Full wwPDB X-ray Structure Validation Report (i)

Jan 14, 2021 – 11:00 AM GMT

PDB ID	:	7BIM
Title	:	A de novo designed nonameric coiled coil
Deposited on	:	2021-01-12
Resolution	:	1.64 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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 (i) symbol.

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

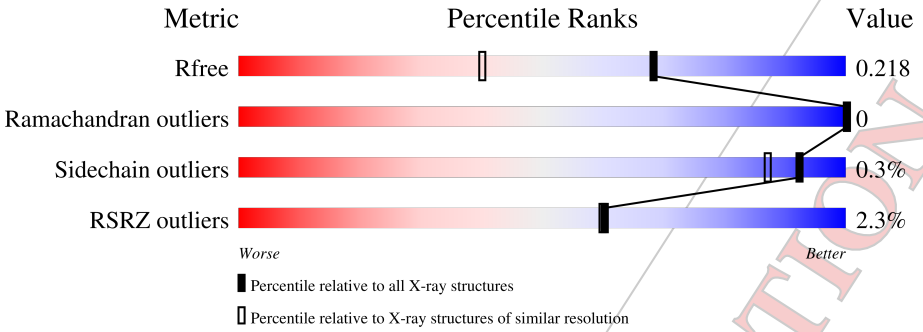
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.16
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

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 1.64 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}	130704	3122 (1.66-1.62)
Ramachandran outliers	138981	3215 (1.66-1.62)
Sidechain outliers	138945	3215 (1.66-1.62)
RSRZ outliers	127900	3079 (1.66-1.62)

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	32	6%, 97%
1	B	32	97%
1	C	32	94%
1	D	32	3%, 94%
1	E	32	3%, 91%, 6%
1	F	32	94%

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Mol	Chain	Length	Quality of chain
1	G	32	94% 6%
1	H	32	6% 94%
1	I	32	3% 94%
1	J	32	91% 6%
1	K	32	97%
1	L	32	94%
1	M	32	97%
1	N	32	94% 6%
1	O	32	3% 94% 6%
1	P	32	94%
1	Q	32	94% 6%
1	R	32	6% 97%
1	S	32	3% 91%
1	T	32	94%
1	U	32	3% 91% 6%
1	V	32	94% 6%
1	W	32	6% 94%
1	X	32	3% 94%
1	Y	32	3% 94%
1	Z	32	6% 97%
1	a	32	3% 97%
1	b	32	94% 6%
1	c	32	97%
1	d	32	97%
1	e	32	3% 94%

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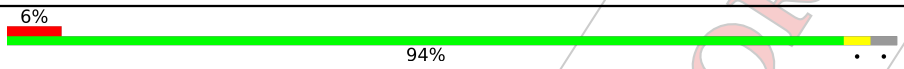
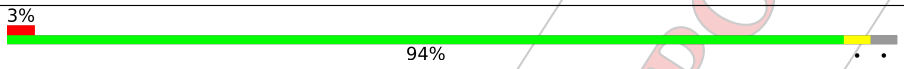
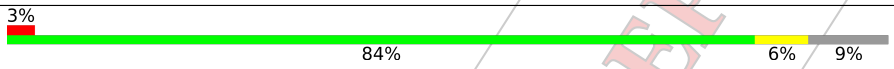
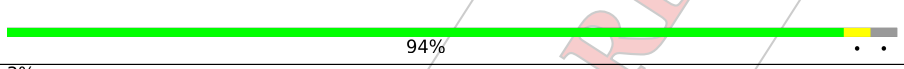
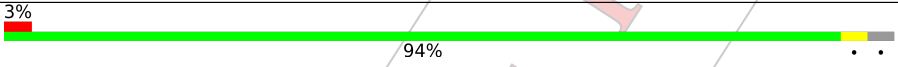
Mol	Chain	Length	Quality of chain
1	f	32	
1	g	32	
1	h	32	
1	i	32	
1	j	32	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8789 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 Nonameric de novo coiled coil CC-Type2-(GgLaId)4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	31	Total	C	N	O	0	1	0
			230	150	39	41			
1	B	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	C	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	D	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	E	30	Total	C	N	O	0	0	0
			220	143	37	40			
1	F	31	Total	C	N	O	0	2	0
			236	153	38	45			
1	G	30	Total	C	N	O	0	1	0
			226	147	37	42			
1	H	31	Total	C	N	O	0	2	0
			236	153	38	45			
1	I	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	J	31	Total	C	N	O	0	2	0
			236	153	38	45			
1	K	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	L	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	M	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	N	30	Total	C	N	O	0	1	0
			226	147	37	42			
1	O	30	Total	C	N	O	0	0	0
			220	143	37	40			
1	P	31	Total	C	N	O	0	1	0
			230	149	38	43			

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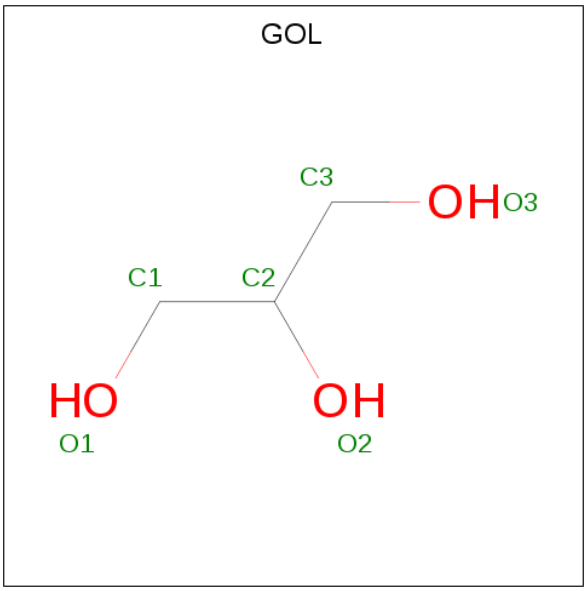
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	Q	30	Total	C	N	O	0	0	0
			220	143	37	40			
1	R	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	S	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	T	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	U	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	V	30	Total	C	N	O	0	0	0
			220	143	37	40			
1	W	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	X	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	Y	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	Z	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	a	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	b	30	Total	C	N	O	0	0	0
			220	143	37	40			
1	c	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	d	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	e	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	f	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	g	31	Total	C	N	O	0	1	0
			230	149	38	43			
1	h	29	Total	C	N	O	0	0	0
			211	137	35	39			
1	i	31	Total	C	N	O	0	0	0
			224	145	38	41			
1	j	31	Total	C	N	O	0	0	0
			224	145	38	41			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	D	1	Total C O 6 3 3	0	0
2	E	1	Total C O 6 3 3	0	0
2	F	1	Total C O 6 3 3	0	0
2	H	1	Total C O 6 3 3	0	0
2	I	1	Total C O 6 3 3	0	0
2	J	1	Total C O 6 3 3	0	0
2	J	1	Total C O 6 3 3	0	0
2	K	1	Total C O 6 3 3	0	0
2	K	1	Total C O 6 3 3	0	0
2	M	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	N	1	Total	C	O	0	0
			6	3	3		
2	N	1	Total	C	O	0	0
			6	3	3		
2	N	1	Total	C	O	0	0
			6	3	3		
2	N	1	Total	C	O	0	0
			6	3	3		
2	P	1	Total	C	O	0	0
			6	3	3		
2	R	1	Total	C	O	0	0
			6	3	3		
2	S	1	Total	C	O	0	0
			6	3	3		
2	S	1	Total	C	O	0	0
			6	3	3		
2	T	1	Total	C	O	0	0
			6	3	3		
2	U	1	Total	C	O	0	0
			6	3	3		
2	V	1	Total	C	O	0	0
			6	3	3		
2	V	1	Total	C	O	0	0
			6	3	3		
2	Y	1	Total	C	O	0	0
			6	3	3		
2	Z	1	Total	C	O	0	0
			6	3	3		
2	Z	1	Total	C	O	0	0
			6	3	3		
2	a	1	Total	C	O	0	0
			6	3	3		
2	c	1	Total	C	O	0	0
			6	3	3		
2	d	1	Total	C	O	0	0
			6	3	3		
2	e	1	Total	C	O	0	0
			6	3	3		
2	f	1	Total	C	O	0	0
			6	3	3		
2	g	1	Total	C	O	0	0
			6	3	3		

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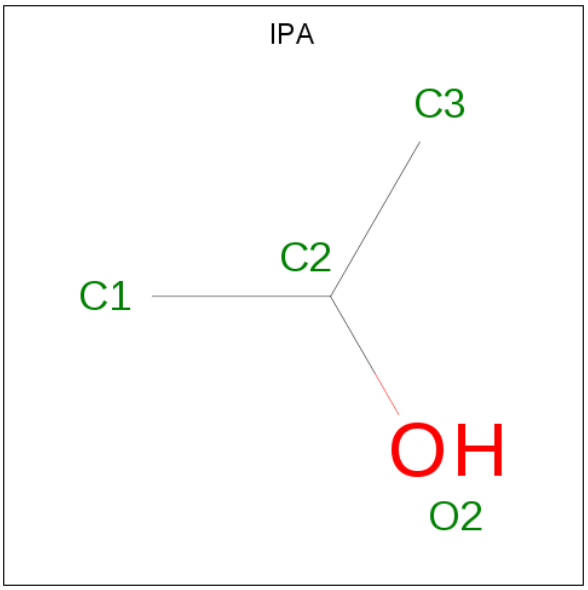
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	g	1	Total C O 6 3 3	0	0
2	g	1	Total C O 6 3 3	0	0
2	h	1	Total C O 6 3 3	0	0
2	j	1	Total C O 6 3 3	0	0

- Molecule 3 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 4 3 1	0	0
3	E	1	Total C O 4 3 1	0	0
3	E	1	Total C O 4 3 1	0	0
3	N	1	Total C O 4 3 1	0	0
3	R	1	Total C O 4 3 1	0	0
3	f	1	Total C O 4 3 1	0	0
3	j	1	Total C O 4 3 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	11	Total O 11 11	0	0
4	B	10	Total O 10 10	0	0
4	C	5	Total O 5 5	0	0
4	D	12	Total O 12 12	0	0
4	E	9	Total O 9 9	0	0
4	F	10	Total O 10 10	0	0
4	G	7	Total O 7 7	0	0
4	H	16	Total O 16 16	0	0
4	I	9	Total O 9 9	0	0
4	J	12	Total O 12 12	0	0
4	K	13	Total O 13 13	0	0
4	L	7	Total O 7 7	0	0
4	M	9	Total O 9 9	0	0
4	N	14	Total O 14 14	0	0
4	O	6	Total O 6 6	0	0
4	P	10	Total O 10 10	0	0
4	Q	13	Total O 13 13	0	0
4	R	6	Total O 6 6	0	0
4	S	14	Total O 14 14	0	0
4	T	10	Total O 10 10	0	0
4	U	15	Total O 15 15	0	0

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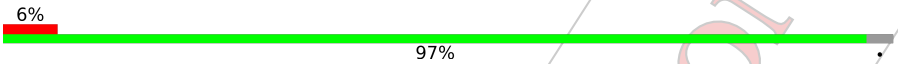
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	V	10	Total O 10 10	0	0
4	W	9	Total O 9 9	0	0
4	X	9	Total O 9 9	0	0
4	Y	7	Total O 7 7	0	0
4	Z	10	Total O 10 10	0	0
4	a	8	Total O 8 8	0	0
4	b	10	Total O 10 10	0	0
4	c	15	Total O 15 15	0	0
4	d	12	Total O 12 12	0	0
4	e	15	Total O 15 15	0	0
4	f	15	Total O 15 15	0	0
4	g	11	Total O 11 11	0	0
4	h	9	Total O 9 9	0	0
4	i	9	Total O 9 9	0	0
4	j	11	Total O 11 11	0	0

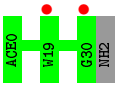
3 Residue-property plots

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: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

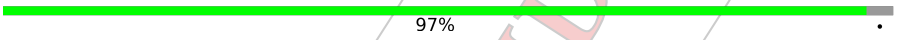
Chain A:





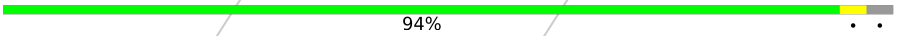
- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain B:



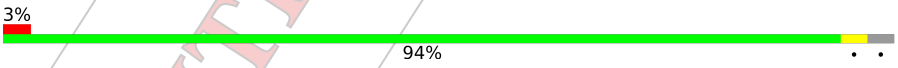
- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

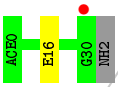
Chain C:



- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

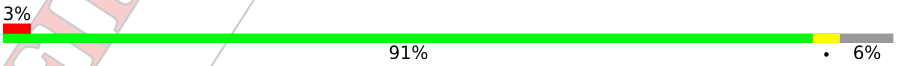
Chain D:

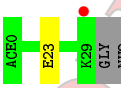




- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

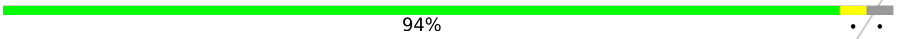
Chain E:

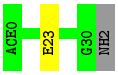




- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

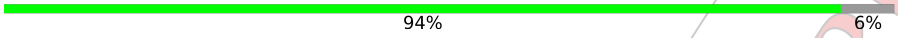
Chain F:





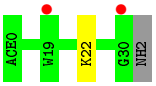
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain G:



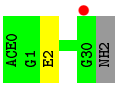
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain H:



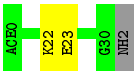
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain I:



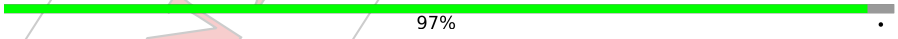
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain J:



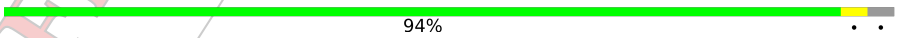
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

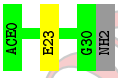
Chain K:



• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

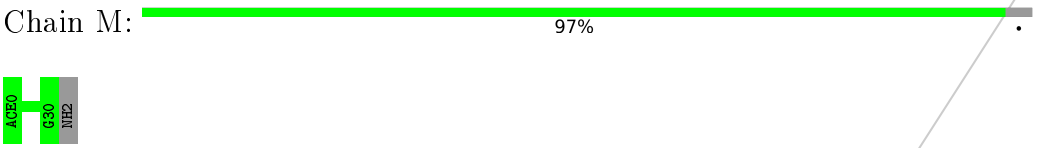
Chain L:





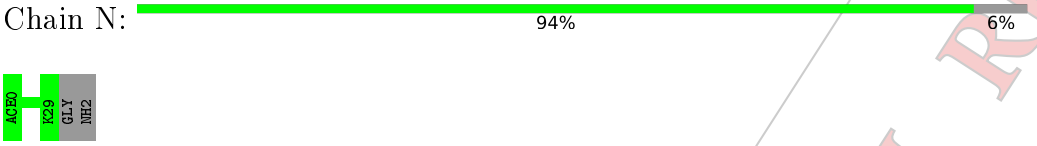
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain M:



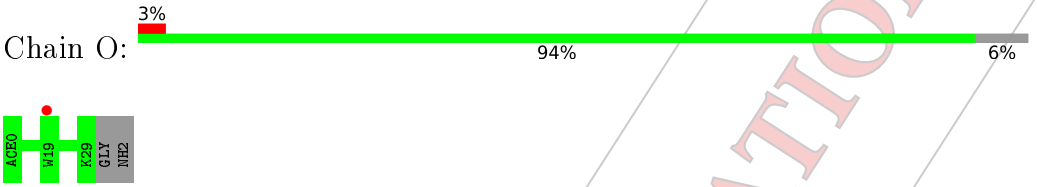
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain N:



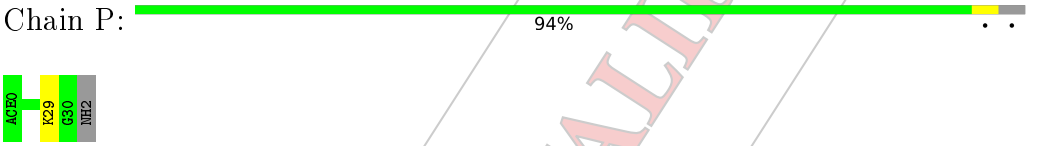
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain O:



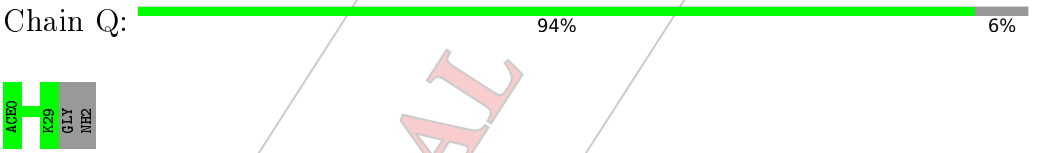
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain P:



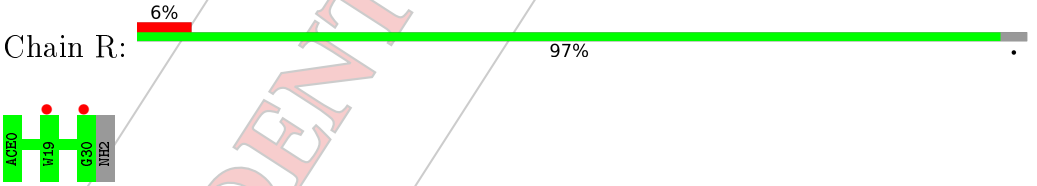
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain Q:



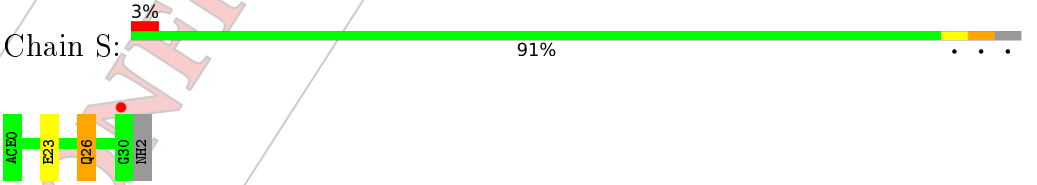
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain R:



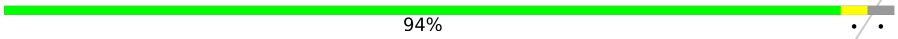
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

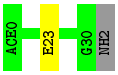
Chain S:



• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

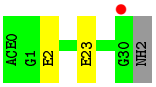
Chain T:





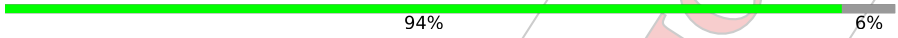
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

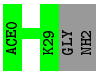
Chain U:



• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

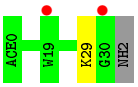
Chain V:





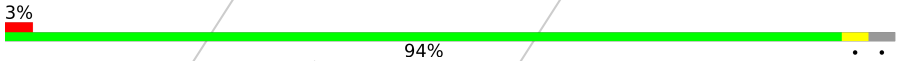
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

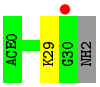
Chain W:



• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

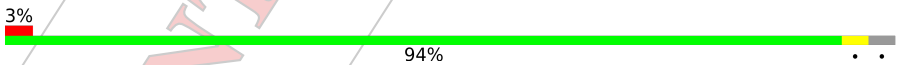
Chain X:

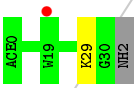




• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

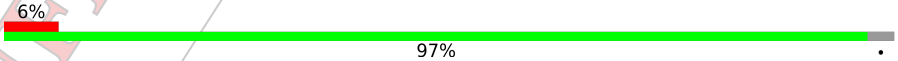
Chain Y:

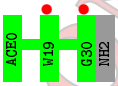




• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

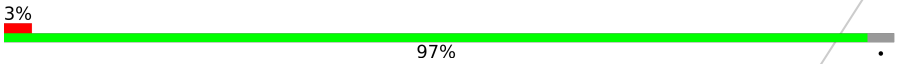
Chain Z:





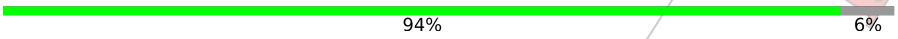
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain a:



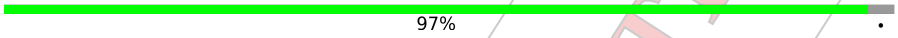
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain b:



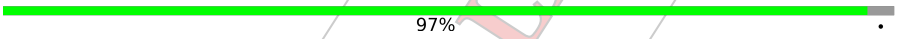
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain c:



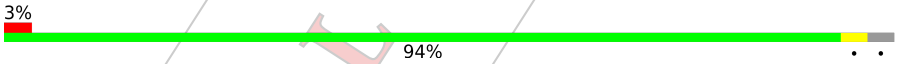
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

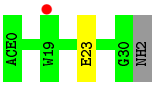
Chain d:



• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

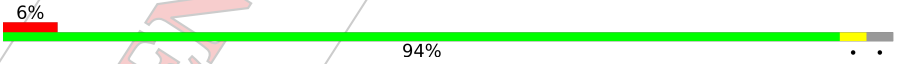
Chain e:

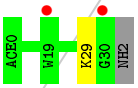




• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

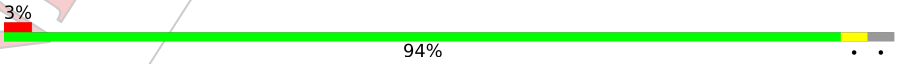
Chain f:





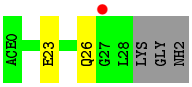
• Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain g:



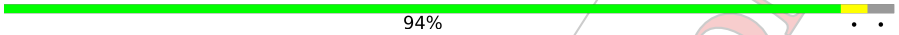
- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

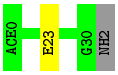
Chain h:



- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

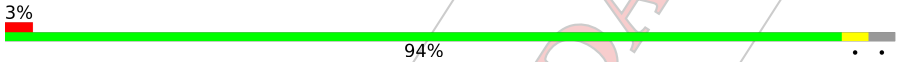
Chain i:

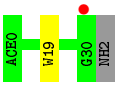




- Molecule 1: Nonameric de novo coiled coil CC-Type2-(GgLaId)4

Chain j:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	71.21Å 128.08Å 71.45Å 90.00° 110.67° 90.00°	Depositor
Resolution (Å)	66.85 – 1.64 66.85 – 1.64	Depositor EDS
% Data completeness (in resolution range)	99.9 (66.85-1.64) 99.9 (66.85-1.64)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.69 (at 1.64Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.182 , 0.205 0.197 , 0.218	Depositor DCC
R_{free} test set	7270 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	23.2	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 54.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.036 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8789	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.76% 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, 0.333 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: GOL, IPA, ACE

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	0.73	0/232	0.62	0/306
1	B	0.77	0/232	0.74	0/307
1	C	0.83	0/223	0.79	1/295 (0.3%)
1	D	0.70	0/223	0.81	1/295 (0.3%)
1	E	0.76	0/219	0.86	1/290 (0.3%)
1	F	1.09	2/241 (0.8%)	0.67	0/319
1	G	0.71	0/228	0.62	0/302
1	H	0.82	0/241	0.83	1/319 (0.3%)
1	I	0.82	0/232	0.86	0/307
1	J	0.78	0/241	0.82	2/319 (0.6%)
1	K	0.75	0/223	0.65	0/295
1	L	0.81	0/223	0.80	1/295 (0.3%)
1	M	0.68	0/223	0.64	0/295
1	N	0.79	0/228	0.69	0/302
1	O	0.68	0/219	0.58	0/290
1	P	0.66	0/232	0.65	1/307 (0.3%)
1	Q	0.81	0/219	0.69	0/290
1	R	0.76	0/232	0.75	0/307
1	S	0.92	1/223 (0.4%)	1.00	2/295 (0.7%)
1	T	0.71	1/232 (0.4%)	0.59	0/307
1	U	0.89	2/232 (0.9%)	0.74	0/307
1	V	0.69	0/219	0.62	0/290
1	W	0.68	0/232	0.76	1/307 (0.3%)
1	X	0.75	0/232	0.71	1/307 (0.3%)
1	Y	0.65	0/223	0.69	1/295 (0.3%)
1	Z	0.78	0/223	0.74	0/295
1	a	0.73	0/223	0.58	0/295
1	b	0.68	0/219	0.63	0/290
1	c	0.86	0/232	0.87	0/307
1	d	0.86	0/223	0.67	0/295
1	e	0.81	1/232 (0.4%)	0.78	0/307
1	f	0.66	0/232	0.73	1/307 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
1	g	0.67	0/232	0.62	1/307 (0.3%)
1	h	0.96	2/210 (1.0%)	0.85	2/279 (0.7%)
1	i	0.74	0/223	0.81	2/295 (0.7%)
1	j	0.94	1/223 (0.4%)	0.72	0/295
All	All	0.78	10/8176 (0.1%)	0.73	19/10820 (0.2%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	h	23	GLU	CD-OE1	-7.88	1.17	1.25
1	F	23[A]	GLU	CD-OE2	7.86	1.34	1.25
1	F	23[B]	GLU	CD-OE2	7.86	1.34	1.25
1	S	23	GLU	CD-OE2	-7.47	1.17	1.25
1	j	19	TRP	CB-CG	-6.41	1.38	1.50
1	e	23	GLU	CD-OE1	-6.37	1.18	1.25
1	U	2	GLU	CD-OE1	5.96	1.32	1.25
1	h	26	GLN	CD-NE2	5.81	1.47	1.32
1	U	23	GLU	CG-CD	5.25	1.59	1.51
1	T	23	GLU	CD-OE2	-5.03	1.20	1.25

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	S	26	GLN	CA-CB-CG	10.68	136.90	113.40
1	J	22	LYS	CD-CE-NZ	7.87	129.80	111.70
1	C	29	LYS	CD-CE-NZ	7.39	128.71	111.70
1	i	23	GLU	OE1-CD-OE2	6.95	131.63	123.30
1	S	23	GLU	OE1-CD-OE2	-6.86	115.06	123.30
1	L	23	GLU	OE1-CD-OE2	-6.86	115.07	123.30
1	J	23	GLU	OE1-CD-OE2	-6.20	115.86	123.30
1	i	23	GLU	CG-CD-OE1	-6.18	105.94	118.30
1	H	22	LYS	CD-CE-NZ	6.16	125.87	111.70
1	P	29	LYS	CD-CE-NZ	6.16	125.87	111.70
1	X	29	LYS	CD-CE-NZ	5.76	124.94	111.70
1	W	29	LYS	CD-CE-NZ	5.70	124.80	111.70
1	D	16	GLU	OE1-CD-OE2	-5.63	116.55	123.30
1	f	29	LYS	CD-CE-NZ	5.35	124.00	111.70
1	h	26	GLN	CG-CD-OE1	-5.32	110.97	121.60
1	E	23	GLU	OE1-CD-OE2	5.20	129.54	123.30
1	h	26	GLN	CA-CB-CG	5.19	124.81	113.40
1	Y	29	LYS	CD-CE-NZ	5.09	123.41	111.70
1	g	29	LYS	CD-CE-NZ	5.06	123.35	111.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	30/32 (94%)	30 (100%)	0	0	100	100
1	B	30/32 (94%)	30 (100%)	0	0	100	100
1	C	29/32 (91%)	29 (100%)	0	0	100	100
1	D	29/32 (91%)	29 (100%)	0	0	100	100
1	E	28/32 (88%)	28 (100%)	0	0	100	100
1	F	31/32 (97%)	31 (100%)	0	0	100	100
1	G	29/32 (91%)	29 (100%)	0	0	100	100
1	H	31/32 (97%)	31 (100%)	0	0	100	100
1	I	30/32 (94%)	30 (100%)	0	0	100	100
1	J	31/32 (97%)	31 (100%)	0	0	100	100
1	K	29/32 (91%)	29 (100%)	0	0	100	100
1	L	29/32 (91%)	29 (100%)	0	0	100	100
1	M	29/32 (91%)	29 (100%)	0	0	100	100
1	N	29/32 (91%)	29 (100%)	0	0	100	100
1	O	28/32 (88%)	28 (100%)	0	0	100	100
1	P	30/32 (94%)	30 (100%)	0	0	100	100
1	Q	28/32 (88%)	28 (100%)	0	0	100	100
1	R	30/32 (94%)	30 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	29/32 (91%)	29 (100%)	0	0	100	100
1	T	30/32 (94%)	30 (100%)	0	0	100	100
1	U	30/32 (94%)	30 (100%)	0	0	100	100
1	V	28/32 (88%)	28 (100%)	0	0	100	100
1	W	30/32 (94%)	30 (100%)	0	0	100	100
1	X	30/32 (94%)	30 (100%)	0	0	100	100
1	Y	29/32 (91%)	29 (100%)	0	0	100	100
1	Z	29/32 (91%)	29 (100%)	0	0	100	100
1	a	29/32 (91%)	29 (100%)	0	0	100	100
1	b	28/32 (88%)	28 (100%)	0	0	100	100
1	c	30/32 (94%)	30 (100%)	0	0	100	100
1	d	29/32 (91%)	29 (100%)	0	0	100	100
1	e	30/32 (94%)	30 (100%)	0	0	100	100
1	f	30/32 (94%)	30 (100%)	0	0	100	100
1	g	30/32 (94%)	30 (100%)	0	0	100	100
1	h	27/32 (84%)	27 (100%)	0	0	100	100
1	i	29/32 (91%)	29 (100%)	0	0	100	100
1	j	29/32 (91%)	29 (100%)	0	0	100	100
All	All	1056/1152 (92%)	1056 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	21/20 (105%)	21 (100%)	0	100	100
1	B	21/20 (105%)	21 (100%)	0	100	100
1	C	20/20 (100%)	20 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	20/20 (100%)	20 (100%)	0	100	100
1	E	20/20 (100%)	20 (100%)	0	100	100
1	F	22/20 (110%)	22 (100%)	0	100	100
1	G	21/20 (105%)	21 (100%)	0	100	100
1	H	22/20 (110%)	22 (100%)	0	100	100
1	I	21/20 (105%)	19 (90%)	2 (10%)	8	1
1	J	22/20 (110%)	22 (100%)	0	100	100
1	K	20/20 (100%)	20 (100%)	0	100	100
1	L	20/20 (100%)	20 (100%)	0	100	100
1	M	20/20 (100%)	20 (100%)	0	100	100
1	N	21/20 (105%)	21 (100%)	0	100	100
1	O	20/20 (100%)	20 (100%)	0	100	100
1	P	21/20 (105%)	21 (100%)	0	100	100
1	Q	20/20 (100%)	20 (100%)	0	100	100
1	R	21/20 (105%)	21 (100%)	0	100	100
1	S	20/20 (100%)	19 (95%)	1 (5%)	24	4
1	T	21/20 (105%)	21 (100%)	0	100	100
1	U	21/20 (105%)	21 (100%)	0	100	100
1	V	20/20 (100%)	20 (100%)	0	100	100
1	W	21/20 (105%)	21 (100%)	0	100	100
1	X	21/20 (105%)	21 (100%)	0	100	100
1	Y	20/20 (100%)	20 (100%)	0	100	100
1	Z	20/20 (100%)	20 (100%)	0	100	100
1	a	20/20 (100%)	20 (100%)	0	100	100
1	b	20/20 (100%)	20 (100%)	0	100	100
1	c	21/20 (105%)	21 (100%)	0	100	100
1	d	20/20 (100%)	20 (100%)	0	100	100
1	e	21/20 (105%)	21 (100%)	0	100	100
1	f	21/20 (105%)	21 (100%)	0	100	100
1	g	21/20 (105%)	21 (100%)	0	100	100
1	h	19/20 (95%)	19 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	i	20/20 (100%)	20 (100%)	0	100 100
1	j	20/20 (100%)	20 (100%)	0	100 100
All	All	740/720 (103%)	737 (100%)	3 (0%)	92 84

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	2[A]	GLU
1	I	2[B]	GLU
1	S	26	GLN

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

46 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	GOL	E	101	-	5,5,5	0.16	0	5,5,5	0.29	0
2	GOL	D	101	-	5,5,5	0.11	0	5,5,5	0.31	0
2	GOL	f	101	-	5,5,5	0.11	0	5,5,5	0.29	0
2	GOL	h	101	-	5,5,5	0.13	0	5,5,5	0.26	0
2	GOL	M	101	-	5,5,5	0.13	0	5,5,5	0.37	0
2	GOL	j	101	-	5,5,5	0.14	0	5,5,5	0.32	0
2	GOL	g	103	-	5,5,5	0.17	0	5,5,5	0.31	0
2	GOL	Y	101	-	5,5,5	0.18	0	5,5,5	0.48	0
2	GOL	Z	101	-	5,5,5	0.11	0	5,5,5	0.28	0
2	GOL	a	101	-	5,5,5	0.20	0	5,5,5	0.30	0
2	GOL	I	101	-	5,5,5	0.13	0	5,5,5	0.30	0
2	GOL	F	101	-	5,5,5	0.09	0	5,5,5	0.19	0
2	GOL	K	101	-	5,5,5	0.17	0	5,5,5	0.46	0
2	GOL	H	101	-	5,5,5	0.15	0	5,5,5	0.32	0
2	GOL	J	101	-	5,5,5	0.09	0	5,5,5	0.31	0
2	GOL	J	102	-	5,5,5	0.16	0	5,5,5	0.44	0
3	IPA	N	105	-	3,3,3	0.28	0	3,3,3	0.08	0
2	GOL	S	101	-	5,5,5	0.16	0	5,5,5	0.38	0
2	GOL	P	101	-	5,5,5	0.13	0	5,5,5	0.29	0
2	GOL	U	101	-	5,5,5	0.15	0	5,5,5	0.36	0
2	GOL	R	101	-	5,5,5	0.11	0	5,5,5	0.31	0
2	GOL	N	103	-	5,5,5	0.11	0	5,5,5	0.36	0
2	GOL	A	101	-	5,5,5	0.13	0	5,5,5	0.33	0
3	IPA	j	102	-	3,3,3	0.21	0	3,3,3	0.13	0
2	GOL	c	101	-	5,5,5	0.16	0	5,5,5	0.33	0
2	GOL	B	101	-	5,5,5	0.12	0	5,5,5	0.37	0
2	GOL	g	101	-	5,5,5	0.09	0	5,5,5	0.26	0
3	IPA	R	102	-	3,3,3	0.23	0	3,3,3	0.10	0
2	GOL	S	102	-	5,5,5	0.12	0	5,5,5	0.36	0
3	IPA	E	103	-	3,3,3	0.18	0	3,3,3	0.07	0
3	IPA	C	101	-	3,3,3	0.36	0	3,3,3	0.30	0
2	GOL	N	101	-	5,5,5	0.16	0	5,5,5	0.57	0
2	GOL	A	103	-	5,5,5	0.12	0	5,5,5	0.33	0
2	GOL	V	101	-	5,5,5	0.09	0	5,5,5	0.24	0
3	IPA	f	102	-	3,3,3	0.18	0	3,3,3	0.07	0
2	GOL	g	102	-	5,5,5	0.06	0	5,5,5	0.38	0
2	GOL	Z	102	-	5,5,5	0.11	0	5,5,5	0.31	0
2	GOL	N	104	-	5,5,5	0.09	0	5,5,5	0.28	0
2	GOL	K	102	-	5,5,5	0.07	0	5,5,5	0.24	0
2	GOL	e	101	-	5,5,5	0.10	0	5,5,5	0.30	0
2	GOL	d	101	-	5,5,5	0.14	0	5,5,5	0.38	0
3	IPA	E	102	-	3,3,3	0.16	0	3,3,3	0.19	0
2	GOL	N	102	-	5,5,5	0.11	0	5,5,5	0.34	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	GOL	T	101	-	5,5,5	0.10	0	5,5,5	0.34	0
2	GOL	V	102	-	5,5,5	0.13	0	5,5,5	0.42	0
2	GOL	A	102	-	5,5,5	0.09	0	5,5,5	0.26	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	E	101	-	-	2/4/4/4	-
2	GOL	D	101	-	-	4/4/4/4	-
2	GOL	f	101	-	-	2/4/4/4	-
2	GOL	h	101	-	-	2/4/4/4	-
2	GOL	M	101	-	-	2/4/4/4	-
2	GOL	j	101	-	-	4/4/4/4	-
2	GOL	g	103	-	-	0/4/4/4	-
2	GOL	Y	101	-	-	2/4/4/4	-
2	GOL	Z	101	-	-	2/4/4/4	-
2	GOL	a	101	-	-	0/4/4/4	-
2	GOL	I	101	-	-	2/4/4/4	-
2	GOL	F	101	-	-	2/4/4/4	-
2	GOL	K	101	-	-	1/4/4/4	-
2	GOL	H	101	-	-	2/4/4/4	-
2	GOL	J	101	-	-	2/4/4/4	-
2	GOL	J	102	-	-	2/4/4/4	-
2	GOL	S	101	-	-	2/4/4/4	-
2	GOL	P	101	-	-	0/4/4/4	-
2	GOL	U	101	-	-	4/4/4/4	-
2	GOL	R	101	-	-	4/4/4/4	-
2	GOL	N	103	-	-	2/4/4/4	-
2	GOL	A	101	-	-	2/4/4/4	-
2	GOL	c	101	-	-	0/4/4/4	-
2	GOL	B	101	-	-	4/4/4/4	-
2	GOL	g	101	-	-	0/4/4/4	-
2	GOL	S	102	-	-	4/4/4/4	-
2	GOL	N	101	-	-	4/4/4/4	-
2	GOL	A	103	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	V	101	-	-	0/4/4/4	-
2	GOL	g	102	-	-	4/4/4/4	-
2	GOL	Z	102	-	-	2/4/4/4	-
2	GOL	N	104	-	-	4/4/4/4	-
2	GOL	K	102	-	-	2/4/4/4	-
2	GOL	e	101	-	-	2/4/4/4	-
2	GOL	d	101	-	-	4/4/4/4	-
2	GOL	N	102	-	-	2/4/4/4	-
2	GOL	T	101	-	-	2/4/4/4	-
2	GOL	V	102	-	-	4/4/4/4	-
2	GOL	A	102	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (86) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	101	GOL	C1-C2-C3-O3
2	D	101	GOL	O1-C1-C2-O2
2	D	101	GOL	O1-C1-C2-C3
2	h	101	GOL	O1-C1-C2-C3
2	M	101	GOL	C1-C2-C3-O3
2	j	101	GOL	O1-C1-C2-C3
2	Y	101	GOL	C1-C2-C3-O3
2	Z	101	GOL	C1-C2-C3-O3
2	I	101	GOL	O1-C1-C2-C3
2	F	101	GOL	O1-C1-C2-C3
2	H	101	GOL	C1-C2-C3-O3
2	H	101	GOL	O2-C2-C3-O3
2	J	102	GOL	C1-C2-C3-O3
2	S	101	GOL	O1-C1-C2-C3
2	U	101	GOL	O1-C1-C2-C3
2	U	101	GOL	C1-C2-C3-O3
2	R	101	GOL	C1-C2-C3-O3
2	N	103	GOL	C1-C2-C3-O3
2	N	103	GOL	O2-C2-C3-O3
2	B	101	GOL	O1-C1-C2-O2
2	B	101	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
2	S	102	GOL	C1-C2-C3-O3
2	N	101	GOL	C1-C2-C3-O3
2	A	103	GOL	O1-C1-C2-C3
2	g	102	GOL	C1-C2-C3-O3
2	N	104	GOL	O1-C1-C2-C3
2	K	102	GOL	C1-C2-C3-O3
2	K	102	GOL	O2-C2-C3-O3
2	d	101	GOL	O1-C1-C2-C3
2	d	101	GOL	C1-C2-C3-O3
2	T	101	GOL	O1-C1-C2-O2
2	T	101	GOL	O1-C1-C2-C3
2	V	102	GOL	O1-C1-C2-C3
2	V	102	GOL	C1-C2-C3-O3
2	F	101	GOL	O1-C1-C2-O2
2	J	102	GOL	O2-C2-C3-O3
2	U	101	GOL	O2-C2-C3-O3
2	R	101	GOL	O2-C2-C3-O3
2	A	103	GOL	O1-C1-C2-O2
2	g	102	GOL	O2-C2-C3-O3
2	d	101	GOL	O2-C2-C3-O3
2	V	102	GOL	O1-C1-C2-O2
2	f	101	GOL	O1-C1-C2-C3
2	j	101	GOL	C1-C2-C3-O3
2	J	101	GOL	O1-C1-C2-C3
2	A	101	GOL	O1-C1-C2-C3
2	S	102	GOL	O1-C1-C2-C3
2	N	101	GOL	O1-C1-C2-C3
2	A	103	GOL	C1-C2-C3-O3
2	g	102	GOL	O1-C1-C2-C3
2	Z	102	GOL	C1-C2-C3-O3
2	N	104	GOL	C1-C2-C3-O3
2	e	101	GOL	C1-C2-C3-O3
2	N	102	GOL	C1-C2-C3-O3
2	h	101	GOL	O1-C1-C2-O2
2	M	101	GOL	O2-C2-C3-O3
2	Y	101	GOL	O2-C2-C3-O3
2	Z	101	GOL	O2-C2-C3-O3
2	A	101	GOL	O1-C1-C2-O2
2	S	102	GOL	O2-C2-C3-O3
2	N	101	GOL	O2-C2-C3-O3
2	e	101	GOL	O2-C2-C3-O3
2	d	101	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	V	102	GOL	O2-C2-C3-O3
2	E	101	GOL	O2-C2-C3-O3
2	S	101	GOL	O1-C1-C2-O2
2	S	102	GOL	O1-C1-C2-O2
2	Z	102	GOL	O2-C2-C3-O3
2	N	104	GOL	O1-C1-C2-O2
2	N	104	GOL	O2-C2-C3-O3
2	N	102	GOL	O2-C2-C3-O3
2	D	101	GOL	O2-C2-C3-O3
2	I	101	GOL	O1-C1-C2-O2
2	J	101	GOL	O1-C1-C2-O2
2	R	101	GOL	O1-C1-C2-O2
2	g	102	GOL	O1-C1-C2-O2
2	B	101	GOL	C1-C2-C3-O3
2	U	101	GOL	O1-C1-C2-O2
2	K	101	GOL	O1-C1-C2-C3
2	R	101	GOL	O1-C1-C2-C3
2	j	101	GOL	O1-C1-C2-O2
2	N	101	GOL	O1-C1-C2-O2
2	j	101	GOL	O2-C2-C3-O3
2	B	101	GOL	O2-C2-C3-O3
2	D	101	GOL	C1-C2-C3-O3
2	f	101	GOL	O1-C1-C2-O2

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, 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	30/32 (93%)	-0.17	2 (6%) 17 15	17, 27, 41, 73	0
1	B	30/32 (93%)	-0.19	0 100 100	19, 26, 39, 79	0
1	C	30/32 (93%)	-0.16	0 100 100	19, 30, 42, 84	0
1	D	30/32 (93%)	-0.05	1 (3%) 46 44	19, 30, 48, 85	0
1	E	29/32 (90%)	-0.15	1 (3%) 45 43	20, 31, 48, 88	0
1	F	30/32 (93%)	-0.24	0 100 100	18, 28, 41, 67	0
1	G	29/32 (90%)	-0.23	0 100 100	17, 25, 41, 56	0
1	H	30/32 (93%)	-0.01	2 (6%) 17 15	17, 27, 48, 83	0
1	I	30/32 (93%)	-0.03	1 (3%) 46 44	18, 27, 54, 90	0
1	J	30/32 (93%)	-0.26	0 100 100	18, 27, 38, 68	0
1	K	30/32 (93%)	-0.30	0 100 100	18, 29, 41, 69	0
1	L	30/32 (93%)	-0.26	0 100 100	19, 29, 37, 62	0
1	M	30/32 (93%)	-0.16	0 100 100	20, 32, 51, 80	0
1	N	29/32 (90%)	-0.08	0 100 100	20, 31, 51, 72	0
1	O	29/32 (90%)	-0.31	1 (3%) 45 43	20, 30, 45, 71	0
1	P	30/32 (93%)	-0.19	0 100 100	19, 28, 43, 85	0
1	Q	29/32 (90%)	-0.18	0 100 100	18, 26, 41, 74	0
1	R	30/32 (93%)	-0.01	2 (6%) 17 15	18, 28, 48, 78	0
1	S	30/32 (93%)	-0.08	1 (3%) 46 44	20, 30, 50, 110	0
1	T	30/32 (93%)	-0.25	0 100 100	20, 30, 49, 91	0
1	U	30/32 (93%)	-0.12	1 (3%) 46 44	20, 32, 42, 66	0
1	V	29/32 (90%)	-0.28	0 100 100	18, 28, 44, 91	0
1	W	30/32 (93%)	-0.06	2 (6%) 17 15	18, 30, 44, 85	0
1	X	30/32 (93%)	-0.14	1 (3%) 46 44	18, 27, 49, 97	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	Y	30/32 (93%)	-0.20	1 (3%) 46 44	19, 30, 48, 102	0
1	Z	30/32 (93%)	-0.06	2 (6%) 17 15	19, 29, 47, 89	0
1	a	30/32 (93%)	-0.12	1 (3%) 46 44	21, 29, 47, 95	0
1	b	29/32 (90%)	-0.24	0 100 100	18, 28, 49, 77	0
1	c	30/32 (93%)	-0.18	0 100 100	18, 28, 39, 74	0
1	d	30/32 (93%)	-0.28	0 100 100	18, 25, 45, 89	0
1	e	30/32 (93%)	-0.22	1 (3%) 46 44	18, 27, 40, 86	0
1	f	30/32 (93%)	-0.09	2 (6%) 17 15	19, 30, 54, 79	0
1	g	30/32 (93%)	-0.12	1 (3%) 46 44	19, 30, 50, 95	0
1	h	28/32 (87%)	-0.09	1 (3%) 42 40	19, 29, 56, 74	0
1	i	30/32 (93%)	-0.20	0 100 100	19, 29, 45, 85	0
1	j	30/32 (93%)	-0.21	1 (3%) 46 44	19, 28, 39, 73	0
All	All	1071/1152 (92%)	-0.16	25 (2%) 60 60	17, 29, 61, 110	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	W	30	GLY	4.8
1	R	30	GLY	4.4
1	a	30	GLY	3.7
1	R	19	TRP	3.6
1	E	29	LYS	3.1
1	U	30	GLY	3.0
1	D	30	GLY	2.9
1	A	19	TRP	2.8
1	S	30	GLY	2.7
1	I	30	GLY	2.7
1	H	19	TRP	2.7
1	Y	19	TRP	2.7
1	f	30	GLY	2.6
1	W	19	TRP	2.5
1	H	30	GLY	2.5
1	f	19	TRP	2.5
1	e	19	TRP	2.5
1	g	30	GLY	2.3
1	j	30	GLY	2.3
1	X	30	GLY	2.3
1	h	27	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	Z	19	TRP	2.2
1	Z	30	GLY	2.2
1	O	19	TRP	2.2
1	A	30	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

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, 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	B-factors(Å^2)	Q<0.9
2	GOL	A	102	6/6	0.57	0.21	55,65,83,112	0
2	GOL	V	101	6/6	0.58	0.18	59,65,72,89	0
3	IPA	f	102	4/4	0.61	0.24	62,68,71,72	0
2	GOL	D	101	6/6	0.65	0.16	56,63,69,77	0
2	GOL	e	101	6/6	0.66	0.18	57,63,68,69	0
3	IPA	R	102	4/4	0.71	0.17	61,61,64,69	0
2	GOL	A	103	6/6	0.72	0.13	57,69,76,98	0
2	GOL	N	102	6/6	0.76	0.24	70,72,77,79	0
2	GOL	Z	102	6/6	0.78	0.11	64,66,78,93	0
3	IPA	j	102	4/4	0.79	0.18	53,54,58,81	0
2	GOL	U	101	6/6	0.80	0.14	47,52,60,63	0
2	GOL	j	101	6/6	0.80	0.14	48,58,70,90	0
2	GOL	M	101	6/6	0.81	0.17	54,65,69,81	0
2	GOL	J	101	6/6	0.81	0.13	57,70,72,80	0
3	IPA	E	103	4/4	0.83	0.22	57,59,63,81	0
2	GOL	R	101	6/6	0.83	0.14	47,57,69,86	0
2	GOL	B	101	6/6	0.85	0.16	40,47,62,66	0
2	GOL	S	102	6/6	0.86	0.13	45,59,64,83	0
2	GOL	N	104	6/6	0.87	0.19	49,56,60,115	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	IPA	E	102	4/4	0.88	0.18	45,49,56,60	0
2	GOL	Y	101	6/6	0.89	0.24	18,56,62,62	0
2	GOL	g	103	6/6	0.89	0.28	26,72,74,75	0
2	GOL	g	101	6/6	0.89	0.13	44,58,69,82	0
2	GOL	P	101	6/6	0.90	0.24	25,53,63,76	0
2	GOL	I	101	6/6	0.91	0.26	27,60,66,71	0
2	GOL	E	101	6/6	0.91	0.26	22,51,69,75	0
3	IPA	N	105	4/4	0.92	0.16	54,55,61,61	0
2	GOL	S	101	6/6	0.92	0.22	20,50,57,61	0
2	GOL	c	101	6/6	0.93	0.24	18,52,60,68	0
2	GOL	a	101	6/6	0.93	0.27	22,55,63,68	0
2	GOL	J	102	6/6	0.93	0.22	19,49,64,66	0
2	GOL	f	101	6/6	0.93	0.24	18,61,66,69	0
2	GOL	V	102	6/6	0.93	0.21	24,58,63,74	0
2	GOL	F	101	6/6	0.93	0.26	17,50,67,74	0
2	GOL	h	101	6/6	0.94	0.24	19,57,68,74	0
2	GOL	K	101	6/6	0.94	0.25	17,52,57,66	0
2	GOL	Z	101	6/6	0.95	0.22	18,55,65,65	0
2	GOL	N	103	6/6	0.95	0.23	16,60,63,72	0
2	GOL	g	102	6/6	0.95	0.23	18,55,71,76	0
2	GOL	d	101	6/6	0.95	0.27	19,52,70,74	0
2	GOL	N	101	6/6	0.96	0.20	20,59,65,70	0
2	GOL	A	101	6/6	0.96	0.24	17,50,57,63	0
2	GOL	H	101	6/6	0.96	0.20	17,54,63,66	0
2	GOL	T	101	6/6	0.96	0.19	17,54,68,68	0
2	GOL	K	102	6/6	0.96	0.21	17,54,59,64	0
3	IPA	C	101	4/4	0.96	0.31	18,47,53,56	0

6.5 Other polymers

There are no such residues in this entry.