



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:35 PM UTC

PDB ID : 5LDR / pdb_00005ldr
Title : Crystal structure of a cold-adapted dimeric beta-D-galactosidase from *Paracoccus* sp. 32d strain in complex with galactose
Authors : Rutkiewicz-Krotewicz, M.; Bujacz, A.; Pietrzyk, A.J.; Sekula, B.; Bujacz, G.
Deposited on : 2016-06-27
Resolution : 3.15 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)	:	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

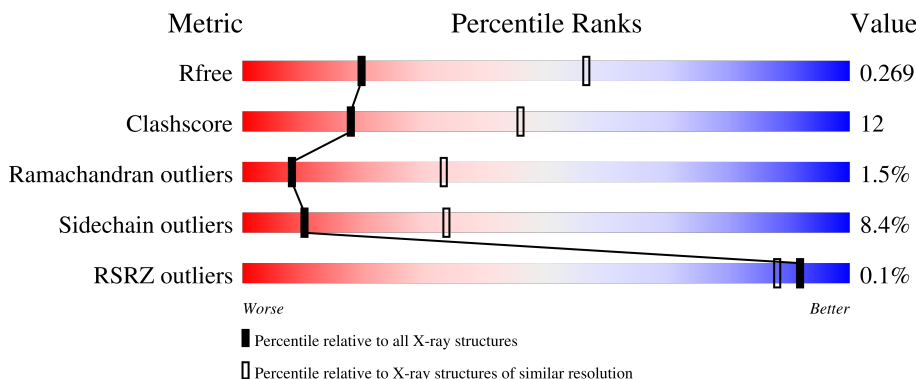
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	732	 65% 29% 5%
2	B	731	 65% 30% 5%

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
5	PEG	B	805	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 11724 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 Beta-D-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	731	5764	3632	1038	1068	26	0	0	0

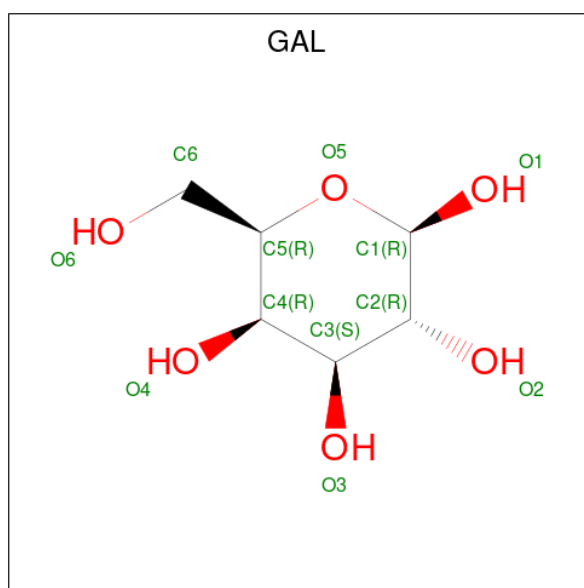
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ASN	-	expression tag	UNP D1LZK0

- Molecule 2 is a protein called Beta-D-galactosidase.

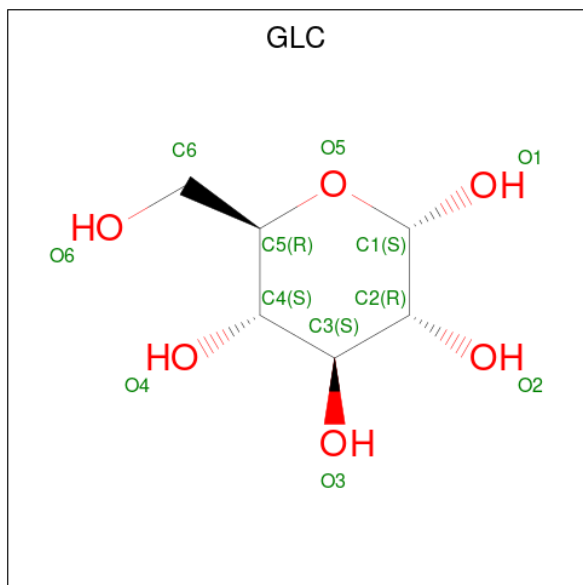
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	731	5763	3632	1038	1067	26	0	0	0

- Molecule 3 is beta-D-galactopyranose (CCD ID: GAL) (formula: C₆H₁₂O₆).



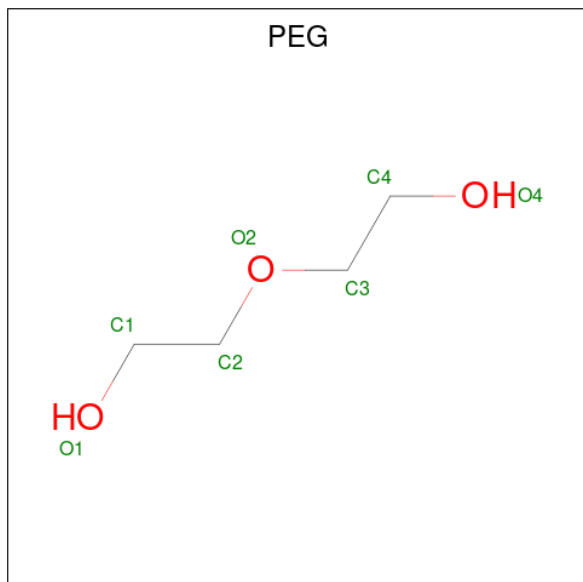
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			12	6	6		
3	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 4 is alpha-D-glucopyranose (CCD ID: GLC) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).

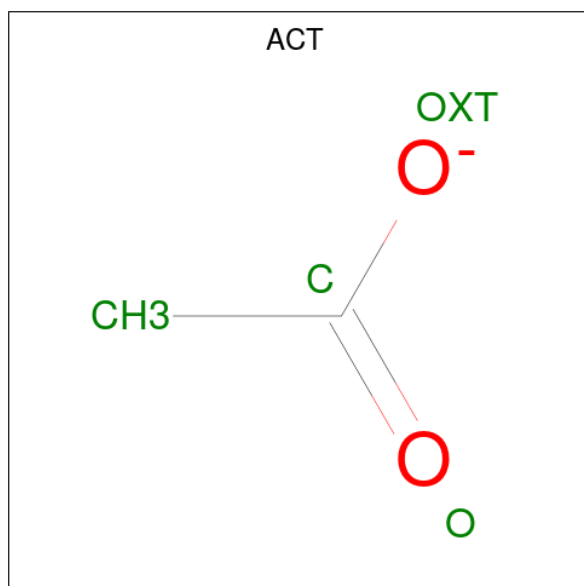


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total Cl 2 2	0	0
6	B	2	Total Cl 2 2	0	0

- Molecule 7 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0

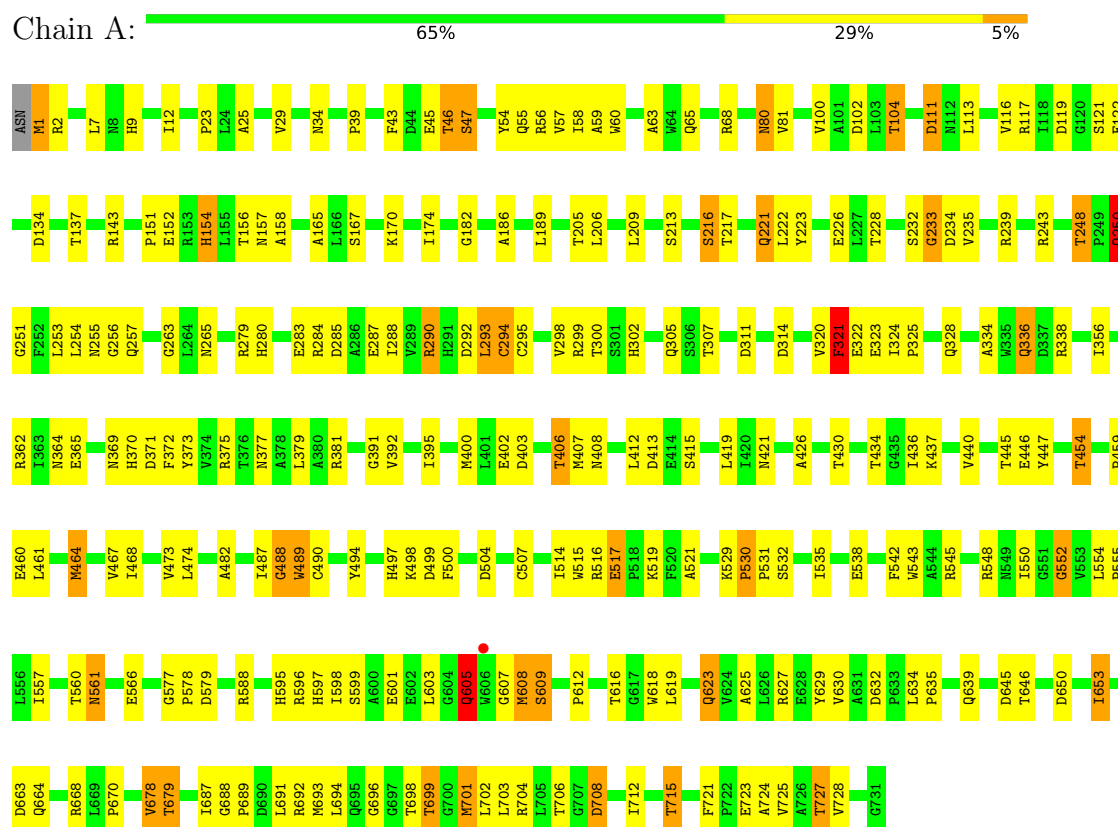
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	66	Total 66	O 66	0	0
8	B	48	Total 48	O 48	0	0

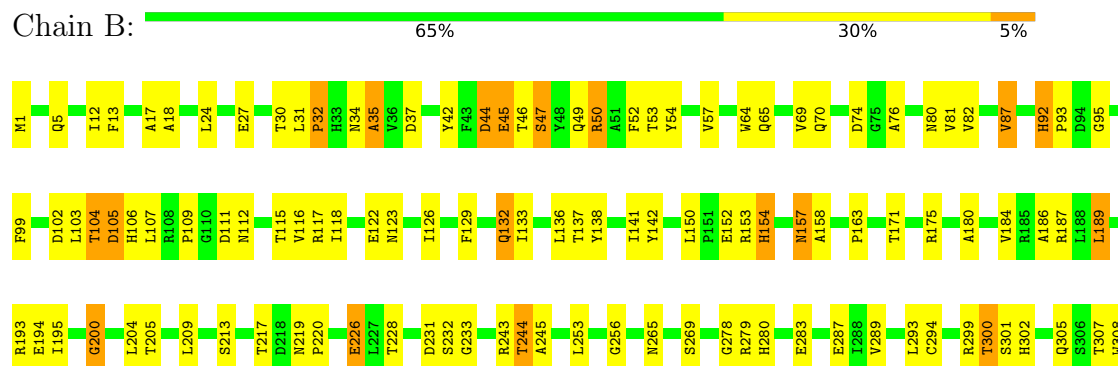
3 Residue-property plots

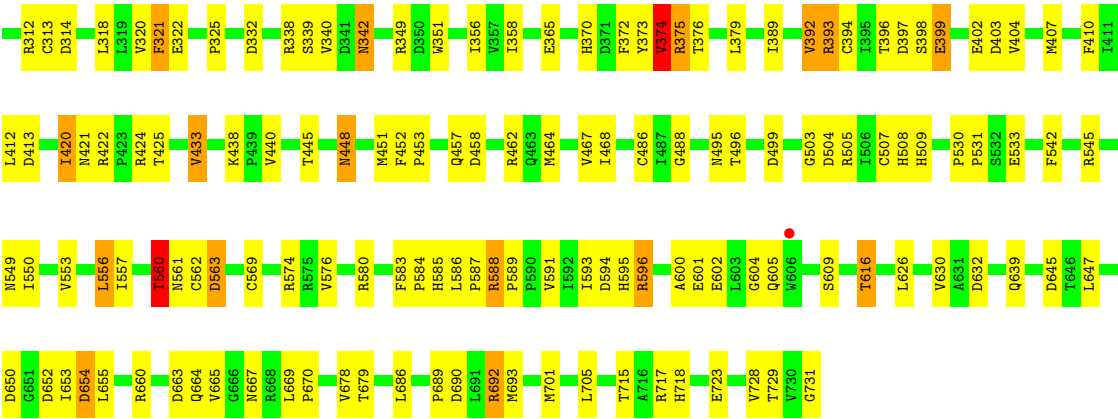
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Beta-D-galactosidase



• Molecule 2: Beta-D-galactosidase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.26Å 107.58Å 201.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.27 – 3.15 46.27 – 3.15	Depositor EDS
% Data completeness (in resolution range)	96.7 (46.27-3.15) 96.7 (46.27-3.15)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.184 , 0.267 0.195 , 0.269	Depositor DCC
R_{free} test set	1480 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	65.9	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11724	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, ACT, CL, PEG, GAL

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	1.20	11/5919 (0.2%)	1.35	40/8084 (0.5%)
2	B	1.22	15/5918 (0.3%)	1.32	40/8084 (0.5%)
All	All	1.21	26/11837 (0.2%)	1.33	80/16168 (0.5%)

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	530	PRO	CA-C	8.91	1.56	1.51
2	B	219	ASN	CA-C	7.67	1.62	1.52
2	B	200	GLY	N-CA	6.25	1.54	1.45
2	B	495	ASN	CA-C	6.20	1.60	1.52
2	B	508	HIS	CA-C	6.07	1.60	1.53
1	A	257	GLN	CA-C	5.97	1.59	1.53
2	B	562	CYS	N-CA	5.93	1.53	1.45
2	B	87	VAL	CA-C	5.81	1.59	1.52
1	A	233	GLY	C-O	-5.80	1.17	1.24
2	B	245	ALA	N-CA	5.78	1.54	1.46
1	A	290	ARG	C-O	-5.76	1.17	1.24
2	B	184	VAL	CA-C	5.71	1.59	1.52
1	A	221	GLN	CA-C	-5.64	1.46	1.52
1	A	232	SER	N-CA	5.53	1.51	1.46
2	B	220	PRO	CA-C	5.53	1.59	1.53
2	B	376	THR	N-CA	5.49	1.52	1.46
1	A	189	LEU	CA-C	5.41	1.59	1.52
1	A	250	GLN	CA-C	5.24	1.60	1.52
1	A	488	GLY	N-CA	5.23	1.51	1.45
2	B	655	LEU	CA-C	-5.23	1.46	1.52
2	B	563	ASP	N-CA	5.21	1.52	1.46
2	B	374	VAL	CA-CB	5.19	1.61	1.54
1	A	727	THR	CA-C	-5.09	1.46	1.52
2	B	57	VAL	CA-CB	5.09	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	549	ASN	CA-C	-5.08	1.46	1.52
1	A	189	LEU	N-CA	5.02	1.52	1.46

All (80) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	ALA	N-CA-C	8.88	122.38	108.79
1	A	154	HIS	N-CA-C	8.82	120.29	108.38
1	A	530	PRO	N-CA-C	8.76	118.88	110.47
1	A	653	ILE	N-CA-C	8.69	121.10	109.37
1	A	560	THR	N-CA-C	8.61	122.36	108.76
1	A	588	ARG	CA-C-N	-7.95	112.20	120.38
1	A	588	ARG	C-N-CA	-7.95	112.20	120.38
2	B	556	LEU	N-CA-C	7.79	121.61	109.07
1	A	577	GLY	CA-C-N	7.70	127.75	119.90
1	A	577	GLY	C-N-CA	7.70	127.75	119.90
2	B	35	ALA	N-CA-C	7.70	119.67	111.28
2	B	269	SER	N-CA-C	-7.14	99.59	110.30
1	A	461	LEU	N-CA-C	7.01	119.81	111.33
1	A	426	ALA	N-CA-C	6.94	118.93	111.36
1	A	688	GLY	CA-C-N	6.71	127.11	119.93
1	A	688	GLY	C-N-CA	6.71	127.11	119.93
1	A	519	LYS	N-CA-C	-6.68	101.92	110.53
2	B	433	VAL	N-CA-C	6.63	117.38	110.62
2	B	452	PHE	CA-C-N	6.57	126.53	119.76
2	B	452	PHE	C-N-CA	6.57	126.53	119.76
1	A	63	ALA	N-CA-C	6.57	121.01	113.19
2	B	496	THR	N-CA-C	6.54	116.70	108.45
1	A	307	THR	N-CA-CB	6.46	119.37	110.01
2	B	111	ASP	N-CA-C	6.38	118.68	108.41
2	B	569	CYS	N-CA-C	6.37	118.77	108.32
2	B	667	ASN	N-CA-C	6.36	119.47	110.50
1	A	46	THR	N-CA-C	-6.35	105.69	113.50
2	B	588	ARG	CA-C-N	-6.35	113.84	120.38
2	B	588	ARG	C-N-CA	-6.35	113.84	120.38
2	B	126	ILE	CA-C-N	-6.30	113.89	120.38
2	B	126	ILE	C-N-CA	-6.30	113.89	120.38
2	B	420	ILE	CB-CA-C	-6.29	103.23	110.41
1	A	561	ASN	N-CA-C	6.28	120.20	112.54
1	A	464	MET	N-CA-C	-6.20	104.14	111.03
2	B	549	ASN	CB-CA-C	-6.15	101.17	109.71
1	A	111	ASP	N-CA-C	6.12	118.67	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	154	HIS	N-CA-C	5.97	117.93	108.79
1	A	557	ILE	CB-CA-C	-5.96	104.10	111.08
2	B	585	HIS	N-CA-C	5.96	120.39	113.18
2	B	591	VAL	CB-CA-C	-5.87	103.64	110.91
1	A	116	VAL	CB-CA-C	-5.85	102.16	110.12
1	A	488	GLY	N-CA-C	5.84	120.02	112.54
1	A	468	ILE	CB-CA-C	-5.72	104.54	112.04
2	B	420	ILE	N-CA-C	5.72	117.07	107.18
1	A	321	PHE	N-CA-C	-5.69	99.14	108.76
2	B	560	THR	N-CA-C	5.60	117.58	109.07
1	A	182	GLY	CA-C-N	-5.54	113.85	119.83
1	A	182	GLY	C-N-CA	-5.54	113.85	119.83
2	B	718	HIS	CA-C-N	-5.54	114.05	119.64
2	B	718	HIS	C-N-CA	-5.54	114.05	119.64
2	B	245	ALA	N-CA-C	5.53	118.38	107.98
2	B	314	ASP	N-CA-C	-5.52	105.35	111.36
1	A	334	ALA	CA-C-N	5.50	127.92	120.44
1	A	334	ALA	C-N-CA	5.50	127.92	120.44
1	A	723	GLU	N-CA-C	5.46	122.43	110.80
2	B	616	THR	CA-C-N	5.42	125.92	122.18
2	B	616	THR	C-N-CA	5.42	125.92	122.18
2	B	404	VAL	N-CA-C	5.41	115.91	108.12
2	B	342	ASN	N-CA-C	5.39	117.23	111.36
1	A	552	GLY	N-CA-C	-5.39	102.88	112.58
1	A	678	VAL	N-CA-C	5.38	117.53	108.81
2	B	693	MET	N-CA-C	5.32	117.42	108.96
2	B	595	HIS	N-CA-C	5.24	117.67	111.33
2	B	563	ASP	N-CA-CB	5.22	117.58	110.01
2	B	141	ILE	N-CA-C	-5.17	98.58	109.34
1	A	415	SER	N-CA-C	-5.16	105.08	111.33
2	B	244	THR	N-CA-C	5.15	116.72	107.80
1	A	489	TRP	CA-C-O	-5.14	115.20	120.54
1	A	137	THR	N-CA-C	5.13	119.82	113.50
2	B	87	VAL	N-CA-C	5.13	115.87	108.48
2	B	458	ASP	N-CA-C	5.10	121.07	109.81
1	A	724	ALA	N-CA-C	5.09	118.02	110.48
2	B	392	VAL	N-CA-C	5.09	115.66	109.30
2	B	488	GLY	N-CA-C	5.07	119.61	111.64
1	A	603	LEU	N-CA-C	-5.04	105.87	111.36
1	A	243	ARG	N-CA-C	5.02	116.69	108.76
1	A	517	GLU	CA-C-N	-5.02	113.57	119.84
1	A	517	GLU	C-N-CA	-5.02	113.57	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	213	SER	N-CA-C	5.01	117.66	109.59
2	B	486	CYS	N-CA-C	5.00	115.91	108.60

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	5764	0	5591	153	0
2	B	5763	0	5591	131	1
3	A	12	0	12	3	0
3	B	12	0	12	0	0
4	A	12	0	12	0	0
5	A	7	0	10	0	0
5	B	28	0	40	5	0
6	A	2	0	0	0	0
6	B	2	0	0	1	0
7	B	8	0	6	0	0
8	A	66	0	0	5	0
8	B	48	0	0	5	0
All	All	11724	0	11274	282	1

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 (282) 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:678:VAL:HG23	1:A:715:THR:O	1.07	1.23
1:A:678:VAL:CG2	1:A:715:THR:O	2.02	1.07
1:A:1:MET:HE3	1:A:235:VAL:HB	1.51	0.90
1:A:157:ASN:HD22	1:A:158:ALA:H	1.19	0.89
1:A:460:GLU:OE2	1:A:548:ARG:NH1	2.12	0.81
1:A:165:ALA:O	1:A:170:LYS:NZ	2.15	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:LEU:HA	2:B:112:ASN:OD1	1.83	0.79
1:A:1:MET:HA	1:A:233:GLY:O	1.83	0.78
1:A:9:HIS:O	1:A:56:ARG:NH1	2.17	0.78
1:A:379:LEU:HD12	1:A:379:LEU:O	1.86	0.75
1:A:517:GLU:HG2	1:A:698:THR:HG21	1.68	0.74
2:B:464:MET:O	2:B:468:ILE:HG12	1.90	0.71
1:A:369:ASN:OD1	1:A:372:PHE:HB3	1.91	0.70
1:A:1:MET:CE	1:A:235:VAL:HB	2.20	0.70
1:A:157:ASN:HD22	1:A:158:ALA:N	1.90	0.70
1:A:601:GLU:HA	1:A:605:GLN:OE1	1.91	0.69
1:A:377:ASN:HD22	1:A:381:ARG:NH1	1.90	0.69
2:B:370:HIS:CD2	5:B:802:PEG:H32	2.28	0.69
1:A:706:THR:OG1	1:A:708:ASP:OD1	2.05	0.68
2:B:393:ARG:NH2	2:B:402:GLU:OE1	2.25	0.68
1:A:221:GLN:NE2	1:A:222:LEU:O	2.27	0.68
2:B:1:MET:N	2:B:233:GLY:O	2.26	0.68
1:A:595:HIS:HA	1:A:598:ILE:O	1.93	0.67
1:A:702:LEU:C	1:A:703:LEU:HD12	2.20	0.67
2:B:365:GLU:OE2	2:B:394:CYS:HB3	1.96	0.66
2:B:312:ARG:NH1	8:B:901:HOH:O	2.23	0.66
2:B:32:PRO:HB3	2:B:142:TYR:O	1.96	0.66
1:A:391:GLY:O	1:A:406:THR:HB	1.97	0.65
2:B:650:ASP:OD2	2:B:652:ASP:N	2.29	0.65
1:A:467:VAL:HG22	1:A:521:ALA:HA	1.80	0.64
1:A:157:ASN:ND2	1:A:158:ALA:H	1.93	0.63
1:A:635:PRO:HB3	1:A:721:PHE:CE1	2.34	0.63
1:A:447:TYR:CD1	1:A:473:VAL:HG11	2.36	0.61
1:A:579:ASP:OD2	1:A:596:ARG:NH2	2.32	0.61
2:B:12:ILE:O	2:B:54:TYR:HA	2.01	0.61
1:A:447:TYR:CE2	1:A:488:GLY:HA2	2.34	0.60
1:A:369:ASN:OD1	1:A:372:PHE:CB	2.50	0.60
2:B:586:LEU:HD23	2:B:587:PRO:HD2	1.84	0.60
2:B:601:GLU:O	2:B:604:GLY:N	2.34	0.60
2:B:115:THR:HG22	2:B:116:VAL:N	2.17	0.60
1:A:464:MET:HE3	8:A:919:HOH:O	2.02	0.59
2:B:42:TYR:CE2	2:B:504:ASP:HB3	2.37	0.59
2:B:49:GLN:NE2	2:B:122:GLU:OE2	2.34	0.58
2:B:300:THR:OG1	2:B:322:GLU:HA	2.03	0.58
2:B:689:PRO:O	2:B:692:ARG:HD3	2.04	0.58
1:A:668:ARG:HG2	8:A:932:HOH:O	2.04	0.58
1:A:279:ARG:O	1:A:283:GLU:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:THR:HB	1:A:305:GLN:CG	2.33	0.58
1:A:668:ARG:HD2	1:A:696:GLY:O	2.04	0.58
2:B:340:VAL:CG1	2:B:379:LEU:HD22	2.34	0.58
1:A:377:ASN:HD22	1:A:381:ARG:HH12	1.51	0.57
1:A:284:ARG:O	1:A:285:ASP:C	2.47	0.57
2:B:17:ALA:HB1	2:B:117:ARG:NE	2.19	0.57
1:A:531:PRO:HG3	1:A:561:ASN:HB3	1.87	0.57
1:A:687:ILE:HD11	1:A:704:ARG:HB2	1.86	0.56
2:B:200:GLY:HA3	2:B:204:LEU:CD2	2.35	0.56
2:B:422:ARG:HD3	5:B:805:PEG:O1	2.04	0.56
1:A:362:ARG:HG2	1:A:373:TYR:CZ	2.39	0.56
1:A:601:GLU:CA	1:A:605:GLN:OE1	2.54	0.56
2:B:293:LEU:O	2:B:294:CYS:C	2.48	0.56
2:B:279:ARG:HD2	2:B:308:TRP:CE3	2.41	0.56
1:A:618:TRP:CD1	1:A:623:GLN:HA	2.41	0.55
2:B:339:SER:O	2:B:340:VAL:C	2.45	0.55
1:A:691:LEU:HD23	1:A:693:MET:HE1	1.89	0.55
1:A:548:ARG:NH2	1:A:555:PRO:O	2.40	0.55
1:A:619:LEU:HA	8:A:904:HOH:O	2.05	0.55
2:B:200:GLY:HA3	2:B:204:LEU:HD21	1.89	0.54
1:A:437:LYS:HA	8:A:933:HOH:O	2.06	0.54
2:B:580:ARG:HD3	8:B:929:HOH:O	2.07	0.54
2:B:542:PHE:CD1	2:B:670:PRO:HG3	2.41	0.54
1:A:205:THR:C	1:A:206:LEU:HG	2.32	0.54
2:B:340:VAL:HG12	2:B:379:LEU:HD22	1.89	0.54
1:A:365:GLU:OE2	3:A:801:GAL:O1	2.25	0.54
2:B:647:LEU:O	2:B:731:GLY:N	2.40	0.54
1:A:635:PRO:HB3	1:A:721:PHE:CZ	2.42	0.53
1:A:221:GLN:HG3	1:A:223:TYR:CE1	2.43	0.53
1:A:447:TYR:CE2	1:A:488:GLY:CA	2.91	0.53
2:B:76:ALA:O	2:B:95:GLY:HA2	2.08	0.53
1:A:538:GLU:OE1	1:A:627:ARG:NH1	2.42	0.53
1:A:290:ARG:O	1:A:294:CYS:HA	2.09	0.53
1:A:377:ASN:HD21	1:A:402:GLU:HG3	1.72	0.53
1:A:694:LEU:HD23	1:A:699:THR:HG22	1.91	0.53
2:B:132:GLN:C	2:B:133:ILE:HG13	2.34	0.53
2:B:321:PHE:C	2:B:321:PHE:CD2	2.86	0.52
1:A:498:LYS:HD2	2:B:632:ASP:HB3	1.90	0.52
1:A:708:ASP:OD1	1:A:708:ASP:N	2.37	0.52
1:A:156:THR:O	1:A:157:ASN:HB2	2.10	0.52
2:B:299:ARG:NH2	2:B:392:VAL:HG21	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:MET:O	1:A:609:SER:CB	2.57	0.52
2:B:35:ALA:HB1	2:B:52:PHE:CE2	2.45	0.52
1:A:678:VAL:HG22	1:A:679:THR:N	2.25	0.52
2:B:420:ILE:HG21	5:B:805:PEG:H22	1.92	0.52
1:A:12:ILE:O	1:A:54:TYR:HA	2.09	0.51
2:B:123:ASN:O	2:B:129:PHE:HB2	2.09	0.51
1:A:379:LEU:HD12	1:A:379:LEU:C	2.36	0.51
2:B:17:ALA:HB1	2:B:117:ARG:HE	1.75	0.51
2:B:189:LEU:HB2	2:B:193:ARG:O	2.10	0.51
2:B:705:LEU:HB3	8:B:909:HOH:O	2.11	0.51
2:B:44:ASP:C	2:B:46:THR:H	2.19	0.51
2:B:321:PHE:C	2:B:321:PHE:HD2	2.18	0.51
1:A:494:TYR:CE2	1:A:507:CYS:HB2	2.45	0.51
2:B:64:TRP:CE3	2:B:69:VAL:HG11	2.46	0.51
2:B:92:HIS:ND1	2:B:99:PHE:HB3	2.24	0.51
2:B:393:ARG:NH1	2:B:398:SER:OG	2.43	0.51
1:A:157:ASN:ND2	1:A:158:ALA:N	2.56	0.51
1:A:446:GLU:OE2	3:A:801:GAL:H1	2.11	0.50
1:A:300:THR:HB	1:A:305:GLN:CD	2.36	0.50
1:A:645:ASP:HA	1:A:728:VAL:HG12	1.92	0.50
1:A:263:GLY:HA2	1:A:295:CYS:HB3	1.94	0.50
2:B:42:TYR:CE2	2:B:504:ASP:CB	2.95	0.50
2:B:647:LEU:N	2:B:729:THR:O	2.44	0.50
1:A:663:ASP:OD1	1:A:663:ASP:C	2.52	0.50
2:B:136:LEU:HB2	2:B:138:TYR:CZ	2.47	0.50
1:A:504:ASP:OD1	1:A:504:ASP:N	2.44	0.50
2:B:507:CYS:HB3	2:B:509:HIS:CE1	2.47	0.50
2:B:265:ASN:OD1	2:B:299:ARG:HD3	2.12	0.50
2:B:195:ILE:HG22	2:B:209:LEU:HD22	1.93	0.49
1:A:712:ILE:O	1:A:727:THR:HA	2.12	0.49
2:B:396:THR:HG22	2:B:433:VAL:HA	1.94	0.49
1:A:288:ILE:O	1:A:292:ASP:HB2	2.12	0.49
2:B:47:SER:O	2:B:50:ARG:NH1	2.45	0.49
1:A:248:THR:O	1:A:251:GLY:O	2.30	0.49
1:A:489:TRP:CD2	1:A:490:CYS:HB3	2.47	0.49
1:A:369:ASN:O	1:A:370:HIS:C	2.55	0.49
1:A:336:GLN:HG2	1:A:372:PHE:CD1	2.48	0.49
1:A:336:GLN:HG2	1:A:372:PHE:CG	2.48	0.49
1:A:545:ARG:NH2	1:A:608:MET:SD	2.85	0.48
1:A:634:LEU:O	1:A:663:ASP:HA	2.12	0.48
2:B:410:PHE:HB3	2:B:451:MET:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:PHE:CD1	1:A:670:PRO:HG3	2.48	0.48
1:A:80:ASN:C	1:A:81:VAL:CG2	2.86	0.48
1:A:517:GLU:HG2	1:A:698:THR:CG2	2.41	0.48
1:A:1:MET:HE2	1:A:235:VAL:O	2.13	0.48
2:B:373:TYR:O	2:B:374:VAL:C	2.56	0.48
1:A:381:ARG:NH2	1:A:403:ASP:OD1	2.45	0.48
2:B:81:VAL:O	2:B:116:VAL:HA	2.14	0.48
1:A:68:ARG:HA	1:A:104:THR:HG21	1.96	0.47
1:A:566:GLU:HB2	1:A:618:TRP:CZ3	2.49	0.47
2:B:115:THR:CG2	2:B:116:VAL:N	2.77	0.47
2:B:278:GLY:N	2:B:654:ASP:OD2	2.36	0.47
2:B:556:LEU:N	2:B:593:ILE:O	2.40	0.47
2:B:574:ARG:NH2	2:B:602:GLU:OE1	2.48	0.47
1:A:302:HIS:O	1:A:325:PRO:HA	2.15	0.47
2:B:424:ARG:HA	5:B:805:PEG:H41	1.97	0.47
1:A:338:ARG:CZ	1:A:338:ARG:HA	2.45	0.47
2:B:34:ASN:HB3	2:B:37:ASP:OD1	2.15	0.47
1:A:298:VAL:HG22	1:A:299:ARG:N	2.29	0.47
2:B:407:MET:HE3	2:B:433:VAL:CG1	2.45	0.46
1:A:499:ASP:O	2:B:545:ARG:HD3	2.15	0.46
2:B:370:HIS:O	2:B:374:VAL:HG12	2.15	0.46
2:B:663:ASP:O	2:B:664:GLN:C	2.58	0.46
1:A:548:ARG:HD3	1:A:552:GLY:O	2.16	0.46
2:B:299:ARG:CZ	2:B:392:VAL:HG21	2.46	0.46
2:B:583:PHE:O	2:B:584:PRO:C	2.58	0.46
1:A:689:PRO:O	1:A:692:ARG:HD3	2.15	0.46
2:B:630:VAL:CG1	2:B:665:VAL:HG11	2.46	0.46
1:A:691:LEU:CD2	1:A:693:MET:HE1	2.45	0.46
2:B:560:THR:HG22	2:B:561:ASN:N	2.31	0.46
2:B:457:GLN:NE2	2:B:670:PRO:O	2.49	0.46
1:A:412:LEU:HA	1:A:413:ASP:HA	1.81	0.45
1:A:515:TRP:HZ3	1:A:702:LEU:HD12	1.81	0.45
2:B:339:SER:O	2:B:342:ASN:N	2.49	0.45
2:B:349:ARG:O	2:B:349:ARG:HG2	2.16	0.45
2:B:542:PHE:CG	2:B:670:PRO:HG3	2.52	0.45
1:A:543:TRP:CG	1:A:629:TYR:HB3	2.52	0.45
1:A:597:HIS:O	1:A:598:ILE:HG13	2.16	0.45
1:A:102:ASP:OD1	1:A:104:THR:OG1	2.34	0.45
1:A:59:ALA:HA	1:A:111:ASP:HA	1.99	0.45
2:B:153:ARG:HB3	2:B:232:SER:HB3	1.99	0.45
2:B:645:ASP:O	2:B:728:VAL:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:GLY:O	1:A:406:THR:CB	2.63	0.45
1:A:446:GLU:HA	1:A:487:ILE:O	2.17	0.45
2:B:103:LEU:O	2:B:104:THR:C	2.59	0.45
2:B:300:THR:HB	2:B:305:GLN:HG3	1.99	0.45
2:B:424:ARG:HA	5:B:805:PEG:C3	2.47	0.45
2:B:279:ARG:O	2:B:280:HIS:C	2.58	0.44
2:B:586:LEU:HD23	2:B:587:PRO:CD	2.47	0.44
1:A:369:ASN:OD1	1:A:369:ASN:O	2.36	0.44
1:A:447:TYR:CE1	1:A:473:VAL:HG11	2.52	0.44
1:A:250:GLN:OE1	1:A:250:GLN:HA	2.16	0.44
1:A:254:LEU:O	1:A:255:ASN:C	2.61	0.44
2:B:530:PRO:O	2:B:531:PRO:C	2.57	0.44
1:A:46:THR:O	1:A:47:SER:C	2.60	0.44
2:B:586:LEU:CD2	2:B:587:PRO:HD2	2.48	0.44
2:B:18:ALA:O	2:B:117:ARG:NH2	2.50	0.44
2:B:31:LEU:HA	2:B:32:PRO:C	2.43	0.44
1:A:400:MET:HE1	1:A:440:VAL:HG21	1.99	0.44
1:A:407:MET:HG3	1:A:408:ASN:N	2.32	0.44
2:B:118:ILE:O	2:B:118:ILE:HG13	2.17	0.44
2:B:503:GLY:N	8:B:906:HOH:O	2.51	0.44
1:A:55:GLN:NE2	1:A:113:LEU:HD22	2.33	0.44
1:A:498:LYS:HG3	1:A:499:ASP:N	2.33	0.44
1:A:650:ASP:HB3	1:A:653:ILE:HD11	2.00	0.44
2:B:372:PHE:O	2:B:375:ARG:HB2	2.18	0.44
2:B:12:ILE:HG22	2:B:24:LEU:HD23	1.99	0.43
2:B:243:ARG:NH1	6:B:806:CL:CL	2.88	0.43
2:B:129:PHE:CE1	2:B:137:THR:HG21	2.53	0.43
2:B:253:LEU:HG	2:B:256:GLY:O	2.18	0.43
1:A:447:TYR:CD2	1:A:488:GLY:HA2	2.52	0.43
2:B:186:ALA:HB2	2:B:204:LEU:HD13	1.99	0.43
1:A:80:ASN:C	1:A:81:VAL:HG23	2.44	0.43
1:A:288:ILE:O	1:A:293:LEU:HD12	2.18	0.43
1:A:320:VAL:HB	1:A:356:ILE:HA	2.01	0.43
1:A:364:ASN:ND2	3:A:801:GAL:O2	2.52	0.43
1:A:430:THR:HG21	1:A:482:ALA:HB1	2.00	0.43
1:A:134:ASP:OD1	1:A:494:TYR:OH	2.23	0.43
2:B:301:SER:HA	2:B:302:HIS:HA	1.85	0.43
2:B:187:ARG:NH1	2:B:226:GLU:OE1	2.51	0.43
2:B:468:ILE:HD11	2:B:557:ILE:HD11	2.00	0.43
1:A:529:LYS:O	1:A:561:ASN:ND2	2.52	0.43
2:B:13:PHE:HA	2:B:53:THR:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:105:ASP:N	2:B:105:ASP:OD1	2.52	0.43
2:B:163:PRO:HG2	2:B:171:THR:HB	2.01	0.43
1:A:284:ARG:O	1:A:287:GLU:N	2.52	0.43
1:A:632:ASP:CG	1:A:632:ASP:O	2.61	0.42
2:B:42:TYR:CZ	2:B:504:ASP:HB3	2.53	0.42
2:B:302:HIS:O	2:B:325:PRO:HA	2.19	0.42
2:B:412:LEU:HA	2:B:413:ASP:HA	1.83	0.42
1:A:25:ALA:HB2	8:A:957:HOH:O	2.20	0.42
1:A:311:ASP:O	1:A:314:ASP:HB2	2.19	0.42
2:B:81:VAL:HG12	2:B:82:VAL:N	2.34	0.42
1:A:554:LEU:HA	1:A:555:PRO:C	2.43	0.42
1:A:1:MET:CG	1:A:2:ARG:H	2.33	0.42
1:A:216:SER:OG	1:A:217:THR:N	2.52	0.42
1:A:362:ARG:HG2	1:A:373:TYR:CE1	2.55	0.42
2:B:321:PHE:CD1	2:B:358:ILE:CG2	3.03	0.42
1:A:39:PRO:HB2	1:A:43:PHE:HD2	1.84	0.42
1:A:57:VAL:HG13	1:A:111:ASP:HB2	2.01	0.42
1:A:122:GLU:OE2	1:A:497:HIS:NE2	2.51	0.42
1:A:154:HIS:CD2	1:A:154:HIS:C	2.98	0.42
1:A:324:ILE:HB	1:A:325:PRO:CD	2.50	0.42
1:A:607:GLY:O	1:A:608:MET:C	2.62	0.42
2:B:70:GLN:NE2	2:B:102:ASP:OD2	2.52	0.42
1:A:514:ILE:O	1:A:514:ILE:CG1	2.67	0.42
1:A:616:THR:HA	1:A:625:ALA:O	2.20	0.42
2:B:150:LEU:HD23	2:B:154:HIS:CG	2.55	0.42
1:A:151:PRO:O	1:A:154:HIS:ND1	2.52	0.42
1:A:701:MET:HE3	1:A:703:LEU:HD11	2.02	0.42
2:B:407:MET:HG2	2:B:433:VAL:HG11	2.02	0.42
2:B:453:PRO:O	2:B:462:ARG:NH2	2.53	0.42
2:B:553:VAL:O	2:B:553:VAL:HG23	2.18	0.42
1:A:228:THR:HA	1:A:234:ASP:O	2.20	0.41
1:A:299:ARG:NH2	1:A:392:VAL:HG21	2.35	0.41
1:A:473:VAL:O	1:A:474:LEU:C	2.63	0.41
2:B:653:ILE:HB	2:B:705:LEU:HD12	2.01	0.41
1:A:500:PHE:CD2	1:A:500:PHE:N	2.88	0.41
2:B:320:VAL:HB	2:B:356:ILE:HA	2.02	0.41
2:B:503:GLY:O	2:B:505:ARG:NH1	2.52	0.41
2:B:594:ASP:OD2	2:B:596:ARG:NH2	2.53	0.41
2:B:283:GLU:O	2:B:287:GLU:HG3	2.20	0.41
2:B:438:LYS:NZ	8:B:902:HOH:O	2.37	0.41
2:B:678:VAL:HG21	2:B:701:MET:HE1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:370:HIS:ND1	2:B:399:GLU:OE2	2.53	0.41
1:A:454:THR:O	1:A:454:THR:HG22	2.20	0.41
1:A:515:TRP:O	1:A:516:ARG:HB2	2.20	0.41
2:B:106:HIS:O	2:B:107:LEU:HD23	2.20	0.41
2:B:122:GLU:HA	2:B:129:PHE:CD1	2.56	0.41
2:B:157:ASN:HD22	2:B:158:ALA:H	1.69	0.41
1:A:170:LYS:HB2	1:A:209:LEU:HB2	2.02	0.41
1:A:265:ASN:ND2	1:A:487:ILE:HG22	2.35	0.41
1:A:174:ILE:HD12	1:A:174:ILE:N	2.36	0.41
1:A:320:VAL:HG12	1:A:321:PHE:N	2.36	0.41
2:B:421:ASN:O	2:B:422:ARG:C	2.64	0.41
2:B:650:ASP:OD2	2:B:650:ASP:C	2.63	0.41
1:A:300:THR:HB	1:A:305:GLN:HG3	2.01	0.41
1:A:459:PRO:O	1:A:460:GLU:C	2.64	0.41
2:B:153:ARG:NH2	2:B:180:ALA:O	2.54	0.41
1:A:60:TRP:HZ2	1:A:65:GLN:HG3	1.86	0.40
1:A:328:GLN:N	1:A:364:ASN:O	2.54	0.40
2:B:313:CYS:SG	2:B:318:LEU:HD23	2.60	0.40
2:B:321:PHE:CD1	2:B:358:ILE:HG21	2.56	0.40
2:B:467:VAL:O	2:B:468:ILE:C	2.65	0.40
1:A:612:PRO:HB3	1:A:630:VAL:HA	2.03	0.40
2:B:588:ARG:O	2:B:589:PRO:C	2.62	0.40
1:A:254:LEU:O	1:A:256:GLY:N	2.54	0.40
1:A:280:HIS:O	1:A:283:GLU:N	2.54	0.40
1:A:372:PHE:O	1:A:375:ARG:HB2	2.21	0.40
1:A:447:TYR:CE2	1:A:488:GLY:N	2.90	0.40
2:B:389:ILE:H	2:B:403:ASP:HB2	1.85	0.40
2:B:639:GLN:HB3	2:B:660:ARG:HB2	2.02	0.40
2:B:321:PHE:CG	2:B:358:ILE:HG23	2.57	0.40
2:B:583:PHE:HB3	2:B:586:LEU:HD12	2.04	0.40

All (1) 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)
2:B:175:ARG:NH1	2:B:679:THR:OG1[3_745]	2.01	0.19

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	729/732 (100%)	621 (85%)	100 (14%)	8 (1%)	11	39
2	B	729/731 (100%)	631 (87%)	84 (12%)	14 (2%)	6	28
All	All	1458/1463 (100%)	1252 (86%)	184 (13%)	22 (2%)	8	33

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	609	SER
2	B	104	THR
2	B	332	ASP
1	A	532	SER
1	A	608	MET
2	B	550	ILE
1	A	152	GLU
1	A	623	GLN
2	B	669	LEU
1	A	605	GLN
2	B	45	GLU
2	B	399	GLU
2	B	600	ALA
2	B	109	PRO
2	B	375	ARG
2	B	448	ASN
1	A	550	ILE
2	B	300	THR
2	B	93	PRO
1	A	23	PRO
2	B	374	VAL
2	B	289	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	611/612 (100%)	560 (92%)	51 (8%)	10	34
2	B	611/611 (100%)	559 (92%)	52 (8%)	10	33
All	All	1222/1223 (100%)	1119 (92%)	103 (8%)	10	33

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	7	LEU
1	A	29	VAL
1	A	34	ASN
1	A	45	GLU
1	A	47	SER
1	A	58	ILE
1	A	80	ASN
1	A	100	VAL
1	A	104	THR
1	A	117	ARG
1	A	119	ASP
1	A	121	SER
1	A	143	ARG
1	A	167	SER
1	A	213	SER
1	A	216	SER
1	A	226	GLU
1	A	239	ARG
1	A	248	THR
1	A	250	GLN
1	A	253	LEU
1	A	293	LEU
1	A	294	CYS
1	A	321	PHE
1	A	322	GLU
1	A	323	GLU

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Mol	Chain	Res	Type
1	A	336	GLN
1	A	371	ASP
1	A	395	ILE
1	A	406	THR
1	A	419	LEU
1	A	421	ASN
1	A	434	THR
1	A	436	ILE
1	A	445	THR
1	A	454	THR
1	A	530	PRO
1	A	535	ILE
1	A	578	PRO
1	A	599	SER
1	A	605	GLN
1	A	639	GLN
1	A	646	THR
1	A	664	GLN
1	A	679	THR
1	A	699	THR
1	A	701	MET
1	A	708	ASP
1	A	715	THR
1	A	725	VAL
2	B	5	GLN
2	B	27	GLU
2	B	30	THR
2	B	32	PRO
2	B	44	ASP
2	B	45	GLU
2	B	47	SER
2	B	50	ARG
2	B	65	GLN
2	B	74	ASP
2	B	80	ASN
2	B	87	VAL
2	B	92	HIS
2	B	105	ASP
2	B	132	GLN
2	B	152	GLU
2	B	157	ASN
2	B	189	LEU

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Mol	Chain	Res	Type
2	B	194	GLU
2	B	205	THR
2	B	217	THR
2	B	226	GLU
2	B	228	THR
2	B	231	ASP
2	B	244	THR
2	B	307	THR
2	B	321	PHE
2	B	338	ARG
2	B	351	TRP
2	B	393	ARG
2	B	397	ASP
2	B	425	THR
2	B	440	VAL
2	B	445	THR
2	B	448	ASN
2	B	499	ASP
2	B	533	GLU
2	B	560	THR
2	B	563	ASP
2	B	576	VAL
2	B	596	ARG
2	B	605	GLN
2	B	609	SER
2	B	616	THR
2	B	626	LEU
2	B	654	ASP
2	B	686	LEU
2	B	690	ASP
2	B	692	ARG
2	B	715	THR
2	B	717	ARG
2	B	723	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	92	HIS
1	A	123	ASN
1	A	157	ASN

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Mol	Chain	Res	Type
1	A	273	GLN
1	A	291	HIS
1	A	302	HIS
1	A	342	ASN
1	A	377	ASN
1	A	408	ASN
1	A	457	GLN
1	A	470	HIS
1	A	495	ASN
1	A	585	HIS
1	A	623	GLN
1	A	720	GLN
2	B	157	ASN
2	B	457	GLN
2	B	509	HIS
2	B	611	HIS

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](#)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 for Mogul analysis.

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
3	GAL	B	801	-	12,12,12	1.44	2 (16%)	17,17,17	2.75	8 (47%)
7	ACT	B	809	-	3,3,3	0.98	0	3,3,3	0.90	0
5	PEG	B	805	-	6,6,6	0.46	0	5,5,5	0.93	0
5	PEG	B	803	-	6,6,6	0.69	0	5,5,5	0.89	0
5	PEG	B	802	-	6,6,6	0.54	0	5,5,5	0.41	0
5	PEG	A	803	-	6,6,6	0.56	0	5,5,5	0.14	0
7	ACT	B	808	-	3,3,3	1.01	0	3,3,3	0.81	0
4	GLC	A	802	-	12,12,12	1.07	0	17,17,17	1.68	4 (23%)
3	GAL	A	801	-	12,12,12	1.01	0	17,17,17	1.77	5 (29%)
5	PEG	B	804	-	6,6,6	0.41	0	5,5,5	0.41	0

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
3	GAL	B	801	-	-	2/2/22/22	0/1/1/1
5	PEG	B	805	-	-	1/4/4/4	-
5	PEG	B	803	-	-	2/4/4/4	-
5	PEG	B	802	-	-	1/4/4/4	-
5	PEG	A	803	-	-	1/4/4/4	-
4	GLC	A	802	-	-	2/2/22/22	0/1/1/1
3	GAL	A	801	-	-	0/2/22/22	0/1/1/1
5	PEG	B	804	-	-	0/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	801	GAL	C6-C5	2.52	1.60	1.51
3	B	801	GAL	C4-C5	2.39	1.58	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	GAL	C1-O5-C5	5.56	124.41	113.65
3	B	801	GAL	C3-C4-C5	5.14	119.55	110.23
3	B	801	GAL	O5-C5-C6	4.69	118.05	106.44
3	A	801	GAL	O3-C3-C2	4.65	121.33	110.38
4	A	802	GLC	C1-O5-C5	4.22	121.82	113.65
3	B	801	GAL	O6-C6-C5	3.62	123.67	111.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	GAL	O5-C1-C2	3.33	116.16	110.30
3	B	801	GAL	O2-C2-C1	3.01	116.18	109.25
3	A	801	GAL	O5-C5-C6	2.83	113.45	106.44
4	A	802	GLC	O5-C5-C6	2.73	113.20	106.44
3	A	801	GAL	O5-C5-C4	-2.67	104.89	109.70
4	A	802	GLC	O5-C1-C2	2.63	114.92	110.30
3	A	801	GAL	O1-C1-C2	2.56	116.41	108.98
3	B	801	GAL	O2-C2-C3	-2.22	105.14	110.38
3	B	801	GAL	O4-C4-C3	-2.18	105.25	110.38
3	A	801	GAL	C4-C3-C2	-2.11	107.13	110.83
4	A	802	GLC	C4-C3-C2	-2.07	107.20	110.83

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	801	GAL	O5-C5-C6-O6
4	A	802	GLC	O5-C5-C6-O6
4	A	802	GLC	C4-C5-C6-O6
5	B	802	PEG	O1-C1-C2-O2
3	B	801	GAL	C4-C5-C6-O6
5	B	805	PEG	C1-C2-O2-C3
5	B	803	PEG	C4-C3-O2-C2
5	A	803	PEG	O2-C3-C4-O4
5	B	803	PEG	C1-C2-O2-C3

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	805	PEG	4	0
5	B	802	PEG	1	0
3	A	801	GAL	3	0

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	731/732 (99%)	-0.46	1 (0%) 92 88	31, 58, 84, 171	0
2	B	731/731 (100%)	-0.36	1 (0%) 92 88	36, 63, 89, 145	0
All	All	1462/1463 (99%)	-0.41	2 (0%) 92 88	31, 60, 87, 171	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	606	TRP	2.4
2	B	606	TRP	2.2

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
5	PEG	B	803	7/7	0.70	0.15	67,71,80,90	0
5	PEG	B	805	7/7	0.78	0.15	113,117,121,122	0
7	ACT	B	808	4/4	0.83	0.13	65,66,70,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GLC	A	802	12/12	0.84	0.10	72,91,102,103	0
5	PEG	A	803	7/7	0.85	0.15	54,66,80,82	0
5	PEG	B	802	7/7	0.86	0.11	59,74,80,80	0
6	CL	A	804	1/1	0.87	0.06	57,57,57,57	0
5	PEG	B	804	7/7	0.88	0.11	67,70,72,72	0
3	GAL	A	801	12/12	0.88	0.10	66,75,79,79	0
7	ACT	B	809	4/4	0.90	0.10	47,54,55,55	0
6	CL	B	807	1/1	0.91	0.06	75,75,75,75	0
3	GAL	B	801	12/12	0.94	0.07	49,56,59,59	0
6	CL	B	806	1/1	0.96	0.05	42,42,42,42	0
6	CL	A	805	1/1	0.96	0.06	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.