



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 18, 2024 – 01:40 AM EDT

PDB ID : 5TLC
Title : Crystal structure of BdsA from Bacillus subtilis WU-S2B
Authors : Okai, M.; Lee, W.C.; Tanokura, M.
Deposited on : 2016-10-11
Resolution : 2.80 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	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

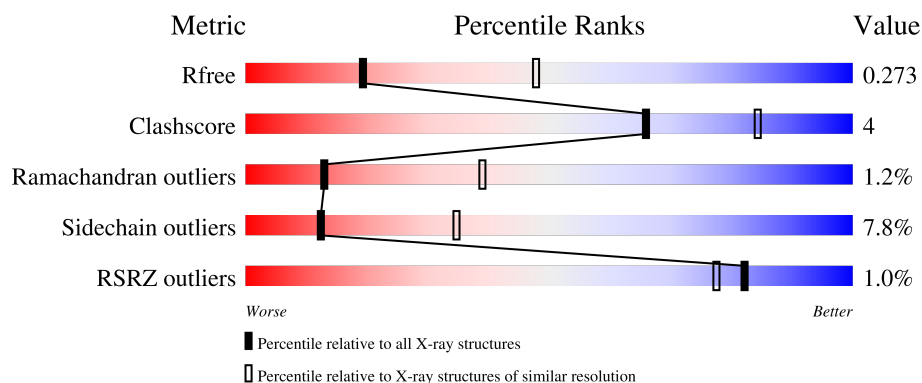
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	453	 78% 16% . .
1	B	453	 80% 14% . .
1	C	453	 75% 10% . 12%
1	D	453	 74% 9% . 15%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12884 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 Dibenzothiophene desulfurization enzyme A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3388	2148	601	634	5			
1	B	436	Total	C	N	O	S	0	0	0
			3379	2144	601	629	5			
1	C	400	Total	C	N	O	S	0	0	0
			3116	1975	557	581	3			
1	D	383	Total	C	N	O	S	0	0	0
			2981	1895	535	548	3			

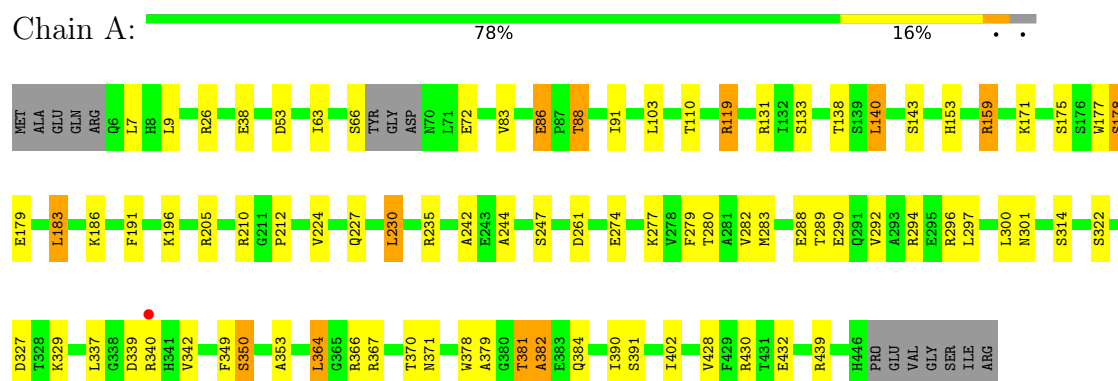
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	11	Total	O	0	0
			11	11		
2	B	5	Total	O	0	0
			5	5		
2	C	2	Total	O	0	0
			2	2		
2	D	2	Total	O	0	0
			2	2		

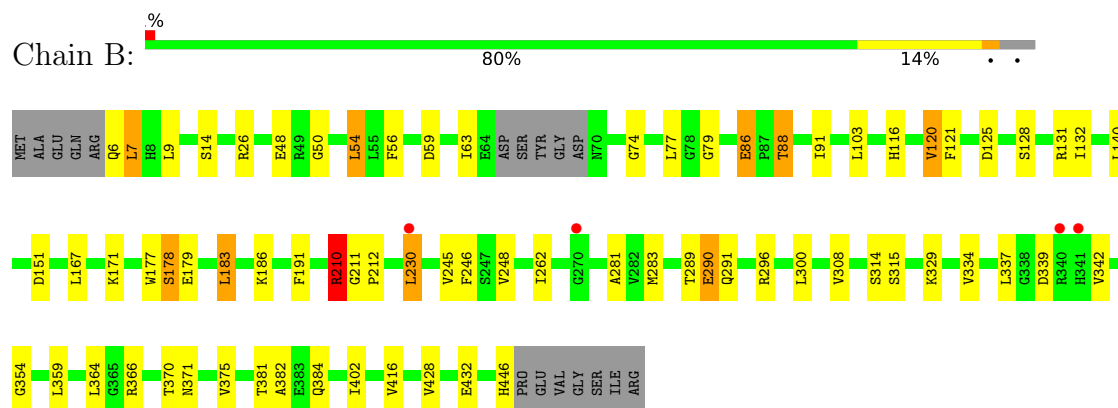
3 Residue-property plots

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.

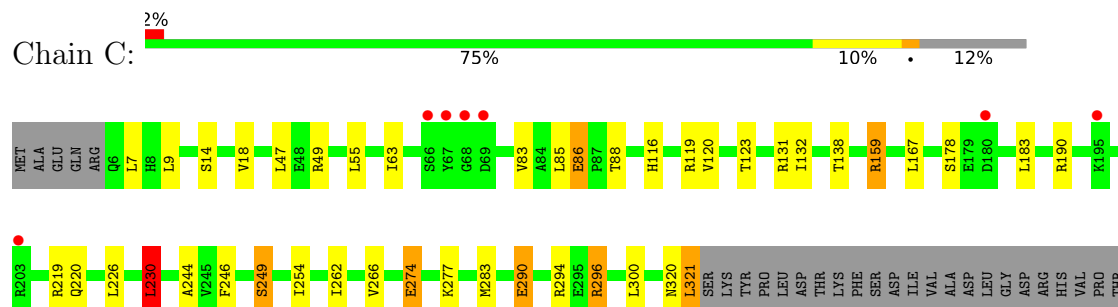
• Molecule 1: Dibenzothiophene desulfurization enzyme A

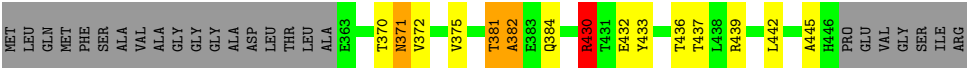


• Molecule 1: Dibenzothiophene desulfurization enzyme A

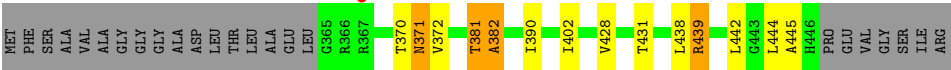
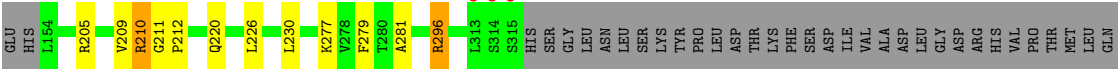
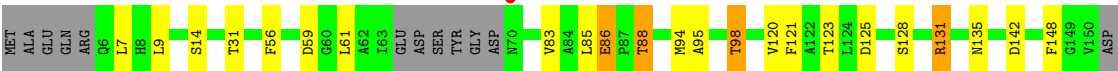


• Molecule 1: Dibenzothiophene desulfurization enzyme A





● Molecule 1: Dibenzothiophene desulfurization enzyme A



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	84.13Å 84.13Å 269.46Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.98 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.80) 99.9 (19.98-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.212 , 0.274 0.214 , 0.273	Depositor DCC
R_{free} test set	2510 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l 0.047 for h,-h-k,-l 0.030 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12884	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.70% 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	0.59	0/3466	0.86	7/4710 (0.1%)
1	B	0.58	0/3458	0.85	4/4699 (0.1%)
1	C	0.56	0/3190	0.84	7/4335 (0.2%)
1	D	0.54	0/3050	0.79	2/4142 (0.0%)
All	All	0.57	0/13164	0.84	20/17886 (0.1%)

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	1

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	119	ARG	NE-CZ-NH1	7.91	124.25	120.30
1	C	296	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	C	296	ARG	NE-CZ-NH2	-6.19	117.20	120.30
1	D	131	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	B	296	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	C	159	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	A	294	ARG	NE-CZ-NH1	5.81	123.20	120.30
1	A	296	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	A	131	ARG	NE-CZ-NH1	5.65	123.13	120.30
1	C	430	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	159	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	C	230	LEU	CA-CB-CG	5.42	127.77	115.30
1	A	296	ARG	NE-CZ-NH2	-5.41	117.59	120.30
1	B	296	ARG	NE-CZ-NH2	-5.34	117.63	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	49	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	C	131	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	B	210	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	A	371	ASN	N-CA-C	-5.13	97.16	111.00
1	D	296	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	B	7	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	53	ASP	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	3388	0	3315	34	0
1	B	3379	0	3311	28	0
1	C	3116	0	3037	28	0
1	D	2981	0	2927	25	0
2	A	11	0	0	0	0
2	B	5	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
All	All	12884	0	12590	102	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 (102) 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:D:94:MET:O	1:D:98:THR:HG23	1.82	0.80
1:C:123:THR:HG23	1:D:85:LEU:HB3	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:290:GLU:OE1	1:C:294:ARG:NH2	2.21	0.73
1:D:210:ARG:HG3	1:D:211:GLY:N	2.02	0.73
1:A:290:GLU:HG3	1:A:384:GLN:OE1	1.93	0.68
1:A:140:LEU:HG	1:A:153:HIS:CE1	2.29	0.67
1:C:116:HIS:O	1:C:120:VAL:HG23	1.95	0.66
1:A:119:ARG:NH2	1:B:59:ASP:OD1	2.29	0.66
1:A:283:MET:CE	1:A:300:LEU:HD21	2.26	0.65
1:C:274:GLU:O	1:C:277:LYS:HE2	1.97	0.64
1:A:183:LEU:O	1:A:191:PHE:O	2.16	0.62
1:A:86:GLU:OE2	1:A:88:THR:HB	2.01	0.60
1:C:85:LEU:HB3	1:D:123:THR:HG23	1.85	0.59
1:C:283:MET:CE	1:C:300:LEU:HD21	2.36	0.55
1:C:320:ASN:OD1	1:C:321:LEU:N	2.38	0.55
1:A:350:SER:HB2	1:A:364:LEU:HD21	1.89	0.55
1:A:177:TRP:O	1:A:178:SER:CB	2.55	0.54
1:D:86:GLU:OE2	1:D:88:THR:HB	2.10	0.52
1:C:226:LEU:HD22	1:C:244:ALA:HB3	1.92	0.52
1:B:6:GLN:O	1:B:428:VAL:O	2.29	0.51
1:D:128:SER:O	1:D:131:ARG:HD3	2.11	0.51
1:C:220:GLN:HG3	1:C:437:THR:HB	1.93	0.50
1:B:121:PHE:O	1:B:125:ASP:HB2	2.12	0.50
1:B:283:MET:HE1	1:B:300:LEU:HD21	1.94	0.49
1:D:277:LYS:HE3	1:D:442:LEU:O	2.12	0.49
1:B:116:HIS:O	1:B:120:VAL:HG23	2.12	0.49
1:C:219:ARG:NH2	1:C:436:THR:OG1	2.41	0.49
1:A:283:MET:HE3	1:A:300:LEU:HD21	1.94	0.49
1:A:26:ARG:HA	1:B:186:LYS:HG2	1.94	0.49
1:C:430:ARG:HD3	1:C:433:TYR:HA	1.95	0.49
1:D:371:ASN:OD1	1:D:371:ASN:N	2.42	0.49
1:C:63:ILE:HD12	1:D:212:PRO:HG2	1.95	0.48
1:C:290:GLU:HG3	1:C:384:GLN:HE22	1.79	0.48
1:D:98:THR:OG1	1:D:131:ARG:NH2	2.47	0.48
1:A:279:PHE:HB3	1:A:402:ILE:HG12	1.94	0.48
1:B:283:MET:CE	1:B:300:LEU:HD21	2.43	0.48
1:C:262:ILE:O	1:C:266:VAL:HG23	2.14	0.48
1:A:301:ASN:OD1	1:A:370:THR:HG23	2.14	0.48
1:B:281:ALA:HA	1:B:402:ILE:HB	1.96	0.48
1:A:91:ILE:HG23	1:A:103:LEU:HB3	1.96	0.47
1:B:128:SER:O	1:B:131:ARG:HG3	2.13	0.47
1:B:210:ARG:CG	1:B:211:GLY:N	2.77	0.47
1:D:220:GLN:HE22	1:D:438:LEU:HB3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:279:PHE:HB3	1:D:402:ILE:HG12	1.97	0.47
1:B:245:VAL:HG11	1:B:262:ILE:HD13	1.97	0.46
1:C:138:THR:O	1:C:159:ARG:HD2	2.16	0.46
1:A:349:PHE:CE1	1:A:353:ALA:HB2	2.51	0.46
1:D:381:THR:O	1:D:382:ALA:CB	2.63	0.46
1:A:138:THR:O	1:A:159:ARG:HD2	2.15	0.46
1:A:212:PRO:HG2	1:B:63:ILE:HD12	1.98	0.45
1:D:121:PHE:O	1:D:125:ASP:HB2	2.16	0.45
1:C:249:SER:HB3	1:C:254:ILE:HG22	1.98	0.45
1:C:430:ARG:HG2	1:C:432:GLU:O	2.17	0.45
1:A:342:VAL:O	1:A:342:VAL:HG13	2.16	0.45
1:A:282:VAL:HG11	1:A:378:TRP:CZ2	2.52	0.45
1:C:123:THR:CG2	1:D:85:LEU:HB3	2.44	0.45
1:A:177:TRP:O	1:A:196:LYS:O	2.34	0.45
1:B:54:LEU:HD11	1:B:56:PHE:HB3	1.98	0.45
1:B:77:LEU:HB2	1:B:308:VAL:HG22	1.98	0.45
1:C:86:GLU:HG2	1:D:120:VAL:HG23	2.00	0.44
1:D:390:ILE:HG12	1:D:428:VAL:HG21	1.99	0.44
1:A:63:ILE:HD12	1:B:212:PRO:HG2	1.99	0.44
1:A:235:ARG:HD2	1:A:261:ASP:OD2	2.17	0.44
1:A:367:ARG:O	1:A:370:THR:HB	2.18	0.44
1:D:281:ALA:HA	1:D:402:ILE:HB	2.00	0.44
1:A:288:GLU:OE1	1:C:296:ARG:HD3	2.18	0.43
1:A:381:THR:O	1:A:382:ALA:CB	2.66	0.43
1:B:183:LEU:O	1:B:191:PHE:O	2.36	0.43
1:B:86:GLU:OE2	1:B:88:THR:HB	2.18	0.43
1:B:177:TRP:O	1:B:178:SER:CB	2.66	0.43
1:B:248:VAL:HG13	1:B:375:VAL:HG22	2.01	0.43
1:D:220:GLN:NE2	1:D:438:LEU:HB3	2.34	0.43
1:A:381:THR:O	1:A:382:ALA:HB2	2.19	0.43
1:B:359:LEU:HD12	1:B:364:LEU:HD13	2.01	0.43
1:A:297:LEU:HD22	1:A:379:ALA:HB2	2.00	0.42
1:B:50:GLY:CA	1:B:416:VAL:HG13	2.49	0.42
1:D:61:LEU:HD13	1:D:148:PHE:CE1	2.54	0.42
1:D:439:ARG:HG3	1:D:444:LEU:HB2	2.00	0.42
1:B:74:GLY:HA2	1:B:79:GLY:HA3	2.00	0.42
1:C:277:LYS:HE3	1:C:442:LEU:O	2.19	0.42
1:C:290:GLU:CG	1:C:384:GLN:HE22	2.33	0.42
1:A:244:ALA:HA	1:A:277:LYS:O	2.20	0.42
1:B:371:ASN:HB2	1:B:375:VAL:HB	2.02	0.42
1:D:135:ASN:HA	1:D:226:LEU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:381:THR:O	1:D:382:ALA:HB3	2.20	0.42
1:C:283:MET:HE3	1:C:300:LEU:HD21	2.02	0.41
1:C:381:THR:O	1:C:382:ALA:HB3	2.21	0.41
1:A:390:ILE:HG12	1:A:428:VAL:HG21	2.03	0.41
1:A:86:GLU:HG2	1:B:120:VAL:HG13	2.03	0.41
1:A:227:GLN:HB3	1:A:242:ALA:HB2	2.01	0.41
1:A:247:SER:O	1:A:280:THR:HA	2.20	0.41
1:A:133:SER:HB3	1:A:224:VAL:HB	2.01	0.41
1:A:289:THR:HG22	1:A:292:VAL:HG23	2.02	0.41
1:B:354:GLY:CA	1:B:359:LEU:HD11	2.51	0.41
1:C:220:GLN:HG2	1:C:439:ARG:HD2	2.02	0.41
1:D:95:ALA:HA	1:D:131:ARG:HH22	1.86	0.41
1:A:186:LYS:HG2	1:B:26:ARG:HA	2.03	0.40
1:B:91:ILE:HD12	1:B:103:LEU:HB3	2.02	0.40
1:B:290:GLU:HG2	1:B:384:GLN:HE22	1.85	0.40
1:C:371:ASN:HB2	1:C:375:VAL:HB	2.03	0.40
1:C:47:LEU:HD12	1:C:55:LEU:HD12	2.02	0.40
1:C:119:ARG:NH2	1:D:59:ASP:OD1	2.51	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	434/453 (96%)	398 (92%)	31 (7%)	5 (1%)	13	39
1	B	432/453 (95%)	401 (93%)	27 (6%)	4 (1%)	17	46
1	C	396/453 (87%)	365 (92%)	25 (6%)	6 (2%)	10	33
1	D	375/453 (83%)	349 (93%)	22 (6%)	4 (1%)	14	41
All	All	1637/1812 (90%)	1513 (92%)	105 (6%)	19 (1%)	13	39

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	D	7	LEU
1	D	382	ALA
1	A	178	SER
1	A	230	LEU
1	A	382	ALA
1	A	430	ARG
1	B	178	SER
1	B	230	LEU
1	B	382	ALA
1	C	7	LEU
1	C	382	ALA
1	C	430	ARG
1	D	445	ALA
1	B	7	LEU
1	C	178	SER
1	C	230	LEU
1	C	445	ALA
1	D	230	LEU

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	350/363 (96%)	318 (91%)	32 (9%)	9	27
1	B	349/363 (96%)	317 (91%)	32 (9%)	9	27
1	C	321/363 (88%)	300 (94%)	21 (6%)	17	44
1	D	306/363 (84%)	287 (94%)	19 (6%)	18	47
All	All	1326/1452 (91%)	1222 (92%)	104 (8%)	12	35

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	38	GLU
1	A	66	SER

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Mol	Chain	Res	Type
1	A	72	GLU
1	A	83	VAL
1	A	86	GLU
1	A	88	THR
1	A	110	THR
1	A	140	LEU
1	A	143	SER
1	A	171	LYS
1	A	175	SER
1	A	179	GLU
1	A	183	LEU
1	A	205	ARG
1	A	210	ARG
1	A	230	LEU
1	A	274	GLU
1	A	314	SER
1	A	322	SER
1	A	327	ASP
1	A	329	LYS
1	A	337	LEU
1	A	339	ASP
1	A	340	ARG
1	A	350	SER
1	A	364	LEU
1	A	366	ARG
1	A	381	THR
1	A	391	SER
1	A	432	GLU
1	A	439	ARG
1	B	9	LEU
1	B	14	SER
1	B	48	GLU
1	B	54	LEU
1	B	86	GLU
1	B	88	THR
1	B	120	VAL
1	B	132	ILE
1	B	140	LEU
1	B	151	ASP
1	B	167	LEU
1	B	171	LYS
1	B	179	GLU

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Mol	Chain	Res	Type
1	B	183	LEU
1	B	210	ARG
1	B	230	LEU
1	B	246	PHE
1	B	289	THR
1	B	290	GLU
1	B	291	GLN
1	B	314	SER
1	B	315	SER
1	B	329	LYS
1	B	334	VAL
1	B	337	LEU
1	B	339	ASP
1	B	342	VAL
1	B	366	ARG
1	B	370	THR
1	B	381	THR
1	B	432	GLU
1	B	446	HIS
1	C	9	LEU
1	C	14	SER
1	C	18	VAL
1	C	83	VAL
1	C	86	GLU
1	C	88	THR
1	C	132	ILE
1	C	167	LEU
1	C	183	LEU
1	C	190	ARG
1	C	230	LEU
1	C	246	PHE
1	C	249	SER
1	C	274	GLU
1	C	290	GLU
1	C	321	LEU
1	C	370	THR
1	C	371	ASN
1	C	372	VAL
1	C	381	THR
1	C	430	ARG
1	D	9	LEU
1	D	14	SER

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Mol	Chain	Res	Type
1	D	31	THR
1	D	56	PHE
1	D	83	VAL
1	D	86	GLU
1	D	88	THR
1	D	98	THR
1	D	142	ASP
1	D	205	ARG
1	D	209	VAL
1	D	210	ARG
1	D	296	ARG
1	D	370	THR
1	D	371	ASN
1	D	372	VAL
1	D	381	THR
1	D	431	THR
1	D	439	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	141	ASN
1	A	153	HIS
1	A	220	GLN
1	A	275	GLN
1	A	441	HIS
1	B	201	ASN
1	B	220	GLN
1	B	301	ASN
1	B	377	GLN
1	B	441	HIS
1	C	32	ASN
1	C	201	ASN
1	C	220	GLN
1	C	275	GLN
1	C	441	HIS
1	D	32	ASN
1	D	220	GLN

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 monosaccharides 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	438/453 (96%)	-0.47	1 (0%) 95 94	25, 40, 66, 103	0
1	B	436/453 (96%)	-0.32	4 (0%) 84 80	29, 46, 71, 106	0
1	C	400/453 (88%)	-0.40	7 (1%) 68 61	28, 43, 69, 100	0
1	D	383/453 (84%)	-0.29	5 (1%) 77 72	31, 49, 79, 95	0
All	All	1657/1812 (91%)	-0.37	17 (1%) 82 77	25, 45, 73, 106	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	314	SER	3.4
1	B	340	ARG	3.4
1	C	69	ASP	3.2
1	A	340	ARG	3.0
1	C	66	SER	2.9
1	B	341	HIS	2.8
1	C	68	GLY	2.8
1	C	203	ARG	2.7
1	D	313	LEU	2.6
1	D	367	ARG	2.5
1	B	230	LEU	2.5
1	C	195	LYS	2.4
1	B	270	GLY	2.2
1	C	180	ASP	2.2
1	C	67	TYR	2.2
1	D	70	ASN	2.1
1	D	315	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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.