



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:04 PM UTC

PDB ID : 8LDH / pdb_00008ldh
Title : REFINED CRYSTAL STRUCTURE OF DOGFISH M4 APO-LACTATE DE-HYDROGENASE
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Deposited on : 1988-01-04
Resolution : 2.80 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

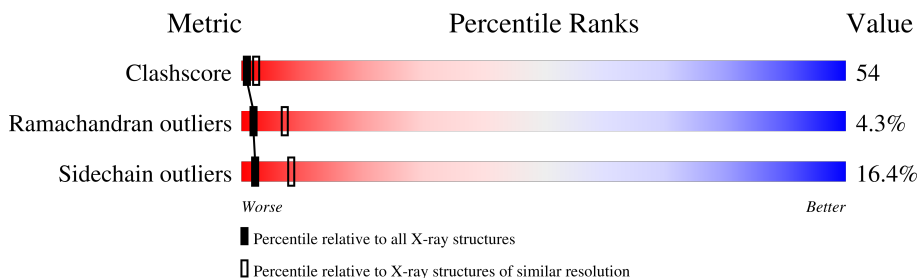
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	330	26% 45% 22% 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	CIT	A	330	-	X	-	-
2	CIT	A	331	-	X	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2852 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.

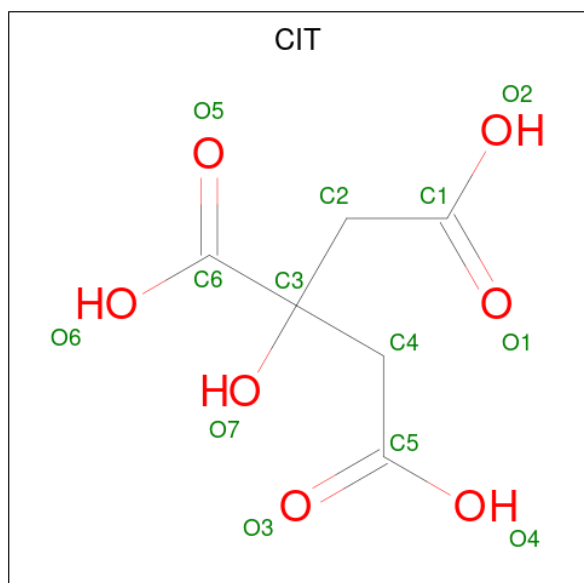
- Molecule 1 is a protein called M4 APO-LACTATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	330	2545	1620	439	468	18	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	ASN	TRP	conflict	UNP P00341
A	206	VAL	ASN	conflict	UNP P00341
A	208	SER	LEU	conflict	UNP P00341
A	209	ILE	LYS	conflict	UNP P00341
A	210	LYS	GLU	conflict	UNP P00341
A	214	LEU	GLU	conflict	UNP P00341
A	215	ASP	LEU	conflict	UNP P00341
A	308	ASN	ASP	conflict	UNP P00341

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is water.

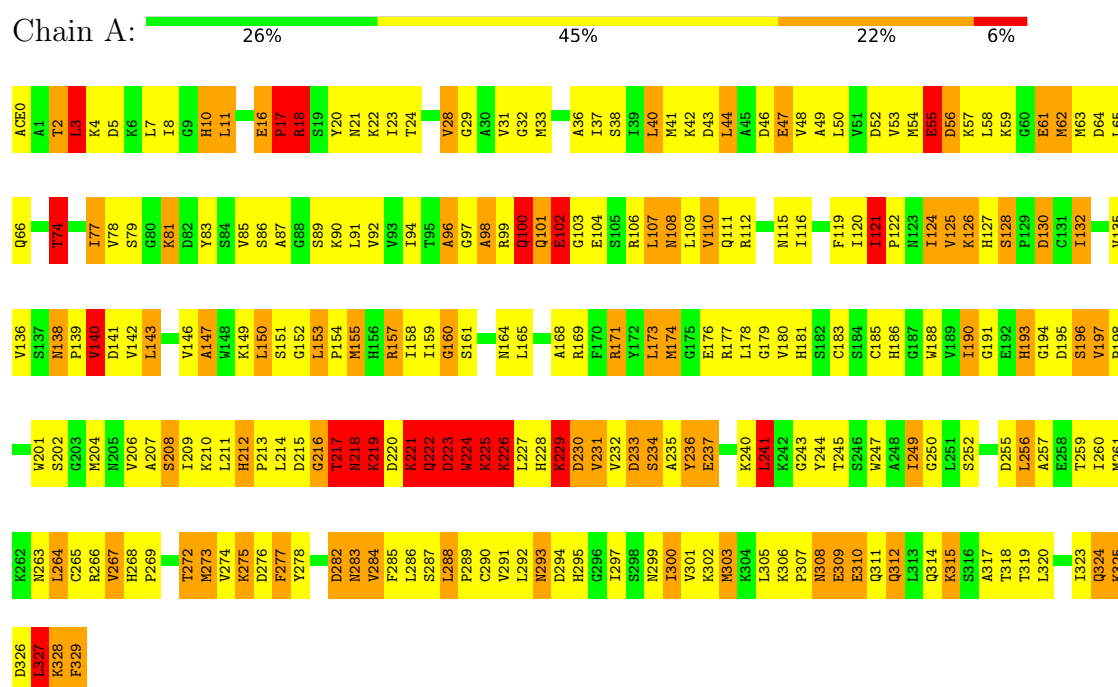
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	281	Total	O	0	0
			281	281		

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. 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. 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.

Note EDS was not executed.

• Molecule 1: M4 APO-LACTATE DEHYDROGENASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	F 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	146.80Å 146.80Å 155.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.191 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2852	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	1.50	12/2590 (0.5%)	2.44	152/3502 (4.3%)

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

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	17	PRO	C-N	-15.60	1.13	1.33
1	A	18	ARG	C-N	-12.36	1.17	1.33
1	A	328	LYS	N-CA	-9.17	1.34	1.46
1	A	18	ARG	CA-CB	8.16	1.67	1.53
1	A	247	TRP	NE1-CE2	-5.53	1.31	1.37
1	A	121	ILE	CA-CB	5.36	1.61	1.54
1	A	62	MET	N-CA	-5.26	1.40	1.46
1	A	196	SER	C-N	5.21	1.39	1.33
1	A	291	VAL	C-O	5.16	1.30	1.24
1	A	128	SER	N-CA	5.14	1.52	1.46
1	A	230	ASP	N-CA	5.10	1.52	1.46
1	A	221	LYS	N-CA	-5.07	1.39	1.46

All (152) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	327	LEU	CA-C-N	25.62	170.48	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	327	LEU	C-N-CA	25.62	170.48	121.54
1	A	115	ASN	CA-CB-CG	13.65	126.25	112.60
1	A	18	ARG	NE-CZ-NH1	13.46	134.96	121.50
1	A	18	ARG	N-CA-C	12.42	128.67	108.55
1	A	195	ASP	CA-CB-CG	12.01	124.61	112.60
1	A	18	ARG	NE-CZ-NH2	-11.96	108.43	119.20
1	A	220	ASP	CA-C-N	11.17	142.88	121.54
1	A	220	ASP	C-N-CA	11.17	142.88	121.54
1	A	216	GLY	N-CA-C	-10.75	99.52	114.67
1	A	18	ARG	CB-CA-C	-9.86	92.11	109.86
1	A	218	ASN	CA-CB-CG	-9.64	102.96	112.60
1	A	324	GLN	CA-C-O	9.48	134.06	120.51
1	A	221	LYS	N-CA-C	9.47	130.97	110.80
1	A	31	VAL	CA-C-N	9.24	130.20	119.94
1	A	31	VAL	C-N-CA	9.24	130.20	119.94
1	A	18	ARG	N-CA-CB	-9.00	95.06	110.99
1	A	327	LEU	CA-C-O	8.65	132.88	120.51
1	A	327	LEU	O-C-N	-8.35	111.49	122.59
1	A	61	GLU	CA-C-N	8.00	131.34	120.54
1	A	61	GLU	C-N-CA	8.00	131.34	120.54
1	A	233	ASP	CA-CB-CG	7.93	120.53	112.60
1	A	157	ARG	NE-CZ-NH2	7.91	126.32	119.20
1	A	100	GLN	OE1-CD-NE2	-7.79	114.81	122.60
1	A	159	ILE	CA-C-N	7.77	129.96	122.73
1	A	159	ILE	C-N-CA	7.77	129.96	122.73
1	A	324	GLN	OE1-CD-NE2	-7.75	114.85	122.60
1	A	138	ASN	CB-CA-C	7.67	120.35	108.61
1	A	119	PHE	CA-CB-CG	-7.66	106.14	113.80
1	A	154	PRO	CB-CA-C	7.55	121.06	111.39
1	A	283	ASN	CB-CG-ND2	7.47	127.60	116.40
1	A	157	ARG	CD-NE-CZ	-7.39	114.05	124.40
1	A	324	GLN	CB-CG-CD	7.29	125.00	112.60
1	A	28	VAL	CB-CA-C	7.22	123.12	111.29
1	A	11	LEU	N-CA-C	-7.19	100.84	110.55
1	A	324	GLN	CB-CA-C	7.16	124.67	110.42
1	A	211	LEU	CB-CA-C	7.07	121.98	110.88
1	A	29	GLY	CA-C-O	-7.07	114.29	121.64
1	A	276	ASP	CA-C-N	6.97	132.99	122.95
1	A	276	ASP	C-N-CA	6.97	132.99	122.95
1	A	310	GLU	CA-CB-CG	6.93	127.95	114.10
1	A	110	VAL	CB-CA-C	6.89	121.47	112.24
1	A	81	LYS	N-CA-C	-6.88	103.56	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	288	LEU	O-C-N	6.78	126.59	121.85
1	A	299	ASN	OD1-CG-ND2	6.75	129.35	122.60
1	A	164	ASN	CA-CB-CG	6.75	119.35	112.60
1	A	3	LEU	CA-C-N	6.74	129.62	120.38
1	A	3	LEU	C-N-CA	6.74	129.62	120.38
1	A	222	GLN	CA-C-N	6.70	134.34	121.54
1	A	222	GLN	C-N-CA	6.70	134.34	121.54
1	A	143	LEU	CB-CA-C	6.58	123.30	110.67
1	A	216	GLY	CA-C-N	6.57	134.09	121.54
1	A	216	GLY	C-N-CA	6.57	134.09	121.54
1	A	77	ILE	CB-CA-C	6.55	120.58	110.83
1	A	160	GLY	CA-C-O	6.50	126.86	120.75
1	A	157	ARG	NE-CZ-NH1	-6.39	115.11	121.50
1	A	277	PHE	CA-CB-CG	6.36	120.16	113.80
1	A	217	THR	N-CA-CB	6.35	121.22	110.49
1	A	222	GLN	N-CA-CB	6.33	121.20	110.49
1	A	193	HIS	CA-C-O	-6.32	114.94	120.88
1	A	11	LEU	CB-CA-C	6.31	122.31	109.76
1	A	236	TYR	N-CA-C	-6.31	104.64	112.90
1	A	127	HIS	CA-CB-CG	-6.25	107.55	113.80
1	A	325	LYS	N-CA-C	-6.24	103.05	110.41
1	A	308	ASN	CA-C-N	6.19	129.05	120.63
1	A	308	ASN	C-N-CA	6.19	129.05	120.63
1	A	40	LEU	CA-C-N	6.19	133.43	121.18
1	A	40	LEU	C-N-CA	6.19	133.43	121.18
1	A	147	ALA	N-CA-C	-6.17	104.64	111.36
1	A	294	ASP	CA-CB-CG	6.15	118.75	112.60
1	A	259	THR	N-CA-CB	6.15	119.16	109.82
1	A	221	LYS	CA-C-N	6.11	133.20	121.54
1	A	221	LYS	C-N-CA	6.11	133.20	121.54
1	A	177	ARG	CD-NE-CZ	6.09	132.93	124.40
1	A	267	VAL	CB-CA-C	6.08	118.32	110.96
1	A	327	LEU	CB-CA-C	6.05	122.47	110.42
1	A	237	GLU	CB-CG-CD	6.05	122.88	112.60
1	A	218	ASN	CA-C-O	6.03	129.13	120.51
1	A	197	VAL	O-C-N	6.01	127.95	121.10
1	A	121	ILE	N-CA-C	6.01	121.85	108.88
1	A	283	ASN	CA-C-N	5.99	131.31	122.99
1	A	283	ASN	C-N-CA	5.99	131.31	122.99
1	A	204	MET	CA-CB-CG	-5.98	102.14	114.10
1	A	328	LYS	N-CA-C	5.98	123.53	110.80
1	A	275	LYS	CA-C-N	5.97	130.64	122.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	275	LYS	C-N-CA	5.97	130.64	122.34
1	A	264	LEU	N-CA-C	5.95	118.72	111.82
1	A	101	GLN	CA-C-O	5.94	129.75	121.73
1	A	18	ARG	NH1-CZ-NH2	-5.93	111.59	119.30
1	A	218	ASN	CA-C-N	5.92	132.84	121.54
1	A	218	ASN	C-N-CA	5.92	132.84	121.54
1	A	276	ASP	CA-C-O	5.92	128.57	121.65
1	A	127	HIS	CA-C-N	-5.91	116.47	122.74
1	A	127	HIS	C-N-CA	-5.91	116.47	122.74
1	A	43	ASP	CA-CB-CG	5.90	118.50	112.60
1	A	18	ARG	CA-CB-CG	-5.89	102.31	114.10
1	A	62	MET	O-C-N	5.85	128.17	122.09
1	A	100	GLN	N-CA-CB	5.82	120.32	110.49
1	A	98	ALA	CA-C-O	-5.82	114.56	121.66
1	A	303	MET	N-CA-C	-5.77	102.92	110.53
1	A	101	GLN	N-CA-C	5.76	118.25	109.95
1	A	46	ASP	O-C-N	5.74	129.80	122.39
1	A	164	ASN	O-C-N	5.73	127.99	122.03
1	A	171	ARG	CA-C-O	-5.73	114.48	120.55
1	A	195	ASP	N-CA-C	-5.65	105.88	112.89
1	A	328	LYS	CA-C-O	5.62	128.55	120.51
1	A	309	GLU	N-CA-C	5.62	117.27	111.03
1	A	282	ASP	CA-C-N	5.58	131.20	122.26
1	A	282	ASP	C-N-CA	5.58	131.20	122.26
1	A	140	VAL	N-CA-C	5.56	116.33	110.72
1	A	10	HIS	CA-CB-CG	-5.53	108.27	113.80
1	A	225	LYS	CA-CB-CG	5.53	125.16	114.10
1	A	55	GLU	CB-CA-C	-5.53	99.42	110.42
1	A	102	GLU	CA-CB-CG	5.51	125.11	114.10
1	A	273	MET	CA-C-O	-5.51	114.07	120.62
1	A	132	ILE	CA-C-O	-5.48	114.09	121.32
1	A	7	LEU	N-CA-CB	-5.45	103.34	110.59
1	A	32	GLY	CA-C-O	-5.43	115.13	121.00
1	A	310	GLU	CG-CD-OE1	5.42	130.88	118.40
1	A	47	GLU	CA-C-O	-5.42	114.04	120.43
1	A	132	ILE	N-CA-C	-5.42	100.51	108.85
1	A	328	LYS	CA-C-N	5.40	131.41	121.70
1	A	328	LYS	C-N-CA	5.40	131.41	121.70
1	A	223	ASP	CA-CB-CG	5.39	117.99	112.60
1	A	132	ILE	CB-CA-C	5.33	119.03	110.82
1	A	236	TYR	O-C-N	5.33	129.93	122.36
1	A	174	MET	CA-C-N	5.33	125.89	119.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	MET	C-N-CA	5.33	125.89	119.98
1	A	291	VAL	CA-C-O	-5.32	114.78	120.85
1	A	241	LEU	N-CA-CB	-5.31	101.41	110.33
1	A	96	ALA	O-C-N	5.30	129.26	123.27
1	A	173	LEU	CB-CA-C	5.30	119.60	110.79
1	A	231	VAL	N-CA-C	-5.28	105.57	110.53
1	A	230	ASP	CA-CB-CG	-5.26	107.34	112.60
1	A	249	ILE	N-CA-CB	5.25	116.59	110.65
1	A	224	TRP	N-CA-CB	5.24	119.34	110.49
1	A	230	ASP	CB-CA-C	5.23	119.68	110.37
1	A	164	ASN	CA-C-O	-5.23	115.51	121.00
1	A	16	GLU	CB-CG-CD	5.19	121.43	112.60
1	A	74	THR	CA-C-O	5.19	126.03	120.32
1	A	226	LYS	O-C-N	5.19	128.11	122.20
1	A	154	PRO	N-CA-C	-5.15	102.92	111.11
1	A	229	LYS	O-C-N	5.13	128.00	122.15
1	A	284	VAL	CA-C-N	5.12	130.28	122.65
1	A	284	VAL	C-N-CA	5.12	130.28	122.65
1	A	8	ILE	CA-C-O	-5.07	114.90	120.48
1	A	130	ASP	N-CA-C	5.07	119.15	112.92
1	A	56	ASP	CA-CB-CG	-5.05	107.55	112.60
1	A	120	ILE	CA-C-N	5.01	131.39	122.13
1	A	120	ILE	C-N-CA	5.01	131.39	122.13
1	A	302	LYS	CA-C-O	5.01	126.39	120.98
1	A	16	GLU	O-C-N	5.00	127.07	121.32

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	PRO	Mainchain
1	A	18	ARG	Sidechain

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	2545	0	2612	283	76
2	A	26	0	10	5	0
3	A	281	0	0	40	19
All	All	2852	0	2622	283	77

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 54.

All (283) 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:273:MET:CE	1:A:275:LYS:HB2	1.75	1.16
1:A:197:VAL:HG23	1:A:228:HIS:HE1	1.13	1.12
1:A:17:PRO:HA	1:A:18:ARG:HD3	1.32	1.11
1:A:273:MET:HE3	1:A:275:LYS:HB2	1.25	1.10
1:A:303:MET:HE3	1:A:305:LEU:HD21	1.15	1.06
1:A:100:GLN:HB2	1:A:109:LEU:HD22	1.35	1.04
1:A:107:LEU:HD11	1:A:325:LYS:CE	1.90	1.01
1:A:197:VAL:HG23	1:A:228:HIS:CE1	1.97	0.99
1:A:190:ILE:O	1:A:198:PRO:HD2	1.63	0.98
1:A:210:LYS:HG2	1:A:213:PRO:HD3	1.47	0.97
1:A:107:LEU:HD11	1:A:325:LYS:HE3	1.44	0.96
1:A:54:MET:HE3	3:A:398:HOH:O	1.65	0.95
1:A:0:ACE:H2	1:A:5:ASP:HB3	1.50	0.94
1:A:190:ILE:C	1:A:190:ILE:HD13	1.96	0.90
1:A:62:MET:HE3	1:A:79:SER:H	1.35	0.89
1:A:230:ASP:HA	1:A:233:ASP:HB2	1.54	0.88
1:A:210:LYS:HG2	1:A:213:PRO:CD	2.02	0.88
1:A:273:MET:HE3	1:A:275:LYS:CB	2.04	0.88
1:A:33:MET:HE1	1:A:65:LEU:HD11	1.55	0.88
1:A:54:MET:CE	3:A:398:HOH:O	2.22	0.87
1:A:229:LYS:HG2	3:A:532:HOH:O	1.74	0.87
1:A:99:ARG:NH2	3:A:574:HOH:O	2.07	0.87
1:A:40:LEU:HD23	1:A:74:THR:HG21	1.57	0.86
1:A:288:LEU:HD23	1:A:300:ILE:HD13	1.56	0.86
1:A:62:MET:HE2	1:A:78:VAL:HA	1.55	0.86
1:A:273:MET:HE1	1:A:283:ASN:HA	1.59	0.85
1:A:303:MET:CE	1:A:305:LEU:HD21	2.05	0.84
1:A:0:ACE:CH3	1:A:5:ASP:HB3	2.08	0.84
1:A:273:MET:CE	1:A:275:LYS:CB	2.56	0.83
1:A:212:HIS:O	1:A:217:THR:HA	1.79	0.83
1:A:62:MET:HE3	1:A:79:SER:N	1.93	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:MET:CE	1:A:78:VAL:HA	2.10	0.82
1:A:100:GLN:HA	1:A:109:LEU:HD13	1.60	0.81
1:A:325:LYS:HA	3:A:376:HOH:O	1.80	0.81
1:A:57:LYS:HE3	3:A:566:HOH:O	1.81	0.80
1:A:215:ASP:HB3	1:A:217:THR:O	1.83	0.79
1:A:106:ARG:HG3	3:A:506:HOH:O	1.82	0.79
1:A:327:LEU:HD13	3:A:545:HOH:O	1.82	0.78
1:A:16:GLU:HB3	3:A:484:HOH:O	1.83	0.78
1:A:52:ASP:OD1	3:A:398:HOH:O	2.02	0.77
1:A:210:LYS:O	1:A:213:PRO:HD2	1.84	0.77
1:A:263:ASN:OD1	1:A:293:ASN:HB2	1.84	0.76
1:A:83:TYR:HE2	1:A:124:ILE:HD11	1.51	0.76
1:A:216:GLY:O	1:A:217:THR:HG23	1.87	0.75
1:A:58:LEU:HD23	3:A:438:HOH:O	1.86	0.75
1:A:219:LYS:HE2	3:A:400:HOH:O	1.86	0.74
1:A:201:TRP:CD1	1:A:219:LYS:HG2	2.22	0.74
1:A:225:LYS:HG3	3:A:556:HOH:O	1.86	0.74
1:A:284:VAL:HG11	1:A:317:ALA:HA	1.69	0.73
1:A:292:LEU:CD2	1:A:297:ILE:HD13	2.19	0.73
1:A:215:ASP:C	1:A:217:THR:H	1.95	0.73
1:A:153:LEU:HD12	1:A:158:ILE:HD11	1.72	0.72
1:A:224:TRP:CZ3	1:A:227:LEU:HD22	2.25	0.72
1:A:288:LEU:HD23	1:A:300:ILE:CD1	2.20	0.72
1:A:81:LYS:O	3:A:430:HOH:O	2.07	0.71
1:A:223:ASP:HB3	3:A:349:HOH:O	1.91	0.70
1:A:210:LYS:NZ	3:A:527:HOH:O	2.21	0.70
1:A:194:GLY:H	1:A:197:VAL:CG1	2.04	0.70
1:A:17:PRO:HA	1:A:18:ARG:CD	2.18	0.69
1:A:190:ILE:O	1:A:198:PRO:CD	2.40	0.69
1:A:236:TYR:C	1:A:240:LYS:HE2	2.18	0.69
1:A:83:TYR:CE2	1:A:124:ILE:HD11	2.28	0.68
1:A:2:THR:HG22	1:A:5:ASP:H	1.59	0.68
1:A:57:LYS:HG3	3:A:566:HOH:O	1.93	0.68
1:A:66:GLN:NE2	3:A:394:HOH:O	2.26	0.67
1:A:121:ILE:O	1:A:125:VAL:HG23	1.94	0.67
1:A:110:VAL:HG11	1:A:142:VAL:HG11	1.76	0.67
1:A:62:MET:HE1	3:A:477:HOH:O	1.96	0.66
1:A:152:GLY:HA2	3:A:449:HOH:O	1.96	0.66
1:A:28:VAL:HG23	3:A:566:HOH:O	1.96	0.66
1:A:149:LYS:O	3:A:450:HOH:O	2.14	0.66
1:A:18:ARG:HH11	1:A:18:ARG:HG2	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:ARG:O	1:A:18:ARG:CG	2.41	0.66
1:A:28:VAL:O	3:A:566:HOH:O	2.14	0.65
1:A:249:ILE:O	1:A:252:SER:HB3	1.97	0.64
1:A:210:LYS:CB	1:A:213:PRO:HD2	2.28	0.64
1:A:210:LYS:HB3	1:A:213:PRO:HD2	1.78	0.64
1:A:289:PRO:HB2	1:A:301:VAL:HB	1.79	0.64
1:A:325:LYS:O	1:A:325:LYS:HG2	1.98	0.64
1:A:141:ASP:OD2	3:A:340:HOH:O	2.15	0.64
1:A:318:THR:HG23	1:A:319:THR:N	2.12	0.63
1:A:210:LYS:NZ	1:A:212:HIS:HB3	2.13	0.63
1:A:323:ILE:O	1:A:325:LYS:N	2.31	0.63
1:A:210:LYS:CG	1:A:213:PRO:CD	2.76	0.62
1:A:206:VAL:O	1:A:207:ALA:HB3	1.97	0.62
1:A:217:THR:O	1:A:218:ASN:HB2	1.99	0.62
1:A:210:LYS:HZ1	1:A:212:HIS:HB3	1.65	0.62
1:A:230:ASP:O	1:A:234:SER:HB2	2.00	0.61
1:A:210:LYS:C	1:A:213:PRO:HD2	2.26	0.61
1:A:264:LEU:HB3	1:A:266:ARG:HG3	1.82	0.61
1:A:173:LEU:HD12	1:A:231:VAL:HG23	1.82	0.61
1:A:326:ASP:O	1:A:327:LEU:HB2	2.00	0.61
1:A:210:LYS:HG2	1:A:213:PRO:HD2	1.83	0.60
1:A:312:GLN:HG2	3:A:553:HOH:O	2.01	0.60
1:A:272:THR:O	1:A:285:PHE:HA	2.02	0.60
1:A:100:GLN:HB2	1:A:109:LEU:CD2	2.22	0.60
1:A:194:GLY:N	1:A:197:VAL:HG13	2.17	0.60
1:A:190:ILE:C	1:A:190:ILE:CD1	2.70	0.60
1:A:0:ACE:CH3	1:A:5:ASP:CB	2.79	0.60
1:A:207:ALA:O	1:A:208:SER:HB3	2.02	0.59
1:A:33:MET:CE	1:A:65:LEU:HD11	2.30	0.59
1:A:188:TRP:CZ3	1:A:269:PRO:HG3	2.38	0.59
1:A:153:LEU:HD12	1:A:158:ILE:CD1	2.33	0.59
1:A:202:SER:O	1:A:210:LYS:HD2	2.03	0.58
1:A:210:LYS:HB3	1:A:213:PRO:CD	2.33	0.58
1:A:38:SER:O	1:A:42:LYS:HB2	2.02	0.58
1:A:287:SER:O	1:A:288:LEU:HD12	2.03	0.58
1:A:50:LEU:O	1:A:79:SER:HA	2.04	0.58
1:A:83:TYR:HD2	1:A:124:ILE:HD13	1.69	0.58
1:A:197:VAL:O	1:A:228:HIS:NE2	2.36	0.57
1:A:179:GLY:HA3	3:A:345:HOH:O	2.04	0.57
1:A:210:LYS:CG	1:A:213:PRO:HD3	2.29	0.57
1:A:273:MET:HE2	1:A:275:LYS:CB	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:GLN:HG2	3:A:521:HOH:O	2.04	0.57
1:A:146:VAL:O	1:A:150:LEU:HB2	2.05	0.57
1:A:243:GLY:O	1:A:244:TYR:HB3	2.04	0.57
1:A:292:LEU:HD21	1:A:297:ILE:HD13	1.85	0.57
1:A:62:MET:HG3	1:A:79:SER:HB3	1.86	0.56
1:A:214:LEU:C	1:A:216:GLY:H	2.13	0.56
1:A:278:TYR:O	1:A:314:GLN:NE2	2.37	0.56
1:A:18:ARG:HG2	1:A:18:ARG:O	2.05	0.56
1:A:98:ALA:HB1	1:A:112:ARG:NH1	2.20	0.56
1:A:293:ASN:C	1:A:293:ASN:HD22	2.13	0.56
1:A:94:ILE:CD1	1:A:121:ILE:HD11	2.36	0.56
1:A:217:THR:OG1	1:A:218:ASN:N	2.36	0.56
1:A:318:THR:CG2	1:A:319:THR:H	2.20	0.55
1:A:197:VAL:O	1:A:228:HIS:CE1	2.59	0.55
1:A:212:HIS:CD2	1:A:217:THR:HB	2.42	0.55
1:A:236:TYR:O	1:A:240:LYS:HE2	2.06	0.55
1:A:210:LYS:HE3	1:A:213:PRO:HD3	1.87	0.55
1:A:107:LEU:CD1	1:A:325:LYS:HE3	2.29	0.55
1:A:315:LYS:O	1:A:318:THR:HG22	2.06	0.55
1:A:173:LEU:HD12	1:A:231:VAL:CG2	2.36	0.55
1:A:194:GLY:N	1:A:197:VAL:CG1	2.70	0.55
1:A:0:ACE:H2	1:A:5:ASP:CB	2.32	0.54
1:A:212:HIS:CD2	1:A:218:ASN:H	2.26	0.54
1:A:107:LEU:HD11	1:A:325:LYS:HE2	1.85	0.54
1:A:20:TYR:O	1:A:90:LYS:HD3	2.07	0.54
1:A:111:GLN:HG2	1:A:329:PHE:C	2.33	0.54
1:A:318:THR:CG2	1:A:319:THR:N	2.70	0.54
1:A:121:ILE:HD12	1:A:147:ALA:HA	1.90	0.54
1:A:194:GLY:H	1:A:197:VAL:HG13	1.72	0.54
1:A:83:TYR:CD2	1:A:124:ILE:HD13	2.43	0.54
1:A:57:LYS:O	1:A:61:GLU:HG2	2.08	0.54
1:A:210:LYS:HB3	1:A:213:PRO:HG2	1.90	0.54
1:A:277:PHE:CE2	1:A:300:ILE:HD12	2.43	0.53
1:A:142:VAL:HG22	1:A:320:LEU:HD22	1.90	0.53
1:A:257:ALA:O	1:A:261:MET:HG2	2.07	0.53
1:A:107:LEU:CD1	1:A:325:LYS:CE	2.79	0.53
1:A:256:LEU:O	1:A:260:ILE:HG13	2.09	0.53
1:A:226:LYS:HB2	1:A:226:LYS:NZ	2.24	0.53
1:A:108:ASN:N	1:A:108:ASN:HD22	2.06	0.53
1:A:142:VAL:O	1:A:146:VAL:HG23	2.09	0.52
1:A:59:LYS:HB2	3:A:439:HOH:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194:GLY:H	1:A:197:VAL:HG11	1.72	0.52
1:A:110:VAL:HG22	1:A:139:PRO:HG3	1.93	0.52
1:A:218:ASN:OD1	1:A:219:LYS:N	2.42	0.52
1:A:142:VAL:HG22	1:A:320:LEU:CD2	2.40	0.51
1:A:232:VAL:HG22	1:A:232:VAL:O	2.08	0.51
1:A:224:TRP:HZ3	1:A:227:LEU:HD22	1.75	0.51
1:A:62:MET:HE3	1:A:78:VAL:HA	1.92	0.51
1:A:312:GLN:CG	3:A:521:HOH:O	2.59	0.51
1:A:138:ASN:HA	1:A:139:PRO:C	2.35	0.50
1:A:190:ILE:O	1:A:190:ILE:HD13	2.11	0.50
1:A:181:HIS:CD2	1:A:183:CYS:H	2.29	0.50
1:A:307:PRO:HA	1:A:310:GLU:HG2	1.92	0.50
1:A:24:THR:OG1	1:A:89:SER:OG	2.27	0.50
1:A:318:THR:HG23	1:A:319:THR:H	1.76	0.50
1:A:24:THR:HG21	1:A:86:SER:HB3	1.94	0.50
1:A:277:PHE:CZ	1:A:300:ILE:HD12	2.47	0.49
1:A:21:ASN:HA	1:A:90:LYS:HG3	1.93	0.49
1:A:83:TYR:CE2	1:A:124:ILE:CD1	2.96	0.49
1:A:42:LYS:CG	1:A:44:LEU:HD13	2.43	0.49
1:A:191:GLY:HA3	1:A:198:PRO:HD2	1.95	0.49
1:A:174:MET:O	1:A:178:LEU:N	2.45	0.49
1:A:22:LYS:HE3	1:A:47:GLU:OE2	2.12	0.49
1:A:111:GLN:CD	1:A:328:LYS:HA	2.38	0.49
1:A:210:LYS:CB	1:A:213:PRO:CD	2.91	0.49
1:A:92:VAL:HG21	1:A:124:ILE:CG2	2.44	0.48
1:A:264:LEU:O	1:A:265:CYS:HB2	2.12	0.48
1:A:237:GLU:HA	1:A:240:LYS:HE2	1.95	0.48
1:A:130:ASP:HA	1:A:157:ARG:HH12	1.78	0.47
1:A:207:ALA:O	1:A:208:SER:CB	2.62	0.47
1:A:196:SER:HB2	3:A:516:HOH:O	2.13	0.47
1:A:237:GLU:O	1:A:241:LEU:HB2	2.15	0.47
1:A:18:ARG:HG2	1:A:18:ARG:NH1	2.26	0.47
1:A:112:ARG:NH1	3:A:426:HOH:O	2.42	0.47
1:A:210:LYS:CG	1:A:213:PRO:HD2	2.42	0.47
1:A:212:HIS:CE1	1:A:219:LYS:HD3	2.50	0.47
1:A:249:ILE:HD11	2:A:330:CIT:H41	1.96	0.47
1:A:121:ILE:CD1	1:A:147:ALA:HB1	2.44	0.47
1:A:255:ASP:OD1	1:A:268:HIS:HE1	1.96	0.47
1:A:226:LYS:HB2	1:A:226:LYS:HZ1	1.80	0.47
1:A:77:ILE:C	1:A:78:VAL:HG13	2.41	0.46
1:A:165:LEU:HD22	1:A:249:ILE:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ARG:HD2	1:A:185:CYS:O	2.15	0.46
1:A:33:MET:HE1	1:A:65:LEU:CD1	2.35	0.46
1:A:233:ASP:C	1:A:235:ALA:N	2.72	0.46
1:A:54:MET:HE1	3:A:398:HOH:O	2.05	0.46
1:A:210:LYS:HB3	1:A:213:PRO:CG	2.46	0.46
1:A:320:LEU:O	1:A:324:GLN:HG3	2.16	0.46
1:A:22:LYS:HB3	1:A:89:SER:HA	1.97	0.46
1:A:28:VAL:HG22	1:A:52:ASP:HB2	1.97	0.46
1:A:249:ILE:HD11	2:A:330:CIT:C4	2.45	0.46
1:A:55:GLU:HB2	1:A:56:ASP:OD1	2.16	0.45
1:A:2:THR:CG2	1:A:4:LYS:HB3	2.46	0.45
1:A:58:LEU:HG	1:A:79:SER:HB2	1.97	0.45
1:A:124:ILE:O	1:A:128:SER:N	2.50	0.45
1:A:229:LYS:HE3	1:A:229:LYS:HB2	1.45	0.45
1:A:0:ACE:H1	1:A:5:ASP:CB	2.47	0.45
1:A:53:VAL:HA	1:A:81:LYS:HD2	1.98	0.45
1:A:100:GLN:CA	1:A:109:LEU:HD13	2.38	0.45
1:A:139:PRO:O	1:A:139:PRO:HG2	2.16	0.45
1:A:157:ARG:O	1:A:158:ILE:HD13	2.16	0.45
1:A:212:HIS:NE2	1:A:217:THR:HB	2.32	0.45
1:A:171:ARG:NH2	2:A:331:CIT:O7	2.47	0.44
1:A:23:ILE:O	1:A:48:VAL:HA	2.17	0.44
1:A:106:ARG:O	1:A:110:VAL:HG23	2.17	0.44
1:A:121:ILE:HB	1:A:122:PRO:HD3	2.00	0.44
1:A:181:HIS:HD2	1:A:183:CYS:SG	2.40	0.44
1:A:28:VAL:HG22	1:A:52:ASP:OD1	2.17	0.44
1:A:212:HIS:HB3	1:A:213:PRO:HD3	2.00	0.44
1:A:206:VAL:C	1:A:208:SER:H	2.26	0.44
1:A:219:LYS:NZ	1:A:219:LYS:CB	2.81	0.44
1:A:155:MET:HE1	1:A:273:MET:HG2	1.99	0.44
1:A:165:LEU:HB3	3:A:515:HOH:O	2.18	0.44
1:A:42:LYS:HG2	1:A:44:LEU:HD13	2.00	0.43
1:A:226:LYS:CA	1:A:226:LYS:HE3	2.47	0.43
1:A:287:SER:O	1:A:288:LEU:CD1	2.66	0.43
1:A:28:VAL:HG22	1:A:52:ASP:CB	2.47	0.43
1:A:171:ARG:HD3	1:A:186:HIS:HA	2.00	0.43
1:A:181:HIS:HD2	1:A:183:CYS:H	1.67	0.43
1:A:190:ILE:CD1	1:A:198:PRO:HB2	2.49	0.43
1:A:111:GLN:NE2	1:A:328:LYS:HA	2.34	0.43
1:A:130:ASP:HA	1:A:157:ARG:NH1	2.34	0.43
1:A:136:VAL:HA	1:A:161:SER:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:LEU:HD23	1:A:143:LEU:HA	1.80	0.43
1:A:210:LYS:HE3	1:A:213:PRO:CG	2.48	0.43
1:A:267:VAL:HA	1:A:290:CYS:O	2.19	0.43
1:A:28:VAL:HG23	3:A:398:HOH:O	2.19	0.43
1:A:83:TYR:CD2	1:A:124:ILE:CD1	3.01	0.42
1:A:306:LYS:O	1:A:309:GLU:HB2	2.19	0.42
1:A:62:MET:CE	3:A:477:HOH:O	2.62	0.42
1:A:325:LYS:O	1:A:325:LYS:CG	2.66	0.42
1:A:210:LYS:HE3	1:A:213:PRO:CD	2.50	0.42
1:A:140:VAL:HG12	1:A:193:HIS:ND1	2.35	0.42
1:A:188:TRP:CE3	1:A:269:PRO:HG3	2.54	0.42
1:A:3:LEU:C	1:A:3:LEU:HD22	2.45	0.42
1:A:201:TRP:CG	1:A:219:LYS:HG2	2.55	0.42
1:A:274:VAL:O	1:A:274:VAL:HG23	2.19	0.42
1:A:22:LYS:HG3	1:A:47:GLU:HB3	2.01	0.42
1:A:125:VAL:HG21	1:A:151:SER:HB2	2.01	0.42
1:A:63:MET:O	1:A:64:ASP:C	2.62	0.42
1:A:165:LEU:O	1:A:168:ALA:HB3	2.19	0.42
1:A:214:LEU:C	1:A:216:GLY:N	2.77	0.42
1:A:0:ACE:H2	3:A:548:HOH:O	2.19	0.42
1:A:229:LYS:CE	3:A:463:HOH:O	2.68	0.42
1:A:124:ILE:H	1:A:124:ILE:HG12	1.71	0.41
1:A:138:ASN:HD22	2:A:330:CIT:C5	2.33	0.41
1:A:194:GLY:O	1:A:197:VAL:HG22	2.20	0.41
1:A:160:GLY:O	1:A:161:SER:C	2.62	0.41
1:A:219:LYS:NZ	1:A:219:LYS:HB2	2.36	0.41
1:A:225:LYS:CD	3:A:556:HOH:O	2.68	0.41
1:A:2:THR:HG22	1:A:5:ASP:N	2.32	0.41
1:A:36:ALA:O	1:A:40:LEU:HD12	2.21	0.41
1:A:233:ASP:C	1:A:235:ALA:H	2.26	0.41
1:A:268:HIS:HA	1:A:269:PRO:HD3	1.87	0.41
1:A:215:ASP:C	1:A:217:THR:N	2.70	0.41
1:A:181:HIS:CD2	1:A:183:CYS:SG	3.14	0.41
1:A:274:VAL:HG21	1:A:286:LEU:HD12	2.01	0.41
1:A:16:GLU:CB	3:A:484:HOH:O	2.57	0.41
1:A:49:ALA:HA	1:A:78:VAL:O	2.21	0.41
1:A:138:ASN:ND2	2:A:330:CIT:O7	2.54	0.41
1:A:210:LYS:CE	1:A:213:PRO:HD3	2.50	0.41
1:A:11:LEU:HD12	1:A:11:LEU:HA	1.82	0.40
1:A:100:GLN:HA	1:A:104:GLU:OE1	2.21	0.40
1:A:10:HIS:HB2	3:A:552:HOH:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:THR:HG21	1:A:86:SER:CB	2.51	0.40
1:A:40:LEU:HD23	1:A:74:THR:CG2	2.39	0.40
1:A:221:LYS:HE3	1:A:221:LYS:HB3	1.77	0.40
1:A:265:CYS:HA	1:A:292:LEU:O	2.20	0.40
1:A:249:ILE:O	1:A:250:GLY:C	2.64	0.40
1:A:293:ASN:ND2	1:A:295:HIS:H	2.19	0.40

All (77) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:LEU:CD2	1:A:329:PHE:CD2[32_555]	0.39	1.81
1:A:107:LEU:CG	1:A:329:PHE:CG[32_555]	0.73	1.47
1:A:103:GLY:O	1:A:112:ARG:O[32_555]	0.78	1.42
1:A:104:GLU:CG	1:A:112:ARG:CG[32_555]	0.78	1.42
1:A:101:GLN:CG	3:A:426:HOH:O[32_555]	0.79	1.41
1:A:111:GLN:C	3:A:497:HOH:O[32_555]	0.80	1.40
1:A:107:LEU:CB	1:A:329:PHE:CB[32_555]	0.83	1.37
1:A:102:GLU:C	1:A:116:ILE:CD1[32_555]	0.89	1.31
1:A:104:GLU:CD	1:A:112:ARG:CD[32_555]	0.89	1.31
1:A:107:LEU:CG	1:A:329:PHE:CB[32_555]	1.00	1.20
1:A:107:LEU:CD1	1:A:329:PHE:CD1[32_555]	1.00	1.20
1:A:102:GLU:O	1:A:116:ILE:CD1[32_555]	1.04	1.16
1:A:329:PHE:N	3:A:419:HOH:O[32_555]	1.11	1.09
1:A:101:GLN:CB	1:A:112:ARG:NH1[32_555]	1.12	1.08
1:A:104:GLU:CD	1:A:112:ARG:NE[32_555]	1.13	1.07
1:A:104:GLU:CG	1:A:112:ARG:CD[32_555]	1.15	1.05
1:A:107:LEU:CD2	1:A:329:PHE:CG[32_555]	1.15	1.05
1:A:111:GLN:O	3:A:497:HOH:O[32_555]	1.17	1.03
1:A:101:GLN:CD	3:A:426:HOH:O[32_555]	1.20	1.00
1:A:103:GLY:C	1:A:112:ARG:O[32_555]	1.25	0.95
1:A:109:LEU:CA	3:A:364:HOH:O[32_555]	1.30	0.90
1:A:108:ASN:OD1	1:A:111:GLN:CB[32_555]	1.32	0.88
1:A:107:LEU:CD1	1:A:329:PHE:CG[32_555]	1.35	0.85
1:A:104:GLU:OE1	1:A:112:ARG:NE[32_555]	1.38	0.82
1:A:107:LEU:CB	1:A:329:PHE:CA[32_555]	1.40	0.80
1:A:101:GLN:OE1	3:A:420:HOH:O[32_555]	1.42	0.78
1:A:104:GLU:OE2	1:A:112:ARG:NE[32_555]	1.43	0.77
1:A:328:LYS:C	3:A:419:HOH:O[32_555]	1.45	0.75
1:A:103:GLY:N	1:A:116:ILE:CG1[32_555]	1.46	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:LEU:CD2	1:A:329:PHE:CE2[32_555]	1.50	0.70
1:A:104:GLU:OE1	1:A:112:ARG:CD[32_555]	1.51	0.69
1:A:103:GLY:CA	1:A:116:ILE:CG1[32_555]	1.58	0.62
1:A:102:GLU:C	1:A:116:ILE:CG1[32_555]	1.59	0.61
1:A:112:ARG:N	3:A:497:HOH:O[32_555]	1.60	0.60
1:A:109:LEU:N	3:A:364:HOH:O[32_555]	1.61	0.59
1:A:108:ASN:ND2	1:A:329:PHE:O[32_555]	1.62	0.58
1:A:103:GLY:O	1:A:112:ARG:C[32_555]	1.66	0.54
1:A:101:GLN:NE2	3:A:426:HOH:O[32_555]	1.70	0.50
1:A:108:ASN:CG	1:A:111:GLN:CB[32_555]	1.71	0.49
1:A:108:ASN:ND2	1:A:329:PHE:C[32_555]	1.72	0.48
1:A:97:GLY:O	1:A:102:GLU:OE2[32_555]	1.73	0.47
1:A:104:GLU:CB	1:A:112:ARG:CD[32_555]	1.75	0.45
1:A:104:GLU:CB	1:A:112:ARG:CG[32_555]	1.75	0.45
1:A:102:GLU:CA	1:A:116:ILE:CD1[32_555]	1.76	0.44
1:A:104:GLU:CD	1:A:112:ARG:CG[32_555]	1.76	0.44
1:A:107:LEU:CD1	1:A:329:PHE:CB[32_555]	1.78	0.42
1:A:101:GLN:CG	1:A:112:ARG:NH1[32_555]	1.79	0.41
1:A:107:LEU:CG	1:A:329:PHE:CD2[32_555]	1.80	0.40
1:A:107:LEU:CG	1:A:329:PHE:CD1[32_555]	1.86	0.34
1:A:102:GLU:O	1:A:116:ILE:CG1[32_555]	1.87	0.33
1:A:104:GLU:OE2	1:A:104:GLU:OE2[32_555]	1.89	0.31
1:A:97:GLY:N	1:A:102:GLU:OE1[32_555]	1.90	0.30
1:A:101:GLN:CA	1:A:112:ARG:NH1[32_555]	1.90	0.30
1:A:108:ASN:N	1:A:329:PHE:O[32_555]	1.93	0.27
1:A:111:GLN:CA	3:A:497:HOH:O[32_555]	1.94	0.26
1:A:101:GLN:N	1:A:112:ARG:NH1[32_555]	1.95	0.25
1:A:107:LEU:CB	1:A:329:PHE:CG[32_555]	1.95	0.25
1:A:108:ASN:C	3:A:364:HOH:O[32_555]	1.96	0.24
1:A:11:LEU:CD2	3:A:471:HOH:O[21_555]	1.97	0.23
1:A:96:ALA:C	1:A:102:GLU:OE1[32_555]	1.97	0.23
1:A:104:GLU:OE2	1:A:112:ARG:CD[32_555]	1.99	0.21
1:A:103:GLY:N	1:A:116:ILE:CD1[32_555]	2.00	0.20
1:A:126:LYS:CG	3:A:597:HOH:O[27_555]	2.00	0.20
1:A:97:GLY:C	1:A:102:GLU:OE2[32_555]	2.01	0.19
1:A:102:GLU:CB	1:A:116:ILE:CD1[32_555]	2.05	0.15
1:A:108:ASN:O	3:A:364:HOH:O[32_555]	2.05	0.15
1:A:108:ASN:OD1	1:A:111:GLN:CA[32_555]	2.05	0.15
1:A:108:ASN:O	1:A:108:ASN:CB[32_555]	2.05	0.15
1:A:329:PHE:CA	3:A:419:HOH:O[32_555]	2.07	0.13
1:A:42:LYS:CE	3:A:567:HOH:O[26_555]	2.11	0.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:GLU:OE2	1:A:112:ARG:CG[32_555]	2.11	0.09
1:A:104:GLU:OE1	1:A:112:ARG:CZ[32_555]	2.12	0.08
1:A:107:LEU:CD2	1:A:329:PHE:CD1[32_555]	2.15	0.05
1:A:101:GLN:CG	1:A:112:ARG:NH2[32_555]	2.16	0.04
1:A:107:LEU:C	1:A:329:PHE:O[32_555]	2.16	0.04
1:A:108:ASN:ND2	1:A:111:GLN:CB[32_555]	2.19	0.01
3:A:572:HOH:O	3:A:591:HOH:O[27_555]	2.19	0.01

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	328/330 (99%)	293 (89%)	21 (6%)	14 (4%)	2 7

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	SER
1	A	217	THR
1	A	218	ASN
1	A	221	LYS
1	A	222	GLN
1	A	223	ASP
1	A	327	LEU
1	A	87	ALA
1	A	102	GLU
1	A	55	GLU
1	A	100	GLN
1	A	219	LYS
1	A	224	TRP
1	A	234	SER

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	286/286 (100%)	239 (84%)	47 (16%)	2 8

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	3	LEU
1	A	17	PRO
1	A	18	ARG
1	A	37	ILE
1	A	41	MET
1	A	44	LEU
1	A	55	GLU
1	A	74	THR
1	A	85	VAL
1	A	91	LEU
1	A	107	LEU
1	A	108	ASN
1	A	121	ILE
1	A	124	ILE
1	A	125	VAL
1	A	126	LYS
1	A	132	ILE
1	A	135	VAL
1	A	140	VAL
1	A	150	LEU
1	A	153	LEU
1	A	155	MET
1	A	169	ARG
1	A	176	GLU
1	A	180	VAL
1	A	190	ILE
1	A	209	ILE
1	A	212	HIS
1	A	219	LYS

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Mol	Chain	Res	Type
1	A	221	LYS
1	A	222	GLN
1	A	225	LYS
1	A	226	LYS
1	A	229	LYS
1	A	241	LEU
1	A	245	THR
1	A	256	LEU
1	A	272	THR
1	A	282	ASP
1	A	293	ASN
1	A	300	ILE
1	A	308	ASN
1	A	311	GLN
1	A	312	GLN
1	A	315	LYS
1	A	329	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	66	GLN
1	A	73	HIS
1	A	108	ASN
1	A	127	HIS
1	A	138	ASN
1	A	181	HIS
1	A	222	GLN
1	A	228	HIS
1	A	268	HIS
1	A	293	ASN
1	A	295	HIS
1	A	308	ASN
1	A	311	GLN
1	A	312	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	CIT	A	331	-	12,12,12	2.48	8 (66%)	17,17,17	3.98	10 (58%)
2	CIT	A	330	-	12,12,12	2.58	6 (50%)	17,17,17	3.93	11 (64%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CIT	A	331	-	-	8/16/16/16	-
2	CIT	A	330	-	-	7/16/16/16	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	330	CIT	C4-C3	-5.12	1.47	1.54
2	A	331	CIT	C4-C3	-3.59	1.49	1.54
2	A	331	CIT	O3-C5	3.46	1.33	1.22
2	A	330	CIT	O5-C6	3.33	1.32	1.22
2	A	330	CIT	O3-C5	3.14	1.32	1.22
2	A	330	CIT	O7-C3	-3.11	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	331	CIT	O1-C1	3.09	1.32	1.22
2	A	331	CIT	O5-C6	2.99	1.31	1.22
2	A	331	CIT	O2-C1	-2.70	1.21	1.30
2	A	331	CIT	C2-C3	2.60	1.57	1.54
2	A	330	CIT	C2-C3	2.34	1.56	1.54
2	A	330	CIT	O6-C6	-2.26	1.22	1.30
2	A	331	CIT	O6-C6	-2.19	1.22	1.30
2	A	331	CIT	O7-C3	2.01	1.47	1.43

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	330	CIT	O5-C6-C3	-7.12	108.31	122.09
2	A	331	CIT	O7-C3-C6	-7.10	98.89	108.96
2	A	331	CIT	O6-C6-C3	7.03	126.63	113.14
2	A	331	CIT	C3-C2-C1	6.76	132.42	113.92
2	A	330	CIT	O7-C3-C6	6.33	117.94	108.96
2	A	330	CIT	C3-C4-C5	6.09	130.57	113.92
2	A	331	CIT	O5-C6-C3	-5.95	110.58	122.09
2	A	330	CIT	O7-C3-C2	-5.91	95.91	109.38
2	A	330	CIT	O6-C6-C3	5.70	124.08	113.14
2	A	331	CIT	O1-C1-C2	-4.99	108.81	122.95
2	A	331	CIT	C4-C3-C6	4.82	120.69	110.03
2	A	330	CIT	O7-C3-C4	-4.14	99.94	109.38
2	A	330	CIT	C3-C2-C1	3.94	124.69	113.92
2	A	331	CIT	C3-C4-C5	3.45	123.34	113.92
2	A	330	CIT	O4-C5-O3	-3.10	115.36	123.33
2	A	331	CIT	O2-C1-C2	3.10	124.16	114.35
2	A	330	CIT	C4-C3-C2	2.79	116.47	109.31
2	A	330	CIT	O1-C1-C2	-2.41	116.13	122.95
2	A	330	CIT	O4-C5-C4	2.28	121.56	114.35
2	A	331	CIT	O7-C3-C4	2.06	114.07	109.38
2	A	331	CIT	C4-C3-C2	-2.05	104.06	109.31

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	330	CIT	C1-C2-C3-O7
2	A	330	CIT	C1-C2-C3-C6
2	A	330	CIT	O7-C3-C6-O5
2	A	330	CIT	O7-C3-C6-O6

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Mol	Chain	Res	Type	Atoms
2	A	331	CIT	C2-C3-C6-O5
2	A	331	CIT	C2-C3-C6-O6
2	A	331	CIT	O7-C3-C6-O5
2	A	331	CIT	O7-C3-C6-O6
2	A	330	CIT	C1-C2-C3-C4
2	A	331	CIT	C6-C3-C4-C5
2	A	330	CIT	C4-C3-C6-O5
2	A	330	CIT	C4-C3-C6-O6
2	A	331	CIT	O1-C1-C2-C3
2	A	331	CIT	O2-C1-C2-C3
2	A	331	CIT	O7-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	331	CIT	1	0
2	A	330	CIT	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	18:ARG	C	19:SER	N	1.17
1	A	17:PRO	C	18:ARG	N	1.13

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.