:237:ASN:OD1	1:C:438:GLN:NE2	2.50	0.45
1:C:102:PRO:HB3	1:C:106:HIS:CE1	2.52	0.44
1:A:74:ARG:NH2	1:A:356:GLY:O	2.43	0.44
1:A:196:LEU:HB3	1:A:231:LEU:HD13	1.99	0.44
1:A:209:ARG:HB2	1:A:209:ARG:NH1	2.33	0.44
1:A:490:ALA:HA	1:B:418:SER:O	2.17	0.44
1:B:112:GLN:HG2	1:B:119:TRP:CE2	2.53	0.44
1:C:422:ARG:NH2	1:A:128:GLY:HA3	2.33	0.44
1:B:158:VAL:O	1:B:209:ARG:NH2	2.50	0.44
1:C:151:LEU:HD12	1:C:201:GLU:HB2	1.99	0.44
1:C:214:SER:O	1:C:276:GLY:HA2	2.17	0.44
1:A:40:ILE:O	1:A:43:TYR:HB3	2.17	0.43
1:A:155:PHE:HA	1:A:205:GLY:O	2.18	0.43
1:B:68:MET:HE1	1:B:81:ARG:NH2	2.33	0.43
1:C:208:TRP:CE2	1:C:282:LYS:HE2	2.53	0.43
1:B:60:ASP:OD2	1:B:64:VAL:HB	2.19	0.43
1:A:155:PHE:HB3	1:A:207:LEU:HD22	2.01	0.43
1:B:105:MET:SD	1:B:152:SER:HB2	2.58	0.43
1:A:239:THR:O	1:A:251:THR:HG22	2.19	0.42
1:C:283:TRP:CD1	1:C:287:ARG:HH11	2.37	0.42
1:A:390:ARG:HG2	1:A:390:ARG:NH2	2.34	0.42
1:B:190:LYS:HA	1:B:190:LYS:HD2	1.79	0.42
1:C:497:GLU:HG3	1:C:502:TRP:CZ3	2.52	0.42
1:A:90:PHE:CZ	1:A:299:ARG:HB2	2.55	0.42
1:A:334:VAL:HG21	1:B:462:MET:HE1	2.02	0.42
1:B:160:PHE:CE1	1:B:171:THR:HG22	2.55	0.41
1:B:208:TRP:CB	1:B:282:LYS:HG2	2.50	0.41
1:B:498:LYS:HD3	1:B:498:LYS:HA	1.82	0.41
1:B:155:PHE:HB3	1:B:207:LEU:HD22	2.01	0.41
1:B:283:TRP:CD1	1:B:287:ARG:HH11	2.38	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:483:PHE:CD1	1:C:489:LEU:HD21	2.55	0.41
1:A:36:TYR:CZ	1:A:255:GLU:HG3	2.56	0.41
1:B:312:LEU:HD23	1:B:330:LEU:HD22	2.03	0.41
1:A:456:LEU:HD12	1:A:459:LEU:HD12	2.04	0.40
1:C:491:ALA:O	1:C:495:GLU:HG2	2.22	0.40
1:A:47:HIS:CE1	1:A:89:TRP:HZ2	2.40	0.40
1:A:474:THR:HG22	1:B:309:GLY:HA2	2.03	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	494/528 (94%)	487 (99%)	6 (1%)	1 (0%)	43	63
1	B	494/528 (94%)	481 (97%)	13 (3%)	0	100	100
1	C	494/528 (94%)	488 (99%)	6 (1%)	0	100	100
All	All	1482/1584 (94%)	1456 (98%)	25 (2%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	ASP

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	420/445 (94%)	419 (100%)	1 (0%)	87	95
1	B	420/445 (94%)	420 (100%)	0	100	100
1	C	420/445 (94%)	419 (100%)	1 (0%)	87	95
All	All	1260/1335 (94%)	1258 (100%)	2 (0%)	87	95

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	390	ARG
1	A	390	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	237	ASN
1	C	274	HIS
1	C	438	GLN
1	C	501	ASN
1	A	122	ASN
1	A	142	GLN
1	A	274	HIS
1	A	499	ASN
1	B	300	HIS
1	B	463	GLN
1	B	499	ASN

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

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, 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	498/528 (94%)	0.68	39 (7%)	19	17	31, 42, 69, 110	0
1	B	498/528 (94%)	0.60	38 (7%)	20	17	30, 43, 74, 104	0
1	C	498/528 (94%)	0.09	31 (6%)	26	23	16, 25, 53, 85	0
All	All	1494/1584 (94%)	0.46	108 (7%)	21	19	16, 39, 67, 110	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	124	VAL	9.8
1	B	283	TRP	8.7
1	A	283	TRP	8.3
1	A	505	VAL	7.4
1	C	283	TRP	7.3
1	A	169	VAL	6.3
1	B	503	ALA	6.3
1	B	505	VAL	6.3
1	C	161	ASP	5.6
1	C	62	ASP	5.3
1	A	161	ASP	5.1
1	C	495	GLU	5.0
1	A	487	GLU	5.0
1	C	499	ASN	4.5
1	C	159	GLN	4.5
1	A	159	GLN	4.5
1	C	487	GLU	4.4
1	B	169	VAL	4.4
1	C	494	ALA	4.1
1	A	501	ASN	4.0
1	A	64	VAL	4.0
1	C	498	LYS	3.9
1	B	132	SER	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	169	VAL	3.8
1	B	496	VAL	3.7
1	C	501	ASN	3.7
1	B	25	ASP	3.6
1	C	123	ALA	3.5
1	A	160	PHE	3.5
1	B	501	ASN	3.5
1	B	486	THR	3.5
1	B	504	SER	3.5
1	A	124	VAL	3.4
1	A	327	GLN	3.4
1	A	74	ARG	3.4
1	A	498	LYS	3.4
1	C	505	VAL	3.4
1	B	130	THR	3.3
1	A	492	ARG	3.3
1	C	25	ASP	3.2
1	C	61	ASP	3.2
1	C	491	ALA	3.2
1	A	488	ALA	3.2
1	A	500	SER	3.2
1	A	417	THR	3.2
1	C	209	ARG	3.1
1	B	59	VAL	3.1
1	B	64	VAL	3.1
1	B	161	ASP	3.0
1	B	120	GLY	3.0
1	C	488	ALA	3.0
1	B	489	LEU	2.9
1	A	502	TRP	2.9
1	B	160	PHE	2.9
1	A	35	GLY	2.9
1	A	209	ARG	2.8
1	C	142	GLN	2.8
1	A	486	THR	2.7
1	B	123	ALA	2.7
1	A	360	LYS	2.7
1	C	64	VAL	2.7
1	A	503	ALA	2.6
1	A	211	GLY	2.6
1	B	62	ASP	2.6
1	B	502	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	496	VAL	2.6
1	C	492	ARG	2.5
1	C	390	ARG	2.5
1	A	489	LEU	2.5
1	C	60	ASP	2.5
1	A	156	VAL	2.5
1	C	490	ALA	2.5
1	C	438	GLN	2.5
1	A	352	PHE	2.5
1	A	504	SER	2.4
1	B	465	THR	2.4
1	B	128	GLY	2.4
1	C	160	PHE	2.4
1	A	279	ASP	2.4
1	B	390	ARG	2.3
1	B	8	LEU	2.3
1	B	117	GLU	2.3
1	B	497	GLU	2.3
1	B	500	SER	2.3
1	B	61	ASP	2.3
1	A	1	MET	2.3
1	B	209	ARG	2.3
1	C	504	SER	2.3
1	A	484	GLY	2.2
1	A	455	TYR	2.2
1	B	53	GLN	2.2
1	B	159	GLN	2.2
1	A	59	VAL	2.2
1	B	125	VAL	2.2
1	C	287	ARG	2.2
1	C	391	GLY	2.1
1	B	35	GLY	2.1
1	B	113	ILE	2.1
1	B	50	PRO	2.1
1	B	459	LEU	2.1
1	A	171	THR	2.1
1	A	451	GLY	2.1
1	B	60	ASP	2.1
1	C	500	SER	2.1
1	A	287	ARG	2.0
1	B	495	GLU	2.0
1	A	485	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	158	VAL	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.