Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:44 AM GMT

PDB ID	:	3BXB
Title	:	Monomeric Far-red Fluorescent Protein mKate Crystallized at pH 7.0
Authors	:	Pletnev, S.; Pletneva, N.; Pletnev, V.
Deposited on	:	2008-01-12
Resolution	:	2.60 Å(reported)

This is a Full wwPDB X-ray Structure 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/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

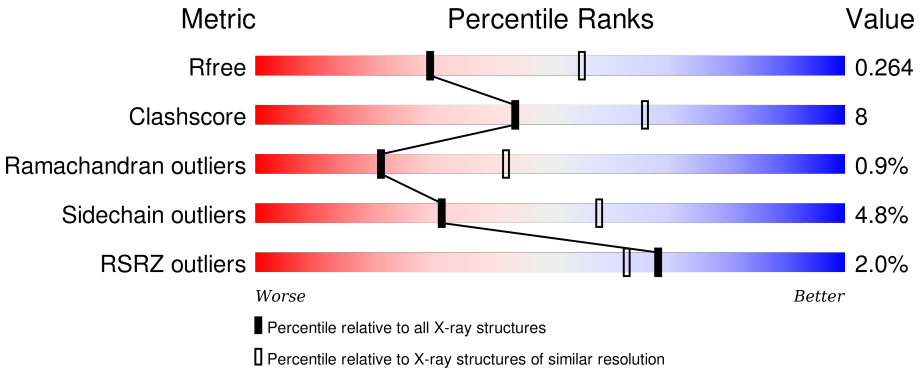
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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 <=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	75% 16% • 8%
1	B	243	77% 14% 8%
1	C	243	71% 20% • 8%
1	D	243	3% 75% 16% 8%
1	E	243	2% 74% 16% • 8%

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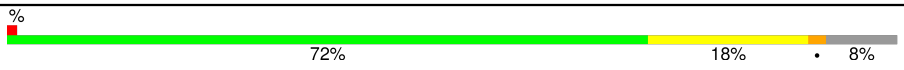
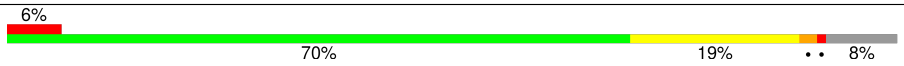
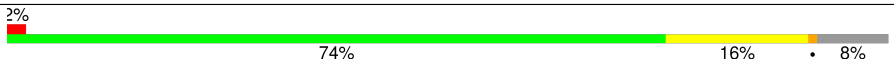
Mol	Chain	Length	Quality of chain
1	F	243	
1	G	243	
1	H	243	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 14615 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 Far-red fluorescent protein mKate.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1776	1129	300	334	13			
1	B	223	Total	C	N	O	S	0	0	0
			1776	1129	300	334	13			
1	C	223	Total	C	N	O	S	0	1	0
			1787	1135	304	335	13			
1	D	223	Total	C	N	O	S	0	2	0
			1799	1144	305	337	13			
1	E	223	Total	C	N	O	S	0	1	0
			1787	1135	304	335	13			
1	F	223	Total	C	N	O	S	0	1	0
			1787	1135	304	335	13			
1	G	223	Total	C	N	O	S	0	0	0
			1776	1129	300	334	13			
1	H	223	Total	C	N	O	S	0	0	0
			1776	1129	300	334	13			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	48	Total	O	0	0
			48	48		
2	B	51	Total	O	0	0
			51	51		
2	C	42	Total	O	0	0
			42	42		
2	D	60	Total	O	0	0
			60	60		
2	E	51	Total	O	0	0
			51	51		
2	F	45	Total	O	0	0
			45	45		

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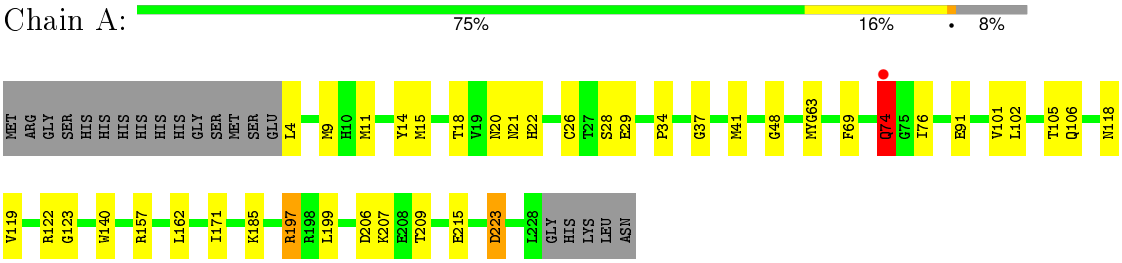
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	25	Total O 25 25	0	0
2	H	29	Total O 29 29	0	0

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 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.

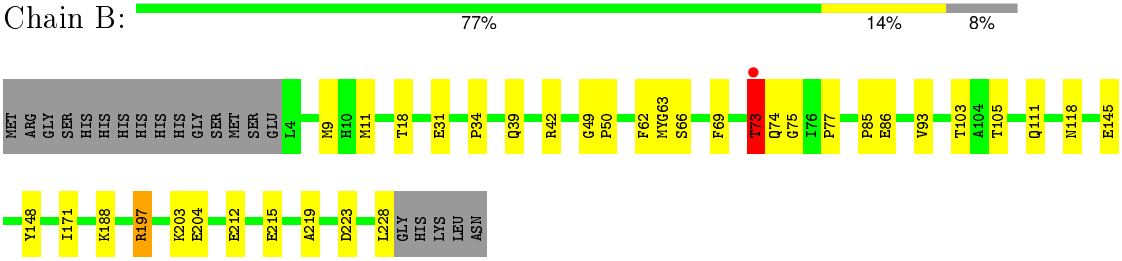
- Molecule 1: Far-red fluorescent protein mKate

Chain A:



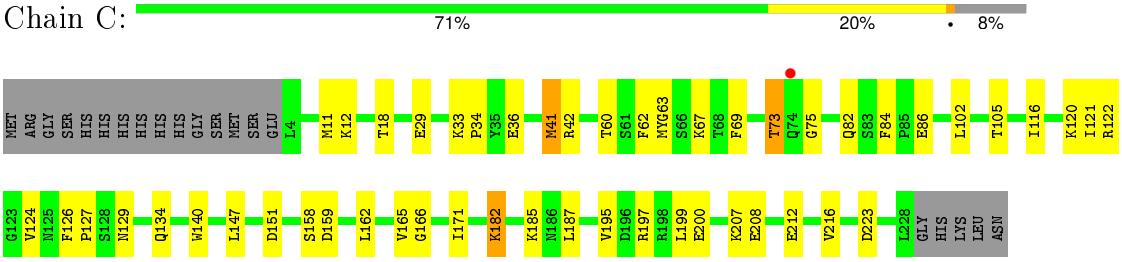
- Molecule 1: Far-red fluorescent protein mKate

Chain B:



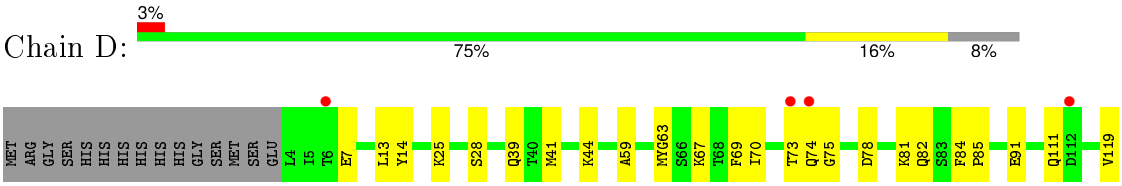
- Molecule 1: Far-red fluorescent protein mKate

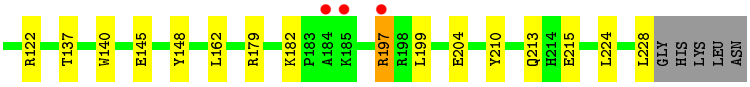
Chain C:



- Molecule 1: Far-red fluorescent protein mKate

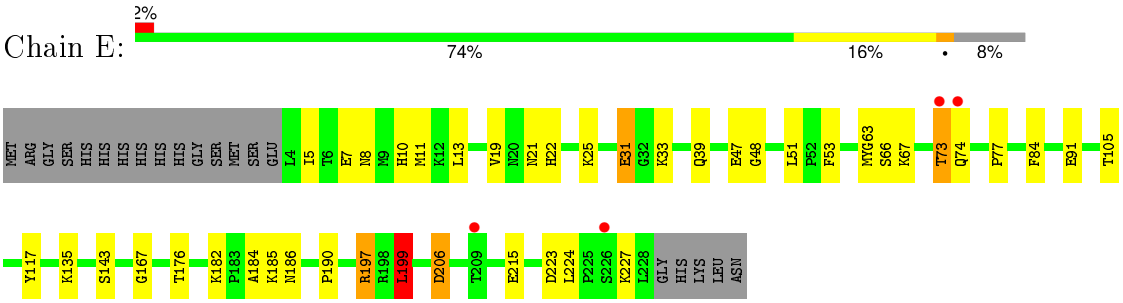
Chain D:





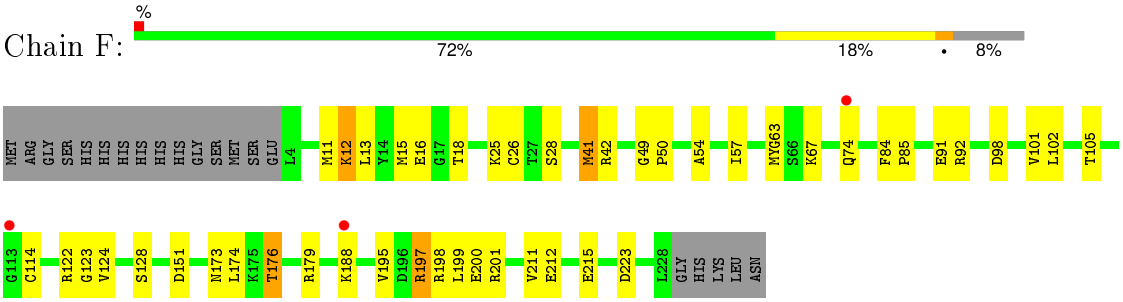
• Molecule 1: Far-red fluorescent protein mKate

Chain E:



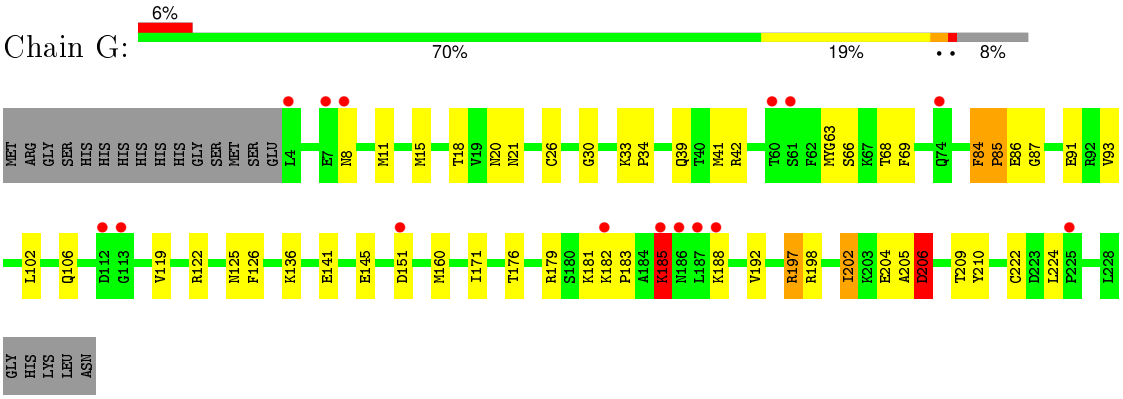
• Molecule 1: Far-red fluorescent protein mKate

Chain F:



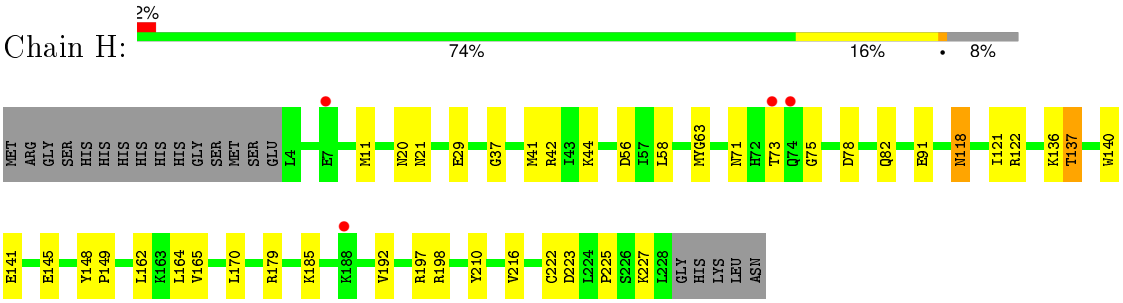
• Molecule 1: Far-red fluorescent protein mKate

Chain G:



• Molecule 1: Far-red fluorescent protein mKate

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	74.18Å 104.97Å 123.03Å 90.00° 105.81° 90.00°	Depositor
Resolution (Å)	29.84 – 2.60 29.84 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.84-2.60) 99.7 (29.84-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.92 (at 2.61Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.170 , 0.263 0.170 , 0.264	Depositor DCC
R_{free} test set	2814 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	41.8	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 47.2	EDS
Estimated twinning fraction	0.020 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	2 of 55744 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	14615	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.89% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: 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	0.60	0/1792	0.67	0/2417
1	B	0.59	0/1792	0.70	1/2417 (0.0%)
1	C	0.62	0/1803	0.66	0/2431
1	D	0.57	0/1816	0.67	0/2449
1	E	0.56	0/1803	0.71	1/2431 (0.0%)
1	F	0.57	0/1803	0.66	0/2431
1	G	0.58	0/1792	0.66	0/2417
1	H	0.52	0/1792	0.64	0/2417
All	All	0.58	0/14393	0.67	2/19410 (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
1	C	0	1
1	F	0	1
1	G	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	199	LEU	CA-CB-CG	5.83	128.71	115.30
1	B	62	PHE	CA-C-O	-5.31	108.95	120.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	84	PHE	Peptide
1	F	74	GLN	Peptide
1	G	84	PHE	Peptide

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	1776	0	1745	31	0
1	B	1776	0	1745	19	0
1	C	1787	0	1757	38	0
1	D	1799	0	1765	24	0
1	E	1787	0	1757	28	0
1	F	1787	0	1757	39	0
1	G	1776	0	1745	41	0
1	H	1776	0	1745	27	0
2	A	48	0	0	1	0
2	B	51	0	0	0	0
2	C	42	0	0	7	0
2	D	60	0	0	1	0
2	E	51	0	0	1	0
2	F	45	0	0	3	0
2	G	25	0	0	5	0
2	H	29	0	0	1	0
All	All	14615	0	14016	227	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 8.

All (227) 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:41:MET:HG3	1:A:63:NRQ:HE3	1.18	1.11
1:A:41:MET:HG3	1:A:63:NRQ:CE	1.85	1.06
1:C:73:THR:HA	2:C:266:HOH:O	1.55	1.05
1:E:67:LYS:NZ	1:E:197[B]:ARG:HH22	1.59	1.00
1:H:78:ASP:O	1:H:82:GLN:HB2	1.62	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:91:GLU:OE2	1:D:179:ARG:NH1	1.99	0.94
1:B:197:ARG:HH11	1:B:197:ARG:HG2	1.37	0.90
1:E:67:LYS:HZ2	1:E:197[B]:ARG:HH22	1.17	0.87
1:H:44:LYS:HE3	1:H:210:TYR:HD2	1.39	0.87
1:F:28:SER:OG	1:F:41:MET:HG2	1.80	0.82
1:H:71:ASN:OD1	1:H:73:THR:HG23	1.84	0.77
1:G:125:ASN:HB2	2:G:247:HOH:O	1.84	0.77
1:H:91:GLU:CD	1:H:179:ARG:HH12	1.88	0.76
1:G:11:MET:HG3	1:G:41:MET:HE3	1.67	0.76
1:G:197:ARG:HH11	1:G:197:ARG:CG	1.98	0.76
1:E:67:LYS:NZ	1:E:197[B]:ARG:NH2	2.33	0.75
1:C:41:MET:CE	1:C:62:PHE:HB3	2.17	0.75
1:G:85:PRO:HD2	1:G:86:GLU:OE2	1.87	0.74
1:B:197:ARG:HH11	1:B:197:ARG:CG	2.01	0.74
1:C:82:GLN:O	1:C:182:LYS:HE2	1.88	0.73
1:C:41:MET:HE1	1:C:62:PHE:HB3	1.71	0.73
1:F:197[A]:ARG:HH11	1:F:197[A]:ARG:HG2	1.53	0.72
1:G:197:ARG:HH11	1:G:197:ARG:HG2	1.55	0.70
1:H:118:ASN:N	1:H:118:ASN:HD22	1.89	0.70
1:F:25:LYS:HB2	1:F:25:LYS:NZ	2.07	0.70
1:F:91:GLU:OE2	1:F:179:ARG:NH1	2.25	0.70
1:E:67:LYS:HZ2	1:E:197[B]:ARG:NH2	1.88	0.67
1:F:67:LYS:HZ1	1:F:197[B]:ARG:HH12	1.42	0.67
1:B:73:THR:OG1	1:B:219:ALA:O	2.13	0.66
1:E:197[B]:ARG:HD3	1:E:215:GLU:OE2	1.96	0.66
1:E:67:LYS:HZ1	1:E:197[B]:ARG:HH22	1.44	0.66
1:G:91:GLU:CD	1:G:179:ARG:HH12	2.00	0.65
1:H:44:LYS:HE3	1:H:210:TYR:CD2	2.27	0.65
1:A:18:THR:HB	1:A:122:ARG:NH1	2.12	0.65
1:D:13:LEU:HB3	1:D:28:SER:OG	1.97	0.64
1:G:205:ALA:HB3	1:G:210:TYR:HB3	1.78	0.64
1:F:92:ARG:HD3	1:F:174:LEU:HD23	1.80	0.64
1:F:25:LYS:HB2	1:F:25:LYS:HZ3	1.63	0.64
1:E:77:PRO:HG2	1:E:190:PRO:HA	1.78	0.63
1:C:151:ASP:HB3	2:C:260:HOH:O	1.97	0.63
1:E:22:HIS:HE1	1:E:48:GLY:O	1.80	0.63
1:F:12:LYS:HD2	1:F:114:CYS:SG	2.39	0.63
1:G:15:MET:HB3	1:G:26:CYS:HB2	1.80	0.63
1:A:122:ARG:HD3	1:C:105:THR:HG23	1.80	0.62
1:H:118:ASN:ND2	1:H:118:ASN:N	2.48	0.62
1:H:227:LYS:HG2	2:H:246:HOH:O	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:136:LYS:HB3	1:H:165:VAL:HB	1.83	0.61
1:C:63:NRQ:CE1	1:C:197[A]:ARG:HE	2.14	0.60
1:F:197[A]:ARG:HH11	1:F:197[A]:ARG:CG	2.14	0.60
1:G:87:GLY:O	1:G:181:LYS:HB2	2.02	0.60
1:A:118:ASN:HB2	2:A:267:HOH:O	2.02	0.60
1:F:63:NRQ:HE2	1:F:199:LEU:HB2	1.84	0.59
1:A:37:GLY:HA2	1:A:69:PHE:O	2.02	0.59
1:D:197[B]:ARG:NH1	2:D:240:HOH:O	2.35	0.58
1:G:20:ASN:HD21	1:G:126:PHE:HB2	1.69	0.58
1:E:63:NRQ:CE2	1:E:197[B]:ARG:HD2	2.34	0.57
1:C:63:NRQ:HE2	1:C:199:LEU:HB2	1.85	0.57
1:B:34:PRO:HA	1:B:69:PHE:HA	1.87	0.57
1:H:37:GLY:O	1:H:216:VAL:HA	2.05	0.57
1:E:39:GLN:HE22	1:E:66:SER:HB3	1.69	0.57
1:F:16:GLU:HG3	1:F:25:LYS:HZ2	1.70	0.57
1:A:140:TRP:CZ3	1:A:162:LEU:HB2	2.40	0.56
1:D:39:GLN:NE2	1:D:69:PHE:HB2	2.20	0.56
1:E:73:THR:HA	2:E:266:HOH:O	2.04	0.56
1:B:145:GLU:HB2	1:B:197:ARG:NH2	2.19	0.55
1:G:145:GLU:HB2	1:G:197:ARG:NH2	2.21	0.55
1:C:67:LYS:NZ	1:C:197[B]:ARG:HH22	2.04	0.55
1:A:11:MET:HG3	1:A:41:MET:HE3	1.88	0.55
1:D:44:LYS:HE3	1:D:210:TYR:HE1	1.71	0.55
1:G:63:NRQ:HA31	1:G:63:NRQ:N1	2.21	0.55
1:G:185:LYS:HE3	1:G:185:LYS:H	1.71	0.55
1:B:203:LYS:H	1:B:212:GLU:HB3	1.71	0.55
1:G:106:GLN:CG	1:G:119:VAL:HG22	2.37	0.54
1:F:212:GLU:HB3	2:F:254:HOH:O	2.07	0.54
1:C:12:LYS:HG2	1:C:29:GLU:OE1	2.08	0.53
1:A:63:NRQ:HE2	1:A:199:LEU:HB2	1.89	0.53
1:B:93:VAL:HG23	1:B:103:THR:HG22	1.90	0.53
1:F:201:ARG:HD3	1:F:211:VAL:HG13	1.91	0.53
1:A:22:HIS:HE1	1:A:48:GLY:O	1.91	0.53
1:H:29:GLU:OE2	1:H:42:ARG:NE	2.39	0.52
1:D:140:TRP:CZ3	1:D:162:LEU:HB2	2.44	0.52
1:F:67:LYS:NZ	1:F:197[B]:ARG:HH12	2.08	0.52
1:D:63:NRQ:CZ	1:D:197[A]:ARG:HG3	2.39	0.52
1:C:63:NRQ:CD2	1:C:197[B]:ARG:HD2	2.40	0.52
1:F:105:THR:HG23	1:G:122:ARG:HD3	1.92	0.52
1:C:34:PRO:HA	1:C:69:PHE:HA	1.92	0.51
1:B:39:GLN:HE22	1:B:66:SER:HB3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:197:ARG:CG	1:G:197:ARG:NH1	2.67	0.51
1:F:42:ARG:HG2	1:F:212:GLU:HG2	1.93	0.51
1:D:84:PHE:HB3	1:D:85:PRO:HA	1.93	0.51
1:D:63:NRQ:HE2	1:D:199:LEU:HB2	1.92	0.51
1:F:13:LEU:HD22	1:F:28:SER:HB3	1.93	0.51
1:E:22:HIS:CE1	1:E:48:GLY:O	2.63	0.51
1:A:223:ASP:OD1	1:A:223:ASP:N	2.37	0.50
1:A:63:NRQ:HG11	1:A:215:GLU:OE1	2.10	0.50
1:G:106:GLN:HG3	1:G:119:VAL:HG22	1.93	0.50
1:E:25:LYS:HB2	1:E:47:GLU:HB2	1.92	0.50
1:C:207:LYS:O	1:C:208:GLU:HB2	2.12	0.50
1:C:63:NRQ:CE2	1:C:197[B]:ARG:HD2	2.41	0.50
1:A:91:GLU:HG3	1:C:124:VAL:HB	1.94	0.50
1:G:224:LEU:O	1:H:198:ARG:NH2	2.41	0.50
1:G:198:ARG:NH2	1:H:222:CYS:SG	2.85	0.49
1:F:85:PRO:HG2	2:F:269:HOH:O	2.11	0.49
1:A:74:GLN:C	1:A:76:ILE:H	2.15	0.49
1:C:29:GLU:HB2	2:C:265:HOH:O	2.12	0.49
1:C:129:ASN:HA	1:C:134:GLN:OE1	2.12	0.49
1:G:151:ASP:N	2:G:256:HOH:O	2.44	0.49
1:E:67:LYS:HZ1	1:E:197[B]:ARG:NH2	2.04	0.49
1:C:33:LYS:HD3	1:C:36:GLU:OE2	2.13	0.49
1:B:105:THR:HG23	1:D:122:ARG:HD3	1.95	0.48
1:F:92:ARG:HB2	1:F:176:THR:HG23	1.95	0.48
1:H:164:LEU:HD21	1:H:170:LEU:HB2	1.94	0.48
1:H:56:ASP:OD1	1:H:137:THR:OG1	2.31	0.48
1:G:18:THR:HB	1:G:122:ARG:NH1	2.29	0.48
1:G:206:ASP:O	1:G:209:THR:OG1	2.22	0.48
1:A:41:MET:CG	1:A:63:NRQ:HE3	2.13	0.48
1:C:75:GLY:HA2	2:C:268:HOH:O	2.14	0.48
1:C:102:LEU:HD21	1:C:121:ILE:HG23	1.96	0.47
1:H:140:TRP:CZ3	1:H:162:LEU:HB2	2.49	0.47
1:F:91:GLU:HG2	2:G:248:HOH:O	2.15	0.47
1:F:63:NRQ:CE1	1:F:197[B]:ARG:HD3	2.44	0.47
1:B:85:PRO:HD2	1:B:86:GLU:OE2	2.14	0.47
1:C:67:LYS:HZ2	1:C:197[B]:ARG:HH22	1.61	0.47
1:B:77:PRO:HG3	1:B:188:LYS:HE3	1.96	0.47
1:C:216:VAL:HG13	1:D:224:LEU:HD13	1.97	0.47
1:C:63:NRQ:N1	1:C:63:NRQ:HA31	2.30	0.47
1:A:105:THR:OG1	1:C:122:ARG:NH1	2.48	0.47
1:B:197:ARG:CG	1:B:197:ARG:NH1	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:207:LYS:HE3	2:C:258:HOH:O	2.14	0.46
1:F:15:MET:HB3	1:F:26:CYS:HB2	1.96	0.46
1:H:145:GLU:HB2	1:H:197:ARG:NH2	2.30	0.46
1:E:5:ILE:HD11	1:E:84:PHE:CD1	2.51	0.46
1:C:63:NRQ:CD1	1:C:197[A]:ARG:HE	2.29	0.46
1:G:106:GLN:HG2	1:G:119:VAL:HG22	1.98	0.46
1:F:195:VAL:HG12	1:F:197[B]:ARG:HG2	1.97	0.46
1:D:137:THR:HB	1:D:162:LEU:HD11	1.97	0.46
1:H:58:LEU:HD22	1:H:121:ILE:HD12	1.98	0.46
1:E:105:THR:HG23	1:H:122:ARG:HD3	1.98	0.46
1:D:197[B]:ARG:HD3	1:D:215:GLU:OE2	2.15	0.46
1:A:20:ASN:O	1:A:21:ASN:HB3	2.16	0.45
1:A:14:TYR:HD2	1:A:118:ASN:HD21	1.64	0.45
1:G:21:ASN:N	2:G:248:HOH:O	2.41	0.45
1:A:15:MET:HB3	1:A:26:CYS:HB2	1.99	0.45
1:E:19:VAL:HB	1:E:53:PHE:CE2	2.52	0.45
1:E:91:GLU:OE1	1:H:20:ASN:HA	2.17	0.45
1:E:13:LEU:HD12	1:E:117:TYR:HD2	1.81	0.45
1:H:148:TYR:HA	1:H:149:PRO:HD3	1.78	0.45
1:F:198:ARG:O	1:F:215:GLU:HA	2.17	0.45
1:G:39:GLN:HE22	1:G:66:SER:HB3	1.82	0.45
1:B:63:NRQ:HD2	1:B:215:GLU:OE1	2.17	0.45
1:C:86:GLU:OE2	1:C:182:LYS:NZ	2.45	0.45
1:F:197[A]:ARG:CG	1:F:197[A]:ARG:NH1	2.77	0.45
1:C:195:VAL:O	1:C:197[A]:ARG:NH1	2.49	0.45
1:A:14:TYR:HD2	1:A:118:ASN:ND2	2.15	0.45
1:G:141:GLU:HG3	1:H:192:VAL:HG21	1.99	0.45
1:E:143:SER:OG	1:E:197[A]:ARG:NH1	2.50	0.45
1:G:222:CYS:SG	1:G:224:LEU:HB2	2.57	0.45
1:F:18:THR:CB	1:F:122:ARG:HH22	2.30	0.45
1:A:171:ILE:HG13	1:B:148:TYR:OH	2.17	0.45
1:F:49:GLY:HA2	1:F:50:PRO:C	2.36	0.45
1:A:63:NRQ:CZ	1:A:197:ARG:HG3	2.47	0.44
1:B:42:ARG:HG2	1:B:212:GLU:HG3	2.00	0.44
1:E:10:HIS:ND1	1:E:31:GLU:HB3	2.32	0.44
1:D:145:GLU:HB2	1:D:197[A]:ARG:CZ	2.48	0.44
1:D:14[A]:TYR:OH	1:D:25:LYS:HE3	2.17	0.44
1:A:63:NRQ:N1	1:A:63:NRQ:HA31	2.31	0.44
1:C:140:TRP:CZ3	1:C:162:LEU:HB2	2.52	0.44
1:G:85:PRO:CD	1:G:86:GLU:OE2	2.63	0.44
1:C:165:VAL:O	1:C:166:GLY:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:51:LEU:O	1:E:135:LYS:NZ	2.40	0.44
1:C:63:NRQ:CE1	1:C:197[A]:ARG:NE	2.80	0.44
1:C:42:ARG:HG2	1:C:212:GLU:HG3	2.00	0.44
1:F:63:NRQ:N1	1:F:63:NRQ:HA31	2.33	0.43
1:F:198:ARG:HD2	1:F:200:GLU:OE2	2.17	0.43
1:E:63:NRQ:CZ	1:E:197[A]:ARG:HG3	2.48	0.43
1:F:25:LYS:HZ3	1:F:25:LYS:CB	2.31	0.43
1:G:91:GLU:OE2	1:G:179:ARG:NH1	2.49	0.43
1:E:184:ALA:O	1:E:186:ASN:N	2.51	0.43
1:D:59:ALA:HA	1:D:213:GLN:HE22	1.84	0.43
1:G:30:GLY:HA2	1:G:42:ARG:NH2	2.33	0.43
1:G:125:ASN:CB	2:G:247:HOH:O	2.53	0.43
1:G:202:ILE:HA	1:G:202:ILE:HD12	1.69	0.43
1:D:67:LYS:HE3	1:D:70:ILE:HD11	2.01	0.43
1:G:192:VAL:HG21	1:H:141:GLU:HG3	1.99	0.43
1:D:41:MET:HB2	1:D:63:NRQ:CE	2.49	0.43
1:F:101:VAL:O	1:F:123:GLY:HA2	2.19	0.43
1:E:63:NRQ:CZ	1:E:197[B]:ARG:HD2	2.48	0.43
1:G:222:CYS:SG	1:H:198:ARG:NH2	2.92	0.43
1:A:74:GLN:H	1:A:74:GLN:HG3	1.62	0.43
1:A:206:ASP:HB2	1:A:209:THR:OG1	2.19	0.43
1:A:101:VAL:O	1:A:123:GLY:HA2	2.19	0.43
1:F:84:PHE:HB3	1:F:85:PRO:HA	2.01	0.42
1:H:20:ASN:O	1:H:21:ASN:CB	2.67	0.42
1:F:25:LYS:HB2	1:F:25:LYS:HZ2	1.83	0.42
1:A:106:GLN:HG3	1:A:119:VAL:HG22	2.01	0.42
1:A:9:MET:HG3	1:A:34:PRO:HG2	2.00	0.42
1:G:63:NRQ:HE1	1:G:160:MET:SD	2.59	0.42
1:D:82:GLN:O	1:D:182:LYS:HE3	2.20	0.42
1:G:39:GLN:NE2	1:G:69:PHE:HB2	2.33	0.42
1:A:157:ARG:HG3	1:B:171:ILE:HG21	2.01	0.42
1:F:92:ARG:HD2	2:F:278:HOH:O	2.19	0.42
1:E:8:ASN:OD1	1:E:33:LYS:NZ	2.52	0.42
1:C:171:ILE:HG13	1:D:148:TYR:OH	2.20	0.41
1:B:73:THR:HB	1:B:74:GLN:H	1.68	0.41
1:F:98:ASP:OD1	1:F:98:ASP:C	2.59	0.41
1:H:63:NRQ:CD1	1:H:197:ARG:HE	2.34	0.41
1:B:49:GLY:HA2	1:B:50:PRO:C	2.40	0.41
1:C:12:LYS:HB2	1:C:116:ILE:HD13	2.02	0.41
1:E:63:NRQ:HE2	1:E:199:LEU:HB2	2.01	0.41
1:G:84:PHE:HB3	1:G:85:PRO:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:60:THR:HG23	2:C:240:HOH:O	2.19	0.41
1:D:78:ASP:OD2	1:D:81:LYS:HD2	2.20	0.41
1:F:54:ALA:O	1:F:57:ILE:HG12	2.21	0.41
1:B:9:MET:HG3	1:B:34:PRO:HG2	2.02	0.41
1:F:13:LEU:HB3	1:F:28:SER:HB3	2.01	0.41
1:G:20:ASN:ND2	1:G:126:PHE:HB2	2.34	0.41
1:E:224:LEU:O	1:F:198:ARG:NH2	2.48	0.41
1:C:200:GLU:HG2	1:D:228:LEU:HD12	2.03	0.41
1:D:74:GLN:O	1:D:75:GLY:C	2.56	0.41
1:C:126:PHE:HA	1:C:127:PRO:HD3	1.97	0.41
1:A:91:GLU:HB2	1:A:105:THR:HG22	2.03	0.40
1:G:182:LYS:HA	1:G:183:PRO:HD3	1.97	0.40
1:G:171:ILE:HG13	1:H:148:TYR:OH	2.20	0.40
1:D:44:LYS:HG2	1:D:210:TYR:CE1	2.57	0.40
1:C:18:THR:HG21	2:C:256:HOH:O	2.22	0.40
1:A:28:SER:OG	1:A:41:MET:CE	2.70	0.40
1:F:124:VAL:HG21	1:G:93:VAL:HB	2.03	0.40

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	218/243 (90%)	211 (97%)	6 (3%)	1 (0%)	34 60
1	B	218/243 (90%)	209 (96%)	7 (3%)	2 (1%)	21 42
1	C	219/243 (90%)	209 (95%)	9 (4%)	1 (0%)	34 60
1	D	220/243 (90%)	211 (96%)	8 (4%)	1 (0%)	34 60
1	E	219/243 (90%)	204 (93%)	10 (5%)	5 (2%)	8 14
1	F	219/243 (90%)	211 (96%)	8 (4%)	0	100 100
1	G	218/243 (90%)	200 (92%)	14 (6%)	4 (2%)	11 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	H	218/243 (90%)	205 (94%)	11 (5%)	2 (1%)	21 42
All	All	1749/1944 (90%)	1660 (95%)	73 (4%)	16 (1%)	21 42

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	THR
1	E	73	THR
1	E	74	GLN
1	G	206	ASP
1	E	185	LYS
1	D	73	THR
1	E	167	GLY
1	G	185	LYS
1	H	225	PRO
1	A	74	GLN
1	C	73	THR
1	E	206	ASP
1	H	75	GLY
1	B	75	GLY
1	G	34	PRO
1	G	85	PRO

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	191/208 (92%)	183 (96%)	8 (4%)	36 65
1	B	191/208 (92%)	181 (95%)	10 (5%)	29 54
1	C	192/208 (92%)	182 (95%)	10 (5%)	29 54
1	D	193/208 (93%)	187 (97%)	6 (3%)	47 76
1	E	192/208 (92%)	180 (94%)	12 (6%)	22 44
1	F	192/208 (92%)	180 (94%)	12 (6%)	22 44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	G	191/208 (92%)	179 (94%)	12 (6%)	22 44
1	H	191/208 (92%)	185 (97%)	6 (3%)	47 76
All	All	1533/1664 (92%)	1457 (95%)	76 (5%)	31 56

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	29	GLU
1	A	74	GLN
1	A	102	LEU
1	A	185	LYS
1	A	197	ARG
1	A	207	LYS
1	A	223	ASP
1	B	11	MET
1	B	18	THR
1	B	31	GLU
1	B	73	THR
1	B	111	GLN
1	B	118	ASN
1	B	197	ARG
1	B	204	GLU
1	B	223	ASP
1	B	228	LEU
1	C	11	MET
1	C	41	MET
1	C	120	LYS
1	C	147	LEU
1	C	158	SER
1	C	159	ASP
1	C	182	LYS
1	C	185	LYS
1	C	187	LEU
1	C	223	ASP
1	D	7	GLU
1	D	111	GLN
1	D	119	VAL
1	D	197[A]	ARG
1	D	197[B]	ARG
1	D	204	GLU

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Mol	Chain	Res	Type
1	E	7	GLU
1	E	11	MET
1	E	21	ASN
1	E	31	GLU
1	E	176	THR
1	E	182	LYS
1	E	197[A]	ARG
1	E	197[B]	ARG
1	E	199	LEU
1	E	206	ASP
1	E	223	ASP
1	E	227	LYS
1	F	11	MET
1	F	12	LYS
1	F	41	MET
1	F	102	LEU
1	F	128	SER
1	F	151	ASP
1	F	173	ASN
1	F	176	THR
1	F	188	LYS
1	F	197[A]	ARG
1	F	197[B]	ARG
1	F	223	ASP
1	G	8	ASN
1	G	33	LYS
1	G	68	THR
1	G	102	LEU
1	G	136	LYS
1	G	176	THR
1	G	185	LYS
1	G	188	LYS
1	G	197	ARG
1	G	202	ILE
1	G	204	GLU
1	G	206	ASP
1	H	11	MET
1	H	41	MET
1	H	118	ASN
1	H	137	THR
1	H	185	LYS
1	H	223	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	118	ASN
1	C	21	ASN
1	C	173	ASN
1	D	21	ASN
1	D	22	HIS
1	D	213	GLN
1	E	22	HIS
1	G	21	ASN
1	G	22	HIS
1	G	74	GLN
1	H	74	GLN
1	H	118	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	NRQ	A	63	1	23,24,25	0.79	1 (4%)	23,32,34	1.36	2 (8%)
1	NRQ	B	63	1	23,24,25	0.82	0	23,32,34	1.53	2 (8%)
1	NRQ	C	63	1	23,24,25	0.78	0	23,32,34	2.14	3 (13%)
1	NRQ	D	63	1	23,24,25	0.84	1 (4%)	23,32,34	1.66	2 (8%)
1	NRQ	E	63	1	23,24,25	0.83	0	23,32,34	2.07	3 (13%)
1	NRQ	F	63	1	23,24,25	0.77	1 (4%)	23,32,34	2.19	2 (8%)
1	NRQ	G	63	1	23,24,25	0.77	1 (4%)	23,32,34	2.58	4 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	NRQ	H	63	1	23,24,25	0.70	0	23,32,34	2.22	2 (8%)

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
1	NRQ	B	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	C	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	D	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	E	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	F	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	G	63	1	-	0/9/31/32	0/2/2/2
1	NRQ	H	63	1	-	0/9/31/32	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	63	NRQ	OH-CZ	-2.20	1.31	1.37
1	G	63	NRQ	OH-CZ	-2.01	1.32	1.37
1	F	63	NRQ	CA1-N1	2.35	1.35	1.28
1	A	63	NRQ	CA1-N1	2.66	1.36	1.28

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	63	NRQ	CB1-CA1-N1	-11.25	104.26	124.94
1	H	63	NRQ	CB1-CA1-N1	-9.84	106.86	124.94
1	F	63	NRQ	CB1-CA1-N1	-9.39	107.69	124.94
1	C	63	NRQ	CB1-CA1-N1	-8.70	108.95	124.94
1	E	63	NRQ	CB1-CA1-N1	-7.55	111.07	124.94
1	D	63	NRQ	CB1-CA1-N1	-6.63	112.75	124.94
1	A	63	NRQ	CB1-CA1-N1	-4.78	116.16	124.94
1	B	63	NRQ	CB1-CA1-N1	-3.96	117.66	124.94
1	C	63	NRQ	CE1-CD1-CG2	-2.61	118.03	121.29
1	G	63	NRQ	CB1-CG1-SD	-2.27	107.31	112.88
1	G	63	NRQ	O2-C2-CA2	-2.04	129.84	130.95
1	G	63	NRQ	C3-CA3-N3	2.16	117.73	113.00
1	H	63	NRQ	C3-CA3-N3	2.35	118.14	113.00
1	A	63	NRQ	C3-CA3-N3	2.64	118.79	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	63	NRQ	C3-CA3-N3	2.71	118.94	113.00
1	E	63	NRQ	CD1-CG2-CD2	2.73	121.81	117.64
1	D	63	NRQ	C3-CA3-N3	2.82	119.17	113.00
1	C	63	NRQ	C3-CA3-N3	2.88	119.30	113.00
1	F	63	NRQ	C3-CA3-N3	3.70	121.09	113.00
1	B	63	NRQ	C3-CA3-N3	4.49	122.84	113.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	63	NRQ	7	0
1	B	63	NRQ	1	0
1	C	63	NRQ	7	0
1	D	63	NRQ	3	0
1	E	63	NRQ	4	0
1	F	63	NRQ	3	0
1	G	63	NRQ	2	0
1	H	63	NRQ	1	0

5.5 Carbohydrates (i)

There are no carbohydrates 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, 95^{th} 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	222/243 (91%)	-0.50	1 (0%)	91 90	23, 39, 62, 85	0
1	B	222/243 (91%)	-0.40	1 (0%)	91 90	23, 36, 64, 88	0
1	C	222/243 (91%)	-0.35	1 (0%)	91 90	25, 42, 66, 82	0
1	D	222/243 (91%)	-0.27	7 (3%)	51 44	23, 39, 68, 94	0
1	E	222/243 (91%)	-0.34	4 (1%)	71 66	22, 39, 68, 88	0
1	F	222/243 (91%)	-0.36	3 (1%)	78 74	24, 40, 68, 91	0
1	G	222/243 (91%)	-0.01	15 (6%)	20 15	26, 49, 78, 90	0
1	H	222/243 (91%)	-0.23	4 (1%)	71 66	28, 52, 73, 97	0
All	All	1776/1944 (91%)	-0.31	36 (2%)	68 63	22, 42, 71, 97	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	73	THR	5.9
1	G	112	ASP	3.8
1	G	113	GLY	3.7
1	E	73	THR	3.7
1	D	112	ASP	3.5
1	G	185	LYS	3.5
1	G	186	ASN	3.4
1	F	74	GLN	3.1
1	G	60	THR	3.1
1	G	188	LYS	3.0
1	G	74	GLN	3.0
1	C	74	GLN	2.8
1	E	74	GLN	2.8
1	D	185	LYS	2.8
1	H	7	GLU	2.5
1	H	74	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	188	LYS	2.3
1	D	6	THR	2.3
1	G	151	ASP	2.3
1	G	61	SER	2.3
1	E	209	THR	2.3
1	H	73	THR	2.3
1	G	8	ASN	2.3
1	G	4	LEU	2.3
1	A	74	GLN	2.3
1	D	74	GLN	2.2
1	G	225	PRO	2.2
1	E	226	SER	2.1
1	G	182	LYS	2.1
1	F	113	GLY	2.1
1	G	187	LEU	2.1
1	D	184	ALA	2.1
1	H	188	LYS	2.1
1	D	197[A]	ARG	2.0
1	B	73	THR	2.0
1	G	7	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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	NRQ	B	63	23/24	0.95	0.31	-	17,40,61,73	0
1	NRQ	D	63	23/24	0.96	0.23	-	28,36,61,89	0
1	NRQ	F	63	23/24	0.96	0.23	-	20,33,69,71	0
1	NRQ	H	63	23/24	0.94	0.27	-	30,62,100,111	0
1	NRQ	E	63	23/24	0.96	0.22	-	23,42,59,73	0
1	NRQ	C	63	23/24	0.95	0.25	-	30,46,57,97	0
1	NRQ	G	63	23/24	0.93	0.30	-	32,51,86,107	0
1	NRQ	A	63	23/24	0.98	0.23	-	25,36,64,79	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.