



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:08 AM GMT

PDB ID : 2VZX
Title : STRUCTURAL AND SPECTROSCOPIC CHARACTERIZATION OF PHO-TOCONVERTING FLUORESCENT PROTEIN DENDRA2
Authors : Adam, V.; Nienhaus, K.; Bourgeois, D.; Nienhaus, G.U.
Deposited on : 2008-08-06
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at 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.

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

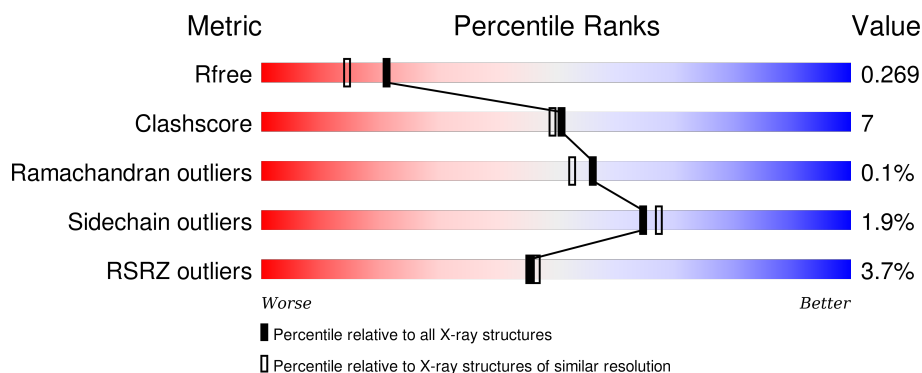
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 ≥ 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	229	<div> <div>2%</div> <div>84%</div> <div>12%</div> <div>•</div> </div>
1	B	229	<div> <div>2%</div> <div>85%</div> <div>11%</div> <div>••</div> </div>
1	C	229	<div> <div>3%</div> <div>86%</div> <div>12%</div> <div>•</div> </div>
1	D	229	<div> <div>3%</div> <div>84%</div> <div>13%</div> <div>•</div> </div>
1	E	229	<div> <div>2%</div> <div>85%</div> <div>11%</div> <div>••</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	229	<div><div></div><div>5%</div><div>87%</div><div>10%</div><div></div><div></div></div>
1	G	229	<div><div></div><div>10%</div><div>79%</div><div>17%</div><div></div><div></div></div>
1	H	229	<div><div></div><div>3%</div><div>86%</div><div>12%</div><div></div><div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15867 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 GREEN FLUORESCENT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	2	0
			1807	1160	308	331	8			
1	B	223	Total	C	N	O	S	0	1	0
			1819	1167	311	333	8			
1	C	225	Total	C	N	O	S	0	2	0
			1845	1182	319	336	8			
1	D	222	Total	C	N	O	S	0	1	0
			1807	1159	307	333	8			
1	E	223	Total	C	N	O	S	0	0	0
			1811	1162	308	333	8			
1	F	221	Total	C	N	O	S	0	1	0
			1799	1155	305	331	8			
1	G	221	Total	C	N	O	S	0	2	0
			1802	1157	305	332	8			
1	H	227	Total	C	N	O	S	0	1	0
			1859	1191	323	337	8			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	ALA	LEU	CONFLICT	UNP Q8T6U0
A	61	VAL	LEU	CONFLICT	UNP Q8T6U0
A	95	PHE	TYR	CONFLICT	UNP Q8T6U0
A	121	LYS	ASN	CONFLICT	UNP Q8T6U0
A	123	THR	MET	CONFLICT	UNP Q8T6U0
A	188	ALA	TYR	CONFLICT	UNP Q8T6U0
A	199	GLY	SER	CONFLICT	UNP Q8T6U0
A	213	ALA	GLY	CONFLICT	UNP Q8T6U0
A	224	VAL	ALA	CONFLICT	UNP Q8T6U0
B	40	ALA	LEU	CONFLICT	UNP Q8T6U0
B	61	VAL	LEU	CONFLICT	UNP Q8T6U0
B	95	PHE	TYR	CONFLICT	UNP Q8T6U0
B	121	LYS	ASN	CONFLICT	UNP Q8T6U0

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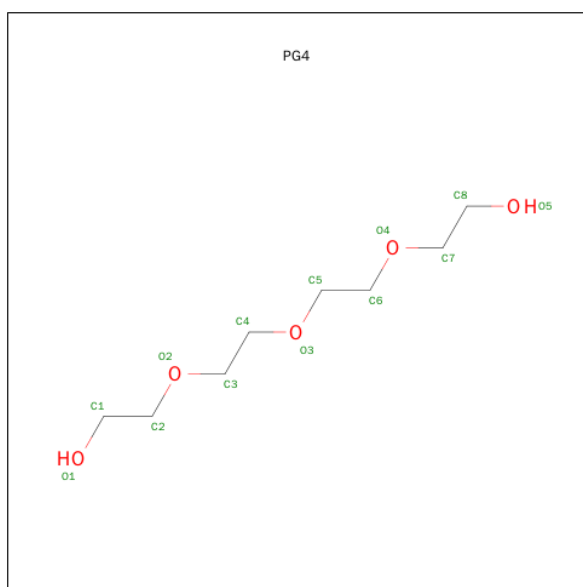
Chain	Residue	Modelled	Actual	Comment	Reference
B	123	THR	MET	CONFLICT	UNP Q8T6U0
B	188	ALA	TYR	CONFLICT	UNP Q8T6U0
B	199	GLY	SER	CONFLICT	UNP Q8T6U0
B	213	ALA	GLY	CONFLICT	UNP Q8T6U0
B	224	VAL	ALA	CONFLICT	UNP Q8T6U0
C	40	ALA	LEU	CONFLICT	UNP Q8T6U0
C	61	VAL	LEU	CONFLICT	UNP Q8T6U0
C	95	PHE	TYR	CONFLICT	UNP Q8T6U0
C	121	LYS	ASN	CONFLICT	UNP Q8T6U0
C	123	THR	MET	CONFLICT	UNP Q8T6U0
C	188	ALA	TYR	CONFLICT	UNP Q8T6U0
C	199	GLY	SER	CONFLICT	UNP Q8T6U0
C	213	ALA	GLY	CONFLICT	UNP Q8T6U0
C	224	VAL	ALA	CONFLICT	UNP Q8T6U0
D	40	ALA	LEU	CONFLICT	UNP Q8T6U0
D	61	VAL	LEU	CONFLICT	UNP Q8T6U0
D	95	PHE	TYR	CONFLICT	UNP Q8T6U0
D	121	LYS	ASN	CONFLICT	UNP Q8T6U0
D	123	THR	MET	CONFLICT	UNP Q8T6U0
D	188	ALA	TYR	CONFLICT	UNP Q8T6U0
D	199	GLY	SER	CONFLICT	UNP Q8T6U0
D	213	ALA	GLY	CONFLICT	UNP Q8T6U0
D	224	VAL	ALA	CONFLICT	UNP Q8T6U0
E	40	ALA	LEU	CONFLICT	UNP Q8T6U0
E	61	VAL	LEU	CONFLICT	UNP Q8T6U0
E	95	PHE	TYR	CONFLICT	UNP Q8T6U0
E	121	LYS	ASN	CONFLICT	UNP Q8T6U0
E	123	THR	MET	CONFLICT	UNP Q8T6U0
E	188	ALA	TYR	CONFLICT	UNP Q8T6U0
E	199	GLY	SER	CONFLICT	UNP Q8T6U0
E	213	ALA	GLY	CONFLICT	UNP Q8T6U0
E	224	VAL	ALA	CONFLICT	UNP Q8T6U0
F	40	ALA	LEU	CONFLICT	UNP Q8T6U0
F	61	VAL	LEU	CONFLICT	UNP Q8T6U0
F	95	PHE	TYR	CONFLICT	UNP Q8T6U0
F	121	LYS	ASN	CONFLICT	UNP Q8T6U0
F	123	THR	MET	CONFLICT	UNP Q8T6U0
F	188	ALA	TYR	CONFLICT	UNP Q8T6U0
F	199	GLY	SER	CONFLICT	UNP Q8T6U0
F	213	ALA	GLY	CONFLICT	UNP Q8T6U0
F	224	VAL	ALA	CONFLICT	UNP Q8T6U0
G	40	ALA	LEU	CONFLICT	UNP Q8T6U0

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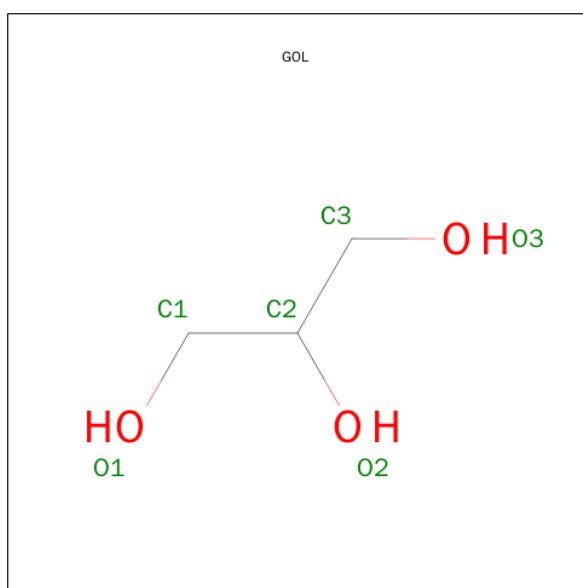
Chain	Residue	Modelled	Actual	Comment	Reference
G	61	VAL	LEU	CONFLICT	UNP Q8T6U0
G	95	PHE	TYR	CONFLICT	UNP Q8T6U0
G	121	LYS	ASN	CONFLICT	UNP Q8T6U0
G	123	THR	MET	CONFLICT	UNP Q8T6U0
G	188	ALA	TYR	CONFLICT	UNP Q8T6U0
G	199	GLY	SER	CONFLICT	UNP Q8T6U0
G	213	ALA	GLY	CONFLICT	UNP Q8T6U0
G	224	VAL	ALA	CONFLICT	UNP Q8T6U0
H	40	ALA	LEU	CONFLICT	UNP Q8T6U0
H	61	VAL	LEU	CONFLICT	UNP Q8T6U0
H	95	PHE	TYR	CONFLICT	UNP Q8T6U0
H	121	LYS	ASN	CONFLICT	UNP Q8T6U0
H	123	THR	MET	CONFLICT	UNP Q8T6U0
H	188	ALA	TYR	CONFLICT	UNP Q8T6U0
H	199	GLY	SER	CONFLICT	UNP Q8T6U0
H	213	ALA	GLY	CONFLICT	UNP Q8T6U0
H	224	VAL	ALA	CONFLICT	UNP Q8T6U0
A	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
A	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
A	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
B	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
B	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
B	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
C	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
C	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
C	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
D	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
D	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
D	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
E	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
E	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
E	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
F	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
F	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
F	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
G	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
G	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
G	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0
H	64	CR8	HIS	CHROMOPHORE	UNP Q8T6U0
H	64	CR8	TYR	CHROMOPHORE	UNP Q8T6U0
H	64	CR8	GLY	CHROMOPHORE	UNP Q8T6U0

- Molecule 2 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	8	5		
2	D	1	Total	C	O	0	0
			13	8	5		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

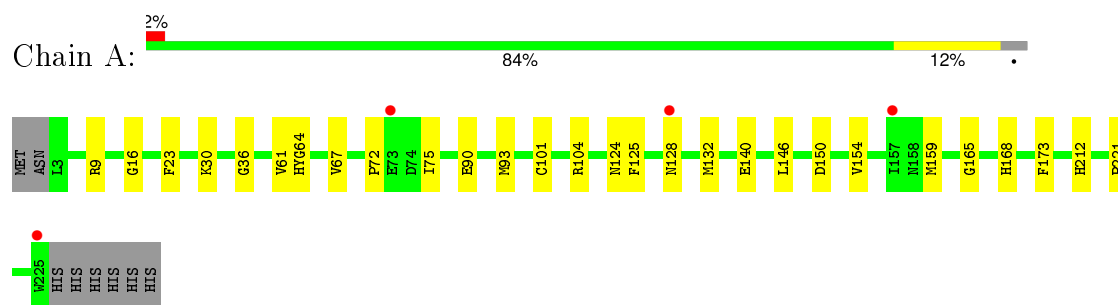
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	185	Total 185	O 185	0	0
4	B	189	Total 189	O 189	0	0
4	C	183	Total 183	O 183	0	0
4	D	148	Total 148	O 148	0	0
4	E	173	Total 173	O 173	0	0
4	F	128	Total 128	O 128	0	0
4	G	113	Total 113	O 113	0	0
4	H	161	Total 161	O 161	0	0

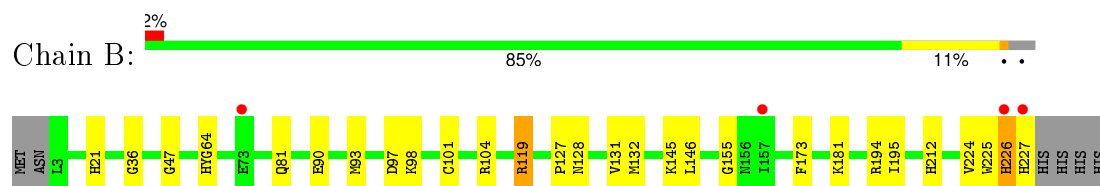
3 Residue-property plots [i](#)

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.

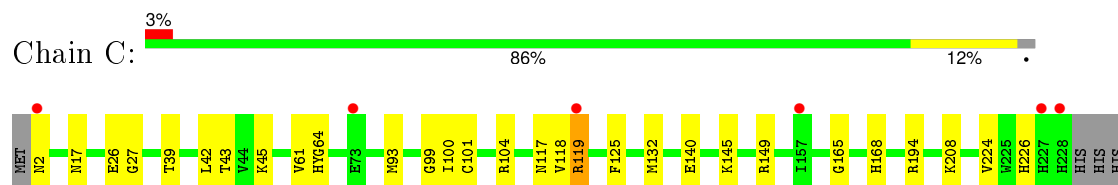
• Molecule 1: GREEN FLUORESCENT PROTEIN



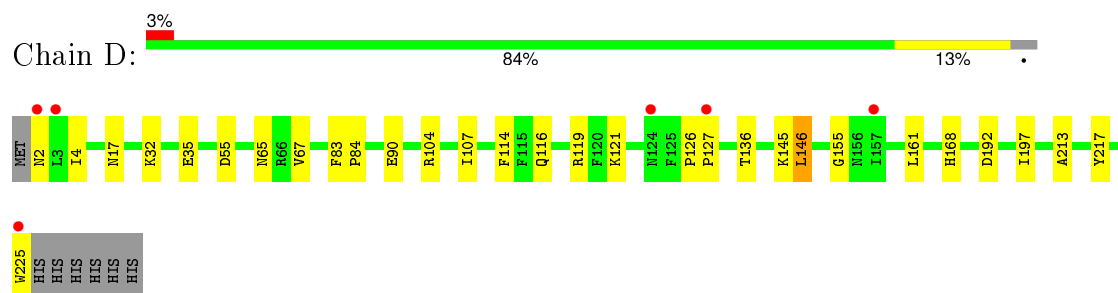
• Molecule 1: GREEN FLUORESCENT PROTEIN



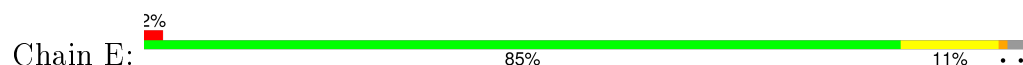
• Molecule 1: GREEN FLUORESCENT PROTEIN



• Molecule 1: GREEN FLUORESCENT PROTEIN

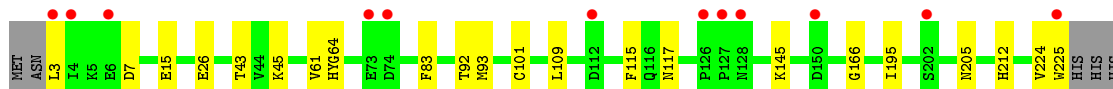
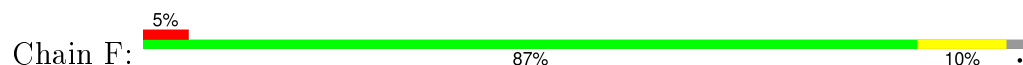


• Molecule 1: GREEN FLUORESCENT PROTEIN

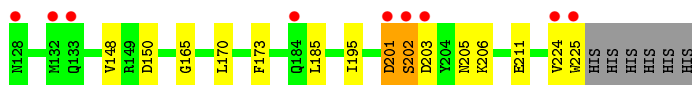
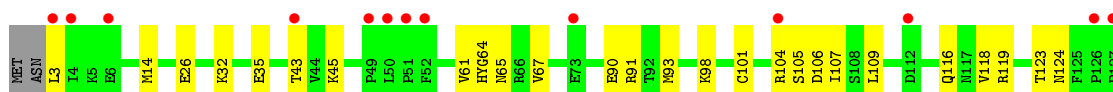
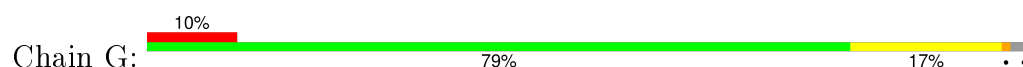




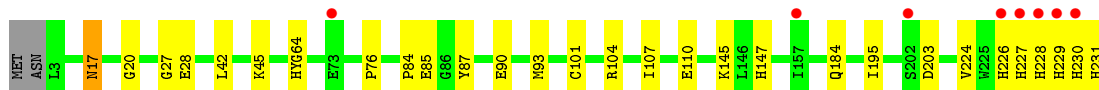
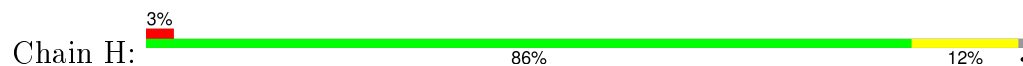
• Molecule 1: GREEN FLUORESCENT PROTEIN



• Molecule 1: GREEN FLUORESCENT PROTEIN



• Molecule 1: GREEN FLUORESCENT PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	71.26 Å 76.85 Å 92.50 Å 90.05° 108.17° 106.58°	Depositor
Resolution (Å)	33.50 – 2.00 33.49 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (33.50-2.00) 91.4 (33.49-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.97 (at 2.00 Å)	Xtriage
Refinement program	REFMAC 5.5.0038	Depositor
R, R_{free}	0.212 , 0.269 0.211 , 0.269	Depositor DCC
R_{free} test set	5661 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.064	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 113213 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	15867	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.27% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CR8, PG4

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	0.49	0/1834	0.60	0/2479
1	B	0.51	0/1845	0.61	0/2495
1	C	0.48	0/1875	0.61	0/2535
1	D	0.48	0/1831	0.63	1/2476 (0.0%)
1	E	0.49	0/1834	0.62	0/2481
1	F	0.45	0/1823	0.59	0/2465
1	G	0.44	0/1829	0.61	0/2473
1	H	0.46	0/1889	0.60	0/2555
All	All	0.48	0/14760	0.61	1/19959 (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	D	146	LEU	CA-CB-CG	6.39	130.01	115.30

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	1807	0	1771	18	0
1	B	1819	0	1772	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1845	0	1798	34	0
1	D	1807	0	1764	24	0
1	E	1811	0	1759	29	0
1	F	1799	0	1758	12	0
1	G	1802	0	1763	39	0
1	H	1859	0	1800	18	0
2	A	13	0	18	3	0
2	D	13	0	18	2	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
4	A	185	0	0	2	0
4	B	189	0	0	4	0
4	C	183	0	0	4	0
4	D	148	0	0	6	0
4	E	173	0	0	9	0
4	F	128	0	0	3	0
4	G	113	0	0	5	0
4	H	161	0	0	4	0
All	All	15867	0	14237	199	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 7.

The worst 5 of 199 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:104[A]:ARG:HH11	1:C:119[A]:ARG:CZ	1.24	1.50
1:G:104[B]:ARG:NH2	1:G:104[B]:ARG:HB2	1.57	1.20
1:C:104[A]:ARG:NH1	1:C:119[A]:ARG:CZ	2.03	1.18
1:G:202:SER:HB3	1:G:203:ASP:HB2	1.26	1.18
1:C:104[A]:ARG:HH11	1:C:119[A]:ARG:NE	1.42	1.17

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	220/229 (96%)	218 (99%)	2 (1%)	0	100	100
1	B	221/229 (96%)	219 (99%)	2 (1%)	0	100	100
1	C	224/229 (98%)	219 (98%)	5 (2%)	0	100	100
1	D	220/229 (96%)	218 (99%)	2 (1%)	0	100	100
1	E	220/229 (96%)	219 (100%)	1 (0%)	0	100	100
1	F	219/229 (96%)	217 (99%)	2 (1%)	0	100	100
1	G	220/229 (96%)	216 (98%)	3 (1%)	1 (0%)	34	26
1	H	225/229 (98%)	220 (98%)	5 (2%)	0	100	100
All	All	1769/1832 (97%)	1746 (99%)	22 (1%)	1 (0%)	56	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	202	SER

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	195/201 (97%)	193 (99%)	2 (1%)	82	85
1	B	196/201 (98%)	194 (99%)	2 (1%)	82	85
1	C	199/201 (99%)	196 (98%)	3 (2%)	72	75
1	D	195/201 (97%)	194 (100%)	1 (0%)	92	94
1	E	195/201 (97%)	189 (97%)	6 (3%)	47	46
1	F	194/201 (96%)	191 (98%)	3 (2%)	72	75
1	G	195/201 (97%)	186 (95%)	9 (5%)	33	28
1	H	200/201 (100%)	196 (98%)	4 (2%)	63	65
All	All	1569/1608 (98%)	1539 (98%)	30 (2%)	65	67

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	226	HIS
1	F	15	GLU
1	H	28	GLU
1	F	7	ASP
1	G	67	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	200	ASN
1	D	128	ASN
1	H	184	GLN
1	D	17	ASN
1	D	21	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 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	64	1	20,27,28	1.72	4 (20%)	16,37,39	1.91	4 (25%)
1	CR8	B	64	1	20,27,28	1.69	4 (20%)	16,37,39	2.08	4 (25%)
1	CR8	C	64	1	20,27,28	1.64	5 (25%)	16,37,39	1.90	6 (37%)
1	CR8	D	64	1	20,27,28	1.72	7 (35%)	16,37,39	2.00	4 (25%)
1	CR8	E	64	1	20,27,28	1.67	5 (25%)	16,37,39	2.18	6 (37%)
1	CR8	F	64	1	20,27,28	1.78	6 (30%)	16,37,39	1.65	3 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CR8	G	64	1	20,27,28	1.83	5 (25%)	16,37,39	1.42	3 (18%)
1	CR8	H	64	1	20,27,28	1.69	3 (15%)	16,37,39	2.18	4 (25%)

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	64	1	-	0/8/25/26	0/3/3/3
1	CR8	B	64	1	-	0/8/25/26	0/3/3/3
1	CR8	C	64	1	-	0/8/25/26	0/3/3/3
1	CR8	D	64	1	-	0/8/25/26	0/3/3/3
1	CR8	E	64	1	-	0/8/25/26	0/3/3/3
1	CR8	F	64	1	-	0/8/25/26	0/3/3/3
1	CR8	G	64	1	-	0/8/25/26	0/3/3/3
1	CR8	H	64	1	-	0/8/25/26	0/3/3/3

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	64	CR8	C4-C1	-2.95	1.39	1.45
1	D	64	CR8	C4-C1	-2.73	1.39	1.45
1	A	64	CR8	C4-C1	-2.71	1.39	1.45
1	G	64	CR8	C4-C1	-2.64	1.39	1.45
1	F	64	CR8	C4-C1	-2.52	1.40	1.45

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	64	CR8	C2-C6-C7	-3.43	118.96	122.00
1	B	64	CR8	C2-C6-C7	-3.26	119.11	122.00
1	D	64	CR8	C2-C6-C7	-3.16	119.19	122.00
1	E	64	CR8	C2-C6-C7	-2.99	119.35	122.00
1	C	64	CR8	C5-C7-C8	-2.87	113.78	121.85

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	64	CR8	1	0
1	B	64	CR8	1	0
1	C	64	CR8	1	0
1	E	64	CR8	2	0
1	F	64	CR8	2	0
1	G	64	CR8	2	0
1	H	64	CR8	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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	PG4	A	1226	-	12,12,12	0.58	0	11,11,11	0.42	0
3	GOL	B	1228	-	5,5,5	0.34	0	5,5,5	0.24	0
3	GOL	C	1229	-	5,5,5	0.38	0	5,5,5	0.32	0
2	PG4	D	1226	-	12,12,12	0.60	0	11,11,11	0.52	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
2	PG4	A	1226	-	-	0/10/10/10	0/0/0/0
3	GOL	B	1228	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1229	-	-	0/4/4/4	0/0/0/0
2	PG4	D	1226	-	-	0/10/10/10	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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
2	A	1226	PG4	3	0
2	D	1226	PG4	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, 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	220/229 (96%)	0.17	4 (1%) 71 72	10, 20, 28, 39	0
1	B	222/229 (96%)	0.07	4 (1%) 71 72	10, 17, 25, 33	0
1	C	224/229 (97%)	0.19	6 (2%) 58 58	10, 20, 30, 39	0
1	D	221/229 (96%)	0.21	6 (2%) 58 58	11, 20, 29, 42	0
1	E	222/229 (96%)	0.05	4 (1%) 71 72	9, 17, 26, 39	0
1	F	220/229 (96%)	0.49	12 (5%) 29 30	13, 26, 37, 42	0
1	G	220/229 (96%)	0.84	22 (10%) 9 10	15, 30, 44, 48	0
1	H	226/229 (98%)	0.18	8 (3%) 48 49	11, 19, 31, 53	0
All	All	1775/1832 (96%)	0.27	66 (3%) 45 47	9, 20, 37, 53	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	225	TRP	7.4
1	A	225	TRP	7.3
1	G	225	TRP	7.0
1	F	225	TRP	6.7
1	H	228	HIS	6.1

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
1	CR8	A	64	25/26	0.91	0.15	-	9,16,17,18	0
1	CR8	H	64	25/26	0.94	0.14	-	7,11,14,15	0
1	CR8	G	64	25/26	0.87	0.15	-	12,23,28,28	0
1	CR8	D	64	25/26	0.94	0.15	-	9,14,17,18	0
1	CR8	F	64	25/26	0.91	0.14	-	15,20,24,24	0
1	CR8	C	64	25/26	0.89	0.15	-	6,16,18,18	0
1	CR8	E	64	25/26	0.95	0.15	-	10,12,14,14	0
1	CR8	B	64	25/26	0.91	0.15	-	10,12,14,15	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	C	1229	6/6	0.73	0.15	0.93	33,35,36,37	0
2	PG4	D	1226	13/13	0.82	0.15	-0.22	32,34,35,35	0
2	PG4	A	1226	13/13	0.85	0.14	-0.23	31,34,36,37	0
3	GOL	B	1228	6/6	0.70	0.15	-0.32	43,43,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.