



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:54 AM UTC

PDB ID : 2ZAV / pdb_00002zav
Title : Arginase I (homo sapiens): native and unliganded structure at 1.70 Å resolution
Authors : Di Costanzo, L.; Christianson, D.W.
Deposited on : 2007-10-11
Resolution : 1.70 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

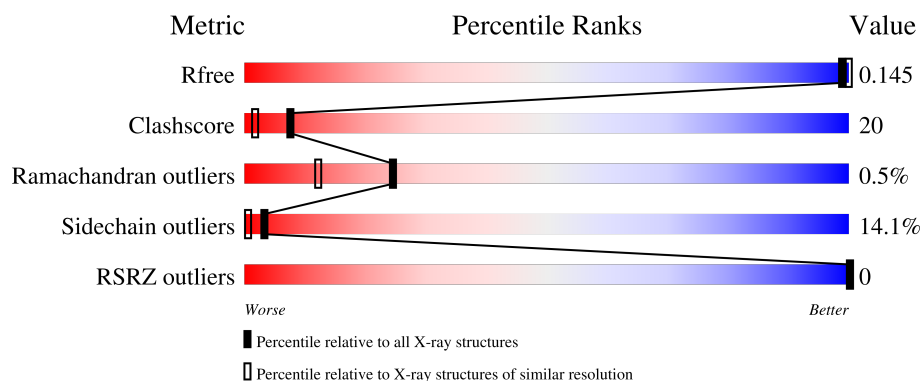
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	322	 64% 24% 9% ..
1	B	322	 53% 32% 10% • 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5067 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 Arginase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2389	1523	407	453	6			
1	B	307	Total	C	N	O	S	0	0	0
			2329	1483	398	442	6			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		
2	B	2	Total	Mn	0	0
			2	2		

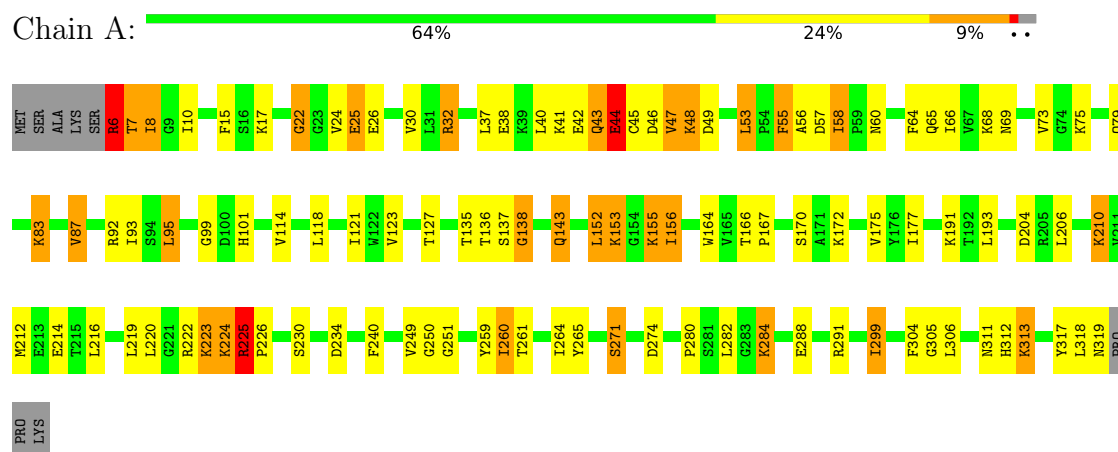
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	197	Total	O	0	0
			197	197		
3	B	148	Total	O	0	0
			148	148		

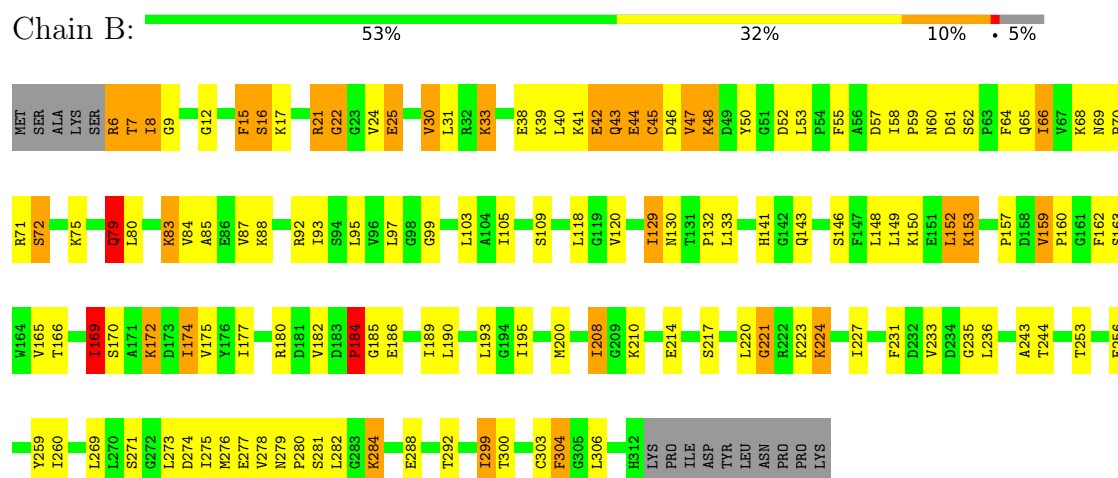
3 Residue-property plots

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: Arginase-1



• Molecule 1: Arginase-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, α , β , γ	90.48Å 90.48Å 69.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.70 50.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-1.70) 97.2 (50.00-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 1.70Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.143 , 0.176 0.145 , 0.145	Depositor DCC
R_{free} test set	3424 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	20.4	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.469 for -h,-k,l 0.126 for h,-h-k,-l 0.126 for -k,-h,-l	Xtriage
Reported twinning fraction	0.500 for -h,-k,l	Depositor
Outliers	0 of 68120 reflections	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	5067	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 3.23% 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 ⓘ

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

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	0.57	0/2439	1.69	41/3310 (1.2%)
1	B	0.52	0/2377	1.65	40/3225 (1.2%)
All	All	0.55	0/4816	1.67	81/6535 (1.2%)

There are no bond length outliers.

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	ARG	CA-CB-CG	15.89	145.87	114.10
1	A	22	GLY	N-CA-C	12.66	127.96	112.64
1	A	318	LEU	CA-C-N	10.84	141.21	121.70
1	A	318	LEU	C-N-CA	10.84	141.21	121.70
1	B	184	PRO	CA-N-CD	-10.33	97.54	112.00
1	B	190	LEU	O-C-N	8.01	130.65	122.08
1	B	22	GLY	N-CA-C	7.58	121.82	112.73
1	A	22	GLY	O-C-N	-7.54	114.67	122.13
1	B	22	GLY	O-C-N	-7.51	114.98	122.19
1	B	190	LEU	CA-C-N	7.49	130.54	120.65
1	B	190	LEU	C-N-CA	7.49	130.54	120.65
1	A	166	THR	CA-C-O	-7.37	113.84	119.59
1	A	220	LEU	CA-C-N	7.26	128.00	119.94
1	A	220	LEU	C-N-CA	7.26	128.00	119.94
1	B	304	PHE	CA-CB-CG	-7.25	106.55	113.80
1	A	47	VAL	N-CA-C	7.04	118.02	107.75
1	A	6	ARG	NE-CZ-NH1	-6.91	114.59	121.50
1	A	225	ARG	CD-NE-CZ	6.83	133.97	124.40
1	A	240	PHE	CA-CB-CG	-6.83	106.97	113.80
1	A	43	GLN	CA-C-N	-6.68	110.22	122.31
1	A	43	GLN	C-N-CA	-6.68	110.22	122.31
1	A	60	ASN	OD1-CG-ND2	6.64	129.24	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	244	THR	CA-C-N	6.50	127.20	119.98
1	B	244	THR	C-N-CA	6.50	127.20	119.98
1	B	182	VAL	CA-C-O	-6.45	113.64	120.48
1	A	6	ARG	CB-CG-CD	6.33	125.85	111.30
1	A	166	THR	O-C-N	6.28	128.32	121.23
1	A	6	ARG	CA-C-N	-6.27	114.15	122.99
1	A	6	ARG	C-N-CA	-6.27	114.15	122.99
1	A	251	GLY	O-C-N	6.20	129.43	122.86
1	A	249	VAL	CA-C-O	-6.19	115.26	122.13
1	B	166	THR	O-C-N	6.19	128.71	121.10
1	B	141	HIS	CA-C-N	6.14	133.44	121.41
1	B	141	HIS	C-N-CA	6.14	133.44	121.41
1	B	15	PHE	CA-CB-CG	-6.09	107.71	113.80
1	B	45	CYS	N-CA-C	6.04	118.25	108.41
1	A	250	GLY	CA-C-N	-5.73	117.33	122.43
1	A	250	GLY	C-N-CA	-5.73	117.33	122.43
1	A	95	LEU	CA-C-N	-5.72	115.22	122.37
1	A	95	LEU	C-N-CA	-5.72	115.22	122.37
1	A	318	LEU	CA-C-O	5.67	126.14	119.28
1	A	282	LEU	CA-C-N	-5.55	114.44	120.71
1	A	282	LEU	C-N-CA	-5.55	114.44	120.71
1	B	159	VAL	CA-C-O	5.55	123.15	119.38
1	A	138	GLY	CA-C-O	5.53	125.25	119.06
1	B	184	PRO	CA-C-N	5.51	126.10	119.98
1	B	184	PRO	C-N-CA	5.51	126.10	119.98
1	B	169	ILE	CA-C-O	5.50	126.84	120.67
1	B	44	GLU	CA-C-N	-5.49	115.27	123.00
1	B	44	GLU	C-N-CA	-5.49	115.27	123.00
1	B	282	LEU	CA-C-N	-5.48	115.13	120.34
1	B	282	LEU	C-N-CA	-5.48	115.13	120.34
1	B	195	ILE	CA-C-O	-5.43	114.85	121.04
1	A	204	ASP	O-C-N	5.38	127.91	122.09
1	B	59	PRO	CA-C-N	-5.36	114.83	122.77
1	B	59	PRO	C-N-CA	-5.36	114.83	122.77
1	A	311	ASN	CA-CB-CG	5.32	117.92	112.60
1	B	177	ILE	CA-C-N	-5.31	115.91	123.08
1	B	177	ILE	C-N-CA	-5.31	115.91	123.08
1	B	130	ASN	CA-CB-CG	-5.28	107.32	112.60
1	B	235	GLY	N-CA-C	-5.23	108.17	114.66
1	A	220	LEU	O-C-N	5.23	128.78	122.35
1	A	55	PHE	CA-C-O	-5.19	116.27	122.13
1	B	165	VAL	CA-C-N	-5.19	114.04	122.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	165	VAL	C-N-CA	-5.19	114.04	122.65
1	B	79	GLN	CA-C-N	5.18	127.22	120.28
1	B	79	GLN	C-N-CA	5.18	127.22	120.28
1	A	143	GLN	CA-C-O	-5.16	113.09	120.16
1	A	234	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	291	ARG	NE-CZ-NH1	-5.13	116.37	121.50
1	A	6	ARG	CB-CA-C	5.11	119.81	110.10
1	B	162	PHE	CA-CB-CG	5.11	118.91	113.80
1	B	85	ALA	CA-C-N	5.11	127.08	120.44
1	B	85	ALA	C-N-CA	5.11	127.08	120.44
1	A	123	VAL	CA-C-O	-5.08	115.05	120.59
1	B	277	GLU	CA-C-N	-5.07	114.67	121.66
1	B	277	GLU	C-N-CA	-5.07	114.67	121.66
1	A	259	TYR	CA-CB-CG	-5.03	104.84	113.90
1	B	21	ARG	CA-C-O	5.02	126.31	120.49
1	A	44	GLU	CA-C-N	-5.01	115.66	122.93
1	A	44	GLU	C-N-CA	-5.01	115.66	122.93

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	2389	0	2433	77	0
1	B	2329	0	2372	115	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	197	0	0	5	0
3	B	148	0	0	10	0
All	All	5067	0	4805	192	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 20.

All (192) 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:208:ILE:HD11	1:B:260:ILE:HG13	1.56	0.87
1:B:16:SER:HB3	1:B:25:GLU:HG2	1.63	0.81
1:B:9:GLY:HA3	1:B:87:VAL:HG21	1.63	0.79
1:B:12:GLY:HA3	1:B:52:ASP:OD1	1.83	0.78
1:B:284:LYS:HD3	1:B:288:GLU:OE1	1.84	0.77
1:A:313:LYS:HG2	1:A:317:TYR:OH	1.84	0.76
1:B:87:VAL:HG22	1:B:92:ARG:HB2	1.68	0.75
1:B:133:LEU:HD12	3:B:2569:HOH:O	1.86	0.75
1:B:53:LEU:HD11	1:B:83:LYS:HG3	1.68	0.74
1:A:219:LEU:O	1:A:225:ARG:HD2	1.87	0.74
1:B:120:VAL:HB	1:B:174:ILE:HD13	1.68	0.74
1:A:75:LYS:O	1:A:79:GLN:HG3	1.87	0.73
1:B:236:LEU:HD11	1:B:299:ILE:HD11	1.71	0.72
1:A:212:MET:SD	1:A:260:ILE:HD13	2.29	0.72
1:B:24:VAL:HG12	1:B:279:ASN:HB2	1.70	0.72
1:A:6:ARG:NH1	1:A:7:THR:H	1.89	0.70
1:B:149:LEU:HD23	1:B:169:ILE:HD12	1.74	0.69
1:B:133:LEU:HD21	1:B:157:PRO:HG3	1.76	0.68
1:B:79:GLN:O	1:B:83:LYS:HG2	1.94	0.67
1:B:53:LEU:HD21	1:B:83:LYS:HG3	1.77	0.67
1:A:53:LEU:HD22	1:A:83:LYS:HG3	1.77	0.67
1:A:68:LYS:HE3	1:A:137:SER:O	1.95	0.66
1:A:261:THR:HG21	1:A:299:ILE:HG23	1.77	0.66
1:B:174:ILE:HD12	1:B:175:VAL:N	2.11	0.65
1:A:10:ILE:HD12	1:A:37:LEU:CD2	2.27	0.65
1:A:25:GLU:OE2	1:A:26:GLU:HG2	1.95	0.65
1:B:15:PHE:HB3	1:B:103:LEU:HD11	1.78	0.65
1:A:10:ILE:HD12	1:A:37:LEU:HD23	1.78	0.64
1:A:210:LYS:NZ	1:A:214:GLU:HG2	2.12	0.64
1:A:38:GLU:O	1:A:42:GLU:HG3	1.97	0.64
1:A:40:LEU:O	1:A:45:CYS:HB2	1.98	0.64
1:B:152:LEU:HD11	1:B:189:ILE:HD12	1.79	0.63
1:B:44:GLU:HB2	3:B:2567:HOH:O	1.99	0.62
1:B:184:PRO:HD3	3:B:2537:HOH:O	2.00	0.62
1:B:174:ILE:HD12	1:B:175:VAL:H	1.65	0.62
1:A:66:ILE:HD11	1:A:136:THR:O	2.01	0.60
1:B:15:PHE:HB2	1:B:55:PHE:CE2	2.35	0.60
1:A:222:ARG:HB3	1:A:223:LYS:NZ	2.16	0.60
1:B:15:PHE:CZ	1:B:17:LYS:HB2	2.36	0.60
1:B:38:GLU:O	1:B:42:GLU:HG3	2.01	0.60
1:B:6:ARG:HG3	1:B:7:THR:H	1.67	0.60
1:A:79:GLN:O	1:A:83:LYS:HG2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ARG:HH11	1:A:32:ARG:HG3	1.67	0.59
1:A:135:THR:HG23	3:A:2548:HOH:O	2.00	0.59
1:B:120:VAL:CB	1:B:174:ILE:HD13	2.33	0.59
1:B:273:LEU:HD21	3:B:2637:HOH:O	2.02	0.58
1:A:30:VAL:HG21	1:A:280:PRO:HG3	1.85	0.58
1:B:9:GLY:HA3	1:B:87:VAL:CG2	2.33	0.57
1:A:210:LYS:HZ2	1:A:214:GLU:HG2	1.69	0.57
1:B:58:ILE:HD12	1:B:72:SER:HA	1.87	0.57
1:A:6:ARG:HD3	1:A:93:ILE:HD11	1.86	0.57
1:A:8:ILE:HD12	1:A:304:PHE:CE1	2.39	0.57
1:A:87:VAL:HG23	1:A:92:ARG:HB2	1.87	0.56
1:B:40:LEU:HA	1:B:43:GLN:HG3	1.88	0.56
1:B:231:PHE:CZ	1:B:299:ILE:HD13	2.40	0.56
1:B:65:GLN:HB2	3:B:2581:HOH:O	2.06	0.55
1:B:133:LEU:CD2	1:B:157:PRO:HG3	2.36	0.54
1:A:32:ARG:HD3	1:A:37:LEU:HD12	1.89	0.54
1:B:208:ILE:HD13	1:B:259:TYR:HD2	1.71	0.54
1:A:152:LEU:HB3	1:A:156:ILE:CD1	2.38	0.54
1:A:155:LYS:HE2	3:A:2563:HOH:O	2.08	0.54
1:A:32:ARG:HH21	1:A:49:ASP:CG	2.14	0.53
1:B:87:VAL:CG2	1:B:92:ARG:HB2	2.36	0.53
1:B:15:PHE:O	1:B:99:GLY:HA2	2.08	0.53
1:B:40:LEU:O	1:B:45:CYS:HB2	2.08	0.53
1:B:129:ILE:HG22	1:B:186:GLU:HG2	1.90	0.53
1:A:210:LYS:O	1:A:214:GLU:HG3	2.09	0.53
1:A:222:ARG:O	1:A:223:LYS:HB3	2.09	0.53
1:B:253:THR:OG1	1:B:256:GLU:HG3	2.08	0.52
1:B:22:GLY:O	1:B:25:GLU:HG3	2.10	0.52
1:B:75:LYS:O	1:B:79:GLN:HG3	2.10	0.52
1:A:156:ILE:HG22	1:A:156:ILE:O	2.09	0.52
1:B:133:LEU:HD11	1:B:157:PRO:HD3	1.92	0.51
1:B:55:PHE:HD1	1:B:79:GLN:OE1	1.93	0.51
1:B:31:LEU:HD13	1:B:97:LEU:HD22	1.93	0.51
1:B:300:THR:O	1:B:303:CYS:HB2	2.10	0.51
1:A:222:ARG:HB3	1:A:223:LYS:HZ3	1.74	0.51
1:B:95:LEU:HD12	1:B:304:PHE:CE2	2.46	0.51
1:B:39:LYS:O	1:B:42:GLU:OE1	2.30	0.50
1:B:8:ILE:HG13	1:B:47:VAL:HB	1.93	0.50
1:B:208:ILE:HD13	1:B:259:TYR:CD2	2.46	0.50
1:A:164:TRP:HB3	3:A:2686:HOH:O	2.11	0.50
1:A:48:LYS:HG2	1:A:92:ARG:NH2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:LEU:CD2	1:A:83:LYS:HG3	2.41	0.49
1:A:172:LYS:HD3	3:A:2526:HOH:O	2.12	0.49
1:B:149:LEU:HD23	1:B:169:ILE:CD1	2.40	0.49
1:B:220:LEU:O	1:B:221:GLY:O	2.29	0.49
1:B:6:ARG:HD2	3:B:2570:HOH:O	2.12	0.49
1:B:220:LEU:HD11	1:B:227:ILE:HD11	1.95	0.49
1:A:7:THR:C	1:A:8:ILE:HD13	2.39	0.48
1:B:275:ILE:HD12	1:B:275:ILE:N	2.28	0.48
1:A:265:TYR:CE2	1:A:305:GLY:HA2	2.49	0.48
1:B:120:VAL:CG1	1:B:174:ILE:HD13	2.44	0.48
1:A:47:VAL:O	1:A:48:LYS:HD3	2.12	0.48
1:B:16:SER:HB2	1:B:24:VAL:HG22	1.95	0.48
1:B:58:ILE:HD12	1:B:72:SER:CA	2.43	0.48
1:B:150:LYS:O	1:B:153:LYS:HB2	2.15	0.47
1:B:66:ILE:HG13	1:B:66:ILE:O	2.14	0.47
1:A:41:LYS:HE3	1:A:47:VAL:HB	1.96	0.47
1:B:39:LYS:HA	1:B:42:GLU:CD	2.40	0.47
1:A:48:LYS:HG2	1:A:92:ARG:CZ	2.45	0.47
1:A:216:LEU:HD21	1:A:264:ILE:CD1	2.45	0.47
1:B:50:TYR:CE1	1:B:87:VAL:HG23	2.49	0.47
1:B:133:LEU:CD1	1:B:157:PRO:HD3	2.45	0.47
1:A:152:LEU:HD13	1:A:193:LEU:HD11	1.96	0.47
1:A:6:ARG:HG3	1:A:93:ILE:CD1	2.44	0.46
1:A:69:ASN:O	1:A:73:VAL:HG23	2.15	0.46
1:A:83:LYS:O	1:A:87:VAL:HG12	2.15	0.46
1:A:226:PRO:HB3	1:A:271:SER:OG	2.15	0.46
1:B:16:SER:HB2	1:B:24:VAL:CG2	2.45	0.46
1:B:170:SER:OG	1:B:172:LYS:HG3	2.15	0.46
1:B:105:ILE:O	1:B:109:SER:OG	2.30	0.46
1:A:164:TRP:CD1	1:A:164:TRP:H	2.33	0.46
1:B:185:GLY:HA3	3:B:2534:HOH:O	2.16	0.46
1:A:56:ALA:O	1:A:58:ILE:HD12	2.15	0.46
1:A:224:LYS:HD2	1:A:224:LYS:HA	1.64	0.46
1:A:22:GLY:O	1:A:25:GLU:HG3	2.16	0.46
1:A:312:HIS:HB2	1:A:317:TYR:CE2	2.51	0.46
1:B:6:ARG:HD2	1:B:6:ARG:HA	1.73	0.46
1:B:64:PHE:CE2	1:B:159:VAL:HG22	2.51	0.46
1:A:138:GLY:N	3:A:2548:HOH:O	2.49	0.45
1:B:46:ASP:OD1	1:B:48:LYS:NZ	2.49	0.45
1:A:46:ASP:OD1	1:A:48:LYS:NZ	2.50	0.45
1:A:58:ILE:HD12	1:A:58:ILE:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:VAL:O	1:B:48:LYS:HD3	2.16	0.45
1:B:61:ASP:OD1	1:B:70:PRO:HD2	2.17	0.45
1:A:121:ILE:CD1	1:A:175:VAL:HB	2.47	0.45
1:A:32:ARG:HG3	1:A:32:ARG:NH1	2.32	0.45
1:B:30:VAL:HG11	1:B:280:PRO:HG3	1.98	0.45
1:B:152:LEU:HD13	1:B:193:LEU:HD11	1.99	0.45
1:B:210:LYS:O	1:B:214:GLU:HG3	2.17	0.45
1:B:233:VAL:HG13	1:B:276:MET:O	2.17	0.45
1:A:6:ARG:N	1:A:44:GLU:OE2	2.50	0.44
1:A:37:LEU:HD23	1:A:47:VAL:HG11	2.00	0.44
1:A:37:LEU:O	1:A:41:LYS:HG3	2.17	0.44
1:A:177:ILE:HG21	1:A:260:ILE:HD11	1.99	0.44
1:B:95:LEU:HD21	1:B:97:LEU:HD21	1.99	0.44
1:B:6:ARG:N	3:B:2567:HOH:O	2.50	0.44
1:B:224:LYS:CG	1:B:269:LEU:HD11	2.47	0.44
1:A:32:ARG:HD3	1:A:37:LEU:CD1	2.47	0.44
1:B:233:VAL:HG11	1:B:278:VAL:HG22	1.98	0.44
1:B:88:LYS:HD2	1:B:88:LYS:HA	1.61	0.44
1:B:300:THR:HA	3:B:2637:HOH:O	2.18	0.44
1:A:64:PHE:O	1:A:65:GLN:HB2	2.18	0.44
1:A:79:GLN:O	1:A:83:LYS:NZ	2.50	0.44
1:B:62:SER:O	1:B:71:ARG:NH1	2.50	0.44
1:B:53:LEU:HD23	1:B:53:LEU:HA	1.82	0.44
1:B:48:LYS:HD3	1:B:48:LYS:HA	1.47	0.43
1:B:33:LYS:HE3	1:B:33:LYS:HB2	1.45	0.43
1:B:53:LEU:HD21	1:B:83:LYS:CD	2.48	0.43
1:B:129:ILE:HD12	1:B:189:ILE:HG21	1.99	0.43
1:B:243:ALA:HB3	1:B:292:THR:HG21	2.00	0.43
1:A:153:LYS:HD3	1:A:167:PRO:HG2	1.99	0.43
1:A:53:LEU:HD12	1:A:55:PHE:CZ	2.53	0.43
1:B:133:LEU:CG	1:B:157:PRO:HG3	2.48	0.43
1:B:159:VAL:HA	1:B:160:PRO:HD3	1.84	0.43
1:A:15:PHE:O	1:A:99:GLY:HA2	2.19	0.43
1:B:224:LYS:HG3	1:B:269:LEU:HD11	2.00	0.43
1:B:233:VAL:HG11	1:B:278:VAL:CG2	2.49	0.43
1:B:61:ASP:HA	1:B:71:ARG:HD2	2.01	0.42
1:B:88:LYS:HE2	1:B:271:SER:OG	2.19	0.42
1:B:236:LEU:HD11	1:B:299:ILE:CD1	2.46	0.42
1:B:180:ARG:HD3	1:B:200:MET:HG3	2.02	0.42
1:B:38:GLU:OE1	1:B:38:GLU:N	2.50	0.42
1:B:41:LYS:NZ	3:B:2620:HOH:O	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:ILE:CD1	1:B:189:ILE:HG21	2.49	0.42
1:B:71:ARG:HD2	1:B:71:ARG:HH11	1.68	0.42
1:A:206:LEU:HB3	1:A:210:LYS:HB3	2.02	0.42
1:B:53:LEU:HD21	1:B:83:LYS:CG	2.44	0.42
1:A:284:LYS:HD2	1:A:288:GLU:OE2	2.19	0.42
1:A:155:LYS:CA	1:A:155:LYS:HE3	2.47	0.41
1:B:148:LEU:CB	1:B:169:ILE:HD11	2.50	0.41
1:B:172:LYS:HG3	1:B:172:LYS:H	1.71	0.41
1:B:210:LYS:HE2	1:B:214:GLU:HG2	2.01	0.41
1:B:132:PRO:HB2	1:B:157:PRO:HG2	2.02	0.41
1:A:10:ILE:HD12	1:A:37:LEU:HD21	2.00	0.41
1:A:17:LYS:HA	1:A:17:LYS:HD3	1.69	0.41
1:B:84:VAL:O	1:B:87:VAL:HG12	2.21	0.41
1:A:8:ILE:HD12	1:A:304:PHE:CD1	2.56	0.41
1:A:25:GLU:HG3	1:A:25:GLU:H	1.41	0.41
1:B:274:ASP:HB3	1:B:276:MET:SD	2.60	0.41
1:B:146:SER:HA	1:B:152:LEU:HD23	2.02	0.41
1:B:152:LEU:HD12	1:B:152:LEU:HA	1.94	0.41
1:B:42:GLU:HG3	1:B:42:GLU:H	1.57	0.40
1:B:61:ASP:OD2	1:B:69:ASN:HA	2.22	0.40
1:B:129:ILE:CG2	1:B:186:GLU:HG2	2.51	0.40
1:A:230:SER:HA	1:A:274:ASP:HB2	2.02	0.40
1:B:7:THR:HG23	1:B:46:ASP:HB3	2.04	0.40
1:B:53:LEU:HD11	1:B:83:LYS:CG	2.45	0.40
1:A:57:ASP:C	1:A:58:ILE:HD12	2.47	0.40
1:A:152:LEU:HD12	1:A:152:LEU:HA	1.96	0.40
1:B:83:LYS:HG2	1:B:83:LYS:H	1.68	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	312/322 (97%)	297 (95%)	14 (4%)	1 (0%)	36	22
1	B	305/322 (95%)	287 (94%)	16 (5%)	2 (1%)	18	7
All	All	617/644 (96%)	584 (95%)	30 (5%)	3 (0%)	24	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	221	GLY
1	A	143	GLN
1	B	143	GLN

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	263/270 (97%)	228 (87%)	35 (13%)	4	1
1	B	256/270 (95%)	218 (85%)	38 (15%)	3	0
All	All	519/540 (96%)	446 (86%)	73 (14%)	3	0

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ARG
1	A	7	THR
1	A	8	ILE
1	A	24	VAL
1	A	25	GLU
1	A	32	ARG
1	A	43	GLN
1	A	44	GLU
1	A	48	LYS
1	A	53	LEU
1	A	58	ILE
1	A	83	LYS
1	A	87	VAL

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Mol	Chain	Res	Type
1	A	95	LEU
1	A	101	HIS
1	A	114	VAL
1	A	118	LEU
1	A	127	THR
1	A	152	LEU
1	A	153	LYS
1	A	155	LYS
1	A	156	ILE
1	A	170	SER
1	A	191	LYS
1	A	210	LYS
1	A	223	LYS
1	A	224	LYS
1	A	225	ARG
1	A	260	ILE
1	A	271	SER
1	A	284	LYS
1	A	299	ILE
1	A	306	LEU
1	A	313	LYS
1	A	319	ASN
1	B	6	ARG
1	B	7	THR
1	B	8	ILE
1	B	16	SER
1	B	21	ARG
1	B	25	GLU
1	B	30	VAL
1	B	33	LYS
1	B	42	GLU
1	B	43	GLN
1	B	47	VAL
1	B	48	LYS
1	B	57	ASP
1	B	60	ASN
1	B	66	ILE
1	B	68	LYS
1	B	72	SER
1	B	79	GLN
1	B	80	LEU
1	B	83	LYS

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Mol	Chain	Res	Type
1	B	93	ILE
1	B	118	LEU
1	B	129	ILE
1	B	152	LEU
1	B	153	LYS
1	B	163	SER
1	B	169	ILE
1	B	172	LYS
1	B	174	ILE
1	B	184	PRO
1	B	208	ILE
1	B	217	SER
1	B	223	LYS
1	B	224	LYS
1	B	281	SER
1	B	284	LYS
1	B	299	ILE
1	B	306	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	139	ASN
1	A	312	HIS
1	B	69	ASN

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

Of 4 ligands modelled in this entry, 4 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	314/322 (97%)	-1.40	0 100 100	14, 23, 39, 66	0
1	B	307/322 (95%)	-1.28	0 100 100	14, 28, 48, 70	0
All	All	621/644 (96%)	-1.34	0 100 100	14, 25, 44, 70	0

There are no RSRZ outliers to report.

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](#)

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. 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	B-factors(Å ²)	Q<0.9
2	MN	A	2514	1/1	1.00	0.01	16,16,16,16	0
2	MN	A	2515	1/1	1.00	0.01	15,15,15,15	0
2	MN	B	2516	1/1	1.00	0.01	19,19,19,19	0
2	MN	B	2517	1/1	1.00	0.01	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.