



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:18 PM UTC

PDB ID : 6H4C / pdb_00006h4c
Title : A polyamorous repressor: deciphering the evolutionary strategy used by the phage-inducible chromosomal islands to spread in nature.
Authors : Ciges-Tomas, J.R.; Alite, C.; Bowring, J.Z.; Donderis, J.; Penades, J.R.; Marina, A.
Deposited on : 2018-07-20
Resolution : 2.52 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:

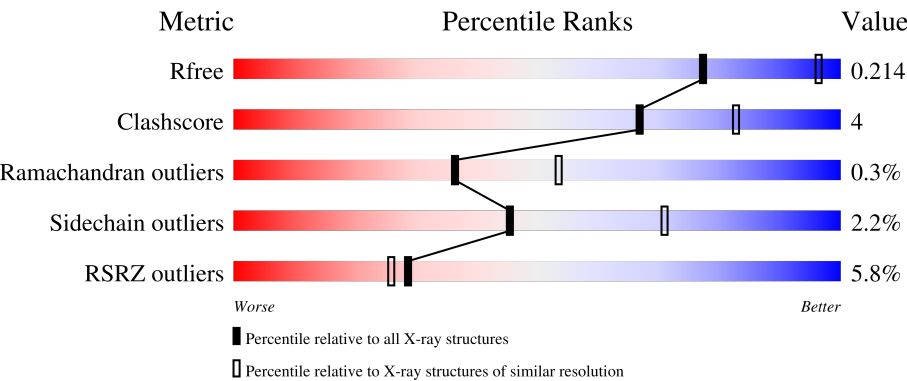
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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.



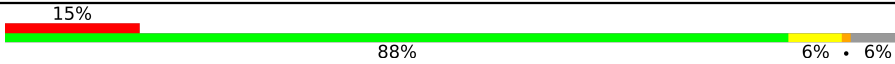
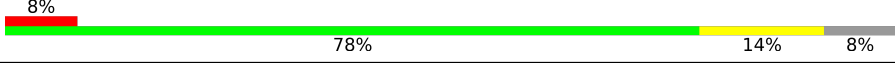
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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	191	2% 72% 7% • 20%
1	C	191	2% 72% 8% • 20%
1	E	191	3% 74% 7% • 19%
1	G	191	4% 77% • • 19%
2	B	157	3% 86% 6% • 6%

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Mol	Chain	Length	Quality of chain
2	D	157	
2	F	157	
2	H	157	

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	C	201	-	-	X	-
5	PEG	E	201	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9321 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 dUTPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1162	735	195	231	1			
1	C	153	Total	C	N	O	S	0	0	0
			1161	735	196	229	1			
1	E	154	Total	C	N	O	S	0	0	0
			1158	732	196	228	2			
1	G	155	Total	C	N	O	S	0	0	0
			1171	741	197	232	1			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP Q8SDV3
A	-20	HIS	-	expression tag	UNP Q8SDV3
A	-19	HIS	-	expression tag	UNP Q8SDV3
A	-18	HIS	-	expression tag	UNP Q8SDV3
A	-17	HIS	-	expression tag	UNP Q8SDV3
A	-16	HIS	-	expression tag	UNP Q8SDV3
A	-15	HIS	-	expression tag	UNP Q8SDV3
A	-14	SER	-	expression tag	UNP Q8SDV3
A	-13	SER	-	expression tag	UNP Q8SDV3
A	-12	GLY	-	expression tag	UNP Q8SDV3
A	-11	VAL	-	expression tag	UNP Q8SDV3
A	-10	ASP	-	expression tag	UNP Q8SDV3
A	-9	LEU	-	expression tag	UNP Q8SDV3
A	-8	GLY	-	expression tag	UNP Q8SDV3
A	-7	THR	-	expression tag	UNP Q8SDV3
A	-6	GLU	-	expression tag	UNP Q8SDV3
A	-5	ASN	-	expression tag	UNP Q8SDV3
A	-4	LEU	-	expression tag	UNP Q8SDV3
A	-3	TYR	-	expression tag	UNP Q8SDV3
A	-2	PHE	-	expression tag	UNP Q8SDV3
A	-1	GLN	-	expression tag	UNP Q8SDV3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q8SDV3
C	-21	MET	-	initiating methionine	UNP Q8SDV3
C	-20	HIS	-	expression tag	UNP Q8SDV3
C	-19	HIS	-	expression tag	UNP Q8SDV3
C	-18	HIS	-	expression tag	UNP Q8SDV3
C	-17	HIS	-	expression tag	UNP Q8SDV3
C	-16	HIS	-	expression tag	UNP Q8SDV3
C	-15	HIS	-	expression tag	UNP Q8SDV3
C	-14	SER	-	expression tag	UNP Q8SDV3
C	-13	SER	-	expression tag	UNP Q8SDV3
C	-12	GLY	-	expression tag	UNP Q8SDV3
C	-11	VAL	-	expression tag	UNP Q8SDV3
C	-10	ASP	-	expression tag	UNP Q8SDV3
C	-9	LEU	-	expression tag	UNP Q8SDV3
C	-8	GLY	-	expression tag	UNP Q8SDV3
C	-7	THR	-	expression tag	UNP Q8SDV3
C	-6	GLU	-	expression tag	UNP Q8SDV3
C	-5	ASN	-	expression tag	UNP Q8SDV3
C	-4	LEU	-	expression tag	UNP Q8SDV3
C	-3	TYR	-	expression tag	UNP Q8SDV3
C	-2	PHE	-	expression tag	UNP Q8SDV3
C	-1	GLN	-	expression tag	UNP Q8SDV3
C	0	SER	-	expression tag	UNP Q8SDV3
E	-21	MET	-	initiating methionine	UNP Q8SDV3
E	-20	HIS	-	expression tag	UNP Q8SDV3
E	-19	HIS	-	expression tag	UNP Q8SDV3
E	-18	HIS	-	expression tag	UNP Q8SDV3
E	-17	HIS	-	expression tag	UNP Q8SDV3
E	-16	HIS	-	expression tag	UNP Q8SDV3
E	-15	HIS	-	expression tag	UNP Q8SDV3
E	-14	SER	-	expression tag	UNP Q8SDV3
E	-13	SER	-	expression tag	UNP Q8SDV3
E	-12	GLY	-	expression tag	UNP Q8SDV3
E	-11	VAL	-	expression tag	UNP Q8SDV3
E	-10	ASP	-	expression tag	UNP Q8SDV3
E	-9	LEU	-	expression tag	UNP Q8SDV3
E	-8	GLY	-	expression tag	UNP Q8SDV3
E	-7	THR	-	expression tag	UNP Q8SDV3
E	-6	GLU	-	expression tag	UNP Q8SDV3
E	-5	ASN	-	expression tag	UNP Q8SDV3
E	-4	LEU	-	expression tag	UNP Q8SDV3
E	-3	TYR	-	expression tag	UNP Q8SDV3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	PHE	-	expression tag	UNP Q8SDV3
E	-1	GLN	-	expression tag	UNP Q8SDV3
E	0	SER	-	expression tag	UNP Q8SDV3
G	-21	MET	-	initiating methionine	UNP Q8SDV3
G	-20	HIS	-	expression tag	UNP Q8SDV3
G	-19	HIS	-	expression tag	UNP Q8SDV3
G	-18	HIS	-	expression tag	UNP Q8SDV3
G	-17	HIS	-	expression tag	UNP Q8SDV3
G	-16	HIS	-	expression tag	UNP Q8SDV3
G	-15	HIS	-	expression tag	UNP Q8SDV3
G	-14	SER	-	expression tag	UNP Q8SDV3
G	-13	SER	-	expression tag	UNP Q8SDV3
G	-12	GLY	-	expression tag	UNP Q8SDV3
G	-11	VAL	-	expression tag	UNP Q8SDV3
G	-10	ASP	-	expression tag	UNP Q8SDV3
G	-9	LEU	-	expression tag	UNP Q8SDV3
G	-8	GLY	-	expression tag	UNP Q8SDV3
G	-7	THR	-	expression tag	UNP Q8SDV3
G	-6	GLU	-	expression tag	UNP Q8SDV3
G	-5	ASN	-	expression tag	UNP Q8SDV3
G	-4	LEU	-	expression tag	UNP Q8SDV3
G	-3	TYR	-	expression tag	UNP Q8SDV3
G	-2	PHE	-	expression tag	UNP Q8SDV3
G	-1	GLN	-	expression tag	UNP Q8SDV3
G	0	SER	-	expression tag	UNP Q8SDV3

- Molecule 2 is a protein called Orf20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	147	Total	C	N	O	S	0	0	0
			1116	716	175	223	2			
2	D	148	Total	C	N	O	S	0	0	0
			1075	690	173	210	2			
2	F	144	Total	C	N	O	S	0	0	0
			1129	728	177	222	2			
2	H	145	Total	C	N	O	S	0	0	0
			1100	712	174	212	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP Q9F0J8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	GLY	-	expression tag	UNP Q9F0J8
F	0	GLY	-	expression tag	UNP Q9F0J8
H	0	GLY	-	expression tag	UNP Q9F0J8

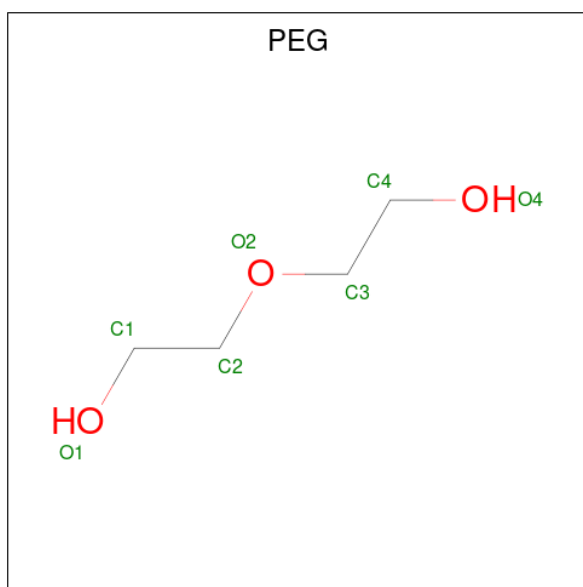
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	G	1	Total Mg 1 1	0	0

- Molecule 4 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Ni 1 1	0	0
4	B	1	Total Ni 1 1	0	0
4	C	1	Total Ni 1 1	0	0
4	E	1	Total Ni 1 1	0	0
4	H	1	Total Ni 1 1	0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	46	Total	O	0	0
			46	46		
6	B	18	Total	O	0	0
			18	18		
6	C	40	Total	O	0	0
			40	40		
6	D	12	Total	O	0	0
			12	12		
6	E	28	Total	O	0	0
			28	28		

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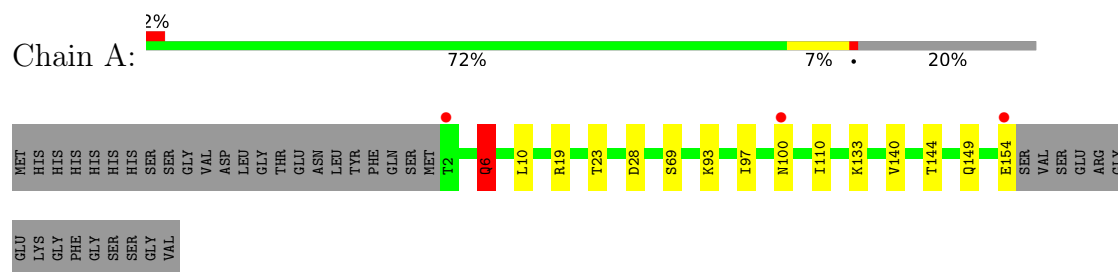
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	13	Total 13	O 13	0	0
6	G	29	Total 29	O 29	0	0
6	H	7	Total 7	O 7	0	0

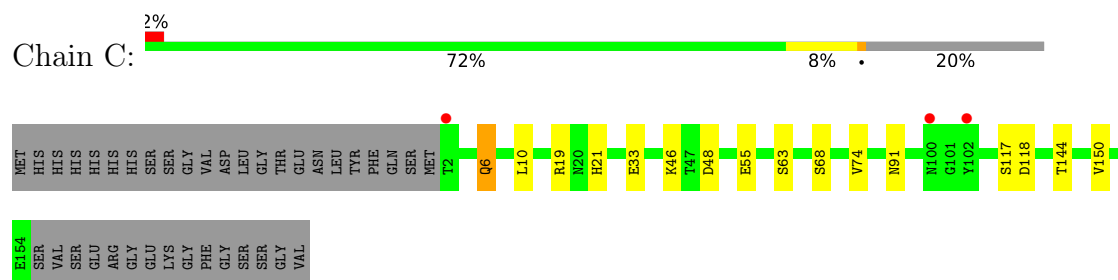
3 Residue-property plots [i](#)

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.

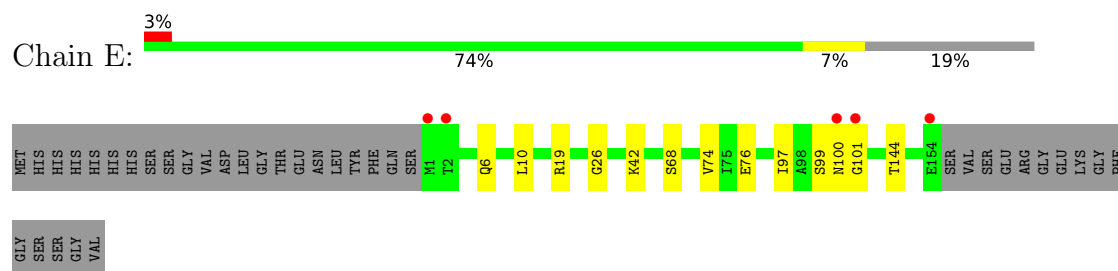
- Molecule 1: dUTPase



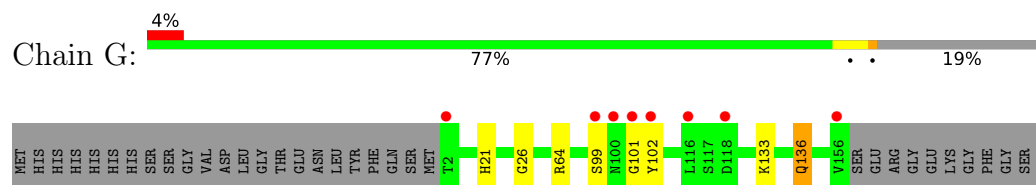
- Molecule 1: dUTPase



- Molecule 1: dUTPase



- Molecule 1: dUTPase



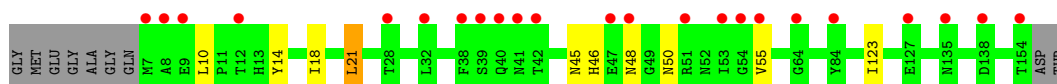
- Molecule 2: Orf20

Chain B:  3% 86% 6% • 6%



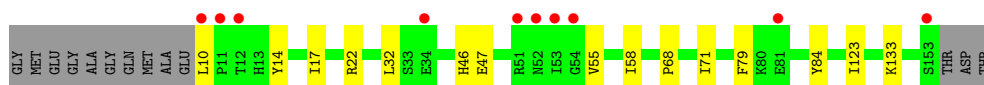
• Molecule 2: Orf20

Chain D:  15% 88% 6% • 6%



• Molecule 2: Orf20

Chain F:  6% 82% 10% 8%



• Molecule 2: Orf20

Chain H:  8% 78% 14% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.49Å 144.49Å 149.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	95.93 – 2.52 95.93 – 2.52	Depositor EDS
% Data completeness (in resolution range)	100.0 (95.93-2.52) 100.0 (95.93-2.52)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.197 , 0.242 0.215 , 0.214	Depositor DCC
R_{free} test set	3122 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.016 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9321	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% 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: MG, PEG, NI

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.66	0/1181	0.93	3/1607 (0.2%)
1	C	0.69	0/1180	0.97	3/1605 (0.2%)
1	E	0.66	0/1177	0.90	1/1602 (0.1%)
1	G	0.67	0/1190	0.96	1/1619 (0.1%)
2	B	0.56	0/1140	0.84	2/1557 (0.1%)
2	D	0.52	0/1098	0.95	2/1501 (0.1%)
2	F	0.56	0/1154	0.86	1/1568 (0.1%)
2	H	0.47	0/1125	0.79	0/1534
All	All	0.60	0/9245	0.90	13/12593 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	46	HIS	N-CA-CB	6.17	119.28	110.16
1	A	6	GLN	N-CA-C	6.08	119.18	110.24
2	D	46	HIS	N-CA-C	-5.89	104.78	111.14
1	A	140	VAL	CA-C-N	5.86	125.76	119.85
1	A	140	VAL	C-N-CA	5.86	125.76	119.85
2	D	46	HIS	N-CA-CB	5.54	118.10	110.07
1	C	6	GLN	N-CA-C	5.52	118.24	110.23
2	B	45	ASN	CA-C-N	5.22	127.53	120.44
2	B	45	ASN	C-N-CA	5.22	127.53	120.44
1	E	26	GLY	N-CA-C	5.17	118.69	111.14
1	G	26	GLY	N-CA-C	5.13	118.59	111.10
1	C	63	SER	N-CA-C	5.10	117.43	110.55
1	C	33	GLU	N-CA-C	5.02	115.67	108.74

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	1162	0	1142	14	0
1	C	1161	0	1147	14	0
1	E	1158	0	1135	10	0
1	G	1171	0	1149	3	0
2	B	1116	0	994	8	0
2	D	1075	0	910	6	0
2	F	1129	0	1037	8	0
2	H	1100	0	980	13	0
3	A	1	0	0	0	0
3	G	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	H	1	0	0	0	0
5	C	21	0	27	9	0
5	D	7	0	10	0	0
5	E	14	0	19	4	0
5	H	7	0	10	0	0
6	A	46	0	0	0	0
6	B	18	0	0	0	0
6	C	40	0	0	0	0
6	D	12	0	0	0	0
6	E	28	0	0	0	0
6	F	13	0	0	0	0
6	G	29	0	0	0	0
6	H	7	0	0	0	0
All	All	9321	0	8560	66	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 (66) 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:C:68:SER:HB2	5:C:201:PEG:H42	1.62	0.80
2:H:36:THR:HG23	2:H:38:PHE:H	1.50	0.76
2:D:45:ASN:HB2	2:D:50:ASN:HB2	1.67	0.75
2:H:20:THR:HG21	2:H:88:LEU:HD21	1.69	0.72
1:C:74:VAL:HG22	5:C:201:PEG:H31	1.75	0.69
2:H:16:THR:O	2:H:20:THR:HG22	1.94	0.67
2:B:44:SER:O	2:B:48:ASN:HB3	1.95	0.67
5:C:201:PEG:H41	1:E:76:GLU:CD	2.18	0.67
1:E:74:VAL:HG22	5:E:201:PEG:H32	1.77	0.66
2:D:45:ASN:HB2	2:D:50:ASN:CB	2.29	0.61
2:B:41:ASN:O	2:B:45:ASN:ND2	2.34	0.60
2:H:33:SER:HA	2:H:36:THR:HG22	1.84	0.59
2:D:10:LEU:HD11	2:D:55:VAL:HA	1.85	0.58
5:C:201:PEG:H12	1:E:42:LYS:NZ	2.17	0.58
2:H:41:ASN:O	2:H:45:ASN:ND2	2.36	0.57
1:A:149:GLN:OE1	2:F:55:VAL:HG11	2.04	0.57
1:A:93:LYS:HD2	5:E:201:PEG:H12	1.87	0.56
1:A:97:ILE:HG12	1:E:97:ILE:HD11	1.87	0.55
2:B:48:ASN:HD21	2:B:50:ASN:ND2	2.06	0.54
2:F:68:PRO:HB2	2:F:71:ILE:HD12	1.90	0.54
1:C:117:SER:OG	1:C:118:ASP:N	2.41	0.53
2:B:22:ARG:NH2	2:B:47:GLU:OE2	2.43	0.52
1:A:19:ARG:NH1	1:C:144:THR:HB	2.24	0.52
1:C:68:SER:CB	5:C:201:PEG:H42	2.35	0.52
2:F:10:LEU:HD11	2:F:55:VAL:HA	1.91	0.52
2:B:48:ASN:ND2	2:B:50:ASN:H	2.07	0.51
1:A:19:ARG:HH12	1:C:144:THR:HB	1.75	0.51
1:A:23:THR:HG22	1:C:55:GLU:HG3	1.92	0.51
1:E:99:SER:O	1:E:101:GLY:N	2.43	0.51
2:H:14:TYR:O	2:H:18:ILE:HG13	2.11	0.51
2:B:48:ASN:HD21	2:B:50:ASN:CG	2.20	0.48
2:D:14:TYR:O	2:D:18:ILE:HG13	2.14	0.47
2:H:35:ARG:NH1	2:H:64:GLY:O	2.47	0.47
1:C:46:LYS:HD2	1:C:48:ASP:OD1	2.15	0.47
1:A:154:GLU:HA	1:A:154:GLU:OE1	2.14	0.47
1:G:64:ARG:NH2	1:G:133:LYS:HE2	2.30	0.47
2:H:32:LEU:O	2:H:36:THR:HG22	2.15	0.47
2:F:22:ARG:HG3	2:F:32:LEU:HD22	1.97	0.46
1:A:6:GLN:HG2	1:C:150:VAL:HG21	1.96	0.46
2:H:22:ARG:NH2	2:H:47:GLU:OE2	2.48	0.46
5:C:201:PEG:H12	1:E:42:LYS:HZ3	1.81	0.44
2:F:22:ARG:NH2	2:F:47:GLU:OE2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:68:SER:HB2	5:E:201:PEG:O4	2.17	0.44
2:H:46:HIS:HD2	2:H:61:TYR:OH	1.99	0.44
1:A:28:ASP:OD2	1:A:133:LYS:HE3	2.19	0.43
1:A:69:SER:HB3	1:C:91:ASN:HD22	1.84	0.43
2:H:45:ASN:OD1	2:H:50:ASN:ND2	2.47	0.43
2:B:10:LEU:HD11	2:B:55:VAL:HA	2.01	0.43
2:B:22:ARG:NH2	2:B:47:GLU:OE1	2.52	0.42
2:D:21:LEU:HA	2:D:21:LEU:HD13	1.81	0.42
1:C:74:VAL:HA	5:C:201:PEG:H31	2.01	0.42
1:A:69:SER:HB3	1:C:91:ASN:ND2	2.34	0.42
1:A:93:LYS:CD	5:E:201:PEG:H12	2.49	0.42
2:H:103:LYS:HD3	2:H:141:TYR:CE1	2.55	0.42
2:F:79:PHE:CE1	2:F:84:TYR:HA	2.55	0.42
1:A:28:ASP:CG	1:A:133:LYS:HE3	2.45	0.42
2:F:58:ILE:HD13	2:F:58:ILE:HA	1.94	0.42
5:C:201:PEG:H12	1:E:42:LYS:HZ2	1.84	0.41
1:A:144:THR:HB	1:E:19:ARG:NH1	2.36	0.41
1:G:64:ARG:HG2	1:G:136:GLN:HG2	2.03	0.41
2:D:48:ASN:CB	2:D:50:ASN:HD22	2.33	0.41
2:F:14:TYR:HA	2:F:17:ILE:HD12	2.02	0.41
1:C:19:ARG:NH1	1:E:144:THR:HB	2.36	0.41
1:C:21:HIS:CE1	5:C:203:PEG:H42	2.57	0.40
2:H:33:SER:HA	2:H:36:THR:CG2	2.52	0.40
1:G:64:ARG:CZ	1:G:133:LYS:HE2	2.52	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	A	151/191 (79%)	148 (98%)	2 (1%)	1 (1%)	18 32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	151/191 (79%)	149 (99%)	2 (1%)	0	100	100
1	E	152/191 (80%)	149 (98%)	2 (1%)	1 (1%)	18	32
1	G	153/191 (80%)	149 (97%)	2 (1%)	2 (1%)	9	17
2	B	145/157 (92%)	145 (100%)	0	0	100	100
2	D	146/157 (93%)	143 (98%)	3 (2%)	0	100	100
2	F	142/157 (90%)	139 (98%)	3 (2%)	0	100	100
2	H	143/157 (91%)	140 (98%)	3 (2%)	0	100	100
All	All	1183/1392 (85%)	1162 (98%)	17 (1%)	4 (0%)	36	53

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	E	100	ASN
1	G	102	TYR
1	G	101	GLY

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	124/162 (76%)	121 (98%)	3 (2%)	43	69
1	C	124/162 (76%)	122 (98%)	2 (2%)	55	78
1	E	122/162 (75%)	120 (98%)	2 (2%)	55	78
1	G	124/162 (76%)	121 (98%)	3 (2%)	43	69
2	B	110/141 (78%)	106 (96%)	4 (4%)	31	55
2	D	94/141 (67%)	92 (98%)	2 (2%)	47	72
2	F	115/141 (82%)	113 (98%)	2 (2%)	53	77
2	H	105/141 (74%)	103 (98%)	2 (2%)	50	74
All	All	918/1212 (76%)	898 (98%)	20 (2%)	45	71

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	10	LEU
1	A	110	ILE
2	B	42	THR
2	B	48	ASN
2	B	124	LYS
2	B	134	ILE
1	C	6	GLN
1	C	10	LEU
2	D	21	LEU
2	D	123	ILE
1	E	6	GLN
1	E	10	LEU
2	F	123	ILE
2	F	133	LYS
1	G	21	HIS
1	G	99	SER
1	G	136	GLN
2	H	69	SER
2	H	123	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	HIS
1	A	127	GLN
1	A	129	ASN
2	B	48	ASN
1	C	13	ASN
1	C	21	HIS
1	C	91	ASN
1	C	127	GLN
1	C	129	ASN
1	C	136	GLN
2	D	50	ASN
1	E	20	ASN
1	E	21	HIS
1	E	127	GLN
1	E	129	ASN
1	G	13	ASN
1	G	122	GLN

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Mol	Chain	Res	Type
2	H	46	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, 7 are monoatomic - leaving 7 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	$\# Z > 2$
5	PEG	C	201	-	6,6,6	1.22	0	5,5,5	0.52	0
5	PEG	C	202	-	6,6,6	0.92	0	5,5,5	0.66	0
5	PEG	C	203	-	6,6,6	0.83	0	5,5,5	0.55	0
5	PEG	H	201	-	6,6,6	0.82	0	5,5,5	0.46	0
5	PEG	D	201	-	6,6,6	0.83	0	5,5,5	0.54	0
5	PEG	E	201	-	6,6,6	1.25	0	5,5,5	0.25	0
5	PEG	E	202	-	6,6,6	0.76	0	5,5,5	0.64	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
5	PEG	C	201	-	-	3/4/4/4	-
5	PEG	C	202	-	-	2/4/4/4	-
5	PEG	C	203	-	-	4/4/4/4	-
5	PEG	H	201	-	-	2/4/4/4	-
5	PEG	D	201	-	-	2/4/4/4	-
5	PEG	E	201	-	-	1/4/4/4	-
5	PEG	E	202	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	203	PEG	O1-C1-C2-O2
5	D	201	PEG	O2-C3-C4-O4
5	D	201	PEG	O1-C1-C2-O2
5	E	201	PEG	O1-C1-C2-O2
5	C	201	PEG	C1-C2-O2-C3
5	C	203	PEG	O2-C3-C4-O4
5	C	201	PEG	O2-C3-C4-O4
5	E	202	PEG	C4-C3-O2-C2
5	E	202	PEG	C1-C2-O2-C3
5	H	201	PEG	C1-C2-O2-C3
5	C	202	PEG	C1-C2-O2-C3
5	C	202	PEG	C4-C3-O2-C2
5	H	201	PEG	C4-C3-O2-C2
5	C	203	PEG	C1-C2-O2-C3
5	C	201	PEG	O1-C1-C2-O2
5	C	203	PEG	C4-C3-O2-C2

There are no ring outliers.

3 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	201	PEG	8	0
5	C	203	PEG	1	0
5	E	201	PEG	4	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	A	153/191 (80%)	-0.27	3 (1%) 65 62	38, 47, 72, 118	0
1	C	153/191 (80%)	-0.23	3 (1%) 65 62	38, 48, 73, 87	0
1	E	154/191 (80%)	-0.15	5 (3%) 50 47	39, 50, 78, 132	0
1	G	155/191 (81%)	-0.08	8 (5%) 33 29	37, 49, 76, 127	0
2	B	147/157 (93%)	0.27	4 (2%) 56 52	39, 64, 91, 102	0
2	D	148/157 (94%)	0.76	23 (15%) 5 4	43, 78, 113, 120	0
2	F	144/157 (91%)	0.36	10 (6%) 23 20	39, 68, 110, 131	0
2	H	145/157 (92%)	0.50	13 (8%) 15 13	42, 74, 109, 140	0
All	All	1199/1392 (86%)	0.14	69 (5%) 29 26	37, 58, 103, 140	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	2	THR	6.0
2	H	135	ASN	4.3
2	F	12	THR	4.0
2	F	52	ASN	3.8
1	A	2	THR	3.7
1	E	154	GLU	3.7
2	D	38	PHE	3.7
1	G	101	GLY	3.7
1	E	101	GLY	3.6
2	H	138	ASP	3.6
2	D	12	THR	3.6
1	E	100	ASN	3.6
2	H	40	GLN	3.5
2	F	53	ILE	3.5
2	D	53	ILE	3.5
1	C	2	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	1	MET	3.4
2	D	32	LEU	3.4
2	D	39	SER	3.4
2	H	52	ASN	3.3
1	C	102	TYR	3.2
2	D	84	TYR	3.2
1	G	100	ASN	3.1
2	H	134	ILE	3.1
2	D	42	THR	3.0
2	D	9	GLU	3.0
2	D	7	MET	3.0
2	B	32	LEU	2.9
2	D	135	ASN	2.9
1	G	116	LEU	2.9
2	F	10	LEU	2.9
2	D	41	ASN	2.9
2	D	54	GLY	2.9
2	D	51	ARG	2.9
1	G	99	SER	2.9
2	D	47	GLU	2.8
2	D	138	ASP	2.7
2	D	40	GLN	2.7
1	G	118	ASP	2.6
1	A	154	GLU	2.6
2	D	154	THR	2.5
2	H	136	VAL	2.5
1	A	100	ASN	2.4
2	F	54	GLY	2.4
2	D	8	ALA	2.4
1	E	2	THR	2.4
2	H	139	ILE	2.4
2	H	9	GLU	2.4
2	H	42	THR	2.3
2	F	11	PRO	2.3
2	H	30	SER	2.3
2	B	9	GLU	2.3
2	F	51	ARG	2.3
2	F	153	SER	2.2
2	D	127	GLU	2.2
1	G	102	TYR	2.2
2	D	28	THR	2.2
2	H	51	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	48	ASN	2.1
2	H	53	ILE	2.1
2	F	34	GLU	2.1
1	C	100	ASN	2.1
2	D	64	GLY	2.1
1	G	156	VAL	2.0
2	B	8	ALA	2.0
2	F	81	GLU	2.0
2	D	55	VAL	2.0
2	H	10	LEU	2.0
2	B	154	THR	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(Å ²)	Q<0.9
5	PEG	E	201	7/7	0.82	0.19	49,55,66,66	0
5	PEG	C	203	7/7	0.85	0.17	81,89,93,98	0
5	PEG	C	201	7/7	0.85	0.18	41,53,58,63	0
5	PEG	C	202	7/7	0.86	0.15	69,77,89,92	0
4	NI	B	201	1/1	0.88	0.11	112,112,112,112	0
5	PEG	D	201	7/7	0.90	0.17	75,82,96,97	0
4	NI	E	203	1/1	0.90	0.11	133,133,133,133	0
5	PEG	H	201	7/7	0.90	0.14	64,75,80,82	0
5	PEG	E	202	7/7	0.92	0.12	81,83,85,86	0
4	NI	C	204	1/1	0.92	0.09	114,114,114,114	0
4	NI	A	202	1/1	0.93	0.10	120,120,120,120	0
4	NI	H	202	1/1	0.96	0.07	110,110,110,110	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	201	1/1	0.98	0.22	43,43,43,43	0
3	MG	G	201	1/1	0.98	0.09	31,31,31,31	1

6.5 Other polymers [i](#)

There are no such residues in this entry.