WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 08:57 AM EST

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)

The following versions of software and data (see references (i)) 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	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36
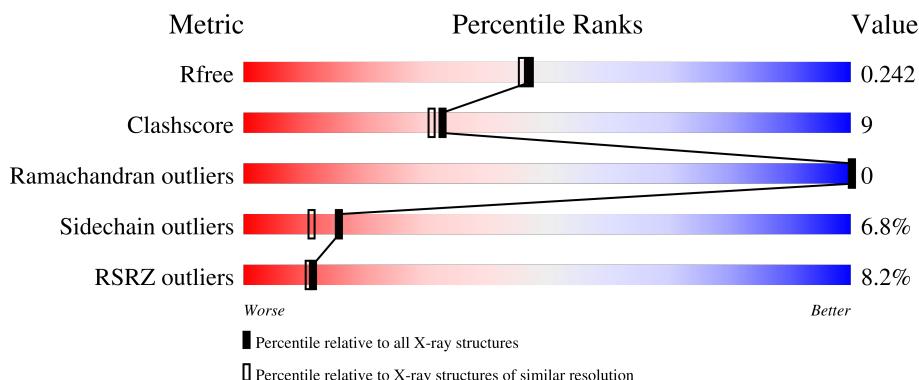
1   Overall quality at a glance   ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
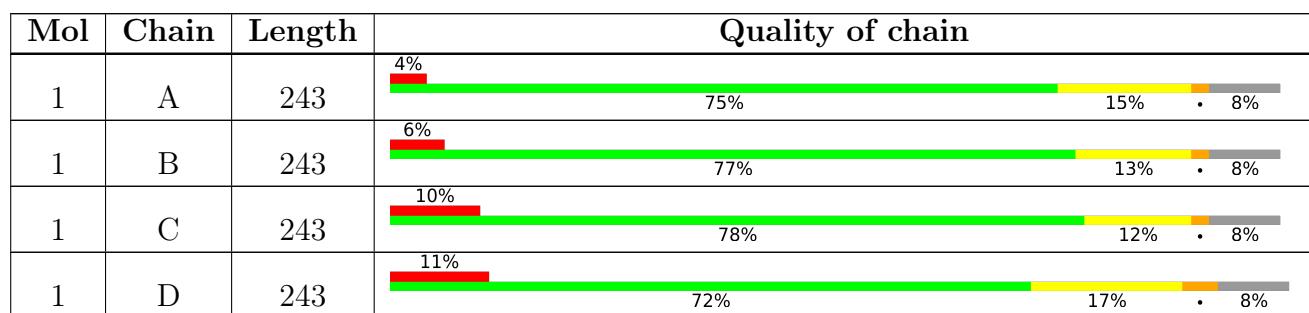
The reported resolution of this entry is 1.99 Å.

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	Percentile Ranks	Value
Rfree		0.242
Clashscore		9
Ramachandran outliers		0
Sidechain outliers		6.8%
RSRZ outliers		8.2%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (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 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 <=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	243	4% 75% 15% • 8%
1	B	243	6% 77% 13% • 8%
1	C	243	10% 78% 12% • 8%
1	D	243	11% 72% 17% • 8%

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
1	NRQ	A	63	-	-	X	-
1	NRQ	B	63	-	-	X	-

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 7632 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 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			
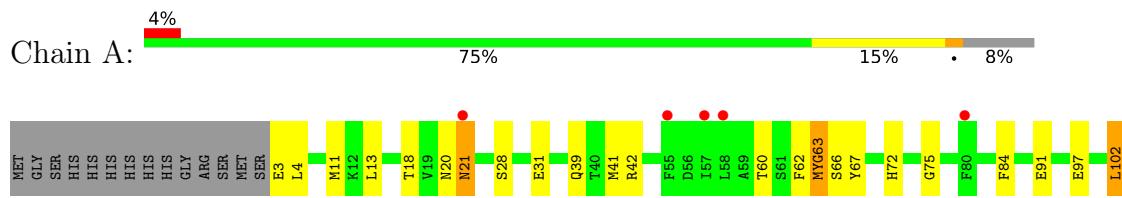
- Molecule 2 is water.

| 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		
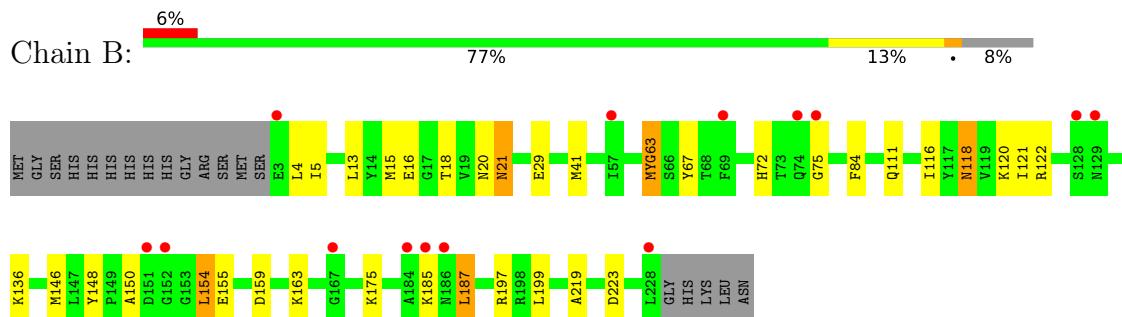
3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, 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.
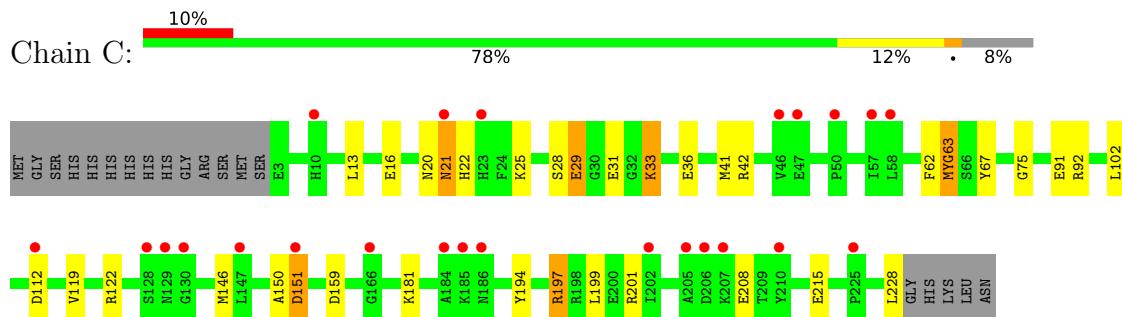
• Molecule 1: LSSmKate1 red fluorescent protein

• Molecule 1: LSSmKate1 red fluorescent protein
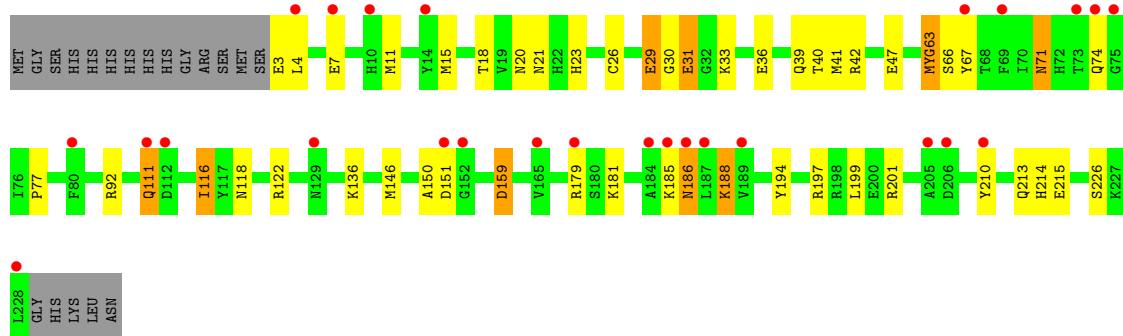
• Molecule 1: LSSmKate1 red fluorescent protein

• Molecule 1: LSSmKate1 red fluorescent protein

4 Data and refinement statistics (i)

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
$< I/\sigma(I) >$ [1]	1.79 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.182 , 0.232 0.191 , 0.242	Depositor DCC
R_{free} test set	3843 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	35.2	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 35.3	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.057 for h,-k,-l	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.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 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(^{o})	Ideal(^{o})
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 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	1808	0	1765	28	0
1	B	1797	0	1753	35	0
1	C	1795	0	1742	26	0
1	D	1795	0	1743	36	0
2	A	136	0	0	6	0
2	B	126	0	0	3	0
2	C	78	0	0	0	0
2	D	97	0	0	2	0
All	All	7632	0	7003	122	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 9.

All (122) 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:B:41:MET:HG3	1:B:63:NRQ:CE	2.04	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:21:ASN:C	1:C:21:ASN:HD22	1.82	0.81
1:B:118:ASN:HB2	2:B:276:HOH:O	1.86	0.76
1:B:18:THR:HG22	2:B:294:HOH:O	1.89	0.71
1:D:146:MET:HG3	1:D:194:TYR:CE1	2.27	0.70
1:B:41:MET:HG3	1:B:63:NRQ:HE1A	1.74	0.69
1:C:67:TYR:OH	1:C:92:ARG:NH2	2.26	0.69
1:D:63[A]:NRQ:CE2	1:D:197:ARG:HD3	2.24	0.68
1:C:21:ASN:HD22	1:C:22:HIS:N	1.92	0.68
1:A:11:MET:HG3	1:A:41:MET:HE3	1.74	0.67
1:C:21:ASN:C	1:C:21:ASN:ND2	2.48	0.67
1:B:41:MET:HG3	1:B:63:NRQ:HE3	1.76	0.66
1:B:63:NRQ:CE2	1:B:197:ARG:HD3	2.26	0.65
1:D:33:LYS:HD2	1:D:36:GLU:OE2	1.99	0.62
1:A:63:NRQ:O2	1:A:67:TYR:HE2	1.83	0.61
1:D:11:MET:HG3	1:D:41:MET:HE3	1.82	0.60
1:D:39:GLN:HE22	1:D:66:SER:CB	2.15	0.60
1:A:197:ARG:HD3	1:A:215:GLU:OE2	2.01	0.59
1:A:97:GLU:OE2	1:B:175:LYS:HE3	2.04	0.58
1:B:150:ALA:HB3	1:B:155:GLU:HG2	1.84	0.58
1:C:16:GLU:HB3	1:C:25:LYS:HG3	1.85	0.57
1:D:150:ALA:O	1:D:151:ASP:HB2	2.04	0.57
1:A:159:ASP:OD2	1:B:159:ASP:OD2	2.23	0.57
1:D:63[A]:NRQ:CZ	1:D:197:ARG:HD2	2.35	0.56
1:A:63:NRQ:CZ	1:A:197:ARG:HD2	2.35	0.56
1:C:29:GLU:OE2	1:C:42:ARG:NH1	2.39	0.56
1:D:214:HIS:HD2	2:D:281:HOH:O	1.88	0.55
1:C:13:LEU:HB3	1:C:28:SER:OG	2.07	0.55
1:B:4:LEU:HD22	1:B:4:LEU:N	2.22	0.54
1:A:11:MET:CG	1:A:41:MET:HE3	2.37	0.54
1:D:29:GLU:OE2	1:D:42:ARG:NH1	2.41	0.54
1:D:42:ARG:HG2	1:D:210:TYR:OH	2.08	0.53
1:B:111:GLN:HG2	1:B:116:ILE:HG13	1.90	0.53
1:B:63:NRQ:CZ	1:B:197:ARG:HD2	2.38	0.53
1:D:63[A]:NRQ:CE1	1:D:197:ARG:HD2	2.38	0.53
1:A:41:MET:HG3	1:A:63:NRQ:CE	2.40	0.52
1:A:11:MET:HG3	1:A:41:MET:CE	2.41	0.51
1:C:146:MET:HG3	1:C:194:TYR:CE1	2.44	0.51
1:D:31:GLU:OE2	1:D:42:ARG:NH2	2.43	0.51
1:A:136:LYS:HE2	2:A:402:HOH:O	2.10	0.51
1:A:31:GLU:OE2	1:A:42:ARG:NH2	2.40	0.50
1:D:77:PRO:CG	1:D:188:LYS:HE3	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:HIS:HA	1:B:219:ALA:HB3	1.92	0.50
2:A:260:HOH:O	1:B:146:MET:HE3	2.12	0.50
1:D:71:ASN:C	1:D:71:ASN:HD22	2.15	0.49
1:D:30:GLY:HA3	1:D:40:THR:O	2.12	0.49
1:A:146:MET:HG3	1:A:194:TYR:CE1	2.47	0.49
1:D:63[A]:NRQ:CZ	1:D:197:ARG:CD	2.89	0.49
1:C:33:LYS:HB2	1:C:36:GLU:HB2	1.96	0.48
1:C:63[A]:NRQ:CE2	1:C:197:ARG:HD3	2.44	0.48
1:B:13:LEU:C	1:B:13:LEU:HD23	2.35	0.47
1:D:63[B]:NRQ:HD2	1:D:67:TYR:OH	2.14	0.47
1:D:77:PRO:HG3	1:D:188:LYS:HE3	1.97	0.47
1:A:84:PHE:O	1:A:182:LYS:NZ	2.47	0.46
1:A:39:GLN:HE22	1:A:66:SER:HB3	1.80	0.46
1:B:63:NRQ:O2	1:B:67:TYR:HE2	1.98	0.46
1:B:63:NRQ:CE1	1:B:197:ARG:HD2	2.46	0.46
1:C:63[A]:NRQ:HD2	1:C:199:LEU:HD12	1.97	0.46
1:A:63:NRQ:CE2	1:A:197:ARG:HD3	2.46	0.46
1:B:148:TYR:CZ	1:B:155:GLU:HB2	2.50	0.45
1:D:186:ASN:H	1:D:186:ASN:HD22	1.64	0.45
2:A:260:HOH:O	1:B:146:MET:CE	2.63	0.45
1:B:63:NRQ:HA31	1:B:63:NRQ:N1	2.31	0.45
1:D:3:GLU:HG2	1:D:4:LEU:N	2.32	0.45
1:D:63[A]:NRQ:CE2	1:D:197:ARG:CD	2.94	0.45
1:B:63:NRQ:N1	1:B:63:NRQ:CA3	2.80	0.45
1:D:20:ASN:O	2:D:332:HOH:O	2.21	0.44
1:C:63[A]:NRQ:CD2	1:C:199:LEU:HD12	2.47	0.44
1:B:63:NRQ:CZ	1:B:197:ARG:CD	2.95	0.44
1:B:150:ALA:HB3	1:B:155:GLU:CG	2.47	0.44
1:A:13:LEU:HB3	1:A:28:SER:OG	2.18	0.43
1:A:214:HIS:HD2	2:A:263:HOH:O	1.99	0.43
1:A:91:GLU:CD	2:A:246:HOH:O	2.56	0.43
1:A:63:NRQ:N1	1:A:63:NRQ:HA31	2.33	0.43
1:C:16:GLU:CB	1:C:25:LYS:HG3	2.48	0.43
1:B:5:ILE:HD11	1:B:84:PHE:CD1	2.54	0.43
1:B:63:NRQ:CE2	1:B:197:ARG:CD	2.95	0.43
1:C:150:ALA:O	1:C:151:ASP:HB2	2.18	0.43
1:D:18:THR:OG1	1:D:122:ARG:NH2	2.52	0.43
1:A:63:NRQ:HD2	1:A:63:NRQ:N2	2.34	0.42
1:B:118:ASN:ND2	2:B:276:HOH:O	2.42	0.42
1:B:15:MET:HG3	1:B:121:ILE:HD12	2.02	0.42
1:B:199:LEU:C	1:B:199:LEU:HD23	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:11:MET:HG3	1:D:41:MET:CE	2.49	0.42
1:C:20:ASN:O	1:C:21:ASN:ND2	2.52	0.42
1:B:16:GLU:HG2	1:B:120:LYS:HE3	2.01	0.42
1:C:41:MET:CE	1:C:62:PHE:HB3	2.50	0.42
1:D:67:TYR:OH	1:D:92:ARG:NH2	2.53	0.42
1:D:15:MET:HB3	1:D:26:CYS:HB2	2.02	0.41
1:A:63:NRQ:N1	1:A:63:NRQ:CA3	2.83	0.41
1:A:199:LEU:C	1:A:199:LEU:HD23	2.40	0.41
1:B:4:LEU:N	1:B:4:LEU:CD2	2.82	0.41
1:A:72:HIS:HA	1:A:219:ALA:HB3	2.03	0.41
1:D:3:GLU:HG2	1:D:4:LEU:H	1.84	0.41
1:A:63:NRQ:CE1	1:A:197:ARG:HD2	2.51	0.41
1:D:111:GLN:HG3	1:D:116:ILE:HD13	2.02	0.41
1:B:20:ASN:HA	1:C:91:GLU:OE2	2.21	0.41
1:B:185:LYS:HD3	1:B:185:LYS:HA	1.90	0.41
1:C:63[A]:NRQ:HE2	1:C:199:LEU:HB2	2.03	0.41
1:A:63:NRQ:CE2	1:A:197:ARG:CD	2.99	0.41
1:B:111:GLN:HG2	1:B:116:ILE:CG1	2.50	0.41
1:A:60:THR:O	1:A:63:NRQ:C2	2.69	0.40
1:C:33:LYS:HB3	1:C:33:LYS:HE2	1.79	0.40
1:D:18:THR:HG22	1:D:23:HIS:HA	2.03	0.40
1:A:20:ASN:O	1:A:21:ASN:CB	2.67	0.40
1:B:18:THR:CG2	1:B:21:ASN:HA	2.51	0.40
1:D:71:ASN:C	1:D:71:ASN:ND2	2.75	0.40
1:A:201:ARG:NH2	2:A:258:HOH:O	2.34	0.40
1:B:223:ASP:OD1	1:B:223:ASP:C	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%)	20	16
1	B	192/207 (93%)	184 (96%)	8 (4%)	30	27
1	C	191/207 (92%)	177 (93%)	14 (7%)	14	9
1	D	191/207 (92%)	172 (90%)	19 (10%)	8	4
All	All	767/828 (93%)	715 (93%)	52 (7%)	16	11

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
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

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	GLN
1	A	214	HIS
1	B	129	ASN
1	C	21	ASN
1	C	129	ASN
1	D	39	GLN
1	D	71	ASN
1	D	186	ASN
1	D	213	GLN
1	D	214	HIS

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	#$|Z| > 2$
1	NRQ	A	63	1	23,24,25	1.54	3 (13%)	23,32,34	3.45	8 (34%)
1	NRQ	C	63[B]	-	23,24,25	1.42	4 (17%)	23,32,34	3.53	4 (17%)
1	NRQ	B	63	1	23,24,25	1.80	4 (17%)	23,32,34	3.16	7 (30%)
1	NRQ	C	63[A]	-	23,24,25	1.32	4 (17%)	23,32,34	1.48	3 (13%)
1	NRQ	D	63[B]	-	23,24,25	1.76	4 (17%)	23,32,34	3.60	5 (21%)
1	NRQ	D	63[A]	-	23,24,25	1.78	4 (17%)	23,32,34	1.94	5 (21%)

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	-	1/9/31/32	0/2/2/2
1	NRQ	C	63[B]	-	-	3/9/31/32	0/2/2/2
1	NRQ	B	63	1	-	2/9/31/32	0/2/2/2
1	NRQ	C	63[A]	-	-	1/9/31/32	0/2/2/2
1	NRQ	D	63[B]	-	-	3/9/31/32	0/2/2/2
1	NRQ	D	63[A]	-	-	1/9/31/32	0/2/2/2

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	63[A]	NRQ	CA1-N1	6.48	1.43	1.27
1	D	63[B]	NRQ	CA1-N1	6.48	1.43	1.27
1	B	63	NRQ	CA3-C3	-4.49	1.33	1.49
1	A	63	NRQ	CA2-C2	-4.21	1.44	1.48
1	B	63	NRQ	CA2-C2	-3.66	1.45	1.48
1	D	63[A]	NRQ	C2-N3	-3.58	1.31	1.39
1	D	63[B]	NRQ	C2-N3	-3.58	1.31	1.39
1	B	63	NRQ	C2-N3	-3.49	1.31	1.39
1	C	63[A]	NRQ	C2-N3	-3.30	1.32	1.39
1	C	63[B]	NRQ	C2-N3	-3.30	1.32	1.39
1	A	63	NRQ	C2-N3	-3.28	1.32	1.39
1	C	63[B]	NRQ	CB2-CA2	2.67	1.37	1.35
1	B	63	NRQ	CA1-N1	2.66	1.33	1.27
1	A	63	NRQ	O3-C3	2.54	1.34	1.19
1	D	63[A]	NRQ	O2-C2	2.50	1.28	1.23
1	D	63[B]	NRQ	O2-C2	2.50	1.28	1.23
1	C	63[A]	NRQ	O3-C3	2.23	1.32	1.19
1	C	63[B]	NRQ	O3-C3	2.23	1.32	1.19
1	C	63[A]	NRQ	CB2-CA2	-2.14	1.33	1.35
1	D	63[A]	NRQ	CA3-C3	2.12	1.56	1.49
1	D	63[B]	NRQ	CA3-C3	2.12	1.56	1.49
1	C	63[A]	NRQ	C1-N3	-2.01	1.35	1.38
1	C	63[B]	NRQ	C1-N3	-2.01	1.35	1.38

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	63	NRQ	O2-C2-CA2	-11.92	124.27	130.96
1	B	63	NRQ	O2-C2-CA2	-11.62	124.44	130.96
1	C	63[B]	NRQ	CB2-CA2-C2	11.55	136.07	122.28
1	D	63[B]	NRQ	CB2-CA2-N2	-11.33	113.12	128.83
1	D	63[B]	NRQ	CB2-CA2-C2	10.82	135.19	122.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	63[B]	NRQ	CB2-CA2-N2	-10.63	114.08	128.83
1	A	63	NRQ	CA2-C2-N3	8.00	107.15	103.37
1	B	63	NRQ	CA2-C2-N3	7.59	106.96	103.37
1	D	63[A]	NRQ	CB2-CA2-C2	-5.56	115.64	122.28
1	A	63	NRQ	CG2-CB2-CA2	-4.05	124.98	129.94
1	D	63[A]	NRQ	C2-CA2-N2	3.79	111.59	108.93
1	D	63[B]	NRQ	C2-CA2-N2	3.79	111.59	108.93
1	C	63[A]	NRQ	CA2-C2-N3	3.66	105.10	103.37
1	C	63[B]	NRQ	CA2-C2-N3	3.66	105.10	103.37
1	C	63[A]	NRQ	CB2-CA2-C2	-3.65	117.91	122.28
1	D	63[B]	NRQ	CG2-CB2-CA2	3.65	134.42	129.94
1	C	63[B]	NRQ	CG2-CB2-CA2	3.45	134.18	129.94
1	A	63	NRQ	CB2-CA2-C2	-3.11	118.56	122.28
1	D	63[A]	NRQ	CB2-CA2-N2	2.84	132.77	128.83
1	A	63	NRQ	CD1-CG2-CD2	2.68	121.61	117.64
1	B	63	NRQ	CB2-CA2-C2	-2.58	119.20	122.28
1	C	63[A]	NRQ	CB2-CA2-N2	2.49	132.27	128.83
1	D	63[A]	NRQ	CD1-CG2-CD2	2.37	121.15	117.64
1	A	63	NRQ	CB2-CA2-N2	2.19	131.87	128.83
1	B	63	NRQ	N3-C1-N2	2.15	116.12	113.28
1	A	63	NRQ	CE1-CD1-CG2	-2.15	118.45	121.25
1	B	63	NRQ	O2-C2-N3	2.13	128.58	124.35
1	B	63	NRQ	CD1-CE1-CZ	2.12	122.20	119.88
1	D	63[A]	NRQ	CE-SD-CG1	2.07	107.51	100.40
1	D	63[B]	NRQ	CE-SD-CG1	2.07	107.51	100.40
1	A	63	NRQ	O2-C2-N3	2.03	128.38	124.35
1	B	63	NRQ	CE1-CD1-CG2	-2.00	118.64	121.25

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	63[B]	NRQ	C2-CA2-CB2-CG2
1	D	63[A]	NRQ	CA1-CB1-CG1-SD
1	D	63[B]	NRQ	CA1-CB1-CG1-SD
1	D	63[B]	NRQ	C2-CA2-CB2-CG2
1	A	63	NRQ	CB1-CG1-SD-CE
1	B	63	NRQ	CB1-CG1-SD-CE
1	C	63[B]	NRQ	N2-CA2-CB2-CG2
1	D	63[B]	NRQ	N2-CA2-CB2-CG2
1	B	63	NRQ	C1-CA1-CB1-CG1
1	C	63[A]	NRQ	C1-CA1-CB1-CG1

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Mol	Chain	Res	Type	Atoms
1	C	63[B]	NRQ	C1-CA1-CB1-CG1

There are no ring outliers.

5 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	63	NRQ	10	0
1	B	63	NRQ	11	0
1	C	63[A]	NRQ	4	0
1	D	63[B]	NRQ	1	0
1	D	63[A]	NRQ	5	0

5.5　Carbohydrates (i)

There are no monosaccharides in this entry.

5.6　Ligand geometry (i)

There are no ligands in this entry.

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	223/243 (91%)	0.30	9 (4%)	38	37	20, 33, 52, 72	0
1	B	223/243 (91%)	0.40	14 (6%)	20	19	19, 35, 53, 71	0
1	C	223/243 (91%)	0.68	24 (10%)	5	5	24, 42, 65, 78	0
1	D	223/243 (91%)	0.71	26 (11%)	4	4	23, 44, 72, 95	0
All	All	892/972 (91%)	0.52	73 (8%)	11	11	19, 38, 64, 95	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	185	LYS	7.3
1	D	184	ALA	6.9
1	C	185	LYS	6.2
1	D	186	ASN	5.8
1	C	206	ASP	5.4
1	A	185	LYS	5.0
1	D	4	LEU	5.0
1	D	206	ASP	5.0
1	D	187	LEU	4.8
1	C	184	ALA	4.5
1	B	186	ASN	4.4
1	C	205	ALA	4.2
1	C	186	ASN	4.1
1	B	75	GLY	4.1
1	D	151	ASP	3.8
1	C	207	LYS	3.8
1	D	75	GLY	3.8
1	B	228	LEU	3.8
1	D	112	ASP	3.8
1	A	186	ASN	3.7
1	D	14	TYR	3.6

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Full wwPDB X-ray Structure Validation Report 3NT9

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Mol	Chain	Res	Type	RSRZ
1	D	210	TYR	3.6
1	D	152	GLY	3.6
1	C	47	GLU	3.4
1	D	205	ALA	3.3
1	D	73	THR	3.2
1	D	7	GLU	3.1
1	D	111	GLN	3.0
1	A	55	PHE	3.0
1	C	129	ASN	3.0
1	D	74	GLN	2.9
1	B	74	GLN	2.9
1	D	228	LEU	2.9
1	B	152	GLY	2.8
1	C	128	SER	2.8
1	C	58	LEU	2.8
1	C	23	HIS	2.7
1	C	210	TYR	2.7
1	C	50	PRO	2.7
1	C	130	GLY	2.7
1	B	129	ASN	2.7
1	C	21	ASN	2.7
1	B	185	LYS	2.6
1	B	3	GLU	2.6
1	C	151	ASP	2.6
1	C	10	HIS	2.5
1	C	46	VAL	2.5
1	B	57	ILE	2.4
1	D	179	ARG	2.4
1	D	69	PHE	2.4
1	A	21	ASN	2.4
1	D	67	TYR	2.4
1	C	57	ILE	2.4
1	C	147	LEU	2.3
1	B	184	ALA	2.3
1	C	112	ASP	2.3
1	A	184	ALA	2.2
1	A	57	ILE	2.2
1	C	202	ILE	2.2
1	D	189	VAL	2.2
1	A	58	LEU	2.2
1	A	187	LEU	2.2
1	B	69	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	128	SER	2.1
1	D	165	VAL	2.1
1	D	10	HIS	2.1
1	D	80	PHE	2.1
1	B	167	GLY	2.1
1	B	151	ASP	2.0
1	A	80	PHE	2.0
1	C	225	PRO	2.0
1	D	129	ASN	2.0
1	C	166	GLY	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. 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
1	NRQ	A	63	23/24	0.94	0.13	25,29,33,35	0
1	NRQ	B	63	23/24	0.94	0.14	29,31,34,37	0
1	NRQ	D	63[A]	23/24	0.95	0.15	32,36,42,47	8
1	NRQ	D	63[B]	23/24	0.95	0.15	27,36,42,47	8
1	NRQ	C	63[A]	23/24	0.96	0.15	28,34,41,43	8
1	NRQ	C	63[B]	23/24	0.96	0.15	20,34,41,43	8

6.3 Carbohydrates ⓘ

There are no monosaccharides 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.