



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 19, 2024 – 04:09 PM JST

PDB ID : 7DNA
Title : Photocleavable Fluorescent Protein in green and red form
Authors : Wen, Y.; Lemieux, J.M.
Deposited on : 2020-12-09
Resolution : 2.30 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.002 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.38.2

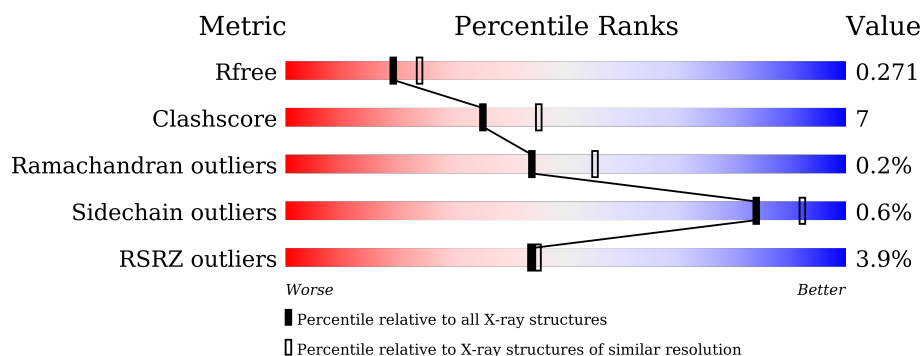
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	240	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>11%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	240	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>15%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	240	<div> <div>6%</div> <div> <div></div> <div>75%</div> <div>12%</div> <div></div> <div>12%</div> </div> </div>
1	K	240	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>10%</div> <div>•</div> <div>11%</div> </div> </div>
2	F	231	<div> <div>3%</div> <div> <div></div> <div>69%</div> <div>16%</div> <div></div> <div>15%</div> </div> </div>
2	I	231	<div> <div>5%</div> <div> <div></div> <div>75%</div> <div>11%</div> <div></div> <div>13%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	J	10	
3	L	10	

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
3	IEY	J	232	X	-	-	-
3	IEY	L	232	X	-	-	-
4	NH2	F	301	-	-	X	-
4	NH2	I	301	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 10676 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-to-red photoconvertible GFP-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	1	3	0
			1741	1116	296	320	9			
1	B	214	Total	C	N	O	S	1	2	0
			1744	1117	297	321	9			
1	D	210	Total	C	N	O	S	1	2	0
			1708	1093	291	315	9			
1	K	213	Total	C	N	O	S	2	3	0
			1738	1114	296	319	9			

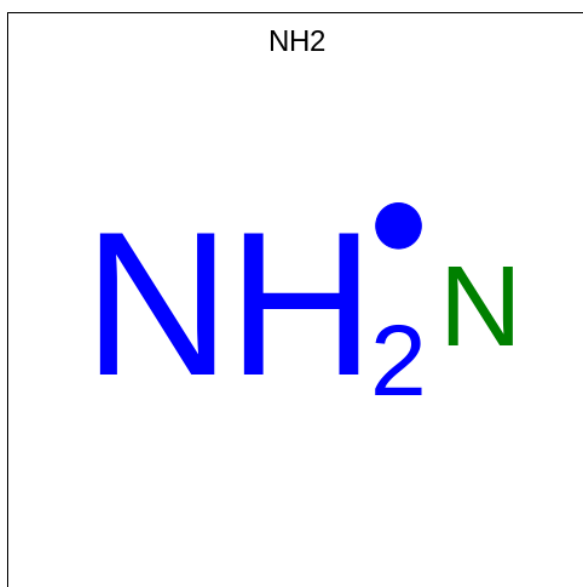
- Molecule 2 is a protein called Green-to-red photoconvertible GFP-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	197	Total	C	N	O	S	1	3	0
			1593	1016	269	299	9			
2	I	200	Total	C	N	O	S	1	2	0
			1609	1028	273	299	9			

- Molecule 3 is a protein called Green-to-red photoconvertible GFP-like protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	J	9	Total	C	N	O	0	0	0
			96	65	17	14			
3	L	9	Total	C	N	O	0	0	0
			96	65	17	14			

- Molecule 4 is AMINO GROUP (three-letter code: NH2) (formula: H₂N).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	F	1	Total N 1 1	0	0
4	I	1	Total N 1 1	0	0

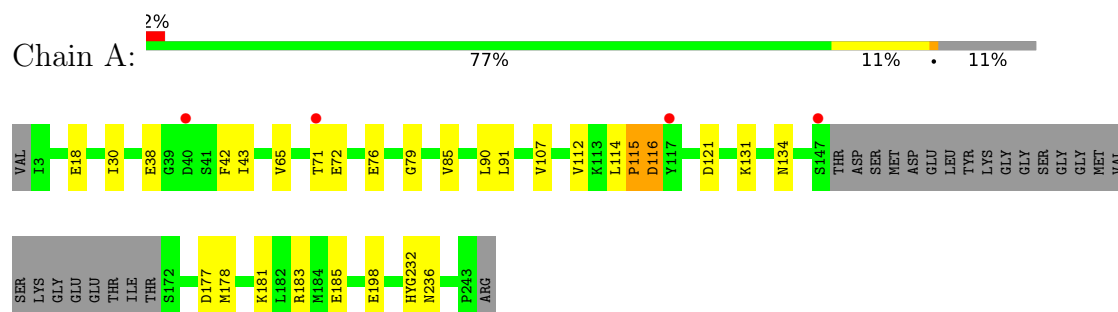
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	64	Total O 64 64	0	0
5	B	57	Total O 57 57	0	0
5	D	68	Total O 68 68	0	0
5	F	60	Total O 60 60	0	0
5	J	1	Total O 1 1	0	0
5	I	50	Total O 50 50	0	0
5	L	1	Total O 1 1	0	0
5	K	48	Total O 48 48	0	0

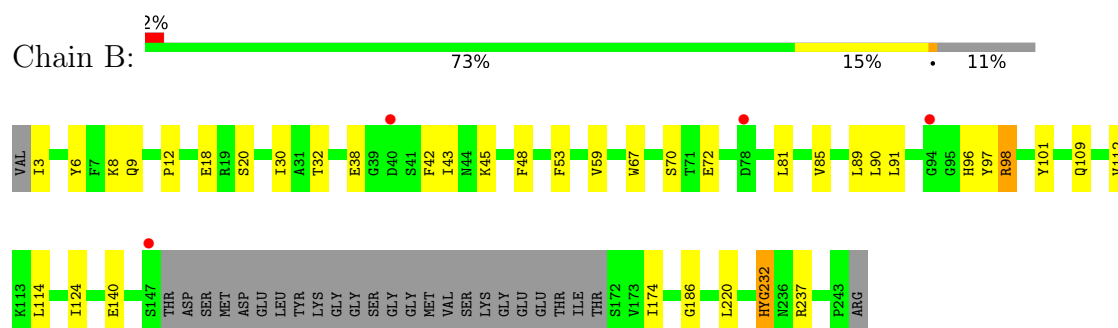
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

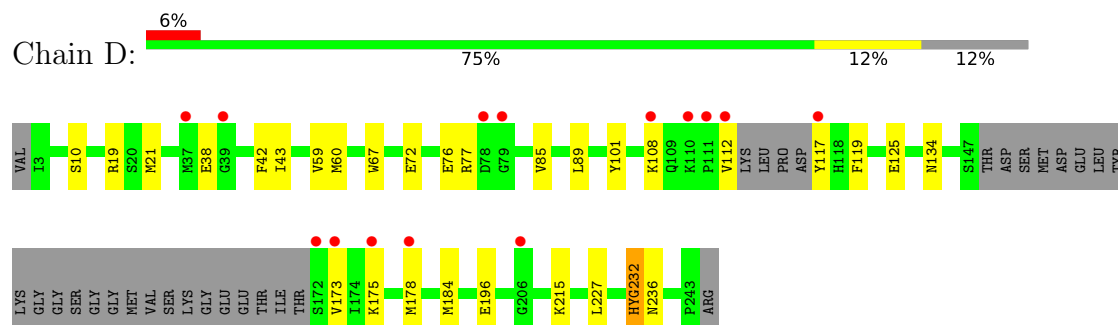
- Molecule 1: Green-to-red photoconvertible GFP-like protein



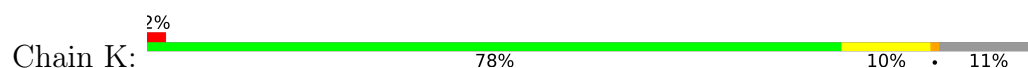
- Molecule 1: Green-to-red photoconvertible GFP-like protein

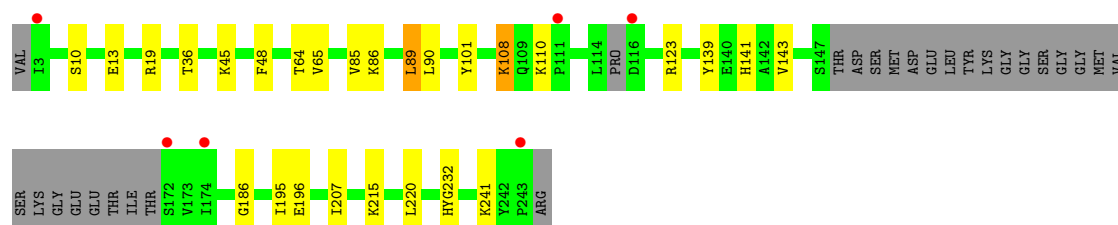


- Molecule 1: Green-to-red photoconvertible GFP-like protein

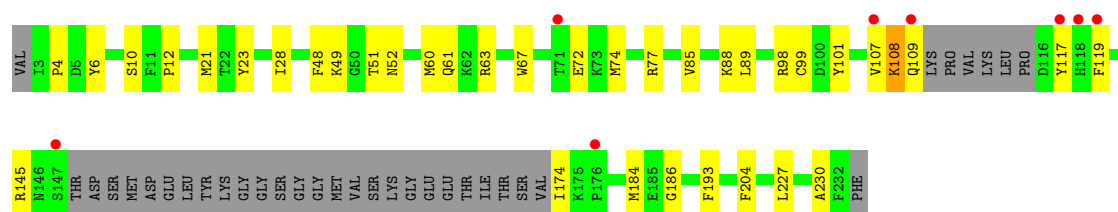


- Molecule 1: Green-to-red photoconvertible GFP-like protein

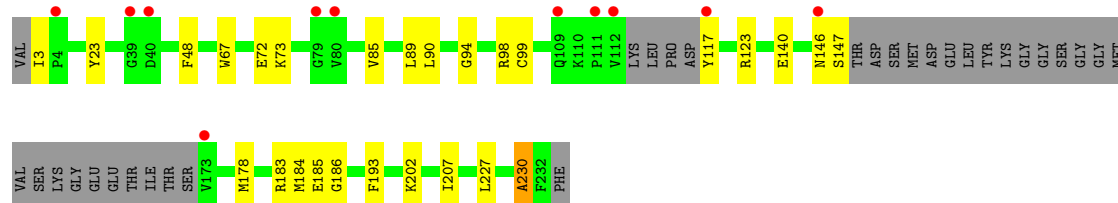
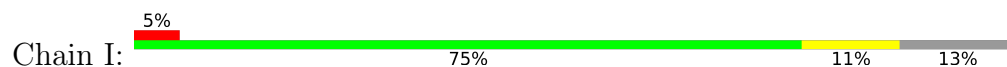




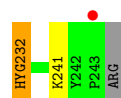
- Molecule 2: Green-to-red photoconvertible GFP-like protein



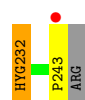
- Molecule 2: Green-to-red photoconvertible GFP-like protein



- Molecule 3: Green-to-red photoconvertible GFP-like protein



- Molecule 3: Green-to-red photoconvertible GFP-like protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.93Å 72.49Å 126.55Å 92.46° 97.31° 92.50°	Depositor
Resolution (Å)	46.27 – 2.30 46.27 – 2.30	Depositor EDS
% Data completeness (in resolution range)	76.4 (46.27-2.30) 76.5 (46.27-2.30)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.94 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.221 , 0.271 0.221 , 0.271	Depositor DCC
R_{free} test set	2599 reflections (4.28%)	wwPDB-VP
Wilson B-factor (Å ²)	23.4	Xtriage
Anisotropy	0.627	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.068 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10676	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.55% 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: CR8, NH2, IEY

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	0.31	0/1762	0.57	2/2373 (0.1%)
1	B	0.32	0/1762	0.54	0/2371
1	D	0.31	0/1724	0.53	0/2319
1	K	0.32	0/1757	0.54	1/2362 (0.0%)
2	F	0.30	0/1637	0.58	2/2201 (0.1%)
2	I	0.32	0/1648	0.57	1/2216 (0.0%)
3	J	0.30	0/74	0.62	0/99
3	L	0.28	0/74	0.50	0/99
All	All	0.31	0/10438	0.55	6/14040 (0.0%)

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
2	I	0	1
3	J	1	0
3	L	1	0
All	All	2	1

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	230	ALA	O-C-N	-8.97	108.34	122.70
2	I	230	ALA	O-C-N	-8.16	109.64	122.70
1	A	115	PRO	C-N-CA	6.61	138.22	121.70
1	K	89	LEU	CA-CB-CG	6.08	129.29	115.30
2	F	230	ALA	CA-C-N	5.92	130.21	117.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	J	232	IEY	CA2
3	L	232	IEY	CA2

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	230	ALA	Mainchain

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	1741	0	1678	28	0
1	B	1744	0	1684	36	0
1	D	1708	0	1637	20	0
1	K	1738	0	1681	18	0
2	F	1593	0	1548	27	0
2	I	1609	0	1567	18	0
3	J	96	0	82	4	0
3	L	96	0	82	5	0
4	F	1	0	0	2	0
4	I	1	0	0	2	0
5	A	64	0	0	4	0
5	B	57	0	0	18	0
5	D	68	0	0	5	0
5	F	60	0	0	6	0
5	I	50	0	0	3	0
5	J	1	0	0	0	0
5	K	48	0	0	5	0
5	L	1	0	0	0	0
All	All	10676	0	9959	148	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 148 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:65:VAL:CG2	1:A:90:LEU:HD12	1.92	0.99
1:B:109:GLN:NE2	5:B:401:HOH:O	1.98	0.97
1:D:38:GLU:OE2	5:D:401:HOH:O	1.84	0.95
1:B:38:GLU:HG2	1:B:43:ILE:HD11	1.60	0.82
1:B:90:LEU:N	5:B:404:HOH:O	2.12	0.82

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	208/240 (87%)	202 (97%)	5 (2%)	1 (0%)	25	32
1	B	207/240 (86%)	204 (99%)	3 (1%)	0	100	100
1	D	201/240 (84%)	194 (96%)	7 (4%)	0	100	100
1	K	205/240 (85%)	198 (97%)	7 (3%)	0	100	100
2	F	193/231 (84%)	187 (97%)	5 (3%)	1 (0%)	25	32
2	I	194/231 (84%)	190 (98%)	4 (2%)	0	100	100
3	J	6/10 (60%)	6 (100%)	0	0	100	100
3	L	6/10 (60%)	6 (100%)	0	0	100	100
All	All	1220/1442 (85%)	1187 (97%)	31 (2%)	2 (0%)	44	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	ASP
2	F	108	LYS

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	185/207 (89%)	184 (100%)	1 (0%)	86	93
1	B	186/207 (90%)	185 (100%)	1 (0%)	86	93
1	D	181/207 (87%)	180 (99%)	1 (1%)	84	92
1	K	185/207 (89%)	183 (99%)	2 (1%)	70	83
2	F	171/199 (86%)	171 (100%)	0	100	100
2	I	173/199 (87%)	171 (99%)	2 (1%)	67	81
3	J	8/9 (89%)	8 (100%)	0	100	100
3	L	8/9 (89%)	8 (100%)	0	100	100
All	All	1097/1244 (88%)	1090 (99%)	7 (1%)	84	92

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	123	ARG
2	I	147	SER
1	K	110	LYS
1	K	108	LYS
1	D	77	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	9	GLN
2	I	146	ASN
2	F	52	ASN
1	B	208	GLN
2	F	146	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	IEY	J	232	3	24,26,27	5.57	8 (33%)	24,35,37	3.40	7 (29%)
1	CR8	K	232	1	20,27,28	2.06	10 (50%)	17,37,39	1.56	2 (11%)
1	CR8	B	232	1	20,27,28	2.10	11 (55%)	17,37,39	1.68	2 (11%)
1	CR8	D	232	1	20,27,28	2.11	9 (45%)	17,37,39	1.73	2 (11%)
3	IEY	L	232	3	24,26,27	5.78	8 (33%)	24,35,37	3.54	5 (20%)
1	CR8	A	232	1	20,27,28	2.10	11 (55%)	17,37,39	1.54	2 (11%)

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
3	IEY	J	232	3	1/1/4/7	4/9/28/29	0/3/3/3
1	CR8	K	232	1	-	5/8/25/26	0/3/3/3
1	CR8	B	232	1	-	2/8/25/26	0/3/3/3
1	CR8	D	232	1	-	4/8/25/26	0/3/3/3
3	IEY	L	232	3	1/1/4/7	5/9/28/29	0/3/3/3
1	CR8	A	232	1	-	5/8/25/26	0/3/3/3

The worst 5 of 57 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	232	IEY	CA2-C2	-22.39	1.36	1.52
3	J	232	IEY	CA2-C2	-21.15	1.37	1.52
3	J	232	IEY	O2-C2	10.41	1.40	1.22
3	L	232	IEY	O2-C2	10.27	1.40	1.22
3	J	232	IEY	CA2-N2	-10.12	1.31	1.47

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	232	IEY	CB2-CA2-N2	15.30	130.94	110.78
3	J	232	IEY	CB2-CA2-N2	13.41	128.45	110.78
3	J	232	IEY	CB2-CA2-C2	5.82	123.99	110.49
1	D	232	CR8	C3-CA3-N3	5.17	119.76	111.92
3	L	232	IEY	CB2-CA2-C2	4.76	121.53	110.49

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	J	232	IEY	CA2
3	L	232	IEY	CA2

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	232	CR8	C7-C8-CA2-C2
1	A	232	CR8	C7-C8-CA2-N2
1	A	232	CR8	CA1-C20-C21-N22
1	A	232	CR8	CA1-C20-C21-C23
1	B	232	CR8	CA1-C20-C21-N22

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	232	IEY	3	0
1	B	232	CR8	1	0
1	D	232	CR8	1	0
3	L	232	IEY	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are modelled with single atom - 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 [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	213/240 (88%)	0.11	4 (1%) 66 67	11, 22, 43, 58	2 (0%)
1	B	213/240 (88%)	0.33	4 (1%) 66 67	12, 26, 46, 60	1 (0%)
1	D	209/240 (87%)	0.47	14 (6%) 25 27	10, 28, 59, 77	1 (0%)
1	K	212/240 (88%)	0.51	6 (2%) 55 56	15, 31, 54, 62	3 (1%)
2	F	197/231 (85%)	0.32	8 (4%) 42 43	10, 27, 53, 64	3 (1%)
2	I	200/231 (86%)	0.43	11 (5%) 32 33	12, 28, 58, 78	2 (1%)
3	J	8/10 (80%)	0.99	1 (12%) 9 10	29, 39, 52, 58	0
3	L	8/10 (80%)	0.79	1 (12%) 9 10	26, 38, 50, 60	0
All	All	1260/1442 (87%)	0.37	49 (3%) 44 45	10, 27, 54, 78	12 (0%)

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	112	VAL	6.6
1	K	116	ASP	3.8
2	I	117	TYR	3.8
2	I	111	PRO	3.6
2	I	79	GLY	3.3

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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	IEY	J	232	24/25	0.84	0.14	21,25,37,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IEY	L	232	24/25	0.85	0.12	21,27,30,32	0
1	CR8	K	232	25/26	0.89	0.10	20,24,30,32	0
1	CR8	D	232	25/26	0.90	0.11	19,25,34,36	0
1	CR8	B	232	25/26	0.91	0.11	16,21,25,28	0
1	CR8	A	232	25/26	0.94	0.08	14,17,23,30	0

6.3 Carbohydrates [i](#)

There are no monosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NH2	I	301	1/1	0.57	0.27	37,37,37,37	0
4	NH2	F	301	1/1	0.62	0.17	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.