



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:13 pm GMT

PDB ID : 4YV0
Title : Crystal structure of Trypanosoma cruzi spermidine synthase in complex with (2S)-N-methyl-N-phenyl-2,3-dihydro-1,4-benzodioxine- 2-carboxamid
Authors : Amano, Y.; Tateishi, Y.
Deposited on : 2015-03-19
Resolution : 1.95 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

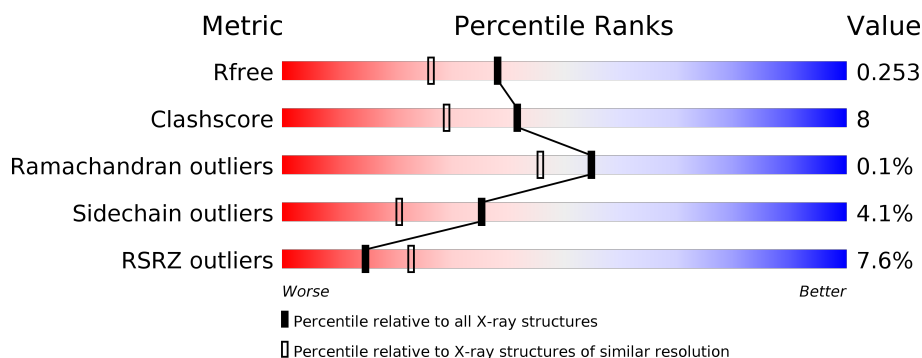
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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 $\leq 5\%$. 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	<div> <div>4%</div> <div> <div></div> <div>71%</div> <div>16%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	304	<div> <div>10%</div> <div> <div></div> <div>78%</div> <div>16%</div> <div>•</div> <div>5%</div> </div> </div>
1	C	304	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>13%</div> <div>•</div> <div>10%</div> </div> </div>
1	D	304	<div> <div>9%</div> <div> <div></div> <div>76%</div> <div>16%</div> <div>•</div> <div>5%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9249 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	269	Total	C	N	O	S	0	0	0
			2124	1350	364	396	14			
1	B	290	Total	C	N	O	S	0	0	0
			2281	1449	389	429	14			
1	C	273	Total	C	N	O	S	0	0	0
			2151	1366	368	403	14			
1	D	290	Total	C	N	O	S	0	0	0
			2281	1449	389	429	14			

There are 32 discrepancies between the modelled and reference sequences:

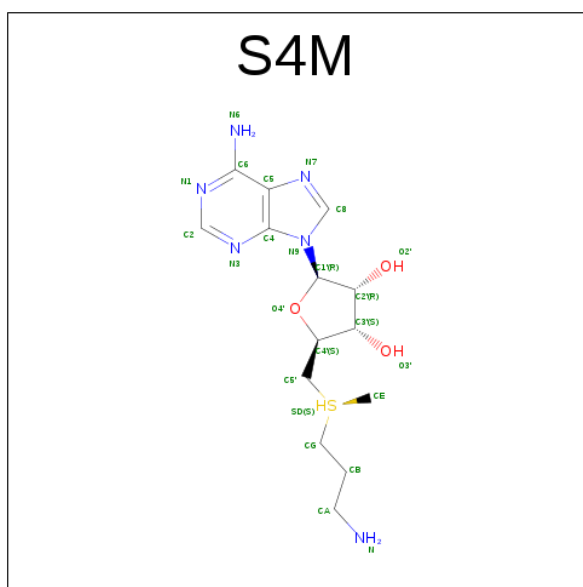
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP Q4DA73
A	-6	ALA	-	expression tag	UNP Q4DA73
A	-5	HIS	-	expression tag	UNP Q4DA73
A	-4	HIS	-	expression tag	UNP Q4DA73
A	-3	HIS	-	expression tag	UNP Q4DA73
A	-2	HIS	-	expression tag	UNP Q4DA73
A	-1	HIS	-	expression tag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

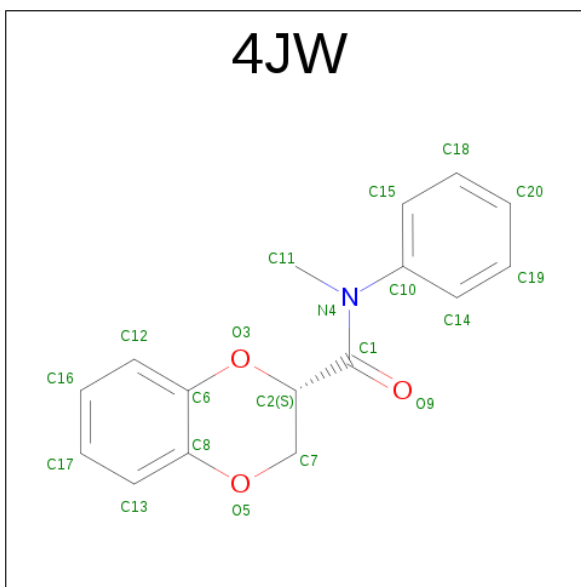
Continued on next page...

Continued from previous page...

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: C₁₄H₂₄N₆O₃S).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			20	16	1	3		
3	D	1	Total	C	N	O	0	0
			20	16	1	3		

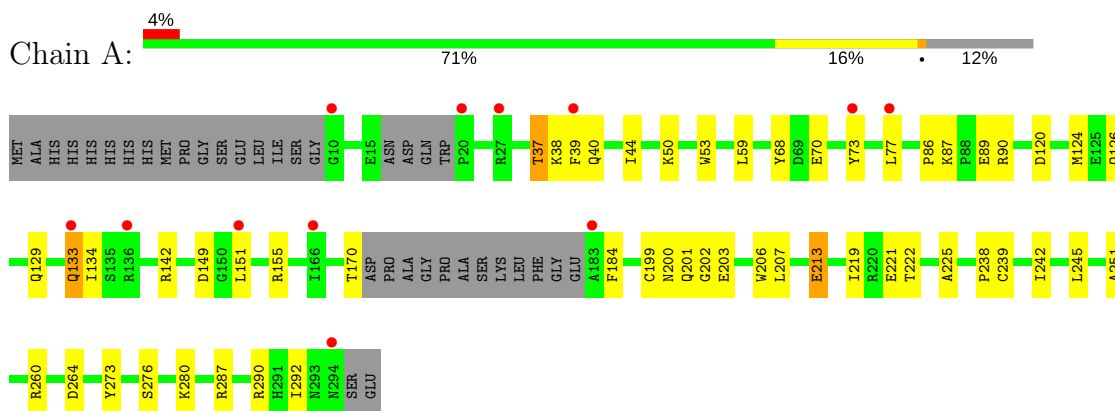
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total	O	0	0
			58	58		
4	B	76	Total	O	0	0
			76	76		
4	C	77	Total	O	0	0
			77	77		
4	D	65	Total	O	0	0
			65	65		

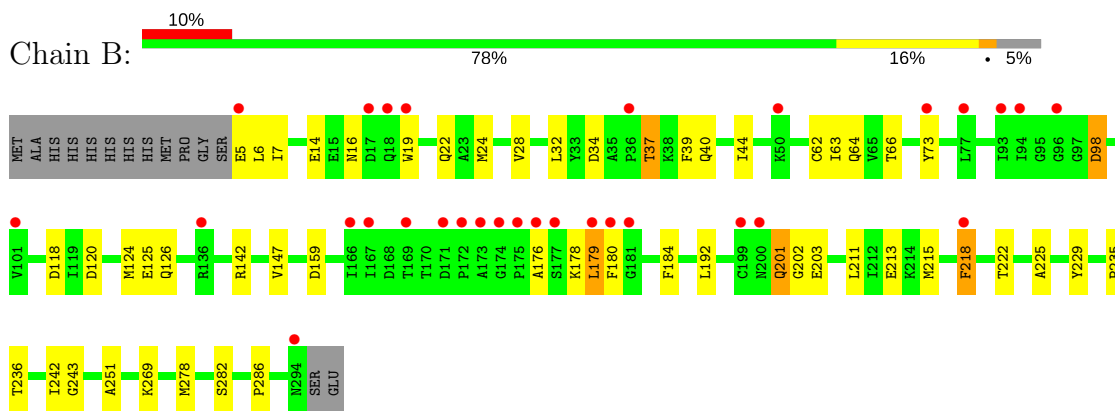
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

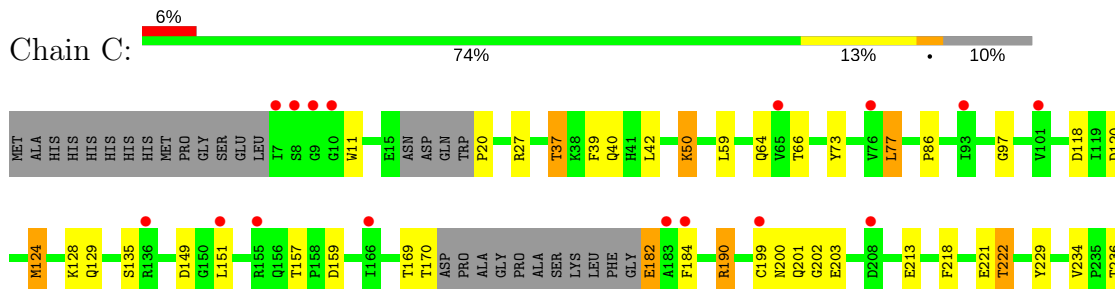
- Molecule 1: Spermidine synthase, putative

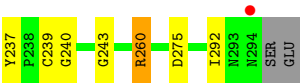


- Molecule 1: Spermidine synthase, putative

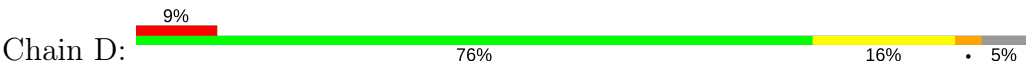


- Molecule 1: Spermidine synthase, putative





● Molecule 1: Spermidine synthase, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.56Å 99.78Å 135.00Å 90.00° 90.64° 90.00°	Depositor
Resolution (Å)	29.41 – 1.95 27.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	96.3 (29.41-1.95) 96.3 (27.00-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.17 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.208 , 0.253 0.208 , 0.253	Depositor DCC
R_{free} test set	4047 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9249	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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 66.74 % 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 5.7553e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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, 4JW

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.94	1/2174 (0.0%)	0.99	6/2944 (0.2%)
1	B	0.99	1/2338 (0.0%)	1.01	7/3172 (0.2%)
1	C	1.00	2/2201 (0.1%)	1.07	9/2980 (0.3%)
1	D	0.98	1/2338 (0.0%)	1.06	8/3172 (0.3%)
All	All	0.98	5/9051 (0.1%)	1.03	30/12268 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	282	SER	CB-OG	6.04	1.50	1.42
1	C	73	TYR	CG-CD1	5.50	1.46	1.39
1	D	213	GLU	CD-OE2	5.45	1.31	1.25
1	A	213	GLU	CG-CD	5.35	1.59	1.51
1	C	199	CYS	CB-SG	-5.05	1.73	1.81

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	190	ARG	NE-CZ-NH2	-17.42	111.59	120.30
1	C	190	ARG	NE-CZ-NH2	-16.97	111.81	120.30
1	D	190	ARG	NE-CZ-NH1	13.74	127.17	120.30
1	C	190	ARG	NE-CZ-NH1	13.19	126.89	120.30
1	A	149	ASP	CB-CG-OD1	8.56	126.00	118.30
1	B	142	ARG	NE-CZ-NH2	-7.97	116.32	120.30
1	C	190	ARG	CG-CD-NE	-7.33	96.42	111.80
1	D	98	ASP	CB-CG-OD1	6.54	124.18	118.30
1	D	159	ASP	CB-CG-OD1	6.45	124.11	118.30
1	D	190	ARG	CG-CD-NE	-6.40	98.36	111.80
1	A	264	ASP	CB-CG-OD2	6.12	123.81	118.30
1	B	142	ARG	NE-CZ-NH1	6.10	123.35	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	190	ARG	CD-NE-CZ	5.92	131.89	123.60
1	C	159	ASP	CB-CG-OD1	5.90	123.61	118.30
1	B	98	ASP	CB-CG-OD1	5.88	123.59	118.30
1	B	278	MET	CG-SD-CE	5.78	109.45	100.20
1	C	275	ASP	CB-CG-OD1	5.73	123.46	118.30
1	A	142	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	B	192	LEU	CB-CG-CD1	-5.62	101.44	111.00
1	C	190	ARG	CD-NE-CZ	5.50	131.29	123.60
1	A	155	ARG	NE-CZ-NH2	5.47	123.03	120.30
1	C	77	LEU	CB-CG-CD1	5.44	120.24	111.00
1	B	213	GLU	OE1-CD-OE2	-5.39	116.83	123.30
1	A	142	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	C	149	ASP	CB-CG-OD1	5.25	123.02	118.30
1	D	142	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	D	107	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	B	159	ASP	CB-CG-OD1	5.10	122.89	118.30
1	C	260	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	A	290	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2124	0	2087	35	0
1	B	2281	0	2230	36	0
1	C	2151	0	2112	43	0
1	D	2281	0	2230	36	0
2	A	24	0	24	1	0
2	B	24	0	24	1	0
2	C	24	0	24	2	0
2	D	24	0	24	0	0
3	B	20	0	15	0	0
3	D	20	0	15	0	0
4	A	58	0	0	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	76	0	0	1	0
4	C	77	0	0	0	0
4	D	65	0	0	2	0
All	All	9249	0	8785	142	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 (142) 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:37:THR:HG22	1:A:40:GLN:H	1.19	1.04
1:C:37:THR:HG21	1:C:120:ASP:OD2	1.60	1.01
1:A:37:THR:HG21	1:A:120:ASP:OD2	1.65	0.97
1:D:37:THR:HG22	1:D:39:PHE:H	1.27	0.96
1:A:37:THR:CG2	1:A:39:PHE:H	1.79	0.95
1:D:203:GLU:HG3	1:D:211:LEU:HD23	1.49	0.95
1:B:37:THR:HG21	1:B:120:ASP:OD2	1.66	0.95
1:C:37:THR:CG2	1:C:39:PHE:H	1.81	0.92
1:A:37:THR:HG23	1:A:39:PHE:H	1.33	0.91
1:B:202:GLY:O	1:B:203:GLU:HB2	1.70	0.91
1:B:37:THR:HG22	1:B:40:GLN:H	1.34	0.91
1:C:37:THR:HG22	1:C:40:GLN:H	1.39	0.86
1:C:37:THR:HG22	1:C:39:PHE:H	1.40	0.84
1:D:37:THR:CG2	1:D:39:PHE:H	1.91	0.83
1:D:37:THR:HG21	1:D:120:ASP:OD2	1.78	0.83
1:D:37:THR:HG22	1:D:39:PHE:N	1.96	0.80
1:A:37:THR:HG22	1:A:40:GLN:N	1.97	0.80
1:B:203:GLU:HG3	1:B:211:LEU:HD23	1.68	0.74
1:D:202:GLY:O	1:D:203:GLU:HB2	1.89	0.72
1:A:90:ARG:NH2	4:A:401:HOH:O	2.22	0.71
1:A:219:ILE:O	1:A:222:THR:HG22	1.91	0.71
1:C:37:THR:HG23	1:C:39:PHE:H	1.57	0.69
1:A:239:CYS:HB3	1:B:235:PRO:HB3	1.74	0.68
1:B:218:PHE:O	1:B:222:THR:HG23	1.93	0.68
1:C:239:CYS:HB3	1:D:235:PRO:HB3	1.76	0.67
1:C:169:THR:O	1:C:201:GLN:OE1	2.12	0.67
1:A:213:GLU:HG3	1:A:292:ILE:HD11	1.77	0.66
1:B:37:THR:CG2	1:B:39:PHE:H	2.09	0.66
1:C:202:GLY:O	1:C:203:GLU:HB2	1.94	0.66
1:B:64:GLN:OE1	2:B:301:S4M:HG1	1.95	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:14:GLU:HG2	1:D:19:TRP:HH2	1.62	0.65
1:A:37:THR:HG22	1:A:39:PHE:H	1.60	0.65
1:A:50:LYS:HE2	4:A:458:HOH:O	1.96	0.64
1:C:218:PHE:O	1:C:222:THR:HG23	1.97	0.64
1:D:172:PRO:O	1:D:177:SER:HB2	1.97	0.64
1:D:133:GLN:HB2	4:D:442:HOH:O	1.97	0.63
1:C:118:ASP:HB3	1:C:124:MET:HE2	1.82	0.61
1:C:37:THR:HG22	1:C:39:PHE:N	2.13	0.61
1:A:207:LEU:HD11	1:A:238:PRO:HB2	1.83	0.61
1:D:213:GLU:HG3	1:D:217:ARG:HH12	1.65	0.60
1:B:14:GLU:OE2	1:B:62:CYS:HA	2.00	0.60
1:C:213:GLU:HG2	1:C:292:ILE:CD1	2.31	0.60
1:D:37:THR:HB	1:D:40:GLN:O	2.03	0.58
1:D:289:ALA:O	1:D:292:ILE:HG12	2.03	0.58
1:C:118:ASP:HB3	1:C:124:MET:CE	2.34	0.57
1:B:37:THR:HG22	1:B:39:PHE:H	1.69	0.57
1:A:87:LYS:HE2	1:A:89:GLU:OE1	2.04	0.56
1:B:229:TYR:CZ	1:B:243:GLY:HA3	2.41	0.56
1:D:157:THR:O	1:D:190:ARG:NH2	2.34	0.56
1:D:202:GLY:O	1:D:203:GLU:CB	2.52	0.56
1:A:202:GLY:O	1:A:203:GLU:HB2	2.05	0.56
1:D:201:GLN:OE1	1:D:242:ILE:HD11	2.06	0.56
1:D:182:GLU:HG3	1:D:218:PHE:CD1	2.42	0.54
1:C:240:GLY:HA3	1:D:240:GLY:HA3	1.90	0.53
1:B:44:ILE:CD1	1:B:126:GLN:HB3	2.38	0.53
1:A:287:ARG:NH1	4:A:403:HOH:O	2.42	0.53
1:B:176:ALA:HA	1:B:179:LEU:CD2	2.39	0.52
1:D:213:GLU:HG2	1:D:214:LYS:N	2.25	0.52
1:C:213:GLU:CG	1:C:292:ILE:HD11	2.39	0.52
1:D:44:ILE:CD1	1:D:126:GLN:HB3	2.40	0.52
1:A:201:GLN:NE2	1:A:242:ILE:HD11	2.25	0.51
1:C:200:ASN:C	1:C:200:ASN:OD1	2.48	0.51
1:C:213:GLU:HG2	1:C:292:ILE:HD11	1.93	0.50
1:C:66:THR:HG21	1:C:236:THR:HG21	1.92	0.50
1:C:37:THR:HG22	1:C:40:GLN:N	2.16	0.50
1:C:50:LYS:HD3	1:C:50:LYS:N	2.27	0.50
1:C:64:GLN:HB3	2:C:301:S4M:HB2	1.93	0.50
1:C:218:PHE:O	1:C:222:THR:CG2	2.60	0.49
1:C:202:GLY:O	1:C:203:GLU:CB	2.58	0.49
1:D:37:THR:HG23	1:D:38:LYS:N	2.28	0.49
1:D:181:GLY:O	1:D:185:TYR:HD2	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:THR:HG23	1:A:38:LYS:N	2.27	0.49
1:C:59:LEU:HD11	2:C:301:S4M:HE3	1.95	0.49
1:D:37:THR:CG2	1:D:38:LYS:N	2.75	0.49
1:C:229:TYR:CZ	1:C:243:GLY:HA3	2.48	0.48
1:B:202:GLY:O	1:B:203:GLU:CB	2.42	0.48
1:D:13:ARG:NE	1:D:15:GLU:OE2	2.38	0.48
1:B:14:GLU:OE2	1:B:63:ILE:N	2.38	0.48
1:A:225:ALA:HB1	1:A:251:ALA:HA	1.96	0.48
1:C:11:TRP:CE2	1:C:27:ARG:HG3	2.48	0.48
1:A:40:GLN:HG3	1:A:59:LEU:HD22	1.95	0.48
1:A:213:GLU:HG3	1:A:292:ILE:CD1	2.43	0.48
1:D:86:PRO:O	1:D:260:ARG:HD3	2.14	0.48
1:A:151:LEU:HD12	1:A:184:PHE:HB2	1.94	0.47
1:D:146:ARG:HG3	4:D:402:HOH:O	2.13	0.47
1:B:6:LEU:O	1:B:7:ILE:HD13	2.14	0.47
1:A:273:TYR:CD1	1:B:286:PRO:HB3	2.49	0.47
1:B:37:THR:HG23	1:B:39:PHE:H	1.78	0.47
1:B:37:THR:CG2	1:B:120:ASP:OD2	2.51	0.47
1:A:206:TRP:CD2	1:B:235:PRO:HG3	2.50	0.47
1:D:167:ILE:HG22	1:D:169:THR:HG23	1.97	0.47
1:B:6:LEU:HD22	1:B:28:VAL:HG21	1.96	0.46
1:C:151:LEU:CD1	1:C:184:PHE:HB2	2.45	0.46
1:A:287:ARG:HG2	1:A:287:ARG:HH11	1.80	0.46
1:B:179:LEU:HA	1:B:184:PHE:CD2	2.51	0.46
1:D:129:GLN:HG2	1:D:130:HIS:NE2	2.30	0.46
1:A:37:THR:CG2	1:A:39:PHE:N	2.63	0.46
1:D:211:LEU:O	1:D:215:MET:HG3	2.17	0.45
1:A:133:GLN:H	1:A:133:GLN:HG2	1.45	0.45
1:B:66:THR:HG21	1:B:236:THR:HG21	1.99	0.45
1:A:200:ASN:HD21	1:A:245:LEU:HD12	1.81	0.45
1:C:86:PRO:O	1:C:260:ARG:HD3	2.17	0.45
1:A:86:PRO:O	1:A:260:ARG:HD3	2.17	0.44
1:A:44:ILE:CD1	1:A:126:GLN:HB3	2.47	0.44
1:A:70:GLU:HG2	1:A:134:ILE:HD11	1.98	0.44
1:A:273:TYR:CE1	1:B:286:PRO:HG3	2.53	0.44
1:C:213:GLU:CG	1:C:292:ILE:CD1	2.95	0.44
1:D:14:GLU:HG2	1:D:19:TRP:CH2	2.48	0.44
1:C:213:GLU:HG2	1:C:292:ILE:HD13	2.00	0.43
1:B:16:ASN:HB3	1:B:19:TRP:CE2	2.54	0.43
1:D:37:THR:HG22	1:D:40:GLN:H	1.83	0.43
1:C:20:PRO:HG2	1:D:50:LYS:CB	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:LEU:HD12	1:B:44:ILE:HG22	2.01	0.43
1:C:97:GLY:HA3	1:C:124:MET:HE2	2.01	0.43
1:D:203:GLU:HB3	1:D:208:ASP:HB2	2.00	0.43
1:B:22:GLN:NE2	4:B:406:HOH:O	2.52	0.43
1:A:276:SER:O	1:A:280:LYS:HG3	2.19	0.43
1:A:73:TYR:CE2	2:A:301:S4M:HA2	2.54	0.42
1:B:24:MET:HE3	1:B:63:ILE:HD12	2.00	0.42
1:A:37:THR:HG22	1:A:39:PHE:N	2.29	0.42
1:A:53:TRP:CZ3	1:A:68:TYR:HD2	2.36	0.42
1:B:211:LEU:O	1:B:215:MET:HG3	2.18	0.42
1:B:73:TYR:OH	1:B:201:GLN:HG2	2.20	0.42
1:B:178:LYS:C	1:B:180:PHE:H	2.22	0.42
1:C:213:GLU:HG3	1:C:292:ILE:HD11	2.01	0.42
1:C:20:PRO:HG2	1:D:50:LYS:HB2	2.02	0.41
1:B:118:ASP:O	1:B:147:VAL:HA	2.20	0.41
1:C:97:GLY:CA	1:C:124:MET:HE2	2.50	0.41
1:B:269:LYS:HE3	1:B:269:LYS:HB3	1.90	0.41
1:B:203:GLU:HG3	1:B:211:LEU:CD2	2.43	0.41
1:B:225:ALA:HB1	1:B:251:ALA:HA	2.03	0.41
1:C:234:VAL:HG11	1:C:237:TYR:CD2	2.56	0.41
1:D:193:LYS:HB3	1:D:194:PRO:HD2	2.02	0.41
1:C:157:THR:O	1:C:190:ARG:NH2	2.27	0.40
1:C:151:LEU:HD11	1:C:184:PHE:HB2	2.03	0.40
1:C:182:GLU:HA	1:C:218:PHE:HZ	1.85	0.40
1:B:5:GLU:N	1:B:34:ASP:OD2	2.54	0.40
1:C:118:ASP:CB	1:C:124:MET:HE2	2.49	0.40
1:C:42:LEU:HD13	1:C:59:LEU:HD21	2.02	0.40
1:D:53:TRP:CZ3	1:D:236:THR:HG23	2.55	0.40
1:C:37:THR:CG2	1:C:40:GLN:H	2.22	0.40
1:C:128:LYS:HA	1:C:135:SER:OG	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	263/304 (86%)	253 (96%)	10 (4%)	0	100	100
1	B	288/304 (95%)	276 (96%)	12 (4%)	0	100	100
1	C	267/304 (88%)	257 (96%)	10 (4%)	0	100	100
1	D	288/304 (95%)	276 (96%)	11 (4%)	1 (0%)	44	33
All	All	1106/1216 (91%)	1062 (96%)	43 (4%)	1 (0%)	55	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	203	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	234/262 (89%)	226 (97%)	8 (3%)	42	29
1	B	250/262 (95%)	242 (97%)	8 (3%)	44	31
1	C	237/262 (90%)	228 (96%)	9 (4%)	38	24
1	D	250/262 (95%)	235 (94%)	15 (6%)	22	9
All	All	971/1048 (93%)	931 (96%)	40 (4%)	35	21

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	THR
1	A	77	LEU
1	A	124	MET
1	A	129	GLN
1	A	133	GLN
1	A	170	THR
1	A	199	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	221	GLU
1	B	37	THR
1	B	98	ASP
1	B	124	MET
1	B	125	GLU
1	B	179	LEU
1	B	201	GLN
1	B	218	PHE
1	B	242	ILE
1	C	37	THR
1	C	50	LYS
1	C	77	LEU
1	C	124	MET
1	C	129	GLN
1	C	170	THR
1	C	182	GLU
1	C	221	GLU
1	C	222	THR
1	D	5	GLU
1	D	6	LEU
1	D	7	ILE
1	D	19	TRP
1	D	37	THR
1	D	77	LEU
1	D	124	MET
1	D	125	GLU
1	D	177	SER
1	D	201	GLN
1	D	213	GLU
1	D	217	ARG
1	D	218	PHE
1	D	220	ARG
1	D	222	THR

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

Mol	Chain	Res	Type
1	A	201	GLN
1	A	233	HIS
1	B	22	GLN
1	B	113	HIS
1	B	129	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	233	HIS
1	C	22	GLN
1	C	113	HIS
1	C	201	GLN
1	D	22	GLN

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	1.01	1 (4%)	20,37,37	1.60	1 (5%)
2	S4M	B	301	-	23,26,26	0.75	1 (4%)	20,37,37	1.02	1 (5%)
3	4JW	B	302	-	22,22,22	0.93	1 (4%)	25,30,30	1.22	3 (12%)
2	S4M	C	301	-	23,26,26	0.91	0	20,37,37	1.03	0
2	S4M	D	301	-	23,26,26	1.03	2 (8%)	20,37,37	1.63	3 (15%)
3	4JW	D	302	-	22,22,22	1.19	2 (9%)	25,30,30	1.28	1 (4%)

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	4JW	B	302	-	-	0/11/21/21	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	4JW	D	302	-	-	0/11/21/21	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	301	S4M	O4'-C1'	2.10	1.44	1.41
2	B	301	S4M	CG-SD	2.11	1.85	1.80
2	A	301	S4M	O4'-C1'	2.43	1.44	1.41
2	D	301	S4M	C2-N3	2.65	1.36	1.32
3	D	302	4JW	O5-C8	2.74	1.40	1.37
3	B	302	4JW	C1-N4	2.82	1.40	1.35
3	D	302	4JW	C1-N4	3.55	1.41	1.35

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	S4M	C4'-O4'-C1'	-5.44	103.97	109.77
2	A	301	S4M	C4'-O4'-C1'	-5.36	104.07	109.77
3	D	302	4JW	C7-O5-C8	-4.43	105.82	115.33
2	B	301	S4M	C4'-O4'-C1'	-3.01	106.57	109.77
3	B	302	4JW	C7-O5-C8	-2.64	109.66	115.33
3	B	302	4JW	O5-C8-C6	-2.22	119.80	122.01
2	D	301	S4M	O4'-C4'-C5'	2.16	114.45	108.87
2	D	301	S4M	N6-C6-N1	2.58	123.89	118.77
3	B	302	4JW	O9-C1-N4	3.07	125.60	121.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	S4M	1	0
2	B	301	S4M	1	0
2	C	301	S4M	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	269/304 (88%)	0.44	12 (4%) 34 44	14, 27, 44, 57	0
1	B	290/304 (95%)	0.53	30 (10%) 7 12	15, 27, 58, 85	0
1	C	273/304 (89%)	0.41	17 (6%) 21 31	12, 26, 45, 67	0
1	D	290/304 (95%)	0.52	26 (8%) 10 17	16, 27, 53, 73	0
All	All	1122/1216 (92%)	0.48	85 (7%) 15 23	12, 27, 49, 85	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	9	GLY	6.2
1	C	7	ILE	5.9
1	D	173	ALA	5.8
1	B	173	ALA	5.5
1	B	174	GLY	5.4
1	A	183	ALA	4.9
1	D	182	GLU	4.8
1	D	174	GLY	4.8
1	B	175	PRO	4.8
1	B	177	SER	4.3
1	C	8	SER	4.3
1	B	166	ILE	4.2
1	D	176	ALA	4.2
1	D	171	ASP	3.7
1	B	180	PHE	3.7
1	B	172	PRO	3.6
1	D	166	ILE	3.5
1	A	136	ARG	3.4
1	B	77	LEU	3.4
1	A	294	ASN	3.4
1	B	93	ILE	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	17	ASP	3.3
1	D	77	LEU	3.3
1	B	294	ASN	3.1
1	B	18	GLN	3.1
1	C	151	LEU	3.0
1	B	19	TRP	3.0
1	D	177	SER	3.0
1	B	73	TYR	3.0
1	A	27	ARG	3.0
1	B	176	ALA	2.9
1	D	181	GLY	2.9
1	A	151	LEU	2.8
1	B	171	ASP	2.8
1	D	18	GLN	2.8
1	B	179	LEU	2.7
1	D	129	GLN	2.7
1	D	169	THR	2.7
1	A	77	LEU	2.7
1	B	5	GLU	2.7
1	D	17	ASP	2.6
1	D	93	ILE	2.6
1	D	294	ASN	2.6
1	C	65	VAL	2.6
1	B	181	GLY	2.6
1	D	116	LEU	2.5
1	C	136	ARG	2.5
1	B	218	PHE	2.5
1	B	94	ILE	2.5
1	D	101	VAL	2.5
1	D	198	CYS	2.5
1	C	166	ILE	2.5
1	B	50	LYS	2.4
1	B	101	VAL	2.4
1	C	101	VAL	2.4
1	D	199	CYS	2.4
1	D	167	ILE	2.4
1	B	199	CYS	2.4
1	C	208	ASP	2.4
1	D	175	PRO	2.3
1	C	294	ASN	2.3
1	A	10	GLY	2.3
1	A	166	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	169	THR	2.3
1	B	200	ASN	2.3
1	B	136	ARG	2.3
1	A	39	PHE	2.2
1	D	19	TRP	2.2
1	A	133	GLN	2.2
1	C	183	ALA	2.2
1	D	218	PHE	2.2
1	C	10	GLY	2.1
1	B	36	PRO	2.1
1	B	96	GLY	2.1
1	C	155	ARG	2.1
1	C	184	PHE	2.1
1	D	133	GLN	2.1
1	A	20	PRO	2.1
1	C	199	CYS	2.1
1	D	50	LYS	2.0
1	A	73	TYR	2.0
1	C	76	VAL	2.0
1	D	183	ALA	2.0
1	B	167	ILE	2.0
1	C	93	ILE	2.0

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 carbohydrates 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. 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(\AA^2)	Q<0.9
2	S4M	A	301	24/24	0.88	0.14	-0.03	23,26,33,43	0
3	4JW	B	302	20/20	0.92	0.12	-0.03	28,35,37,38	0
2	S4M	C	301	24/24	0.92	0.13	-0.29	25,29,45,55	0
3	4JW	D	302	20/20	0.93	0.11	-0.34	26,31,34,34	0
2	S4M	B	301	24/24	0.90	0.14	-0.39	26,28,37,44	0
2	S4M	D	301	24/24	0.90	0.13	-0.68	24,30,47,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.