Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:42 PM GMT

PDB ID : 4YV1
Title : Crystal structure of Trypanosoma cruzi spermidine synthase in complex with quinolin-8-yl piperidine-1-carboxylate
Authors : Amano, Y.; Tateishi, Y.
Deposited on : 2015-03-19
Resolution : 1.85 Å(reported)

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

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

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 1.85 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		0.246
Clashscore		8
Ramachandran outliers		0.2%
Sidechain outliers		4.0%
RSRZ outliers		7.7%

Worse   *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
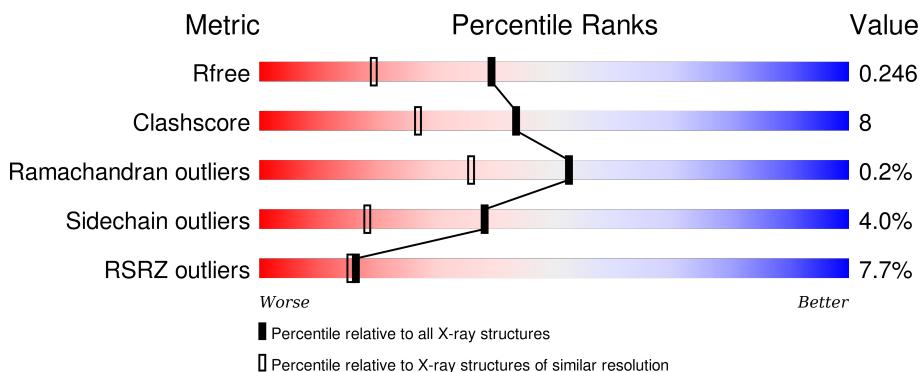
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	304	7% ... 71% / 17% / • / 10%
1	B	304	8% ... 79% / 14% / • / 5%
1	C	304	6% ... 76% / 12% / • / 10%
1	D	304	7% ... 81% / 12% / • / 5%
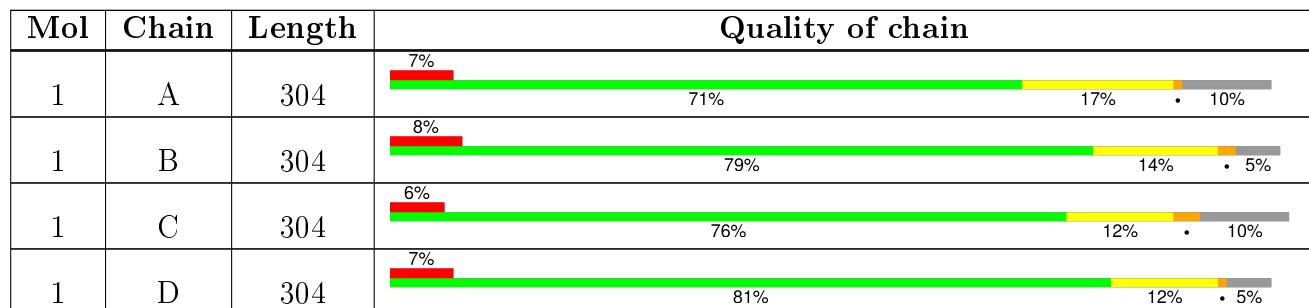
2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9421 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 Spermidine synthase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total 2163	C 1374	N 371	O 404	S 14	0	0	0
1	B	288	Total 2268	C 1442	N 387	O 425	S 14	0	0	0
1	C	275	Total 2173	C 1379	N 373	O 407	S 14	0	0	0
1	D	288	Total 2268	C 1442	N 387	O 425	S 14	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP Q4DA73
A	-6	ALA	-	expression tag	UNP Q4DA73
A	-5	HIS	-	expression tag	UNP Q4DA73
A	-4	HIS	-	expression tag	UNP Q4DA73
A	-3	HIS	-	expression tag	UNP Q4DA73
A	-2	HIS	-	expression tag	UNP Q4DA73
A	-1	HIS	-	expression tag	UNP Q4DA73
A	0	HIS	-	expression tag	UNP Q4DA73
B	-7	MET	-	initiating methionine	UNP Q4DA73
B	-6	ALA	-	expression tag	UNP Q4DA73
B	-5	HIS	-	expression tag	UNP Q4DA73
B	-4	HIS	-	expression tag	UNP Q4DA73
B	-3	HIS	-	expression tag	UNP Q4DA73
B	-2	HIS	-	expression tag	UNP Q4DA73
B	-1	HIS	-	expression tag	UNP Q4DA73
B	0	HIS	-	expression tag	UNP Q4DA73
C	-7	MET	-	initiating methionine	UNP Q4DA73
C	-6	ALA	-	expression tag	UNP Q4DA73
C	-5	HIS	-	expression tag	UNP Q4DA73
C	-4	HIS	-	expression tag	UNP Q4DA73
C	-3	HIS	-	expression tag	UNP Q4DA73

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP Q4DA73
C	-1	HIS	-	expression tag	UNP Q4DA73
C	0	HIS	-	expression tag	UNP Q4DA73
D	-7	MET	-	initiating methionine	UNP Q4DA73
D	-6	ALA	-	expression tag	UNP Q4DA73
D	-5	HIS	-	expression tag	UNP Q4DA73
D	-4	HIS	-	expression tag	UNP Q4DA73
D	-3	HIS	-	expression tag	UNP Q4DA73
D	-2	HIS	-	expression tag	UNP Q4DA73
D	-1	HIS	-	expression tag	UNP Q4DA73
D	0	HIS	-	expression tag	UNP Q4DA73

- Molecule 2 is 5'-[(S)-(3-AMINOPROPYL)(METHYL)-LAMBDA 4 -SULFANYL]-5'-DEOXYADENOSINE (three-letter code: S4M) (formula: $C_{14}H_{24}N_6O_3S$).
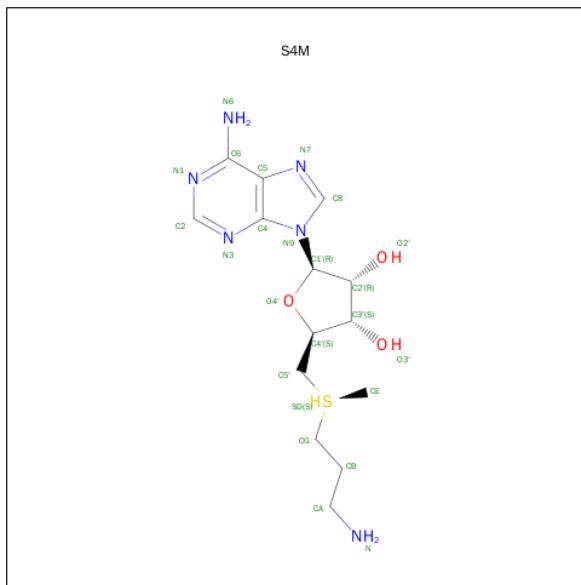
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			24	14	6	3	1		
2	B	1	Total	C	N	O	S	0	0
			24	14	6	3	1		
2	C	1	Total	C	N	O	S	0	0
			24	14	6	3	1		
2	D	1	Total	C	N	O	S	0	0
			24	14	6	3	1		

- Molecule 3 is quinolin-8-yl piperidine-1-carboxylate (three-letter code: 4K2) (formula: $C_{15}H_{16}N_2O_2$).
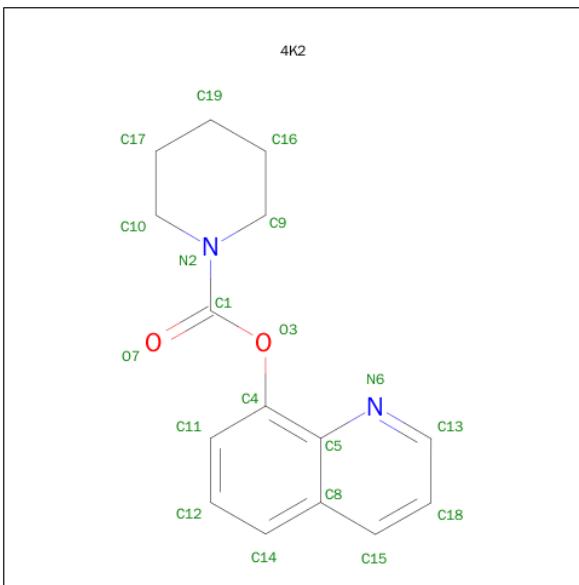
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total 19	C 15	N 2	O 2	0	0
3	D	1	Total 19	C 15	N 2	O 2	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	94	Total 94	O 94	0	0
4	B	105	Total 105	O 105	0	0
4	C	111	Total 111	O 111	0	0
4	D	105	Total 105	O 105	0	0

3 Residue-property plots ⓘ

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

- Molecule 1: Spermidine synthase, putative

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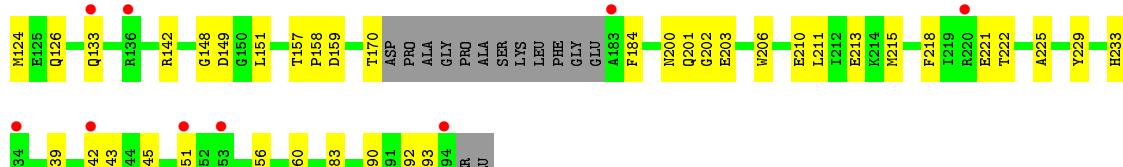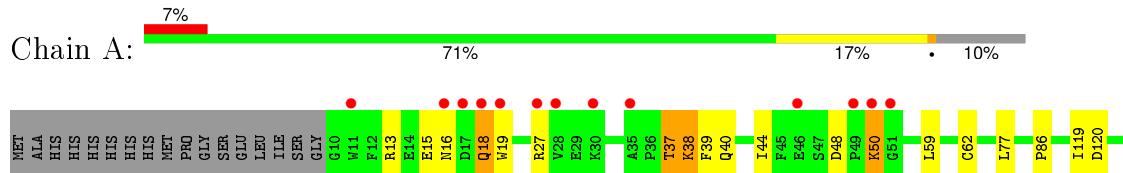
- Molecule 1: Spermidine synthase, putative
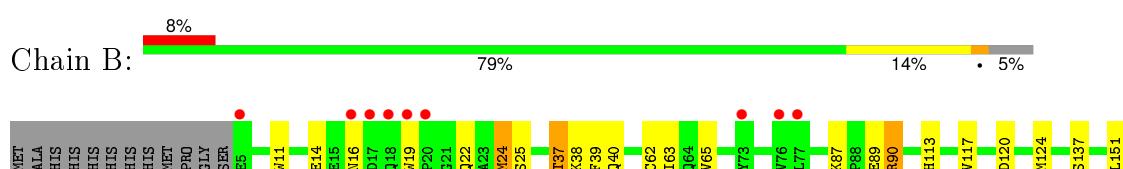
- Molecule 1: Spermidine synthase, putative
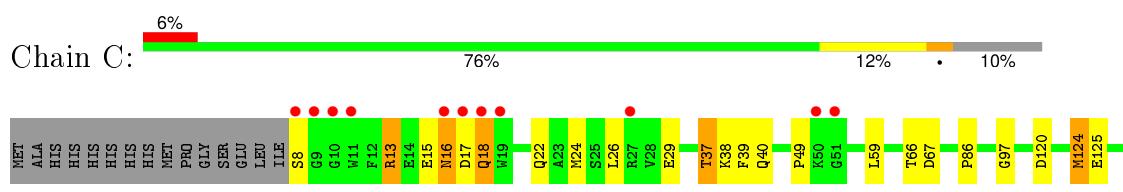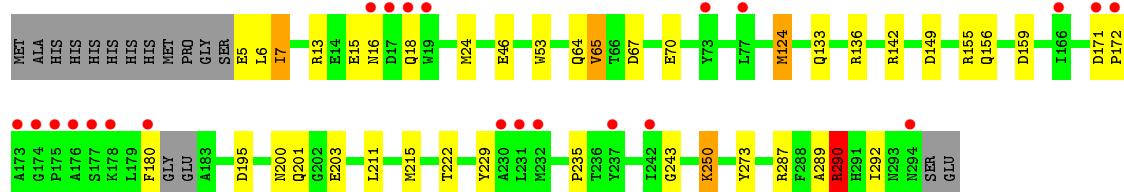
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	43.42Å 99.27Å 135.06Å 90.00° 90.54° 90.00°	Depositor
Resolution (Å)	34.15 – 1.85 34.15 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.5 (34.15-1.85) 99.5 (34.15-1.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	3.32 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.196 , 0.245 0.196 , 0.246	Depositor DCC
R_{free} test set	4858 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	20.9	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.43 , 51.7	EDS
Estimated twinning fraction	0.023 for h,-k,-l	Xtriage
L-test for twinning [2]	$<|L|> = 0.50, <L^2> = 0.33$	Xtriage
Outliers	2 of 97158 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9421	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 61.39 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.3205e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: S4M, 4K2

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	0.91	1/2216 (0.0%)	0.97	4/3005 (0.1%)
1	B	0.96	1/2324 (0.0%)	0.99	5/3152 (0.2%)
1	C	0.93	0/2226	0.99	4/3018 (0.1%)
1	D	0.92	1/2324 (0.0%)	1.01	10/3152 (0.3%)
All	All	0.93	3/9090 (0.0%)	0.99	23/12327 (0.2%)

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	C	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	206	TRP	CE3-CZ3	5.23	1.47	1.38
1	B	248	SER	CB-OG	5.16	1.49	1.42
1	D	273	TYR	CE1-CZ	5.12	1.45	1.38

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	290	ARG	NE-CZ-NH1	10.88	125.74	120.30
1	D	159	ASP	CB-CG-OD1	9.11	126.50	118.30
1	D	290	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	D	287	ARG	NE-CZ-NH2	-7.84	116.38	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	290	ARG	NE-CZ-NH1	7.59	124.09	120.30
1	D	67	ASP	CB-CG-OD1	7.06	124.66	118.30
1	A	142	ARG	NE-CZ-NH2	-7.04	116.78	120.30
1	D	142	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	B	159	ASP	CB-CG-OD1	6.32	123.99	118.30
1	D	159	ASP	CB-CG-OD2	-6.29	112.64	118.30
1	D	65	VAL	CG1-CB-CG2	-6.08	101.17	110.90
1	D	149	ASP	CB-CG-OD1	6.00	123.70	118.30
1	B	275	ASP	CB-CG-OD1	5.83	123.54	118.30
1	A	149	ASP	CB-CG-OD1	5.59	123.33	118.30
1	C	142	ARG	NE-CZ-NH2	-5.57	117.51	120.30
1	B	290	ARG	CD-NE-CZ	5.51	131.32	123.60
1	B	192	LEU	CB-CG-CD1	-5.30	101.98	111.00
1	C	67	ASP	CB-CG-OD1	5.20	122.98	118.30
1	D	287	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	C	260	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	D	290	ARG	NE-CZ-NH2	-5.03	117.78	120.30
1	A	159	ASP	CB-CG-OD1	5.02	122.82	118.30
1	C	151	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	293	ASN	Peptide
1	C	17	ASP	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	2163	0	2115	43	0
1	B	2268	0	2220	42	0
1	C	2173	0	2123	34	0
1	D	2268	0	2220	30	0
2	A	24	0	24	0	0
2	B	24	0	24	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	24	0	24	2	0
2	D	24	0	24	1	0
3	B	19	0	16	2	0
3	D	19	0	16	2	0
4	A	94	0	0	2	0
4	B	105	0	0	4	0
4	C	111	0	0	1	0
4	D	105	0	0	6	0
All	All	9421	0	8806	144	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 (144) 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:62:CYS:HB3	4:A:428:HOH:O	1.56	1.03
1:D:203:GLU:HG3	1:D:211:LEU:HD23	1.40	0.99
1:C:37:THR:HG21	1:C:120:ASP:OD2	1.63	0.99
1:B:37:THR:HG21	1:B:120:ASP:OD2	1.61	0.98
1:A:37:THR:HG21	1:A:120:ASP:OD2	1.62	0.98
1:A:37:THR:CG2	1:A:39:PHE:H	1.79	0.94
1:A:251:ALA:HB3	1:D:156:GLN:OE1	1.69	0.93
1:A:37:THR:HG22	1:A:40:GLN:H	1.35	0.91
1:C:37:THR:HG22	1:C:40:GLN:H	1.35	0.90
1:C:37:THR:HG22	1:C:39:PHE:H	1.39	0.88
1:D:46:GLU:HG2	4:D:488:HOH:O	1.76	0.84
1:A:210:GLU:HG3	4:A:412:HOH:O	1.76	0.83
1:A:37:THR:HG23	1:A:39:PHE:H	1.45	0.82
1:C:37:THR:CG2	1:C:39:PHE:H	1.93	0.82
1:D:215:MET:HG2	4:D:462:HOH:O	1.78	0.81
1:D:13:ARG:NH2	1:D:15:GLU:OE1	2.13	0.81
1:C:22:GLN:NE2	1:D:53:TRP:HE1	1.81	0.78
1:B:90:ARG:HG3	1:B:90:ARG:HH11	1.49	0.77
1:B:37:THR:HG22	1:B:40:GLN:H	1.50	0.77
1:A:48:ASP:OD1	1:A:50:LYS:HG2	1.86	0.76
1:A:201:GLN:NE2	1:A:242:ILE:HD11	2.01	0.76
1:D:171:ASP:HB2	1:D:172:PRO:CD	2.17	0.75
1:A:37:THR:HG22	1:A:39:PHE:H	1.49	0.74
1:B:176:ALA:HA	1:B:179:LEU:HD22	1.69	0.74
1:B:37:THR:HG22	1:B:39:PHE:H	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:13:ARG:NH2	1:C:15:GLU:OE2	2.23	0.71
1:A:13:ARG:HD3	1:A:15:GLU:OE2	1.90	0.71
1:B:202:GLY:O	1:B:203:GLU:HB2	1.89	0.71
1:C:24:MET:HE2	1:C:238:PRO:HG3	1.72	0.71
1:A:16:ASN:HB3	1:A:18:GLN:HE21	1.55	0.71
1:B:269:LYS:HB2	4:B:467:HOH:O	1.92	0.70
1:B:37:THR:CG2	1:B:39:PHE:H	2.05	0.69
1:A:218:PHE:O	1:A:222:THR:HG23	1.93	0.69
1:D:215:MET:CG	4:D:462:HOH:O	2.39	0.68
1:A:13:ARG:NH2	1:A:15:GLU:OE2	2.16	0.68
1:A:202:GLY:O	1:A:203:GLU:HB2	1.94	0.68
1:C:22:GLN:HE21	1:D:53:TRP:HE1	1.44	0.66
1:A:225:ALA:HB1	1:A:251:ALA:HA	1.77	0.65
1:A:225:ALA:CB	1:A:251:ALA:HA	2.26	0.65
1:B:90:ARG:CG	1:B:90:ARG:HH11	2.08	0.65
1:B:203:GLU:HG3	1:B:211:LEU:HD23	1.79	0.65
1:A:40:GLN:HG3	1:A:59:LEU:HD22	1.79	0.62
1:B:169:THR:HG21	1:B:179:LEU:HD23	1.81	0.62
1:B:180:PHE:C	4:B:432:HOH:O	2.38	0.61
1:A:16:ASN:HB2	1:A:19:TRP:NE1	2.15	0.61
1:C:242:ILE:HG13	1:C:243:GLY:H	1.66	0.60
1:C:200:ASN:C	1:C:200:ASN:OD1	2.41	0.58
1:A:37:THR:HG22	1:A:40:GLN:N	2.15	0.56
1:D:171:ASP:HB2	1:D:172:PRO:HD2	1.87	0.56
1:C:203:GLU:HG3	1:C:211:LEU:HD23	1.87	0.56
1:D:16:ASN:ND2	1:D:18:GLN:HB2	2.21	0.56
1:B:117:VAL:HG21	1:B:153:PHE:CD2	2.41	0.55
1:B:219:ILE:HG23	1:B:224:PHE:CD1	2.44	0.53
1:A:37:THR:HG22	1:A:39:PHE:N	2.21	0.53
1:C:16:ASN:HB3	1:C:18:GLN:CB	2.39	0.53
1:C:59:LEU:HD11	2:C:301:S4M:HE3	1.90	0.53
1:B:202:GLY:O	1:B:203:GLU:CB	2.56	0.52
1:C:37:THR:HG22	1:C:40:GLN:N	2.16	0.52
1:B:16:ASN:HB3	1:B:19:TRP:CE3	2.45	0.52
1:D:16:ASN:HD22	1:D:18:GLN:HB2	1.74	0.52
1:D:171:ASP:HB2	1:D:172:PRO:HD3	1.91	0.52
1:D:64:GLN:OE1	2:D:301:S4M:HG1	2.10	0.52
1:B:37:THR:HG23	1:B:38:LYS:N	2.26	0.51
1:D:133:GLN:HB2	4:D:463:HOH:O	2.10	0.51
1:B:171:ASP:HB2	1:B:172:PRO:HD2	1.93	0.51
1:A:86:PRO:O	1:A:260:ARG:HD3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:ILE:HD13	1:D:7:ILE:O	2.12	0.50
1:B:14:GLU:OE2	1:B:63:ILE:N	2.37	0.49
1:A:151:LEU:CD1	1:A:184:PHE:HB2	2.42	0.49
1:D:195:ASP:OD1	1:D:195:ASP:N	2.36	0.49
1:C:97:GLY:O	1:C:124:MET:HG3	2.13	0.49
1:C:170:THR:HG21	4:C:427:HOH:O	2.12	0.49
1:C:37:THR:HB	1:C:40:GLN:O	2.12	0.48
1:B:229:TYR:CZ	1:B:243:GLY:HA3	2.47	0.48
1:C:66:THR:HG21	1:C:236:THR:HG21	1.95	0.48
1:A:44:ILE:CD1	1:A:126:GLN:HB3	2.43	0.48
1:C:37:THR:HG22	1:C:39:PHE:N	2.18	0.48
1:B:87:LYS:HE3	1:B:89:GLU:OE1	2.13	0.48
1:D:250:LYS:NZ	4:D:402:HOH:O	2.39	0.48
1:B:287:ARG:O	1:B:290:ARG:HG2	2.14	0.47
1:A:40:GLN:CG	1:A:59:LEU:HD22	2.44	0.47
1:A:16:ASN:HB3	1:A:18:GLN:NE2	2.28	0.47
1:A:239:CYS:HB3	1:B:235:PRO:HB3	1.96	0.47
1:A:251:ALA:CB	1:D:156:GLN:OE1	2.52	0.47
1:B:218:PHE:C	1:B:218:PHE:CD1	2.88	0.47
1:D:229:TYR:CZ	1:D:243:GLY:HA3	2.49	0.47
1:B:171:ASP:HB2	1:B:172:PRO:CD	2.45	0.46
1:D:290:ARG:HH11	1:D:290:ARG:CG	2.28	0.46
1:B:290:ARG:HG3	1:B:290:ARG:HH11	1.81	0.46
1:A:37:THR:HG23	1:A:38:LYS:N	2.31	0.46
1:C:26:LEU:HD21	3:D:302:4K2:H7	1.98	0.46
1:C:203:GLU:HA	1:C:242:ILE:HD11	1.98	0.45
1:D:65:VAL:HG13	1:D:70:GLU:HB3	1.97	0.45
1:D:180:PHE:HD2	1:D:215:MET:CE	2.29	0.45
1:A:44:ILE:HD12	1:A:126:GLN:HB3	1.98	0.45
1:C:242:ILE:HG13	1:C:243:GLY:N	2.31	0.45
1:B:90:ARG:NH1	1:B:113:HIS:HD2	2.15	0.44
1:C:86:PRO:O	1:C:260:ARG:HD3	2.16	0.44
1:C:37:THR:HG23	1:C:38:LYS:N	2.32	0.44
1:B:151:LEU:CD1	1:B:179:LEU:HD12	2.47	0.44
1:C:237:TYR:CE2	1:C:242:ILE:HD13	2.53	0.44
1:B:137:SER:HA	4:B:498:HOH:O	2.17	0.44
1:A:229:TYR:CZ	1:A:243:GLY:HA3	2.53	0.43
1:A:202:GLY:O	1:A:203:GLU:CB	2.61	0.43
1:D:200:ASN:C	1:D:200:ASN:OD1	2.55	0.43
1:B:169:THR:CG2	1:B:179:LEU:HD23	2.47	0.43
1:D:46:GLU:CG	4:D:488:HOH:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:MET:HB2	3:B:302:4K2:C11	2.48	0.43
1:D:289:ALA:O	1:D:292:ILE:HG12	2.18	0.43
1:B:16:ASN:CB	1:B:19:TRP:CE3	3.02	0.43
1:C:239:CYS:HB3	1:D:235:PRO:HB3	1.99	0.43
1:B:38:LYS:HE2	1:B:38:LYS:HB3	1.65	0.43
1:A:225:ALA:CB	1:A:251:ALA:CA	2.96	0.43
1:C:128:LYS:HA	1:C:135:SER:OG	2.18	0.43
1:B:200:ASN:OD1	1:B:200:ASN:C	2.55	0.43
1:C:125:GLU:O	1:C:129:GLN:HG2	2.19	0.43
1:B:90:ARG:NH1	1:B:90:ARG:CG	2.73	0.42
2:C:301:S4M:HB1	2:C:301:S4M:HE1	1.81	0.42
1:C:16:ASN:HB3	1:C:18:GLN:HB2	2.00	0.42
1:B:151:LEU:HD13	1:B:179:LEU:CD1	2.50	0.42
1:B:203:GLU:HG3	1:B:211:LEU:CD2	2.47	0.42
1:A:215:MET:HE2	1:A:245:LEU:HD12	2.01	0.42
1:C:16:ASN:HB3	1:C:18:GLN:HB3	2.01	0.42
1:C:37:THR:CG2	1:C:120:ASP:OD2	2.51	0.42
1:B:37:THR:HB	1:B:40:GLN:O	2.20	0.41
1:A:203:GLU:HG3	1:A:211:LEU:HD23	2.03	0.41
1:D:7:ILE:C	1:D:7:ILE:HD13	2.40	0.41
1:D:124:MET:H	1:D:124:MET:HG2	1.67	0.41
1:C:229:TYR:CZ	1:C:243:GLY:HA3	2.55	0.41
1:A:256:THR:HA	1:A:283:PHE:CD2	2.56	0.41
1:A:48:ASP:OD1	1:A:50:LYS:HE2	2.20	0.41
1:D:24:MET:HB2	3:D:302:4K2:C11	2.50	0.41
1:A:213:GLU:HG3	1:A:292:ILE:HD11	2.01	0.41
1:C:29:GLU:HB2	1:C:49:PRO:HD3	2.01	0.41
1:B:14:GLU:OE2	1:B:62:CYS:HA	2.21	0.41
1:A:233:HIS:HE1	4:B:502:HOH:O	2.04	0.41
1:A:200:ASN:OD1	1:A:200:ASN:C	2.59	0.41
1:A:157:THR:HA	1:A:158:PRO:HD3	1.94	0.40
1:B:11:TRP:HE3	1:B:25:SER:HB3	1.86	0.40
1:B:37:THR:CG2	1:B:38:LYS:N	2.84	0.40
1:B:22:GLN:HB2	3:B:302:4K2:H16	2.02	0.40
1:A:119:ILE:HA	1:A:148:GLY:O	2.22	0.40
1:C:37:THR:HG23	1:C:39:PHE:H	1.79	0.40
1:A:151:LEU:HD12	1:A:184:PHE:HB2	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	269/304 (88%)	260 (97%)	9 (3%)	0	100	100
1	B	284/304 (93%)	273 (96%)	10 (4%)	1 (0%)	39	22
1	C	271/304 (89%)	262 (97%)	8 (3%)	1 (0%)	39	22
1	D	284/304 (93%)	274 (96%)	10 (4%)	0	100	100
All	All	1108/1216 (91%)	1069 (96%)	37 (3%)	2 (0%)	52	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	18	GLN
1	B	170	THR

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	238/262 (91%)	228 (96%)	10 (4%)	36	16
1	B	249/262 (95%)	240 (96%)	9 (4%)	42	21
1	C	239/262 (91%)	229 (96%)	10 (4%)	36	16
1	D	249/262 (95%)	239 (96%)	10 (4%)	38	18
All	All	975/1048 (93%)	936 (96%)	39 (4%)	38	18

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	27	ARG
1	A	37	THR
1	A	38	LYS
1	A	50	LYS
1	A	77	LEU
1	A	124	MET
1	A	133	GLN
1	A	170	THR
1	A	221	GLU
1	B	24	MET
1	B	37	THR
1	B	65	VAL
1	B	90	ARG
1	B	124	MET
1	B	179	LEU
1	B	201	GLN
1	B	218	PHE
1	B	290	ARG
1	C	8	SER
1	C	13	ARG
1	C	16	ASN
1	C	37	THR
1	C	124	MET
1	C	129	GLN
1	C	133	GLN
1	C	170	THR
1	C	201	GLN
1	C	221	GLU
1	D	5	GLU
1	D	6	LEU
1	D	7	ILE
1	D	124	MET
1	D	136	ARG
1	D	155	ARG
1	D	201	GLN
1	D	222	THR
1	D	250	LYS
1	D	290	ARG

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	18	GLN
1	A	22	GLN
1	A	129	GLN
1	A	201	GLN
1	A	233	HIS
1	B	22	GLN
1	B	113	HIS
1	B	129	GLN
1	C	18	GLN
1	C	22	GLN
1	C	233	HIS
1	D	16	ASN
1	D	113	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

6 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	S4M	A	301	-	23,26,26	0.90	1 (4%)	17,37,37	1.69	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	S4M	B	301	-	23,26,26	0.87	1 (4%)	17,37,37	1.40	1 (5%)
3	4K2	B	302	-	21,21,21	1.28	3 (14%)	27,28,28	1.60	4 (14%)
2	S4M	C	301	-	23,26,26	0.82	0	17,37,37	1.44	5 (29%)
2	S4M	D	301	-	23,26,26	0.87	0	17,37,37	2.21	3 (17%)
3	4K2	D	302	-	21,21,21	1.36	3 (14%)	27,28,28	0.99	2 (7%)

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	S4M	A	301	-	-	0/7/28/28	0/3/3/3
2	S4M	B	301	-	-	0/7/28/28	0/3/3/3
3	4K2	B	302	-	-	0/8/16/16	0/3/3/3
2	S4M	C	301	-	-	0/7/28/28	0/3/3/3
2	S4M	D	301	-	-	0/7/28/28	0/3/3/3
3	4K2	D	302	-	-	0/8/16/16	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	302	4K2	C4-C5	-3.31	1.38	1.42
3	B	302	4K2	C4-C5	-2.78	1.38	1.42
3	B	302	4K2	C8-C5	-2.33	1.39	1.42
2	B	301	S4M	CG-SD	2.00	1.85	1.80
3	D	302	4K2	C1-N2	2.01	1.38	1.35
2	A	301	S4M	O4'-C1'	2.16	1.44	1.41
3	D	302	4K2	O7-C1	2.19	1.24	1.21
3	B	302	4K2	C1-N2	2.55	1.39	1.35

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	301	S4M	C4'-O4'-C1'	-7.72	101.46	109.64
2	A	301	S4M	C4'-O4'-C1'	-5.36	103.96	109.64
2	B	301	S4M	C4'-O4'-C1'	-4.61	104.76	109.64
3	B	302	4K2	C4-O3-C1	-3.77	106.97	117.83
2	C	301	S4M	CB-CG-SD	-2.40	106.74	112.17
3	D	302	4K2	C4-O3-C1	-2.14	111.65	117.83
2	C	301	S4M	N3-C2-N1	-2.03	127.28	128.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	S4M	O3'-C3'-C4'	-2.02	104.99	111.01
3	D	302	4K2	C14-C8-C5	2.03	121.77	118.27
2	A	301	S4M	O4'-C1'-N9	2.05	111.97	108.11
2	A	301	S4M	O4'-C4'-C5'	2.13	114.58	108.90
3	B	302	4K2	C11-C4-C5	2.17	123.05	120.23
2	D	301	S4M	N6-C6-N1	2.21	122.22	118.52
2	C	301	S4M	O4'-C4'-C5'	2.48	115.50	108.90
2	D	301	S4M	C1'-N9-C4	2.51	129.60	126.81
2	C	301	S4M	O4'-C1'-N9	2.58	112.98	108.11
3	B	302	4K2	C9-N2-C10	2.75	117.61	112.57
3	B	302	4K2	C4-C5-N6	4.06	122.32	118.86

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	302	4K2	2	0
2	C	301	S4M	2	0
2	D	301	S4M	1	0
3	D	302	4K2	2	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	273/304 (89%)	0.38	22 (8%)	15	14	11, 24, 44, 78	0
1	B	288/304 (94%)	0.37	25 (8%)	13	12	12, 22, 47, 72	0
1	C	275/304 (90%)	0.23	17 (6%)	24	22	11, 20, 42, 71	0
1	D	288/304 (94%)	0.37	22 (7%)	17	16	11, 22, 47, 77	0
All	All	1124/1216 (92%)	0.34	86 (7%)	16	15	11, 22, 44, 78	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	173	ALA	8.6
1	C	9	GLY	6.6
1	C	19	TRP	6.2
1	B	173	ALA	5.5
1	A	294	ASN	5.4
1	A	17	ASP	5.1
1	A	16	ASN	4.9
1	C	17	ASP	4.8
1	D	171	ASP	4.7
1	B	19	TRP	4.5
1	A	18	GLN	4.5
1	A	27	ARG	4.4
1	C	8	SER	4.3
1	D	177	SER	4.2
1	B	18	GLN	4.2
1	D	174	GLY	4.1
1	B	17	ASP	4.1
1	D	18	GLN	4.0
1	D	176	ALA	4.0
1	C	294	ASN	3.9
1	B	5	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	177	SER	3.9
1	A	19	TRP	3.7
1	B	176	ALA	3.6
1	A	251	ALA	3.4
1	B	16	ASN	3.3
1	C	10	GLY	3.3
1	D	19	TRP	3.3
1	B	20	PRO	3.3
1	D	17	ASP	3.2
1	C	16	ASN	3.2
1	C	51	GLY	3.1
1	C	18	GLN	3.1
1	D	172	PRO	3.1
1	B	242	ILE	3.0
1	D	294	ASN	3.0
1	D	175	PRO	3.0
1	A	51	GLY	2.9
1	C	27	ARG	2.9
1	D	180	PHE	2.9
1	C	11	TRP	2.9
1	B	180	PHE	2.9
1	A	50	LYS	2.8
1	A	183	ALA	2.8
1	A	242	ILE	2.8
1	A	253	VAL	2.8
1	B	175	PRO	2.7
1	D	242	ILE	2.7
1	B	171	ASP	2.6
1	B	76	VAL	2.6
1	C	170	THR	2.6
1	A	220	ARG	2.6
1	B	174	GLY	2.6
1	B	183	ALA	2.6
1	C	234	VAL	2.5
1	C	50	LYS	2.5
1	D	77	LEU	2.5
1	D	178	LYS	2.5
1	A	133	GLN	2.5
1	B	77	LEU	2.5
1	B	199	CYS	2.4
1	A	11	TRP	2.4
1	D	73	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	235	PRO	2.4
1	A	28	VAL	2.4
1	B	166	ILE	2.3
1	B	172	PRO	2.3
1	B	179	LEU	2.3
1	D	231	LEU	2.3
1	C	242	ILE	2.2
1	A	46	GLU	2.2
1	A	49	PRO	2.2
1	B	294	ASN	2.2
1	B	73	TYR	2.2
1	A	35	ALA	2.1
1	A	136	ARG	2.1
1	C	169	THR	2.1
1	D	232	MET	2.1
1	D	230	ALA	2.1
1	B	232	MET	2.1
1	D	16	ASN	2.0
1	A	234	VAL	2.0
1	A	30	LYS	2.0
1	D	166	ILE	2.0
1	D	237	TYR	2.0
1	C	133	GLN	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	4K2	B	302	19/19	0.87	0.16	-0.11	40,49,54,55	0
2	S4M	C	301	24/24	0.93	0.11	-0.12	21,26,43,52	0
2	S4M	B	301	24/24	0.92	0.11	-0.41	20,23,32,38	0
2	S4M	D	301	24/24	0.90	0.12	-0.42	22,30,40,48	0
2	S4M	A	301	24/24	0.94	0.10	-0.46	22,24,31,42	0
3	4K2	D	302	19/19	0.94	0.11	-0.73	28,36,41,41	0

6.5 Other polymers (i)

There are no such residues in this entry.