



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:31 AM UTC

PDB ID : 1LL7 / pdb_00001ll7
Title : STRUCTURE OF THE E171Q MUTANT OF C. IMMITIS CHITINASE 1
Authors : Bortone, K.; Monzingo, A.F.; Ernst, S.; Robertus, J.D.
Deposited on : 2002-04-26
Resolution : 2.00 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

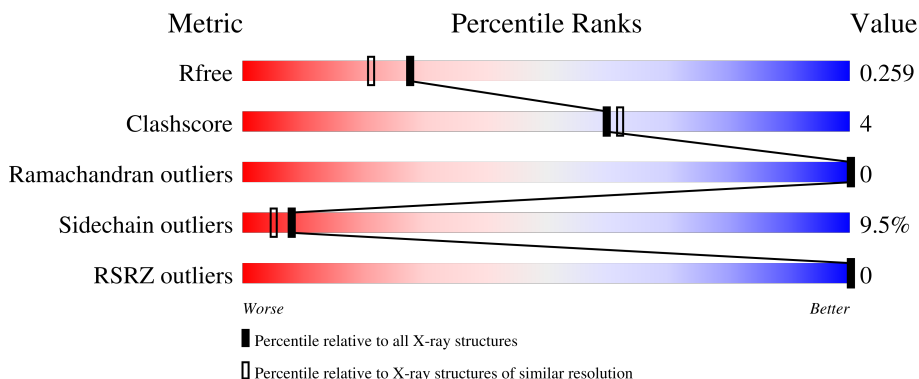
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	392	
1	B	392	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6506 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 CHITINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	0	0
			3083	1963	511	597	12			
1	B	392	Total	C	N	O	S	0	0	0
			3083	1963	511	597	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	GLN	GLU	engineered mutation	UNP P54196
B	171	GLN	GLU	engineered mutation	UNP P54196

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	177	Total	O	0	0
			177	177		
2	B	163	Total	O	0	0
			163	163		

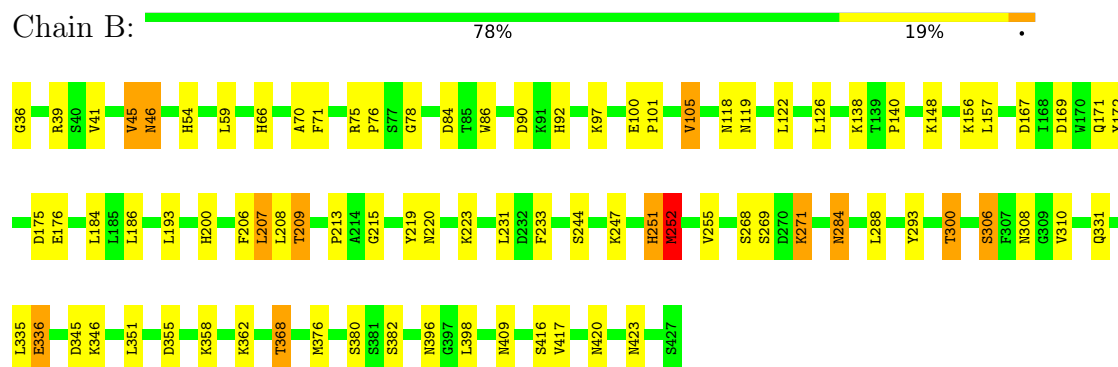
3 Residue-property plots

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: CHITINASE 1



• Molecule 1: CHITINASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	90.33Å 90.33Å 95.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	5.00 – 2.00 5.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (5.00-2.00) 91.6 (5.00-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.01Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.207 , 0.267 0.202 , 0.259	Depositor DCC
R_{free} test set	2367 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 32.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.213 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6506	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.43% 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

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	0.90	5/3165 (0.2%)	1.55	40/4282 (0.9%)
1	B	0.91	5/3165 (0.2%)	1.56	43/4282 (1.0%)
All	All	0.90	10/6330 (0.2%)	1.55	83/8564 (1.0%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	251	HIS	CD2-NE2	-7.08	1.30	1.37
1	A	92	HIS	CD2-NE2	-6.86	1.30	1.37
1	A	251	HIS	CD2-NE2	-6.73	1.30	1.37
1	B	200	HIS	CD2-NE2	-6.44	1.30	1.37
1	B	54	HIS	CD2-NE2	-6.01	1.31	1.37
1	B	66	HIS	CD2-NE2	-5.97	1.31	1.37
1	A	200	HIS	CD2-NE2	-5.88	1.31	1.37
1	B	92	HIS	CD2-NE2	-5.73	1.31	1.37
1	A	66	HIS	CD2-NE2	-5.38	1.31	1.37
1	A	54	HIS	CD2-NE2	-5.38	1.31	1.37

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	45	VAL	N-CA-CB	-10.77	98.07	110.99
1	A	45	VAL	N-CA-CB	-10.68	98.17	110.99
1	A	46	ASN	CA-CB-CG	7.89	120.49	112.60
1	B	92	HIS	CB-CG-CD2	-7.69	121.20	131.20
1	B	284	ASN	OD1-CG-ND2	-7.64	114.96	122.60
1	B	46	ASN	CA-CB-CG	7.56	120.16	112.60
1	B	380	SER	N-CA-C	7.55	121.59	112.38
1	B	284	ASN	CB-CG-ND2	7.44	127.56	116.40
1	A	284	ASN	CB-CG-ND2	7.42	127.52	116.40
1	B	308	ASN	OD1-CG-ND2	-7.29	115.31	122.60
1	A	382	SER	N-CA-C	7.22	121.80	112.92
1	A	380	SER	N-CA-C	7.14	121.09	112.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	HIS	CB-CG-CD2	-7.14	121.92	131.20
1	A	45	VAL	CB-CA-C	7.08	120.47	110.84
1	B	45	VAL	CB-CA-C	7.03	120.39	110.84
1	A	284	ASN	OD1-CG-ND2	-7.01	115.59	122.60
1	A	233	PHE	CA-CB-CG	6.90	120.70	113.80
1	B	382	SER	N-CA-C	6.86	121.36	112.92
1	B	368	THR	N-CA-CB	-6.83	99.94	109.91
1	A	368	THR	N-CA-CB	-6.79	100.00	109.91
1	B	247	LYS	N-CA-C	-6.62	105.50	113.97
1	A	355	ASP	CA-CB-CG	6.53	119.13	112.60
1	B	355	ASP	CA-CB-CG	6.52	119.12	112.60
1	B	251	HIS	CB-CG-CD2	-6.47	122.79	131.20
1	B	206	PHE	CA-CB-CG	-6.43	107.37	113.80
1	A	105	VAL	CB-CA-C	-6.43	101.03	110.81
1	B	420	ASN	CA-CB-CG	6.40	119.00	112.60
1	B	105	VAL	CB-CA-C	-6.35	101.15	110.81
1	B	92	HIS	CB-CG-ND1	6.32	132.18	122.70
1	B	90	ASP	N-CA-C	6.30	120.99	113.12
1	A	206	PHE	CA-CB-CG	-6.26	107.54	113.80
1	A	396	ASN	OD1-CG-ND2	-6.19	116.41	122.60
1	A	308	ASN	OD1-CG-ND2	-6.18	116.42	122.60
1	A	54	HIS	CB-CG-CD2	-6.16	123.19	131.20
1	A	251	HIS	CB-CG-CD2	-6.14	123.22	131.20
1	A	215	GLY	CA-C-N	6.11	125.59	119.24
1	A	215	GLY	C-N-CA	6.11	125.59	119.24
1	B	84	ASP	CA-CB-CG	6.06	118.66	112.60
1	B	215	GLY	CA-C-N	6.05	125.53	119.24
1	B	215	GLY	C-N-CA	6.05	125.53	119.24
1	A	252	MET	CG-SD-CE	-6.03	87.63	100.90
1	A	176	GLU	CA-C-O	-6.03	114.45	120.90
1	B	396	ASN	OD1-CG-ND2	-6.03	116.57	122.60
1	A	84	ASP	CA-CB-CG	5.93	118.53	112.60
1	A	420	ASN	CA-CB-CG	5.90	118.50	112.60
1	B	233	PHE	CA-CB-CG	5.87	119.67	113.80
1	B	54	HIS	CB-CG-CD2	-5.83	123.62	131.20
1	B	175	ASP	CA-CB-CG	5.77	118.37	112.60
1	A	247	LYS	N-CA-C	-5.76	106.41	113.50
1	A	92	HIS	CB-CG-ND1	5.75	131.32	122.70
1	A	208	LEU	N-CA-C	-5.71	99.11	108.76
1	B	284	ASN	CA-CB-CG	5.69	118.29	112.60
1	B	252	MET	CG-SD-CE	-5.61	88.56	100.90
1	B	368	THR	CA-CB-OG1	-5.54	101.29	109.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	284	ASN	CA-CB-CG	5.53	118.13	112.60
1	B	409	ASN	OD1-CG-ND2	-5.53	117.07	122.60
1	B	423	ASN	CA-CB-CG	-5.46	107.14	112.60
1	A	175	ASP	CA-CB-CG	5.45	118.05	112.60
1	A	118	ASN	CA-CB-CG	-5.42	107.18	112.60
1	A	423	ASN	CA-CB-CG	-5.41	107.19	112.60
1	A	203	GLY	O-C-N	-5.38	118.52	122.71
1	B	208	LEU	N-CA-C	-5.35	99.22	108.69
1	A	200	HIS	CA-C-N	5.34	125.41	119.32
1	A	200	HIS	C-N-CA	5.34	125.41	119.32
1	B	220	ASN	OD1-CG-ND2	-5.34	117.26	122.60
1	A	368	THR	CA-CB-OG1	-5.31	101.64	109.60
1	A	54	HIS	CB-CG-ND1	5.30	130.65	122.70
1	A	90	ASP	N-CA-C	5.30	119.74	113.12
1	B	219	TYR	CA-CB-CG	5.30	123.43	113.90
1	B	118	ASN	CA-CB-CG	-5.26	107.34	112.60
1	A	98	TRP	CE2-CD2-CG	-5.23	100.93	107.20
1	B	54	HIS	CB-CG-ND1	5.22	130.53	122.70
1	B	200	HIS	CA-C-N	5.17	125.21	119.32
1	B	200	HIS	C-N-CA	5.17	125.21	119.32
1	B	345	ASP	CA-C-N	5.14	127.42	120.38
1	B	345	ASP	C-N-CA	5.14	127.42	120.38
1	A	86	TRP	CE2-CD2-CG	-5.12	101.06	107.20
1	B	416	SER	CA-C-O	5.10	126.87	121.16
1	A	131	TRP	CE2-CD2-CG	-5.10	101.08	107.20
1	B	368	THR	CB-CA-C	5.08	118.78	110.96
1	B	409	ASN	CA-CB-CG	5.06	117.66	112.60
1	B	86	TRP	CE2-CD2-CG	-5.03	101.17	107.20
1	A	252	MET	N-CA-C	5.02	119.40	113.28

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	3083	0	2963	26	0
1	B	3083	0	2963	26	0
2	A	177	0	0	8	0
2	B	163	0	0	8	0
All	All	6506	0	5926	52	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 (52) 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:176:GLU:HB3	2:B:523:HOH:O	1.92	0.70
1:A:300:THR:HG23	1:A:306:SER:O	2.04	0.57
1:B:207:LEU:HD13	2:B:543:HOH:O	2.06	0.55
1:A:192:ALA:HB2	2:A:598:HOH:O	2.07	0.55
1:A:138:LYS:HG2	2:A:541:HOH:O	2.07	0.55
1:B:167:ASP:OD2	1:B:209:THR:HG22	2.07	0.54
1:B:300:THR:HG23	1:B:306:SER:O	2.08	0.54
1:A:119:ASN:HB2	2:A:561:HOH:O	2.09	0.52
1:A:335:LEU:HD22	2:A:545:HOH:O	2.09	0.52
1:A:271:LYS:HB2	1:A:271:LYS:NZ	2.25	0.52
1:B:172:TYR:CE2	1:B:213:PRO:HB3	2.45	0.52
1:A:167:ASP:OD2	1:A:209:THR:HG22	2.10	0.51
1:A:172:TYR:CE2	1:A:213:PRO:HB3	2.46	0.51
1:B:41:VAL:O	1:B:376:MET:HA	2.10	0.51
1:A:252:MET:HE1	1:A:293:TYR:CE2	2.46	0.50
1:A:251:HIS:HE1	2:A:508:HOH:O	1.95	0.50
1:A:41:VAL:O	1:A:376:MET:HA	2.12	0.50
1:A:251:HIS:HD2	2:A:491:HOH:O	1.95	0.49
1:B:251:HIS:HD2	2:B:499:HOH:O	1.96	0.49
1:B:271:LYS:HB2	1:B:271:LYS:NZ	2.28	0.48
1:B:251:HIS:HE1	2:B:500:HOH:O	1.95	0.48
1:B:252:MET:HE1	1:B:293:TYR:CE2	2.50	0.47
1:A:100:GLU:HB2	2:A:552:HOH:O	2.14	0.47
1:B:70:ALA:HA	1:B:71:PHE:HA	1.65	0.47
1:B:138:LYS:HG2	2:B:453:HOH:O	2.14	0.47
1:B:169:ASP:HB3	1:B:171:GLN:HE21	1.80	0.46
1:B:39:ARG:NH1	2:B:554:HOH:O	2.49	0.46
1:B:100:GLU:HA	1:B:101:PRO:HD2	1.77	0.46
1:B:255:VAL:O	1:B:268:SER:HB2	2.16	0.46
1:A:97:LYS:HB2	1:A:100:GLU:HG3	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:ARG:HH11	1:A:39:ARG:HD3	1.69	0.44
1:A:255:VAL:O	1:A:268:SER:HB2	2.18	0.43
1:B:97:LYS:HB2	1:B:100:GLU:HG3	1.99	0.43
1:A:169:ASP:HB3	1:A:171:GLN:HE21	1.82	0.43
1:A:70:ALA:HA	1:A:71:PHE:HA	1.64	0.43
1:B:244:SER:HB3	1:B:310:VAL:HG11	1.99	0.43
1:B:36:GLY:HA3	2:B:536:HOH:O	2.17	0.43
1:B:213:PRO:HA	2:B:444:HOH:O	2.18	0.43
1:A:155:LEU:HD23	1:A:193:LEU:HD12	2.01	0.42
1:A:78:GLY:HA2	1:A:140:PRO:HB3	2.01	0.42
1:B:148:LYS:HD3	1:B:148:LYS:HA	1.80	0.42
1:A:119:ASN:ND2	1:A:122:LEU:HB2	2.34	0.42
1:A:252:MET:HG3	2:A:492:HOH:O	2.19	0.41
1:A:255:VAL:HA	1:A:269:SER:OG	2.21	0.41
1:B:255:VAL:HA	1:B:269:SER:OG	2.21	0.41
1:A:330:ALA:HB1	1:A:343:SER:HB2	2.01	0.41
1:B:362:LYS:HD3	1:B:362:LYS:HA	1.90	0.41
1:A:148:LYS:HD3	1:A:148:LYS:HA	1.80	0.41
1:A:336:GLU:H	1:A:336:GLU:CD	2.29	0.41
1:B:119:ASN:ND2	1:B:122:LEU:HB2	2.35	0.41
1:B:78:GLY:HA2	1:B:140:PRO:HB3	2.03	0.40
1:B:336:GLU:H	1:B:336:GLU:CD	2.28	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	390/392 (100%)	380 (97%)	10 (3%)	0	100	100
1	B	390/392 (100%)	381 (98%)	9 (2%)	0	100	100
All	All	780/784 (100%)	761 (98%)	19 (2%)	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	326/326 (100%)	295 (90%)	31 (10%)	8	5
1	B	326/326 (100%)	295 (90%)	31 (10%)	8	5
All	All	652/652 (100%)	590 (90%)	62 (10%)	8	5

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	VAL
1	A	46	ASN
1	A	59	LEU
1	A	75	ARG
1	A	76	PRO
1	A	105	VAL
1	A	126	LEU
1	A	156	LYS
1	A	157	LEU
1	A	184	LEU
1	A	186	LEU
1	A	193	LEU
1	A	209	THR
1	A	223	LYS
1	A	231	LEU
1	A	252	MET
1	A	271	LYS
1	A	284	ASN
1	A	288	LEU
1	A	300	THR
1	A	306	SER
1	A	328	GLN
1	A	331	GLN
1	A	335	LEU
1	A	336	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	346	LYS
1	A	351	LEU
1	A	358	LYS
1	A	368	THR
1	A	398	LEU
1	A	417	VAL
1	B	45	VAL
1	B	46	ASN
1	B	59	LEU
1	B	75	ARG
1	B	76	PRO
1	B	105	VAL
1	B	126	LEU
1	B	156	LYS
1	B	157	LEU
1	B	184	LEU
1	B	186	LEU
1	B	193	LEU
1	B	207	LEU
1	B	209	THR
1	B	223	LYS
1	B	231	LEU
1	B	252	MET
1	B	271	LYS
1	B	284	ASN
1	B	288	LEU
1	B	300	THR
1	B	306	SER
1	B	331	GLN
1	B	335	LEU
1	B	336	GLU
1	B	346	LYS
1	B	351	LEU
1	B	358	LYS
1	B	368	THR
1	B	398	LEU
1	B	417	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	66	HIS
1	A	171	GLN
1	A	200	HIS
1	A	235	ASN
1	A	251	HIS
1	A	284	ASN
1	A	347	ASN
1	A	387	ASN
1	A	406	GLN
1	B	66	HIS
1	B	111	GLN
1	B	171	GLN
1	B	200	HIS
1	B	251	HIS
1	B	284	ASN
1	B	423	ASN

5.3.3 RNA [i](#)

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 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 ⓘ

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	392/392 (100%)	-1.61	0 100 100	8, 16, 26, 34	0
1	B	392/392 (100%)	-1.59	0 100 100	10, 17, 26, 35	0
All	All	784/784 (100%)	-1.60	0 100 100	8, 17, 26, 35	0

There are no RSRZ outliers to report.

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.