



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:47 AM GMT

PDB ID : 3C6M
Title : Crystal structure of human spermine synthase in complex with spermine and 5-methylthioadenosine
Authors : Min, J.; Wu, H.; Zeng, H.; Loppnau, P.; Weigelt, J.; Sundstrom, M.; Arrowsmith, C.H.; Edwards, A.M.; Bochkarev, A.; Pegg, A.E.; Plotnikov, A.N.; Structural Genomics Consortium (SGC)
Deposited on : 2008-02-04
Resolution : 2.45 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

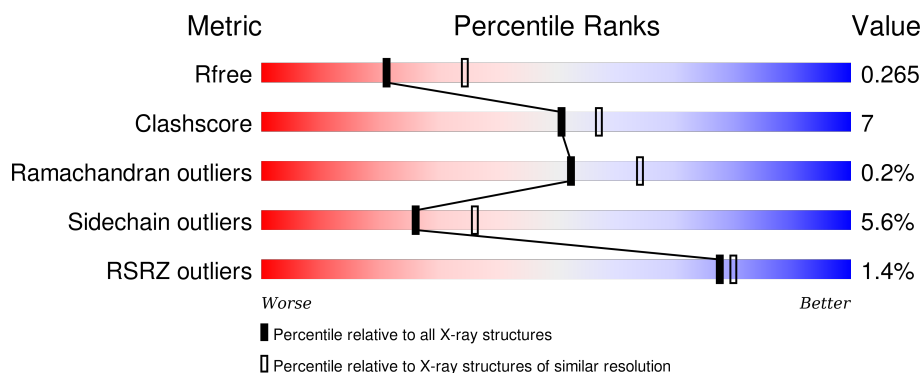
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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	381	
1	B	381	
1	C	381	
1	D	381	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SPM	A	501	-	-	-	X
2	SPM	D	501	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10378 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 Spermine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2676	1714	436	509	17			
1	B	342	Total	C	N	O	S	0	0	0
			2719	1738	446	518	17			
1	C	291	Total	C	N	O	S	0	0	0
			2325	1490	379	440	16			
1	D	278	Total	C	N	O	S	0	0	0
			2222	1430	362	415	15			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	EXPRESSION TAG	UNP P52788
A	-13	GLY	-	EXPRESSION TAG	UNP P52788
A	-12	SER	-	EXPRESSION TAG	UNP P52788
A	-11	SER	-	EXPRESSION TAG	UNP P52788
A	-10	HIS	-	EXPRESSION TAG	UNP P52788
A	-9	HIS	-	EXPRESSION TAG	UNP P52788
A	-8	HIS	-	EXPRESSION TAG	UNP P52788
A	-7	HIS	-	EXPRESSION TAG	UNP P52788
A	-6	HIS	-	EXPRESSION TAG	UNP P52788
A	-5	HIS	-	EXPRESSION TAG	UNP P52788
A	-4	SER	-	EXPRESSION TAG	UNP P52788
A	-3	SER	-	EXPRESSION TAG	UNP P52788
A	-2	GLY	-	EXPRESSION TAG	UNP P52788
A	-1	LEU	-	EXPRESSION TAG	UNP P52788
A	0	VAL	-	EXPRESSION TAG	UNP P52788
A	1	PRO	-	EXPRESSION TAG	UNP P52788
A	2	ARG	-	EXPRESSION TAG	UNP P52788
A	3	GLY	-	EXPRESSION TAG	UNP P52788
A	4	SER	-	EXPRESSION TAG	UNP P52788
B	-14	MET	-	EXPRESSION TAG	UNP P52788
B	-13	GLY	-	EXPRESSION TAG	UNP P52788

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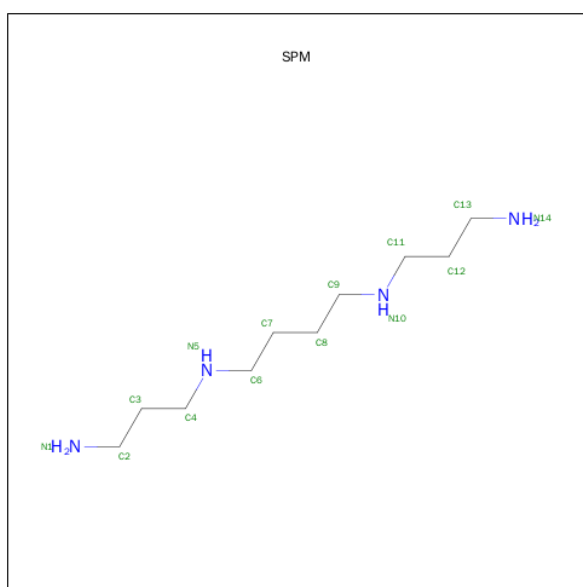
Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	SER	-	EXPRESSION TAG	UNP P52788
B	-11	SER	-	EXPRESSION TAG	UNP P52788
B	-10	HIS	-	EXPRESSION TAG	UNP P52788
B	-9	HIS	-	EXPRESSION TAG	UNP P52788
B	-8	HIS	-	EXPRESSION TAG	UNP P52788
B	-7	HIS	-	EXPRESSION TAG	UNP P52788
B	-6	HIS	-	EXPRESSION TAG	UNP P52788
B	-5	HIS	-	EXPRESSION TAG	UNP P52788
B	-4	SER	-	EXPRESSION TAG	UNP P52788
B	-3	SER	-	EXPRESSION TAG	UNP P52788
B	-2	GLY	-	EXPRESSION TAG	UNP P52788
B	-1	LEU	-	EXPRESSION TAG	UNP P52788
B	0	VAL	-	EXPRESSION TAG	UNP P52788
B	1	PRO	-	EXPRESSION TAG	UNP P52788
B	2	ARG	-	EXPRESSION TAG	UNP P52788
B	3	GLY	-	EXPRESSION TAG	UNP P52788
B	4	SER	-	EXPRESSION TAG	UNP P52788
C	-14	MET	-	EXPRESSION TAG	UNP P52788
C	-13	GLY	-	EXPRESSION TAG	UNP P52788
C	-12	SER	-	EXPRESSION TAG	UNP P52788
C	-11	SER	-	EXPRESSION TAG	UNP P52788
C	-10	HIS	-	EXPRESSION TAG	UNP P52788
C	-9	HIS	-	EXPRESSION TAG	UNP P52788
C	-8	HIS	-	EXPRESSION TAG	UNP P52788
C	-7	HIS	-	EXPRESSION TAG	UNP P52788
C	-6	HIS	-	EXPRESSION TAG	UNP P52788
C	-5	HIS	-	EXPRESSION TAG	UNP P52788
C	-4	SER	-	EXPRESSION TAG	UNP P52788
C	-3	SER	-	EXPRESSION TAG	UNP P52788
C	-2	GLY	-	EXPRESSION TAG	UNP P52788
C	-1	LEU	-	EXPRESSION TAG	UNP P52788
C	0	VAL	-	EXPRESSION TAG	UNP P52788
C	1	PRO	-	EXPRESSION TAG	UNP P52788
C	2	ARG	-	EXPRESSION TAG	UNP P52788
C	3	GLY	-	EXPRESSION TAG	UNP P52788
C	4	SER	-	EXPRESSION TAG	UNP P52788
D	-14	MET	-	EXPRESSION TAG	UNP P52788
D	-13	GLY	-	EXPRESSION TAG	UNP P52788
D	-12	SER	-	EXPRESSION TAG	UNP P52788
D	-11	SER	-	EXPRESSION TAG	UNP P52788
D	-10	HIS	-	EXPRESSION TAG	UNP P52788
D	-9	HIS	-	EXPRESSION TAG	UNP P52788

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	HIS	-	EXPRESSION TAG	UNP P52788
D	-7	HIS	-	EXPRESSION TAG	UNP P52788
D	-6	HIS	-	EXPRESSION TAG	UNP P52788
D	-5	HIS	-	EXPRESSION TAG	UNP P52788
D	-4	SER	-	EXPRESSION TAG	UNP P52788
D	-3	SER	-	EXPRESSION TAG	UNP P52788
D	-2	GLY	-	EXPRESSION TAG	UNP P52788
D	-1	LEU	-	EXPRESSION TAG	UNP P52788
D	0	VAL	-	EXPRESSION TAG	UNP P52788
D	1	PRO	-	EXPRESSION TAG	UNP P52788
D	2	ARG	-	EXPRESSION TAG	UNP P52788
D	3	GLY	-	EXPRESSION TAG	UNP P52788
D	4	SER	-	EXPRESSION TAG	UNP P52788

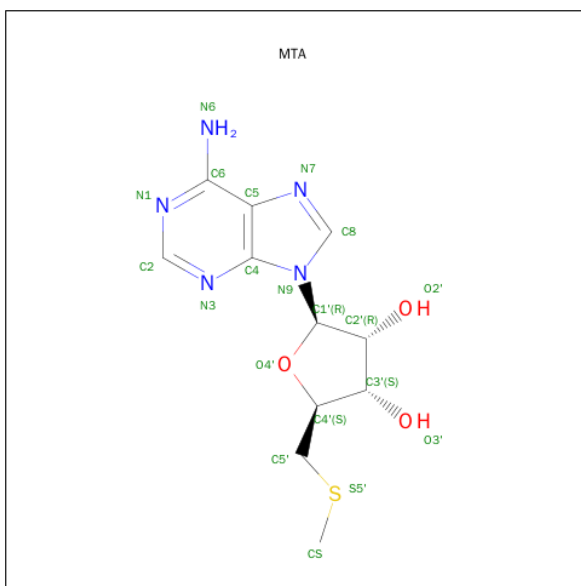
- Molecule 2 is SPERMINE (three-letter code: SPM) (formula: $C_{10}H_{26}N_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			14	10	4		
2	B	1	Total	C	N	0	0
			14	10	4		
2	C	1	Total	C	N	0	0
			14	10	4		
2	D	1	Total	C	N	0	0
			14	10	4		

- Molecule 3 is 5'-DEOXY-5'-METHYLTHIOADENOSINE (three-letter code: MTA)

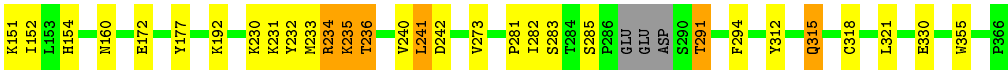
(formula: C₁₁H₁₅N₅O₃S).



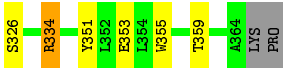
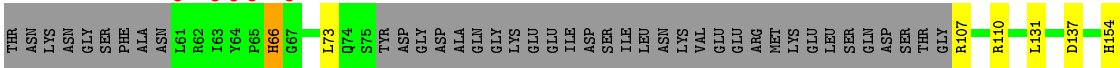
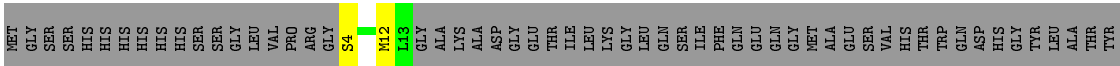
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			20	11	5	3	1		
3	B	1	Total	C	N	O	S	0	0
			20	11	5	3	1		
3	C	1	Total	C	N	O	S	0	0
			20	11	5	3	1		
3	D	1	Total	C	N	O	S	0	0
			20	11	5	3	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	75	Total	O	0	0
			75	75		
4	B	100	Total	O	0	0
			100	100		
4	C	67	Total	O	0	0
			67	67		
4	D	58	Total	O	0	0
			58	58		



• Molecule 1: Spermine synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	88.26 Å 88.26 Å 197.67 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.65 – 2.45 33.06 – 2.45	Depositor EDS
% Data completeness (in resolution range)	97.1 (35.65-2.45) 97.1 (33.06-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.45 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.271 0.206 , 0.265	Depositor DCC
R_{free} test set	3045 reflections (5.23%)	DCC
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 8.5	EDS
Estimated twinning fraction	0.045 for -h,-k,l 0.069 for h,-h-k,-l 0.135 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 61243 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10378	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: MTA, SPM

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	0.62	0/2724	0.71	1/3677 (0.0%)
1	B	0.62	0/2766	0.71	0/3731
1	C	0.65	0/2363	0.71	0/3186
1	D	0.61	0/2262	0.71	1/3056 (0.0%)
All	All	0.63	0/10115	0.71	2/13650 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	234	ARG	NE-CZ-NH2	-7.54	116.53	120.30
1	A	234	ARG	NE-CZ-NH2	-6.46	117.07	120.30

There are no chirality outliers.

There are no planarity outliers.

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	2676	0	2671	39	0
1	B	2719	0	2719	38	0
1	C	2325	0	2356	30	0
1	D	2222	0	2249	37	0
2	A	14	0	26	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	14	0	26	1	0
2	C	14	0	26	1	0
2	D	14	0	26	7	0
3	A	20	0	15	0	0
3	B	20	0	15	0	0
3	C	20	0	15	2	0
3	D	20	0	15	1	0
4	A	75	0	0	6	0
4	B	100	0	0	6	0
4	C	67	0	0	1	0
4	D	58	0	0	3	0
All	All	10378	0	10159	139	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 7.

All (139) 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:D:334:ARG:HH11	1:D:334:ARG:HG2	1.19	1.04
1:A:44:ASP:HB2	4:A:562:HOH:O	1.56	1.03
1:A:12:MET:HG2	4:B:581:HOH:O	1.61	0.98
1:C:315:GLN:HE21	1:C:355:TRP:HE1	1.21	0.88
1:A:137:ASP:OD1	1:A:154:HIS:HD2	1.57	0.87
1:A:315:GLN:HE21	1:A:355:TRP:HE1	1.21	0.84
1:B:212:LYS:HG3	4:B:599:HOH:O	1.78	0.83
1:B:172:GLU:HA	1:B:236:THR:HG22	1.60	0.83
1:D:351:TYR:O	2:D:501:SPM:H21	1.80	0.82
1:A:325:LEU:O	1:A:329:GLU:HG3	1.83	0.79
1:A:42:TRP:HB3	1:A:45:HIS:HB2	1.67	0.75
1:D:334:ARG:HH11	1:D:334:ARG:CG	2.00	0.74
1:C:282:ILE:HD12	3:C:401:MTA:C8	2.20	0.72
1:B:315:GLN:HE21	1:B:355:TRP:HE1	1.38	0.71
1:D:172:GLU:HA	1:D:236:THR:HG22	1.76	0.67
1:C:315:GLN:NE2	1:C:355:TRP:HE1	1.90	0.66
1:C:231:LYS:HE3	1:C:232:TYR:OH	1.96	0.66
1:C:172:GLU:OE2	1:C:235:LYS:HB2	1.95	0.66
1:D:315:GLN:HE21	1:D:355:TRP:HE1	1.43	0.65
1:A:42:TRP:CB	1:A:45:HIS:HB2	2.26	0.64
1:D:137:ASP:OD1	1:D:154:HIS:HD2	1.80	0.64
1:D:334:ARG:NH1	1:D:334:ARG:HG2	2.00	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:LYS:NZ	1:D:107:ARG:HH22	1.96	0.63
1:A:234:ARG:NH2	1:A:242:ASP:OD1	2.31	0.62
1:C:85:GLU:O	1:C:89:ILE:HD12	1.98	0.62
1:A:74:GLN:HA	1:A:75:SER:HB3	1.83	0.61
1:A:154:HIS:HE1	1:C:330:GLU:OE1	1.84	0.61
1:C:230:LYS:HG3	1:C:241:LEU:HB3	1.83	0.61
1:A:74:GLN:HA	1:A:75:SER:CB	2.32	0.60
1:D:169:ASN:ND2	2:D:501:SPM:H112	2.16	0.60
1:B:4:SER:HB2	1:B:116:ARG:O	2.02	0.60
1:A:167:ASP:OD1	2:A:501:SPM:H71	2.01	0.60
1:B:20:GLU:N	4:B:600:HOH:O	2.34	0.59
1:A:169:ASN:HD22	2:A:501:SPM:H132	1.66	0.59
1:D:262:ARG:O	1:D:266:GLU:HG2	2.02	0.59
1:B:161:ILE:HG12	1:B:171:ALA:HB2	1.83	0.59
1:A:226:ILE:HG23	1:A:241:LEU:HG	1.84	0.58
1:D:315:GLN:NE2	1:D:355:TRP:HE1	2.01	0.58
1:A:353:GLU:OE2	2:A:501:SPM:H32	2.03	0.58
1:D:313:PHE:CE1	1:D:359:THR:HG23	2.39	0.58
1:B:88:SER:O	1:B:92:LYS:HD3	2.03	0.58
1:C:151:LYS:HZ2	1:D:107:ARG:HH22	1.52	0.57
1:B:296:ARG:NH1	1:B:300:ASP:OD2	2.38	0.56
1:B:27:GLN:HG2	1:B:37:GLU:OE1	2.04	0.56
1:D:211:LEU:HA	4:D:594:HOH:O	2.05	0.56
1:D:355:TRP:CH2	2:D:501:SPM:H61	2.40	0.56
1:B:177:TYR:CZ	2:B:501:SPM:H131	2.40	0.56
1:C:231:LYS:HE3	1:C:232:TYR:CZ	2.40	0.55
1:A:6:HIS:HE1	1:A:72:ASP:OD1	1.90	0.55
1:B:141:TYR:O	1:B:151:LYS:HA	2.08	0.54
1:A:236:THR:HB	4:A:504:HOH:O	2.08	0.54
1:C:177:TYR:CZ	2:C:501:SPM:H131	2.42	0.54
1:B:23:LEU:HD22	1:B:27:GLN:HG3	1.90	0.54
1:A:108:VAL:N	4:A:516:HOH:O	2.41	0.53
1:D:230:LYS:HD2	1:D:241:LEU:O	2.09	0.53
1:C:89:ILE:O	1:C:93:VAL:HG23	2.07	0.53
1:A:36:ALA:O	1:A:51:TYR:HA	2.08	0.53
1:D:189:TYR:O	1:D:192:LYS:HB2	2.10	0.52
1:B:273:VAL:O	1:B:312:TYR:HA	2.10	0.52
1:B:73:LEU:HD13	1:B:90:LEU:HD21	1.90	0.52
1:D:353:GLU:OE2	2:D:501:SPM:H32	2.09	0.52
1:D:234:ARG:HG3	4:D:557:HOH:O	2.09	0.51
1:C:230:LYS:HD2	1:C:241:LEU:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:231:LYS:HD3	1:D:232:TYR:CZ	2.46	0.51
1:A:60:ASN:OD1	1:B:60:ASN:OD1	2.29	0.51
1:D:172:GLU:HG2	1:D:235:LYS:HB3	1.91	0.51
1:A:137:ASP:OD1	1:A:154:HIS:CD2	2.50	0.50
1:B:73:LEU:HD22	1:B:86:ILE:HG23	1.92	0.50
1:A:35:MET:HA	1:A:52:THR:O	2.11	0.50
1:B:37:GLU:HG3	1:B:51:TYR:CE1	2.47	0.50
1:B:147:TYR:HB3	1:B:282:ILE:HD13	1.92	0.50
1:A:40:HIS:HE1	4:A:529:HOH:O	1.93	0.50
1:C:234:ARG:NH2	1:C:242:ASP:OD2	2.45	0.49
1:D:110:ARG:O	1:D:110:ARG:HG2	2.11	0.49
1:D:291:THR:N	4:D:609:HOH:O	2.45	0.49
1:C:233:MET:HB3	1:C:236:THR:HG23	1.93	0.49
1:A:351:TYR:O	2:A:501:SPM:H21	2.13	0.49
1:B:137:ASP:OD1	1:B:154:HIS:HD2	1.95	0.48
1:B:234:ARG:NH2	1:B:242:ASP:OD2	2.44	0.48
2:A:501:SPM:H72	4:A:576:HOH:O	2.14	0.48
1:B:365:LYS:H	1:B:365:LYS:HD2	1.79	0.48
1:D:355:TRP:CZ2	2:D:501:SPM:H61	2.49	0.48
1:B:281:PRO:HB2	1:B:294:PHE:CE2	2.48	0.47
1:B:235:LYS:HD3	4:B:569:HOH:O	2.14	0.47
1:A:136:ILE:HA	1:A:154:HIS:O	2.15	0.47
1:A:276:ASP:OD1	2:A:501:SPM:H122	2.15	0.47
1:D:187:GLU:OE1	1:D:311:LYS:HE3	2.15	0.46
1:C:318:CYS:SG	1:C:321:LEU:HG	2.55	0.46
1:D:234:ARG:NH2	1:D:242:ASP:OD1	2.47	0.46
1:B:44:ASP:N	1:B:44:ASP:OD2	2.49	0.46
1:B:318:CYS:SG	1:B:321:LEU:HG	2.56	0.46
1:A:41:THR:HG22	1:A:47:TYR:CD1	2.51	0.46
1:C:291:THR:HG22	4:C:565:HOH:O	2.17	0.45
1:D:172:GLU:HA	1:D:236:THR:CG2	2.44	0.45
1:B:177:TYR:CD2	1:B:177:TYR:C	2.90	0.45
1:A:11:PHE:CZ	1:A:97:MET:HG3	2.52	0.45
1:A:279:ALA:O	1:A:281:PRO:HD3	2.15	0.45
1:A:130:ARG:NH2	1:B:157:GLN:HE22	2.14	0.45
1:C:68:LEU:HD11	1:C:70:LEU:HD21	1.97	0.45
1:D:172:GLU:CG	1:D:235:LYS:HB3	2.47	0.44
1:C:11:PHE:O	1:C:68:LEU:HA	2.17	0.44
1:C:282:ILE:HD12	3:C:401:MTA:H8	1.98	0.44
1:B:179:ARG:NH1	4:B:525:HOH:O	2.50	0.44
1:D:217:THR:HG23	1:D:250:GLN:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:PHE:HB2	1:A:69:VAL:HB	1.99	0.44
1:D:257:ILE:HB	1:D:258:PRO:CD	2.48	0.44
1:A:42:TRP:CG	1:A:45:HIS:HB2	2.53	0.43
1:C:154:HIS:HB2	1:C:160:ASN:ND2	2.33	0.43
1:B:216:VAL:O	1:B:249:TYR:HA	2.17	0.43
1:C:273:VAL:O	1:C:312:TYR:HA	2.18	0.43
1:C:141:TYR:HB3	1:C:152:ILE:HB	1.98	0.43
1:B:246:GLY:HA3	1:B:249:TYR:CE2	2.54	0.43
1:C:112:PRO:HA	1:C:113:PRO:HD2	1.92	0.43
1:A:233:MET:HB3	1:A:236:THR:HG23	2.01	0.42
1:D:240:VAL:HG13	1:D:241:LEU:HD13	2.01	0.42
1:B:60:ASN:HA	1:B:60:ASN:HD22	1.56	0.42
1:A:223:GLN:HB2	1:A:253:ILE:HG21	2.01	0.42
1:A:12:MET:HE2	4:A:516:HOH:O	2.19	0.42
1:D:12:MET:SD	1:D:12:MET:N	2.93	0.42
1:A:6:HIS:CE1	1:A:72:ASP:OD1	2.70	0.42
1:D:201:ASP:O	1:D:237:CYS:HB3	2.19	0.42
1:C:321:LEU:HA	1:C:321:LEU:HD23	1.91	0.42
1:B:245:LYS:HG2	4:B:598:HOH:O	2.19	0.42
1:D:177:TYR:OH	2:D:501:SPM:H122	2.20	0.41
1:C:281:PRO:HB2	1:C:294:PHE:CE2	2.55	0.41
1:D:169:ASN:ND2	2:D:501:SPM:C11	2.84	0.41
1:A:234:ARG:HH22	1:A:242:ASP:CG	2.22	0.41
1:C:154:HIS:HB2	1:C:160:ASN:HD21	1.85	0.41
1:B:275:ASN:HB3	1:B:314:THR:OG1	2.21	0.41
1:B:169:ASN:HD21	1:B:278:THR:HG22	1.85	0.41
1:B:330:GLU:OE1	1:D:154:HIS:HE1	2.03	0.41
1:C:85:GLU:O	1:C:88:SER:HB3	2.21	0.41
1:B:201:ASP:O	1:B:237:CYS:HB3	2.21	0.41
1:B:315:GLN:NE2	1:B:355:TRP:HE1	2.12	0.41
1:C:154:HIS:HA	1:C:160:ASN:HD22	1.85	0.41
1:D:164:LEU:CD1	3:D:401:MTA:H3'	2.51	0.40
1:B:42:TRP:CB	1:B:45:HIS:HB2	2.51	0.40
1:A:41:THR:HG22	1:A:47:TYR:HD1	1.86	0.40
1:A:246:GLY:HA3	1:A:249:TYR:CE2	2.57	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	326/381 (86%)	312 (96%)	13 (4%)	1 (0%)	46	57
1	B	332/381 (87%)	319 (96%)	13 (4%)	0	100	100
1	C	281/381 (74%)	268 (95%)	13 (5%)	0	100	100
1	D	270/381 (71%)	252 (93%)	16 (6%)	2 (1%)	26	32
All	All	1209/1524 (79%)	1151 (95%)	55 (4%)	3 (0%)	52	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	SER
1	D	66	HIS
1	D	200	GLY

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	296/333 (89%)	277 (94%)	19 (6%)	22	29
1	B	301/333 (90%)	285 (95%)	16 (5%)	28	39
1	C	261/333 (78%)	249 (95%)	12 (5%)	33	46
1	D	248/333 (74%)	233 (94%)	15 (6%)	24	33
All	All	1106/1332 (83%)	1044 (94%)	62 (6%)	26	36

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	28	SER
1	A	31	GLN
1	A	32	GLU
1	A	38	SER
1	A	44	ASP
1	A	88	SER
1	A	92	LYS
1	A	101	SER
1	A	190	THR
1	A	208	ILE
1	A	214	LYS
1	A	223	GLN
1	A	236	THR
1	A	240	VAL
1	A	241	LEU
1	A	265	LYS
1	A	315	GLN
1	A	319	VAL
1	B	23	LEU
1	B	28	SER
1	B	31	GLN
1	B	42	TRP
1	B	44	ASP
1	B	60	ASN
1	B	74	GLN
1	B	83	LYS
1	B	88	SER
1	B	236	THR
1	B	240	VAL
1	B	241	LEU
1	B	296	ARG
1	B	315	GLN
1	B	340	GLU
1	B	365	LYS
1	C	92	LYS
1	C	131	LEU
1	C	192	LYS
1	C	234	ARG
1	C	235	LYS
1	C	236	THR
1	C	240	VAL
1	C	241	LEU

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Mol	Chain	Res	Type
1	C	283	SER
1	C	285	SER
1	C	291	THR
1	C	315	GLN
1	D	4	SER
1	D	66	HIS
1	D	73	LEU
1	D	131	LEU
1	D	192	LYS
1	D	234	ARG
1	D	236	THR
1	D	240	VAL
1	D	241	LEU
1	D	243	ASN
1	D	284	THR
1	D	291	THR
1	D	315	GLN
1	D	326	SER
1	D	334	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	31	GLN
1	A	60	ASN
1	A	154	HIS
1	A	160	ASN
1	A	169	ASN
1	A	315	GLN
1	B	6	HIS
1	B	33	GLN
1	B	154	HIS
1	B	160	ASN
1	B	169	ASN
1	B	315	GLN
1	C	81	GLN
1	C	154	HIS
1	C	160	ASN
1	C	169	ASN
1	C	223	GLN
1	C	315	GLN

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Mol	Chain	Res	Type
1	D	6	HIS
1	D	154	HIS
1	D	160	ASN
1	D	169	ASN
1	D	315	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](#)

8 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	$\# Z > 2$
3	MTA	A	401	-	17,22,22	1.28	2 (11%)	17,32,32	3.54	7 (41%)
2	SPM	A	501	-	13,13,13	0.66	0	12,12,12	1.84	4 (33%)
3	MTA	B	401	-	17,22,22	1.26	2 (11%)	17,32,32	3.26	7 (41%)
2	SPM	B	501	-	13,13,13	0.44	0	12,12,12	0.95	0
3	MTA	C	401	-	17,22,22	1.21	1 (5%)	17,32,32	3.27	9 (52%)
2	SPM	C	501	-	13,13,13	0.30	0	12,12,12	0.93	0
3	MTA	D	401	-	17,22,22	1.15	2 (11%)	17,32,32	3.93	9 (52%)
2	SPM	D	501	-	13,13,13	0.35	0	12,12,12	1.22	2 (16%)

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
3	MTA	A	401	-	-	0/3/23/23	0/3/3/3
2	SPM	A	501	-	-	0/11/11/11	0/0/0/0
3	MTA	B	401	-	-	0/3/23/23	0/3/3/3
2	SPM	B	501	-	-	0/11/11/11	0/0/0/0
3	MTA	C	401	-	-	0/3/23/23	0/3/3/3
2	SPM	C	501	-	-	0/11/11/11	0/0/0/0
3	MTA	D	401	-	-	0/3/23/23	0/3/3/3
2	SPM	D	501	-	-	0/11/11/11	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	MTA	C5'-S5'	-3.63	1.76	1.80
3	D	401	MTA	C5'-S5'	-3.03	1.77	1.80
3	A	401	MTA	C2-N3	2.20	1.36	1.32
3	B	401	MTA	C5-C4	2.68	1.46	1.40
3	D	401	MTA	C5-C4	2.85	1.46	1.40
3	C	401	MTA	C5-C4	3.18	1.47	1.40
3	A	401	MTA	C5-C4	3.40	1.48	1.40

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	401	MTA	CS-S5'-C5'	-12.07	81.60	101.21
3	A	401	MTA	CS-S5'-C5'	-10.16	84.69	101.21
3	B	401	MTA	N3-C2-N1	-9.83	121.37	128.89
3	C	401	MTA	CS-S5'-C5'	-8.12	88.02	101.21
3	D	401	MTA	N3-C2-N1	-7.74	122.97	128.89
3	A	401	MTA	N3-C2-N1	-6.52	123.90	128.89
3	B	401	MTA	CS-S5'-C5'	-5.63	92.06	101.21
3	C	401	MTA	N3-C2-N1	-5.52	124.67	128.89
3	A	401	MTA	C4'-O4'-C1'	-4.96	104.27	109.72
3	C	401	MTA	C4'-O4'-C1'	-4.76	104.49	109.72
3	D	401	MTA	C4'-O4'-C1'	-3.66	105.69	109.72
3	B	401	MTA	C1'-N9-C4	-3.50	121.66	126.94
3	B	401	MTA	C4'-O4'-C1'	-3.07	106.34	109.72
3	C	401	MTA	C4-C5-N7	-3.00	106.72	109.48
3	C	401	MTA	C1'-N9-C4	-2.92	122.53	126.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	MTA	C4-C5-N7	-2.92	106.80	109.48
3	D	401	MTA	C1'-N9-C4	-2.80	122.71	126.94
3	C	401	MTA	C2'-C1'-N9	-2.75	110.09	114.29
3	D	401	MTA	C4-C5-N7	-2.67	107.02	109.48
3	B	401	MTA	C4-C5-N7	-2.67	107.03	109.48
3	A	401	MTA	C4'-C5'-S5'	-2.10	107.39	113.52
3	D	401	MTA	O3'-C3'-C4'	-2.01	105.01	111.05
2	D	501	SPM	C6-N5-C4	2.06	120.64	113.35
3	C	401	MTA	C2-N1-C6	2.13	122.58	118.77
2	D	501	SPM	C7-C6-N5	2.15	117.34	111.96
3	D	401	MTA	O4'-C4'-C5'	2.16	114.74	108.85
2	A	501	SPM	C12-C11-N10	2.20	117.45	111.96
3	D	401	MTA	C2-N1-C6	2.36	122.98	118.77
3	B	401	MTA	O4'-C1'-N9	2.43	113.18	108.10
3	D	401	MTA	O4'-C1'-N9	2.48	113.28	108.10
3	B	401	MTA	C2-N1-C6	2.49	123.22	118.77
3	C	401	MTA	O4'-C1'-N9	2.83	114.03	108.10
2	A	501	SPM	C6-N5-C4	2.84	123.41	113.35
3	A	401	MTA	O4'-C1'-N9	2.93	114.23	108.10
3	A	401	MTA	O4'-C4'-C5'	3.11	117.32	108.85
2	A	501	SPM	C11-N10-C9	3.29	125.00	113.35
3	C	401	MTA	O4'-C4'-C5'	3.35	117.97	108.85
2	A	501	SPM	C7-C6-N5	3.36	120.36	111.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	SPM	6	0
2	B	501	SPM	1	0
3	C	401	MTA	2	0
2	C	501	SPM	1	0
3	D	401	MTA	1	0
2	D	501	SPM	7	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	336/381 (88%)	-0.20	4 (1%) 81 83	11, 26, 63, 69	0
1	B	342/381 (89%)	-0.28	4 (1%) 81 83	7, 22, 50, 58	0
1	C	291/381 (76%)	-0.28	5 (1%) 73 75	13, 25, 71, 78	0
1	D	278/381 (72%)	-0.20	5 (1%) 71 74	14, 29, 64, 80	0
All	All	1247/1524 (81%)	-0.24	18 (1%) 78 80	7, 26, 61, 80	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	65	PRO	5.0
1	C	86	ILE	4.6
1	D	67	GLY	3.6
1	D	64	TYR	3.6
1	A	30	PHE	3.0
1	B	66	HIS	3.0
1	B	290	SER	2.8
1	C	73	LEU	2.5
1	C	92	LYS	2.5
1	C	71	LEU	2.5
1	D	63	ILE	2.5
1	B	34	GLY	2.4
1	D	61	LEU	2.3
1	B	39	VAL	2.3
1	A	47	TYR	2.1
1	A	64	TYR	2.1
1	A	75	SER	2.1
1	C	88	SER	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(Å ²)	Q<0.9
2	SPM	A	501	14/14	0.90	0.18	5.95	6,13,20,20	0
2	SPM	D	501	14/14	0.91	0.16	2.93	17,22,27,27	0
2	SPM	B	501	14/14	0.97	0.13	1.88	9,14,17,17	0
2	SPM	C	501	14/14	0.96	0.14	1.06	13,17,19,20	0
3	MTA	C	401	20/20	0.98	0.12	-0.36	17,19,21,21	0
3	MTA	B	401	20/20	0.99	0.11	-0.43	9,14,17,18	0
3	MTA	A	401	20/20	0.98	0.11	-0.56	16,21,22,23	0
3	MTA	D	401	20/20	0.98	0.11	-0.60	19,23,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.