



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:17 PM GMT

PDB ID : 4HQ9  
Title : Crystal structure of a green-to-red photoconvertible DRONPA, pcDRONPA  
in the green-off-state  
Authors : Nguyen Bich, N.; Van Meervelt, L.  
Deposited on : 2012-10-25  
Resolution : 2.07 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

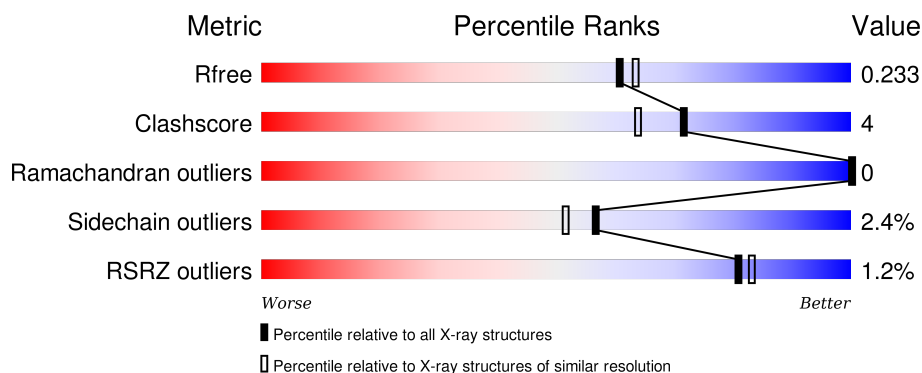
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.07 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))
$R_{free}$	91344	1799 (2.08-2.04)
Clashscore	102246	1910 (2.08-2.04)
Ramachandran outliers	100387	1893 (2.08-2.04)
Sidechain outliers	100360	1893 (2.08-2.04)
RSRZ outliers	91569	1802 (2.08-2.04)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	258	 78% 5% 16%
1	B	258	 76% 7% 16%
1	C	258	 79% 5% 16%
1	D	258	 2% 72% 12% 16%
1	E	258	 2% 74% 10% 16%

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Mol	Chain	Length	Quality of chain
1	F	258	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PEG	A	301	-	-	-	X
2	PEG	B	301	-	-	-	X
2	PEG	D	301	-	-	-	X
3	PGE	A	302	-	-	-	X
4	PG4	C	301	-	-	-	X
4	PG4	F	302	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11101 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	217	Total	C	N	O	S	0	2	0
			1756	1124	298	325	9			
1	B	216	Total	C	N	O	S	0	1	0
			1734	1112	292	321	9			
1	C	218	Total	C	N	O	S	0	3	0
			1763	1128	295	330	10			
1	D	216	Total	C	N	O	S	0	0	0
			1730	1108	290	323	9			
1	E	217	Total	C	N	O	S	0	0	0
			1732	1111	289	323	9			
1	F	214	Total	C	N	O	S	0	0	0
			1721	1101	290	321	9			

There are 258 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	EXPRESSION TAG	UNP Q5TLG6
A	-34	ARG	-	EXPRESSION TAG	UNP Q5TLG6
A	-33	GLY	-	EXPRESSION TAG	UNP Q5TLG6
A	-32	SER	-	EXPRESSION TAG	UNP Q5TLG6
A	-31	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	-30	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	-29	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	-28	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	-27	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	-26	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	-25	GLY	-	EXPRESSION TAG	UNP Q5TLG6
A	-24	MET	-	EXPRESSION TAG	UNP Q5TLG6
A	-23	ALA	-	EXPRESSION TAG	UNP Q5TLG6
A	-22	SER	-	EXPRESSION TAG	UNP Q5TLG6
A	-21	MET	-	EXPRESSION TAG	UNP Q5TLG6
A	-20	THR	-	EXPRESSION TAG	UNP Q5TLG6
A	-19	GLY	-	EXPRESSION TAG	UNP Q5TLG6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	EXPRESSION TAG	UNP Q5TLG6
A	-17	GLN	-	EXPRESSION TAG	UNP Q5TLG6
A	-16	GLN	-	EXPRESSION TAG	UNP Q5TLG6
A	-15	MET	-	EXPRESSION TAG	UNP Q5TLG6
A	-14	GLY	-	EXPRESSION TAG	UNP Q5TLG6
A	-13	ARG	-	EXPRESSION TAG	UNP Q5TLG6
A	-12	ASN	-	EXPRESSION TAG	UNP Q5TLG6
A	-11	LEU	-	EXPRESSION TAG	UNP Q5TLG6
A	-10	TYR	-	EXPRESSION TAG	UNP Q5TLG6
A	-9	ASP	-	EXPRESSION TAG	UNP Q5TLG6
A	-8	ASP	-	EXPRESSION TAG	UNP Q5TLG6
A	-7	ASP	-	EXPRESSION TAG	UNP Q5TLG6
A	-6	ASP	-	EXPRESSION TAG	UNP Q5TLG6
A	-5	LYS	-	EXPRESSION TAG	UNP Q5TLG6
A	-4	ASP	-	EXPRESSION TAG	UNP Q5TLG6
A	-3	PRO	-	EXPRESSION TAG	UNP Q5TLG6
A	-2	GLY	-	EXPRESSION TAG	UNP Q5TLG6
A	-1	SER	-	EXPRESSION TAG	UNP Q5TLG6
A	0	HIS	-	EXPRESSION TAG	UNP Q5TLG6
A	60	ALA	VAL	ENGINEERED MUTATION	UNP Q5TLG6
A	63	CR8	CYS	CHROMOPHORE	UNP Q5TLG6
A	63	CR8	TYR	CHROMOPHORE	UNP Q5TLG6
A	63	CR8	GLY	CHROMOPHORE	UNP Q5TLG6
A	94	SER	ASN	ENGINEERED MUTATION	UNP Q5TLG6
A	102	ILE	ASN	ENGINEERED MUTATION	UNP Q5TLG6
A	218	GLY	GLU	ENGINEERED MUTATION	UNP Q5TLG6
B	-35	MET	-	EXPRESSION TAG	UNP Q5TLG6
B	-34	ARG	-	EXPRESSION TAG	UNP Q5TLG6
B	-33	GLY	-	EXPRESSION TAG	UNP Q5TLG6
B	-32	SER	-	EXPRESSION TAG	UNP Q5TLG6
B	-31	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	-30	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	-29	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	-28	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	-27	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	-26	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	-25	GLY	-	EXPRESSION TAG	UNP Q5TLG6
B	-24	MET	-	EXPRESSION TAG	UNP Q5TLG6
B	-23	ALA	-	EXPRESSION TAG	UNP Q5TLG6
B	-22	SER	-	EXPRESSION TAG	UNP Q5TLG6
B	-21	MET	-	EXPRESSION TAG	UNP Q5TLG6
B	-20	THR	-	EXPRESSION TAG	UNP Q5TLG6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	GLY	-	EXPRESSION TAG	UNP Q5TLG6
B	-18	GLY	-	EXPRESSION TAG	UNP Q5TLG6
B	-17	GLN	-	EXPRESSION TAG	UNP Q5TLG6
B	-16	GLN	-	EXPRESSION TAG	UNP Q5TLG6
B	-15	MET	-	EXPRESSION TAG	UNP Q5TLG6
B	-14	GLY	-	EXPRESSION TAG	UNP Q5TLG6
B	-13	ARG	-	EXPRESSION TAG	UNP Q5TLG6
B	-12	ASN	-	EXPRESSION TAG	UNP Q5TLG6
B	-11	LEU	-	EXPRESSION TAG	UNP Q5TLG6
B	-10	TYR	-	EXPRESSION TAG	UNP Q5TLG6
B	-9	ASP	-	EXPRESSION TAG	UNP Q5TLG6
B	-8	ASP	-	EXPRESSION TAG	UNP Q5TLG6
B	-7	ASP	-	EXPRESSION TAG	UNP Q5TLG6
B	-6	ASP	-	EXPRESSION TAG	UNP Q5TLG6
B	-5	LYS	-	EXPRESSION TAG	UNP Q5TLG6
B	-4	ASP	-	EXPRESSION TAG	UNP Q5TLG6
B	-3	PRO	-	EXPRESSION TAG	UNP Q5TLG6
B	-2	GLY	-	EXPRESSION TAG	UNP Q5TLG6
B	-1	SER	-	EXPRESSION TAG	UNP Q5TLG6
B	0	HIS	-	EXPRESSION TAG	UNP Q5TLG6
B	60	ALA	VAL	ENGINEERED MUTATION	UNP Q5TLG6
B	63	CR8	CYS	CHROMOPHORE	UNP Q5TLG6
B	63	CR8	TYR	CHROMOPHORE	UNP Q5TLG6
B	63	CR8	GLY	CHROMOPHORE	UNP Q5TLG6
B	94	SER	ASN	ENGINEERED MUTATION	UNP Q5TLG6
B	102	ILE	ASN	ENGINEERED MUTATION	UNP Q5TLG6
B	218	GLY	GLU	ENGINEERED MUTATION	UNP Q5TLG6
C	-35	MET	-	EXPRESSION TAG	UNP Q5TLG6
C	-34	ARG	-	EXPRESSION TAG	UNP Q5TLG6
C	-33	GLY	-	EXPRESSION TAG	UNP Q5TLG6
C	-32	SER	-	EXPRESSION TAG	UNP Q5TLG6
C	-31	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	-30	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	-29	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	-28	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	-27	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	-26	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	-25	GLY	-	EXPRESSION TAG	UNP Q5TLG6
C	-24	MET	-	EXPRESSION TAG	UNP Q5TLG6
C	-23	ALA	-	EXPRESSION TAG	UNP Q5TLG6
C	-22	SER	-	EXPRESSION TAG	UNP Q5TLG6
C	-21	MET	-	EXPRESSION TAG	UNP Q5TLG6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-20	THR	-	EXPRESSION TAG	UNP Q5TLG6
C	-19	GLY	-	EXPRESSION TAG	UNP Q5TLG6
C	-18	GLY	-	EXPRESSION TAG	UNP Q5TLG6
C	-17	GLN	-	EXPRESSION TAG	UNP Q5TLG6
C	-16	GLN	-	EXPRESSION TAG	UNP Q5TLG6
C	-15	MET	-	EXPRESSION TAG	UNP Q5TLG6
C	-14	GLY	-	EXPRESSION TAG	UNP Q5TLG6
C	-13	ARG	-	EXPRESSION TAG	UNP Q5TLG6
C	-12	ASN	-	EXPRESSION TAG	UNP Q5TLG6
C	-11	LEU	-	EXPRESSION TAG	UNP Q5TLG6
C	-10	TYR	-	EXPRESSION TAG	UNP Q5TLG6
C	-9	ASP	-	EXPRESSION TAG	UNP Q5TLG6
C	-8	ASP	-	EXPRESSION TAG	UNP Q5TLG6
C	-7	ASP	-	EXPRESSION TAG	UNP Q5TLG6
C	-6	ASP	-	EXPRESSION TAG	UNP Q5TLG6
C	-5	LYS	-	EXPRESSION TAG	UNP Q5TLG6
C	-4	ASP	-	EXPRESSION TAG	UNP Q5TLG6
C	-3	PRO	-	EXPRESSION TAG	UNP Q5TLG6
C	-2	GLY	-	EXPRESSION TAG	UNP Q5TLG6
C	-1	SER	-	EXPRESSION TAG	UNP Q5TLG6
C	0	HIS	-	EXPRESSION TAG	UNP Q5TLG6
C	60	ALA	VAL	ENGINEERED MUTATION	UNP Q5TLG6
C	63	CR8	CYS	CHROMOPHORE	UNP Q5TLG6
C	63	CR8	TYR	CHROMOPHORE	UNP Q5TLG6
C	63	CR8	GLY	CHROMOPHORE	UNP Q5TLG6
C	94	SER	ASN	ENGINEERED MUTATION	UNP Q5TLG6
C	102	ILE	ASN	ENGINEERED MUTATION	UNP Q5TLG6
C	218	GLY	GLU	ENGINEERED MUTATION	UNP Q5TLG6
D	-35	MET	-	EXPRESSION TAG	UNP Q5TLG6
D	-34	ARG	-	EXPRESSION TAG	UNP Q5TLG6
D	-33	GLY	-	EXPRESSION TAG	UNP Q5TLG6
D	-32	SER	-	EXPRESSION TAG	UNP Q5TLG6
D	-31	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	-30	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	-29	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	-28	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	-27	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	-26	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	-25	GLY	-	EXPRESSION TAG	UNP Q5TLG6
D	-24	MET	-	EXPRESSION TAG	UNP Q5TLG6
D	-23	ALA	-	EXPRESSION TAG	UNP Q5TLG6
D	-22	SER	-	EXPRESSION TAG	UNP Q5TLG6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-21	MET	-	EXPRESSION TAG	UNP Q5TLG6
D	-20	THR	-	EXPRESSION TAG	UNP Q5TLG6
D	-19	GLY	-	EXPRESSION TAG	UNP Q5TLG6
D	-18	GLY	-	EXPRESSION TAG	UNP Q5TLG6
D	-17	GLN	-	EXPRESSION TAG	UNP Q5TLG6
D	-16	GLN	-	EXPRESSION TAG	UNP Q5TLG6
D	-15	MET	-	EXPRESSION TAG	UNP Q5TLG6
D	-14	GLY	-	EXPRESSION TAG	UNP Q5TLG6
D	-13	ARG	-	EXPRESSION TAG	UNP Q5TLG6
D	-12	ASN	-	EXPRESSION TAG	UNP Q5TLG6
D	-11	LEU	-	EXPRESSION TAG	UNP Q5TLG6
D	-10	TYR	-	EXPRESSION TAG	UNP Q5TLG6
D	-9	ASP	-	EXPRESSION TAG	UNP Q5TLG6
D	-8	ASP	-	EXPRESSION TAG	UNP Q5TLG6
D	-7	ASP	-	EXPRESSION TAG	UNP Q5TLG6
D	-6	ASP	-	EXPRESSION TAG	UNP Q5TLG6
D	-5	LYS	-	EXPRESSION TAG	UNP Q5TLG6
D	-4	ASP	-	EXPRESSION TAG	UNP Q5TLG6
D	-3	PRO	-	EXPRESSION TAG	UNP Q5TLG6
D	-2	GLY	-	EXPRESSION TAG	UNP Q5TLG6
D	-1	SER	-	EXPRESSION TAG	UNP Q5TLG6
D	0	HIS	-	EXPRESSION TAG	UNP Q5TLG6
D	60	ALA	VAL	ENGINEERED MUTATION	UNP Q5TLG6
D	63	CR8	CYS	CHROMOPHORE	UNP Q5TLG6
D	63	CR8	TYR	CHROMOPHORE	UNP Q5TLG6
D	63	CR8	GLY	CHROMOPHORE	UNP Q5TLG6
D	94	SER	ASN	ENGINEERED MUTATION	UNP Q5TLG6
D	102	ILE	ASN	ENGINEERED MUTATION	UNP Q5TLG6
D	218	GLY	GLU	ENGINEERED MUTATION	UNP Q5TLG6
E	-35	MET	-	EXPRESSION TAG	UNP Q5TLG6
E	-34	ARG	-	EXPRESSION TAG	UNP Q5TLG6
E	-33	GLY	-	EXPRESSION TAG	UNP Q5TLG6
E	-32	SER	-	EXPRESSION TAG	UNP Q5TLG6
E	-31	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	-30	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	-29	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	-28	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	-27	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	-26	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	-25	GLY	-	EXPRESSION TAG	UNP Q5TLG6
E	-24	MET	-	EXPRESSION TAG	UNP Q5TLG6
E	-23	ALA	-	EXPRESSION TAG	UNP Q5TLG6

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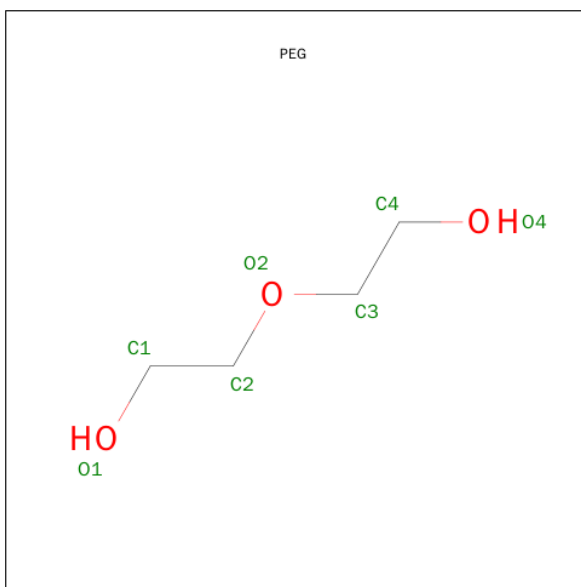
Chain	Residue	Modelled	Actual	Comment	Reference
E	-22	SER	-	EXPRESSION TAG	UNP Q5TLG6
E	-21	MET	-	EXPRESSION TAG	UNP Q5TLG6
E	-20	THR	-	EXPRESSION TAG	UNP Q5TLG6
E	-19	GLY	-	EXPRESSION TAG	UNP Q5TLG6
E	-18	GLY	-	EXPRESSION TAG	UNP Q5TLG6
E	-17	GLN	-	EXPRESSION TAG	UNP Q5TLG6
E	-16	GLN	-	EXPRESSION TAG	UNP Q5TLG6
E	-15	MET	-	EXPRESSION TAG	UNP Q5TLG6
E	-14	GLY	-	EXPRESSION TAG	UNP Q5TLG6
E	-13	ARG	-	EXPRESSION TAG	UNP Q5TLG6
E	-12	ASN	-	EXPRESSION TAG	UNP Q5TLG6
E	-11	LEU	-	EXPRESSION TAG	UNP Q5TLG6
E	-10	TYR	-	EXPRESSION TAG	UNP Q5TLG6
E	-9	ASP	-	EXPRESSION TAG	UNP Q5TLG6
E	-8	ASP	-	EXPRESSION TAG	UNP Q5TLG6
E	-7	ASP	-	EXPRESSION TAG	UNP Q5TLG6
E	-6	ASP	-	EXPRESSION TAG	UNP Q5TLG6
E	-5	LYS	-	EXPRESSION TAG	UNP Q5TLG6
E	-4	ASP	-	EXPRESSION TAG	UNP Q5TLG6
E	-3	PRO	-	EXPRESSION TAG	UNP Q5TLG6
E	-2	GLY	-	EXPRESSION TAG	UNP Q5TLG6
E	-1	SER	-	EXPRESSION TAG	UNP Q5TLG6
E	0	HIS	-	EXPRESSION TAG	UNP Q5TLG6
E	60	ALA	VAL	ENGINEERED MUTATION	UNP Q5TLG6
E	63	CR8	CYS	CHROMOPHORE	UNP Q5TLG6
E	63	CR8	TYR	CHROMOPHORE	UNP Q5TLG6
E	63	CR8	GLY	CHROMOPHORE	UNP Q5TLG6
E	94	SER	ASN	ENGINEERED MUTATION	UNP Q5TLG6
E	102	ILE	ASN	ENGINEERED MUTATION	UNP Q5TLG6
E	218	GLY	GLU	ENGINEERED MUTATION	UNP Q5TLG6
F	-35	MET	-	EXPRESSION TAG	UNP Q5TLG6
F	-34	ARG	-	EXPRESSION TAG	UNP Q5TLG6
F	-33	GLY	-	EXPRESSION TAG	UNP Q5TLG6
F	-32	SER	-	EXPRESSION TAG	UNP Q5TLG6
F	-31	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	-30	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	-29	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	-28	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	-27	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	-26	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	-25	GLY	-	EXPRESSION TAG	UNP Q5TLG6
F	-24	MET	-	EXPRESSION TAG	UNP Q5TLG6

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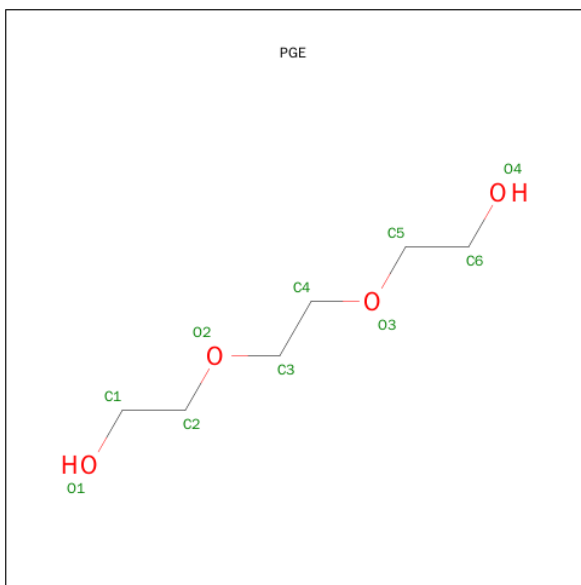
Chain	Residue	Modelled	Actual	Comment	Reference
F	-23	ALA	-	EXPRESSION TAG	UNP Q5TLG6
F	-22	SER	-	EXPRESSION TAG	UNP Q5TLG6
F	-21	MET	-	EXPRESSION TAG	UNP Q5TLG6
F	-20	THR	-	EXPRESSION TAG	UNP Q5TLG6
F	-19	GLY	-	EXPRESSION TAG	UNP Q5TLG6
F	-18	GLY	-	EXPRESSION TAG	UNP Q5TLG6
F	-17	GLN	-	EXPRESSION TAG	UNP Q5TLG6
F	-16	GLN	-	EXPRESSION TAG	UNP Q5TLG6
F	-15	MET	-	EXPRESSION TAG	UNP Q5TLG6
F	-14	GLY	-	EXPRESSION TAG	UNP Q5TLG6
F	-13	ARG	-	EXPRESSION TAG	UNP Q5TLG6
F	-12	ASN	-	EXPRESSION TAG	UNP Q5TLG6
F	-11	LEU	-	EXPRESSION TAG	UNP Q5TLG6
F	-10	TYR	-	EXPRESSION TAG	UNP Q5TLG6
F	-9	ASP	-	EXPRESSION TAG	UNP Q5TLG6
F	-8	ASP	-	EXPRESSION TAG	UNP Q5TLG6
F	-7	ASP	-	EXPRESSION TAG	UNP Q5TLG6
F	-6	ASP	-	EXPRESSION TAG	UNP Q5TLG6
F	-5	LYS	-	EXPRESSION TAG	UNP Q5TLG6
F	-4	ASP	-	EXPRESSION TAG	UNP Q5TLG6
F	-3	PRO	-	EXPRESSION TAG	UNP Q5TLG6
F	-2	GLY	-	EXPRESSION TAG	UNP Q5TLG6
F	-1	SER	-	EXPRESSION TAG	UNP Q5TLG6
F	0	HIS	-	EXPRESSION TAG	UNP Q5TLG6
F	60	ALA	VAL	ENGINEERED MUTATION	UNP Q5TLG6
F	63	CR8	CYS	CHROMOPHORE	UNP Q5TLG6
F	63	CR8	TYR	CHROMOPHORE	UNP Q5TLG6
F	63	CR8	GLY	CHROMOPHORE	UNP Q5TLG6
F	94	SER	ASN	ENGINEERED MUTATION	UNP Q5TLG6
F	102	ILE	ASN	ENGINEERED MUTATION	UNP Q5TLG6
F	218	GLY	GLU	ENGINEERED MUTATION	UNP Q5TLG6

- Molecule 2 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



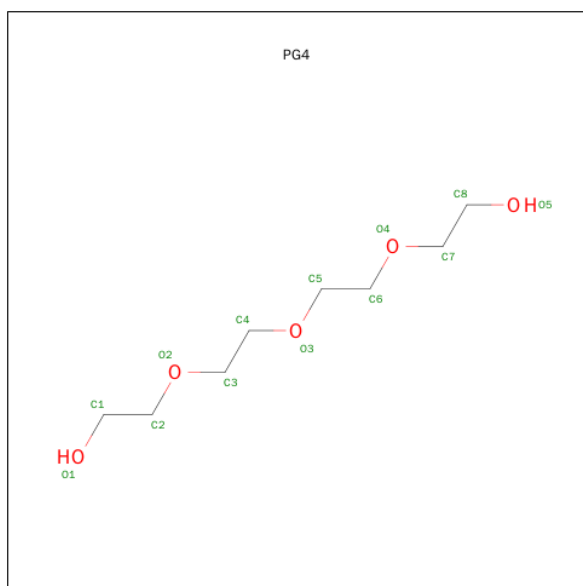
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			7	4	3		
2	B	1	Total	C	O	0	0
			7	4	3		
2	D	1	Total	C	O	0	0
			7	4	3		
2	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 3 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 4 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			13	8	5		
4	F	1	Total	C	O	0	0
			13	8	5		

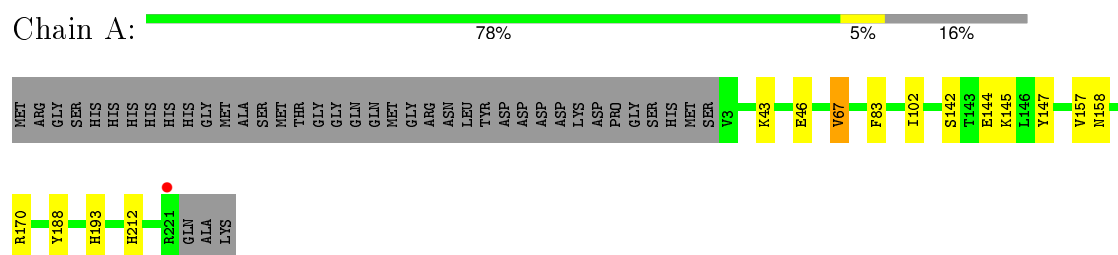
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	126	Total	O	0	0
			126	126		
5	B	84	Total	O	0	0
			84	84		
5	C	111	Total	O	0	0
			111	111		
5	D	98	Total	O	0	0
			98	98		
5	E	83	Total	O	0	0
			83	83		
5	F	99	Total	O	0	0
			99	99		

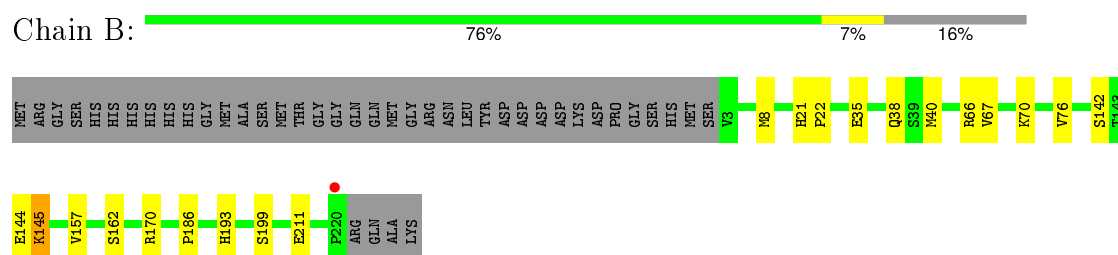
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

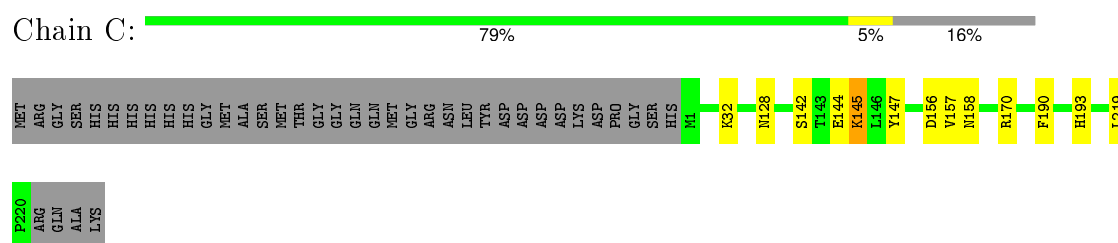
- Molecule 1: Fluorescent protein Dronpa



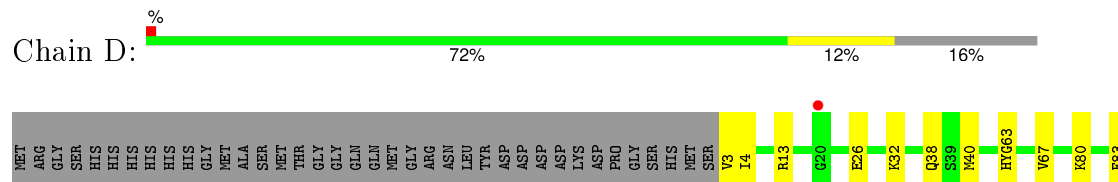
- Molecule 1: Fluorescent protein Dronpa

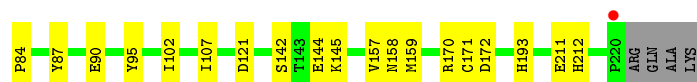


- Molecule 1: Fluorescent protein Dronpa

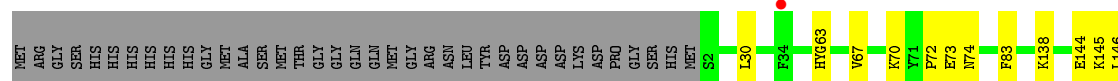
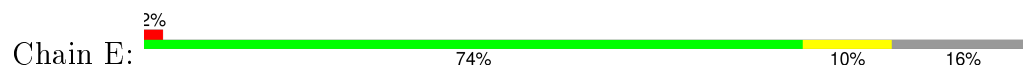


- Molecule 1: Fluorescent protein Dronpa

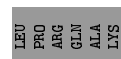
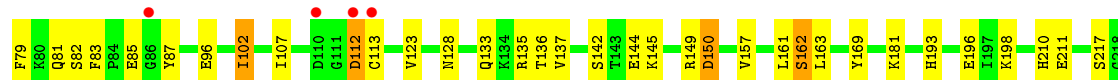
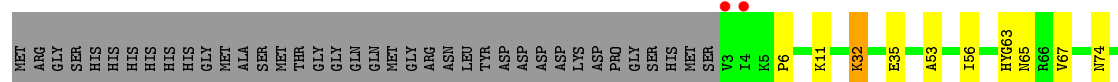




- Molecule 1: Fluorescent protein Dronpa



- Molecule 1: Fluorescent protein Dronpa



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.18Å 103.55Å 176.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	64.43 – 2.07 64.43 – 2.07	Depositor EDS
% Data completeness (in resolution range)	98.4 (64.43-2.07) 98.4 (64.43-2.07)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.70 (at 2.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.189 , 0.234 0.193 , 0.233	Depositor DCC
$R_{free}$ test set	3881 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	33.5	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 46.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	2 of 77037 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11101	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.36% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: PG4, CR8, PEG, PGE

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	0.56	0/1785	0.64	0/2410
1	B	0.51	0/1759	0.63	0/2379
1	C	0.53	0/1794	0.61	0/2422
1	D	0.56	0/1751	0.65	0/2367
1	E	0.52	0/1753	0.63	0/2369
1	F	0.53	0/1741	0.68	1/2350 (0.0%)
All	All	0.54	0/10583	0.64	1/14297 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	150	ASP	CB-CA-C	-6.83	96.74	110.40

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	1756	0	1683	12	0
1	B	1734	0	1649	11	0
1	C	1763	0	1692	9	0
1	D	1730	0	1644	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1732	0	1649	12	0
1	F	1721	0	1644	29	0
2	A	7	0	10	0	0
2	B	7	0	10	0	0
2	D	7	0	10	0	0
2	F	7	0	10	2	0
3	A	10	0	14	3	0
4	C	13	0	18	0	0
4	F	13	0	18	0	0
5	A	126	0	0	2	0
5	B	84	0	0	2	0
5	C	111	0	0	2	0
5	D	98	0	0	2	0
5	E	83	0	0	0	0
5	F	99	0	0	3	0
All	All	11101	0	10051	88	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 (88) 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:170:ARG:NH1	5:D:488:HOH:O	2.19	0.76
1:D:158:ASN:ND2	1:D:172:ASP:OD2	2.19	0.75
1:F:128:ASN:ND2	5:F:459:HOH:O	2.20	0.75
1:C:219:LEU:HD13	1:D:212:HIS:HD2	1.52	0.74
1:D:142:SER:OG	1:D:193:HIS:NE2	2.23	0.71
1:A:43:LYS:HZ1	3:A:302:PGE:H32	1.54	0.70
1:D:142:SER:HG	1:D:193:HIS:HE2	1.38	0.69
1:F:133:GLN:OE1	1:F:135:ARG:NH2	2.24	0.69
1:E:70:LYS:HB3	1:E:214:GLU:HG2	1.76	0.66
1:D:38:GLN:OE1	5:D:498:HOH:O	2.14	0.64
1:B:38:GLN:OE1	5:B:481:HOH:O	2.15	0.63
1:E:73:GLU:CD	1:E:73:GLU:H	2.02	0.63
1:A:212:HIS:ND1	5:A:504:HOH:O	2.31	0.61
1:C:142:SER:OG	1:C:193:HIS:NE2	2.34	0.60
1:E:146:LEU:HD23	1:E:153:LEU:HD21	1.83	0.60
1:B:145:LYS:HD3	5:B:471:HOH:O	2.02	0.59
1:F:67:VAL:HG11	1:F:83:PHE:CE1	2.37	0.59
1:F:67:VAL:HG11	1:F:83:PHE:HE1	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:158:ASN:ND2	1:E:172:ASP:OD2	2.36	0.58
1:F:81:GLN:O	1:F:181:LYS:NZ	2.34	0.58
1:F:144:GLU:HA	1:F:157:VAL:HB	1.85	0.57
1:F:112:ASP:OD2	1:F:112:ASP:N	2.36	0.57
1:A:43:LYS:NZ	3:A:302:PGE:H5	2.20	0.55
1:D:144:GLU:HA	1:D:157:VAL:HB	1.87	0.55
1:B:38:GLN:NE2	1:B:211:GLU:OE1	2.39	0.55
1:E:63:CR8:H4	1:E:177:TYR:OH	2.06	0.54
1:E:67:VAL:HG11	1:E:83:PHE:CE1	2.42	0.54
1:E:149:ARG:HG2	1:E:154:LYS:HE2	1.91	0.53
1:F:85:GLU:CD	1:F:181:LYS:HD3	2.28	0.53
1:F:11:LYS:HG3	1:F:113:CYS:SG	2.49	0.53
1:C:147:TYR:OH	1:D:170:ARG:NE	2.36	0.52
1:B:142:SER:OG	1:B:193:HIS:NE2	2.42	0.52
1:C:145:LYS:HG3	1:C:190:PHE:CE2	2.44	0.52
1:D:13:ARG:NH1	1:D:26:GLU:OE2	2.41	0.51
1:A:43:LYS:HE3	3:A:302:PGE:H4	1.93	0.51
1:E:144:GLU:HA	1:E:157:VAL:HB	1.93	0.51
1:A:142:SER:OG	1:A:193:HIS:NE2	2.44	0.50
1:F:6:PRO:O	5:F:466:HOH:O	2.19	0.50
1:B:35:GLU:HA	1:B:70:LYS:HD3	1.93	0.49
1:D:142:SER:HG	1:D:193:HIS:CD2	2.30	0.49
1:F:149:ARG:O	1:F:150:ASP:HB2	2.13	0.49
1:A:158:ASN:HB3	1:A:170:ARG:CZ	2.42	0.49
1:A:144:GLU:HA	1:A:157:VAL:HB	1.94	0.49
1:D:142:SER:OG	1:D:159:MET:SD	2.71	0.49
1:A:158:ASN:HB3	1:A:170:ARG:NH2	2.29	0.48
1:C:144:GLU:HA	1:C:157:VAL:HB	1.95	0.48
1:F:137:VAL:HB	1:F:162:SER:HB3	1.96	0.48
1:F:65:ASN:OD1	1:F:67:VAL:HG13	2.14	0.48
1:B:144:GLU:HA	1:B:157:VAL:HB	1.95	0.47
1:B:145:LYS:N	1:B:145:LYS:HE2	2.30	0.47
1:A:147:TYR:HB3	1:A:188:TYR:CD1	2.51	0.46
1:F:142:SER:OG	1:F:193:HIS:NE2	2.47	0.46
1:F:163:LEU:HD11	1:F:169:TYR:HB2	1.96	0.46
1:F:96:GLU:HA	2:F:301:PEG:H32	1.97	0.46
1:C:128:ASN:ND2	5:C:497:HOH:O	2.48	0.46
1:C:32:LYS:HB3	1:C:32:LYS:HE2	1.74	0.46
1:C:219:LEU:CD1	1:D:212:HIS:HD2	2.26	0.45
1:D:95:TYR:CD2	1:D:171:CYS:HB2	2.51	0.45
1:F:79:PHE:O	1:F:82:SER:OG	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:72:PRO:HB2	1:E:74:ASN:OD1	2.18	0.44
1:B:170:ARG:HB3	1:B:170:ARG:CZ	2.48	0.43
1:A:67:VAL:HG21	1:A:83:PHE:CE1	2.53	0.43
1:F:53:ALA:O	1:F:56:ILE:HG12	2.18	0.43
1:F:96:GLU:HB3	2:F:301:PEG:H21	2.00	0.42
1:F:210:HIS:HB2	5:F:487:HOH:O	2.19	0.42
5:C:507:HOH:O	1:D:142:SER:HB3	2.19	0.42
1:D:4:ILE:HD13	1:D:80:LYS:HB3	2.00	0.42
1:F:87:TYR:CZ	1:F:107:ILE:HD12	2.54	0.42
1:A:46:GLU:OE1	5:A:438:HOH:O	2.22	0.42
1:D:83:PHE:HB3	1:D:84:PRO:HA	2.01	0.42
1:F:63:CR8:H23	1:F:211:GLU:HB2	2.01	0.42
1:D:102:ILE:HD13	1:F:102:ILE:HG23	2.02	0.41
1:F:136:THR:HG21	1:F:161:LEU:HD13	2.01	0.41
1:E:201:ASP:OD2	1:E:206:ASN:HB2	2.20	0.41
1:E:148:VAL:HG21	1:E:185:LEU:HB3	2.02	0.41
1:D:90:GLU:HB3	1:F:123:VAL:HB	2.01	0.41
1:E:196:GLU:HG3	1:E:198:LYS:HD3	2.03	0.41
1:D:121:ASP:C	1:F:102:ILE:HD11	2.41	0.41
1:B:170:ARG:HB3	1:B:170:ARG:NH1	2.36	0.41
1:B:21[A]:HIS:HA	1:B:22:PRO:HD3	1.76	0.41
1:F:74:ASN:N	1:F:74:ASN:OD1	2.48	0.41
1:F:32:LYS:HG2	1:F:35:GLU:OE2	2.21	0.40
1:D:87:TYR:CZ	1:D:107:ILE:HD12	2.57	0.40
1:C:158:ASN:HB3	1:C:170:ARG:CZ	2.51	0.40
1:F:198:LYS:HB3	1:F:198:LYS:HE3	1.69	0.40
1:A:102:ILE:HD13	1:A:102:ILE:HG21	1.85	0.40
1:B:76:VAL:HB	1:B:186:PRO:HB3	2.03	0.40
1:D:40:MET:HG2	1:D:63:CR8:C10	2.51	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	216/258 (84%)	211 (98%)	5 (2%)	0	100	100
1	B	214/258 (83%)	212 (99%)	2 (1%)	0	100	100
1	C	218/258 (84%)	215 (99%)	3 (1%)	0	100	100
1	D	213/258 (83%)	211 (99%)	2 (1%)	0	100	100
1	E	214/258 (83%)	211 (99%)	3 (1%)	0	100	100
1	F	211/258 (82%)	209 (99%)	2 (1%)	0	100	100
All	All	1286/1548 (83%)	1269 (99%)	17 (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	186/218 (85%)	184 (99%)	2 (1%)	80	79
1	B	181/218 (83%)	174 (96%)	7 (4%)	39	31
1	C	188/218 (86%)	186 (99%)	2 (1%)	80	79
1	D	181/218 (83%)	176 (97%)	5 (3%)	51	45
1	E	181/218 (83%)	178 (98%)	3 (2%)	68	65
1	F	181/218 (83%)	174 (96%)	7 (4%)	39	31
All	All	1098/1308 (84%)	1072 (98%)	26 (2%)	57	51

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	VAL
1	A	145	LYS
1	B	8	MET
1	B	40	MET
1	B	66	ARG
1	B	67	VAL
1	B	145	LYS

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Mol	Chain	Res	Type
1	B	162	SER
1	B	199	SER
1	C	145	LYS
1	C	156	ASP
1	D	3	VAL
1	D	32	LYS
1	D	67	VAL
1	D	145	LYS
1	D	211	GLU
1	E	30	LEU
1	E	138	LYS
1	E	145	LYS
1	F	32	LYS
1	F	102	ILE
1	F	112	ASP
1	F	145	LYS
1	F	162	SER
1	F	196	GLU
1	F	217	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	194	HIS
1	D	38	GLN
1	D	74	ASN
1	D	206	ASN
1	E	158	ASN
1	E	194	HIS
1	E	212	HIS

### 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	CR8	A	63	1	20,27,28	1.97	5 (25%)	16,37,39	1.22	0
1	CR8	B	63	1	20,27,28	1.96	5 (25%)	16,37,39	1.78	5 (31%)
1	CR8	C	63	1	20,27,28	1.96	5 (25%)	16,37,39	1.51	4 (25%)
1	CR8	D	63	1	20,27,28	1.95	7 (35%)	16,37,39	1.68	6 (37%)
1	CR8	E	63	1	20,27,28	2.04	5 (25%)	16,37,39	1.27	2 (12%)
1	CR8	F	63	1	20,27,28	1.93	6 (30%)	16,37,39	1.55	3 (18%)

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	CR8	A	63	1	-	1/8/25/26	0/3/3/3
1	CR8	B	63	1	-	1/8/25/26	0/3/3/3
1	CR8	C	63	1	-	1/8/25/26	0/3/3/3
1	CR8	D	63	1	-	1/8/25/26	0/3/3/3
1	CR8	E	63	1	-	1/8/25/26	0/3/3/3
1	CR8	F	63	1	-	1/8/25/26	0/3/3/3

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	63	CR8	C4-C1	-2.97	1.39	1.45
1	B	63	CR8	C4-C1	-2.96	1.39	1.45
1	D	63	CR8	C4-C1	-2.91	1.39	1.45
1	E	63	CR8	C4-C1	-2.89	1.39	1.45
1	C	63	CR8	C4-C1	-2.79	1.39	1.45
1	F	63	CR8	C4-C1	-2.62	1.39	1.45
1	A	63	CR8	C2-C1	-2.44	1.40	1.45
1	D	63	CR8	C14-N15	-2.41	1.30	1.34
1	F	63	CR8	C2-C1	-2.36	1.40	1.45
1	C	63	CR8	C2-C1	-2.29	1.40	1.45
1	E	63	CR8	C2-C1	-2.26	1.40	1.45
1	D	63	CR8	C2-C1	-2.26	1.40	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	63	CR8	C17-N13	-2.22	1.45	1.49
1	B	63	CR8	C2-C1	-2.09	1.41	1.45
1	D	63	CR8	C17-N13	-2.04	1.45	1.49
1	D	63	CR8	C8-C7	3.14	1.44	1.36
1	F	63	CR8	C8-C7	3.43	1.44	1.36
1	B	63	CR8	C8-C7	3.48	1.44	1.36
1	A	63	CR8	C8-C7	3.80	1.45	1.36
1	C	63	CR8	C8-C7	3.88	1.45	1.36
1	E	63	CR8	C8-C7	3.94	1.46	1.36
1	C	63	CR8	C9-C12	3.98	1.49	1.39
1	F	63	CR8	O3-C1	4.03	1.37	1.24
1	A	63	CR8	C9-C12	4.03	1.49	1.39
1	D	63	CR8	O3-C1	4.20	1.37	1.24
1	D	63	CR8	C9-C12	4.20	1.49	1.39
1	B	63	CR8	C9-C12	4.21	1.49	1.39
1	F	63	CR8	C9-C12	4.24	1.49	1.39
1	B	63	CR8	O3-C1	4.27	1.37	1.24
1	E	63	CR8	C9-C12	4.32	1.50	1.39
1	A	63	CR8	O3-C1	4.37	1.38	1.24
1	C	63	CR8	O3-C1	4.40	1.38	1.24
1	E	63	CR8	O3-C1	4.72	1.39	1.24

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	63	CR8	C2-C6-C7	-3.13	119.22	122.00
1	D	63	CR8	C2-C6-C7	-3.08	119.26	122.00
1	B	63	CR8	O3-C1-C4	-2.71	117.24	121.51
1	F	63	CR8	C4-C5-C7	-2.49	119.79	122.00
1	D	63	CR8	O3-C1-C4	-2.42	117.69	121.51
1	C	63	CR8	C2-C6-C7	-2.40	119.87	122.00
1	D	63	CR8	C16-C14-N15	-2.27	118.76	123.77
1	F	63	CR8	C2-C6-C7	-2.24	120.01	122.00
1	B	63	CR8	C16-C14-N15	-2.16	119.00	123.77
1	C	63	CR8	C16-C14-N15	-2.08	119.18	123.77
1	D	63	CR8	C4-C5-C7	-2.06	120.17	122.00
1	D	63	CR8	C6-C7-C5	2.00	120.50	116.13
1	B	63	CR8	C4-C1-C2	2.03	120.54	116.77
1	E	63	CR8	C17-N13-C12	2.04	128.40	124.74
1	C	63	CR8	C17-N13-C12	2.05	128.41	124.74
1	E	63	CR8	C-C17-N13	2.10	115.78	112.37
1	F	63	CR8	C4-C1-C2	2.23	120.91	116.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	63	CR8	C4-C1-C2	2.46	121.33	116.77
1	C	63	CR8	C-C17-N13	3.26	117.67	112.37
1	B	63	CR8	C-C17-N13	3.40	117.89	112.37

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	63	CR8	C7-C8-C9-N15
1	B	63	CR8	C7-C8-C9-N15
1	F	63	CR8	C7-C8-C9-N15
1	A	63	CR8	C7-C8-C9-N15
1	C	63	CR8	C7-C8-C9-N15
1	E	63	CR8	C7-C8-C9-N15

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	63	CR8	1	0
1	E	63	CR8	1	0
1	F	63	CR8	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PEG	A	301	-	6,6,6	0.50	0	5,5,5	0.69	0
3	PGE	A	302	-	9,9,9	0.54	0	8,8,8	0.97	1 (12%)
2	PEG	B	301	-	6,6,6	0.44	0	5,5,5	1.17	1 (20%)
4	PG4	C	301	-	12,12,12	0.71	0	11,11,11	0.73	0
2	PEG	D	301	-	6,6,6	0.43	0	5,5,5	0.73	0
2	PEG	F	301	-	6,6,6	0.52	0	5,5,5	0.78	0
4	PG4	F	302	-	12,12,12	0.72	0	11,11,11	0.99	1 (9%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PEG	A	301	-	-	0/4/4/4	0/0/0/0
3	PGE	A	302	-	-	0/7/7/7	0/0/0/0
2	PEG	B	301	-	-	0/4/4/4	0/0/0/0
4	PG4	C	301	-	-	0/10/10/10	0/0/0/0
2	PEG	D	301	-	-	0/4/4/4	0/0/0/0
2	PEG	F	301	-	-	0/4/4/4	0/0/0/0
4	PG4	F	302	-	-	0/10/10/10	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	PGE	C5-O3-C4	2.15	122.57	113.31
4	F	302	PG4	C5-O3-C4	2.33	123.32	113.31
2	B	301	PEG	C3-O2-C2	2.51	124.10	113.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	302	PGE	3	0
2	F	301	PEG	2	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	216/258 (83%)	-0.30	1 (0%) 91 93	21, 31, 49, 73	0
1	B	215/258 (83%)	-0.15	1 (0%) 91 93	21, 34, 54, 79	0
1	C	217/258 (84%)	-0.20	0 100 100	20, 31, 49, 69	0
1	D	215/258 (83%)	-0.19	2 (0%) 85 87	22, 32, 51, 66	0
1	E	216/258 (83%)	-0.19	5 (2%) 64 67	22, 34, 52, 77	0
1	F	213/258 (82%)	-0.13	6 (2%) 56 62	22, 34, 51, 65	0
All	All	1292/1548 (83%)	-0.19	15 (1%) 81 83	20, 33, 52, 79	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	112	ASP	5.2
1	F	110	ASP	3.0
1	E	220	PRO	2.9
1	F	4	ILE	2.9
1	D	220	PRO	2.5
1	E	219	LEU	2.5
1	F	3	VAL	2.5
1	A	221	ARG	2.5
1	B	220	PRO	2.4
1	E	218	GLY	2.2
1	F	86	GLY	2.2
1	F	113	CYS	2.2
1	E	165	GLY	2.1
1	E	34	PHE	2.1
1	D	20	GLY	2.1

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	CR8	F	63	25/26	0.95	0.11	-	22,35,45,47	0
1	CR8	D	63	25/26	0.95	0.12	-	20,34,45,57	0
1	CR8	B	63	25/26	0.95	0.12	-	24,35,51,57	0
1	CR8	C	63	25/26	0.95	0.10	-	20,29,45,51	0
1	CR8	A	63	25/26	0.96	0.10	-	21,31,43,49	0
1	CR8	E	63	25/26	0.94	0.13	-	25,34,43,50	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	PG4	C	301	13/13	0.84	0.23	6.65	40,48,56,56	0
2	PEG	B	301	7/7	0.73	0.21	5.91	43,45,55,65	0
2	PEG	D	301	7/7	0.82	0.17	4.00	47,50,59,59	0
2	PEG	A	301	7/7	0.88	0.14	3.58	46,52,55,57	0
3	PGE	A	302	10/10	0.85	0.22	2.78	48,57,60,61	0
4	PG4	F	302	13/13	0.83	0.14	2.08	40,52,57,65	0
2	PEG	F	301	7/7	0.89	0.14	1.97	38,41,50,52	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.