



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 09:20 pm BST

PDB ID : 5ZW0
Title : Apo-form PigA
Authors : Lee, C.-C.; Ko, T.-P.; Wang, A.H.J.
Deposited on : 2018-05-14
Resolution : 2.54 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

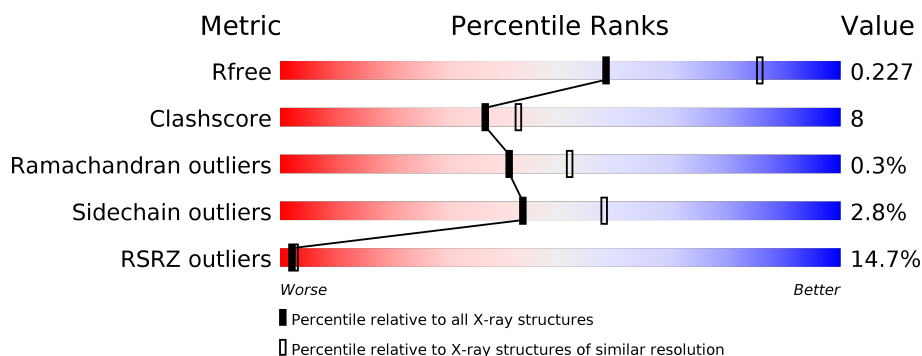
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 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	402	<div> <div>15%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>5%</div> </div> </div>
1	B	402	<div> <div>13%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>7%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6043 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 L-prolyl-[peptidyl-carrier protein] dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	382	Total	C	N	O	S	0	0	0
			2927	1858	498	551	20			
1	B	375	Total	C	N	O	S	0	0	0
			2871	1822	488	541	20			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	387	GLY	-	expression tag	UNP Q5W271
A	388	SER	-	expression tag	UNP Q5W271
A	389	LEU	-	expression tag	UNP Q5W271
A	390	VAL	-	expression tag	UNP Q5W271
A	391	PRO	-	expression tag	UNP Q5W271
A	392	ARG	-	expression tag	UNP Q5W271
A	393	GLY	-	expression tag	UNP Q5W271
A	394	SER	-	expression tag	UNP Q5W271
A	395	HIS	-	expression tag	UNP Q5W271
A	396	HIS	-	expression tag	UNP Q5W271
A	397	HIS	-	expression tag	UNP Q5W271
A	398	HIS	-	expression tag	UNP Q5W271
A	399	HIS	-	expression tag	UNP Q5W271
A	400	HIS	-	expression tag	UNP Q5W271
A	401	HIS	-	expression tag	UNP Q5W271
A	402	HIS	-	expression tag	UNP Q5W271
B	387	GLY	-	expression tag	UNP Q5W271
B	388	SER	-	expression tag	UNP Q5W271
B	389	LEU	-	expression tag	UNP Q5W271
B	390	VAL	-	expression tag	UNP Q5W271
B	391	PRO	-	expression tag	UNP Q5W271
B	392	ARG	-	expression tag	UNP Q5W271
B	393	GLY	-	expression tag	UNP Q5W271
B	394	SER	-	expression tag	UNP Q5W271
B	395	HIS	-	expression tag	UNP Q5W271

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	396	HIS	-	expression tag	UNP Q5W271
B	397	HIS	-	expression tag	UNP Q5W271
B	398	HIS	-	expression tag	UNP Q5W271
B	399	HIS	-	expression tag	UNP Q5W271
B	400	HIS	-	expression tag	UNP Q5W271
B	401	HIS	-	expression tag	UNP Q5W271
B	402	HIS	-	expression tag	UNP Q5W271

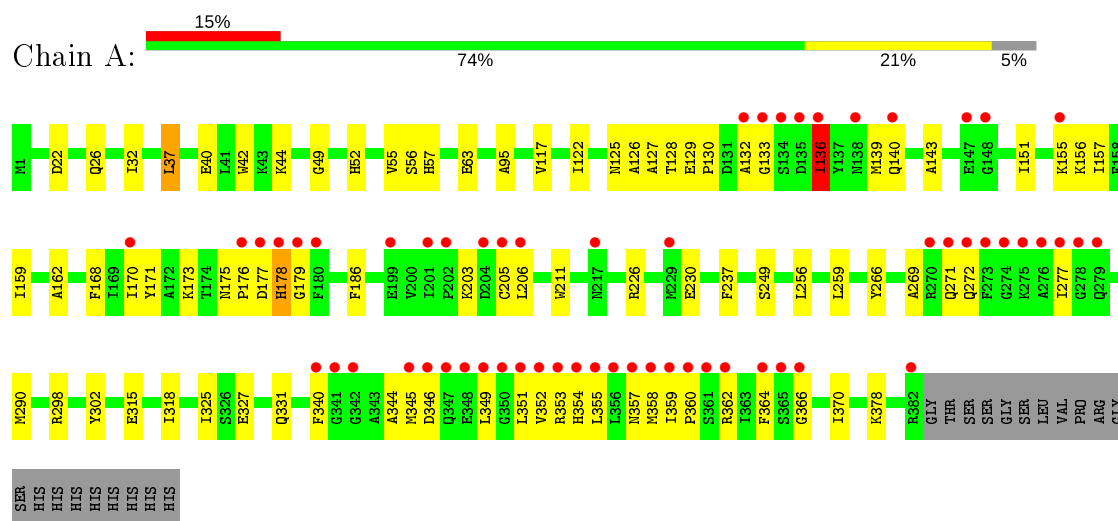
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	143	Total	O	0	0
			143	143		
2	B	102	Total	O	0	0
			102	102		

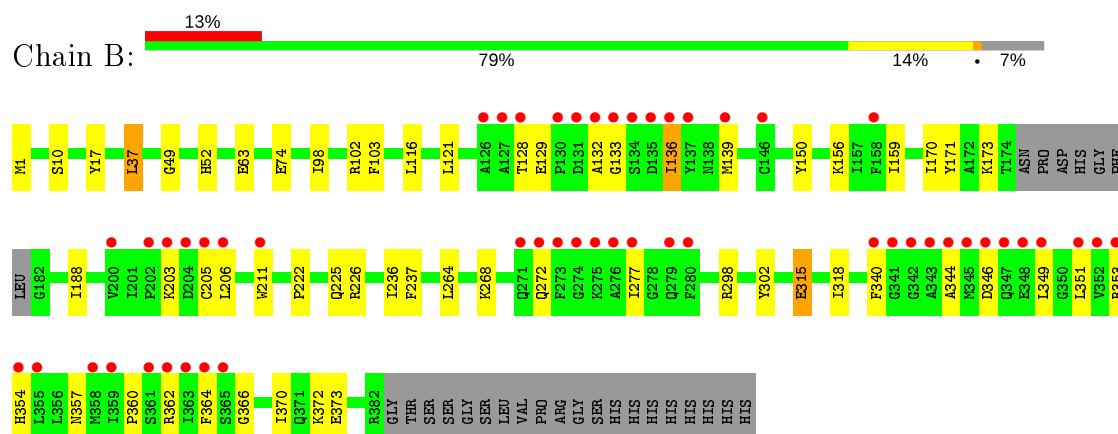
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: L-prolyl-[peptidyl-carrier protein] dehydrogenase



- Molecule 1: L-prolyl-[peptidyl-carrier protein] dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	79.22Å 163.02Å 146.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.90 – 2.54 19.91 – 2.54	Depositor EDS
% Data completeness (in resolution range)	90.4 (19.90-2.54) 90.4 (19.91-2.54)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.89 (at 2.53Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.179 , 0.227 0.179 , 0.227	Depositor DCC
R_{free} test set	1429 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 75.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6043	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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	0.44	0/2981	0.61	1/4022 (0.0%)
1	B	0.44	0/2921	0.59	1/3938 (0.0%)
All	All	0.44	0/5902	0.60	2/7960 (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	A	37	LEU	CA-CB-CG	-5.97	101.58	115.30
1	B	37	LEU	CA-CB-CG	-5.00	103.80	115.30

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	2927	0	2921	58	0
1	B	2871	0	2873	34	0
2	A	143	0	0	1	0
2	B	102	0	0	2	0
All	All	6043	0	5794	92	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 8.

All (92) 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:129:GLU:HB2	1:A:132:ALA:HB3	1.55	0.87
1:B:129:GLU:HB2	1:B:132:ALA:HB3	1.57	0.85
1:A:56:SER:HA	1:A:63:GLU:HG2	1.61	0.83
1:B:372:LYS:NZ	2:B:501:HOH:O	2.16	0.77
1:A:366:GLY:HA2	1:A:370:ILE:HD12	1.70	0.73
1:B:139:MET:H	1:B:173:LYS:HE3	1.61	0.66
1:A:139:MET:H	1:A:173:LYS:NZ	1.96	0.64
1:B:203:LYS:HD3	1:B:211:TRP:HE1	1.65	0.62
1:B:340:PHE:HB2	1:B:344:ALA:HB2	1.83	0.60
1:B:49:GLY:HA2	1:B:52:HIS:CE1	2.37	0.59
1:A:340:PHE:HB2	1:A:344:ALA:HB2	1.85	0.59
1:A:175:ASN:O	1:A:177:ASP:N	2.36	0.59
1:B:203:LYS:HD3	1:B:211:TRP:NE1	2.17	0.59
1:B:366:GLY:HA2	1:B:370:ILE:HD12	1.85	0.58
1:A:125:ASN:O	1:A:159:ILE:HG23	2.04	0.58
1:A:203:LYS:HB2	1:A:211:TRP:HE1	1.69	0.57
1:A:346:ASP:HB3	1:A:349:LEU:HB2	1.88	0.55
1:A:206:LEU:HD12	1:A:360:PRO:HG2	1.88	0.55
1:B:132:ALA:HB1	1:B:139:MET:HG2	1.88	0.55
1:B:103:PHE:CG	1:B:236:ILE:HG12	2.40	0.55
1:A:127:ALA:O	1:A:136:ILE:HD13	2.07	0.55
1:B:128:THR:HA	1:B:133:GLY:HA2	1.88	0.54
1:B:170:ILE:HG13	1:B:188:ILE:HD12	1.88	0.54
1:B:206:LEU:HD12	1:B:360:PRO:HG2	1.89	0.54
1:A:353:ARG:HG2	1:A:357:ASN:HD21	1.73	0.53
1:A:259:LEU:HG	1:A:290:MET:HE1	1.92	0.51
1:A:130:PRO:HD2	1:A:140:GLN:NE2	2.26	0.51
1:A:136:ILE:HD12	1:A:237:PHE:CE2	2.46	0.51
1:B:340:PHE:CD1	1:B:351:LEU:HD22	2.46	0.50
1:A:130:PRO:HD3	1:A:157:ILE:HG12	1.93	0.50
1:A:126:ALA:HA	1:A:159:ILE:HD12	1.92	0.50
1:A:249:SER:HB3	1:A:325:ILE:HD13	1.92	0.50
1:A:346:ASP:HB3	1:A:349:LEU:CB	2.41	0.50
1:A:42:TRP:CZ3	1:A:122:ILE:HG12	2.47	0.49
1:B:98:ILE:HG23	1:B:102:ARG:HD2	1.93	0.49
1:A:32:ILE:HG21	1:A:353:ARG:CZ	2.43	0.49
1:A:55:VAL:HG11	1:A:117:VAL:HG21	1.95	0.49
1:A:186:PHE:CE2	1:A:226:ARG:HG3	2.47	0.49
1:A:298:ARG:HD2	1:A:302:TYR:OH	2.13	0.49
1:B:132:ALA:HB2	1:B:139:MET:HA	1.95	0.49
1:B:136:ILE:HD12	1:B:237:PHE:CZ	2.48	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ALA:O	1:A:271:GLN:HG3	2.13	0.48
1:A:340:PHE:CD1	1:A:351:LEU:HD22	2.49	0.48
1:B:264:LEU:HD22	1:B:268:LYS:HE3	1.96	0.48
1:B:298:ARG:HG3	1:B:302:TYR:CE2	2.49	0.48
1:B:150:TYR:OH	1:B:226:ARG:NH1	2.46	0.48
1:A:203:LYS:HE2	1:A:205:CYS:O	2.13	0.47
1:B:156:LYS:HB3	1:B:159:ILE:HD11	1.97	0.47
1:B:298:ARG:HD2	1:B:302:TYR:OH	2.14	0.47
1:B:272:GLN:HB2	1:B:277:ILE:HG22	1.97	0.46
1:B:346:ASP:HB3	1:B:349:LEU:HB2	1.98	0.46
1:B:203:LYS:HE2	1:B:205:CYS:O	2.15	0.46
1:A:128:THR:HA	1:A:133:GLY:HA2	1.98	0.46
1:A:362:ARG:HG2	1:A:362:ARG:H	1.59	0.45
1:A:249:SER:HB3	1:A:325:ILE:CD1	2.46	0.45
1:A:345:MET:HG2	1:A:352:VAL:HG21	1.99	0.45
1:B:17:TYR:OH	2:B:502:HOH:O	2.18	0.45
1:B:340:PHE:HD1	1:B:351:LEU:HD22	1.82	0.45
1:A:331:GLN:HG3	2:A:607:HOH:O	2.18	0.44
1:A:355:LEU:O	1:A:359:ILE:HG13	2.18	0.43
1:A:178:HIS:HB3	1:A:179:GLY:H	1.71	0.43
1:A:40:GLU:OE2	1:A:44:LYS:NZ	2.50	0.43
1:B:362:ARG:HG2	1:B:362:ARG:H	1.61	0.42
1:A:171:TYR:CE1	1:A:237:PHE:HB2	2.53	0.42
1:A:327:GLU:HG2	1:A:362:ARG:HH22	1.84	0.42
1:B:116:LEU:HD23	1:B:121:LEU:HB2	2.02	0.42
1:A:203:LYS:HD3	1:A:211:TRP:NE1	2.35	0.42
1:A:129:GLU:HG2	1:A:155:LYS:O	2.20	0.42
1:A:129:GLU:CG	1:A:156:LYS:HD3	2.50	0.42
1:A:354:HIS:O	1:A:358:MET:HG3	2.19	0.42
1:A:22:ASP:HA	1:A:26:GLN:HE21	1.85	0.42
1:A:57:HIS:ND1	1:A:63:GLU:OE2	2.49	0.41
1:A:159:ILE:O	1:A:211:TRP:HA	2.20	0.41
1:B:315:GLU:O	1:B:318:ILE:HG22	2.20	0.41
1:A:353:ARG:O	1:A:357:ASN:ND2	2.54	0.41
1:A:49:GLY:HA2	1:A:52:HIS:CE1	2.55	0.41
1:A:139:MET:H	1:A:173:LYS:HZ1	1.67	0.41
1:B:222:PRO:HD2	1:B:225:GLN:HG3	2.02	0.41
1:A:168:PHE:HB3	1:A:170:ILE:HD11	2.02	0.41
1:A:95:ALA:HB1	1:A:125:ASN:CG	2.41	0.41
1:A:143:ALA:HA	1:A:151:ILE:O	2.21	0.41
1:B:353:ARG:O	1:B:357:ASN:ND2	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:ASN:C	1:A:177:ASP:H	2.24	0.41
1:A:136:ILE:HD12	1:A:237:PHE:CZ	2.56	0.41
1:A:266:TYR:CE2	1:A:277:ILE:HD11	2.55	0.41
1:B:171:TYR:CE1	1:B:237:PHE:HB2	2.56	0.41
1:B:74:GLU:OE1	1:B:302:TYR:OH	2.27	0.41
1:A:256:LEU:HA	1:A:256:LEU:HD12	1.78	0.41
1:A:129:GLU:HG3	1:A:156:LYS:HD3	2.01	0.40
1:A:159:ILE:CG2	1:A:162:ALA:HB2	2.52	0.40
1:A:340:PHE:CE1	1:A:351:LEU:HD22	2.56	0.40
1:A:272:GLN:HB2	1:A:277:ILE:HG22	2.04	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	380/402 (94%)	356 (94%)	22 (6%)	2 (0%)	29	40
1	B	371/402 (92%)	351 (95%)	20 (5%)	0	100	100
All	All	751/804 (93%)	707 (94%)	42 (6%)	2 (0%)	41	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	176	PRO
1	A	136	ILE

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	308/325 (95%)	300 (97%)	8 (3%)	46	61
1	B	302/325 (93%)	293 (97%)	9 (3%)	41	55
All	All	610/650 (94%)	593 (97%)	17 (3%)	43	58

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LEU
1	A	136	ILE
1	A	178	HIS
1	A	230	GLU
1	A	315	GLU
1	A	318	ILE
1	A	364	PHE
1	A	378	LYS
1	B	1	MET
1	B	10	SER
1	B	37	LEU
1	B	63	GLU
1	B	136	ILE
1	B	315	GLU
1	B	354	HIS
1	B	364	PHE
1	B	373	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	34	GLN
1	A	296	GLN
1	A	354	HIS
1	A	368	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	382/402 (95%)	0.41	59 (15%) 2 2	10, 44, 200, 287	0
1	B	375/402 (93%)	0.34	52 (13%) 2 3	13, 45, 217, 263	0
All	All	757/804 (94%)	0.38	111 (14%) 2 3	10, 44, 212, 287	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	347	GLN	19.1
1	A	205	CYS	17.1
1	B	133	GLY	14.2
1	B	134	SER	13.6
1	B	345	MET	13.4
1	A	341	GLY	12.6
1	A	348	GLU	11.7
1	B	273	PHE	11.7
1	B	364	PHE	11.5
1	B	341	GLY	10.7
1	A	134	SER	10.4
1	A	132	ALA	10.3
1	B	365	SER	8.5
1	B	348	GLU	8.4
1	A	272	GLN	8.0
1	B	342	GLY	8.0
1	B	347	GLN	7.8
1	A	133	GLY	7.6
1	B	272	GLN	7.6
1	A	273	PHE	7.5
1	B	275	LYS	7.3
1	A	345	MET	7.3
1	B	277	ILE	7.3
1	B	136	ILE	6.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	271	GLN	6.4
1	B	279	GLN	6.0
1	A	274	GLY	5.7
1	B	128	THR	5.7
1	B	205	CYS	5.7
1	B	137	TYR	5.6
1	B	276	ALA	5.5
1	B	132	ALA	5.4
1	A	277	ILE	5.3
1	A	271	GLN	5.3
1	B	358	MET	5.3
1	A	270	ARG	5.2
1	B	274	GLY	5.1
1	A	364	PHE	5.1
1	B	139	MET	5.0
1	A	201	ILE	5.0
1	A	346	ASP	5.0
1	A	275	LYS	5.0
1	A	204	ASP	5.0
1	A	276	ALA	4.9
1	A	358	MET	4.9
1	B	130	PRO	4.9
1	B	203	LYS	4.9
1	B	202	PRO	4.9
1	A	359	ILE	4.8
1	B	206	LEU	4.8
1	B	344	ALA	4.7
1	A	360	PRO	4.7
1	A	361	SER	4.5
1	A	178	HIS	4.5
1	A	279	GLN	4.4
1	A	342	GLY	4.3
1	A	349	LEU	4.2
1	B	352	VAL	4.2
1	A	206	LEU	4.1
1	A	148	GLY	4.1
1	A	278	GLY	4.1
1	A	355	LEU	4.0
1	B	131	ASP	4.0
1	A	357	ASN	3.9
1	B	127	ALA	3.8
1	A	353	ARG	3.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	180	PHE	3.7
1	A	365	SER	3.7
1	A	179	GLY	3.7
1	B	280	PHE	3.4
1	B	353	ARG	3.4
1	A	217	ASN	3.3
1	A	362	ARG	3.2
1	A	356	LEU	3.2
1	A	354	HIS	3.2
1	B	351	LEU	3.2
1	A	147	GLU	3.1
1	A	140	GLN	3.1
1	B	343	ALA	2.9
1	A	382	ARG	2.9
1	B	355	LEU	2.9
1	A	351	LEU	2.9
1	A	199	GLU	2.8
1	B	346	ASP	2.8
1	B	126	ALA	2.7
1	B	204	ASP	2.7
1	A	352	VAL	2.6
1	B	359	ILE	2.6
1	B	135	ASP	2.6
1	B	361	SER	2.5
1	A	350	GLY	2.5
1	A	177	ASP	2.5
1	B	340	PHE	2.4
1	A	135	ASP	2.4
1	A	340	PHE	2.3
1	B	354	HIS	2.3
1	B	362	ARG	2.3
1	B	158	PHE	2.3
1	B	146	CYS	2.3
1	A	176	PRO	2.3
1	A	155	LYS	2.3
1	B	349	LEU	2.2
1	B	211	TRP	2.2
1	A	366	GLY	2.2
1	A	138	ASN	2.1
1	A	136	ILE	2.1
1	B	363	ILE	2.1
1	B	200	VAL	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	170	ILE	2.1
1	A	229	MET	2.0
1	A	202	PRO	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 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.