



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:50 PM GMT

PDB ID : 4DNG
Title : Crystal structure of putative aldehyde dehydrogenase from *Bacillus subtilis* subsp. *subtilis* str. 168
Authors : Malashkevich, V.N.; Bhosle, R.; Toro, R.; Seidel, R.; Almo, S.C.; New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2012-02-08
Resolution : 2.50 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

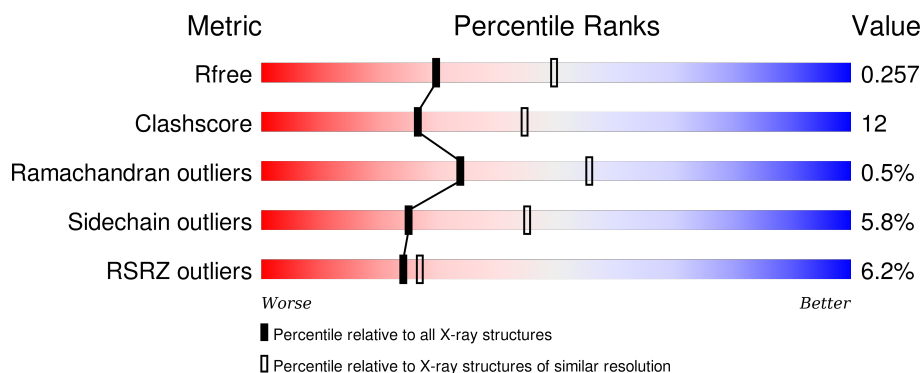
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	485	<div> <div>7%</div> <div> <div></div> <div>73%</div> <div>17%</div> <div>•</div> <div>7%</div> </div> </div>
1	B	485	<div> <div>5%</div> <div> <div></div> <div>71%</div> <div>20%</div> <div>•</div> <div>8%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6977 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 Uncharacterized aldehyde dehydrogenase AldY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	2	0
			3480	2200	588	680	12			
1	B	447	Total	C	N	O	S	0	1	0
			3427	2165	580	669	13			

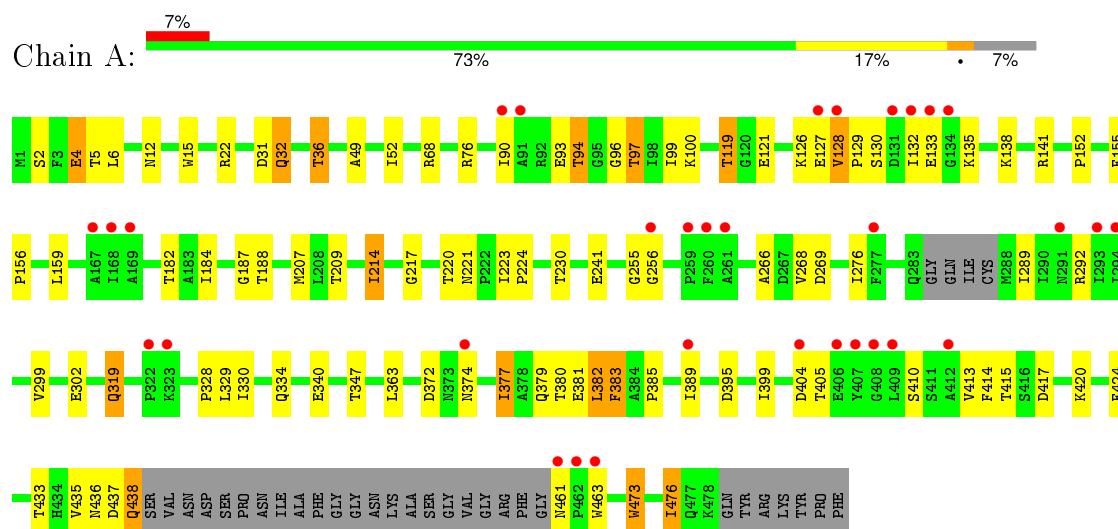
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	32	Total	O	0	0
			32	32		
2	B	38	Total	O	0	0
			38	38		

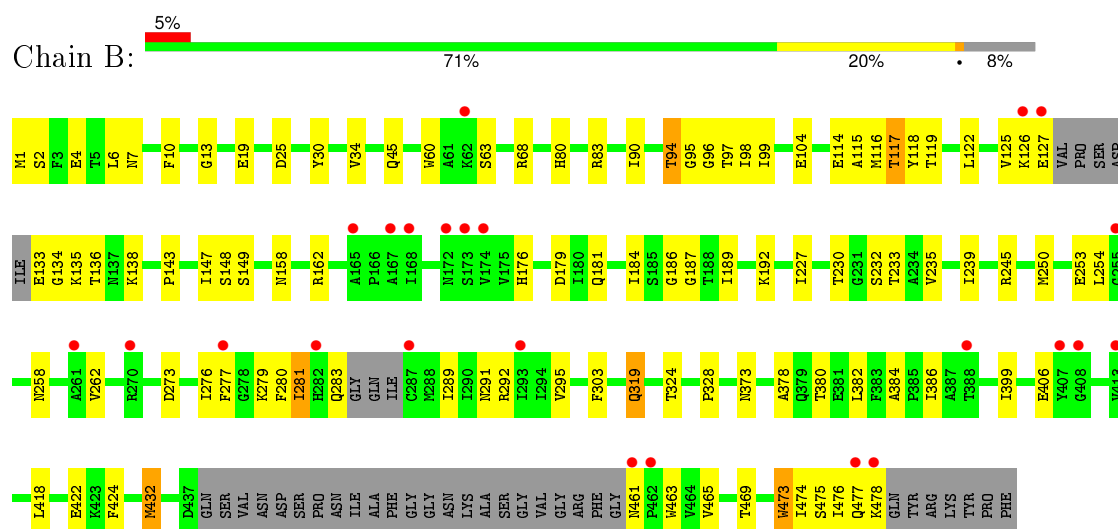
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Uncharacterized aldehyde dehydrogenase AldY



- Molecule 1: Uncharacterized aldehyde dehydrogenase AldY



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.20Å 90.52Å 86.86Å 90.00° 108.44° 90.00°	Depositor
Resolution (Å)	19.84 – 2.50 19.84 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.84-2.50) 98.8 (19.84-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.182 , 0.256 0.184 , 0.257	Depositor DCC
R_{free} test set	1631 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	70.8	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 58.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 32293 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6977	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.55	3/3541 (0.1%)	0.69	2/4790 (0.0%)
1	B	0.57	2/3482 (0.1%)	0.68	0/4707
All	All	0.56	5/7023 (0.1%)	0.68	2/9497 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	15	TRP	CD2-CE2	5.31	1.47	1.41
1	A	473	TRP	CD2-CE2	5.30	1.47	1.41
1	A	463	TRP	CD2-CE2	5.28	1.47	1.41
1	B	463	TRP	CD2-CE2	5.27	1.47	1.41
1	B	473	TRP	CD2-CE2	5.25	1.47	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	ARG	NE-CZ-NH2	-5.11	117.74	120.30
1	A	363	LEU	CA-CB-CG	5.00	126.81	115.30

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	3480	0	3504	105	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3427	0	3448	78	0
2	A	32	0	0	0	0
2	B	38	0	0	0	0
All	All	6977	0	6952	169	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 12.

All (169) 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:B:94:THR:HG22	1:B:96:GLY:H	1.24	1.02
1:A:380:THR:O	1:A:382:LEU:HD21	1.66	0.96
1:B:90:ILE:O	1:B:94:THR:HB	1.67	0.95
1:A:292:ARG:NH1	1:A:405:THR:CG2	2.33	0.91
1:B:30:TYR:HB2	1:B:319:GLN:NE2	1.86	0.90
1:A:473:TRP:HE3	1:B:432:MET:HB3	1.35	0.89
1:A:381:GLU:C	1:A:382:LEU:HD23	1.94	0.88
1:A:268:VAL:CG2	1:A:299:VAL:CG1	2.53	0.87
1:A:292:ARG:NH1	1:A:405:THR:HG22	1.93	0.84
1:A:90:ILE:O	1:A:94:THR:HB	1.79	0.81
1:A:435:VAL:CG2	1:B:476:ILE:HA	2.11	0.80
1:A:380:THR:O	1:A:382:LEU:CD2	2.30	0.79
1:A:268:VAL:CG2	1:A:299:VAL:HG11	2.12	0.79
1:A:268:VAL:HG21	1:A:299:VAL:CG1	2.12	0.79
1:A:4:GLU:HB2	1:A:36:THR:HG23	1.66	0.77
1:A:127:GLU:C	1:A:128:VAL:CG2	2.53	0.77
1:A:473:TRP:CE3	1:B:432:MET:HB3	2.20	0.77
1:B:149:SER:OG	1:B:176:HIS:HD2	1.69	0.76
1:A:94:THR:HG22	1:A:96:GLY:H	1.51	0.75
1:B:399:ILE:HG12	1:B:424:PHE:CD1	2.19	0.75
1:A:127:GLU:O	1:A:128:VAL:HG23	1.87	0.74
1:B:280:PHE:O	1:B:283:GLN:HG2	1.87	0.74
1:A:127:GLU:C	1:A:128:VAL:HG23	2.08	0.73
1:A:127:GLU:C	1:A:129:PRO:HD3	2.09	0.73
1:B:6:LEU:HD11	1:B:192:LYS:HG3	1.71	0.72
1:A:127:GLU:HB3	1:A:128:VAL:HG22	1.72	0.72
1:B:179:ASP:OD1	1:B:181[B]:GLN:HG2	1.90	0.70
1:B:176:HIS:HE1	1:B:186:GLY:O	1.76	0.69
1:A:126:LYS:HE2	1:A:138:LYS:HD3	1.75	0.68
1:A:292:ARG:HH11	1:A:405:THR:CG2	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:GLY:N	1:A:381:GLU:OE2	2.26	0.68
1:A:4:GLU:O	1:A:36:THR:HG21	1.95	0.67
1:B:99:ILE:HD12	1:B:99:ILE:H	1.60	0.67
1:B:122:LEU:HD23	1:B:143:PRO:HD3	1.76	0.66
1:A:128:VAL:N	1:A:129:PRO:CD	2.59	0.66
1:A:132:ILE:HG22	1:A:133:GLU:O	1.96	0.66
1:A:437:ASP:OD2	1:A:438:GLN:N	2.30	0.65
1:B:279:LYS:HG3	1:B:279:LYS:O	1.95	0.65
1:A:292:ARG:NH1	1:A:405:THR:HG21	2.11	0.64
1:B:384:ALA:HB3	1:B:386:ILE:HD12	1.80	0.64
1:A:435:VAL:HG23	1:B:476:ILE:HA	1.80	0.64
1:A:49:ALA:CB	1:A:207:MET:CE	2.76	0.63
1:B:30:TYR:HB2	1:B:319:GLN:HE22	1.64	0.63
1:A:126:LYS:HG2	1:A:138:LYS:HG2	1.80	0.62
1:A:138:LYS:NZ	1:B:422:GLU:OE1	2.30	0.62
1:B:104:GLU:HG3	1:B:158:ASN:HB2	1.81	0.62
1:A:31:ASP:O	1:A:32:GLN:HB2	1.99	0.62
1:B:97:THR:HG21	1:B:324:THR:O	2.00	0.61
1:A:330:ILE:CG2	1:A:334:GLN:HG3	2.31	0.61
1:A:128:VAL:HG11	1:B:461:ASN:OD1	2.01	0.61
1:A:49:ALA:CB	1:A:207:MET:HE1	2.31	0.61
1:B:97:THR:HG22	1:B:98:ILE:N	2.17	0.59
1:A:241:GLU:HB2	1:B:245:ARG:HD3	1.86	0.58
1:B:30:TYR:HB2	1:B:319:GLN:HE21	1.67	0.58
1:A:121:GLU:OE1	1:A:121:GLU:HA	2.03	0.58
1:B:114:GLU:O	1:B:117:THR:HB	2.03	0.57
1:A:49:ALA:HB2	1:A:207:MET:HE1	1.87	0.57
1:A:319:GLN:HG2	1:A:328:PRO:HD3	1.85	0.57
1:B:94:THR:HG22	1:B:96:GLY:N	2.08	0.56
1:A:330:ILE:HG22	1:A:334:GLN:HG3	1.87	0.56
1:A:381:GLU:O	1:A:382:LEU:HD23	2.05	0.56
1:A:94:THR:CG2	1:A:96:GLY:H	2.17	0.56
1:A:268:VAL:HG11	1:A:302:GLU:HG2	1.88	0.56
1:A:292:ARG:HH11	1:A:405:THR:HG21	1.68	0.55
1:B:291:ASN:ND2	1:B:380:THR:O	2.40	0.55
1:A:292:ARG:HH12	1:A:405:THR:CG2	2.18	0.54
1:A:255:GLY:C	1:A:381:GLU:OE2	2.46	0.54
1:A:221:ASN:OD1	1:A:223:ILE:HG12	2.08	0.54
1:A:68:ARG:HB3	1:A:119:THR:HG21	1.89	0.54
1:A:399:ILE:HG13	1:A:424:PHE:CD1	2.43	0.54
1:A:437:ASP:CG	1:A:438:GLN:N	2.61	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395:ASP:O	1:A:399:ILE:HG12	2.08	0.53
1:A:268:VAL:HG22	1:A:299:VAL:CG1	2.36	0.53
1:A:435:VAL:HG22	1:B:476:ILE:HA	1.88	0.53
1:A:404:ASP:OD1	1:A:404:ASP:C	2.45	0.53
1:A:68:ARG:HH11	1:A:119:THR:HG22	1.72	0.53
1:A:49:ALA:CB	1:A:207:MET:HE3	2.37	0.53
1:A:184:ILE:HA	1:A:188:THR:OG1	2.08	0.53
1:B:99:ILE:HD12	1:B:99:ILE:N	2.23	0.53
1:A:49:ALA:HB1	1:A:207:MET:CE	2.38	0.52
1:A:97:THR:HG22	1:A:100:LYS:H	1.74	0.52
1:A:417:ASP:HB3	1:A:420:LYS:HB3	1.91	0.52
1:B:60:TRP:CZ2	1:B:68:ARG:HG3	2.45	0.51
1:A:268:VAL:HG22	1:A:299:VAL:HG11	1.90	0.51
1:A:374:ASN:HA	1:A:379:GLN:HE21	1.75	0.51
1:B:292:ARG:HH21	1:B:373:ASN:HD21	1.57	0.51
1:B:148:SER:HB3	1:B:227:ILE:HD13	1.91	0.51
1:B:233:THR:HG22	1:B:254:LEU:HB3	1.92	0.51
1:A:435:VAL:HG21	1:B:476:ILE:HG12	1.93	0.51
1:B:116:MET:O	1:B:119:THR:HG22	2.11	0.51
1:A:437:ASP:CG	1:A:438:GLN:H	2.14	0.51
1:A:4:GLU:O	1:A:36:THR:CG2	2.58	0.50
1:B:262:VAL:HB	1:B:295:VAL:HG13	1.93	0.50
1:A:435:VAL:HG21	1:B:476:ILE:HG23	1.93	0.50
1:A:5:THR:HG23	1:A:6:LEU:HD23	1.94	0.50
1:B:30:TYR:CB	1:B:319:GLN:NE2	2.70	0.50
1:A:128:VAL:N	1:A:129:PRO:HD3	2.27	0.49
1:A:404:ASP:OD1	1:A:404:ASP:O	2.30	0.49
1:B:10:PHE:CZ	1:B:13:GLY:HA2	2.47	0.49
1:A:49:ALA:HB1	1:A:207:MET:HE3	1.95	0.48
1:B:97:THR:HG22	1:B:98:ILE:H	1.77	0.48
1:A:268:VAL:HG21	1:A:299:VAL:HG13	1.95	0.47
1:B:19:GLU:HG2	1:B:45:GLN:CD	2.34	0.47
1:A:99:ILE:H	1:A:99:ILE:HD12	1.80	0.47
1:B:277:PHE:HA	1:B:281:ILE:HG13	1.97	0.47
1:B:6:LEU:CD1	1:B:192:LYS:HG3	2.43	0.47
1:B:30:TYR:CB	1:B:319:GLN:HE22	2.26	0.47
1:B:135:LYS:HG2	1:B:477:GLN:OE1	2.15	0.47
1:B:184:ILE:O	1:B:189:ILE:HG12	2.14	0.47
1:A:209:THR:HG21	1:A:214:ILE:HD12	1.97	0.47
1:A:121:GLU:O	1:A:141:ARG:HG2	2.15	0.46
1:B:19:GLU:HG2	1:B:45:GLN:OE1	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:GLY:O	1:B:478:LYS:HG3	2.15	0.46
1:B:319:GLN:HG3	1:B:328:PRO:HD2	1.97	0.46
1:A:382:LEU:HD23	1:A:382:LEU:N	2.28	0.46
1:A:476:ILE:HD13	1:B:418:LEU:HD13	1.97	0.46
1:B:176:HIS:CE1	1:B:186:GLY:O	2.63	0.45
1:A:209:THR:HG21	1:A:214:ILE:CD1	2.47	0.45
1:B:126:LYS:HB3	1:B:138:LYS:HZ1	1.81	0.45
1:A:159:LEU:HD13	1:A:230:THR:HG21	1.98	0.45
1:A:377:ILE:H	1:A:377:ILE:HG13	1.54	0.45
1:A:414:PHE:CE2	1:A:436:ASN:HA	2.51	0.45
1:A:31:ASP:O	1:A:32:GLN:CB	2.63	0.45
1:B:7:ASN:OD1	1:B:7:ASN:N	2.44	0.45
1:A:68:ARG:HB3	1:A:119:THR:CG2	2.46	0.45
1:A:2:SER:HA	1:A:4:GLU:OE1	2.17	0.45
1:B:235:VAL:HG12	1:B:239:ILE:HD12	1.99	0.45
1:B:230:THR:HA	1:B:253:GLU:O	2.17	0.44
1:B:465:VAL:O	1:B:469:THR:OG1	2.28	0.44
1:B:303:PHE:CD1	1:B:303:PHE:C	2.90	0.44
1:A:266:ALA:HB2	1:A:414:PHE:O	2.18	0.44
1:B:25:ASP:HB3	1:B:34:VAL:HG22	2.00	0.44
1:A:292:ARG:HH11	1:A:405:THR:HG22	1.74	0.43
1:B:232:SER:OG	1:B:235:VAL:HG23	2.18	0.43
1:A:12:ASN:HB2	1:A:52:ILE:HD13	1.99	0.43
1:A:268:VAL:CG2	1:A:299:VAL:HG12	2.44	0.43
1:B:292:ARG:HD2	1:B:378:ALA:O	2.19	0.43
1:B:258:ASN:HB2	1:B:289:ILE:O	2.18	0.43
1:B:97:THR:HG21	1:B:99:ILE:HD13	2.00	0.43
1:B:68:ARG:NH2	1:B:122:LEU:HD13	2.34	0.43
1:A:413:VAL:HG13	1:A:435:VAL:HG12	2.00	0.42
1:B:95:GLY:HA2	1:B:319:GLN:HG2	2.01	0.42
1:A:435:VAL:CG2	1:B:476:ILE:HG12	2.50	0.42
1:A:97:THR:HG22	1:A:99:ILE:N	2.34	0.42
1:B:126:LYS:HD3	1:B:138:LYS:HZ3	1.83	0.42
1:A:289:ILE:HG12	1:A:383:PHE:CE1	2.54	0.42
1:B:399:ILE:HG12	1:B:424:PHE:HD1	1.75	0.42
1:B:95:GLY:O	1:B:319:GLN:HG2	2.20	0.42
1:A:329:LEU:HD21	1:A:385:PRO:HD3	2.02	0.42
1:A:127:GLU:C	1:A:128:VAL:HG22	2.37	0.42
1:A:319:GLN:HG2	1:A:328:PRO:CD	2.49	0.42
1:B:80:HIS:O	1:B:83:ARG:HG2	2.20	0.42
1:A:155:PHE:N	1:A:156:PRO:CD	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:VAL:HG12	1:B:127:GLU:HG2	2.02	0.41
1:B:115:ALA:HA	1:B:118:TYR:CZ	2.55	0.41
1:A:241:GLU:OE1	1:B:245:ARG:NH2	2.53	0.41
1:B:95:GLY:C	1:B:319:GLN:HG2	2.41	0.41
1:A:220:THR:HG22	1:A:220:THR:O	2.20	0.41
1:A:127:GLU:C	1:A:129:PRO:CD	2.83	0.41
1:A:128:VAL:O	1:A:129:PRO:C	2.56	0.41
1:B:122:LEU:HD12	1:B:122:LEU:N	2.36	0.41
1:A:94:THR:HG22	1:A:96:GLY:N	2.27	0.41
1:A:93:GLU:CD	1:A:182:THR:HA	2.40	0.41
1:A:221:ASN:O	1:A:224:PRO:HD2	2.21	0.40
1:A:130:SER:HB2	1:A:135:LYS:HD3	2.03	0.40
1:B:63:SER:O	1:B:68:ARG:NH1	2.55	0.40
1:A:289:ILE:CD1	1:A:383:PHE:HE1	2.35	0.40
1:B:99:ILE:CD1	1:B:99:ILE:H	2.31	0.40
1:A:433:THR:O	1:B:474:ILE:HA	2.22	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	448/485 (92%)	435 (97%)	10 (2%)	3 (1%)	26	46
1	B	440/485 (91%)	430 (98%)	9 (2%)	1 (0%)	52	75
All	All	888/970 (92%)	865 (97%)	19 (2%)	4 (0%)	34	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	GLY
1	A	217	GLY

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Mol	Chain	Res	Type
1	B	187	GLY
1	A	152	PRO

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	376/399 (94%)	352 (94%)	24 (6%)	22	39
1	B	369/399 (92%)	350 (95%)	19 (5%)	29	52
All	All	745/798 (93%)	702 (94%)	43 (6%)	25	45

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLU
1	A	32	GLN
1	A	36	THR
1	A	76	ARG
1	A	94	THR
1	A	97	THR
1	A	119	THR
1	A	128	VAL
1	A	214	ILE
1	A	269	ASP
1	A	276	ILE
1	A	319	GLN
1	A	340	GLU
1	A	347	THR
1	A	372	ASP
1	A	377	ILE
1	A	382	LEU
1	A	383	PHE
1	A	389	ILE
1	A	410	SER
1	A	415	THR

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Mol	Chain	Res	Type
1	A	438	GLN
1	A	461	ASN
1	A	476	ILE
1	B	1	MET
1	B	2	SER
1	B	4	GLU
1	B	94	THR
1	B	117	THR
1	B	133	GLU
1	B	136	THR
1	B	147	ILE
1	B	162	ARG
1	B	250	MET
1	B	273	ASP
1	B	276	ILE
1	B	281	ILE
1	B	319	GLN
1	B	382	LEU
1	B	406	GLU
1	B	432	MET
1	B	473	TRP
1	B	475	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	107	GLN
1	A	154	ASN
1	A	291	ASN
1	A	319	GLN
1	A	379	GLN
1	B	154	ASN
1	B	176	HIS
1	B	319	GLN
1	B	373	ASN

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 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	452/485 (93%)	0.23	32 (7%) 19 21	52, 80, 123, 187	0
1	B	447/485 (92%)	0.06	24 (5%) 29 33	51, 75, 110, 161	0
All	All	899/970 (92%)	0.14	56 (6%) 24 27	51, 77, 120, 187	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	478	LYS	5.8
1	A	132	ILE	5.5
1	B	407	TYR	5.1
1	A	131	ASP	5.0
1	A	293	ILE	5.0
1	A	407	TYR	5.0
1	A	463	TRP	4.8
1	A	133	GLU	4.7
1	A	134	GLY	4.7
1	A	260	PHE	4.6
1	B	461	ASN	4.2
1	A	261	ALA	4.1
1	B	167	ALA	4.0
1	A	277	PHE	4.0
1	B	255	GLY	4.0
1	B	168	ILE	3.5
1	A	406	GLU	3.5
1	A	409	LEU	3.4
1	B	462	PRO	3.4
1	A	294	ILE	3.4
1	B	282	HIS	3.2
1	B	62	LYS	3.1
1	A	256	GLY	3.0
1	A	291	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	174	VAL	2.9
1	B	127	GLU	2.8
1	B	388	THR	2.8
1	B	277	PHE	2.8
1	B	126	LYS	2.7
1	A	259	PRO	2.6
1	A	167	ALA	2.6
1	A	128	VAL	2.5
1	B	293	ILE	2.5
1	A	127	GLU	2.5
1	A	169	ALA	2.5
1	B	477	GLN	2.4
1	A	374	ASN	2.4
1	A	168	ILE	2.4
1	B	173	SER	2.4
1	A	462	PRO	2.4
1	B	408	GLY	2.3
1	B	413	VAL	2.3
1	A	90	ILE	2.3
1	B	261	ALA	2.3
1	B	287	CYS	2.2
1	A	412	ALA	2.2
1	A	404	ASP	2.2
1	A	322	PRO	2.2
1	A	323	LYS	2.2
1	B	270	ARG	2.2
1	A	91	ALA	2.2
1	A	408	GLY	2.1
1	A	389	ILE	2.1
1	A	461	ASN	2.1
1	B	172	ASN	2.1
1	B	165	ALA	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.