



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:24 AM GMT

PDB ID : 2QLE
Title : GFP/S205V mutant
Authors : Shu, X.; Remington, S.J.
Deposited on : 2007-07-12
Resolution : 1.59 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

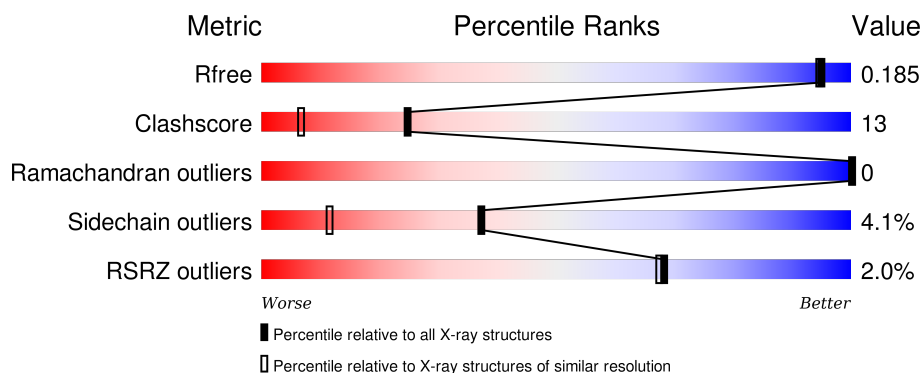
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	236	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>22%</div> <div>• •</div> </div> </div>
1	B	236	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>17%</div> <div>• •</div> </div> </div>
1	C	236	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>20%</div> <div>• •</div> </div> </div>
1	D	236	<div> <div>%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>•</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7961 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 fluorescence protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	9	0
			1818	1165	300	347	6			
1	B	226	Total	C	N	O	S	0	4	0
			1756	1130	300	320	6			
1	C	226	Total	C	N	O	S	0	2	0
			1774	1138	301	329	6			
1	D	226	Total	C	N	O	S	0	3	0
			1729	1105	292	326	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	CRO	SER	CHROMOPHORE	UNP Q8GHE2
A	205	VAL	SER	ENGINEERED	UNP Q8GHE2
B	66	CRO	SER	CHROMOPHORE	UNP Q8GHE2
B	205	VAL	SER	ENGINEERED	UNP Q8GHE2
C	66	CRO	SER	CHROMOPHORE	UNP Q8GHE2
C	205	VAL	SER	ENGINEERED	UNP Q8GHE2
D	66	CRO	SER	CHROMOPHORE	UNP Q8GHE2
D	205	VAL	SER	ENGINEERED	UNP Q8GHE2

- Molecule 2 is IMIDAZOLE (three-letter code: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			5	3	2		
2	B	1	Total	C	N	0	0
			5	3	2		
2	C	1	Total	C	N	0	0
			5	3	2		
2	D	1	Total	C	N	0	0
			5	3	2		

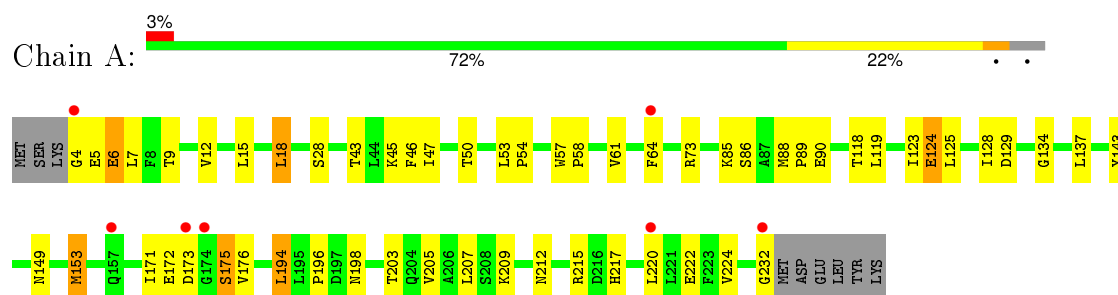
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	238	Total	O	0	0
			238	238		
3	B	237	Total	O	0	3
			240	240		
3	C	213	Total	O	0	0
			213	213		
3	D	171	Total	O	0	2
			173	173		

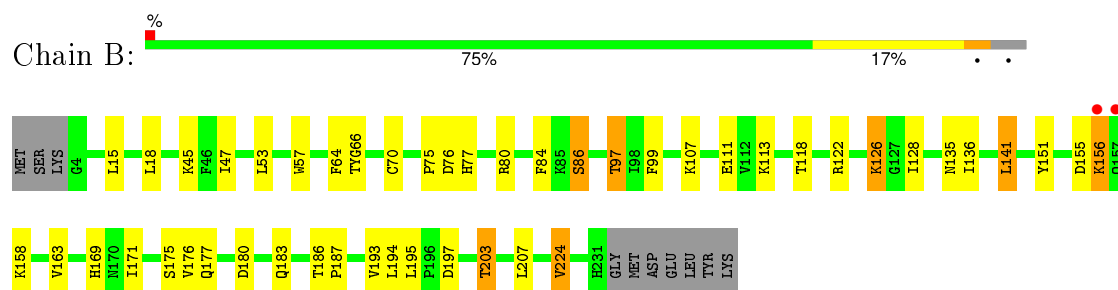
3 Residue-property plots [i](#)

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.

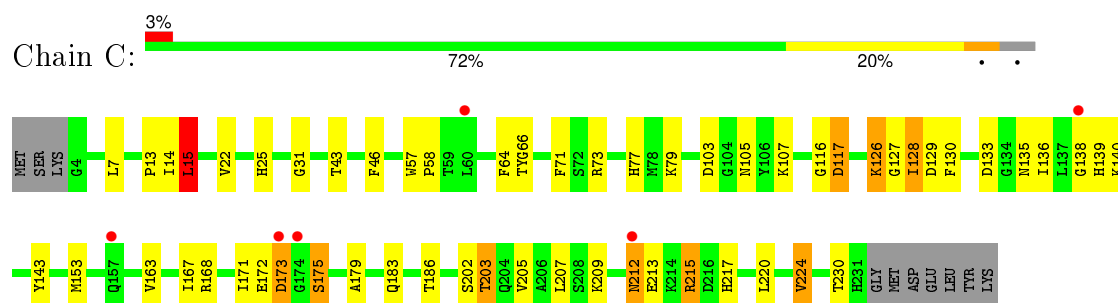
- Molecule 1: Green fluorescence protein



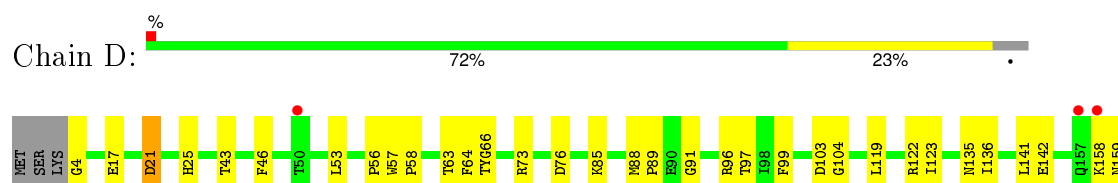
- Molecule 1: Green fluorescence protein



- Molecule 1: Green fluorescence protein



- Molecule 1: Green fluorescence protein



R168	H169	N170	I171	S175	V176	Q177	Y182	Q183	T186	P187	I188	D197	T203	Q204	L207	D210	E213	K214	R215	L220	L221	T225	I229	T230	H231	GLY	MET	ASP	GLU	LEU	TYR	LYS
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.83Å 151.50Å 59.73Å 90.00° 110.23° 90.00°	Depositor
Resolution (Å)	10.00 – 1.59 29.22 – 1.59	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.59) 98.1 (29.22-1.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 1.59Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.176 , 0.256 0.185 , 0.185	Depositor DCC
R_{free} test set	5998 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 128.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 119117 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7961	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IMD, 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	0.92	1/1869 (0.1%)	1.04	3/2534 (0.1%)
1	B	0.94	1/1789 (0.1%)	1.05	4/2426 (0.2%)
1	C	0.92	0/1801	1.10	4/2439 (0.2%)
1	D	0.91	0/1759	1.01	1/2388 (0.0%)
All	All	0.92	2/7218 (0.0%)	1.05	12/9787 (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	B	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	61	VAL	CB-CG1	5.14	1.63	1.52
1	B	64	PHE	CE1-CZ	5.06	1.47	1.37

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	15	LEU	CB-CG-CD2	-7.97	97.44	111.00
1	B	180	ASP	CB-CG-OD1	7.34	124.91	118.30
1	A	215	ARG	NE-CZ-NH1	-6.85	116.87	120.30
1	C	128	ILE	CB-CA-C	-6.71	98.17	111.60
1	B	97	THR	N-CA-C	-6.48	93.50	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	156	LYS	Peptide

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	1818	0	1739	49	0
1	B	1756	0	1664	42	0
1	C	1774	0	1684	49	0
1	D	1729	0	1593	42	0
2	A	5	0	5	1	0
2	B	5	0	5	1	0
2	C	5	0	5	1	0
2	D	5	0	5	1	0
3	A	238	0	0	10	0
3	B	240	0	0	8	0
3	C	213	0	0	11	0
3	D	173	0	0	9	0
All	All	7961	0	6700	177	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 13.

The worst 5 of 177 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:A:153:MET:SD	1:A:153:MET:CE	2.04	1.43
1:C:215:ARG:HH11	1:C:215:ARG:HG3	1.27	0.97
1:D:207:LEU:H	2:D:239:IMD:HN3	1.14	0.91
1:C:207:LEU:H	2:C:239:IMD:HN1	1.19	0.91
1:A:207:LEU:H	2:A:239:IMD:HN3	1.23	0.85

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	232/236 (98%)	230 (99%)	2 (1%)	0	100	100
1	B	225/236 (95%)	219 (97%)	6 (3%)	0	100	100
1	C	223/236 (94%)	216 (97%)	7 (3%)	0	100	100
1	D	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
All	All	904/944 (96%)	886 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	195/206 (95%)	186 (95%)	9 (5%)	33	9
1	B	178/206 (86%)	174 (98%)	4 (2%)	60	31
1	C	184/206 (89%)	171 (93%)	13 (7%)	18	3
1	D	175/206 (85%)	172 (98%)	3 (2%)	68	44
All	All	732/824 (89%)	703 (96%)	29 (4%)	37	12

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	13	PRO
1	C	117	ASP
1	D	76	ASP

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Mol	Chain	Res	Type
1	C	15	LEU
1	C	126	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	149	ASN
1	C	164	ASN
1	D	149	ASN
1	B	170	ASN
1	C	184	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	22,22,24	2.51	7 (31%)	27,30,34	1.74	10 (37%)
1	CRO	B	66	1	22,22,24	2.39	6 (27%)	27,30,34	2.48	9 (33%)
1	CRO	C	66	1	22,22,24	2.53	6 (27%)	27,30,34	1.90	8 (29%)
1	CRO	D	66	1	22,22,24	2.86	7 (31%)	27,30,34	2.24	8 (29%)

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	-	0/8/29/32	0/2/2/2
1	CRO	B	66	1	-	0/8/29/32	0/2/2/2
1	CRO	C	66	1	-	0/8/29/32	0/2/2/2
1	CRO	D	66	1	-	0/8/29/32	0/2/2/2

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	66	CRO	CB2-CA2	-2.05	1.33	1.35
1	C	66	CRO	CA3-N3	-2.03	1.43	1.47
1	D	66	CRO	CG2-CB2	2.11	1.51	1.46
1	A	66	CRO	CA2-C2	2.31	1.51	1.48
1	A	66	CRO	CA2-N2	2.34	1.43	1.38

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	CRO	CA2-C2-N3	-6.66	100.06	103.40
1	D	66	CRO	N3-C1-N2	-6.27	106.71	111.56
1	D	66	CRO	CG2-CB2-CA2	-5.47	123.11	130.22
1	B	66	CRO	N3-C1-N2	-5.12	107.60	111.56
1	B	66	CRO	CA3-N3-C1	-4.63	121.98	127.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	66	CRO	1	0
1	C	66	CRO	1	0
1	D	66	CRO	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	IMD	A	239	-	3,5,5	0.46	0	4,5,5	0.64	0
2	IMD	B	239	-	3,5,5	0.19	0	4,5,5	0.64	0
2	IMD	C	239	-	3,5,5	0.20	0	4,5,5	0.56	0
2	IMD	D	239	-	3,5,5	0.16	0	4,5,5	0.67	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	IMD	A	239	-	-	0/0/0/0	0/1/1/1
2	IMD	B	239	-	-	0/0/0/0	0/1/1/1
2	IMD	C	239	-	-	0/0/0/0	0/1/1/1
2	IMD	D	239	-	-	0/0/0/0	0/1/1/1

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.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	239	IMD	1	0
2	B	239	IMD	1	0
2	C	239	IMD	1	0
2	D	239	IMD	1	0

5.7 Other polymers ⓘ

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	226/236 (95%)	-0.02	7 (3%) 52 50	18, 27, 58, 84	0
1	B	225/236 (95%)	-0.09	2 (0%) 85 85	17, 27, 50, 70	0
1	C	225/236 (95%)	0.03	6 (2%) 58 56	19, 28, 55, 89	0
1	D	225/236 (95%)	0.04	3 (1%) 79 79	19, 30, 57, 76	0
All	All	901/944 (95%)	-0.01	18 (1%) 68 67	17, 28, 54, 89	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	174	GLY	4.6
1	C	173	ASP	3.3
1	B	156	LYS	3.3
1	C	212	ASN	2.7
1	A	4	GLY	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(Å ²)	Q<0.9
1	CRO	B	66	21/23	0.99	0.14	-	16,20,22,24	0
1	CRO	A	66	21/23	0.98	0.13	-	12,19,24,25	0
1	CRO	D	66	21/23	0.97	0.13	-	19,23,30,36	0
1	CRO	C	66	21/23	0.98	0.12	-	15,21,24,28	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	IMD	B	239	5/5	0.93	0.10	1.57	26,32,50,53	0
2	IMD	A	239	5/5	0.93	0.09	1.39	20,25,38,46	0
2	IMD	C	239	5/5	0.95	0.09	1.01	28,32,47,82	0
2	IMD	D	239	5/5	0.96	0.08	0.55	23,29,46,99	0

6.5 Other polymers [i](#)

There are no such residues in this entry.