



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:12 PM UTC

PDB ID : 5NEN / pdb_00005nen
Title : Crystal structure of the soluble domain of LipC, a membrane fusion protein of a type I secretion system
Authors : Murata, D.; Akutsu, M.; Takano, K.
Deposited on : 2017-03-11
Resolution : 2.90 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

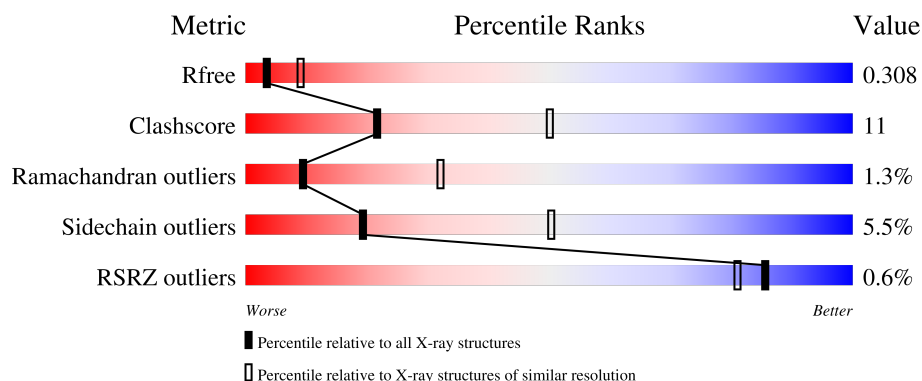
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	448	
1	B	448	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3604 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 Lipase C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			1982	1220	360	396	6			
1	B	213	Total	C	N	O	S	0	0	0
			1622	1000	292	325	5			

There are 94 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	MET	deletion	UNP Q54457
A	?	-	GLY	deletion	UNP Q54457
A	?	-	TRP	deletion	UNP Q54457
A	?	-	LEU	deletion	UNP Q54457
A	?	-	VAL	deletion	UNP Q54457
A	?	-	VAL	deletion	UNP Q54457
A	?	-	GLY	deletion	UNP Q54457
A	?	-	ILE	deletion	UNP Q54457
A	?	-	GLY	deletion	UNP Q54457
A	?	-	LEU	deletion	UNP Q54457
A	?	-	PHE	deletion	UNP Q54457
A	?	-	GLY	deletion	UNP Q54457
A	?	-	PHE	deletion	UNP Q54457
A	?	-	LEU	deletion	UNP Q54457
A	?	-	ALA	deletion	UNP Q54457
A	?	-	TRP	deletion	UNP Q54457
A	?	-	ALA	deletion	UNP Q54457
A	?	-	ALA	deletion	UNP Q54457
A	?	-	PHE	deletion	UNP Q54457
A	?	-	ALA	deletion	UNP Q54457
A	?	-	PRO	deletion	UNP Q54457
A	423	LEU	-	expression tag	UNP Q54457
A	424	GLU	-	expression tag	UNP Q54457
A	425	ILE	-	expression tag	UNP Q54457
A	426	LYS	-	expression tag	UNP Q54457

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Chain	Residue	Modelled	Actual	Comment	Reference
A	427	ARG	-	expression tag	UNP Q54457
A	428	ALA	-	expression tag	UNP Q54457
A	429	SER	-	expression tag	UNP Q54457
A	430	GLN	-	expression tag	UNP Q54457
A	431	PRO	-	expression tag	UNP Q54457
A	432	GLU	-	expression tag	UNP Q54457
A	433	LEU	-	expression tag	UNP Q54457
A	434	ALA	-	expression tag	UNP Q54457
A	435	PRO	-	expression tag	UNP Q54457
A	436	GLU	-	expression tag	UNP Q54457
A	437	ASP	-	expression tag	UNP Q54457
A	438	PRO	-	expression tag	UNP Q54457
A	439	GLU	-	expression tag	UNP Q54457
A	440	ASP	-	expression tag	UNP Q54457
A	441	VAL	-	expression tag	UNP Q54457
A	442	GLU	-	expression tag	UNP Q54457
A	443	HIS	-	expression tag	UNP Q54457
A	444	HIS	-	expression tag	UNP Q54457
A	445	HIS	-	expression tag	UNP Q54457
A	446	HIS	-	expression tag	UNP Q54457
A	447	HIS	-	expression tag	UNP Q54457
A	448	HIS	-	expression tag	UNP Q54457
B	?	-	MET	deletion	UNP Q54457
B	?	-	GLY	deletion	UNP Q54457
B	?	-	TRP	deletion	UNP Q54457
B	?	-	LEU	deletion	UNP Q54457
B	?	-	VAL	deletion	UNP Q54457
B	?	-	VAL	deletion	UNP Q54457
B	?	-	GLY	deletion	UNP Q54457
B	?	-	ILE	deletion	UNP Q54457
B	?	-	GLY	deletion	UNP Q54457
B	?	-	LEU	deletion	UNP Q54457
B	?	-	PHE	deletion	UNP Q54457
B	?	-	GLY	deletion	UNP Q54457
B	?	-	PHE	deletion	UNP Q54457
B	?	-	LEU	deletion	UNP Q54457
B	?	-	ALA	deletion	UNP Q54457
B	?	-	TRP	deletion	UNP Q54457
B	?	-	ALA	deletion	UNP Q54457
B	?	-	ALA	deletion	UNP Q54457
B	?	-	PHE	deletion	UNP Q54457
B	?	-	ALA	deletion	UNP Q54457

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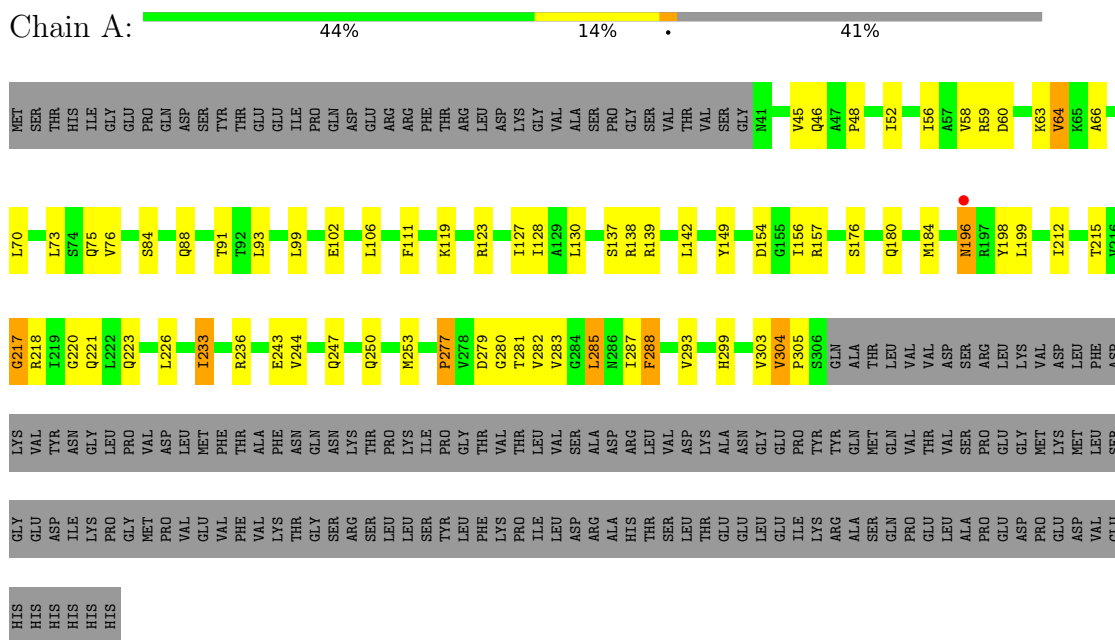
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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP Q54457
B	423	LEU	-	expression tag	UNP Q54457
B	424	GLU	-	expression tag	UNP Q54457
B	425	ILE	-	expression tag	UNP Q54457
B	426	LYS	-	expression tag	UNP Q54457
B	427	ARG	-	expression tag	UNP Q54457
B	428	ALA	-	expression tag	UNP Q54457
B	429	SER	-	expression tag	UNP Q54457
B	430	GLN	-	expression tag	UNP Q54457
B	431	PRO	-	expression tag	UNP Q54457
B	432	GLU	-	expression tag	UNP Q54457
B	433	LEU	-	expression tag	UNP Q54457
B	434	ALA	-	expression tag	UNP Q54457
B	435	PRO	-	expression tag	UNP Q54457
B	436	GLU	-	expression tag	UNP Q54457
B	437	ASP	-	expression tag	UNP Q54457
B	438	PRO	-	expression tag	UNP Q54457
B	439	GLU	-	expression tag	UNP Q54457
B	440	ASP	-	expression tag	UNP Q54457
B	441	VAL	-	expression tag	UNP Q54457
B	442	GLU	-	expression tag	UNP Q54457
B	443	HIS	-	expression tag	UNP Q54457
B	444	HIS	-	expression tag	UNP Q54457
B	445	HIS	-	expression tag	UNP Q54457
B	446	HIS	-	expression tag	UNP Q54457
B	447	HIS	-	expression tag	UNP Q54457
B	448	HIS	-	expression tag	UNP Q54457

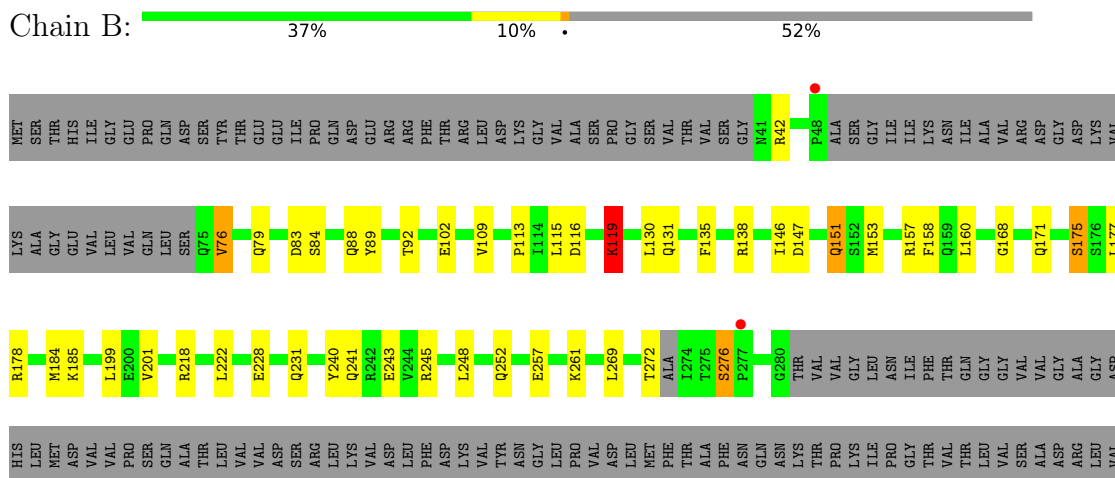
3 Residue-property plots

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: Lipase C



• Molecule 1: Lipase C



ASP	LEU
LYS	THR
ALA	GLU
ASN	GLU
GLY	LEU
GLY	GLU
PRO	ILE
TYR	LYS
ARG	ARG
GLN	ALA
MET	SER
GLN	SER
VAL	PRO
THR	GLU
VAL	ALA
SER	LEU
PRO	PRO
GLU	GLU
GLY	ASP
MET	PRO
LYS	GLU
MET	ASP
LEU	VAL
SER	GLU
GLY	HIS
GLU	HIS
ASP	HIS
ILE	HIS
LYS	HIS
PRO	HIS
GLY	
MET	
PRO	
VAL	
GLU	
VAL	
PHE	
VAL	
LYS	
THR	
GLY	
SER	
ARG	
SER	
LEU	
LEU	
SER	
TYR	
LEU	
PHE	
LYS	
PRO	
ILE	
LEU	
ASP	
ARG	
ALA	
HIS	
THR	
SER	

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	126.31Å 126.31Å 71.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.35 – 2.90 41.35 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (41.35-2.90) 100.0 (41.35-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.81 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.252 , 0.301 0.261 , 0.308	Depositor DCC
R_{free} test set	1382 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	82.5	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 41.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.080 for -h,-k,l 0.345 for h,-h-k,-l 0.087 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3604	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.17% 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	0.70	0/1998	1.06	5/2706 (0.2%)
1	B	0.70	0/1635	1.15	5/2202 (0.2%)
All	All	0.70	0/3633	1.11	10/4908 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	276	SER	CA-C-N	-14.16	106.43	120.31
1	B	276	SER	C-N-CA	-14.16	106.43	120.31
1	A	304	VAL	CA-C-N	9.31	131.48	119.84
1	A	304	VAL	C-N-CA	9.31	131.48	119.84
1	B	76	VAL	N-CA-C	7.35	119.02	111.00
1	A	217	GLY	N-CA-C	-6.28	105.20	112.73
1	B	119	LYS	CB-CA-C	-5.83	100.78	110.68
1	A	196	ASN	N-CA-C	5.65	117.44	111.28
1	B	175	SER	N-CA-C	-5.17	105.54	111.07
1	A	233	ILE	CB-CA-C	-5.03	105.54	111.97

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	1982	0	1914	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1622	0	1537	34	0
All	All	3604	0	3451	76	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 11.

All (76) 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:73:LEU:HD23	1:A:75:GLN:H	1.34	0.92
1:A:88:GLN:OE1	1:B:218:ARG:NH1	2.17	0.77
1:B:113:PRO:HA	1:B:116:ASP:HB3	1.68	0.76
1:A:102:GLU:OE1	1:A:138:ARG:NH1	2.22	0.72
1:A:154:ASP:OD1	1:A:157:ARG:NH1	2.27	0.68
1:A:63:LYS:HA	1:A:281:THR:HA	1.77	0.67
1:B:241:GLN:OE1	1:B:245:ARG:NH1	2.27	0.65
1:A:282:VAL:HG12	1:A:303:VAL:HG12	1.79	0.64
1:A:277:PRO:HD2	1:A:303:VAL:HG21	1.81	0.63
1:B:147:ASP:O	1:B:151:GLN:HG2	1.99	0.62
1:B:184:MET:HE1	1:B:201:VAL:HG21	1.82	0.62
1:A:250:GLN:HA	1:A:253:MET:HE3	1.82	0.60
1:A:59:ARG:HA	1:A:285:LEU:HD21	1.83	0.60
1:A:64:VAL:HB	1:A:280:GLY:H	1.68	0.59
1:B:102:GLU:HB3	1:B:240:TYR:OH	2.04	0.57
1:A:52:ILE:HG12	1:A:293:VAL:HG12	1.86	0.56
1:A:60:ASP:H	1:A:285:LEU:HD11	1.69	0.56
1:A:102:GLU:CD	1:A:138:ARG:HH11	2.13	0.56
1:B:138:ARG:NH2	1:B:243:GLU:OE2	2.38	0.56
1:A:137:SER:OG	1:B:151:GLN:NE2	2.38	0.56
1:B:228:GLU:O	1:B:231:GLN:HG2	2.07	0.55
1:A:123:ARG:NH2	1:B:158:PHE:O	2.31	0.53
1:A:156:ILE:HG21	1:A:226:LEU:HG	1.89	0.53
1:A:64:VAL:HB	1:A:280:GLY:O	2.08	0.53
1:B:84:SER:O	1:B:88:GLN:HG3	2.09	0.53
1:A:56:ILE:HG22	1:A:58:VAL:H	1.74	0.53
1:A:243:GLU:O	1:A:247:GLN:HG3	2.09	0.52
1:B:245:ARG:HG3	1:B:245:ARG:HH11	1.74	0.52
1:A:84:SER:O	1:A:88:GLN:HG3	2.09	0.52
1:A:184:MET:HE2	1:A:198:TYR:HA	1.92	0.52
1:A:130:LEU:HD21	1:B:151:GLN:O	2.10	0.51
1:B:116:ASP:O	1:B:119:LYS:HD3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:176:SER:O	1:A:180:GLN:HG2	2.12	0.50
1:A:220:GLY:HA2	1:A:223:GLN:OE1	2.11	0.50
1:A:196:ASN:OD1	1:A:196:ASN:C	2.54	0.50
1:B:184:MET:CE	1:B:201:VAL:HG21	2.41	0.49
1:A:106:LEU:O	1:A:139:ARG:NH2	2.45	0.49
1:A:46:GLN:HA	1:A:299:HIS:HA	1.94	0.49
1:B:109:VAL:HG23	1:B:135:PHE:CD2	2.48	0.48
1:B:79:GLN:NE2	1:B:83:ASP:OD1	2.44	0.48
1:B:151:GLN:HG2	1:B:151:GLN:H	1.40	0.48
1:B:175:SER:O	1:B:178:ARG:HB3	2.14	0.47
1:B:248:LEU:O	1:B:252:GLN:HG3	2.15	0.47
1:A:73:LEU:O	1:A:75:GLN:HG3	2.14	0.47
1:B:89:TYR:O	1:B:92:THR:OG1	2.25	0.47
1:B:130:LEU:HD12	1:B:130:LEU:HA	1.76	0.46
1:B:228:GLU:HA	1:B:231:GLN:HG2	1.98	0.46
1:B:269:LEU:O	1:B:272:THR:HG23	2.15	0.46
1:B:113:PRO:HA	1:B:116:ASP:CB	2.44	0.46
1:B:102:GLU:OE2	1:B:138:ARG:NH1	2.42	0.45
1:A:64:VAL:N	1:A:280:GLY:O	2.50	0.45
1:A:218:ARG:HH22	1:B:261:LYS:HZ1	1.64	0.45
1:A:243:GLU:CG	1:A:247:GLN:HE21	2.29	0.45
1:A:217:GLY:O	1:A:221:GLN:HG2	2.17	0.45
1:A:243:GLU:HG2	1:A:247:GLN:HE21	1.82	0.45
1:A:111:PHE:CE2	1:A:128:ILE:HG23	2.52	0.44
1:A:99:LEU:HD23	1:A:99:LEU:HA	1.69	0.44
1:B:160:LEU:HD21	1:B:222:LEU:HB2	1.99	0.44
1:A:226:LEU:HD23	1:A:226:LEU:HA	1.79	0.44
1:B:116:ASP:OD1	1:B:119:LYS:HE3	2.18	0.43
1:A:64:VAL:HG12	1:A:279:ASP:HA	2.01	0.42
1:A:91:THR:HG23	1:A:127:ILE:HG12	2.01	0.42
1:A:93:LEU:HA	1:A:93:LEU:HD23	1.74	0.42
1:A:149:TYR:HB3	1:A:233:ILE:HD11	2.00	0.42
1:B:199:LEU:HD12	1:B:199:LEU:H	1.84	0.42
1:B:177:LEU:HA	1:B:177:LEU:HD23	1.78	0.42
1:A:142:LEU:HD13	1:A:236:ARG:HH12	1.85	0.42
1:A:58:VAL:HG21	1:A:70:LEU:HD22	2.02	0.41
1:B:160:LEU:HD23	1:B:160:LEU:HA	1.83	0.41
1:A:288:PHE:CD1	1:A:288:PHE:N	2.86	0.41
1:A:127:ILE:HD12	1:A:127:ILE:HA	1.83	0.41
1:A:58:VAL:HG23	1:A:70:LEU:HA	2.02	0.40
1:B:168:GLY:O	1:B:171:GLN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:VAL:HG12	1:A:282:VAL:HG21	2.02	0.40
1:A:287:ILE:HG23	1:A:288:PHE:CD1	2.57	0.40
1:B:153:MET:HE2	1:B:157:ARG:NH2	2.35	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	264/448 (59%)	248 (94%)	12 (4%)	4 (2%)	8	28
1	B	207/448 (46%)	202 (98%)	3 (1%)	2 (1%)	12	39
All	All	471/896 (53%)	450 (96%)	15 (3%)	6 (1%)	9	32

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	305	PRO
1	A	66	ALA
1	B	276	SER
1	A	48	PRO
1	A	277	PRO
1	B	42	ARG

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	202/388 (52%)	190 (94%)	12 (6%)	18	48
1	B	163/388 (42%)	155 (95%)	8 (5%)	22	54
All	All	365/776 (47%)	345 (94%)	20 (6%)	19	50

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	VAL
1	A	64	VAL
1	A	76	VAL
1	A	119	LYS
1	A	199	LEU
1	A	212	ILE
1	A	215	THR
1	A	244	VAL
1	A	283	VAL
1	A	285	LEU
1	A	288	PHE
1	A	304	VAL
1	B	76	VAL
1	B	115	LEU
1	B	119	LYS
1	B	131	GLN
1	B	146	ILE
1	B	151	GLN
1	B	185	LYS
1	B	257	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	230	GLN
1	A	241	GLN
1	A	247	GLN
1	B	140	GLN
1	B	151	GLN

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 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	266/448 (59%)	-0.89	1 (0%) 88 85	48, 88, 161, 201	0
1	B	213/448 (47%)	-0.93	2 (0%) 81 75	52, 79, 123, 187	0
All	All	479/896 (53%)	-0.91	3 (0%) 85 81	48, 83, 151, 201	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	277	PRO	3.3
1	A	196	ASN	2.8
1	B	48	PRO	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.