



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:11 AM UTC

PDB ID : 5AOE / pdb_00005aoe
Title : Crystal structure of pneumolysin D168A mutant.
Authors : van Pee, K.; Yildiz, O.
Deposited on : 2015-09-10
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

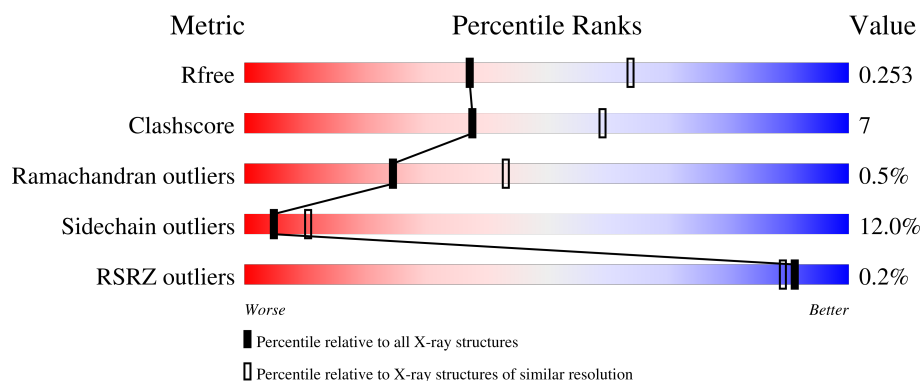
1 Overall quality at a glance

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	488	77% 17% 5%
1	B	488	74% 22% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7878 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 PNEUMOLYSIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	488	Total	C	N	O	S	0	0	0
			3862	2432	666	757	7			
1	B	488	Total	C	N	O	S	0	0	0
			3862	2432	666	757	7			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	ALA	-	expression tag	UNP Q04IN8
A	-15	HIS	-	expression tag	UNP Q04IN8
A	-14	HIS	-	expression tag	UNP Q04IN8
A	-13	HIS	-	expression tag	UNP Q04IN8
A	-12	HIS	-	expression tag	UNP Q04IN8
A	-11	HIS	-	expression tag	UNP Q04IN8
A	-10	HIS	-	expression tag	UNP Q04IN8
A	-9	SER	-	expression tag	UNP Q04IN8
A	-8	SER	-	expression tag	UNP Q04IN8
A	-7	GLY	-	expression tag	UNP Q04IN8
A	-6	LEU	-	expression tag	UNP Q04IN8
A	-5	VAL	-	expression tag	UNP Q04IN8
A	-4	PRO	-	expression tag	UNP Q04IN8
A	-3	ARG	-	expression tag	UNP Q04IN8
A	-2	GLY	-	expression tag	UNP Q04IN8
A	-1	SER	-	expression tag	UNP Q04IN8
A	0	HIS	-	expression tag	UNP Q04IN8
A	151	GLU	ASP	engineered mutation	UNP Q04IN8
B	-16	ALA	-	expression tag	UNP Q04IN8
B	-15	HIS	-	expression tag	UNP Q04IN8
B	-14	HIS	-	expression tag	UNP Q04IN8
B	-13	HIS	-	expression tag	UNP Q04IN8
B	-12	HIS	-	expression tag	UNP Q04IN8
B	-11	HIS	-	expression tag	UNP Q04IN8
B	-10	HIS	-	expression tag	UNP Q04IN8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	SER	-	expression tag	UNP Q04IN8
B	-8	SER	-	expression tag	UNP Q04IN8
B	-7	GLY	-	expression tag	UNP Q04IN8
B	-6	LEU	-	expression tag	UNP Q04IN8
B	-5	VAL	-	expression tag	UNP Q04IN8
B	-4	PRO	-	expression tag	UNP Q04IN8
B	-3	ARG	-	expression tag	UNP Q04IN8
B	-2	GLY	-	expression tag	UNP Q04IN8
B	-1	SER	-	expression tag	UNP Q04IN8
B	0	HIS	-	expression tag	UNP Q04IN8
B	151	GLU	ASP	engineered mutation	UNP Q04IN8

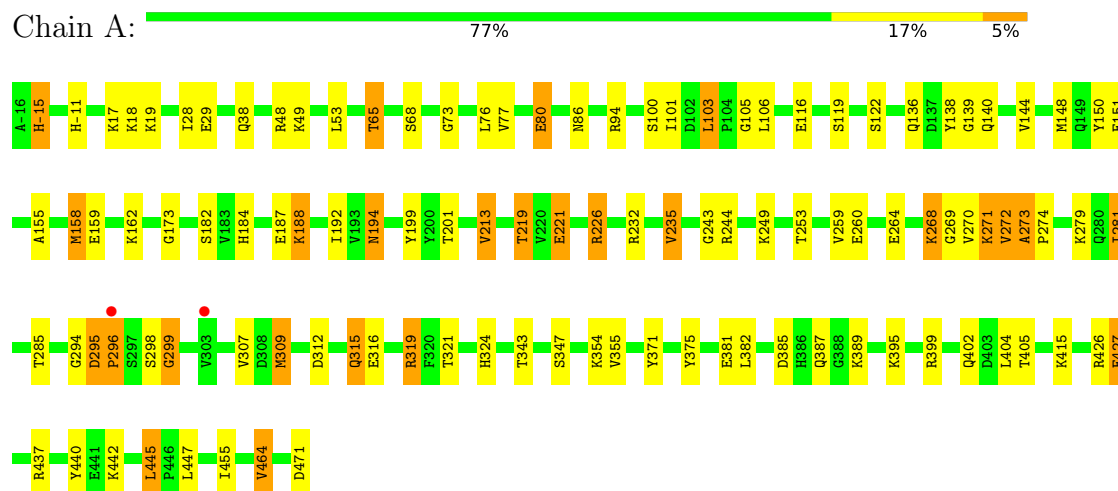
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	80	Total O 80 80	0	0
2	B	74	Total O 74 74	0	0

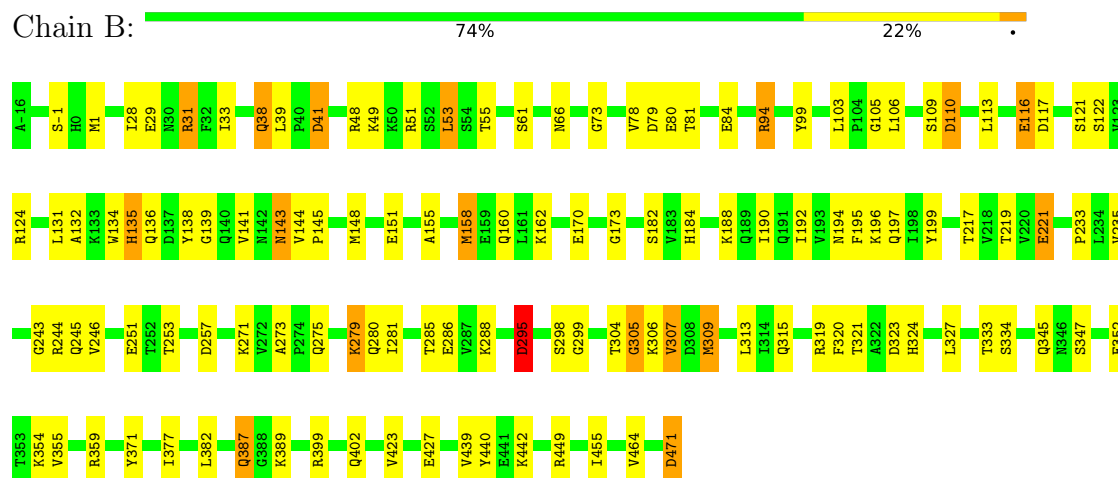
3 Residue-property plots

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 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: PNEUMOLYSIN



• Molecule 1: PNEUMOLYSIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	160.86Å 24.66Å 208.35Å 90.00° 90.26° 90.00°	Depositor
Resolution (Å)	49.49 – 2.50 49.49 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (49.49-2.50) 98.3 (49.49-2.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.51Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.222 , 0.250 0.225 , 0.253	Depositor DCC
R_{free} test set	2962 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.409 for h,-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7878	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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	0.27	0/3943	0.72	6/5359 (0.1%)
1	B	0.29	0/3943	0.73	3/5359 (0.1%)
All	All	0.28	0/7886	0.73	9/10718 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	295	ASP	CA-C-N	-7.09	113.39	120.98
1	B	295	ASP	C-N-CA	-7.09	113.39	120.98
1	A	295	ASP	CA-C-N	6.88	128.43	119.84
1	A	295	ASP	C-N-CA	6.88	128.43	119.84
1	A	86	ASN	CA-C-N	5.91	125.87	119.78
1	A	86	ASN	C-N-CA	5.91	125.87	119.78
1	A	273	ALA	CA-C-N	-5.77	113.84	119.78
1	A	273	ALA	C-N-CA	-5.77	113.84	119.78
1	B	305	GLY	N-CA-C	-5.18	105.46	112.14

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	3862	0	3793	45	0
1	B	3862	0	3793	62	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	80	0	0	3	0
2	B	74	0	0	0	0
All	All	7878	0	7586	107	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 7.

All (107) 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:38:GLN:HE21	1:B:38:GLN:HA	1.40	0.84
1:B:73:GLY:O	1:B:94:ARG:NH2	2.16	0.78
1:B:151:GLU:HB2	1:B:194:ASN:HB3	1.69	0.74
1:B:273:ALA:O	1:B:275:GLN:NE2	2.24	0.71
1:A:73:GLY:O	1:A:94:ARG:NH2	2.23	0.71
1:A:295:ASP:HB3	1:A:296:PRO:HD2	1.71	0.71
1:B:321:THR:H	1:B:324:HIS:CE1	2.12	0.68
1:B:105:GLY:HA3	1:B:138:TYR:HE2	1.61	0.66
1:B:116:GLU:OE1	1:B:117:ASP:N	2.27	0.66
1:B:131:LEU:O	1:B:135:HIS:ND1	2.29	0.65
1:B:257:ASP:OD2	1:B:354:LYS:NZ	2.30	0.65
1:A:319:ARG:HE	1:A:324:HIS:HE1	1.43	0.65
1:B:455:ILE:HG22	1:B:464:VAL:HG12	1.79	0.65
1:B:399:ARG:NH1	1:B:402:GLN:OE1	2.30	0.64
1:A:94:ARG:NH1	2:A:2038:HOH:O	2.28	0.63
1:A:48:ARG:NH1	1:A:184:HIS:O	2.32	0.63
1:A:65:THR:HG21	1:A:299:GLY:HA2	1.80	0.63
1:B:324:HIS:O	1:B:324:HIS:ND1	2.31	0.62
1:B:158:MET:HE1	1:B:173:GLY:HA3	1.82	0.62
1:B:41:ASP:OD1	1:B:41:ASP:N	2.32	0.62
1:A:182:SER:HB3	1:A:188:LYS:HG3	1.81	0.61
1:A:150:TYR:OH	1:A:268:LYS:NZ	2.34	0.61
1:B:143:ASN:OD1	1:B:145:PRO:HG3	1.99	0.61
1:B:320:PHE:HA	1:B:324:HIS:HE1	1.67	0.60
1:B:80:GLU:O	1:B:84:GLU:HG2	2.03	0.59
1:B:29:GLU:OE2	1:B:31:ARG:NH1	2.35	0.59
1:A:259:VAL:HG22	1:A:281:ILE:HD12	1.85	0.58
1:A:151:GLU:HB2	1:A:194:ASN:HB2	1.86	0.57
1:B:281:ILE:O	1:B:285:THR:OG1	2.21	0.57
1:B:251:GLU:HG3	1:B:286:GLU:HB2	1.86	0.57
1:B:219:THR:HG22	1:B:221:GLU:H	1.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:GLN:HE21	1:B:38:GLN:CA	2.17	0.56
1:B:196:LYS:HG2	1:B:245:GLN:HG3	1.88	0.56
1:B:449:ARG:HE	1:B:471:ASP:H	1.53	0.55
1:B:288:LYS:HG3	1:B:304:THR:HG22	1.88	0.55
1:A:159:GLU:OE2	1:A:162:LYS:NZ	2.39	0.55
1:B:103:LEU:HB2	1:B:106:LEU:HD12	1.88	0.55
1:B:79:ASP:OD1	1:B:81:THR:OG1	2.21	0.54
1:B:51:ARG:NE	1:B:352:GLU:OE1	2.40	0.54
1:A:309:MET:HE3	1:A:309:MET:H	1.72	0.54
1:A:269:GLY:O	1:A:271:LYS:NZ	2.36	0.54
1:B:440:TYR:CZ	1:B:442:LYS:HG3	2.43	0.53
1:B:134:TRP:HE3	1:B:135:HIS:CE1	2.26	0.53
1:B:110:ASP:OD1	1:B:110:ASP:N	2.40	0.53
1:B:48:ARG:NH2	1:B:184:HIS:O	2.37	0.50
1:B:305:GLY:HA3	1:B:309:MET:SD	2.51	0.50
1:B:-1:SER:HB2	1:B:1:MET:HE3	1.93	0.50
1:A:399:ARG:NH1	1:A:402:GLN:OE1	2.43	0.49
1:A:199:TYR:CD2	1:A:243:GLY:HA2	2.47	0.49
1:A:268:LYS:HB3	1:A:270:VAL:HG23	1.95	0.48
1:B:144:VAL:O	1:B:144:VAL:HG23	2.12	0.48
1:B:275:GLN:HB3	1:B:279:LYS:HD3	1.96	0.48
1:A:281:ILE:O	1:A:285:THR:OG1	2.26	0.48
1:B:190:ILE:HG12	1:B:251:GLU:HB3	1.96	0.48
1:B:195:PHE:HB2	1:B:246:VAL:HB	1.95	0.48
1:B:199:TYR:CD2	1:B:243:GLY:HA2	2.49	0.48
1:B:298:SER:OG	1:B:299:GLY:N	2.45	0.48
1:B:235:VAL:CG1	1:B:333:THR:HB	2.44	0.47
1:A:272:VAL:HB	1:A:274:PRO:HD2	1.97	0.47
1:B:53:LEU:HD12	1:B:160:GLN:HG2	1.95	0.47
1:B:182:SER:HB3	1:B:188:LYS:HG2	1.95	0.47
1:B:135:HIS:HA	1:B:139:GLY:HA3	1.97	0.47
1:A:-15:HIS:O	1:A:-11:HIS:ND1	2.42	0.47
1:A:38:GLN:NE2	1:A:415:LYS:HB3	2.30	0.47
1:B:295:ASP:HA	1:B:324:HIS:CD2	2.50	0.46
1:A:119:SER:H	1:A:122:SER:HB2	1.79	0.46
1:B:321:THR:H	1:B:324:HIS:HE1	1.62	0.46
1:A:38:GLN:HE22	1:A:415:LYS:HB3	1.80	0.46
1:A:309:MET:HE2	1:A:309:MET:HB3	1.71	0.46
1:A:105:GLY:HA3	1:A:138:TYR:CD1	2.49	0.46
1:B:306:LYS:HA	1:B:306:LYS:HD2	1.69	0.46
1:B:29:GLU:H	1:B:29:GLU:CD	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:THR:HG23	1:A:221:GLU:H	1.81	0.46
1:A:440:TYR:CZ	1:A:442:LYS:HG3	2.51	0.46
1:A:371:TYR:CG	1:A:427:GLU:HG3	2.50	0.45
1:B:279:LYS:HB3	1:B:279:LYS:NZ	2.32	0.45
1:A:226:ARG:NH1	2:A:2036:HOH:O	2.45	0.45
1:A:381:GLU:HG3	1:A:395:LYS:HG3	1.97	0.45
1:A:77:VAL:HG11	1:A:232:ARG:CZ	2.47	0.44
1:A:94:ARG:NH1	1:A:213:VAL:HG22	2.32	0.44
1:B:78:VAL:HB	1:B:233:PRO:HD2	1.99	0.44
1:A:151:GLU:HB2	1:A:194:ASN:CB	2.47	0.44
1:B:99:TYR:O	1:B:113:LEU:N	2.50	0.44
1:B:155:ALA:HB2	1:B:192:ILE:HD12	2.00	0.44
1:A:76:LEU:HB2	1:A:235:VAL:HG12	2.00	0.43
1:A:244:ARG:NH2	1:A:316:GLU:OE1	2.52	0.43
1:A:272:VAL:HG12	1:A:273:ALA:H	1.84	0.43
1:A:455:ILE:HG22	1:A:464:VAL:HG13	1.99	0.43
1:B:321:THR:OG1	1:B:323:ASP:OD1	2.34	0.43
1:A:294:GLY:C	1:A:324:HIS:HD2	2.26	0.42
1:A:80:GLU:H	1:A:80:GLU:HG3	1.49	0.42
1:B:387:GLN:HB2	1:B:389:LYS:HD2	2.00	0.42
1:A:445:LEU:HD12	1:A:445:LEU:HA	1.87	0.42
1:B:235:VAL:HG13	1:B:334:SER:C	2.44	0.42
1:B:132:ALA:O	1:B:136:GLN:HG2	2.20	0.41
1:B:377:ILE:HG12	1:B:423:VAL:HG13	2.02	0.41
1:A:347:SER:HB3	2:A:2022:HOH:O	2.19	0.41
1:A:103:LEU:HD12	1:A:103:LEU:HA	1.82	0.41
1:A:312:ASP:HA	1:A:315:GLN:HB2	2.02	0.41
1:A:155:ALA:HB2	1:A:192:ILE:HD12	2.02	0.41
1:B:304:THR:O	1:B:304:THR:OG1	2.31	0.41
1:A:158:MET:HE1	1:A:173:GLY:HA3	2.03	0.40
1:A:375:TYR:CD1	1:A:404:LEU:HD12	2.57	0.40
1:B:162:LYS:HD3	1:B:170:GLU:HB2	2.03	0.40
1:B:244:ARG:NH1	1:B:313:LEU:O	2.43	0.40
1:B:78:VAL:HG21	1:B:233:PRO:HG2	2.03	0.40
1:B:371:TYR:CG	1:B:427:GLU:HG3	2.56	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	486/488 (100%)	467 (96%)	15 (3%)	4 (1%)	16	31
1	B	486/488 (100%)	465 (96%)	20 (4%)	1 (0%)	43	63
All	All	972/976 (100%)	932 (96%)	35 (4%)	5 (0%)	24	43

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	296	PRO
1	B	307	VAL
1	A	-15	HIS
1	A	299	GLY
1	A	139	GLY

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	429/429 (100%)	370 (86%)	59 (14%)	3	7
1	B	429/429 (100%)	385 (90%)	44 (10%)	7	14
All	All	858/858 (100%)	755 (88%)	103 (12%)	5	10

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	LYS

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Mol	Chain	Res	Type
1	A	18	LYS
1	A	19	LYS
1	A	28	ILE
1	A	29	GLU
1	A	49	LYS
1	A	53	LEU
1	A	65	THR
1	A	68	SER
1	A	80	GLU
1	A	100	SER
1	A	101	ILE
1	A	103	LEU
1	A	106	LEU
1	A	116	GLU
1	A	136	GLN
1	A	140	GLN
1	A	144	VAL
1	A	148	MET
1	A	158	MET
1	A	187	GLU
1	A	188	LYS
1	A	194	ASN
1	A	201	THR
1	A	213	VAL
1	A	219	THR
1	A	221	GLU
1	A	226	ARG
1	A	235	VAL
1	A	249	LYS
1	A	253	THR
1	A	260	GLU
1	A	264	GLU
1	A	268	LYS
1	A	271	LYS
1	A	272	VAL
1	A	279	LYS
1	A	281	ILE
1	A	298	SER
1	A	307	VAL
1	A	309	MET
1	A	315	GLN
1	A	319	ARG

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Mol	Chain	Res	Type
1	A	321	THR
1	A	343	THR
1	A	354	LYS
1	A	355	VAL
1	A	382	LEU
1	A	385	ASP
1	A	387	GLN
1	A	389	LYS
1	A	405	THR
1	A	426	ARG
1	A	427	GLU
1	A	437	ARG
1	A	445	LEU
1	A	447	LEU
1	A	464	VAL
1	A	471	ASP
1	B	28	ILE
1	B	31	ARG
1	B	33	ILE
1	B	38	GLN
1	B	39	LEU
1	B	41	ASP
1	B	49	LYS
1	B	53	LEU
1	B	55	THR
1	B	61	SER
1	B	66	ASN
1	B	94	ARG
1	B	109	SER
1	B	110	ASP
1	B	116	GLU
1	B	121	SER
1	B	122	SER
1	B	124	ARG
1	B	135	HIS
1	B	141	VAL
1	B	143	ASN
1	B	148	MET
1	B	158	MET
1	B	197	GLN
1	B	217	THR
1	B	221	GLU

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Mol	Chain	Res	Type
1	B	253	THR
1	B	271	LYS
1	B	279	LYS
1	B	280	GLN
1	B	295	ASP
1	B	307	VAL
1	B	309	MET
1	B	315	GLN
1	B	319	ARG
1	B	327	LEU
1	B	345	GLN
1	B	347	SER
1	B	355	VAL
1	B	359	ARG
1	B	382	LEU
1	B	387	GLN
1	B	439	VAL
1	B	471	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	156	HIS
1	A	189	GLN
1	A	191	GLN
1	A	315	GLN
1	A	324	HIS
1	B	37	ASN
1	B	38	GLN
1	B	156	HIS
1	B	197	GLN
1	B	324	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	488/488 (100%)	-0.57	2 (0%) 88 86	27, 67, 131, 188	0
1	B	488/488 (100%)	-0.56	0 100 100	24, 63, 136, 196	0
All	All	976/976 (100%)	-0.57	2 (0%) 91 89	24, 65, 135, 196	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	PRO	2.2
1	A	303	VAL	2.1

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.