



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:52 PM GMT

PDB ID : 1VJ0
Title : Crystal structure of Alcohol dehydrogenase (TM0436) from *Thermotoga maritima* at 2.00 Å resolution
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2003-12-02
Resolution : 2.00 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

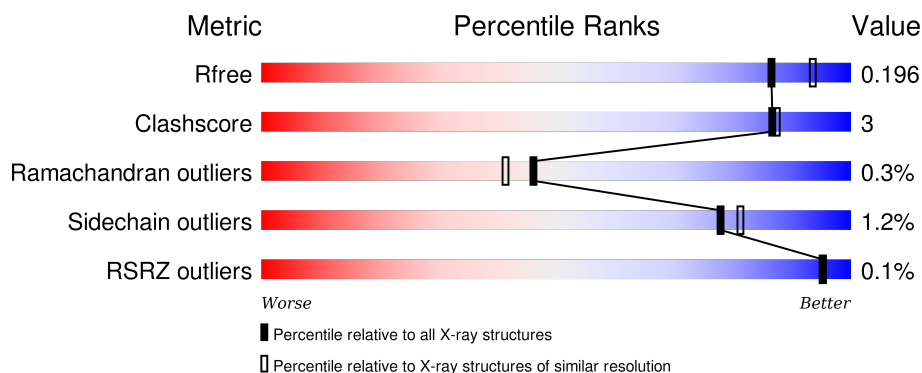
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	380	 90% 7% •
1	B	380	 88% 7% • •
1	C	380	 89% 7% • •
1	D	380	 90% 6% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ZN	B	401	-	-	-	X
3	UNL	C	2003	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12514 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 alcohol dehydrogenase, zinc-containing.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	4	0
			2830	1801	482	531	16			
1	B	364	Total	C	N	O	S	0	3	0
			2821	1796	484	526	15			
1	C	364	Total	C	N	O	S	0	3	0
			2827	1799	488	525	15			
1	D	365	Total	C	N	O	S	0	5	0
			2824	1796	488	525	15			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	LEADER SEQUENCE	UNP Q9WYR7
A	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYR7
A	-9	SER	-	LEADER SEQUENCE	UNP Q9WYR7
A	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYR7
A	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYR7
A	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYR7
A	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
A	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
A	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
A	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
A	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
A	0	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
B	-11	MET	-	LEADER SEQUENCE	UNP Q9WYR7
B	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYR7
B	-9	SER	-	LEADER SEQUENCE	UNP Q9WYR7
B	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYR7
B	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYR7
B	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYR7
B	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
B	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
B	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYR7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
B	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
B	0	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
C	-11	MET	-	LEADER SEQUENCE	UNP Q9WYR7
C	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYR7
C	-9	SER	-	LEADER SEQUENCE	UNP Q9WYR7
C	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYR7
C	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYR7
C	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYR7
C	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
C	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
C	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
C	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
C	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
C	0	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
D	-11	MET	-	LEADER SEQUENCE	UNP Q9WYR7
D	-10	GLY	-	LEADER SEQUENCE	UNP Q9WYR7
D	-9	SER	-	LEADER SEQUENCE	UNP Q9WYR7
D	-8	ASP	-	LEADER SEQUENCE	UNP Q9WYR7
D	-7	LYS	-	LEADER SEQUENCE	UNP Q9WYR7
D	-6	ILE	-	LEADER SEQUENCE	UNP Q9WYR7
D	-5	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
D	-4	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
D	-3	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
D	-2	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
D	-1	HIS	-	LEADER SEQUENCE	UNP Q9WYR7
D	0	HIS	-	LEADER SEQUENCE	UNP Q9WYR7

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Zn 2 2	0	0
2	A	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0
2	C	2	Total Zn 2 2	0	0

- Molecule 3 is UNKNOWN LIGAND (three-letter code: UNL) (formula:).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total O 2 2	0	0
3	A	1	Total O 3 3	0	0
3	D	1	Total O 3 3	0	0
3	C	1	Total O 4 4	0	0

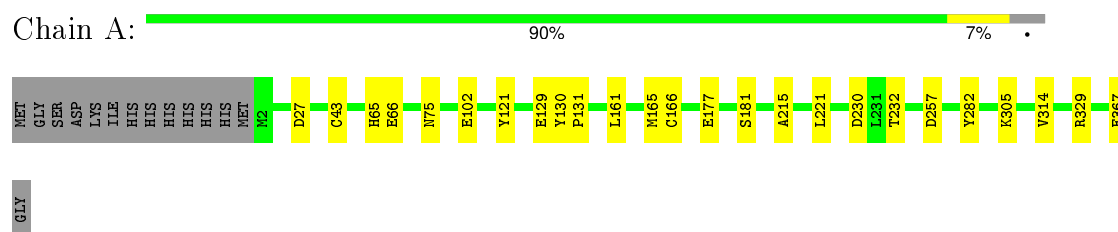
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	324	Total O 326 326	0	2
4	B	285	Total O 288 288	0	3
4	C	307	Total O 312 312	0	5
4	D	262	Total O 266 266	0	5

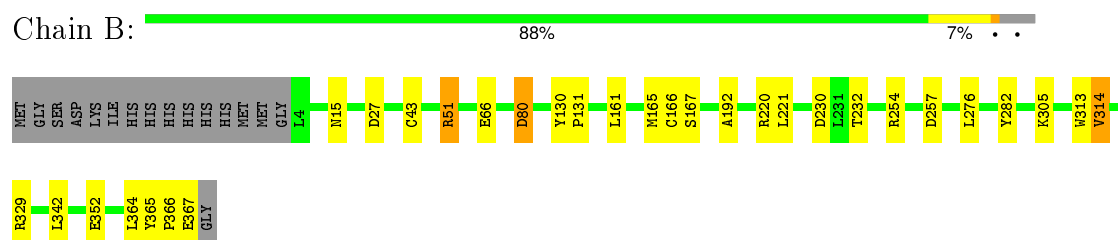
3 Residue-property plots [i](#)

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.

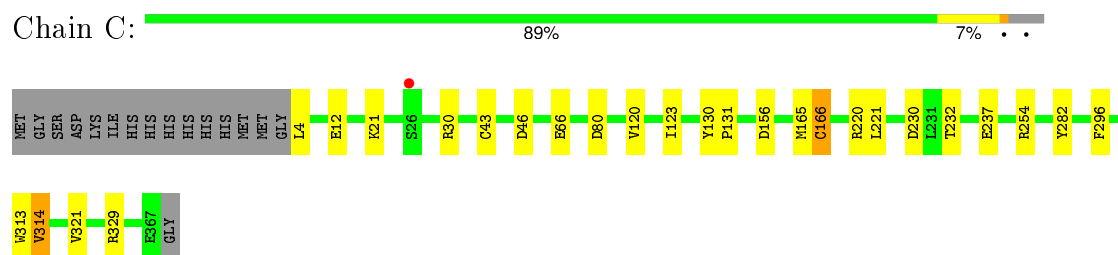
- Molecule 1: alcohol dehydrogenase, zinc-containing



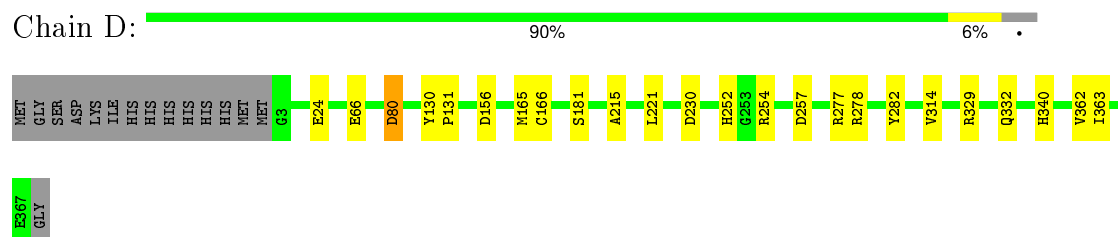
- Molecule 1: alcohol dehydrogenase, zinc-containing



- Molecule 1: alcohol dehydrogenase, zinc-containing



- Molecule 1: alcohol dehydrogenase, zinc-containing



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.88Å 104.92Å 161.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.53 – 2.00 92.88 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (80.53-2.00) 99.0 (92.88-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.1.9999	Depositor
R, R_{free}	0.145 , 0.194 0.157 , 0.196	Depositor DCC
R_{free} test set	2090 reflections (2.01%)	DCC
Wilson B-factor (Å ²)	24.1	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 106259 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12514	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, UNL

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	0.79	0/2904	0.88	3/3936 (0.1%)
1	B	0.81	0/2891	0.89	6/3917 (0.2%)
1	C	0.86	5/2897 (0.2%)	0.91	8/3923 (0.2%)
1	D	0.78	0/2904	0.88	7/3936 (0.2%)
All	All	0.81	5/11596 (0.0%)	0.89	24/15712 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	321	VAL	CB-CG2	-6.31	1.39	1.52
1	C	166[A]	CYS	CB-SG	-6.29	1.71	1.82
1	C	166[B]	CYS	CB-SG	-6.29	1.71	1.82
1	C	237	GLU	CD-OE1	5.18	1.31	1.25
1	C	296	PHE	CE2-CZ	5.08	1.47	1.37

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	254	ARG	NE-CZ-NH2	-6.81	116.89	120.30
1	B	80	ASP	CB-CG-OD1	6.74	124.37	118.30
1	B	257	ASP	CB-CG-OD2	6.59	124.23	118.30
1	A	257	ASP	CB-CG-OD2	6.25	123.92	118.30
1	A	27	ASP	CB-CG-OD2	6.21	123.89	118.30
1	D	277	ARG	NE-CZ-NH2	-6.19	117.21	120.30
1	C	230	ASP	CB-CG-OD2	6.17	123.86	118.30
1	D	277	ARG	NE-CZ-NH1	6.10	123.35	120.30
1	B	27	ASP	CB-CG-OD2	6.02	123.72	118.30
1	D	80	ASP	CB-CG-OD1	6.00	123.70	118.30
1	A	230	ASP	CB-CG-OD2	5.98	123.69	118.30
1	C	46	ASP	CB-CG-OD2	5.98	123.68	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	156	ASP	CB-CG-OD2	5.70	123.43	118.30
1	C	254	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	B	51	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	D	156	ASP	CB-CG-OD2	5.48	123.23	118.30
1	B	230	ASP	CB-CG-OD2	5.47	123.23	118.30
1	C	166[A]	CYS	CA-CB-SG	-5.42	104.24	114.00
1	C	166[B]	CYS	CA-CB-SG	-5.42	104.24	114.00
1	D	230	ASP	CB-CG-OD2	5.39	123.15	118.30
1	D	257	ASP	CB-CG-OD2	5.33	123.09	118.30
1	C	4	LEU	CA-CB-CG	5.15	127.15	115.30
1	C	220	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	B	254	ARG	NE-CZ-NH1	5.01	122.80	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2830	0	2812	21	0
1	B	2821	0	2825	14	0
1	C	2827	0	2844	12	0
1	D	2824	0	2814	11	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	3	0	0	1	0
3	B	2	0	0	0	0
3	C	4	0	0	3	0
3	D	3	0	0	0	0
4	A	326	0	0	5	0
4	B	288	0	0	3	0
4	C	312	0	0	4	0
4	D	266	0	0	4	0
All	All	12514	0	11295	62	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 3.

All (62) 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)
3:A:2001:UNL:O1	3:A:2001:UNL:O2	1.55	1.20
1:A:166[B]:CYS:SG	4:A:2179:HOH:O	2.25	0.94
1:A:66:GLU:CD	1:A:166[B]:CYS:SG	2.52	0.89
1:B:43:CYS:HB2	1:B:66:GLU:OE2	1.72	0.88
3:C:2003:UNL:O4	3:C:2003:UNL:O3	1.97	0.83
3:C:2003:UNL:O1	3:C:2003:UNL:O3	1.95	0.82
3:C:2003:UNL:O2	3:C:2003:UNL:O3	2.02	0.77
1:C:43:CYS:HB2	1:C:66:GLU:OE2	1.91	0.71
1:A:66:GLU:OE2	1:A:166[B]:CYS:SG	2.50	0.69
1:B:166[B]:CYS:SG	1:B:167:SER:N	2.67	0.68
1:A:43:CYS:HB2	1:A:66:GLU:OE2	1.95	0.67
1:C:165:MET:HG3	4:C:2152:HOH:O	1.95	0.65
1:D:332:GLN:HG3	4:D:2154:HOH:O	1.99	0.62
4:B:2108:HOH:O	1:D:278:ARG:HD3	1.99	0.62
1:D:252:HIS:ND1	4:D:2235:HOH:O	2.33	0.55
1:C:66:GLU:OE2	1:C:166[B]:CYS:SG	2.64	0.55
1:C:12:GLU:OE2	1:C:21:LYS:NZ	2.36	0.54
1:D:66:GLU:CD	1:D:166[B]:CYS:SG	2.88	0.52
1:D:130:TYR:CG	1:D:131:PRO:HA	2.45	0.52
1:D:165:MET:HA	1:D:165:MET:CE	2.39	0.51
1:B:66:GLU:CD	1:B:166[B]:CYS:SG	2.88	0.51
1:C:66:GLU:CD	1:C:166[B]:CYS:SG	2.90	0.50
1:A:367:GLU:HG2	4:A:2243:HOH:O	2.10	0.50
1:A:102[B]:GLU:HG3	4:B:2046:HOH:O	2.13	0.49
1:D:215:ALA:HB3	1:D:221:LEU:HD21	1.95	0.48
1:A:165:MET:HB3	4:A:2084:HOH:O	2.14	0.47
1:C:165:MET:CG	4:C:2152:HOH:O	2.60	0.47
1:B:342:LEU:O	1:B:364:LEU:HA	2.15	0.47
1:A:130:TYR:CG	1:A:131:PRO:HA	2.50	0.47
1:A:161:LEU:O	1:A:165:MET:HG2	2.15	0.46
1:C:130:TYR:CG	1:C:131:PRO:HA	2.50	0.46
1:B:192:ALA:O	1:B:220:ARG:HD3	2.16	0.46
1:C:221:LEU:HD22	1:C:232:THR:HB	1.98	0.45
1:A:215:ALA:HB3	1:A:221:LEU:HD21	1.97	0.45
1:D:340:HIS:HB2	1:D:362:VAL:HG22	1.99	0.45
1:C:329:ARG:HD2	4:C:2161:HOH:O	2.17	0.44
1:A:221:LEU:HD22	1:A:232:THR:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:329:ARG:NH1	4:C:2184:HOH:O	2.51	0.44
1:B:165:MET:CE	1:B:165:MET:HA	2.48	0.44
1:B:313:TRP:CD1	1:B:314:VAL:HG22	2.53	0.43
1:A:102[B]:GLU:CG	4:B:2046:HOH:O	2.66	0.43
1:B:15:ASN:OD1	1:B:51:ARG:HD3	2.18	0.43
1:A:329:ARG:NE	4:A:2277:HOH:O	2.32	0.43
1:C:313:TRP:CD1	1:C:314:VAL:HG22	2.54	0.42
1:B:276:LEU:O	1:B:305:LYS:NZ	2.48	0.42
1:A:329:ARG:HD3	4:D:2026:HOH:O	2.19	0.42
1:A:165:MET:HA	1:A:165:MET:CE	2.50	0.42
1:A:75:ASN:OD1	1:A:75:ASN:O	2.37	0.42
1:B:130:TYR:CG	1:B:131:PRO:HA	2.53	0.42
1:D:329[B]:ARG:NE	4:D:2223:HOH:O	2.38	0.42
1:A:129:GLU:CD	1:A:129:GLU:H	2.23	0.42
1:D:66:GLU:OE2	1:D:166[B]:CYS:SG	2.77	0.41
1:B:161:LEU:O	1:B:165:MET:HG2	2.21	0.41
1:A:65:HIS:HB3	1:A:121:TYR:O	2.20	0.41
1:A:177:GLU:CD	4:A:2024:HOH:O	2.58	0.41
1:B:221:LEU:HD22	1:B:232:THR:HB	2.02	0.41
1:C:120:VAL:HG11	1:C:123:ILE:HD12	2.03	0.41
1:A:66:GLU:CG	1:A:166[B]:CYS:SG	3.09	0.40
1:B:365:TYR:HA	1:B:366:PRO:HD3	1.96	0.40
1:A:75:ASN:OD1	1:A:75:ASN:C	2.59	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	368/380 (97%)	359 (98%)	8 (2%)	1 (0%)	46	41
1	B	365/380 (96%)	353 (97%)	11 (3%)	1 (0%)	46	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	365/380 (96%)	356 (98%)	8 (2%)	1 (0%)	46	41
1	D	368/380 (97%)	357 (97%)	10 (3%)	1 (0%)	46	41
All	All	1466/1520 (96%)	1425 (97%)	37 (2%)	4 (0%)	46	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	314	VAL
1	A	314	VAL
1	B	314	VAL
1	C	314	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	304/319 (95%)	301 (99%)	3 (1%)	82	85
1	B	305/319 (96%)	301 (99%)	4 (1%)	76	79
1	C	307/319 (96%)	304 (99%)	3 (1%)	82	85
1	D	305/319 (96%)	300 (98%)	5 (2%)	70	73
All	All	1221/1276 (96%)	1206 (99%)	15 (1%)	78	81

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	181	SER
1	A	282	TYR
1	A	305	LYS
1	B	80	ASP
1	B	282	TYR
1	B	352	GLU
1	B	367	GLU
1	C	30	ARG

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Mol	Chain	Res	Type
1	C	80	ASP
1	C	282	TYR
1	D	24	GLU
1	D	80	ASP
1	D	181	SER
1	D	282	TYR
1	D	363	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	210	ASN
1	A	219	ASN
1	B	16	GLN
1	B	219	ASN
1	C	219	ASN
1	D	219	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 4 are unknown and 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	366/380 (96%)	-0.09	0	100 100	24, 29, 38, 46	0
1	B	364/380 (95%)	-0.06	0	100 100	23, 29, 39, 45	0
1	C	364/380 (95%)	-0.07	1 (0%)	94 94	24, 29, 38, 51	0
1	D	365/380 (96%)	-0.03	0	100 100	24, 29, 39, 47	0
All	All	1459/1520 (95%)	-0.06	1 (0%)	95 95	23, 29, 39, 51	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	26	SER	2.3

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ZN	B	401	1/1	0.91	0.17	2.83	26,26,26,26	1
3	UNL	C	2003	4/-	0.96	0.17	1.39	23,26,36,38	0
2	ZN	A	401	1/1	0.80	0.14	1.05	35,35,35,35	1
2	ZN	C	401	1/1	0.97	0.15	0.65	33,33,33,33	1
3	UNL	D	2004	3/-	0.94	0.13	-0.03	23,23,32,58	0
3	UNL	B	2002	2/-	0.99	0.10	-0.86	21,21,21,29	0
3	UNL	A	2001	3/-	0.96	0.09	-1.62	23,23,28,53	0
2	ZN	D	400	1/1	1.00	0.07	-1.95	23,23,23,23	0
2	ZN	D	401	1/1	0.91	0.08	-1.97	34,34,34,34	1
2	ZN	C	400	1/1	1.00	0.05	-2.25	22,22,22,22	0
2	ZN	B	400	1/1	0.99	0.05	-2.54	22,22,22,22	0
2	ZN	A	400	1/1	1.00	0.05	-2.98	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.