



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:59 AM UTC

PDB ID : 4A73 / pdb_00004a73
Title : SINGLE POINT MUTANT OF THERMUS THERMOPHILUS LACTATE
DEHYDROGENASE
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Deposited on : 2011-11-10
Resolution : 3.00 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

<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

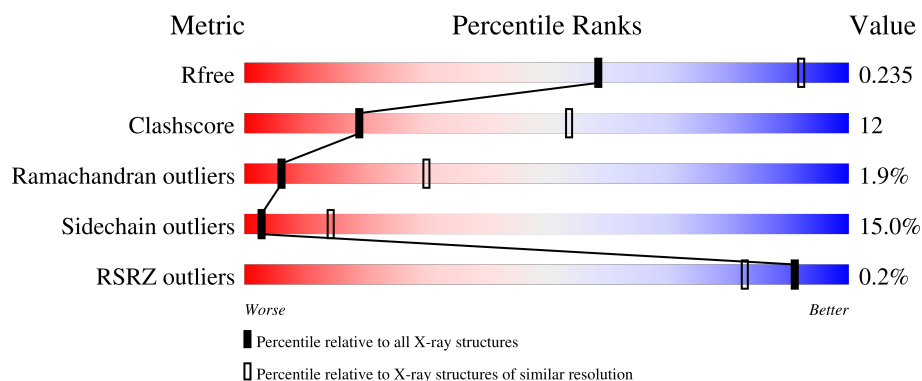
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 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	310	 69% 26% 5%
1	B	310	 71% 24% 5% 5%
1	C	310	 64% 29% 7%
1	D	310	 61% 34% 5% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9440 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 L-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	1	0
			2316	1470	414	429	3			
1	B	309	Total	C	N	O	S	0	3	0
			2320	1471	417	429	3			
1	C	309	Total	C	N	O	S	0	1	0
			2308	1465	413	427	3			
1	D	310	Total	C	N	O	S	0	2	0
			2325	1475	418	429	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	218	ALA	ARG	engineered mutation	UNP Q5SJA1
B	218	ALA	ARG	engineered mutation	UNP Q5SJA1
C	218	ALA	ARG	engineered mutation	UNP Q5SJA1
D	218	ALA	ARG	engineered mutation	UNP Q5SJA1

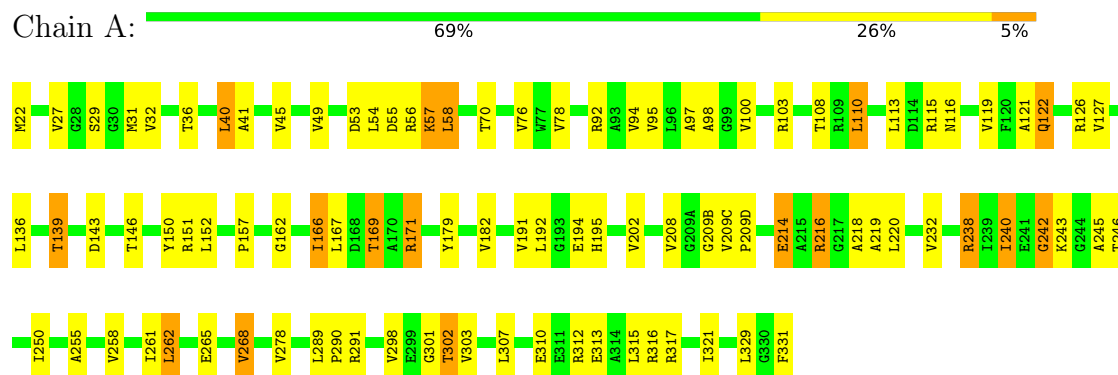
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	59	Total	O	0	0
			59	59		
2	B	60	Total	O	0	0
			60	60		
2	C	19	Total	O	0	0
			19	19		
2	D	33	Total	O	0	0
			33	33		

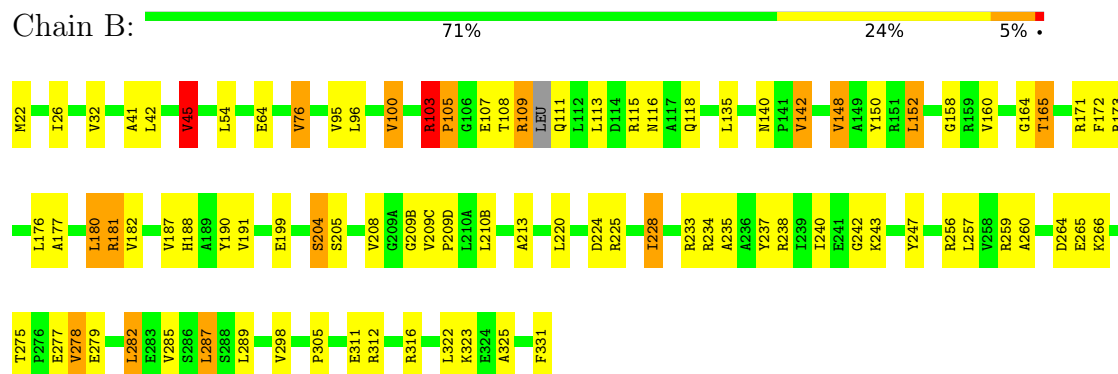
3 Residue-property plots

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.

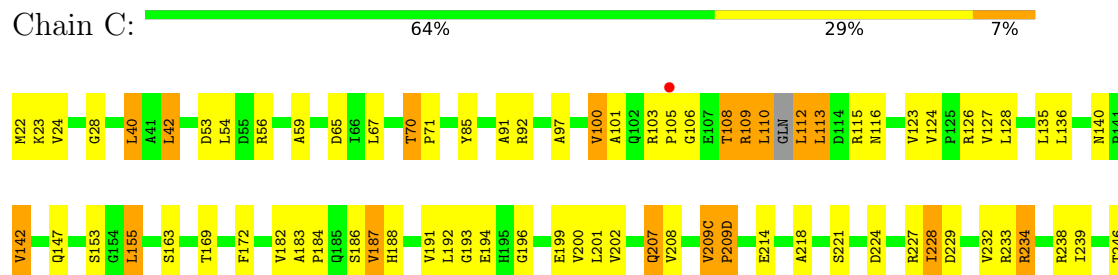
• Molecule 1: L-LACTATE DEHYDROGENASE

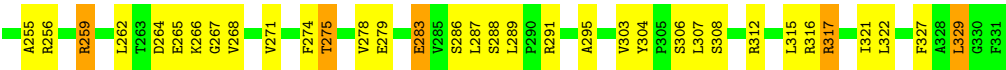


• Molecule 1: L-LACTATE DEHYDROGENASE

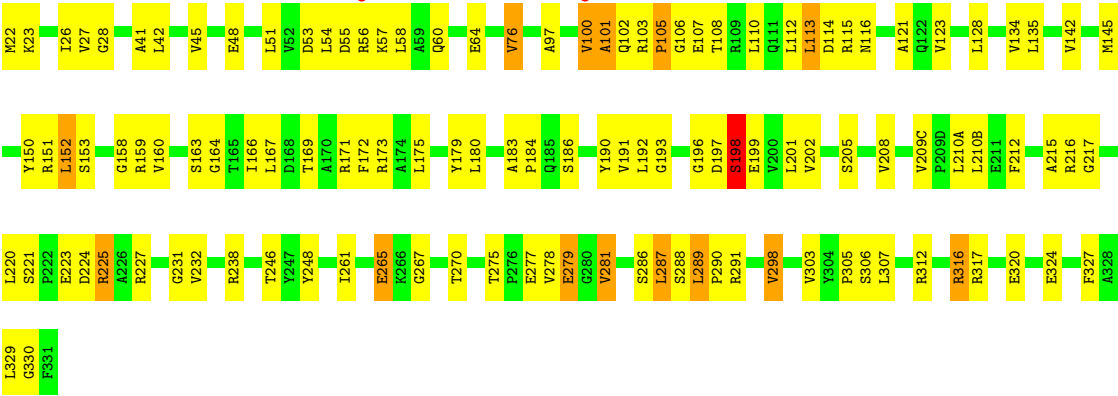


• Molecule 1: L-LACTATE DEHYDROGENASE





● Molecule 1: L-LACTATE DEHYDROGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	158.04Å 158.04Å 142.11Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.29 – 3.00 49.29 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (49.29-3.00) 99.1 (49.29-3.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.2_869)	Depositor
R, R_{free}	0.170 , 0.235 0.165 , 0.235	Depositor DCC
R_{free} test set	1999 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	80.3	Xtriage
Anisotropy	0.252	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 76.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.040 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9440	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% 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	0.61	0/2360	0.99	4/3211 (0.1%)
1	B	0.58	0/2369	0.97	4/3221 (0.1%)
1	C	0.55	0/2351	0.95	6/3198 (0.2%)
1	D	0.57	0/2371	0.91	0/3224
All	All	0.58	0/9451	0.96	14/12854 (0.1%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	103	ARG	CA-C-N	6.88	128.44	119.84
1	B	103	ARG	C-N-CA	6.88	128.44	119.84
1	B	109	ARG	N-CA-C	-6.24	105.83	113.50
1	C	304	TYR	CA-C-N	-6.04	114.39	120.31
1	C	304	TYR	C-N-CA	-6.04	114.39	120.31
1	C	42	LEU	N-CA-C	-5.84	106.28	113.41
1	A	70	THR	CA-C-N	-5.73	113.92	119.87
1	A	70	THR	C-N-CA	-5.73	113.92	119.87
1	A	166	ILE	N-CA-CB	5.47	116.95	110.55
1	B	100	VAL	N-CA-C	5.36	115.06	108.53
1	C	142	VAL	N-CA-C	5.31	116.68	110.62
1	C	124	VAL	CA-C-N	-5.23	113.31	119.84
1	C	124	VAL	C-N-CA	-5.23	113.31	119.84
1	A	166	ILE	CB-CA-C	-5.15	105.37	111.97

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	2316	0	2363	51	0
1	B	2320	0	2376	54	0
1	C	2308	0	2361	62	0
1	D	2325	0	2382	66	0
2	A	59	0	0	6	0
2	B	60	0	0	3	0
2	C	19	0	0	2	0
2	D	33	0	0	2	0
All	All	9440	0	9482	221	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 (221) 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:22:MET:N	2:D:2001:HOH:O	2.05	0.89
1:D:142:VAL:HG11	1:D:164:GLY:H	1.37	0.88
1:C:224:ASP:OD1	1:C:227:ARG:NH2	2.11	0.83
1:B:173:ARG:HH21	1:B:190:TYR:HE1	1.29	0.80
1:C:112:LEU:O	1:C:116:ASN:N	2.15	0.78
1:C:22:MET:N	2:C:2001:HOH:O	2.18	0.76
1:C:22:MET:SD	1:C:92[A]:ARG:NH1	2.59	0.74
1:A:143:ASP:OD2	2:A:2029:HOH:O	2.06	0.74
1:A:238:ARG:NH1	1:B:64:GLU:OE2	2.19	0.73
1:C:110:LEU:HD12	1:C:112:LEU:H	1.53	0.73
1:C:194:GLU:HG3	1:C:322:LEU:HD21	1.70	0.73
1:D:101:ALA:HB1	1:D:115:ARG:HH11	1.56	0.70
1:B:209(B):GLY:HA2	1:C:207:GLN:HE21	1.58	0.68
1:A:22:MET:N	2:A:2001:HOH:O	2.25	0.68
1:D:60:GLN:NE2	1:D:64:GLU:OE1	2.28	0.67
1:C:275:THR:OG1	1:C:291:ARG:NH2	2.28	0.66
1:D:279:GLU:OE2	1:D:312:ARG:NH2	2.29	0.66
1:D:224:ASP:HA	1:D:227:ARG:HG2	1.77	0.65
1:A:291:ARG:HG2	1:A:302:THR:HB	1.79	0.65
1:A:49:VAL:HB	1:A:78:VAL:HG22	1.79	0.65
1:C:110:LEU:O	1:C:113:LEU:N	2.30	0.65
1:D:113:LEU:HD21	1:D:329:LEU:HG	1.79	0.64
1:B:199:GLU:O	1:B:233[A]:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:172:PHE:CD1	1:D:201:LEU:HD13	2.34	0.63
1:C:153:SER:HB2	1:C:155:LEU:HD22	1.81	0.63
1:D:105:PRO:HB2	1:D:106:GLY:HA3	1.81	0.63
1:D:196:GLY:O	1:D:198:SER:N	2.32	0.62
1:B:204:SER:OG	1:B:311:GLU:OE1	2.19	0.61
1:B:22:MET:N	2:B:2002:HOH:O	2.32	0.61
1:D:105:PRO:CB	1:D:106:GLY:HA3	2.31	0.60
1:D:169:THR:HA	1:D:191:VAL:HG23	1.84	0.59
1:C:279:GLU:HB3	1:C:316:ARG:HG3	1.85	0.59
1:A:268:VAL:HA	1:A:291:ARG:O	2.03	0.58
1:A:57:LYS:H	1:A:57:LYS:HD2	1.67	0.58
1:C:278:VAL:HG11	1:C:287:LEU:HD21	1.85	0.58
1:A:53:ASP:OD1	2:A:2008:HOH:O	2.17	0.57
1:A:95:VAL:HG22	1:A:136:LEU:HD23	1.86	0.57
1:A:179:TYR:OH	1:A:219:ALA:O	2.20	0.57
1:A:40:LEU:HD12	1:A:45:VAL:HB	1.88	0.56
1:C:110:LEU:HD13	1:C:115:ARG:HD3	1.86	0.56
1:A:29:SER:O	1:A:29:SER:OG	2.09	0.56
1:A:209(B):GLY:N	2:A:2042:HOH:O	2.36	0.55
1:D:150:TYR:HA	1:D:160:VAL:HG21	1.89	0.55
1:D:265:GLU:HG2	1:D:267:GLY:H	1.72	0.55
1:A:97:ALA:HA	1:A:139:THR:HG22	1.89	0.55
1:C:233:ARG:O	1:C:234:ARG:NH1	2.40	0.54
1:A:303:VAL:HG22	1:D:212:PHE:HE1	1.72	0.53
1:A:243:LYS:HE3	1:A:245:ALA:O	2.07	0.53
1:C:109:ARG:NH1	1:C:110:LEU:HD23	2.23	0.53
1:B:264:ASP:OD1	1:B:266:LYS:NZ	2.41	0.53
1:A:31:MET:HE1	2:B:2051:HOH:O	2.09	0.53
1:B:173:ARG:HG2	1:B:187:VAL:O	2.08	0.53
1:C:265:GLU:HG2	1:C:267:GLY:H	1.74	0.53
1:B:173:ARG:NH1	2:B:2047:HOH:O	2.41	0.52
1:D:275:THR:OG1	1:D:291:ARG:NH2	2.41	0.52
1:A:171:ARG:NH1	2:A:2034:HOH:O	2.42	0.52
1:B:282:LEU:O	1:B:323:LYS:HE3	2.08	0.52
1:B:177:ALA:HB1	1:B:182:VAL:O	2.10	0.52
1:A:121:ALA:HA	1:A:152:LEU:HD13	1.92	0.51
1:B:172:PHE:O	1:B:176:LEU:HB2	2.10	0.51
1:D:209(C):VAL:HG13	1:D:212:PHE:HB2	1.92	0.51
1:A:291:ARG:HH11	1:A:302:THR:HG21	1.75	0.51
1:C:274:PHE:HZ	1:C:283:GLU:HB3	1.74	0.51
1:D:53:ASP:OD1	1:D:54:LEU:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:PHE:CE1	1:B:228:ILE:HD11	2.46	0.51
1:C:110:LEU:CD1	1:C:112:LEU:H	2.22	0.51
1:C:196:GLY:O	1:C:199:GLU:HG2	2.11	0.50
1:D:290:PRO:HB2	1:D:303:VAL:HB	1.94	0.50
1:D:265:GLU:HG2	1:D:267:GLY:N	2.27	0.50
1:B:158:GLY:HA2	1:B:298:VAL:HG22	1.94	0.50
1:D:128:LEU:HD11	1:D:153:SER:HB2	1.94	0.50
1:D:172:PHE:CE1	1:D:201:LEU:HD13	2.46	0.50
1:B:256:ARG:CZ	1:B:259:ARG:HH11	2.24	0.49
1:C:92[B]:ARG:HH22	1:C:295:ALA:HB1	1.77	0.49
1:B:109:ARG:O	1:B:113:LEU:HB3	2.12	0.49
1:A:58:LEU:HA	1:B:242:GLY:O	2.12	0.49
1:A:150:TYR:CE1	1:A:157:PRO:HA	2.47	0.49
1:A:36:THR:O	1:A:40:LEU:HB2	2.12	0.49
1:B:224:ASP:O	1:B:228:ILE:HG23	2.12	0.49
1:A:100:VAL:HG22	1:A:116:ASN:OD1	2.12	0.49
1:A:268:VAL:HG13	1:D:186:SER:HB3	1.94	0.49
1:B:220:LEU:O	1:B:225[A]:ARG:NH1	2.46	0.48
1:C:109:ARG:HB2	1:C:110:LEU:HA	1.95	0.48
1:D:158:GLY:HA2	1:D:298:VAL:HG22	1.95	0.48
1:B:235:ALA:HA	1:B:238:ARG:NH1	2.28	0.48
1:B:188:HIS:CE1	1:C:188:HIS:CE1	3.02	0.48
1:B:233[B]:ARG:HH22	1:B:234:ARG:HH11	1.60	0.48
1:A:166:ILE:HG13	1:A:167:LEU:HD13	1.96	0.48
1:C:274:PHE:CZ	1:C:283:GLU:HB3	2.48	0.48
1:B:26:ILE:HG12	1:B:95:VAL:HB	1.94	0.48
1:A:301:GLY:HA3	1:D:216[B]:ARG:NH1	2.29	0.48
1:A:307:LEU:HD23	1:A:312:ARG:HA	1.95	0.48
1:C:172:PHE:HD1	1:C:232:VAL:HG21	1.78	0.47
1:D:278:VAL:O	1:D:281:VAL:HG23	2.14	0.47
1:B:260:ALA:HA	1:B:265:GLU:HB2	1.97	0.47
1:B:165:THR:O	1:B:165:THR:HG23	2.14	0.47
1:C:23:LYS:HB3	1:C:91:ALA:HA	1.96	0.47
1:C:28:GLY:HA3	1:C:97:ALA:O	2.14	0.47
1:C:239:ILE:HG21	1:C:246:THR:HG22	1.96	0.47
1:C:327:PHE:C	1:C:329:LEU:H	2.22	0.47
1:D:191:VAL:HG22	1:D:201:LEU:HD22	1.97	0.47
1:C:202:VAL:O	1:C:202:VAL:HG13	2.15	0.46
1:A:265:GLU:O	1:D:183:ALA:HB2	2.16	0.46
1:D:41:ALA:HA	1:D:76:VAL:HG11	1.96	0.46
1:A:313:GLU:HG3	1:A:316:ARG:NH2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:112:LEU:HD12	1:C:112:LEU:HA	1.78	0.46
1:D:105:PRO:CG	1:D:106:GLY:HA3	2.46	0.46
1:D:135:LEU:HD12	1:D:160:VAL:HG22	1.97	0.46
1:B:165:THR:HG21	1:B:191:VAL:O	2.16	0.46
1:C:306:SER:O	1:C:307:LEU:HD12	2.15	0.46
1:C:256:ARG:HH11	1:C:259:ARG:HG2	1.81	0.46
1:D:193:GLY:HA2	1:D:287:LEU:HB2	1.97	0.46
1:B:142:VAL:HG11	1:B:164:GLY:H	1.80	0.46
1:A:55:ASP:OD1	1:A:57:LYS:HD2	2.15	0.46
1:D:55:ASP:O	1:D:58:LEU:N	2.48	0.46
1:A:40:LEU:HD13	1:A:255:ALA:HB1	1.99	0.45
1:C:147:GLN:HB2	1:C:286:SER:OG	2.16	0.45
1:D:28:GLY:HA3	1:D:97:ALA:O	2.16	0.45
1:D:205:SER:HB3	1:D:306:SER:HB3	1.98	0.45
1:D:305:PRO:O	1:D:307:LEU:HG	2.17	0.45
1:B:135:LEU:HD12	1:B:160:VAL:HG22	1.99	0.45
1:C:192:LEU:HD22	1:C:289:LEU:HA	1.98	0.45
1:C:274:PHE:HA	1:C:286:SER:HB3	1.98	0.45
1:D:327:PHE:C	1:D:330:GLY:H	2.25	0.45
1:B:305:PRO:HA	1:C:209(C):VAL:HG23	1.99	0.45
1:A:146:THR:OG1	1:A:162:GLY:HA3	2.17	0.45
1:B:172:PHE:CD1	1:B:228:ILE:HD11	2.52	0.45
1:A:103:ARG:HG3	1:A:115:ARG:HH12	1.81	0.44
1:C:65:ASP:OD2	1:D:248:TYR:N	2.50	0.44
1:C:264:ASP:O	1:C:266:LYS:HG3	2.17	0.44
1:C:271:VAL:O	1:C:288:SER:HA	2.17	0.44
1:A:301:GLY:HA3	1:D:216[B]:ARG:HH12	1.82	0.44
1:C:307:LEU:HB3	1:C:308:SER:H	1.64	0.44
1:D:288:SER:O	1:D:289:LEU:HD13	2.17	0.44
1:A:110:LEU:HD12	1:A:110:LEU:HA	1.59	0.44
1:B:279:GLU:CD	1:B:312:ARG:HG3	2.42	0.44
1:C:53:ASP:O	1:C:56:ARG:HD3	2.18	0.44
1:D:163:SER:O	1:D:166:ILE:HG23	2.18	0.44
1:A:313:GLU:HG2	1:A:317:ARG:HE	1.83	0.44
1:A:92:ARG:HD3	1:A:262:LEU:HD22	1.99	0.44
1:C:289:LEU:HA	1:C:289:LEU:HD23	1.76	0.44
1:B:199:GLU:OE2	1:B:233[A]:ARG:HG3	2.18	0.44
1:C:40:LEU:HD13	1:C:255:ALA:HA	1.99	0.44
1:B:107:GLU:HB2	1:B:111:GLN:HG2	1.99	0.43
1:B:322:LEU:O	1:B:325:ALA:HB3	2.18	0.43
1:A:169:THR:OG1	1:A:191:VAL:N	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210(B):LEU:HD21	1:B:225[A]:ARG:NH1	2.33	0.43
1:D:191:VAL:O	1:D:192:LEU:HD23	2.18	0.43
1:B:279:GLU:OE1	1:B:312:ARG:HG3	2.18	0.43
1:C:279:GLU:CD	1:C:312:ARG:HG2	2.43	0.43
1:D:169:THR:O	1:D:173:ARG:HG3	2.19	0.43
1:D:183:ALA:HA	1:D:184:PRO:HD3	1.89	0.43
1:C:67:LEU:O	1:C:70:THR:HG22	2.18	0.43
1:D:223:GLU:C	1:D:225:ARG:H	2.26	0.43
1:B:181:ARG:HG2	1:B:181:ARG:HH11	1.83	0.43
1:D:116:ASN:HB3	1:D:145:MET:HE2	2.01	0.43
1:A:214:GLU:C	1:A:216:ARG:H	2.27	0.43
1:B:22:MET:HA	1:B:22:MET:HE2	2.01	0.43
1:C:127:VAL:HG12	1:C:128:LEU:HD23	2.00	0.43
1:A:303:VAL:HG22	1:D:212:PHE:CE1	2.52	0.43
1:D:215:ALA:C	1:D:217:GLY:H	2.26	0.42
1:B:233[B]:ARG:NH2	1:B:234:ARG:HH11	2.17	0.42
1:B:152:LEU:HD12	1:B:152:LEU:HA	1.78	0.42
1:B:275:THR:HG21	1:B:278:VAL:HG22	2.01	0.42
1:D:184:PRO:C	1:D:186:SER:H	2.27	0.42
1:D:199:GLU:OE2	1:D:232:VAL:HG12	2.20	0.42
1:D:215:ALA:HB3	2:D:2028:HOH:O	2.19	0.42
1:C:169:THR:HA	1:C:191:VAL:HG23	2.01	0.42
1:D:23:LYS:HE3	1:D:48:GLU:OE2	2.18	0.42
1:A:329:LEU:HD12	1:A:329:LEU:HA	1.68	0.42
1:B:150:TYR:N	1:B:160:VAL:HG11	2.35	0.42
1:D:121:ALA:HA	1:D:152:LEU:HD21	2.00	0.42
1:A:56:ARG:NH2	2:A:2011:HOH:O	2.46	0.42
1:A:240:ILE:C	1:A:242:GLY:H	2.28	0.42
1:A:289:LEU:O	1:A:291:ARG:HG3	2.20	0.42
1:D:159:ARG:HE	1:D:159:ARG:HB3	1.71	0.42
1:B:289:LEU:HD23	1:B:289:LEU:HA	1.77	0.42
1:B:148:VAL:HB	1:B:331:PHE:CE2	2.55	0.41
1:C:265:GLU:HG2	1:C:267:GLY:N	2.35	0.41
1:C:53:ASP:HB3	1:C:59:ALA:HB2	2.03	0.41
1:D:329:LEU:HD23	1:D:329:LEU:HA	1.76	0.41
1:B:41:ALA:HA	1:B:76:VAL:HG11	2.02	0.41
1:C:54:LEU:HD23	2:C:2009:HOH:O	2.20	0.41
1:C:92[B]:ARG:HH22	1:C:295:ALA:CB	2.33	0.41
1:C:268:VAL:HA	1:C:291:ARG:O	2.20	0.41
1:D:26:ILE:HB	1:D:51:LEU:HD23	2.02	0.41
1:D:199:GLU:H	1:D:199:GLU:HG2	1.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:LEU:HD22	1:A:290:PRO:HD3	2.03	0.41
1:B:234:ARG:O	1:B:238:ARG:HG3	2.19	0.41
1:C:209(C):VAL:HG22	1:C:209(D):PRO:HD2	2.02	0.41
1:C:317:ARG:O	1:C:321:ILE:HG13	2.20	0.41
1:D:221:SER:O	1:D:225:ARG:HB3	2.20	0.41
1:C:187:VAL:HA	1:C:208:VAL:HG22	2.02	0.41
1:D:190:TYR:HB3	1:D:270:THR:HG21	2.02	0.41
1:A:41:ALA:HA	1:A:76:VAL:HG21	2.02	0.41
1:B:115:ARG:O	1:B:118:GLN:HB2	2.21	0.41
1:C:183:ALA:HA	1:C:184:PRO:HD3	1.95	0.41
1:C:140:ASN:HA	1:C:142:VAL:N	2.36	0.41
1:A:40:LEU:HD12	1:A:40:LEU:HA	1.87	0.41
1:D:105:PRO:HG2	1:D:106:GLY:HA3	2.02	0.41
1:D:316:ARG:HG3	1:D:317:ARG:N	2.36	0.41
1:A:122:GLN:HG3	1:A:126:ARG:NH2	2.36	0.41
1:C:103:ARG:O	1:C:106:GLY:N	2.53	0.41
1:C:228:ILE:HG13	1:C:229:ASP:N	2.35	0.41
1:D:102:GLN:O	1:D:103:ARG:HG3	2.20	0.41
1:B:100:VAL:HG22	1:B:116:ASN:OD1	2.20	0.41
1:D:27:VAL:HG11	1:D:123:VAL:HG11	2.03	0.41
1:D:134:VAL:HG11	1:D:261:ILE:HD13	2.03	0.41
1:B:45:VAL:CG1	1:B:259:ARG:HG3	2.51	0.40
1:D:105:PRO:HD2	1:D:107:GLU:H	1.86	0.40
1:B:287:LEU:HB3	1:B:322:LEU:HD12	2.03	0.40
1:C:70:THR:HG22	1:C:71:PRO:HD3	2.03	0.40
1:A:194:GLU:HG2	1:A:195:HIS:C	2.46	0.40
1:B:176:LEU:O	1:B:180:LEU:HB2	2.21	0.40
1:B:180:LEU:HD11	1:B:213:ALA:HB2	2.02	0.40
1:B:322:LEU:HD23	1:B:322:LEU:HA	1.88	0.40
1:C:85:TYR:CD2	1:C:126:ARG:HG2	2.57	0.40
1:D:179:TYR:HD1	1:D:180:LEU:HD23	1.87	0.40
1:A:151:ARG:HG3	1:A:331:PHE:HB3	2.02	0.40
1:B:54:LEU:HA	1:B:54:LEU:HD23	1.84	0.40
1:C:193:GLY:HA2	1:C:287:LEU:HD13	2.02	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	309/310 (100%)	288 (93%)	17 (6%)	4 (1%)	9	38
1	B	310/310 (100%)	287 (93%)	18 (6%)	5 (2%)	7	34
1	C	308/310 (99%)	275 (89%)	25 (8%)	8 (3%)	4	23
1	D	310/310 (100%)	272 (88%)	32 (10%)	6 (2%)	6	30
All	All	1237/1240 (100%)	1122 (91%)	92 (7%)	23 (2%)	6	30

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	ALA
1	B	105	PRO
1	C	101	ALA
1	C	112	LEU
1	C	218	ALA
1	D	100	VAL
1	D	105	PRO
1	A	216	ARG
1	C	329	LEU
1	D	198	SER
1	B	103	ARG
1	B	243	LYS
1	C	105	PRO
1	C	283	GLU
1	D	197	ASP
1	D	231	GLY
1	A	98	ALA
1	C	108	THR
1	D	101	ALA
1	B	247	TYR
1	C	100	VAL
1	A	242	GLY
1	B	45	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	232/231 (100%)	194 (84%)	38 (16%)	2	12
1	B	233/231 (101%)	202 (87%)	31 (13%)	4	18
1	C	231/231 (100%)	198 (86%)	33 (14%)	3	16
1	D	233/231 (101%)	196 (84%)	37 (16%)	2	13
All	All	929/924 (100%)	790 (85%)	139 (15%)	3	14

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	VAL
1	A	32	VAL
1	A	40	LEU
1	A	54	LEU
1	A	57	LYS
1	A	58	LEU
1	A	94	VAL
1	A	108	THR
1	A	110	LEU
1	A	113	LEU
1	A	119	VAL
1	A	122	GLN
1	A	127	VAL
1	A	139	THR
1	A	169	THR
1	A	171	ARG
1	A	182	VAL
1	A	202	VAL
1	A	208	VAL
1	A	209(C)	VAL
1	A	209(D)	PRO
1	A	214	GLU
1	A	220	LEU
1	A	232	VAL

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Mol	Chain	Res	Type
1	A	238	ARG
1	A	240	ILE
1	A	246	THR
1	A	250	ILE
1	A	258	VAL
1	A	261	ILE
1	A	262	LEU
1	A	268	VAL
1	A	278	VAL
1	A	298	VAL
1	A	302	THR
1	A	310	GLU
1	A	315	LEU
1	A	321	ILE
1	B	32	VAL
1	B	42	LEU
1	B	45	VAL
1	B	76	VAL
1	B	96	LEU
1	B	103	ARG
1	B	105	PRO
1	B	108	THR
1	B	140	ASN
1	B	142	VAL
1	B	148	VAL
1	B	152	LEU
1	B	165	THR
1	B	171	ARG
1	B	180	LEU
1	B	181	ARG
1	B	204	SER
1	B	205	SER
1	B	208	VAL
1	B	209(C)	VAL
1	B	209(D)	PRO
1	B	228	ILE
1	B	237	TYR
1	B	240	ILE
1	B	257	LEU
1	B	277	GLU
1	B	278	VAL
1	B	282	LEU

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Mol	Chain	Res	Type
1	B	285	VAL
1	B	287	LEU
1	B	316	ARG
1	C	24	VAL
1	C	40	LEU
1	C	42	LEU
1	C	70	THR
1	C	100	VAL
1	C	108	THR
1	C	109	ARG
1	C	110	LEU
1	C	113	LEU
1	C	123	VAL
1	C	135	LEU
1	C	136	LEU
1	C	155	LEU
1	C	163	SER
1	C	182	VAL
1	C	186	SER
1	C	187	VAL
1	C	200	VAL
1	C	201	LEU
1	C	207	GLN
1	C	209(C)	VAL
1	C	209(D)	PRO
1	C	214	GLU
1	C	221	SER
1	C	228	ILE
1	C	234	ARG
1	C	238	ARG
1	C	259	ARG
1	C	262	LEU
1	C	275	THR
1	C	303	VAL
1	C	315	LEU
1	C	317	ARG
1	D	42	LEU
1	D	45	VAL
1	D	56[A]	ARG
1	D	56[B]	ARG
1	D	57	LYS
1	D	76	VAL

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Mol	Chain	Res	Type
1	D	100	VAL
1	D	108	THR
1	D	110	LEU
1	D	112	LEU
1	D	113	LEU
1	D	114	ASP
1	D	151	ARG
1	D	152	LEU
1	D	167	LEU
1	D	171	ARG
1	D	175	LEU
1	D	198	SER
1	D	202	VAL
1	D	208	VAL
1	D	210(A)	LEU
1	D	210(B)	LEU
1	D	220	LEU
1	D	225	ARG
1	D	238	ARG
1	D	246	THR
1	D	265	GLU
1	D	277	GLU
1	D	279	GLU
1	D	281	VAL
1	D	286	SER
1	D	287	LEU
1	D	289	LEU
1	D	298	VAL
1	D	316	ARG
1	D	320	GLU
1	D	324	GLU

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

Mol	Chain	Res	Type
1	A	68	HIS
1	B	102	GLN
1	B	122	GLN
1	C	68	HIS
1	C	140	ASN
1	C	207	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 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	310/310 (100%)	-0.79	0	100 100	44, 82, 116, 166	1 (0%)
1	B	309/310 (99%)	-0.84	0	100 100	44, 80, 119, 147	3 (0%)
1	C	309/310 (99%)	-0.70	1 (0%)	90 79	54, 97, 152, 208	1 (0%)
1	D	310/310 (100%)	-0.71	2 (0%)	85 69	48, 88, 141, 175	2 (0%)
All	All	1238/1240 (99%)	-0.76	3 (0%)	91 83	44, 86, 137, 208	7 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	105	PRO	3.3
1	D	56[A]	ARG	2.1
1	D	100	VAL	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.