



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 05:23 am BST

PDB ID : 3DRD
Title : Crystal Structure of 7,8 Diaminopelargonic Acid Synthase Apoenzyme in Bacillus subtilis
Authors : Dey, S.; Sacchettini, J.C.
Deposited on : 2008-07-11
Resolution : 2.17 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 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	:	2.11
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)	:	2.11

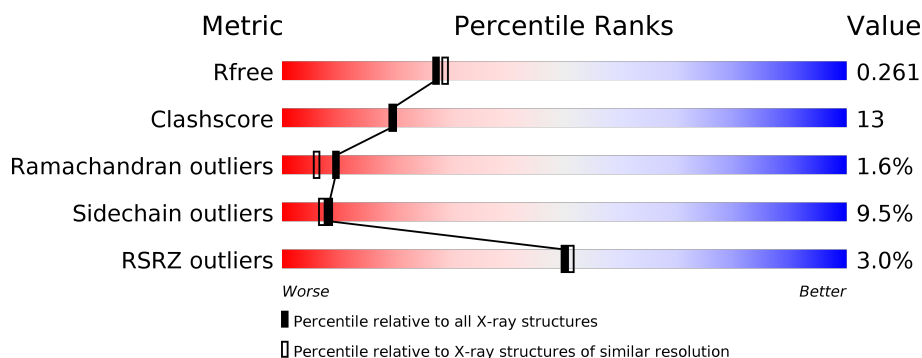
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.17 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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 on 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	<div> <div>3%</div> <div> <div></div> <div>66%</div> <div>23%</div> <div>• 6%</div> </div> </div>
1	B	448	<div> <div>3%</div> <div> <div></div> <div>68%</div> <div>21%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6826 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 Adenosylmethionine-8-amino-7-oxononanoate aminotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3296	2102	546	625	23			
1	B	417	Total	C	N	O	S	0	0	0
			3280	2093	544	621	22			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	121	Total	O	0	0
			121	121		
2	B	129	Total	O	0	0
			129	129		

- Molecule 1: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.17Å 102.84Å 74.56Å 90.00° 105.15° 90.00°	Depositor
Resolution (Å)	35.00 – 2.17 37.92 – 2.17	Depositor EDS
% Data completeness (in resolution range)	93.0 (35.00-2.17) 93.0 (37.92-2.17)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.33 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.205 , 0.265 0.202 , 0.261	Depositor DCC
R_{free} test set	2098 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.304	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6826	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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	0.45	0/3363	0.64	0/4536
1	B	0.45	0/3347	0.62	2/4515 (0.0%)
All	All	0.45	0/6710	0.63	2/9051 (0.0%)

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	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	106	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	B	106	ARG	NE-CZ-NH1	5.45	123.02	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	ARG	Peptide
1	A	383	GLU	Peptide
1	B	390	ALA	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	3296	0	3292	92	0
1	B	3280	0	3276	88	0
2	A	121	0	0	3	0
2	B	129	0	0	6	0
All	All	6826	0	6568	168	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 13.

All (168) 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:117:MET:HE2	1:A:277:ALA:HB2	1.38	1.03
1:B:188:ASP:OD1	1:B:191:GLU:HG3	1.65	0.97
1:A:350:LYS:HD3	2:A:630:HOH:O	1.65	0.97
1:A:447:GLU:O	1:A:448:ASP:HB2	1.71	0.90
1:A:2:THR:O	1:A:6:ILE:HG13	1.71	0.90
1:B:440:ILE:O	1:B:444:THR:HB	1.74	0.86
1:B:393:ARG:O	1:B:397:LYS:HG2	1.77	0.84
1:A:383:GLU:O	1:A:383:GLU:HG2	1.78	0.82
1:A:117:MET:HE2	1:A:277:ALA:CB	2.09	0.82
1:B:350:LYS:HD2	1:B:350:LYS:H	1.44	0.80
1:A:19:GLN:HE21	1:A:21:LYS:H	1.28	0.79
1:B:77:ALA:HA	1:B:323:LEU:HD13	1.66	0.77
1:B:110:SER:HB2	1:B:316:HIS:HE1	1.52	0.74
1:B:28:LEU:HD22	1:B:403:ARG:HD2	1.70	0.74
1:B:16:PRO:O	1:B:18:THR:CG2	2.36	0.74
1:A:117:MET:CE	1:A:277:ALA:HB2	2.18	0.73
1:B:134:PRO:HG3	2:B:686:HOH:O	1.91	0.71
1:B:19:GLN:HE21	1:B:21:LYS:H	1.37	0.71
1:A:106:ARG:HG2	1:A:299:TYR:CD1	2.26	0.70
1:B:350:LYS:HD2	1:B:350:LYS:N	2.08	0.69
1:B:363:HIS:HB2	1:B:444:THR:HG21	1.75	0.69
1:A:83:GLY:H	1:B:18:THR:HG21	1.57	0.68
1:A:118:GLU:O	1:A:122:LYS:HG2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:381:SER:OG	1:B:384:THR:HG21	1.94	0.68
1:B:16:PRO:O	1:B:18:THR:HG22	1.92	0.68
1:A:425:THR:HG22	1:A:428:GLU:H	1.59	0.68
1:B:2:THR:OG1	1:B:3:HIS:N	2.26	0.67
1:B:86:ASN:ND2	1:B:89:ALA:H	1.92	0.67
1:A:308:ASN:N	1:A:308:ASN:OD1	2.26	0.66
1:A:117:MET:CE	1:A:277:ALA:CB	2.72	0.66
1:B:188:ASP:OD1	1:B:191:GLU:CG	2.43	0.65
1:A:87:VAL:HB	1:A:88:PRO:HD3	1.78	0.65
1:A:16:PRO:HG2	1:B:82:LEU:HD22	1.77	0.65
1:A:19:GLN:NE2	1:A:21:LYS:H	1.95	0.64
1:A:307:GLU:HG2	1:A:308:ASN:OD1	1.97	0.64
1:A:18:THR:HG21	1:B:83:GLY:H	1.62	0.63
1:A:383:GLU:O	1:A:383:GLU:CG	2.46	0.63
1:A:384:THR:OG1	1:A:386:GLU:HG2	1.99	0.62
1:B:383:GLU:CD	1:B:383:GLU:H	2.04	0.61
1:A:447:GLU:O	1:A:448:ASP:CB	2.49	0.59
1:A:26:ASN:O	1:A:403:ARG:NH2	2.35	0.59
1:A:16:PRO:O	1:A:18:THR:HG22	2.02	0.59
1:B:389:PRO:HB2	1:B:391:ASP:HB2	1.86	0.58
1:A:315:GLY:HA3	1:B:16:PRO:HB3	1.85	0.58
1:A:1:MET:HG3	1:A:3:HIS:H	1.68	0.58
1:B:2:THR:N	1:B:5:LEU:HD12	2.17	0.58
1:B:384:THR:OG1	1:B:386:GLU:HB2	2.04	0.58
1:B:444:THR:C	1:B:446:LEU:H	2.07	0.57
1:B:304:ASP:HB2	1:B:310:LYS:HE2	1.87	0.57
1:A:86:ASN:HD22	1:A:88:PRO:HD2	1.69	0.57
1:B:381:SER:OG	1:B:384:THR:CG2	2.51	0.57
1:A:440:ILE:O	1:A:444:THR:HB	2.04	0.57
1:A:142:MET:SD	1:A:176:ALA:HB3	2.45	0.57
1:A:93:ALA:O	1:A:97:ILE:HG12	2.05	0.56
1:B:427:GLU:O	1:B:431:GLU:HG3	2.06	0.56
1:A:316:HIS:HB2	1:A:319:THR:HG23	1.88	0.56
1:A:315:GLY:HA3	1:B:16:PRO:CB	2.36	0.55
1:A:1:MET:HG3	1:A:2:THR:N	2.21	0.55
1:B:110:SER:CB	1:B:316:HIS:HE1	2.17	0.55
1:B:16:PRO:O	1:B:18:THR:HG23	2.05	0.55
1:B:110:SER:HB2	1:B:316:HIS:CE1	2.38	0.55
1:B:33:GLY:O	1:B:61:ARG:HD3	2.06	0.55
1:A:133:LYS:HB2	1:A:135:GLU:OE1	2.07	0.55
1:B:248:MET:CE	1:B:273:PRO:HA	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:389:PRO:HB2	1:B:391:ASP:CB	2.37	0.54
1:B:54:TRP:N	1:B:54:TRP:CD1	2.74	0.54
1:A:380:ARG:HB3	1:A:388:TYR:CE2	2.42	0.54
1:A:1:MET:HB3	1:A:4:ASP:OD2	2.08	0.54
1:B:425:THR:OG1	1:B:427:GLU:HG2	2.08	0.54
1:B:401:LYS:HA	1:B:401:LYS:HE3	1.88	0.54
1:A:307:GLU:CG	1:A:308:ASN:OD1	2.56	0.53
1:A:285:GLY:HA2	1:B:318:TYR:OH	2.09	0.53
1:A:21:LYS:O	1:A:25:GLU:HG2	2.09	0.53
1:A:373:MET:HG3	1:A:419:LEU:HD21	1.90	0.52
1:A:50:PHE:H	1:A:50:PHE:HD2	1.57	0.52
1:B:86:ASN:HD21	1:B:89:ALA:H	1.57	0.52
1:B:363:HIS:ND1	1:B:444:THR:HG23	2.23	0.52
1:B:87:VAL:HB	1:B:88:PRO:HD3	1.92	0.51
1:A:351:LEU:HD22	1:A:355:LEU:HG	1.91	0.51
1:A:136:LYS:NZ	1:A:245:ASP:O	2.43	0.51
1:A:16:PRO:O	1:A:18:THR:CG2	2.60	0.49
1:B:393:ARG:HD2	2:B:693:HOH:O	2.12	0.49
1:A:259:ARG:HD2	1:A:419:LEU:HD23	1.95	0.49
1:B:118:GLU:O	1:B:122:LYS:HG3	2.13	0.49
1:B:106:ARG:HG2	1:B:299:TYR:CD1	2.48	0.49
1:A:380:ARG:HD2	1:A:386:GLU:OE2	2.13	0.49
1:A:117:MET:CE	1:A:277:ALA:HB3	2.43	0.49
1:B:260:THR:HB	1:B:370:LEU:HG	1.94	0.49
1:A:313:PHE:O	1:A:314:HIS:CG	2.66	0.48
1:A:18:THR:HG21	1:B:83:GLY:N	2.28	0.48
1:B:248:MET:HE3	1:B:273:PRO:HA	1.95	0.48
1:A:361:LEU:HB2	1:A:364:VAL:HG23	1.95	0.48
1:B:394:ILE:O	1:B:398:VAL:HG23	2.14	0.48
1:A:405:LEU:HB3	1:A:435:ILE:HG23	1.96	0.48
1:B:195:GLN:O	1:B:199:GLU:HG3	2.13	0.48
1:B:356:GLN:O	1:B:359:HIS:HB2	2.14	0.47
1:B:315:GLY:HA2	2:B:514:HOH:O	2.14	0.47
1:A:303:TYR:HA	1:B:19:GLN:HE22	1.80	0.47
1:B:34:THR:HG22	1:B:61:ARG:NH2	2.29	0.47
1:A:296:GLU:O	1:A:300:LYS:HG2	2.15	0.47
1:A:117:MET:HE1	1:A:249:ILE:CG2	2.45	0.47
1:B:133:LYS:N	1:B:134:PRO:HD3	2.30	0.47
1:A:133:LYS:HG3	1:A:136:LYS:HG3	1.96	0.47
1:A:16:PRO:CG	1:B:82:LEU:HD22	2.42	0.47
1:B:82:LEU:HD23	1:B:82:LEU:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:318:TYR:OH	1:B:285:GLY:HA2	2.16	0.46
1:B:363:HIS:HB2	1:B:444:THR:CG2	2.44	0.46
1:A:86:ASN:ND2	1:A:88:PRO:HD2	2.31	0.46
1:B:444:THR:HG22	1:B:445:SER:N	2.30	0.46
1:B:412:LEU:CD2	1:B:417:ALA:HB2	2.46	0.46
1:A:118:GLU:HG2	1:A:122:LYS:HE3	1.98	0.45
1:B:359:HIS:O	1:B:382:LYS:NZ	2.49	0.45
1:B:233:TYR:O	1:B:237:VAL:HG12	2.16	0.45
1:B:422:LEU:N	1:B:422:LEU:HD12	2.31	0.45
1:A:392:ARG:NH2	1:A:447:GLU:OE2	2.48	0.45
1:A:218:SER:HB2	1:A:250:VAL:CG1	2.46	0.45
1:A:50:PHE:N	1:A:50:PHE:CD2	2.85	0.45
1:A:22:ASP:CG	1:A:393:ARG:HH22	2.21	0.45
1:A:330:GLU:HA	1:A:330:GLU:OE2	2.17	0.45
1:A:361:LEU:HD11	1:A:437:LYS:HG3	1.99	0.45
1:B:125:PHE:CE1	1:B:137:GLN:HB2	2.52	0.45
1:B:393:ARG:CD	2:B:693:HOH:O	2.65	0.45
1:A:287:LEU:HD23	1:B:321:ASN:HD21	1.83	0.44
1:B:65:LEU:HG	1:B:327:VAL:HG22	1.99	0.44
1:A:51:SER:HB2	1:A:54:TRP:HA	2.00	0.44
1:B:339:ASN:O	1:B:343:GLN:HG2	2.18	0.44
1:A:126:GLN:HE22	1:A:312:PHE:HA	1.83	0.44
1:A:86:ASN:ND2	1:A:89:ALA:H	2.16	0.43
1:B:218:SER:O	1:B:255:THR:HG21	2.18	0.43
2:A:555:HOH:O	1:B:60:HIS:HD2	2.00	0.43
1:B:354:LEU:HD22	2:B:696:HOH:O	2.17	0.43
1:A:338:GLU:O	1:A:339:ASN:C	2.56	0.43
1:A:78:HIS:CE1	1:A:318:TYR:HA	2.53	0.43
1:A:97:ILE:HD11	1:A:107:VAL:HG23	2.01	0.42
1:B:380:ARG:NH2	1:B:389:PRO:HD3	2.35	0.42
1:B:335:PHE:HA	1:B:340:ILE:HG12	1.99	0.42
1:A:358:LEU:O	1:A:364:VAL:HG21	2.19	0.42
1:A:122:LYS:HZ3	1:A:314:HIS:CD2	2.38	0.42
1:A:401:LYS:O	1:A:405:LEU:HD23	2.19	0.42
1:A:425:THR:HG22	1:A:427:GLU:N	2.34	0.42
1:A:81:LEU:HA	1:A:84:MET:O	2.19	0.42
1:B:397:LYS:HG2	1:B:397:LYS:H	1.63	0.42
1:B:18:THR:HB	2:B:748:HOH:O	2.19	0.42
1:A:364:VAL:O	1:A:379:VAL:HG22	2.20	0.42
1:B:266:CYS:HB2	1:B:271:VAL:HG22	2.02	0.42
1:B:444:THR:C	1:B:446:LEU:N	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:ASP:HB2	1:A:308:ASN:OD1	2.19	0.41
1:A:110:SER:HA	1:A:319:THR:HG22	2.02	0.41
1:B:78:HIS:HA	1:B:322:GLN:OE1	2.20	0.41
1:B:238:ARG:NH1	1:B:248:MET:HE2	2.34	0.41
1:B:109:TYR:HB2	1:B:319:THR:HG23	2.01	0.41
1:A:288:PRO:HG2	1:B:288:PRO:HG2	2.01	0.41
1:A:323:LEU:HA	1:A:323:LEU:HD12	1.85	0.41
1:A:425:THR:CG2	1:A:427:GLU:H	2.34	0.41
1:B:446:LEU:O	1:B:447:GLU:C	2.58	0.41
1:B:422:LEU:N	1:B:422:LEU:CD1	2.84	0.41
1:A:22:ASP:OD2	1:A:393:ARG:NH2	2.54	0.41
1:B:138:LYS:HD3	1:B:174:TYR:CE1	2.56	0.41
1:B:143:LYS:HD3	1:B:176:ALA:O	2.21	0.41
1:A:122:LYS:NZ	1:A:314:HIS:CD2	2.89	0.41
1:A:203:LEU:O	1:A:203:LEU:HD23	2.20	0.41
1:A:364:VAL:O	1:A:377:GLU:O	2.39	0.41
1:A:444:THR:CG2	2:A:563:HOH:O	2.69	0.40
1:B:110:SER:CB	1:B:316:HIS:CE1	3.02	0.40
1:A:253:VAL:O	1:A:280:LYS:HD2	2.21	0.40
1:A:106:ARG:O	1:A:293:PHE:HA	2.21	0.40
1:A:380:ARG:HB3	1:A:388:TYR:CD2	2.56	0.40
1:A:2:THR:HG21	1:A:42:ASN:ND2	2.36	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	415/448 (93%)	393 (95%)	15 (4%)	7 (2%)	9	5
1	B	413/448 (92%)	394 (95%)	13 (3%)	6 (2%)	10	7
All	All	828/896 (92%)	787 (95%)	28 (3%)	13 (2%)	9	6

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	383	GLU
1	B	391	ASP
1	A	339	ASN
1	A	364	VAL
1	B	445	SER
1	A	184	SER
1	A	280	LYS
1	A	304	ASP
1	B	280	LYS
1	B	339	ASN
1	A	53	VAL
1	B	76	ILE
1	B	53	VAL

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	355/378 (94%)	318 (90%)	37 (10%)	7	5
1	B	353/378 (93%)	323 (92%)	30 (8%)	10	9
All	All	708/756 (94%)	641 (90%)	67 (10%)	8	7

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	10	LYS
1	A	18	THR
1	A	25	GLU
1	A	50	PHE
1	A	54	TRP
1	A	55	LEU
1	A	61	ARG
1	A	63	LYS
1	A	65	LEU

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Mol	Chain	Res	Type
1	A	79	SER
1	A	86	ASN
1	A	106	ARG
1	A	143	LYS
1	A	183	ARG
1	A	184	SER
1	A	200	LEU
1	A	204	LEU
1	A	206	GLU
1	A	234	LEU
1	A	237	VAL
1	A	271	VAL
1	A	308	ASN
1	A	323	LEU
1	A	336	GLU
1	A	338	GLU
1	A	351	LEU
1	A	374	CYS
1	A	380	ARG
1	A	394	ILE
1	A	400	LEU
1	A	403	ARG
1	A	412	LEU
1	A	422	LEU
1	A	425	THR
1	A	444	THR
1	A	448	ASP
1	B	2	THR
1	B	7	GLU
1	B	18	THR
1	B	50	PHE
1	B	54	TRP
1	B	82	LEU
1	B	86	ASN
1	B	106	ARG
1	B	143	LYS
1	B	180	TYR
1	B	183	ARG
1	B	234	LEU
1	B	237	VAL
1	B	316	HIS
1	B	338	GLU

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Mol	Chain	Res	Type
1	B	347	LYS
1	B	351	LEU
1	B	357	ASP
1	B	358	LEU
1	B	359	HIS
1	B	379	VAL
1	B	380	ARG
1	B	384	THR
1	B	397	LYS
1	B	400	LEU
1	B	401	LYS
1	B	405	LEU
1	B	444	THR
1	B	446	LEU
1	B	447	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	42	ASN
1	A	60	HIS
1	A	86	ASN
1	A	91	GLN
1	A	126	GLN
1	A	137	GLN
1	A	314	HIS
1	A	343	GLN
1	A	352	HIS
1	B	19	GLN
1	B	60	HIS
1	B	86	ASN
1	B	91	GLN
1	B	195	GLN
1	B	316	HIS
1	B	321	ASN
1	B	331	ASN
1	B	343	GLN
1	B	363	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 carbohydrates 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	419/448 (93%)	0.24	12 (2%) 51 52	14, 26, 44, 60	1 (0%)
1	B	417/448 (93%)	0.21	13 (3%) 49 50	14, 25, 41, 61	1 (0%)
All	All	836/896 (93%)	0.23	25 (2%) 50 51	14, 25, 42, 61	2 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	313	PHE	6.4
1	B	309	LEU	5.3
1	B	2	THR	4.9
1	B	307	GLU	4.0
1	A	3	HIS	3.9
1	A	143	LYS	3.7
1	B	313	PHE	3.5
1	B	308	ASN	3.4
1	B	306	TYR	3.3
1	A	307	GLU	3.3
1	A	314	HIS	3.2
1	A	308	ASN	3.1
1	A	306	TYR	3.1
1	B	3	HIS	2.8
1	B	118	GLU	2.8
1	A	305	ASP	2.7
1	A	309	LEU	2.6
1	A	383	GLU	2.6
1	B	316	HIS	2.5
1	B	315	GLY	2.3
1	B	191	GLU	2.2
1	B	314	HIS	2.2
1	A	448	ASP	2.1
1	A	381	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	356	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 carbohydrates 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.