



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 07:23 PM UTC

PDB ID : 5TLC / pdb_00005tlc
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	:	4-5-2 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

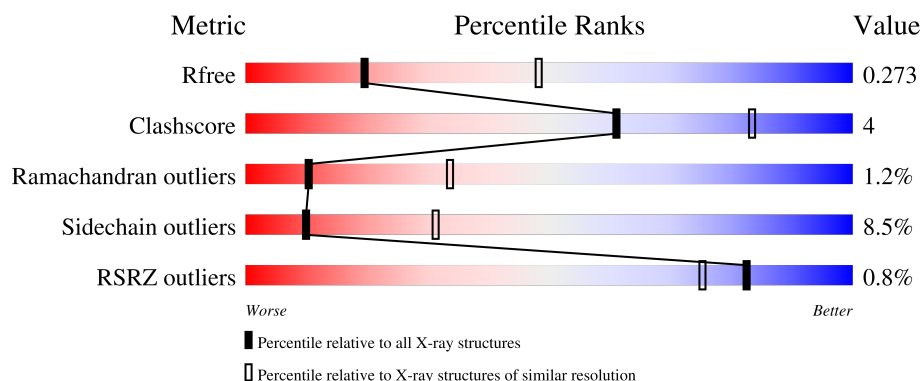
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (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	0.2% 78% 16% . .
1	B	453	79% 14% . .
1	C	453	2% 75% 11% . 12%
1	D	453	0.2% 73% 10% . 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			

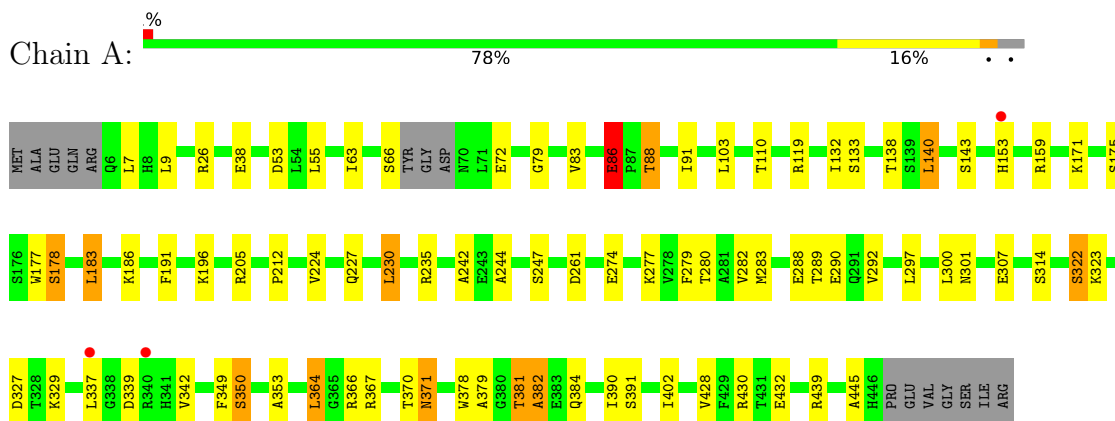
- Molecule 2 is water.

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		

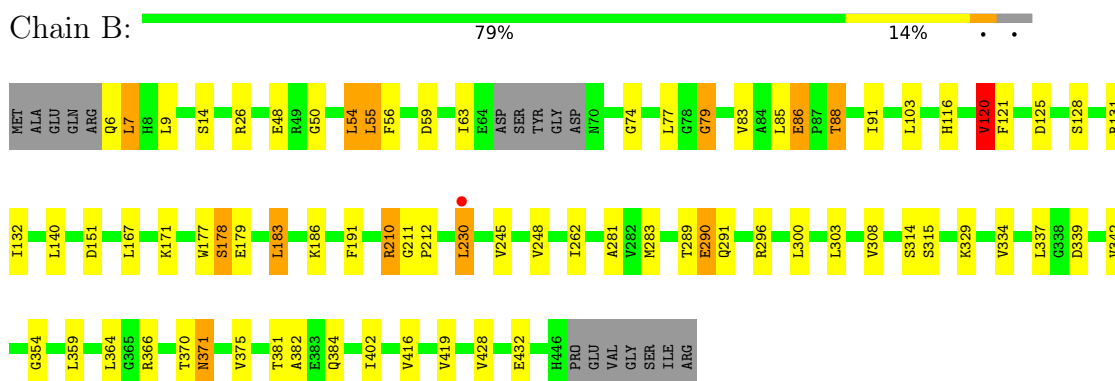
3 Residue-property plots

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.

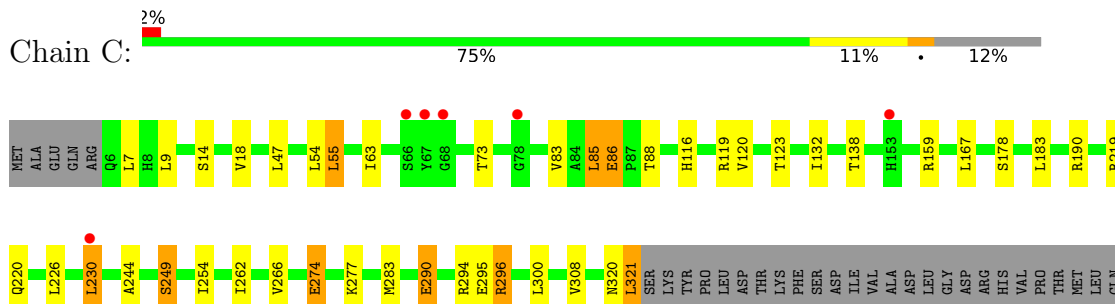
• Molecule 1: Dibenzothiophene desulfurization enzyme A

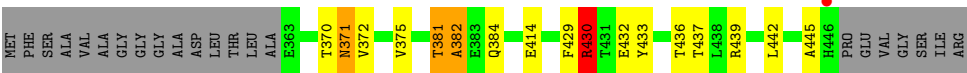


• Molecule 1: Dibenzothiophene desulfurization enzyme A

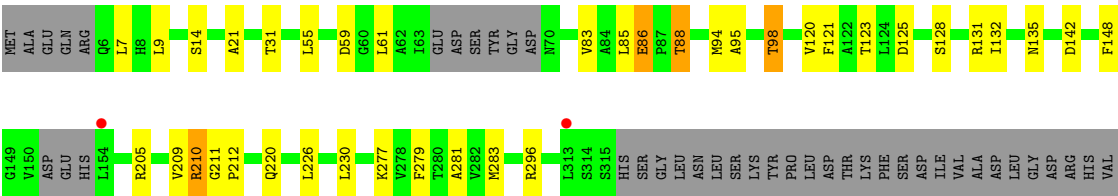


• Molecule 1: Dibenzothiophene desulfurization enzyme A





● 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 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-2.80) 99.6 (20.00-2.80)	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)	0.31 , 26.7	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	0.82	0/3466	1.08	7/4710 (0.1%)
1	B	0.83	0/3458	1.07	5/4699 (0.1%)
1	C	0.79	0/3190	1.05	0/4335
1	D	0.78	0/3050	1.02	0/4142
All	All	0.81	0/13164	1.06	12/17886 (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 (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	371	ASN	N-CA-C	-7.65	98.50	109.29
1	A	445	ALA	N-CA-C	6.45	121.03	111.04
1	A	371	ASN	N-CA-C	-6.40	97.16	110.80
1	A	79	GLY	N-CA-C	5.83	118.17	111.36
1	A	439	ARG	N-CA-C	-5.35	105.48	112.23
1	B	79	GLY	N-CA-C	5.25	117.97	111.93
1	A	307	GLU	N-CA-C	5.15	117.63	111.71
1	A	86	GLU	CA-C-N	5.12	125.16	119.32
1	A	86	GLU	C-N-CA	5.12	125.16	119.32
1	B	120	VAL	CB-CA-C	-5.09	102.95	111.29
1	B	303	LEU	N-CA-C	5.04	118.69	112.54
1	B	419	VAL	N-CA-C	5.03	115.70	110.82

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	35	0
1	B	3379	0	3311	29	0
1	C	3116	0	3037	30	0
1	D	2981	0	2927	26	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	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 4.

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: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
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	0.72
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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
1:D:21:ALA:HB2	1:D:283:MET:HE1	1.97	0.47
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:B:283:MET:HE1	1:B:300:LEU:HD21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:283:MET:HE3	1:A:300:LEU:HD21	1.96	0.44
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:C:283:MET:HE3	1:C:300:LEU:HD21	2.00	0.43
1:A:322:SER:O	1:A:323:LYS:C	2.60	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:C:296:ARG:HH22	1:C:414:GLU:CD	2.26	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:55:LEU:C	1:B:55:LEU:HD23	2.44	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
1:D:381:THR:O	1:D:382:ALA:HB3	2.20	0.42
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:C:429:PHE:O	1:C:430:ARG:C	2.63	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%)	10	34
1	B	432/453 (95%)	401 (93%)	27 (6%)	4 (1%)	14	41
1	C	396/453 (87%)	365 (92%)	25 (6%)	6 (2%)	8	28
1	D	375/453 (83%)	349 (93%)	22 (6%)	4 (1%)	11	36
All	All	1637/1812 (90%)	1513 (92%)	105 (6%)	19 (1%)	10	34

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	D	7	LEU
1	D	382	ALA

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Mol	Chain	Res	Type
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%)	319 (91%)	31 (9%)	9	29
1	B	349/363 (96%)	314 (90%)	35 (10%)	7	24
1	C	321/363 (88%)	294 (92%)	27 (8%)	10	32
1	D	306/363 (84%)	286 (94%)	20 (6%)	15	43
All	All	1326/1452 (91%)	1213 (92%)	113 (8%)	10	31

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	38	GLU
1	A	55	LEU
1	A	66	SER
1	A	72	GLU

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Mol	Chain	Res	Type
1	A	83	VAL
1	A	86	GLU
1	A	88	THR
1	A	110	THR
1	A	132	ILE
1	A	140	LEU
1	A	143	SER
1	A	171	LYS
1	A	175	SER
1	A	183	LEU
1	A	205	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	350	SER
1	A	364	LEU
1	A	366	ARG
1	A	371	ASN
1	A	381	THR
1	A	391	SER
1	A	432	GLU
1	B	7	LEU
1	B	9	LEU
1	B	14	SER
1	B	48	GLU
1	B	54	LEU
1	B	55	LEU
1	B	83	VAL
1	B	85	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

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Mol	Chain	Res	Type
1	B	179	GLU
1	B	183	LEU
1	B	210	ARG
1	B	230	LEU
1	B	289	THR
1	B	290	GLU
1	B	291	GLN
1	B	296	ARG
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	C	9	LEU
1	C	14	SER
1	C	18	VAL
1	C	54	LEU
1	C	55	LEU
1	C	73	THR
1	C	83	VAL
1	C	85	LEU
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	249	SER
1	C	274	GLU
1	C	290	GLU
1	C	295	GLU
1	C	296	ARG
1	C	308	VAL
1	C	321	LEU
1	C	370	THR

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Mol	Chain	Res	Type
1	C	371	ASN
1	C	372	VAL
1	C	381	THR
1	C	430	ARG
1	D	9	LEU
1	D	14	SER
1	D	31	THR
1	D	55	LEU
1	D	83	VAL
1	D	86	GLU
1	D	88	THR
1	D	98	THR
1	D	132	ILE
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 (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	135	ASN
1	A	201	ASN
1	A	220	GLN
1	A	265	HIS
1	A	441	HIS
1	B	80	GLN
1	B	198	GLN
1	B	220	GLN
1	B	291	GLN
1	B	384	GLN
1	B	418	GLN
1	B	441	HIS
1	C	70	ASN

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Mol	Chain	Res	Type
1	C	80	GLN
1	C	135	ASN
1	C	220	GLN
1	C	441	HIS
1	D	32	ASN
1	D	126	ASN
1	D	135	ASN
1	D	384	GLN
1	D	446	HIS

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 [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	438/453 (96%)	-0.37	3 (0%) 84 77	25, 40, 66, 103	0
1	B	436/453 (96%)	-0.20	1 (0%) 91 88	29, 46, 71, 106	0
1	C	400/453 (88%)	-0.30	7 (1%) 67 58	28, 43, 69, 100	0
1	D	383/453 (84%)	-0.12	3 (0%) 82 75	31, 49, 79, 95	0
All	All	1657/1812 (91%)	-0.25	14 (0%) 82 75	25, 45, 73, 106	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	153	HIS	4.0
1	A	340	ARG	3.3
1	C	153	HIS	2.9
1	D	154	LEU	2.6
1	C	66	SER	2.4
1	D	365	GLY	2.3
1	D	313	LEU	2.2
1	C	67	TYR	2.2
1	C	78	GLY	2.2
1	A	337	LEU	2.1
1	B	230	LEU	2.1
1	C	446	HIS	2.1
1	C	68	GLY	2.1
1	C	230	LEU	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.