



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:45 AM UTC

PDB ID : 1AZW / pdb_00001azw
Title : PROLINE IMINOPEPTIDASE FROM XANTHOMONAS CAMPESTRIS
PV. CITRI
Authors : Medrano, F.J.; Alonso, J.; Garcia, J.L.; Romero, A.; Bode, W.; Gomis-Ruth,
F.X.
Deposited on : 1997-11-22
Resolution : 2.70 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

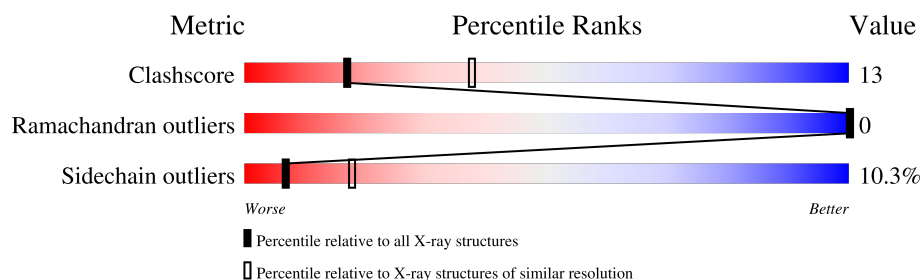
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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))
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	313	 66% 28% . .
1	B	313	 69% 25% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5227 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 PROLINE IMINOPEPTIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	29	0	0
			2514	1599	452	456	7			
1	B	313	Total	C	N	O	S	26	0	0
			2514	1599	452	456	7			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	121	GLN	ALA	conflict	UNP P52279
A	122	THR	ASP	conflict	UNP P52279
A	123	HIS	PRO	conflict	UNP P52279
A	124	PRO	SER	conflict	UNP P52279
A	125	GLN	ALA	conflict	UNP P52279
A	126	GLN	ALA	conflict	UNP P52279
A	127	VAL	GLY	conflict	UNP P52279
A	128	THR	HIS	conflict	UNP P52279
A	129	GLU	GLN	conflict	UNP P52279
B	121	GLN	ALA	conflict	UNP P52279
B	122	THR	ASP	conflict	UNP P52279
B	123	HIS	PRO	conflict	UNP P52279
B	124	PRO	SER	conflict	UNP P52279
B	125	GLN	ALA	conflict	UNP P52279
B	126	GLN	ALA	conflict	UNP P52279
B	127	VAL	GLY	conflict	UNP P52279
B	128	THR	HIS	conflict	UNP P52279
B	129	GLU	GLN	conflict	UNP P52279

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	91	Total	O	0	0
			91	91		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	108	Total 108	O 108	0	0

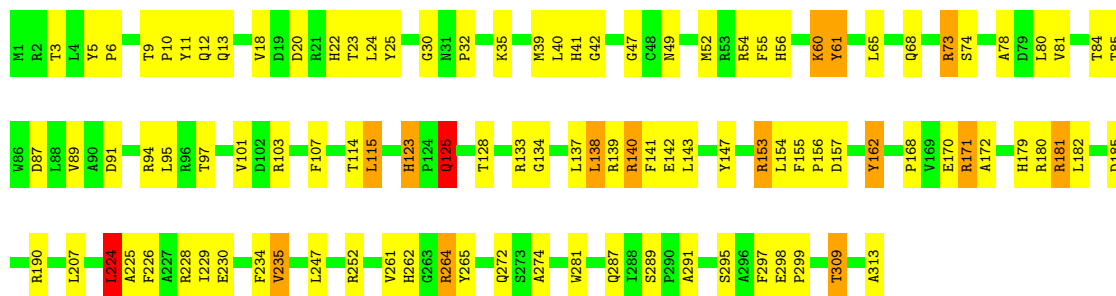
3 Residue-property plots

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

Note EDS was not executed.

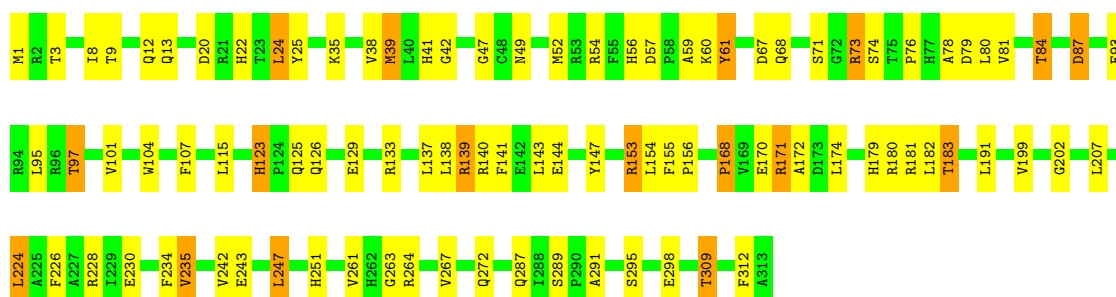
• Molecule 1: PROLINE IMINOPEPTIDASE

Chain A: 



• Molecule 1: PROLINE IMINOPEPTIDASE

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	147.20Å 167.80Å 85.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 2.70	Depositor
% Data completeness (in resolution range)	94.5 (7.00-2.70)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.192 , 0.253	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5227	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

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	0.63	0/2591	1.11	21/3525 (0.6%)
1	B	0.58	0/2591	1.04	10/3525 (0.3%)
All	All	0.61	0/5182	1.07	31/7050 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	298	GLU	N-CA-C	-9.46	98.15	110.07
1	A	54	ARG	N-CA-C	8.43	123.13	113.02
1	B	147	TYR	N-CA-C	7.46	122.38	113.28
1	A	289	SER	CA-C-N	6.96	128.53	119.84
1	A	289	SER	C-N-CA	6.96	128.53	119.84
1	A	87	ASP	N-CA-C	-6.88	103.01	111.40
1	A	298	GLU	N-CA-C	-6.59	100.07	109.62
1	A	61	TYR	N-CA-C	6.57	119.60	108.90
1	B	139	ARG	N-CA-C	-6.41	100.99	110.48
1	B	54	ARG	N-CA-C	6.25	120.52	113.02
1	A	125	GLN	N-CA-C	6.09	118.72	111.71
1	A	155	PHE	CA-C-N	6.03	125.51	119.24
1	A	155	PHE	C-N-CA	6.03	125.51	119.24
1	B	123	HIS	CA-C-N	5.94	125.15	118.97
1	B	123	HIS	C-N-CA	5.94	125.15	118.97
1	A	185	ASP	N-CA-C	-5.92	104.77	112.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	224	LEU	N-CA-C	5.84	117.32	111.07
1	A	281	TRP	CA-C-N	5.68	125.36	119.05
1	A	281	TRP	C-N-CA	5.68	125.36	119.05
1	B	61	TYR	N-CA-C	5.65	118.62	109.40
1	A	123	HIS	CA-C-N	5.64	125.11	119.24
1	A	123	HIS	C-N-CA	5.64	125.11	119.24
1	B	295	SER	N-CA-C	5.62	118.21	110.35
1	B	87	ASP	N-CA-C	-5.55	104.62	111.40
1	A	295	SER	N-CA-C	5.50	118.06	110.35
1	A	74	SER	N-CA-C	-5.41	102.03	110.42
1	A	138	LEU	N-CA-C	5.41	119.45	112.86
1	A	298	GLU	CA-C-N	5.33	126.50	119.84
1	A	298	GLU	C-N-CA	5.33	126.50	119.84
1	A	140	ARG	N-CA-C	5.24	117.74	111.71
1	A	224	LEU	N-CA-C	5.20	117.35	111.11

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	162	TYR	Sidechain

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	2514	0	2386	66	0
1	B	2514	0	2386	62	0
2	A	91	0	0	5	0
2	B	108	0	0	3	0
All	All	5227	0	4772	123	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 13.

All (123) 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:49:ASN:OD1	1:A:52:MET:HG3	1.79	0.82
1:B:138:LEU:HD23	1:B:143:LEU:HD21	1.68	0.75
1:B:153:ARG:HH11	1:B:153:ARG:HG3	1.54	0.72
1:A:168:PRO:HA	1:A:171:ARG:HD3	1.73	0.71
1:B:41:HIS:HE1	1:B:68:GLN:H	1.38	0.70
1:B:39:MET:HE1	1:B:56:HIS:CE1	2.28	0.69
1:A:262:HIS:ND1	1:A:274:ALA:HB2	2.09	0.68
1:A:172:ALA:CB	1:B:140:ARG:HD2	2.24	0.67
1:A:41:HIS:HE1	1:A:68:GLN:H	1.42	0.66
1:A:226:PHE:O	1:A:230:GLU:HB2	1.96	0.65
1:A:56:HIS:HA	1:A:309:THR:HG21	1.79	0.64
1:B:139:ARG:NH1	1:B:141:PHE:CZ	2.66	0.64
1:B:41:HIS:HD2	1:B:42:GLY:O	1.80	0.64
1:A:154:LEU:C	1:A:156:PRO:HD3	2.24	0.63
1:A:123:HIS:HE1	2:A:324:HOH:O	1.83	0.62
1:B:139:ARG:NH1	1:B:141:PHE:CE2	2.68	0.61
1:A:252:ARG:HD3	2:A:352:HOH:O	2.02	0.60
1:B:138:LEU:CD2	1:B:143:LEU:HD21	2.32	0.60
1:B:56:HIS:HA	1:B:309:THR:HG21	1.84	0.60
1:B:68:GLN:O	1:B:71:SER:HB3	2.01	0.60
1:B:154:LEU:C	1:B:156:PRO:HD3	2.28	0.59
1:B:140:ARG:O	1:B:140:ARG:HG3	2.02	0.59
1:B:76:PRO:HG2	1:B:79:ASP:HB2	1.85	0.59
1:A:85:THR:O	1:A:89:VAL:HG23	2.03	0.59
1:B:25:TYR:CG	1:B:73:ARG:HG3	2.37	0.59
1:B:35:LYS:HD3	1:B:61:TYR:HE1	1.69	0.58
1:A:39:MET:HE1	1:A:56:HIS:HE1	1.68	0.58
1:B:140:ARG:HD3	1:B:144:GLU:OE2	2.03	0.58
1:B:35:LYS:HD3	1:B:61:TYR:CE1	2.38	0.58
1:B:84:THR:HG21	2:B:332:HOH:O	2.03	0.58
1:A:39:MET:HE2	1:A:107:PHE:HB3	1.85	0.57
1:B:226:PHE:O	1:B:230:GLU:HB2	2.03	0.57
1:A:35:LYS:HD3	1:A:61:TYR:CE1	2.39	0.57
1:A:230:GLU:HG2	1:A:234:PHE:CE2	2.40	0.56
1:B:171:ARG:HG3	1:B:174:LEU:HD21	1.87	0.56
1:A:264:ARG:HG2	1:A:265:TYR:CE1	2.41	0.56
1:A:224:LEU:HD12	1:A:228:ARG:HD2	1.88	0.56
1:A:39:MET:CE	1:A:107:PHE:HB3	2.35	0.56
1:A:114:THR:HG21	1:A:138:LEU:HD12	1.88	0.56
1:B:170:GLU:HA	2:B:322:HOH:O	2.06	0.55
1:A:9:THR:HG22	1:A:10:PRO:HD2	1.89	0.54
1:B:8:ILE:HG12	1:B:9:THR:N	2.23	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:MET:HE3	1:B:107:PHE:CD1	2.43	0.54
1:B:57:ASP:OD2	1:B:59:ALA:HB3	2.08	0.54
1:A:170:GLU:CD	1:A:181:ARG:HH22	2.15	0.53
1:A:41:HIS:CE1	1:A:68:GLN:H	2.26	0.53
1:B:179:HIS:O	1:B:183:THR:HB	2.07	0.53
1:A:30:GLY:O	1:A:32:PRO:HD3	2.10	0.52
1:A:103:ARG:HD2	1:A:125:GLN:O	2.09	0.52
1:A:153:ARG:HH11	1:A:153:ARG:HG3	1.73	0.52
1:B:207:LEU:HD22	1:B:291:ALA:O	2.09	0.52
1:A:55:PHE:O	1:A:309:THR:HG21	2.08	0.52
1:B:123:HIS:HB3	1:B:126:GLN:HG2	1.92	0.51
1:A:9:THR:CG2	1:A:10:PRO:HD2	2.41	0.51
1:B:139:ARG:HA	1:B:243:GLU:HG3	1.92	0.51
1:A:39:MET:HE1	1:A:56:HIS:CE1	2.46	0.50
1:A:140:ARG:HD2	1:B:172:ALA:CB	2.42	0.50
1:A:139:ARG:NH1	1:A:141:PHE:CZ	2.81	0.49
1:A:139:ARG:HG3	1:A:142:GLU:OE2	2.13	0.49
1:A:133:ARG:HD2	1:A:134:GLY:N	2.28	0.48
1:B:168:PRO:O	1:B:171:ARG:HB2	2.14	0.48
1:A:235:VAL:HG13	1:B:180:ARG:CZ	2.44	0.48
1:B:129:GLU:HG2	1:B:312:PHE:CD1	2.49	0.48
1:B:22:HIS:HE1	1:B:81:VAL:O	1.96	0.48
1:B:191:LEU:HD12	1:B:224:LEU:CD2	2.44	0.47
1:A:41:HIS:HD2	1:A:42:GLY:O	1.98	0.47
1:B:39:MET:HE1	1:B:56:HIS:HE1	1.75	0.47
1:B:78:ALA:O	1:B:228:ARG:NH1	2.47	0.47
1:A:25:TYR:CD1	1:A:25:TYR:C	2.92	0.47
1:A:25:TYR:CG	1:A:73:ARG:HG3	2.50	0.47
1:B:93:GLU:O	1:B:97:THR:HB	2.14	0.47
1:B:251:HIS:HE1	2:B:384:HOH:O	1.98	0.47
1:A:39:MET:HG3	1:A:65:LEU:HG	1.97	0.47
1:A:41:HIS:CE1	1:A:47:GLY:HA2	2.50	0.47
1:A:180:ARG:CZ	1:B:235:VAL:HG13	2.45	0.47
1:A:138:LEU:HD23	1:A:143:LEU:HD21	1.96	0.46
1:A:190:ARG:HD3	1:A:224:LEU:HD11	1.97	0.46
1:B:76:PRO:HG2	1:B:79:ASP:CB	2.46	0.46
1:A:78:ALA:O	1:A:228:ARG:NH1	2.49	0.46
1:A:22:HIS:HE1	1:A:81:VAL:O	1.99	0.45
1:A:123:HIS:CD2	2:A:387:HOH:O	2.69	0.45
1:A:91:ASP:OD1	1:A:94:ARG:NH1	2.50	0.45
1:B:140:ARG:HG3	1:B:144:GLU:HG3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLN:NE2	1:A:115:LEU:HD12	2.32	0.45
1:B:234:PHE:CD1	1:B:234:PHE:N	2.82	0.45
1:B:25:TYR:CD1	1:B:25:TYR:C	2.95	0.44
1:A:5:TYR:HB3	1:A:6:PRO:HD2	1.98	0.44
1:A:107:PHE:CD1	1:A:107:PHE:C	2.95	0.44
1:A:141:PHE:CD1	1:A:141:PHE:C	2.95	0.44
1:B:24:LEU:HA	1:B:74:SER:OG	2.18	0.44
1:A:157:ASP:OD1	1:A:157:ASP:N	2.51	0.44
1:A:230:GLU:HG2	1:A:234:PHE:CZ	2.51	0.44
1:A:207:LEU:HD22	1:A:291:ALA:O	2.18	0.44
1:B:49:ASN:OD1	1:B:52:MET:HG3	2.17	0.44
1:A:147:TYR:HB3	1:A:162:TYR:OH	2.17	0.43
1:A:123:HIS:CE1	2:A:324:HOH:O	2.66	0.43
1:B:41:HIS:CD2	1:B:47:GLY:H	2.35	0.43
1:A:12:GLN:NE2	1:A:13:GLN:C	2.76	0.43
1:A:224:LEU:CD1	1:A:228:ARG:HD2	2.48	0.43
1:B:133:ARG:HA	1:B:261:VAL:O	2.18	0.43
1:B:139:ARG:HH21	1:B:247:LEU:HD21	1.84	0.43
1:B:84:THR:HB	1:B:87:ASP:OD2	2.19	0.42
1:A:225:ALA:O	1:A:229:ILE:HG13	2.19	0.42
1:B:247:LEU:HD12	1:B:247:LEU:HA	1.72	0.42
1:B:155:PHE:CE2	1:B:267:VAL:HG21	2.53	0.42
1:A:55:PHE:CZ	1:A:297:PHE:CE1	3.07	0.42
1:A:40:LEU:HD13	1:A:115:LEU:HB3	2.02	0.42
1:A:133:ARG:HA	1:A:261:VAL:O	2.19	0.42
1:A:11:TYR:CE2	1:A:32:PRO:HG3	2.55	0.41
1:B:199:VAL:O	1:B:202:GLY:N	2.52	0.41
1:A:179:HIS:HE1	2:A:329:HOH:O	2.03	0.41
1:B:8:ILE:HG12	1:B:9:THR:H	1.85	0.41
1:A:133:ARG:HD2	1:A:133:ARG:C	2.45	0.41
1:A:18:VAL:HG11	1:A:24:LEU:HD22	2.03	0.41
1:A:172:ALA:HB1	1:B:140:ARG:HD2	2.02	0.41
1:B:263:GLY:HA2	1:B:289:SER:HB2	2.03	0.41
1:A:60:LYS:HE2	1:A:313:ALA:HB1	2.03	0.40
1:B:57:ASP:OD2	1:B:60:LYS:HD3	2.21	0.40
1:B:12:GLN:NE2	1:B:13:GLN:O	2.54	0.40
1:B:38:VAL:HB	1:B:104:TRP:CZ3	2.56	0.40
1:B:67:ASP:HB3	1:B:71:SER:O	2.20	0.40
1:B:154:LEU:O	1:B:156:PRO:HD3	2.22	0.40
1:B:155:PHE:HE2	1:B:267:VAL:HG21	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	311/313 (99%)	294 (94%)	17 (6%)	0	100	100
1	B	311/313 (99%)	293 (94%)	18 (6%)	0	100	100
All	All	622/626 (99%)	587 (94%)	35 (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	258/258 (100%)	232 (90%)	26 (10%)	7	18
1	B	258/258 (100%)	231 (90%)	27 (10%)	6	17
All	All	516/516 (100%)	463 (90%)	53 (10%)	7	18

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	A	20	ASP
1	A	23	THR
1	A	60	LYS
1	A	73	ARG
1	A	80	LEU
1	A	84	THR
1	A	95	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	97	THR
1	A	101	VAL
1	A	115	LEU
1	A	125	GLN
1	A	128	THR
1	A	137	LEU
1	A	153	ARG
1	A	171	ARG
1	A	181	ARG
1	A	182	LEU
1	A	224	LEU
1	A	235	VAL
1	A	247	LEU
1	A	264	ARG
1	A	272	GLN
1	A	287	GLN
1	A	299	PRO
1	A	309	THR
1	B	1	MET
1	B	3	THR
1	B	20	ASP
1	B	24	LEU
1	B	39	MET
1	B	73	ARG
1	B	80	LEU
1	B	84	THR
1	B	95	LEU
1	B	97	THR
1	B	101	VAL
1	B	115	LEU
1	B	125	GLN
1	B	137	LEU
1	B	153	ARG
1	B	168	PRO
1	B	171	ARG
1	B	181	ARG
1	B	182	LEU
1	B	183	THR
1	B	235	VAL
1	B	242	VAL
1	B	247	LEU
1	B	264	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	272	GLN
1	B	287	GLN
1	B	309	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	41	HIS
1	A	123	HIS
1	A	126	GLN
1	A	217	HIS
1	A	272	GLN
1	A	278	HIS
1	A	285	GLN
1	A	287	GLN
1	A	301	ASN
1	B	22	HIS
1	B	41	HIS
1	B	77	HIS
1	B	121	GLN
1	B	164	ASN
1	B	179	HIS
1	B	217	HIS
1	B	232	HIS
1	B	251	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 ⓘ

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.