



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:10 AM UTC

PDB ID : 3DO9 / pdb_00003do9
Title : Crystal structure of protein ba1542 from bacillus anthracis str.ames
Authors : Patskovsky, Y.; Ozyurt, S.; Freeman, J.; Iizuka, M.; Maletic, M.; Smith, D.; Wasserman, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2008-07-03
Resolution : 2.75 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

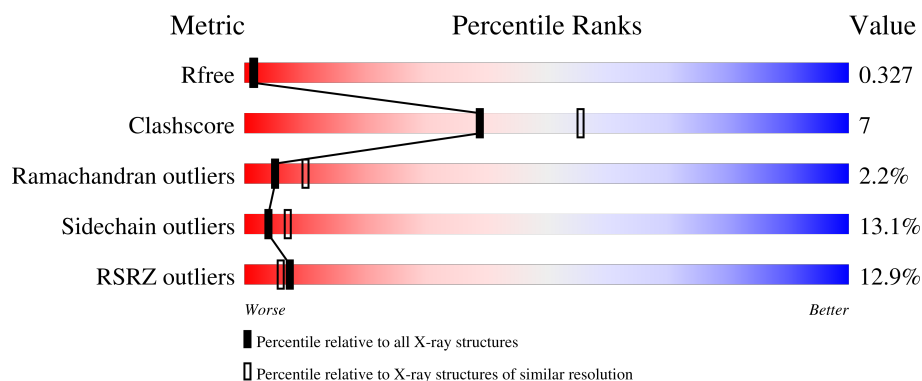
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	188	3% 67% 23% 5% 5%
1	B	188	16% 67% 23% • • 6%
1	C	188	16% 66% 18% • 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4463 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 UPF0302 protein BA_1542/GBAA1542/BAS1430.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	5	0
			1554	992	272	282	8			
1	B	177	Total	C	N	O	S	0	1	0
			1505	961	265	271	8			
1	C	164	Total	C	N	O	S	0	0	0
			1395	894	245	249	7			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q81SV3
A	1	LEU	-	expression tag	UNP Q81SV3
A	179	GLU	-	expression tag	UNP Q81SV3
A	180	GLY	-	expression tag	UNP Q81SV3
A	181	HIS	-	expression tag	UNP Q81SV3
A	182	HIS	-	expression tag	UNP Q81SV3
A	183	HIS	-	expression tag	UNP Q81SV3
A	184	HIS	-	expression tag	UNP Q81SV3
A	185	HIS	-	expression tag	UNP Q81SV3
A	186	HIS	-	expression tag	UNP Q81SV3
B	0	SER	-	expression tag	UNP Q81SV3
B	1	LEU	-	expression tag	UNP Q81SV3
B	179	GLU	-	expression tag	UNP Q81SV3
B	180	GLY	-	expression tag	UNP Q81SV3
B	181	HIS	-	expression tag	UNP Q81SV3
B	182	HIS	-	expression tag	UNP Q81SV3
B	183	HIS	-	expression tag	UNP Q81SV3
B	184	HIS	-	expression tag	UNP Q81SV3
B	185	HIS	-	expression tag	UNP Q81SV3
B	186	HIS	-	expression tag	UNP Q81SV3
C	0	SER	-	expression tag	UNP Q81SV3
C	1	LEU	-	expression tag	UNP Q81SV3
C	179	GLU	-	expression tag	UNP Q81SV3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	180	GLY	-	expression tag	UNP Q81SV3
C	181	HIS	-	expression tag	UNP Q81SV3
C	182	HIS	-	expression tag	UNP Q81SV3
C	183	HIS	-	expression tag	UNP Q81SV3
C	184	HIS	-	expression tag	UNP Q81SV3
C	185	HIS	-	expression tag	UNP Q81SV3
C	186	HIS	-	expression tag	UNP Q81SV3

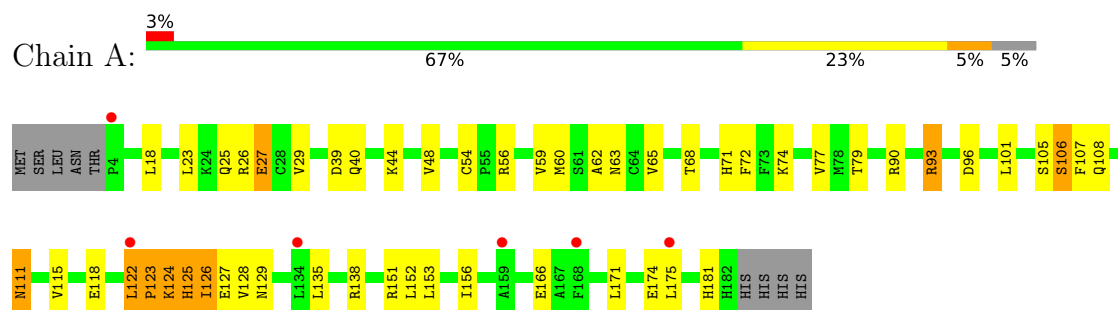
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total O 4 4	0	0
2	B	5	Total O 5 5	0	0

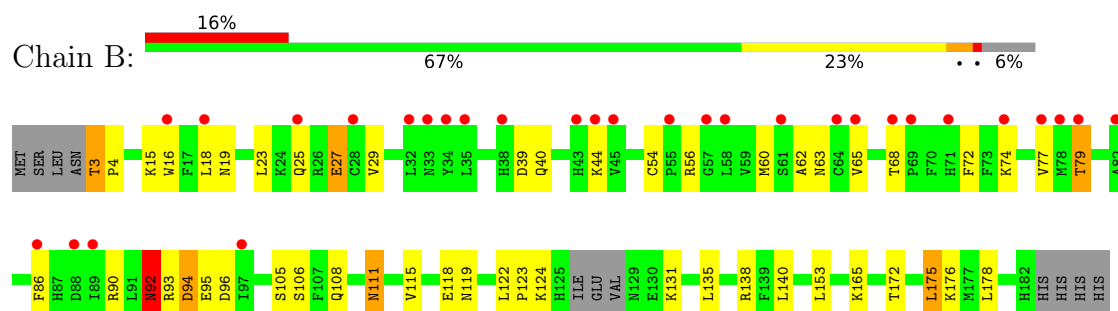
3 Residue-property plots [i](#)

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.

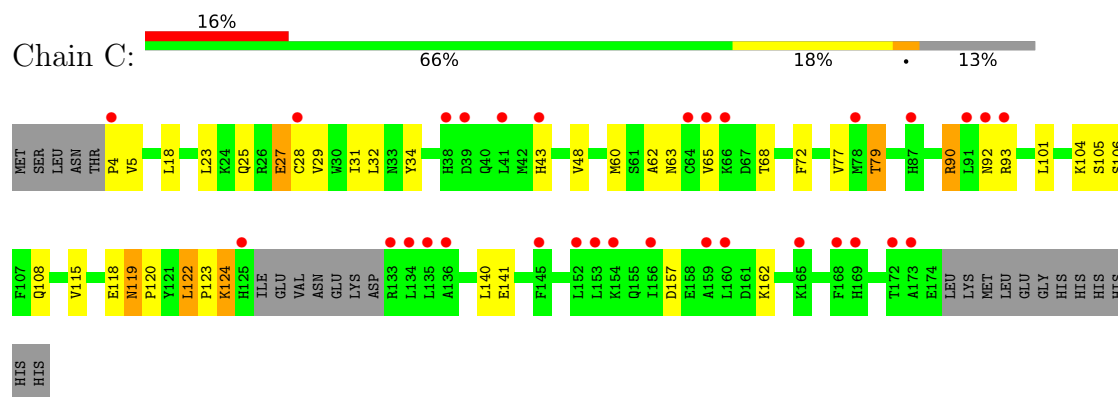
- Molecule 1: UPF0302 protein BA_1542/GBAA1542/BAS1430



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4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	127.74Å 127.74Å 196.07Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.75 20.00 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-2.75) 99.5 (20.00-2.75)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.264 , 0.312 0.292 , 0.327	Depositor DCC
R_{free} test set	847 reflections (3.18%)	wwPDB-VP
Wilson B-factor (Å ²)	50.1	Xtriage
Anisotropy	0.130	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4463	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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	0.43	0/1598	0.92	5/2150 (0.2%)
1	B	0.43	0/1544	0.92	5/2076 (0.2%)
1	C	0.44	0/1429	0.93	2/1922 (0.1%)
All	All	0.43	0/4571	0.92	12/6148 (0.2%)

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	2
1	B	0	2
1	C	0	1
All	All	0	5

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	135	LEU	N-CA-C	-6.50	103.70	111.69
1	A	54	CYS	CA-C-N	6.17	126.63	119.47
1	A	54	CYS	C-N-CA	6.17	126.63	119.47
1	B	54	CYS	CA-C-N	5.95	127.27	119.84
1	B	54	CYS	C-N-CA	5.95	127.27	119.84
1	B	68	THR	CA-C-N	5.61	126.86	119.84
1	B	68	THR	C-N-CA	5.61	126.86	119.84
1	C	68	THR	CA-C-N	5.53	124.99	119.24
1	C	68	THR	C-N-CA	5.53	124.99	119.24
1	B	131	LYS	N-CA-C	-5.24	106.89	113.28
1	A	68	THR	CA-C-N	5.07	124.51	119.24
1	A	68	THR	C-N-CA	5.07	124.51	119.24

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	124	LYS	Peptide
1	A	93	ARG	Peptide
1	B	3	THR	Peptide
1	B	94	ASP	Peptide
1	C	92	ASN	Peptide

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	1554	0	1514	31	0
1	B	1505	0	1471	18	0
1	C	1395	0	1364	13	0
2	A	4	0	0	0	0
2	B	5	0	0	1	0
All	All	4463	0	4349	60	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 (60) 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:124:LYS:HG2	1:A:125:HIS:HB2	1.33	1.10
1:A:124:LYS:HG2	1:A:125:HIS:CB	2.06	0.85
1:A:124:LYS:CG	1:A:125:HIS:N	2.43	0.80
1:A:126:ILE:O	1:A:128:VAL:N	2.23	0.72
1:A:111:ASN:H	1:A:111:ASN:HD22	1.44	0.66
1:A:124:LYS:HG2	1:A:125:HIS:N	2.13	0.64
1:A:126:ILE:C	1:A:128:VAL:H	2.05	0.64
1:B:105:SER:HB2	1:B:108:GLN:HB3	1.83	0.60
1:A:111:ASN:HD22	1:A:111:ASN:N	2.03	0.57
1:B:111:ASN:HD22	1:B:111:ASN:H	1.51	0.57
1:B:94:ASP:O	1:B:95:GLU:CD	2.48	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:LYS:HG3	1:A:125:HIS:H	1.70	0.56
1:A:124:LYS:HG3	1:A:125:HIS:N	2.21	0.55
1:B:44:LYS:HB3	1:B:96:ASP:HA	1.88	0.55
1:B:3:THR:HB	1:B:4:PRO:CD	2.38	0.54
1:A:44:LYS:HB3	1:A:96:ASP:HA	1.89	0.54
1:C:119:ASN:HD21	1:C:122:LEU:HD23	1.74	0.52
1:C:34:TYR:CE1	1:C:90:ARG:HD2	2.46	0.51
1:A:105:SER:O	1:A:106:SER:C	2.54	0.51
1:C:105:SER:HB2	1:C:108:GLN:HB3	1.93	0.51
1:B:86:PHE:O	1:B:90:ARG:HG2	2.11	0.51
1:B:165:LYS:HB2	2:B:187:HOH:O	2.10	0.51
1:B:3:THR:HB	1:B:4:PRO:HD2	1.92	0.50
1:A:124:LYS:O	1:A:126:ILE:N	2.44	0.50
1:B:111:ASN:HD22	1:B:111:ASN:N	2.09	0.48
1:B:18:LEU:HD22	1:B:29:VAL:HG13	1.96	0.48
1:A:23:LEU:HA	1:A:62:ALA:HA	1.96	0.47
1:B:23:LEU:HA	1:B:62:ALA:HA	1.95	0.47
1:C:4:PRO:HB2	1:C:5:VAL:H	1.58	0.47
1:A:108:GLN:O	1:A:108:GLN:HG2	2.14	0.47
1:A:56:ARG:HD2	1:A:74:LYS:HZ2	1.79	0.47
1:A:105:SER:O	1:A:107:PHE:N	2.48	0.46
1:A:124:LYS:HG2	1:A:125:HIS:CA	2.45	0.46
1:A:18:LEU:HD22	1:A:29:VAL:HG13	1.98	0.45
1:B:72:PHE:HB3	1:B:79:THR:HG23	1.96	0.45
1:C:23:LEU:HA	1:C:62:ALA:HA	1.96	0.45
1:C:25:GLN:HG2	1:C:27:GLU:HG2	1.97	0.45
1:C:18:LEU:HD22	1:C:29:VAL:HG13	1.98	0.44
1:C:28:CYS:HA	1:C:31:ILE:HD12	1.98	0.44
1:A:153:LEU:HA	1:A:156:ILE:HD12	1.99	0.44
1:C:32:LEU:HG	1:C:60:MET:HE1	1.98	0.44
1:A:72:PHE:HB3	1:A:79:THR:HG23	2.00	0.44
1:C:28:CYS:HB3	1:C:60:MET:HE3	2.00	0.44
1:B:25:GLN:HG2	1:B:27:GLU:HG2	2.00	0.44
1:A:26:ARG:HD2	1:B:153:LEU:HD21	1.99	0.43
1:A:124:LYS:C	1:A:126:ILE:N	2.76	0.43
1:C:119:ASN:HA	1:C:120:PRO:HD3	1.86	0.43
1:B:92:ASN:HD22	1:B:92:ASN:N	2.17	0.43
1:C:72:PHE:HB3	1:C:79:THR:HG23	2.00	0.43
1:C:124:LYS:HB2	1:C:124:LYS:HE3	1.80	0.42
1:A:122:LEU:HD22	1:A:122:LEU:HA	1.87	0.42
1:A:25:GLN:HG2	1:A:27:GLU:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ARG:NH2	1:B:175:LEU:HD21	2.36	0.41
1:B:15:LYS:O	1:B:19:ASN:ND2	2.52	0.41
1:A:122:LEU:HA	1:A:123:PRO:HD3	1.91	0.41
1:B:172:THR:HG22	1:B:176:LYS:HE2	2.03	0.41
1:A:151:ARG:HD2	1:A:151:ARG:HA	1.87	0.41
1:A:59:VAL:HB	1:A:71:HIS:HB2	2.02	0.41
1:A:171:LEU:HA	1:A:174:GLU:HB2	2.04	0.40
1:A:124:LYS:H	1:A:125:HIS:HB3	1.86	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	182/188 (97%)	167 (92%)	9 (5%)	6 (3%)	3	5
1	B	174/188 (93%)	163 (94%)	8 (5%)	3 (2%)	7	14
1	C	160/188 (85%)	146 (91%)	12 (8%)	2 (1%)	9	18
All	All	516/564 (92%)	476 (92%)	29 (6%)	11 (2%)	5	11

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	PRO
1	A	106	SER
1	A	125	HIS
1	B	92	ASN
1	B	123	PRO
1	C	106	SER
1	C	123	PRO
1	A	127	GLU
1	B	106	SER

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Mol	Chain	Res	Type
1	A	93	ARG
1	A	126	ILE

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	172/177 (97%)	152 (88%)	20 (12%)	5	10
1	B	167/177 (94%)	143 (86%)	24 (14%)	3	5
1	C	154/177 (87%)	134 (87%)	20 (13%)	4	7
All	All	493/531 (93%)	429 (87%)	64 (13%)	4	7

All (64) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	GLU
1	A	39	ASP
1	A	40	GLN
1	A	48	VAL
1	A	60	MET
1	A	63	ASN
1	A	65	VAL
1	A	77	VAL
1	A	90	ARG
1	A	101	LEU
1	A	111	ASN
1	A	115	VAL
1	A	118	GLU
1	A	122	LEU
1	A	129	ASN
1	A	138	ARG
1	A	152	LEU
1	A	166	GLU
1	A	175	LEU
1	A	181	HIS

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Mol	Chain	Res	Type
1	B	16	TRP
1	B	27	GLU
1	B	39	ASP
1	B	40	GLN
1	B	56	ARG
1	B	60	MET
1	B	63	ASN
1	B	65	VAL
1	B	74	LYS
1	B	77	VAL
1	B	79	THR
1	B	92	ASN
1	B	93	ARG
1	B	111	ASN
1	B	115	VAL
1	B	118	GLU
1	B	119	ASN
1	B	122	LEU
1	B	124	LYS
1	B	135	LEU
1	B	138	ARG
1	B	140	LEU
1	B	175	LEU
1	B	178	LEU
1	C	27	GLU
1	C	43	HIS
1	C	48	VAL
1	C	63	ASN
1	C	65	VAL
1	C	77	VAL
1	C	79	THR
1	C	90	ARG
1	C	93	ARG
1	C	101	LEU
1	C	104	LYS
1	C	115	VAL
1	C	118	GLU
1	C	119	ASN
1	C	122	LEU
1	C	124	LYS
1	C	140	LEU
1	C	141	GLU

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Mol	Chain	Res	Type
1	C	157	ASP
1	C	162	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	40	GLN
1	A	100	GLN
1	A	102	ASN
1	A	108	GLN
1	A	111	ASN
1	A	119	ASN
1	B	43	HIS
1	B	63	ASN
1	B	111	ASN
1	B	119	ASN
1	C	50	HIS
1	C	63	ASN
1	C	111	ASN
1	C	119	ASN
1	C	125	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 [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	179/188 (95%)	0.49	6 (3%)	48 46	20, 72, 133, 174	5 (2%)
1	B	177/188 (94%)	0.97	30 (16%)	4 4	23, 90, 137, 158	1 (0%)
1	C	164/188 (87%)	1.00	31 (18%)	3 3	37, 85, 160, 194	0
All	All	520/564 (92%)	0.81	67 (12%)	7 6	20, 81, 151, 194	6 (1%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	97	ILE	4.7
1	C	41	LEU	4.5
1	B	64	CYS	4.4
1	B	65	VAL	4.2
1	B	79	THR	4.0
1	C	153	LEU	3.9
1	C	38	HIS	3.4
1	B	58	LEU	3.4
1	C	125	HIS	3.4
1	C	160	LEU	3.3
1	C	173	ALA	3.3
1	B	34	TYR	3.2
1	C	152	LEU	3.1
1	B	82	ALA	3.0
1	B	61	SER	2.8
1	B	78	MET	2.8
1	A	4	PRO	2.7
1	C	165	LYS	2.7
1	A	168	PHE	2.7
1	B	89	ILE	2.7
1	C	134	LEU	2.7
1	C	136	ALA	2.7
1	C	39	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	169	HIS	2.7
1	B	74	LYS	2.6
1	B	69	PRO	2.6
1	B	43	HIS	2.6
1	B	57	GLY	2.6
1	B	33	ASN	2.6
1	C	43	HIS	2.6
1	C	154	LYS	2.5
1	C	65	VAL	2.5
1	C	28	CYS	2.5
1	C	156	ILE	2.5
1	C	78	MET	2.5
1	C	64	CYS	2.5
1	B	18	LEU	2.5
1	C	159	ALA	2.5
1	B	28	CYS	2.4
1	B	45	VAL	2.4
1	A	134	LEU	2.4
1	B	38	HIS	2.4
1	C	87	HIS	2.4
1	B	16	TRP	2.4
1	C	145	PHE	2.4
1	C	172	THR	2.4
1	B	71	HIS	2.3
1	B	68	THR	2.3
1	C	4	PRO	2.2
1	B	77	VAL	2.2
1	C	168	PHE	2.2
1	B	55	PRO	2.2
1	C	66	LYS	2.2
1	C	133	ARG	2.2
1	B	44	LYS	2.1
1	B	32	LEU	2.1
1	B	35	LEU	2.1
1	C	135	LEU	2.1
1	B	86	PHE	2.1
1	C	93	ARG	2.1
1	C	91	LEU	2.1
1	A	175	LEU	2.1
1	C	92	ASN	2.0
1	A	159	ALA	2.0
1	B	88	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	122	LEU	2.0
1	B	25	GLN	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 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.