



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:56 AM GMT

PDB ID : 3NT9
Title : CRYSTAL STRUCTURE OF LSSmKate1 red fluorescent proteins with large Stokes shift
Authors : Malashkevich, V.N.; Piatkevich, K.; Almo, S.C.; Verkhusha, V.
Deposited on : 2010-07-03
Resolution : 1.99 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

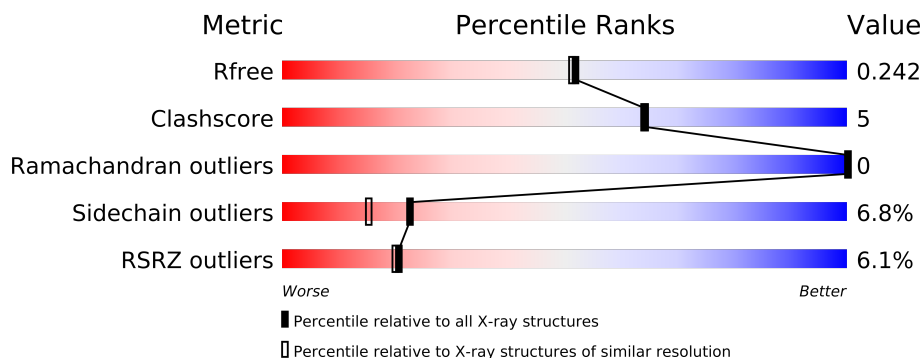
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.99 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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	243	
1	B	243	
1	C	243	
1	D	243	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7632 atoms, of which 0 are hydrogen and 0 are deuterium.

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 LSSmKate1 red fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	2	0
			1808	1148	308	341	11			
1	B	224	Total	C	N	O	S	0	1	0
			1797	1142	304	340	11			
1	C	224	Total	C	N	O	S	0	1	0
			1795	1143	301	340	11			
1	D	224	Total	C	N	O	S	0	1	0
			1795	1143	301	340	11			

- Molecule 2 is water.

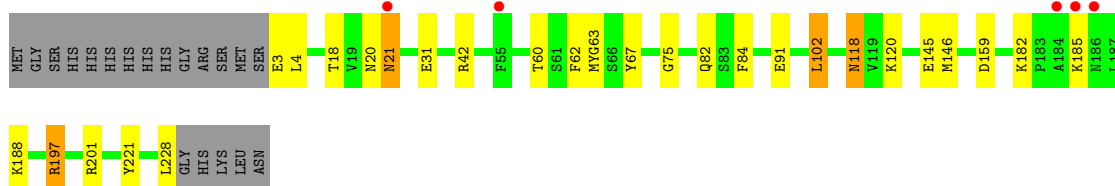
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	136	Total	O	0	0
			136	136		
2	B	126	Total	O	0	0
			126	126		
2	C	78	Total	O	0	0
			78	78		
2	D	97	Total	O	0	0
			97	97		

3 Residue-property plots

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.

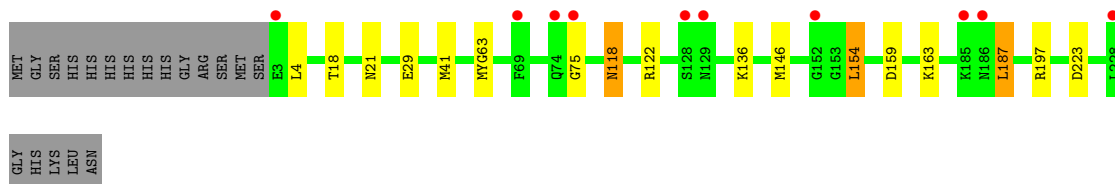
- Molecule 1: LSSmKate1 red fluorescent protein

Chain A: 



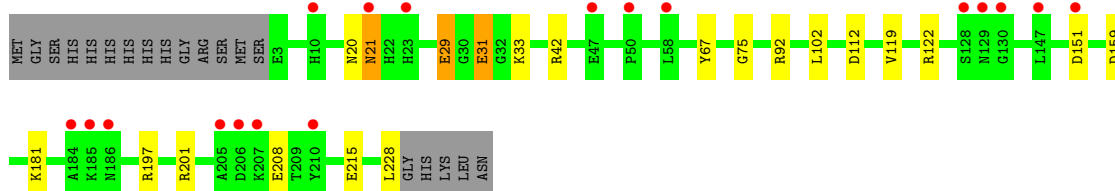
- Molecule 1: LSSmKate1 red fluorescent protein

Chain B: 



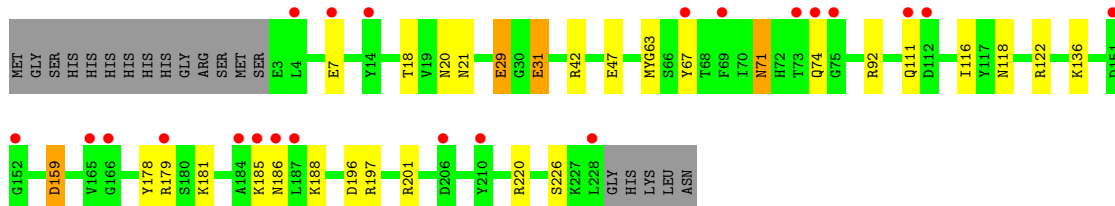
- Molecule 1: LSSmKate1 red fluorescent protein

Chain C: 



- Molecule 1: LSSmKate1 red fluorescent protein

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	72.18Å 72.18Å 226.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.81 – 1.99 19.71 – 1.99	Depositor EDS
% Data completeness (in resolution range)	97.3 (19.81-1.99) 97.3 (19.71-1.99)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.5.0089	Depositor
R, R_{free}	0.182 , 0.232 0.192 , 0.242	Depositor DCC
R_{free} test set	3843 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 29.6	EDS
Estimated twinning fraction	0.057 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 76295 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7632	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 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NRQ

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	0.94	4/1825 (0.2%)	0.81	3/2461 (0.1%)
1	B	0.85	0/1814	0.78	2/2447 (0.1%)
1	C	0.79	0/1803	0.74	1/2432 (0.0%)
1	D	0.77	0/1803	0.74	1/2432 (0.0%)
All	All	0.84	4/7245 (0.1%)	0.77	7/9772 (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	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	62	PHE	C-O	6.35	1.35	1.23
1	A	145	GLU	CD-OE1	-5.91	1.19	1.25
1	A	145	GLU	CD-OE2	-5.42	1.19	1.25
1	A	221	TYR	CD1-CE1	-5.37	1.31	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	102	LEU	CA-CB-CG	6.87	131.10	115.30
1	A	146	MET	CG-SD-CE	-6.83	89.28	100.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	PHE	CA-C-O	-6.79	105.85	120.10
1	D	159	ASP	CB-CG-OD1	5.58	123.32	118.30
1	B	154	LEU	CA-CB-CG	5.55	128.06	115.30
1	B	187	LEU	CA-CB-CG	5.45	127.84	115.30
1	C	102	LEU	CA-CB-CG	5.03	126.87	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	75	GLY	Peptide
1	B	75	GLY	Peptide
1	C	75	GLY	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1808	0	0	12	0
1	B	1797	0	0	11	0
1	C	1795	0	0	6	0
1	D	1795	0	0	10	0
2	A	136	0	0	4	0
2	B	126	0	0	3	0
2	C	78	0	0	0	0
2	D	97	0	0	1	0
All	All	7632	0	0	38	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (38) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:67:TYR:OH	1:C:92:ARG:NH2	2.26	0.69
1:C:21:ASN:ND2	1:C:21:ASN:C	2.48	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:201:ARG:NH2	2:A:258:HOH:O	2.34	0.61
1:A:159:ASP:OD2	1:B:159:ASP:OD2	2.23	0.57
1:C:29:GLU:OE2	1:C:42:ARG:NH1	2.39	0.56
1:A:31:GLU:OE2	1:A:42:ARG:NH2	2.40	0.54
1:D:29:GLU:OE2	1:D:42:ARG:NH1	2.41	0.54
1:B:118:ASN:ND2	2:B:276:HOH:O	2.42	0.52
1:C:31:GLU:OE2	1:C:42:ARG:NH2	2.43	0.52
1:D:31:GLU:OE2	1:D:42:ARG:NH2	2.43	0.51
1:D:63[A]:NRQ:CZ	1:D:197:ARG:CD	2.89	0.49
1:A:118:ASN:ND2	2:A:383:HOH:O	2.46	0.48
1:A:84:PHE:O	1:A:182:LYS:NZ	2.47	0.47
1:B:18:THR:CG2	2:B:294:HOH:O	2.64	0.45
1:D:67:TYR:OH	1:D:178:TYR:OH	2.34	0.45
2:A:260:HOH:O	1:B:146:MET:CE	2.63	0.45
1:D:63[A]:NRQ:CE2	1:D:197:ARG:CD	2.94	0.45
1:B:63:NRQ:CA3	1:B:63:NRQ:N1	2.80	0.45
1:D:20:ASN:O	2:D:332:HOH:O	2.21	0.44
1:B:63:NRQ:CZ	1:B:197:ARG:CD	2.95	0.44
1:B:63:NRQ:CE2	1:B:197:ARG:CD	2.95	0.43
1:A:91:GLU:CD	2:A:246:HOH:O	2.56	0.43
1:D:196:ASP:OD2	1:D:220:ARG:NE	2.52	0.43
1:D:18:THR:OG1	1:D:122:ARG:NH2	2.52	0.43
1:A:82:GLN:O	1:A:182:LYS:NZ	2.52	0.42
1:C:20:ASN:O	1:C:21:ASN:ND2	2.52	0.42
1:B:4:LEU:N	1:B:4:LEU:CD2	2.82	0.42
1:D:67:TYR:OH	1:D:92:ARG:NH2	2.53	0.42
1:A:63:NRQ:CA3	1:A:63:NRQ:N1	2.83	0.41
1:B:118:ASN:CB	2:B:276:HOH:O	2.68	0.41
1:B:41:MET:CG	1:B:63:NRQ:CE	2.99	0.41
1:A:63:NRQ:CE2	1:A:197:ARG:CD	2.99	0.41
1:A:60:THR:O	1:A:63:NRQ:C2	2.69	0.40
1:A:63:NRQ:O2	1:A:67:TYR:CE2	2.73	0.40
1:A:20:ASN:O	1:A:21:ASN:CB	2.67	0.40
1:D:71:ASN:C	1:D:71:ASN:ND2	2.75	0.40
1:B:223:ASP:C	1:B:223:ASP:OD1	2.59	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	221/243 (91%)	215 (97%)	6 (3%)	0	100	100
1	B	220/243 (90%)	216 (98%)	4 (2%)	0	100	100
1	C	219/243 (90%)	214 (98%)	5 (2%)	0	100	100
1	D	219/243 (90%)	214 (98%)	5 (2%)	0	100	100
All	All	879/972 (90%)	859 (98%)	20 (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	193/207 (93%)	182 (94%)	11 (6%)	29	21
1	B	192/207 (93%)	184 (96%)	8 (4%)	40	34
1	C	191/207 (92%)	177 (93%)	14 (7%)	20	13
1	D	191/207 (92%)	172 (90%)	19 (10%)	11	6
All	All	767/828 (93%)	715 (93%)	52 (7%)	22	15

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	4	LEU
1	A	18	THR
1	A	21	ASN
1	A	102	LEU

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Mol	Chain	Res	Type
1	A	118	ASN
1	A	120	LYS
1	A	185	LYS
1	A	188	LYS
1	A	197	ARG
1	A	228	LEU
1	B	21	ASN
1	B	29	GLU
1	B	118	ASN
1	B	122	ARG
1	B	136	LYS
1	B	154	LEU
1	B	163	LYS
1	B	187	LEU
1	C	21	ASN
1	C	29	GLU
1	C	31	GLU
1	C	33	LYS
1	C	112	ASP
1	C	119	VAL
1	C	122	ARG
1	C	151	ASP
1	C	159	ASP
1	C	181	LYS
1	C	197	ARG
1	C	201	ARG
1	C	208	GLU
1	C	228	LEU
1	D	7	GLU
1	D	21	ASN
1	D	29	GLU
1	D	31	GLU
1	D	47	GLU
1	D	71	ASN
1	D	74	GLN
1	D	111	GLN
1	D	116	ILE
1	D	118	ASN
1	D	136	LYS
1	D	159	ASP
1	D	179	ARG
1	D	181	LYS

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Mol	Chain	Res	Type
1	D	185	LYS
1	D	186	ASN
1	D	188	LYS
1	D	201	ARG
1	D	226	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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	NRQ	A	63	1	24,24,25	6.85	3 (12%)	30,32,34	3.05	9 (30%)
1	NRQ	B	63	1	24,24,25	4.54	5 (20%)	30,32,34	2.81	7 (23%)
1	NRQ	C	63[A]	-	7,8,25	0.51	0	8,10,34	0.39	0
1	NRQ	C	63[B]	-	7,8,25	0.64	0	8,10,34	0.65	0
1	NRQ	D	63[A]	-	7,8,25	0.34	0	8,10,34	0.58	0
1	NRQ	D	63[B]	-	7,8,25	0.49	0	8,10,34	0.47	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
1	NRQ	A	63	1	-	0/9/31/32	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	NRQ	B	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	C	63[A]	-	-	0/0/0/32	0/1/1/2
1	NRQ	C	63[B]	-	-	0/0/0/32	0/1/1/2
1	NRQ	D	63[A]	-	-	0/0/0/32	0/1/1/2
1	NRQ	D	63[B]	-	-	0/0/0/32	0/1/1/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	63	NRQ	O3-C3	32.87	1.34	1.11
1	B	63	NRQ	O3-C3	18.10	1.23	1.11
1	B	63	NRQ	CA3-C3	-10.74	1.33	1.48
1	B	63	NRQ	C2-N3	-3.84	1.31	1.39
1	A	63	NRQ	CA2-C2	-3.71	1.44	1.48
1	A	63	NRQ	C2-N3	-3.60	1.32	1.39
1	B	63	NRQ	CA2-C2	-3.22	1.45	1.48
1	B	63	NRQ	CA1-N1	2.61	1.33	1.27

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	63	NRQ	O2-C2-CA2	-11.58	124.27	130.96
1	B	63	NRQ	O2-C2-CA2	-11.28	124.44	130.96
1	A	63	NRQ	CA2-C2-N3	6.52	107.15	103.44
1	B	63	NRQ	CA2-C2-N3	6.19	106.96	103.44
1	A	63	NRQ	CA3-N3-C1	4.67	131.05	124.10
1	A	63	NRQ	CG2-CB2-CA2	-4.46	124.98	130.10
1	B	63	NRQ	CA3-N3-C1	3.93	129.95	124.10
1	B	63	NRQ	N3-C1-N2	3.69	116.12	113.24
1	A	63	NRQ	N3-C1-N2	3.05	115.62	113.24
1	A	63	NRQ	CD1-CG2-CD2	2.55	121.61	117.66
1	A	63	NRQ	CB2-CA2-C2	-2.54	118.56	122.46
1	A	63	NRQ	CE1-CD1-CG2	-2.26	118.45	121.30
1	B	63	NRQ	C1-CA1-N1	-2.25	119.17	121.83
1	B	63	NRQ	CB2-CA2-C2	-2.12	119.20	122.46
1	B	63	NRQ	CE1-CD1-CG2	-2.11	118.64	121.30
1	A	63	NRQ	C1-CA1-N1	-2.03	119.43	121.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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	224/243 (92%)	0.21	5 (2%) 59 59	20, 33, 52, 72	0
1	B	224/243 (92%)	0.30	10 (4%) 32 31	19, 35, 53, 71	0
1	C	224/243 (92%)	0.54	18 (8%) 12 12	24, 42, 65, 78	0
1	D	224/243 (92%)	0.57	22 (9%) 8 7	23, 44, 72, 95	0
All	All	896/972 (92%)	0.41	55 (6%) 21 20	19, 38, 64, 95	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	184	ALA	6.2
1	D	185	LYS	5.7
1	C	185	LYS	5.3
1	D	186	ASN	5.1
1	C	206	ASP	4.6
1	D	4	LEU	4.4
1	D	206	ASP	4.1
1	A	185	LYS	4.1
1	B	186	ASN	3.9
1	D	75	GLY	3.8
1	C	207	LYS	3.7
1	C	205	ALA	3.7
1	D	187	LEU	3.7
1	C	186	ASN	3.6
1	D	152	GLY	3.5
1	D	151	ASP	3.5
1	B	228	LEU	3.5
1	B	75	GLY	3.4
1	A	186	ASN	3.4
1	C	184	ALA	3.3
1	D	210	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	112	ASP	3.2
1	D	7	GLU	3.2
1	D	14	TYR	3.0
1	C	47	GLU	3.0
1	D	73	THR	2.8
1	B	152	GLY	2.8
1	C	129	ASN	2.8
1	D	111	GLN	2.8
1	D	74	GLN	2.6
1	C	128	SER	2.5
1	B	3	GLU	2.4
1	B	74	GLN	2.4
1	D	165	VAL	2.4
1	B	185	LYS	2.4
1	D	228	LEU	2.4
1	B	129	ASN	2.4
1	C	23	HIS	2.4
1	C	210	TYR	2.3
1	A	184	ALA	2.3
1	C	147	LEU	2.3
1	C	130	GLY	2.3
1	C	50	PRO	2.3
1	C	21	ASN	2.3
1	C	10	HIS	2.2
1	A	21	ASN	2.1
1	A	55	PHE	2.1
1	D	166	GLY	2.1
1	D	179	ARG	2.1
1	D	69	PHE	2.1
1	C	151	ASP	2.1
1	C	58	LEU	2.0
1	B	69	PHE	2.0
1	B	128	SER	2.0
1	D	67	TYR	2.0

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	NRQ	C	63[B]	8/24	0.15	1.35	20,25,31,32	8
1	NRQ	C	63[A]	8/24	0.15	1.35	28,29,34,35	8
1	NRQ	D	63[A]	8/24	0.14	0.84	32,33,34,34	8
1	NRQ	D	63[B]	8/24	0.14	0.84	27,32,34,35	8
1	NRQ	B	63	23/24	0.14	0.73	29,31,34,37	0
1	NRQ	A	63	23/24	0.12	0.59	25,29,33,35	0

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.