



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 01:17 PM UTC

PDB ID : 7RRH / pdb_00007rrh
Title : Crystal structure of fast switching R66M/M159T mutant of fluorescent protein Dronpa (Dronpa2)
Authors : Lin, C.-Y.; Romei, M.G.; Mathews, I.I.; Boxer, S.G.
Deposited on : 2021-08-09
Resolution : 1.75 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

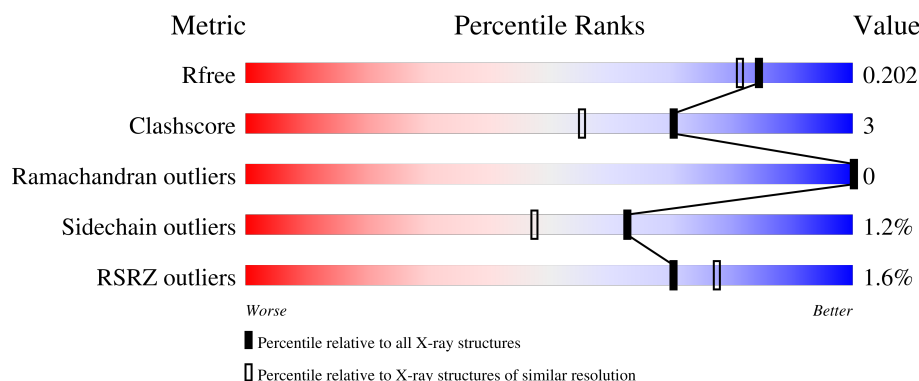
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1187 (1.74-1.74)
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	255	
1	B	255	
1	C	255	
1	D	255	
1	E	255	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	255	% 69% 13% • 16%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11331 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 Fluorescent protein Dronpa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	7	0
			1776	1137	296	333	10			
1	B	215	Total	C	N	O	S	0	5	0
			1756	1121	293	332	10			
1	C	216	Total	C	N	O	S	0	2	0
			1744	1115	290	329	10			
1	D	216	Total	C	N	O	S	0	1	0
			1738	1111	290	327	10			
1	E	213	Total	C	N	O	S	0	4	0
			1734	1103	290	331	10			
1	F	214	Total	C	N	O	S	0	2	0
			1722	1099	287	326	10			

There are 246 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	GLY	-	expression tag	UNP Q5TLG6
A	-26	SER	-	expression tag	UNP Q5TLG6
A	-25	SER	-	expression tag	UNP Q5TLG6
A	-24	HIS	-	expression tag	UNP Q5TLG6
A	-23	HIS	-	expression tag	UNP Q5TLG6
A	-22	HIS	-	expression tag	UNP Q5TLG6
A	-21	HIS	-	expression tag	UNP Q5TLG6
A	-20	HIS	-	expression tag	UNP Q5TLG6
A	-19	HIS	-	expression tag	UNP Q5TLG6
A	-18	SER	-	expression tag	UNP Q5TLG6
A	-17	SER	-	expression tag	UNP Q5TLG6
A	-16	GLY	-	expression tag	UNP Q5TLG6
A	-15	LEU	-	expression tag	UNP Q5TLG6
A	-14	VAL	-	expression tag	UNP Q5TLG6
A	-13	PRO	-	expression tag	UNP Q5TLG6
A	-12	GLY	-	expression tag	UNP Q5TLG6
A	-11	GLY	-	expression tag	UNP Q5TLG6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	SER	-	expression tag	UNP Q5TLG6
A	-9	HIS	-	expression tag	UNP Q5TLG6
A	-8	MET	-	expression tag	UNP Q5TLG6
A	-7	VAL	-	expression tag	UNP Q5TLG6
A	-6	SER	-	expression tag	UNP Q5TLG6
A	-5	LYS	-	expression tag	UNP Q5TLG6
A	-4	GLY	-	expression tag	UNP Q5TLG6
A	-3	GLU	-	expression tag	UNP Q5TLG6
A	-2	GLU	-	expression tag	UNP Q5TLG6
A	-1	ASN	-	expression tag	UNP Q5TLG6
A	0	ASN	-	expression tag	UNP Q5TLG6
A	1	MET	-	expression tag	UNP Q5TLG6
A	2	ALA	-	expression tag	UNP Q5TLG6
A	63	GYC	CYS	chromophore	UNP Q5TLG6
A	63	GYC	TYR	chromophore	UNP Q5TLG6
A	63	GYC	GLY	chromophore	UNP Q5TLG6
A	66	MET	ARG	engineered mutation	UNP Q5TLG6
A	159	THR	MET	engineered mutation	UNP Q5TLG6
A	218	GLY	GLU	conflict	UNP Q5TLG6
A	224	MET	-	insertion	UNP Q5TLG6
A	225	ASP	-	insertion	UNP Q5TLG6
A	226	GLU	-	insertion	UNP Q5TLG6
A	227	LEU	-	insertion	UNP Q5TLG6
A	228	TYR	-	insertion	UNP Q5TLG6
B	-27	GLY	-	expression tag	UNP Q5TLG6
B	-26	SER	-	expression tag	UNP Q5TLG6
B	-25	SER	-	expression tag	UNP Q5TLG6
B	-24	HIS	-	expression tag	UNP Q5TLG6
B	-23	HIS	-	expression tag	UNP Q5TLG6
B	-22	HIS	-	expression tag	UNP Q5TLG6
B	-21	HIS	-	expression tag	UNP Q5TLG6
B	-20	HIS	-	expression tag	UNP Q5TLG6
B	-19	HIS	-	expression tag	UNP Q5TLG6
B	-18	SER	-	expression tag	UNP Q5TLG6
B	-17	SER	-	expression tag	UNP Q5TLG6
B	-16	GLY	-	expression tag	UNP Q5TLG6
B	-15	LEU	-	expression tag	UNP Q5TLG6
B	-14	VAL	-	expression tag	UNP Q5TLG6
B	-13	PRO	-	expression tag	UNP Q5TLG6
B	-12	GLY	-	expression tag	UNP Q5TLG6
B	-11	GLY	-	expression tag	UNP Q5TLG6
B	-10	SER	-	expression tag	UNP Q5TLG6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	HIS	-	expression tag	UNP Q5TLG6
B	-8	MET	-	expression tag	UNP Q5TLG6
B	-7	VAL	-	expression tag	UNP Q5TLG6
B	-6	SER	-	expression tag	UNP Q5TLG6
B	-5	LYS	-	expression tag	UNP Q5TLG6
B	-4	GLY	-	expression tag	UNP Q5TLG6
B	-3	GLU	-	expression tag	UNP Q5TLG6
B	-2	GLU	-	expression tag	UNP Q5TLG6
B	-1	ASN	-	expression tag	UNP Q5TLG6
B	0	ASN	-	expression tag	UNP Q5TLG6
B	1	MET	-	expression tag	UNP Q5TLG6
B	2	ALA	-	expression tag	UNP Q5TLG6
B	63	GYC	CYS	chromophore	UNP Q5TLG6
B	63	GYC	TYR	chromophore	UNP Q5TLG6
B	63	GYC	GLY	chromophore	UNP Q5TLG6
B	66	MET	ARG	engineered mutation	UNP Q5TLG6
B	159	THR	MET	engineered mutation	UNP Q5TLG6
B	218	GLY	GLU	conflict	UNP Q5TLG6
B	224	MET	-	insertion	UNP Q5TLG6
B	225	ASP	-	insertion	UNP Q5TLG6
B	226	GLU	-	insertion	UNP Q5TLG6
B	227	LEU	-	insertion	UNP Q5TLG6
B	228	TYR	-	insertion	UNP Q5TLG6
C	-27	GLY	-	expression tag	UNP Q5TLG6
C	-26	SER	-	expression tag	UNP Q5TLG6
C	-25	SER	-	expression tag	UNP Q5TLG6
C	-24	HIS	-	expression tag	UNP Q5TLG6
C	-23	HIS	-	expression tag	UNP Q5TLG6
C	-22	HIS	-	expression tag	UNP Q5TLG6
C	-21	HIS	-	expression tag	UNP Q5TLG6
C	-20	HIS	-	expression tag	UNP Q5TLG6
C	-19	HIS	-	expression tag	UNP Q5TLG6
C	-18	SER	-	expression tag	UNP Q5TLG6
C	-17	SER	-	expression tag	UNP Q5TLG6
C	-16	GLY	-	expression tag	UNP Q5TLG6
C	-15	LEU	-	expression tag	UNP Q5TLG6
C	-14	VAL	-	expression tag	UNP Q5TLG6
C	-13	PRO	-	expression tag	UNP Q5TLG6
C	-12	GLY	-	expression tag	UNP Q5TLG6
C	-11	GLY	-	expression tag	UNP Q5TLG6
C	-10	SER	-	expression tag	UNP Q5TLG6
C	-9	HIS	-	expression tag	UNP Q5TLG6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-8	MET	-	expression tag	UNP Q5TLG6
C	-7	VAL	-	expression tag	UNP Q5TLG6
C	-6	SER	-	expression tag	UNP Q5TLG6
C	-5	LYS	-	expression tag	UNP Q5TLG6
C	-4	GLY	-	expression tag	UNP Q5TLG6
C	-3	GLU	-	expression tag	UNP Q5TLG6
C	-2	GLU	-	expression tag	UNP Q5TLG6
C	-1	ASN	-	expression tag	UNP Q5TLG6
C	0	ASN	-	expression tag	UNP Q5TLG6
C	1	MET	-	expression tag	UNP Q5TLG6
C	2	ALA	-	expression tag	UNP Q5TLG6
C	63	GYC	CYS	chromophore	UNP Q5TLG6
C	63	GYC	TYR	chromophore	UNP Q5TLG6
C	63	GYC	GLY	chromophore	UNP Q5TLG6
C	66	MET	ARG	engineered mutation	UNP Q5TLG6
C	159	THR	MET	engineered mutation	UNP Q5TLG6
C	218	GLY	GLU	conflict	UNP Q5TLG6
C	224	MET	-	insertion	UNP Q5TLG6
C	225	ASP	-	insertion	UNP Q5TLG6
C	226	GLU	-	insertion	UNP Q5TLG6
C	227	LEU	-	insertion	UNP Q5TLG6
C	228	TYR	-	insertion	UNP Q5TLG6
D	-27	GLY	-	expression tag	UNP Q5TLG6
D	-26	SER	-	expression tag	UNP Q5TLG6
D	-25	SER	-	expression tag	UNP Q5TLG6
D	-24	HIS	-	expression tag	UNP Q5TLG6
D	-23	HIS	-	expression tag	UNP Q5TLG6
D	-22	HIS	-	expression tag	UNP Q5TLG6
D	-21	HIS	-	expression tag	UNP Q5TLG6
D	-20	HIS	-	expression tag	UNP Q5TLG6
D	-19	HIS	-	expression tag	UNP Q5TLG6
D	-18	SER	-	expression tag	UNP Q5TLG6
D	-17	SER	-	expression tag	UNP Q5TLG6
D	-16	GLY	-	expression tag	UNP Q5TLG6
D	-15	LEU	-	expression tag	UNP Q5TLG6
D	-14	VAL	-	expression tag	UNP Q5TLG6
D	-13	PRO	-	expression tag	UNP Q5TLG6
D	-12	GLY	-	expression tag	UNP Q5TLG6
D	-11	GLY	-	expression tag	UNP Q5TLG6
D	-10	SER	-	expression tag	UNP Q5TLG6
D	-9	HIS	-	expression tag	UNP Q5TLG6
D	-8	MET	-	expression tag	UNP Q5TLG6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	-7	VAL	-	expression tag	UNP Q5TLG6
D	-6	SER	-	expression tag	UNP Q5TLG6
D	-5	LYS	-	expression tag	UNP Q5TLG6
D	-4	GLY	-	expression tag	UNP Q5TLG6
D	-3	GLU	-	expression tag	UNP Q5TLG6
D	-2	GLU	-	expression tag	UNP Q5TLG6
D	-1	ASN	-	expression tag	UNP Q5TLG6
D	0	ASN	-	expression tag	UNP Q5TLG6
D	1	MET	-	expression tag	UNP Q5TLG6
D	2	ALA	-	expression tag	UNP Q5TLG6
D	63	GYC	CYS	chromophore	UNP Q5TLG6
D	63	GYC	TYR	chromophore	UNP Q5TLG6
D	63	GYC	GLY	chromophore	UNP Q5TLG6
D	66	MET	ARG	engineered mutation	UNP Q5TLG6
D	159	THR	MET	engineered mutation	UNP Q5TLG6
D	218	GLY	GLU	conflict	UNP Q5TLG6
D	224	MET	-	insertion	UNP Q5TLG6
D	225	ASP	-	insertion	UNP Q5TLG6
D	226	GLU	-	insertion	UNP Q5TLG6
D	227	LEU	-	insertion	UNP Q5TLG6
D	228	TYR	-	insertion	UNP Q5TLG6
E	-27	GLY	-	expression tag	UNP Q5TLG6
E	-26	SER	-	expression tag	UNP Q5TLG6
E	-25	SER	-	expression tag	UNP Q5TLG6
E	-24	HIS	-	expression tag	UNP Q5TLG6
E	-23	HIS	-	expression tag	UNP Q5TLG6
E	-22	HIS	-	expression tag	UNP Q5TLG6
E	-21	HIS	-	expression tag	UNP Q5TLG6
E	-20	HIS	-	expression tag	UNP Q5TLG6
E	-19	HIS	-	expression tag	UNP Q5TLG6
E	-18	SER	-	expression tag	UNP Q5TLG6
E	-17	SER	-	expression tag	UNP Q5TLG6
E	-16	GLY	-	expression tag	UNP Q5TLG6
E	-15	LEU	-	expression tag	UNP Q5TLG6
E	-14	VAL	-	expression tag	UNP Q5TLG6
E	-13	PRO	-	expression tag	UNP Q5TLG6
E	-12	GLY	-	expression tag	UNP Q5TLG6
E	-11	GLY	-	expression tag	UNP Q5TLG6
E	-10	SER	-	expression tag	UNP Q5TLG6
E	-9	HIS	-	expression tag	UNP Q5TLG6
E	-8	MET	-	expression tag	UNP Q5TLG6
E	-7	VAL	-	expression tag	UNP Q5TLG6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-6	SER	-	expression tag	UNP Q5TLG6
E	-5	LYS	-	expression tag	UNP Q5TLG6
E	-4	GLY	-	expression tag	UNP Q5TLG6
E	-3	GLU	-	expression tag	UNP Q5TLG6
E	-2	GLU	-	expression tag	UNP Q5TLG6
E	-1	ASN	-	expression tag	UNP Q5TLG6
E	0	ASN	-	expression tag	UNP Q5TLG6
E	1	MET	-	expression tag	UNP Q5TLG6
E	2	ALA	-	expression tag	UNP Q5TLG6
E	63	GYC	CYS	chromophore	UNP Q5TLG6
E	63	GYC	TYR	chromophore	UNP Q5TLG6
E	63	GYC	GLY	chromophore	UNP Q5TLG6
E	66	MET	ARG	engineered mutation	UNP Q5TLG6
E	159	THR	MET	engineered mutation	UNP Q5TLG6
E	218	GLY	GLU	conflict	UNP Q5TLG6
E	224	MET	-	insertion	UNP Q5TLG6
E	225	ASP	-	insertion	UNP Q5TLG6
E	226	GLU	-	insertion	UNP Q5TLG6
E	227	LEU	-	insertion	UNP Q5TLG6
E	228	TYR	-	insertion	UNP Q5TLG6
F	-27	GLY	-	expression tag	UNP Q5TLG6
F	-26	SER	-	expression tag	UNP Q5TLG6
F	-25	SER	-	expression tag	UNP Q5TLG6
F	-24	HIS	-	expression tag	UNP Q5TLG6
F	-23	HIS	-	expression tag	UNP Q5TLG6
F	-22	HIS	-	expression tag	UNP Q5TLG6
F	-21	HIS	-	expression tag	UNP Q5TLG6
F	-20	HIS	-	expression tag	UNP Q5TLG6
F	-19	HIS	-	expression tag	UNP Q5TLG6
F	-18	SER	-	expression tag	UNP Q5TLG6
F	-17	SER	-	expression tag	UNP Q5TLG6
F	-16	GLY	-	expression tag	UNP Q5TLG6
F	-15	LEU	-	expression tag	UNP Q5TLG6
F	-14	VAL	-	expression tag	UNP Q5TLG6
F	-13	PRO	-	expression tag	UNP Q5TLG6
F	-12	GLY	-	expression tag	UNP Q5TLG6
F	-11	GLY	-	expression tag	UNP Q5TLG6
F	-10	SER	-	expression tag	UNP Q5TLG6
F	-9	HIS	-	expression tag	UNP Q5TLG6
F	-8	MET	-	expression tag	UNP Q5TLG6
F	-7	VAL	-	expression tag	UNP Q5TLG6
F	-6	SER	-	expression tag	UNP Q5TLG6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	-5	LYS	-	expression tag	UNP Q5TLG6
F	-4	GLY	-	expression tag	UNP Q5TLG6
F	-3	GLU	-	expression tag	UNP Q5TLG6
F	-2	GLU	-	expression tag	UNP Q5TLG6
F	-1	ASN	-	expression tag	UNP Q5TLG6
F	0	ASN	-	expression tag	UNP Q5TLG6
F	1	MET	-	expression tag	UNP Q5TLG6
F	2	ALA	-	expression tag	UNP Q5TLG6
F	63	GYC	CYS	chromophore	UNP Q5TLG6
F	63	GYC	TYR	chromophore	UNP Q5TLG6
F	63	GYC	GLY	chromophore	UNP Q5TLG6
F	66	MET	ARG	engineered mutation	UNP Q5TLG6
F	159	THR	MET	engineered mutation	UNP Q5TLG6
F	218	GLY	GLU	conflict	UNP Q5TLG6
F	224	MET	-	insertion	UNP Q5TLG6
F	225	ASP	-	insertion	UNP Q5TLG6
F	226	GLU	-	insertion	UNP Q5TLG6
F	227	LEU	-	insertion	UNP Q5TLG6
F	228	TYR	-	insertion	UNP Q5TLG6

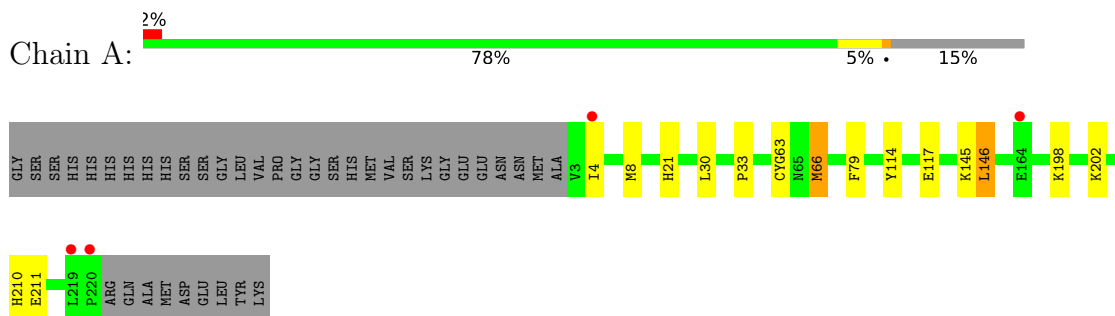
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	166	Total O 166 166	0	0
2	B	193	Total O 193 193	0	0
2	C	162	Total O 162 162	0	0
2	D	145	Total O 145 145	0	0
2	E	123	Total O 123 123	0	0
2	F	72	Total O 72 72	0	0

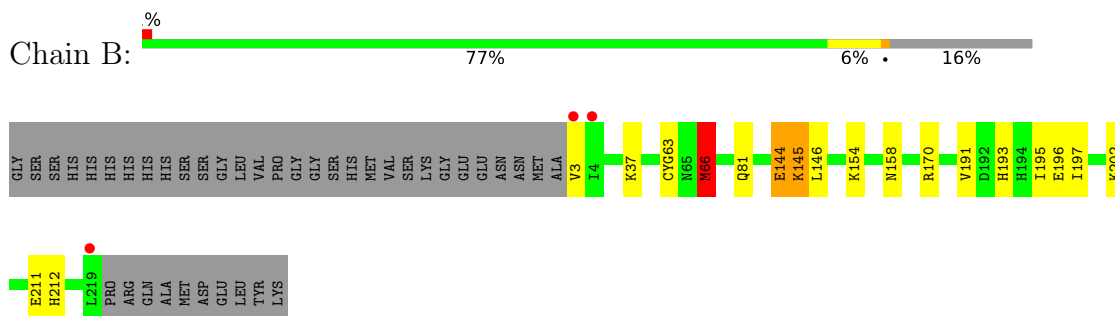
3 Residue-property plots

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.

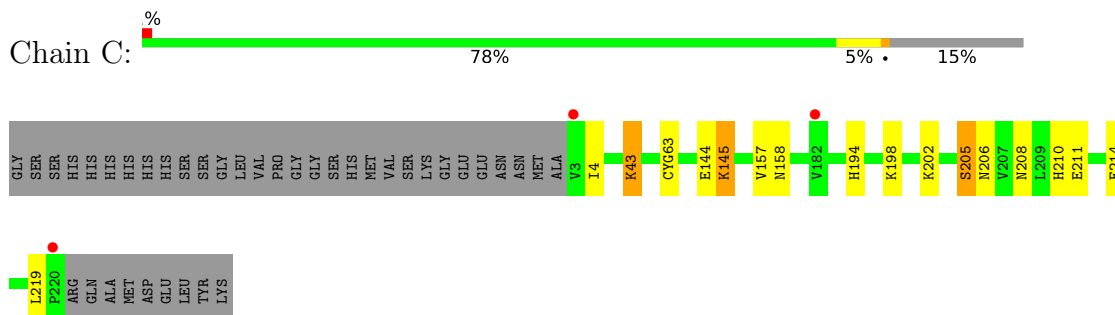
- Molecule 1: Fluorescent protein Dronpa



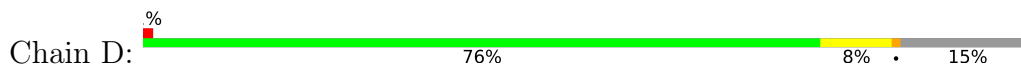
- Molecule 1: Fluorescent protein Dronpa

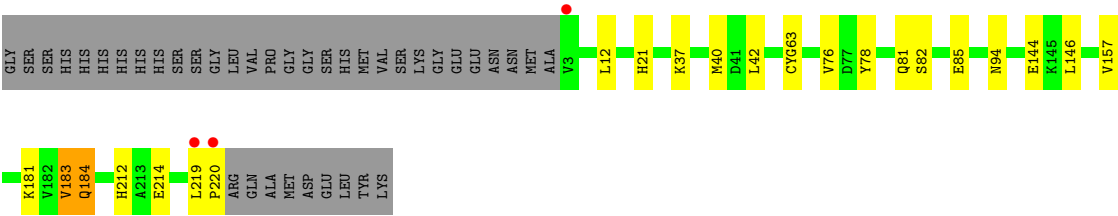


- Molecule 1: Fluorescent protein Dronpa

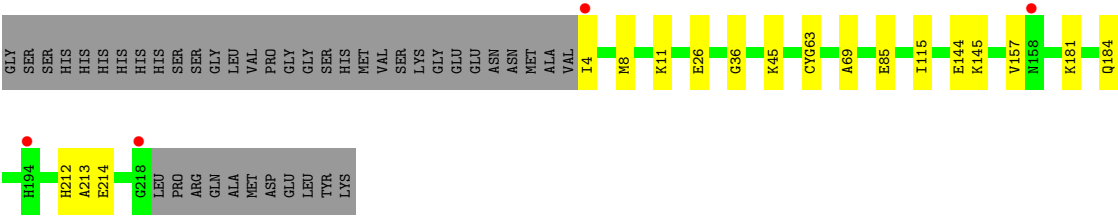
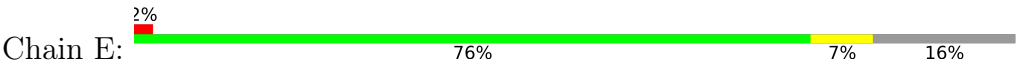


- Molecule 1: Fluorescent protein Dronpa

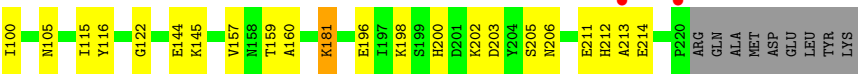
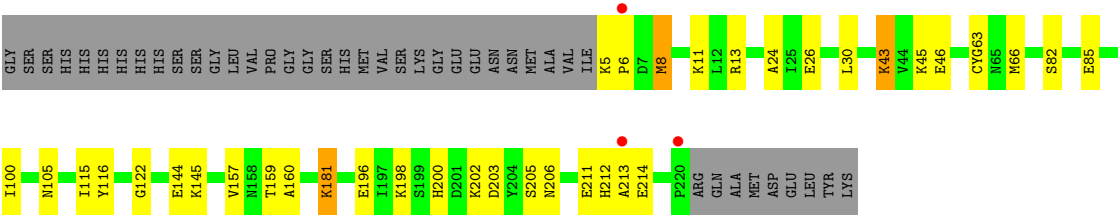




• Molecule 1: Fluorescent protein Dronpa



• Molecule 1: Fluorescent protein Dronpa



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.63Å 71.54Å 108.27Å 90.00° 110.12° 90.00°	Depositor
Resolution (Å)	37.77 – 1.75 37.77 – 1.75	Depositor EDS
% Data completeness (in resolution range)	97.8 (37.77-1.75) 89.8 (37.77-1.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.83 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.13rc2_2986	Depositor
R, R_{free}	0.176 , 0.202 0.179 , 0.202	Depositor DCC
R_{free} test set	6643 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.5	Xtriage
Anisotropy	0.582	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 33.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11331	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: GYC

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	0.53	6/1814 (0.3%)	0.64	1/2450 (0.0%)
1	B	0.67	9/1787 (0.5%)	0.65	3/2414 (0.1%)
1	C	0.68	9/1772 (0.5%)	0.65	0/2395
1	D	0.68	4/1763 (0.2%)	0.67	0/2383
1	E	0.51	1/1758 (0.1%)	0.58	0/2376
1	F	0.57	2/1750 (0.1%)	0.61	1/2366 (0.0%)
All	All	0.61	31/10644 (0.3%)	0.63	5/14384 (0.0%)

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	197	ILE	C-O	-7.32	1.15	1.23
1	C	4	ILE	C-O	-7.07	1.16	1.24
1	A	117	GLU	C-O	-6.99	1.16	1.24
1	C	43	LYS	C-O	-6.57	1.16	1.23
1	D	94	ASN	C-O	-6.33	1.16	1.23
1	D	214	GLU	C-O	-6.31	1.16	1.23
1	B	158	ASN	C-O	-6.16	1.16	1.24
1	C	214	GLU	C-O	-6.11	1.17	1.23
1	E	214	GLU	C-O	-6.01	1.17	1.23
1	C	158	ASN	C-O	-5.90	1.17	1.24
1	B	170	ARG	C-O	-5.86	1.16	1.23
1	B	195	ILE	C-O	-5.84	1.18	1.24
1	A	21	HIS	C-O	-5.67	1.17	1.24
1	A	66	MET	C-O	-5.58	1.17	1.24
1	C	202	LYS	C-O	-5.36	1.17	1.24
1	F	145	LYS	C-O	-5.34	1.17	1.24
1	B	202	LYS	C-O	-5.29	1.17	1.24
1	F	43	LYS	C-O	-5.25	1.17	1.23
1	C	194	HIS	C-O	-5.24	1.17	1.24
1	A	30	LEU	C-O	-5.16	1.17	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	202	LYS	C-O	-5.14	1.18	1.24
1	B	145	LYS	C-O	-5.13	1.17	1.24
1	B	66	MET	C-O	-5.12	1.17	1.24
1	D	21	HIS	C-O	-5.10	1.18	1.24
1	D	146	LEU	C-O	-5.10	1.17	1.24
1	C	208	ASN	C-O	-5.05	1.18	1.24
1	B	196	GLU	C-O	-5.03	1.17	1.23
1	C	145	LYS	C-O	-5.03	1.18	1.24
1	C	205	SER	C-O	-5.03	1.17	1.24
1	B	144	GLU	C-O	-5.02	1.17	1.23
1	A	146	LEU	C-O	-5.00	1.17	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	202	LYS	N-CA-C	6.86	119.63	111.33
1	F	8	MET	N-CA-C	6.14	119.05	109.52
1	A	202	LYS	N-CA-C	5.91	118.20	111.11
1	B	196	GLU	N-CA-C	5.68	117.75	108.55
1	B	170	ARG	N-CA-C	5.28	118.29	110.48

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1776	0	1706	8	0
1	B	1756	0	1668	9	0
1	C	1744	0	1660	7	0
1	D	1738	0	1654	13	0
1	E	1734	0	1628	10	0
1	F	1722	0	1628	23	0
2	A	166	0	0	1	0
2	B	193	0	0	1	0
2	C	162	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	145	0	0	0	0
2	E	123	0	0	0	0
2	F	72	0	0	0	0
All	All	11331	0	9944	70	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 3.

All (70) 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:D:12:LEU:HD21	1:D:40:MET:HE1	1.51	0.93
1:B:193:HIS:HD2	1:B:211:GLU:OE2	1.65	0.79
1:D:81:GLN:O	1:D:181:LYS:NZ	2.19	0.74
1:D:76:VAL:HG11	1:D:184:GLN:HG2	1.70	0.73
1:F:85:GLU:CD	1:F:181:LYS:HD3	2.14	0.72
1:E:4:ILE:HA	1:E:8:MET:HE2	1.73	0.71
1:F:30:LEU:HD12	1:F:30:LEU:C	2.17	0.70
1:F:26:GLU:HG3	1:F:45:LYS:HG3	1.72	0.70
1:F:85:GLU:OE1	1:F:181:LYS:HD3	1.92	0.68
1:D:219:LEU:HD12	1:D:220:PRO:HD2	1.76	0.68
1:B:37:LYS:HE3	1:B:212[B]:HIS:CD2	2.29	0.67
1:F:24:ALA:HB3	1:F:46:GLU:HG3	1.75	0.67
1:E:26:GLU:HG3	1:E:45:LYS:HG3	1.77	0.66
1:C:198:LYS:HE3	1:C:210:HIS:HB2	1.78	0.66
1:F:11:LYS:HG2	1:F:115:ILE:HG22	1.77	0.65
1:F:202:LYS:HG3	1:F:203:ASP:N	2.13	0.62
1:A:198:LYS:HG3	1:A:210[A]:HIS:CD2	2.36	0.61
1:E:85:GLU:N	1:E:85:GLU:OE1	2.32	0.59
1:D:82:SER:HA	1:D:181:LYS:HZ2	1.67	0.57
1:D:12:LEU:CD2	1:D:40:MET:HE1	2.30	0.57
1:A:211:GLU:OE2	2:A:301:HOH:O	2.18	0.56
1:A:4:ILE:HD13	1:A:114:TYR:OH	2.06	0.56
1:A:146:LEU:HD12	1:A:146:LEU:N	2.21	0.55
1:B:66:MET:HE1	1:B:193:HIS:NE2	2.22	0.54
1:F:202:LYS:HG3	1:F:203:ASP:H	1.73	0.53
1:A:4:ILE:HD11	1:A:33:PRO:HG2	1.88	0.53
1:F:196:GLU:CD	1:F:198:LYS:HE3	2.33	0.53
1:F:43:LYS:HA	1:F:205:SER:O	2.10	0.52
1:D:40:MET:HE2	1:D:42:LEU:HD21	1.92	0.52
1:D:85:GLU:OE2	1:D:181:LYS:HE3	2.08	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:MET:HE1	1:B:191:VAL:HG11	1.90	0.52
1:F:30:LEU:HD12	1:F:30:LEU:O	2.09	0.51
1:B:66:MET:CE	1:B:193:HIS:NE2	2.73	0.51
1:D:82:SER:HA	1:D:181:LYS:NZ	2.25	0.51
1:D:85:GLU:OE2	1:D:181:LYS:CE	2.60	0.50
1:F:11:LYS:O	1:F:115:ILE:HA	2.11	0.50
1:C:43:LYS:NZ	1:C:206:ASN:OD1	2.44	0.50
1:B:81:GLN:NE2	2:B:307:HOH:O	2.42	0.49
1:F:159:THR:OG1	1:F:160:ALA:N	2.45	0.48
1:C:198:LYS:HE3	1:C:210:HIS:CB	2.43	0.47
1:A:4:ILE:HD11	1:A:8:MET:HG3	1.95	0.47
1:F:5:LYS:N	1:F:6:PRO:HD2	2.29	0.47
1:C:211:GLU:OE2	2:C:301:HOH:O	2.21	0.47
1:F:144:GLU:HA	1:F:157:VAL:HB	1.97	0.46
1:B:193:HIS:CD2	1:B:211:GLU:OE2	2.57	0.46
1:C:144:GLU:HA	1:C:157:VAL:HB	1.98	0.45
1:F:13:ARG:NH1	1:F:26:GLU:OE1	2.42	0.45
1:E:181:LYS:HD3	1:E:181:LYS:HA	1.56	0.45
1:C:198:LYS:HD2	1:C:210:HIS:CD2	2.52	0.44
1:B:146:LEU:HD23	1:B:154:LYS:O	2.17	0.44
1:E:4:ILE:HA	1:E:8:MET:CE	2.44	0.44
1:F:213:ALA:C	1:F:214:GLU:CG	2.91	0.44
1:F:100:ILE:O	1:F:122:GLY:HA2	2.18	0.44
1:A:66:MET:HG2	1:A:79:PHE:CE1	2.52	0.43
1:F:196:GLU:OE1	1:F:198:LYS:HE3	2.18	0.43
1:F:211:GLU:HG2	1:F:212:HIS:H	1.84	0.43
1:C:219:LEU:HD12	1:C:219:LEU:HA	1.89	0.43
1:F:105:ASN:OD1	1:F:116:TYR:HB3	2.20	0.42
1:E:144:GLU:HA	1:E:157:VAL:HB	2.01	0.42
1:E:11:LYS:O	1:E:115:ILE:HA	2.20	0.42
1:D:37:LYS:HD3	1:D:212:HIS:HB2	2.01	0.42
1:F:5:LYS:O	1:F:5:LYS:HG3	2.19	0.42
1:B:144:GLU:OE2	1:B:193:HIS:HE1	2.03	0.42
1:D:78:TYR:CD2	1:D:183:VAL:HG22	2.55	0.41
1:D:144:GLU:HA	1:D:157:VAL:HB	2.02	0.41
1:E:69:ALA:HA	1:E:213:ALA:O	2.21	0.41
1:A:198:LYS:HE2	1:A:210[A]:HIS:ND1	2.36	0.41
1:E:184:GLN:HA	1:E:184:GLN:OE1	2.20	0.41
1:F:200:HIS:HA	1:F:206:ASN:O	2.21	0.40
1:E:36:GLY:O	1:E:212:HIS:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	218/255 (86%)	216 (99%)	2 (1%)	0	100	100
1	B	215/255 (84%)	214 (100%)	1 (0%)	0	100	100
1	C	213/255 (84%)	211 (99%)	2 (1%)	0	100	100
1	D	212/255 (83%)	210 (99%)	2 (1%)	0	100	100
1	E	212/255 (83%)	210 (99%)	2 (1%)	0	100	100
1	F	211/255 (83%)	208 (99%)	3 (1%)	0	100	100
All	All	1281/1530 (84%)	1269 (99%)	12 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	192/217 (88%)	191 (100%)	1 (0%)	81	75
1	B	188/217 (87%)	185 (98%)	3 (2%)	55	35
1	C	186/217 (86%)	184 (99%)	2 (1%)	65	50
1	D	185/217 (85%)	183 (99%)	2 (1%)	65	50
1	E	184/217 (85%)	183 (100%)	1 (0%)	81	75
1	F	183/217 (84%)	179 (98%)	4 (2%)	45	22
All	All	1118/1302 (86%)	1105 (99%)	13 (1%)	63	47

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	145	LYS
1	B	3	VAL
1	B	66	MET
1	B	145	LYS
1	C	145	LYS
1	C	205	SER
1	D	183	VAL
1	D	184	GLN
1	E	145	LYS
1	F	8	MET
1	F	66	MET
1	F	82	SER
1	F	181	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	HIS
1	B	193	HIS
1	C	208	ASN
1	D	208	ASN
1	F	193	HIS
1	F	208	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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
1	GYC	A	63	1	21,22,23	1.09	3 (14%)	26,30,32	1.94	7 (26%)
1	GYC	F	63	1	21,22,23	1.05	1 (4%)	26,30,32	2.29	6 (23%)
1	GYC	D	63	1	21,22,23	1.14	2 (9%)	26,30,32	2.41	8 (30%)
1	GYC	B	63	1	21,22,23	1.19	3 (14%)	26,30,32	2.30	8 (30%)
1	GYC	E	63	1	21,22,23	1.03	2 (9%)	26,30,32	2.17	8 (30%)
1	GYC	C	63	1	21,22,23	1.03	3 (14%)	26,30,32	2.17	10 (38%)

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
1	GYC	A	63	1	-	3/10/29/30	0/2/2/2
1	GYC	F	63	1	-	3/10/29/30	0/2/2/2
1	GYC	D	63	1	-	3/10/29/30	0/2/2/2
1	GYC	B	63	1	-	3/10/29/30	0/2/2/2
1	GYC	E	63	1	-	3/10/29/30	0/2/2/2
1	GYC	C	63	1	-	3/10/29/30	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	63	GYC	CB2-CA2	3.62	1.38	1.35
1	B	63	GYC	CB2-CA2	3.44	1.38	1.35
1	D	63	GYC	CB2-CA2	3.41	1.38	1.35
1	E	63	GYC	CB2-CA2	3.21	1.38	1.35
1	C	63	GYC	CB2-CA2	3.08	1.38	1.35
1	A	63	GYC	CB2-CA2	2.64	1.37	1.35
1	A	63	GYC	CA2-C2	-2.48	1.45	1.48
1	A	63	GYC	C2-N3	-2.39	1.34	1.40
1	B	63	GYC	C2-N3	-2.33	1.34	1.40
1	B	63	GYC	CA2-C2	-2.22	1.46	1.48
1	E	63	GYC	C2-N3	-2.22	1.34	1.40
1	D	63	GYC	C2-N3	-2.21	1.34	1.40
1	C	63	GYC	C2-N3	-2.14	1.35	1.40
1	C	63	GYC	CA2-C2	-2.01	1.46	1.48

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	63	GYC	O2-C2-CA2	-8.99	125.28	131.02
1	F	63	GYC	O2-C2-CA2	-7.57	126.19	131.02
1	B	63	GYC	O2-C2-CA2	-7.44	126.28	131.02
1	C	63	GYC	O2-C2-CA2	-7.22	126.41	131.02
1	E	63	GYC	O2-C2-CA2	-7.09	126.49	131.02
1	A	63	GYC	O2-C2-CA2	-6.51	126.86	131.02
1	F	63	GYC	C2-CA2-N2	-4.39	105.81	108.95
1	F	63	GYC	CA2-N2-C1	4.29	109.15	105.80
1	B	63	GYC	CB2-CA2-N2	3.87	134.02	128.76
1	B	63	GYC	C2-CA2-N2	-3.52	106.43	108.95
1	E	63	GYC	C2-CA2-N2	-3.49	106.45	108.95
1	F	63	GYC	CG2-CB2-CA2	-3.46	125.76	129.87
1	D	63	GYC	CB2-CA2-N2	3.28	133.22	128.76
1	E	63	GYC	CG2-CB2-CA2	-3.15	126.12	129.87
1	E	63	GYC	CA2-N2-C1	2.97	108.12	105.80
1	B	63	GYC	CA2-N2-C1	2.97	108.12	105.80
1	B	63	GYC	CA2-C2-N3	2.94	105.97	103.50
1	C	63	GYC	CB2-CA2-N2	2.91	132.71	128.76
1	D	63	GYC	C2-CA2-N2	-2.77	106.97	108.95
1	A	63	GYC	CA1-CB1-SG1	-2.76	108.50	114.40
1	C	63	GYC	C2-CA2-N2	-2.72	107.00	108.95
1	D	63	GYC	CA2-N2-C1	2.65	107.87	105.80
1	A	63	GYC	CB2-CA2-N2	2.48	132.12	128.76
1	D	63	GYC	O2-C2-N3	2.44	129.40	124.31
1	E	63	GYC	CB2-CA2-N2	2.43	132.06	128.76
1	E	63	GYC	CA1-CB1-SG1	-2.41	109.24	114.40
1	A	63	GYC	CG2-CB2-CA2	-2.41	127.00	129.87
1	B	63	GYC	CA1-CB1-SG1	-2.40	109.27	114.40
1	D	63	GYC	CG2-CB2-CA2	-2.35	127.07	129.87
1	B	63	GYC	CB2-CA2-C2	-2.33	119.53	122.36
1	C	63	GYC	CA2-N2-C1	2.30	107.60	105.80
1	E	63	GYC	CA2-C2-N3	2.28	105.42	103.50
1	C	63	GYC	CA1-CB1-SG1	-2.27	109.54	114.40
1	A	63	GYC	C2-N3-C1	2.24	109.11	108.07
1	C	63	GYC	CA1-C1-N3	-2.21	121.96	124.84
1	E	63	GYC	CA1-C1-N3	-2.20	121.98	124.84
1	C	63	GYC	CA2-C2-N3	2.18	105.33	103.50
1	D	63	GYC	CA2-C2-N3	2.17	105.32	103.50
1	F	63	GYC	CA2-C2-N3	2.16	105.32	103.50
1	B	63	GYC	CG2-CB2-CA2	-2.16	127.30	129.87
1	C	63	GYC	CD2-CG2-CD1	2.14	120.82	117.65
1	D	63	GYC	CB2-CA2-C2	-2.10	119.81	122.36
1	A	63	GYC	CA2-N2-C1	2.10	107.44	105.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	63	GYC	O3-C3-CA3	-2.08	116.12	125.47
1	A	63	GYC	C2-CA2-N2	-2.03	107.49	108.95
1	C	63	GYC	CG2-CB2-CA2	-2.01	127.48	129.87
1	F	63	GYC	O2-C2-N3	2.00	128.49	124.31

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	63	GYC	C3-CA3-N3-C2
1	A	63	GYC	N2-CA2-CB2-CG2
1	A	63	GYC	C2-CA2-CB2-CG2
1	B	63	GYC	N2-CA2-CB2-CG2
1	B	63	GYC	C2-CA2-CB2-CG2
1	C	63	GYC	C3-CA3-N3-C2
1	C	63	GYC	N2-CA2-CB2-CG2
1	C	63	GYC	C2-CA2-CB2-CG2
1	D	63	GYC	N2-CA2-CB2-CG2
1	D	63	GYC	C2-CA2-CB2-CG2
1	E	63	GYC	C3-CA3-N3-C2
1	E	63	GYC	N2-CA2-CB2-CG2
1	E	63	GYC	C2-CA2-CB2-CG2
1	F	63	GYC	C3-CA3-N3-C2
1	F	63	GYC	N2-CA2-CB2-CG2
1	F	63	GYC	C2-CA2-CB2-CG2
1	B	63	GYC	C3-CA3-N3-C2
1	D	63	GYC	C3-CA3-N3-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	215/255 (84%)	-0.07	4 (1%)	66	73	14, 37, 56, 102	7 (3%)
1	B	214/255 (83%)	-0.02	3 (1%)	73	80	14, 38, 60, 83	5 (2%)
1	C	215/255 (84%)	0.02	3 (1%)	73	80	15, 41, 59, 83	2 (0%)
1	D	215/255 (84%)	0.29	3 (1%)	73	80	16, 46, 72, 112	1 (0%)
1	E	212/255 (83%)	0.38	4 (1%)	66	73	16, 49, 78, 98	4 (1%)
1	F	213/255 (83%)	0.60	3 (1%)	73	80	22, 61, 92, 117	2 (0%)
All	All	1284/1530 (83%)	0.20	20 (1%)	70	77	14, 44, 79, 117	21 (1%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	220	PRO	4.6
1	D	219	LEU	4.4
1	D	3	VAL	4.0
1	B	4	ILE	3.7
1	C	3	VAL	3.7
1	B	219	LEU	3.6
1	A	220	PRO	3.5
1	E	218	GLY	3.4
1	B	3	VAL	3.2
1	C	220	PRO	3.1
1	E	4	ILE	2.9
1	F	220	PRO	2.8
1	A	219	LEU	2.5
1	C	182	VAL	2.4
1	E	194	HIS	2.2
1	A	4	ILE	2.2
1	E	158[A]	ASN	2.2
1	F	213	ALA	2.2
1	F	6	PRO	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	164	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	GYC	F	63	21/22	0.92	0.10	60,65,69,73	0
1	GYC	D	63	21/22	0.94	0.11	35,43,57,65	0
1	GYC	B	63	21/22	0.94	0.10	27,37,49,49	0
1	GYC	C	63	21/22	0.95	0.09	34,39,50,54	0
1	GYC	E	63	21/22	0.96	0.10	42,47,53,61	0
1	GYC	A	63	21/22	0.97	0.07	26,34,44,47	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.