



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:19 PM UTC

PDB ID : 1LTA / pdb_00001lta
Title : 2.2 ANGSTROMS CRYSTAL STRUCTURE OF E. COLI HEAT-LABILE ENTEROTOXIN (LT) WITH BOUND GALACTOSE
Authors : Merritt, E.A.; Sixma, T.K.; Kalk, K.H.; Van Zanten, B.A.M.; Hol, W.G.J.
Deposited on : 1993-09-15
Resolution : 2.20 Å(reported)

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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

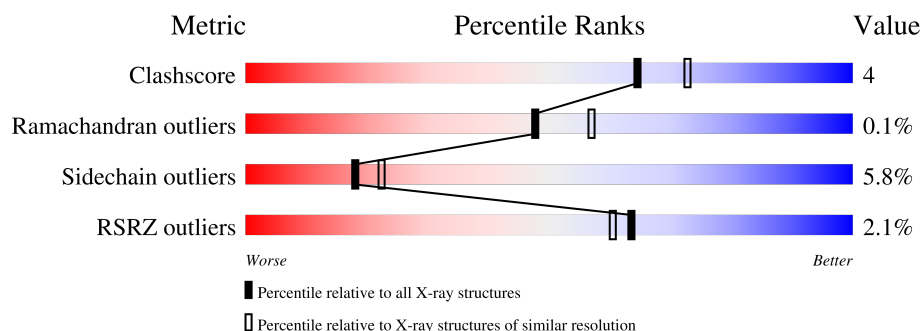
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	D	103	
1	E	103	
1	F	103	
1	G	103	
1	H	103	
2	A	188	

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Mol	Chain	Length	Quality of chain
3	C	49	12% 71% 12% 6% • 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6390 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 HEAT-LABILE ENTEROTOXIN, SUBUNIT B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	103	Total	C	N	O	S	0	0	0
			824	516	139	163	6			
1	E	103	Total	C	N	O	S	0	0	0
			824	516	139	163	6			
1	F	103	Total	C	N	O	S	0	0	0
			824	516	139	163	6			
1	G	103	Total	C	N	O	S	0	0	0
			824	516	139	163	6			
1	H	103	Total	C	N	O	S	0	0	0
			824	516	139	163	6			

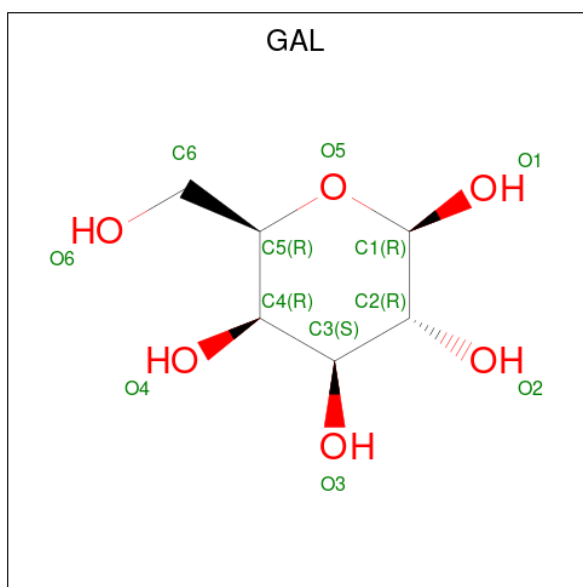
- Molecule 2 is a protein called HEAT-LABILE ENTEROTOXIN, SUBUNIT A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	188	Total	C	N	O	S	0	0	0
			1531	963	280	284	4			

- Molecule 3 is a protein called HEAT-LABILE ENTEROTOXIN, SUBUNIT A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	45	Total	C	N	O	S	0	0	0
			384	235	66	82	1			

- Molecule 4 is beta-D-galactopyranose (CCD ID: GAL) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			12	6	6		
4	E	1	Total	C	O	0	0
			12	6	6		
4	F	1	Total	C	O	0	0
			12	6	6		
4	G	1	Total	C	O	0	0
			12	6	6		
4	H	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is water.

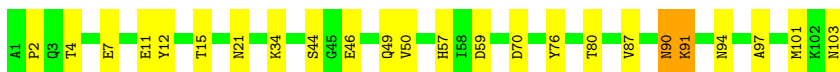
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	52	Total	O	0	0
			52	52		
5	E	44	Total	O	0	0
			44	44		
5	F	29	Total	O	0	0
			29	29		
5	G	52	Total	O	0	0
			52	52		
5	H	39	Total	O	0	0
			39	39		
5	A	58	Total	O	0	0
			58	58		
5	C	21	Total	O	0	0
			21	21		

3 Residue-property plots [i](#)

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.

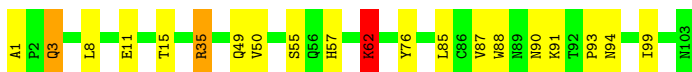
- Molecule 1: HEAT-LABILE ENTEROTOXIN, SUBUNIT B

Chain D: 



- Molecule 1: HEAT-LABILE ENTEROTOXIN, SUBUNIT B

Chain E: 



- Molecule 1: HEAT-LABILE ENTEROTOXIN, SUBUNIT B

Chain F: 



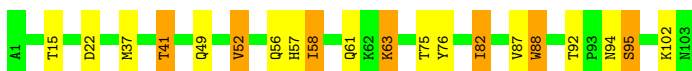
- Molecule 1: HEAT-LABILE ENTEROTOXIN, SUBUNIT B

Chain G: 



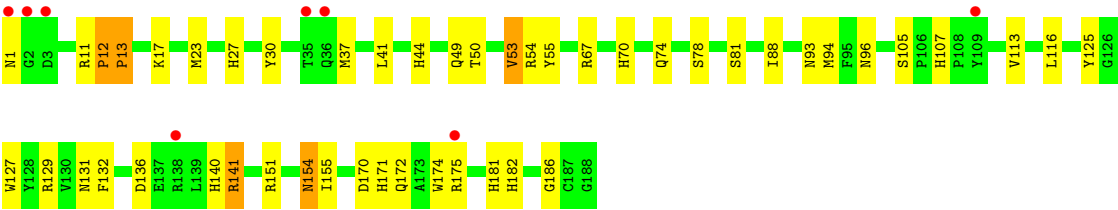
- Molecule 1: HEAT-LABILE ENTEROTOXIN, SUBUNIT B

Chain H: 



- Molecule 2: HEAT-LABILE ENTEROTOXIN, SUBUNIT A

Chain A: 



● Molecule 3: HEAT-LABILE ENTEROTOXIN, SUBUNIT A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.70Å 73.50Å 163.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.20 81.65 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.20) 87.8 (81.65-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.74 (at 2.20Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.175 , (Not available) 0.162 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 71.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6390	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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: 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	D	0.96	1/835 (0.1%)	1.67	11/1124 (1.0%)
1	E	0.99	1/835 (0.1%)	1.72	10/1124 (0.9%)
1	F	0.96	1/835 (0.1%)	1.71	12/1124 (1.1%)
1	G	1.00	1/835 (0.1%)	1.81	23/1124 (2.0%)
1	H	1.00	1/835 (0.1%)	1.84	19/1124 (1.7%)
2	A	1.12	9/1579 (0.6%)	1.77	37/2147 (1.7%)
3	C	0.93	0/388	1.84	11/520 (2.1%)
All	All	1.02	14/6142 (0.2%)	1.76	123/8287 (1.5%)

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	D	0	1
1	E	0	1
1	H	0	1
All	All	0	3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	44	HIS	CD2-NE2	-7.04	1.30	1.37
1	F	57	HIS	CD2-NE2	-6.76	1.30	1.37
2	A	182	HIS	CD2-NE2	-6.58	1.30	1.37
2	A	27	HIS	CD2-NE2	-6.58	1.30	1.37
1	H	57	HIS	CD2-NE2	-6.52	1.30	1.37
2	A	70	HIS	CD2-NE2	-6.52	1.30	1.37
2	A	181	HIS	CD2-NE2	-6.30	1.30	1.37
2	A	171	HIS	CD2-NE2	-6.18	1.31	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	140	HIS	CD2-NE2	-6.05	1.31	1.37
1	D	57	HIS	CD2-NE2	-5.71	1.31	1.37
1	E	57	HIS	CD2-NE2	-5.70	1.31	1.37
2	A	107	HIS	CD2-NE2	-5.40	1.31	1.37
1	G	99	ILE	CB-CG1	-5.13	1.43	1.53
2	A	44	HIS	CG-ND1	-5.02	1.32	1.38

All (123) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	103	ASN	CA-CB-CG	8.42	121.02	112.60
2	A	170	ASP	CA-CB-CG	8.03	120.63	112.60
1	G	99	ILE	CB-CG1-CD1	-7.94	97.13	113.80
1	G	103	ASN	CA-CB-CG	-7.73	104.87	112.60
1	G	50	VAL	N-CA-C	-7.72	96.72	107.99
1	G	21	ASN	OD1-CG-ND2	-7.71	114.89	122.60
1	G	102	LYS	O-C-N	7.65	132.70	123.36
3	C	237	ARG	CA-CB-CG	7.60	129.30	114.10
1	E	50	VAL	N-CA-C	-7.55	96.97	107.99
1	F	57	HIS	CB-CG-CD2	-7.40	121.58	131.20
1	H	94	ASN	OD1-CG-ND2	-7.36	115.24	122.60
1	F	70	ASP	CA-CB-CG	7.25	119.85	112.60
1	D	57	HIS	CB-CG-CD2	-7.17	121.87	131.20
3	C	197	ASP	CA-CB-CG	7.13	119.73	112.60
1	E	1	ALA	CA-C-N	7.11	127.10	119.78
1	E	1	ALA	C-N-CA	7.11	127.10	119.78
1	H	57	HIS	CB-CG-CD2	-7.00	122.09	131.20
1	H	102	LYS	CA-C-N	6.97	134.25	121.70
1	H	102	LYS	C-N-CA	6.97	134.25	121.70
1	D	70	ASP	CA-CB-CG	6.96	119.56	112.60
1	E	3	GLN	CA-CB-CG	-6.95	100.21	114.10
3	C	215	GLN	OE1-CD-NE2	-6.82	115.78	122.60
1	H	61	GLN	OE1-CD-NE2	-6.76	115.84	122.60
1	H	94	ASN	CB-CG-ND2	6.75	126.53	116.40
2	A	78	SER	N-CA-C	6.63	119.35	111.33
2	A	49	GLN	OE1-CD-NE2	-6.60	116.00	122.60
1	G	1	ALA	CA-C-O	-6.56	109.64	120.80
1	G	69	LYS	CG-CD-CE	6.56	126.38	111.30
1	G	90	ASN	OD1-CG-ND2	-6.54	116.06	122.60
1	H	95	SER	CB-CA-C	-6.53	99.09	109.80
1	G	73	ARG	NE-CZ-NH2	-6.49	113.36	119.20
1	H	58	ILE	N-CA-C	-6.43	103.04	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	93	ASN	OD1-CG-ND2	-6.36	116.24	122.60
1	F	57	HIS	CB-CG-ND1	6.35	132.22	122.70
2	A	171	HIS	CB-CG-CD2	-6.33	122.97	131.20
1	D	94	ASN	OD1-CG-ND2	-6.32	116.28	122.60
1	E	57	HIS	CB-CG-CD2	-6.29	123.02	131.20
2	A	53	VAL	N-CA-C	-6.29	101.46	109.58
1	E	62	LYS	CG-CD-CE	-6.20	97.03	111.30
1	H	58	ILE	CB-CG1-CD1	6.20	126.82	113.80
2	A	12	PRO	CA-C-N	6.16	125.65	119.24
2	A	12	PRO	C-N-CA	6.16	125.65	119.24
2	A	154	ASN	CA-CB-CG	-6.13	106.47	112.60
2	A	93	ASN	CA-CB-CG	6.12	118.72	112.60
3	C	234	ASN	CA-CB-CG	6.10	118.70	112.60
3	C	214	TYR	N-CA-C	-6.08	104.73	111.36
3	C	236	ILE	CA-CB-CG1	-6.07	100.09	110.40
1	G	102	LYS	CA-C-N	6.07	132.62	121.70
1	G	102	LYS	C-N-CA	6.07	132.62	121.70
1	F	13	ARG	CA-CB-CG	6.06	126.21	114.10
2	A	27	HIS	CB-CG-CD2	-6.04	123.35	131.20
2	A	37	MET	N-CA-CB	-6.02	101.00	110.69
1	F	82	ILE	N-CA-C	-6.02	99.76	108.36
1	G	86	CYS	N-CA-C	-5.98	99.49	109.24
1	G	99	ILE	CB-CA-C	-5.95	100.06	110.71
1	D	90	ASN	OD1-CG-ND2	-5.94	116.66	122.60
2	A	105	SER	CA-C-N	5.91	125.61	119.05
2	A	105	SER	C-N-CA	5.91	125.61	119.05
1	G	89	ASN	OD1-CG-ND2	-5.85	116.75	122.60
1	H	88	TRP	CG-CD2-CE3	5.82	139.72	133.90
1	F	51	GLU	CA-CB-CG	5.82	125.74	114.10
1	H	49	GLN	OE1-CD-NE2	-5.79	116.81	122.60
2	A	182	HIS	CB-CG-CD2	-5.79	123.67	131.20
1	E	88	TRP	CB-CG-CD1	-5.79	118.22	126.90
1	H	41	THR	N-CA-CB	-5.78	100.77	111.53
1	D	50	VAL	N-CA-C	-5.76	99.58	107.99
2	A	44	HIS	CB-CG-CD2	-5.73	123.75	131.20
1	H	22	ASP	CA-CB-CG	5.72	118.32	112.60
2	A	93	ASN	CB-CG-ND2	5.72	124.98	116.40
1	G	100	SER	CA-CB-OG	-5.70	99.69	111.10
2	A	174	TRP	CG-CD2-CE3	5.70	139.60	133.90
2	A	96	ASN	OD1-CG-ND2	-5.70	116.90	122.60
2	A	107	HIS	CB-CG-CD2	-5.69	123.80	131.20
1	H	95	SER	N-CA-CB	5.66	119.49	110.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	102	LYS	O-C-N	5.65	129.92	123.31
1	G	1	ALA	CA-C-N	5.65	125.65	119.89
1	G	1	ALA	C-N-CA	5.65	125.65	119.89
1	H	61	GLN	CG-CD-NE2	5.64	124.86	116.40
1	G	3	GLN	OE1-CD-NE2	-5.63	116.97	122.60
1	E	94	ASN	OD1-CG-ND2	-5.62	116.98	122.60
2	A	107	HIS	CA-C-N	5.62	124.81	118.97
2	A	107	HIS	C-N-CA	5.62	124.81	118.97
2	A	41	LEU	N-CA-C	5.61	117.40	111.28
1	D	57	HIS	CB-CG-ND1	5.61	131.11	122.70
1	D	80	THR	CA-CB-OG1	-5.58	101.22	109.60
3	C	235	ARG	CG-CD-NE	-5.57	99.75	112.00
1	E	88	TRP	CG-CD2-CE3	5.51	139.41	133.90
2	A	107	HIS	CB-CG-ND1	5.51	130.97	122.70
2	A	132	PHE	CA-CB-CG	-5.51	108.28	113.80
2	A	140	HIS	N-CA-C	-5.45	100.35	109.24
2	A	113	VAL	O-C-N	-5.44	117.43	123.20
2	A	74	GLN	OE1-CD-NE2	-5.43	117.17	122.60
1	G	9	CYS	CA-C-N	5.37	128.22	120.38
1	G	9	CYS	C-N-CA	5.37	128.22	120.38
3	C	235	ARG	NE-CZ-NH2	-5.36	114.38	119.20
3	C	239	GLU	CA-C-N	5.36	131.34	121.70
3	C	239	GLU	C-N-CA	5.36	131.34	121.70
1	D	94	ASN	CB-CG-ND2	5.35	124.43	116.40
2	A	174	TRP	CE2-CD2-CG	-5.33	100.80	107.20
2	A	140	HIS	CB-CG-CD2	-5.32	124.28	131.20
3	C	239	GLU	O-C-N	5.28	129.61	122.59
1	H	57	HIS	CB-CG-ND1	5.27	130.60	122.70
1	D	97	ALA	N-CA-C	-5.26	106.54	113.12
1	F	52	VAL	CA-C-N	5.25	125.17	119.76
1	F	52	VAL	C-N-CA	5.25	125.17	119.76
1	F	50	VAL	N-CA-C	-5.24	100.34	107.99
1	G	17	ILE	N-CA-C	-5.24	100.84	108.17
1	F	94	ASN	OD1-CG-ND2	-5.23	117.37	122.60
2	A	127	TRP	CG-CD2-CE3	5.22	139.12	133.90
2	A	1	ASN	CA-C-N	5.21	125.05	120.10
2	A	1	ASN	C-N-CA	5.21	125.05	120.10
2	A	11	ARG	CA-C-N	5.20	125.73	120.38
2	A	11	ARG	C-N-CA	5.20	125.73	120.38
1	H	52	VAL	N-CA-C	-5.13	104.25	109.02
1	D	49	GLN	OE1-CD-NE2	-5.13	117.47	122.60
1	D	103	ASN	CA-CB-CG	5.10	117.70	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	90	ASN	OD1-CG-ND2	-5.10	117.50	122.60
1	G	59	ASP	N-CA-C	5.08	117.71	111.82
2	A	136	ASP	N-CA-C	-5.08	100.80	108.67
1	G	90	ASN	CA-CB-CG	5.07	117.67	112.60
2	A	181	HIS	CB-CG-CD2	-5.05	124.64	131.20
1	H	82	ILE	CA-CB-CG1	-5.04	101.83	110.40
1	F	35	ARG	N-CA-C	-5.03	104.41	110.44

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	76	TYR	Sidechain
1	E	76	TYR	Sidechain
1	H	76	TYR	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	D	824	0	841	9	0
1	E	824	0	841	9	0
1	F	824	0	841	8	0
1	G	824	0	841	5	0
1	H	824	0	841	7	0
2	A	1531	0	1423	15	0
3	C	384	0	361	3	0
4	D	12	0	12	0	0
4	E	12	0	12	0	0
4	F	12	0	12	1	0
4	G	12	0	12	0	0
4	H	12	0	12	0	0
5	A	58	0	0	0	0
5	C	21	0	0	0	0
5	D	52	0	0	1	0
5	E	44	0	0	0	0
5	F	29	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	52	0	0	0	0
5	H	39	0	0	1	0
All	All	6390	0	6049	47	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 4.

All (47) 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:G:3:GLN:HE22	1:H:92:THR:HG22	1.43	0.83
1:E:85:LEU:HD23	1:E:99:ILE:HG22	1.64	0.80
1:F:103:ASN:HB2	2:A:151:ARG:HH12	1.64	0.63
1:H:37:MET:HE2	1:H:52:VAL:HG23	1.81	0.62
2:A:94:MET:HB2	2:A:155:ILE:HD12	1.81	0.61
1:D:44:SER:OG	1:D:46:GLU:HG3	2.01	0.60
1:F:25:LEU:HB2	1:F:43:LYS:HD2	1.85	0.59
1:H:75:THR:HG21	1:H:82:ILE:HD11	1.83	0.59
1:E:85:LEU:CD2	1:E:99:ILE:HG22	2.33	0.57
1:E:49:GLN:HB3	1:E:93:PRO:HG2	1.86	0.57
1:G:20:ILE:HG21	1:G:42:PHE:CE1	2.42	0.54
1:G:3:GLN:NE2	1:H:92:THR:HG22	2.18	0.53
1:F:91:LYS:HD3	4:F:104:GAL:O3	2.09	0.53
1:D:11:GLU:OE1	1:E:35:ARG:HD2	2.08	0.53
1:H:63:LYS:HG3	5:H:130:HOH:O	2.09	0.52
1:E:3:GLN:HG2	1:F:93:PRO:HD3	1.91	0.52
1:D:90:ASN:O	1:D:91:LYS:HD2	2.10	0.51
1:F:82:ILE:HD12	1:F:99:ILE:HD11	1.94	0.50
2:A:23:MET:HE1	2:A:30:TYR:CD1	2.47	0.49
1:G:15:THR:HA	1:G:87:VAL:O	2.13	0.48
2:A:125:TYR:CZ	2:A:141:ARG:HD3	2.47	0.48
1:E:62:LYS:HE3	3:C:240:LEU:HA	1.94	0.48
1:F:14:ASN:O	1:F:88:TRP:HA	2.13	0.48
2:A:172:GLN:HA	2:A:175:ARG:HE	1.79	0.48
1:E:15:THR:HA	1:E:87:VAL:O	2.14	0.48
1:H:88:TRP:HE3	1:H:95:SER:HB2	1.79	0.47
1:H:15:THR:HA	1:H:87:VAL:O	2.15	0.47
2:A:23:MET:HE1	2:A:30:TYR:HD1	1.79	0.47
2:A:129:ARG:HH12	2:A:131:ASN:HD21	1.63	0.47
2:A:94:MET:CB	2:A:155:ILE:HD12	2.46	0.46
1:D:4:THR:HB	5:D:143:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:99:ILE:HD13	1:E:99:ILE:HG21	1.75	0.45
1:D:2:PRO:HA	1:D:7:GLU:OE2	2.17	0.45
1:F:15:THR:HA	1:F:87:VAL:O	2.16	0.44
1:D:12:TYR:OH	1:E:35:ARG:HG3	2.18	0.44
2:A:129:ARG:NH1	2:A:131:ASN:HD21	2.16	0.44
2:A:186:GLY:O	3:C:199:CYS:HB2	2.18	0.43
1:D:15:THR:HA	1:D:87:VAL:O	2.18	0.42
1:G:102:LYS:O	1:G:103:ASN:HB2	2.19	0.42
2:A:155:ILE:HD13	2:A:155:ILE:HA	1.75	0.42
1:F:71:THR:O	1:F:75:THR:HG23	2.20	0.42
2:A:172:GLN:HA	2:A:175:ARG:NE	2.35	0.42
2:A:125:TYR:O	2:A:141:ARG:HD2	2.20	0.42
1:D:34:LYS:HE2	1:D:34:LYS:HB2	1.84	0.41
1:D:59:ASP:HB3	3:C:239:GLU:HG2	2.01	0.41
2:A:12:PRO:HA	2:A:13:PRO:HD3	1.86	0.41
2:A:53:VAL:O	2:A:54:ARG:C	2.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
1	E	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
1	F	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
1	G	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
1	H	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
2	A	186/188 (99%)	179 (96%)	7 (4%)	0	100	100
3	C	43/49 (88%)	41 (95%)	1 (2%)	1 (2%)	5	3
All	All	734/752 (98%)	716 (98%)	17 (2%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	237	ARG

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	D	95/95 (100%)	92 (97%)	3 (3%)	34	47
1	E	95/95 (100%)	89 (94%)	6 (6%)	16	19
1	F	95/95 (100%)	89 (94%)	6 (6%)	16	19
1	G	95/95 (100%)	88 (93%)	7 (7%)	13	14
1	H	95/95 (100%)	91 (96%)	4 (4%)	26	36
2	A	157/157 (100%)	147 (94%)	10 (6%)	16	19
3	C	44/48 (92%)	41 (93%)	3 (7%)	14	17
All	All	676/680 (99%)	637 (94%)	39 (6%)	18	22

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	21	ASN
1	D	91	LYS
1	D	101	MET
1	E	8	LEU
1	E	11	GLU
1	E	35	ARG
1	E	55	SER
1	E	62	LYS
1	E	91	LYS
1	F	6	THR
1	F	43	LYS
1	F	55	SER
1	F	59	ASP
1	F	91	LYS
1	F	103	ASN

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Mol	Chain	Res	Type
1	G	11	GLU
1	G	35	ARG
1	G	55	SER
1	G	91	LYS
1	G	99	ILE
1	G	100	SER
1	G	103	ASN
1	H	41	THR
1	H	56	GLN
1	H	58	ILE
1	H	63	LYS
2	A	13	PRO
2	A	17	LYS
2	A	50	THR
2	A	55	TYR
2	A	67	ARG
2	A	81	SER
2	A	88	ILE
2	A	116	LEU
2	A	141	ARG
2	A	154	ASN
3	C	234	ASN
3	C	235	ARG
3	C	239	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	16	GLN
1	D	21	ASN
1	D	49	GLN
1	E	49	GLN
1	E	103	ASN
1	G	3	GLN
1	G	49	GLN
1	H	49	GLN
2	A	1	ASN
2	A	27	HIS
2	A	131	ASN
3	C	215	GLN
3	C	234	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 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$
4	GAL	G	104	-	12,12,12	0.86	0	17,17,17	0.68	0
4	GAL	H	104	-	12,12,12	0.74	0	17,17,17	0.90	0
4	GAL	F	104	-	12,12,12	1.01	1 (8%)	17,17,17	0.87	1 (5%)
4	GAL	D	104	-	12,12,12	0.69	0	17,17,17	0.66	0
4	GAL	E	104	-	12,12,12	0.66	0	17,17,17	0.54	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
4	GAL	G	104	-	-	0/2/22/22	0/1/1/1
4	GAL	H	104	-	-	0/2/22/22	0/1/1/1
4	GAL	F	104	-	-	2/2/22/22	0/1/1/1
4	GAL	D	104	-	-	0/2/22/22	0/1/1/1
4	GAL	E	104	-	-	0/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	104	GAL	C4-C3	2.09	1.57	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	104	GAL	O5-C5-C6	2.02	111.44	106.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	104	GAL	O5-C5-C6-O6
4	F	104	GAL	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	104	GAL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	D	103/103 (100%)	-0.78	0 100 100	6, 16, 33, 52	0
1	E	103/103 (100%)	-0.75	0 100 100	8, 16, 32, 49	0
1	F	103/103 (100%)	-0.53	2 (1%) 66 63	9, 21, 40, 52	0
1	G	103/103 (100%)	-0.58	0 100 100	8, 19, 36, 48	0
1	H	103/103 (100%)	-0.61	0 100 100	9, 18, 36, 53	0
2	A	188/188 (100%)	-0.16	8 (4%) 40 36	10, 24, 56, 109	0
3	C	45/49 (91%)	0.19	6 (13%) 7 5	11, 23, 90, 99	0
All	All	748/752 (99%)	-0.47	16 (2%) 63 60	6, 20, 47, 109	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	240	LEU	8.8
2	A	1	ASN	7.3
2	A	2	GLY	5.3
3	C	239	GLU	4.8
3	C	238	ASP	4.1
2	A	36	GLN	3.8
2	A	175	ARG	3.1
1	F	103	ASN	3.0
3	C	197	ASP	3.0
3	C	196	GLY	2.8
2	A	109	TYR	2.7
2	A	35	THR	2.6
2	A	138	ARG	2.4
3	C	237	ARG	2.1
1	F	43	LYS	2.0
2	A	3	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
4	GAL	E	104	12/12	0.91	0.09	26,34,38,40	0
4	GAL	G	104	12/12	0.91	0.09	31,37,43,45	0
4	GAL	H	104	12/12	0.91	0.09	32,34,40,41	0
4	GAL	D	104	12/12	0.92	0.07	25,27,33,40	0
4	GAL	F	104	12/12	0.92	0.08	39,40,42,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.