



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 17, 2017 – 05:46 AM EDT

PDB ID : 4W74
Title : Crystal Structure of Full-Length Split GFP Mutant E115C/T118H With Metal Mediated Crystal Contacts, P 1 21 1 Space Group
Authors : Leibly, D.J.; Waldo, G.S.; Yeates, T.O.
Deposited on : unknown
Resolution : 2.10 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029824

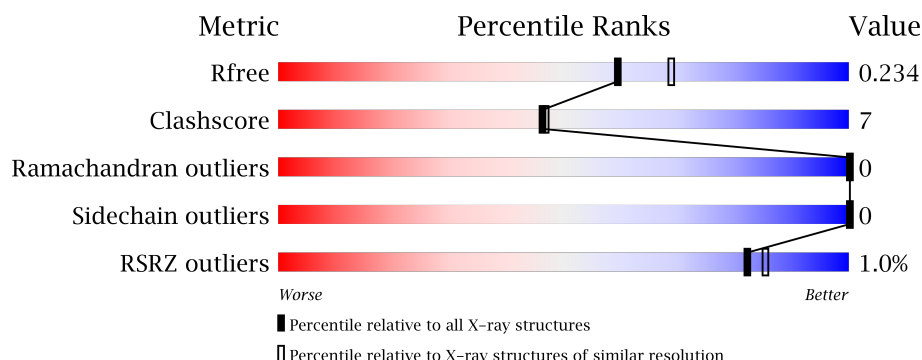
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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 style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 12%, green 85%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 85% 12% .. </div> </div>
1	B	229	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 11%, green 86%, grey 11%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 86% 11% . </div> </div>
1	C	229	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 7%, green 91%, grey 2%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 91% 7% . </div> </div>
1	D	229	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 12%, green 85%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 85% 12% . </div> </div>
1	E	229	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 10%, green 87%, grey 12%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 87% 10% . </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	229	<div><div><div>%</div><div><div></div><div>88%</div><div>10%</div><div></div></div><div></div></div></div>
1	G	229	<div><div><div>%</div><div><div></div><div>85%</div><div>12%</div><div></div></div><div></div></div></div>
1	H	229	<div><div><div></div><div><div></div><div>84%</div><div>13%</div><div></div></div><div></div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14583 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 E115C/T118H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1799	1146	306	343	4			
1	B	224	Total	C	N	O	S	0	0	0
			1795	1144	306	341	4			
1	C	225	Total	C	N	O	S	0	0	0
			1801	1146	308	343	4			
1	D	222	Total	C	N	O	S	0	0	0
			1781	1135	302	340	4			
1	E	224	Total	C	N	O	S	0	0	0
			1799	1146	306	343	4			
1	F	225	Total	C	N	O	S	0	0	0
			1796	1145	303	344	4			
1	G	225	Total	C	N	O	S	0	0	0
			1806	1150	307	345	4			
1	H	224	Total	C	N	O	S	0	0	0
			1799	1146	306	343	4			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		

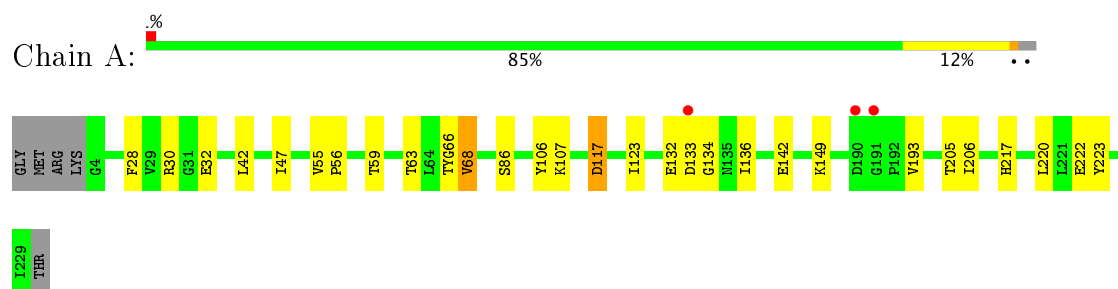
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	27	Total 27	O 27	0	0
3	B	24	Total 24	O 24	0	0
3	C	21	Total 21	O 21	0	0
3	D	26	Total 26	O 26	0	0
3	E	29	Total 29	O 29	0	0
3	F	20	Total 20	O 20	0	0
3	G	22	Total 22	O 22	0	0
3	H	32	Total 32	O 32	0	0

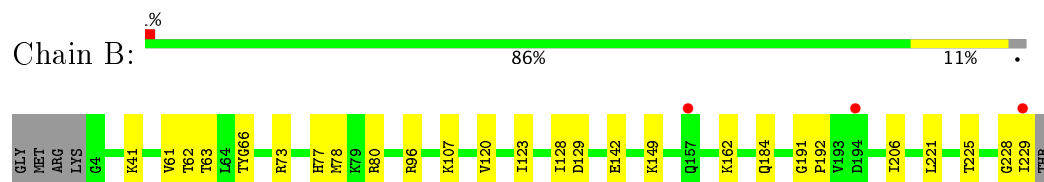
3 Residue-property plots [i](#)

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

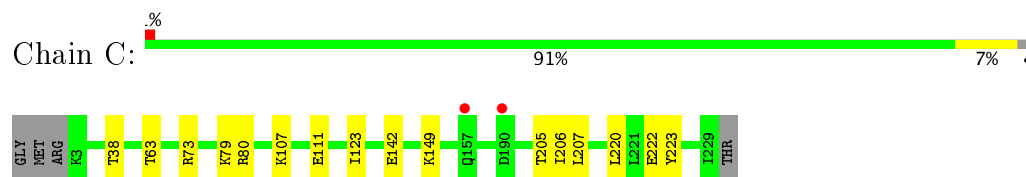
- Molecule 1: fluorescent protein E115C/T118H



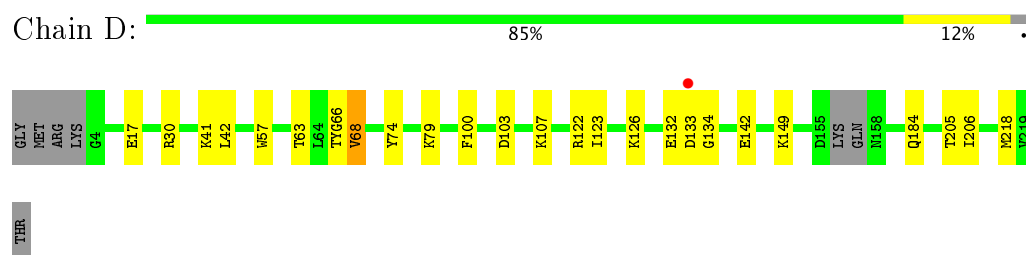
- Molecule 1: fluorescent protein E115C/T118H



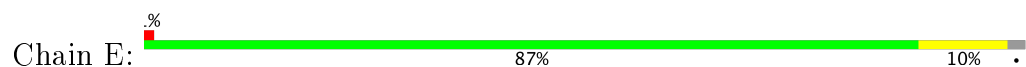
- Molecule 1: fluorescent protein E115C/T118H



- Molecule 1: fluorescent protein E115C/T118H

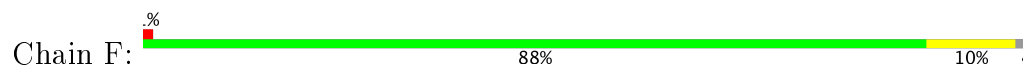


- Molecule 1: fluorescent protein E115C/T118H

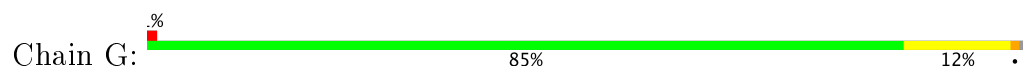




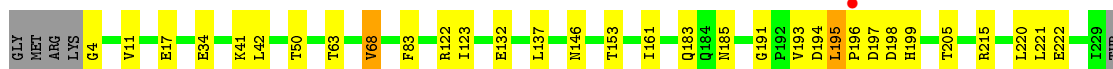
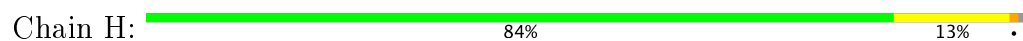
- Molecule 1: fluorescent protein E115C/T118H



- Molecule 1: fluorescent protein E115C/T118H



- Molecule 1: fluorescent protein E115C/T118H



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.44Å 119.79Å 130.57Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	88.27 – 2.10 88.27 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.7 (88.27-2.10) 98.8 (88.27-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_1555)	Depositor
R, R_{free}	0.212 , 0.235 0.212 , 0.234	Depositor DCC
R_{free} test set	11939 reflections (10.00%)	DCC
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.790	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.468 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14583	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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: ZN, CRO

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	0.57	1/1817 (0.1%)	0.73	2/2457 (0.1%)
1	B	0.56	0/1813	0.72	0/2452
1	C	0.58	0/1818	0.75	1/2457 (0.0%)
1	D	0.62	1/1798 (0.1%)	0.76	2/2431 (0.1%)
1	E	0.61	1/1817 (0.1%)	0.74	1/2457 (0.0%)
1	F	0.55	0/1814	0.72	2/2455 (0.1%)
1	G	0.58	1/1824 (0.1%)	0.78	3/2467 (0.1%)
1	H	0.59	1/1817 (0.1%)	0.77	2/2457 (0.1%)
All	All	0.58	5/14518 (0.0%)	0.75	13/19633 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	68	VAL	N-CA	-7.26	1.31	1.46
1	A	68	VAL	N-CA	-7.06	1.32	1.46
1	E	68	VAL	N-CA	-7.00	1.32	1.46
1	G	68	VAL	N-CA	-6.75	1.32	1.46
1	D	68	VAL	N-CA	-5.76	1.34	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	195	LEU	C-N-CD	-6.19	106.98	120.60
1	C	79	LYS	CD-CE-NZ	6.13	125.80	111.70
1	H	4	GLY	N-CA-C	6.01	128.14	113.10
1	G	30	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	A	132	GLU	CB-CA-C	5.68	121.76	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	190	ASP	Mainchain

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	1799	0	1746	33	0
1	B	1795	0	1742	25	0
1	C	1801	0	1751	17	1
1	D	1781	0	1724	29	0
1	E	1799	0	1747	35	0
1	F	1796	0	1737	18	1
1	G	1806	0	1752	38	0
1	H	1799	0	1746	32	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
3	A	27	0	0	2	0
3	B	24	0	0	1	0
3	C	21	0	0	0	0
3	D	26	0	0	1	0
3	E	29	0	0	1	0
3	F	20	0	0	3	0
3	G	22	0	0	3	0
3	H	32	0	0	3	0
All	All	14583	0	13945	205	1

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 205 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:E:77:HIS:CE1	1:E:229:ILE:HD11	1.57	1.37
1:D:57:TRP:HB3	1:D:218:MET:CE	1.54	1.34
1:E:77:HIS:CE1	1:E:229:ILE:CD1	2.26	1.17
1:D:57:TRP:HB3	1:D:218:MET:HE2	1.29	1.14
1:E:77:HIS:ND1	1:E:229:ILE:HD11	1.65	1.10

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:111:GLU:OE1	1:F:158:ASN:ND2[2_455]	1.88	0.32

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	219/229 (96%)	214 (98%)	5 (2%)	0	100	100
1	B	219/229 (96%)	214 (98%)	5 (2%)	0	100	100
1	C	220/229 (96%)	217 (99%)	3 (1%)	0	100	100
1	D	215/229 (94%)	210 (98%)	5 (2%)	0	100	100
1	E	219/229 (96%)	214 (98%)	5 (2%)	0	100	100
1	F	220/229 (96%)	216 (98%)	4 (2%)	0	100	100
1	G	220/229 (96%)	217 (99%)	3 (1%)	0	100	100
1	H	219/229 (96%)	217 (99%)	2 (1%)	0	100	100
All	All	1751/1832 (96%)	1719 (98%)	32 (2%)	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	193/197 (98%)	193 (100%)	0	100	100
1	B	192/197 (98%)	192 (100%)	0	100	100
1	C	193/197 (98%)	193 (100%)	0	100	100
1	D	191/197 (97%)	191 (100%)	0	100	100
1	E	193/197 (98%)	193 (100%)	0	100	100
1	F	192/197 (98%)	192 (100%)	0	100	100
1	G	194/197 (98%)	194 (100%)	0	100	100
1	H	193/197 (98%)	193 (100%)	0	100	100
All	All	1541/1576 (98%)	1541 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	146	ASN
1	H	185	ASN
1	H	146	ASN
1	F	94	GLN
1	H	159	ASN

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	CRO	A	66	1	23,23,24	1.66	5 (21%)	27,32,34	3.06	9 (33%)
1	CRO	B	66	1	23,23,24	3.47	4 (17%)	27,32,34	4.00	7 (25%)
1	CRO	C	66	1	23,23,24	1.98	7 (30%)	27,32,34	2.94	6 (22%)
1	CRO	D	66	1	23,23,24	1.63	4 (17%)	27,32,34	3.44	11 (40%)
1	CRO	E	66	1	23,23,24	1.75	5 (21%)	27,32,34	3.08	8 (29%)
1	CRO	F	66	1	23,23,24	3.47	4 (17%)	27,32,34	3.98	7 (25%)
1	CRO	G	66	1	23,23,24	1.63	4 (17%)	27,32,34	3.47	9 (33%)
1	CRO	H	66	1	23,23,24	1.95	7 (30%)	27,32,34	3.25	7 (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	CRO	A	66	1	-	0/12/31/32	0/2/2/2
1	CRO	B	66	1	-	0/12/31/32	0/2/2/2
1	CRO	C	66	1	-	0/12/31/32	0/2/2/2
1	CRO	D	66	1	-	0/12/31/32	0/2/2/2
1	CRO	E	66	1	-	0/12/31/32	0/2/2/2
1	CRO	F	66	1	-	0/12/31/32	0/2/2/2
1	CRO	G	66	1	-	0/12/31/32	0/2/2/2
1	CRO	H	66	1	-	0/12/31/32	0/2/2/2

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	66	CRO	CA1-N1	-3.89	1.35	1.47
1	E	66	CRO	CA3-N3	-3.02	1.40	1.47
1	C	66	CRO	OG1-CB1	-2.77	1.35	1.43
1	F	66	CRO	C2-N3	-2.74	1.33	1.39
1	B	66	CRO	C2-N3	-2.74	1.33	1.39

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	66	CRO	O2-C2-CA2	-11.99	124.50	130.97
1	G	66	CRO	O2-C2-CA2	-11.18	124.94	130.97
1	H	66	CRO	O2-C2-CA2	-10.15	125.50	130.97
1	B	66	CRO	O2-C2-CA2	-10.04	125.56	130.97
1	F	66	CRO	O2-C2-CA2	-10.02	125.57	130.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	66	CRO	3	0
1	B	66	CRO	5	0
1	D	66	CRO	1	0
1	F	66	CRO	2	0
1	G	66	CRO	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	223/229 (97%)	-0.15	3 (1%) 77 81	26, 37, 52, 83	0
1	B	223/229 (97%)	-0.11	3 (1%) 77 81	25, 38, 64, 82	0
1	C	224/229 (97%)	-0.16	2 (0%) 84 86	24, 37, 61, 76	0
1	D	221/229 (96%)	-0.18	1 (0%) 90 92	25, 36, 53, 68	0
1	E	223/229 (97%)	-0.18	2 (0%) 84 86	26, 35, 55, 105	0
1	F	224/229 (97%)	-0.13	2 (0%) 84 86	27, 38, 59, 80	0
1	G	224/229 (97%)	-0.10	3 (1%) 77 81	28, 39, 59, 81	0
1	H	223/229 (97%)	-0.22	1 (0%) 92 93	27, 35, 54, 92	0
All	All	1785/1832 (97%)	-0.15	17 (0%) 82 85	24, 37, 58, 105	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	191	GLY	5.9
1	B	157	GLN	4.1
1	D	133	ASP	3.2
1	E	192	PRO	2.8
1	A	133	ASP	2.7

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	CRO	B	66	22/23	0.91	0.14	-	28,36,45,52	0
1	CRO	D	66	22/23	0.93	0.10	-	29,34,41,50	0
1	CRO	F	66	22/23	0.90	0.14	-	23,37,44,44	0
1	CRO	C	66	22/23	0.94	0.12	-	32,38,41,44	0
1	CRO	G	66	22/23	0.94	0.11	-	34,35,39,45	0
1	CRO	A	66	22/23	0.96	0.10	-	26,32,36,39	0
1	CRO	E	66	22/23	0.92	0.11	-	26,33,39,45	0
1	CRO	H	66	22/23	0.94	0.11	-	30,36,42,50	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
2	ZN	D	301	1/1	0.98	0.14	-	42,42,42,42	0
2	ZN	A	301	1/1	0.94	0.14	-	45,45,45,45	0
2	ZN	C	301	1/1	0.99	0.08	-	43,43,43,43	0
2	ZN	E	301	1/1	0.99	0.06	-	42,42,42,42	0
2	ZN	B	302	1/1	0.99	0.12	-	43,43,43,43	0
2	ZN	B	301	1/1	0.98	0.09	-	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.