Full wwPDB X-ray Structure Validation Report (i)

Mar 22, 2016 – 07:29 PM EDT

PDB ID	:	1M6Y
Title	:	Crystal Structure Analysis of TM0872, a Putative SAM-dependent Methyltransferase, Complexed with SAH
Authors	:	Miller, D.J.; Anderson, W.F.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2002-07-17
Resolution	:	1.90 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 (i) symbol.

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

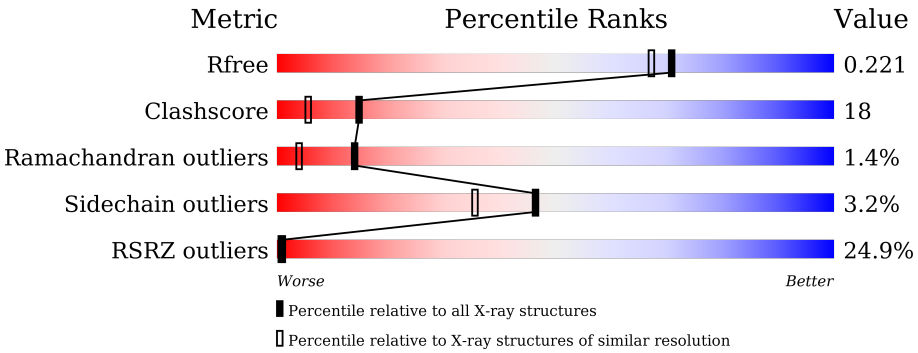
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027107
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0122
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027107

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 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	301	5% 82% 14%
1	B	301	41% 54% 36% 8%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5064 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.

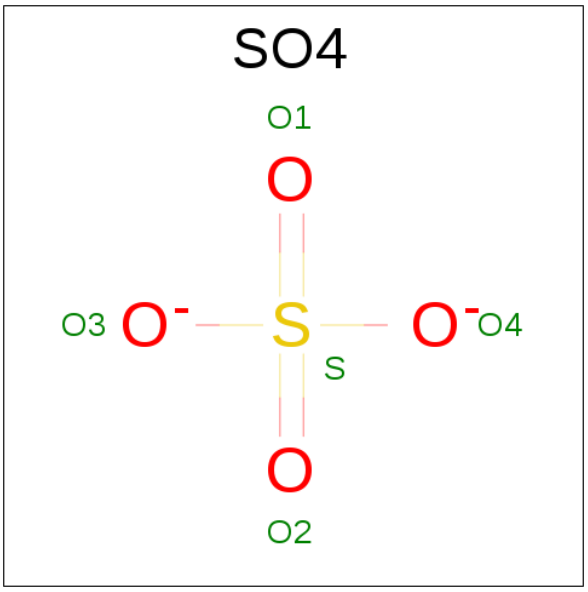
- Molecule 1 is a protein called S-adenosyl-methyltransferase mraW.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	Se	0	3	0
			2427	1531	443	446	3	4			
1	B	278	Total	C	N	O	S	Se	0	0	0
			2208	1401	396	404	3	4			

There are 14 discrepancies between the modelled and reference sequences:

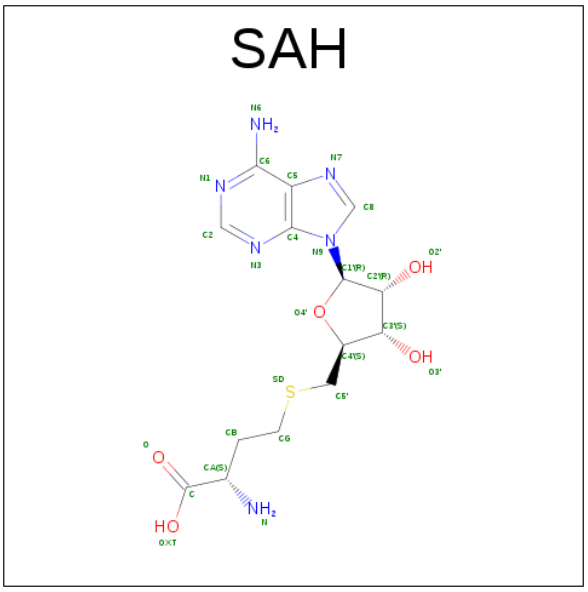
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	CLONING ARTIFACT	UNP Q9WZX6
A	0	HIS	-	CLONING ARTIFACT	UNP Q9WZX6
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
A	12	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
A	102	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
A	128	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
A	130	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
B	-1	GLY	-	CLONING ARTIFACT	UNP Q9WZX6
B	0	HIS	-	CLONING ARTIFACT	UNP Q9WZX6
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
B	12	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
B	102	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
B	128	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6
B	130	MSE	MET	MODIFIED RESIDUE	UNP Q9WZX6

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: $C_{14}H_{20}N_6O_5S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O S 26 14 6 5 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 4 is water.

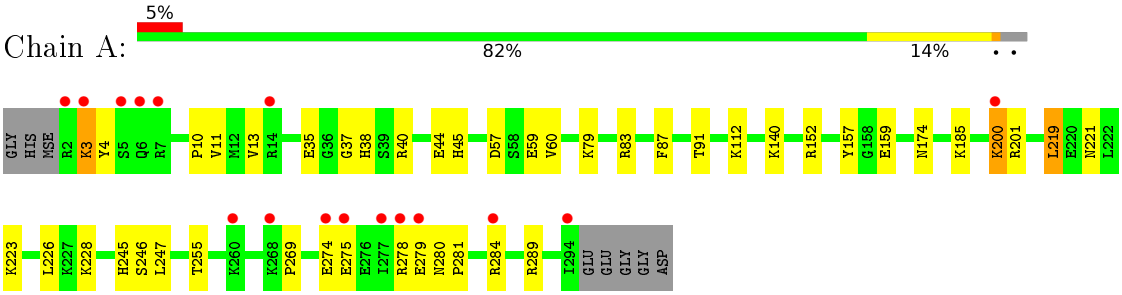
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	264	Total	O	0	0
			264	264		
4	B	103	Total	O	0	0
			103	103		

3 Residue-property plots (i)

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

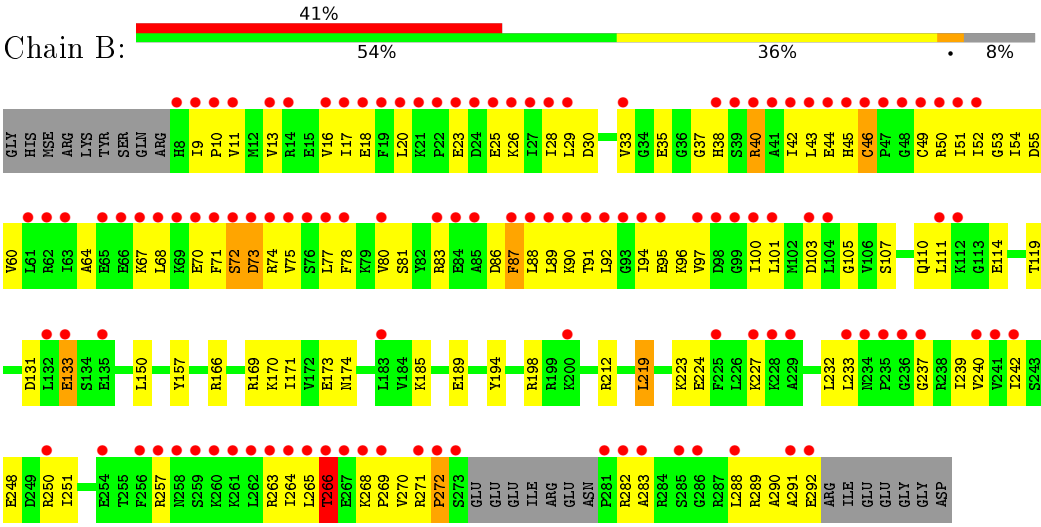
- Molecule 1: S-adenosyl-methyltransferase mraW

Chain A:



- Molecule 1: S-adenosyl-methyltransferase mraW

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α, β, γ	133.40Å 133.40Å 133.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 1.90 19.89 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.3 (19.89-1.90) 99.9 (19.89-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.01 (at 1.90Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.197 , 0.212 0.205 , 0.221	Depositor DCC
R_{free} test set	3138 reflections (5.05%)	DCC
Wilson B-factor (Å^2)	23.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 49.4	EDS
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 62185 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5064	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.31% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SAH, SO4

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	0.45	0/2457	0.64	0/3289
1	B	0.36	0/2235	0.60	1/2998 (0.0%)
All	All	0.41	0/4692	0.62	1/6287 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	272	PRO	N-CA-CB	5.40	109.78	103.30

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	2427	0	2503	42	0
1	B	2208	0	2244	127	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	26	0	19	2	0
3	B	26	0	19	4	0
4	A	264	0	0	5	0
4	B	103	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5064	0	4785	169	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 18.

All (169) 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:B:257:ARG:HA	1:B:264:ILE:HD11	1.46	0.96
1:B:128:MSE:HE1	1:B:212:ARG:HB2	1.47	0.95
1:B:270:VAL:HB	1:B:288:LEU:HB3	1.46	0.92
1:B:11:VAL:HG22	1:B:283:ALA:HB2	1.51	0.91
1:B:128:MSE:CE	1:B:212:ARG:HB2	2.06	0.85
1:B:40:ARG:HG2	1:B:40:ARG:HH21	1.43	0.84
1:B:16:VAL:HG22	1:B:20:LEU:HD12	1.62	0.81
1:B:247:LEU:HD12	1:B:250:ARG:HH12	1.44	0.81
1:A:10:PRO:HB2	1:A:13[B]:VAL:CG1	2.10	0.81
1:B:174:ASN:HD21	1:B:185:LYS:NZ	1.78	0.81
1:B:269:PRO:HG3	1:B:289:ARG:HH12	1.45	0.80
1:B:10:PRO:HB3	1:B:38:HIS:HD2	1.46	0.80
1:B:245:HIS:CD2	1:B:247:LEU:HB3	2.16	0.80
1:B:128:MSE:HE3	4:B:537:HOH:O	1.82	0.79
1:B:70:GLU:HG3	1:B:71:PHE:HD1	1.46	0.79
1:B:10:PRO:HB3	1:B:38:HIS:CD2	2.20	0.77
1:B:174:ASN:HD21	1:B:185:LYS:HZ2	1.31	0.74
1:A:269:PRO:HG3	1:A:289:ARG:NH2	2.03	0.73
1:B:92:LEU:HD12	1:B:94:ILE:HG13	1.69	0.73
1:B:100:ILE:HG13	1:B:233:LEU:HD11	1.72	0.72
1:B:264:ILE:HG22	1:B:266:THR:H	1.54	0.71
1:B:265:LEU:HG	1:B:291:ALA:HA	1.72	0.71
1:B:11:VAL:HG21	1:B:244:PHE:HZ	1.52	0.71
1:B:128:MSE:CE	4:B:537:HOH:O	2.38	0.71
1:B:42:ILE:HB	1:B:51:ILE:HD11	1.73	0.70
1:A:157:TYR:O	1:A:245:HIS:HE1	1.75	0.70
1:B:13:VAL:O	1:B:16:VAL:HG12	1.92	0.70
1:A:201:ARG:HD3	1:A:284:ARG:HH22	1.56	0.69
1:B:240:VAL:HG22	1:B:290:ALA:HB2	1.75	0.67
1:B:70:GLU:HG3	1:B:71:PHE:CD1	2.29	0.67
1:B:16:VAL:O	1:B:20:LEU:HB2	1.94	0.67
1:B:26:LYS:O	1:B:49:CYS:HA	1.96	0.66
1:B:43:LEU:HG	1:B:51:ILE:HD12	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ILE:HD12	1:B:233:LEU:HD21	1.76	0.66
1:B:223:LYS:O	1:B:227:LYS:HG3	1.96	0.66
1:A:200:LYS:HE3	1:A:200:LYS:HA	1.79	0.65
1:B:35:GLU:O	1:B:64:ALA:HA	1.96	0.64
1:B:247:LEU:O	1:B:251:ILE:HG13	1.97	0.64
1:B:10:PRO:HG3	1:B:37:GLY:HA3	1.80	0.64
1:A:284:ARG:HB3	1:A:284:ARG:NH2	2.13	0.64
1:A:4:TYR:HB2	1:A:112:LYS:HE2	1.80	0.63
1:B:92:LEU:HD13	1:B:92:LEU:O	1.99	0.62
1:B:71:PHE:HD2	1:B:74:ARG:HH21	1.46	0.62
1:A:4:TYR:O	1:A:112:LYS:HE3	1.99	0.62
1:B:40:ARG:HD3	1:B:40:ARG:O	2.00	0.61
1:B:245:HIS:NE2	1:B:247:LEU:HB3	2.15	0.61
1:B:17:ILE:HG13	1:B:18:GLU:N	2.15	0.61
1:B:29:LEU:HD21	1:B:97:VAL:HG11	1.81	0.61
1:B:242:ILE:HG12	1:B:288:LEU:HD23	1.83	0.61
1:A:3:LYS:HA	1:A:3:LYS:HE3	1.84	0.60
1:B:269:PRO:HG3	1:B:289:ARG:NH1	2.15	0.60
1:B:107:SER:OG	1:B:110:GLN:HG3	2.02	0.60
1:B:11:VAL:HG13	1:B:283:ALA:HB1	1.84	0.60
1:B:57:ASP:HB3	1:B:60:VAL:HG22	1.84	0.60
1:B:269:PRO:CG	1:B:289:ARG:HH12	2.15	0.59
1:B:28:ILE:HB	1:B:51:ILE:HG12	1.83	0.59
1:B:247:LEU:CD1	1:B:250:ARG:HH12	2.14	0.59
1:B:50:ARG:HH21	1:B:52:ILE:HD11	1.68	0.59
1:A:10:PRO:HB2	1:A:13[B]:VAL:HG12	1.84	0.58
1:A:200:LYS:HE3	1:A:200:LYS:CA	2.33	0.58
1:B:83:ARG:HD2	1:B:224:GLU:OE1	2.03	0.58
1:B:87:PHE:O	1:B:91:THR:HG23	2.04	0.58
1:B:11:VAL:HG21	1:B:244:PHE:CZ	2.38	0.57
1:B:111:LEU:HD22	1:B:119:THR:CG2	2.35	0.57
1:B:128:MSE:CE	1:B:212:ARG:CB	2.80	0.57
1:B:288:LEU:HD13	1:B:289:ARG:N	2.20	0.57
1:B:89:LEU:HD21	1:B:97:VAL:HG13	1.88	0.56
1:B:67:LYS:C	1:B:68:LEU:HD12	2.27	0.56
1:A:38:HIS:HD2	3:A:401:SAH:N	2.04	0.55
1:B:240:VAL:HG22	1:B:290:ALA:CB	2.37	0.55
1:A:11:VAL:O	1:A:38:HIS:HE1	1.90	0.55
1:B:40:ARG:NH2	1:B:40:ARG:HG2	2.18	0.55
1:B:11:VAL:HG22	1:B:283:ALA:CB	2.30	0.54
1:B:269:PRO:HG3	1:B:289:ARG:HH22	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:HIS:CD2	1:A:247:LEU:HB3	2.43	0.54
1:A:40:ARG:O	1:A:44:GLU:HG3	2.08	0.54
1:B:80:VAL:HG11	1:B:88:LEU:HD22	1.90	0.53
1:B:219:LEU:HD11	1:B:251:ILE:HD11	1.90	0.53
1:B:128:MSE:HE2	1:B:212:ARG:CB	2.39	0.53
1:A:278:ARG:HG2	1:A:278:ARG:HH21	1.75	0.52
1:A:59:GLU:HG3	4:A:578:HOH:O	2.08	0.52
1:B:38:HIS:ND1	1:B:101:LEU:HD21	2.24	0.52
1:B:64:ALA:O	1:B:68:LEU:HD13	2.10	0.51
1:B:67:LYS:O	1:B:68:LEU:HD12	2.10	0.51
1:A:174:ASN:HD21	1:A:185:LYS:NZ	2.09	0.51
1:A:40:ARG:NH1	1:A:44:GLU:OE2	2.44	0.51
1:B:100:ILE:HB	1:B:239:ILE:HG13	1.93	0.51
1:B:46:CYS:SG	1:B:46:CYS:O	2.69	0.51
1:A:269:PRO:HG3	1:A:289:ARG:CZ	2.42	0.50
1:A:57:ASP:HB3	1:A:60[A]:VAL:HG22	1.93	0.49
1:B:94:ILE:HG22	1:B:95:GLU:N	2.28	0.49
1:B:289:ARG:HG3	1:B:289:ARG:HH11	1.77	0.49
1:B:38:HIS:O	1:B:42:ILE:HG13	2.12	0.49
1:B:29:LEU:CD1	1:B:97:VAL:HG21	2.43	0.49
1:A:281:PRO:O	1:A:284:ARG:HG3	2.13	0.49
1:B:11:VAL:HG13	1:B:283:ALA:CB	2.41	0.49
1:B:233:LEU:N	1:B:233:LEU:HD22	2.28	0.49
1:B:81:SER:C	1:B:83:ARG:H	2.14	0.49
1:B:50:ARG:NH2	1:B:52:ILE:HD11	2.28	0.48
1:B:185:LYS:O	1:B:189:GLU:HG3	2.14	0.48
1:B:29:LEU:CD2	1:B:97:VAL:HG11	2.43	0.48
1:B:86:ASP:HB2	1:B:90:LYS:NZ	2.29	0.48
1:A:38:HIS:HD2	3:A:401:SAH:HN2	1.59	0.48
1:B:40:ARG:HH21	1:B:40:ARG:CG	2.21	0.48
1:A:284:ARG:HH21	1:A:284:ARG:HB3	1.78	0.48
1:A:79:LYS:HE2	4:A:513:HOH:O	2.14	0.48
1:B:42:ILE:CB	1:B:51:ILE:HD11	2.41	0.48
1:B:20:LEU:HG	1:B:240:VAL:HG21	1.95	0.48
1:B:50:ARG:HG2	1:B:51:ILE:H	1.79	0.48
1:B:131:ASP:OD1	1:B:133:GLU:HB2	2.14	0.47
1:B:288:LEU:C	1:B:288:LEU:HD13	2.34	0.47
1:B:105:GLY:O	3:B:402:SAH:H5'1	2.15	0.47
1:B:194:TYR:CZ	1:B:198:ARG:HB3	2.49	0.47
1:A:159:GLU:OE2	1:A:246:SER:HB2	2.15	0.47
1:B:42:ILE:CG2	1:B:51:ILE:HD11	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:53:GLY:O	1:B:77:LEU:HA	2.14	0.47
1:B:51:ILE:O	1:B:75:VAL:HA	2.15	0.47
1:A:274:GLU:HG3	1:A:278:ARG:HH22	1.80	0.47
1:B:170:LYS:HE2	4:B:542:HOH:O	2.15	0.47
1:B:54:ILE:HA	1:B:78:PHE:O	2.15	0.47
1:A:83:ARG:HD2	1:A:221:ASN:HA	1.98	0.46
1:B:264:ILE:HG22	1:B:265:LEU:N	2.31	0.46
1:B:174:ASN:ND2	1:B:185:LYS:HZ2	2.07	0.46
1:B:97:VAL:HG22	1:B:232:LEU:O	2.15	0.46
1:B:245:HIS:HD2	1:B:248:GLU:H	1.64	0.46
1:B:242:ILE:HG12	1:B:288:LEU:CD2	2.44	0.46
1:B:174:ASN:ND2	1:B:185:LYS:NZ	2.56	0.46
1:B:174:ASN:HD21	1:B:185:LYS:HZ1	1.62	0.45
1:A:10:PRO:HB2	1:A:13[B]:VAL:HG13	1.91	0.45
1:A:226:LEU:HB3	1:A:255:THR:HG21	1.99	0.45
1:A:13[B]:VAL:HG22	4:A:714:HOH:O	2.17	0.44
1:A:219:LEU:CD1	1:A:223:LYS:HE2	2.47	0.44
1:B:81:SER:HA	3:B:402:SAH:N1	2.33	0.44
1:B:157:TYR:O	1:B:245:HIS:HE1	2.01	0.44
1:A:10:PRO:HG3	1:A:37:GLY:HA3	1.98	0.44
1:A:200:LYS:HE3	1:A:200:LYS:O	2.17	0.44
1:A:87:PHE:O	1:A:91:THR:HG23	2.18	0.44
1:B:55:ASP:OD2	3:B:402:SAH:H1'	2.17	0.44
1:B:103:ASP:HB3	3:B:402:SAH:HG1	1.99	0.44
1:B:166:ARG:HD3	4:B:583:HOH:O	2.16	0.44
1:B:86:ASP:O	1:B:90:LYS:HG3	2.18	0.44
1:B:20:LEU:HG	1:B:240:VAL:CG2	2.47	0.43
1:A:4:TYR:O	1:A:112:LYS:CE	2.67	0.43
1:B:29:LEU:HG	1:B:97:VAL:HG21	2.00	0.43
1:B:247:LEU:HA	1:B:250:ARG:NH1	2.34	0.43
1:B:75:VAL:O	1:B:75:VAL:HG13	2.19	0.43
1:B:9:ILE:HA	1:B:10:PRO:HD3	1.94	0.43
1:A:174:ASN:HD21	1:A:185:LYS:HZ2	1.67	0.42
1:B:30:ASP:HB3	1:B:33:VAL:HG22	2.01	0.42
1:B:128:MSE:HE2	1:B:212:ARG:HG3	2.01	0.42
1:B:269:PRO:HG3	1:B:289:ARG:NH2	2.35	0.42
1:A:245:HIS:CD2	1:A:247:LEU:H	2.38	0.42
1:B:81:SER:C	1:B:83:ARG:N	2.73	0.42
1:A:278:ARG:HG3	1:A:279:GLU:N	2.35	0.42
1:A:45:HIS:HD2	4:A:687:HOH:O	2.03	0.42
1:A:35:GLU:HG3	1:A:60[B]:VAL:CG2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:SER:O	1:B:74:ARG:N	2.52	0.42
1:A:140:LYS:HD2	4:A:712:HOH:O	2.19	0.41
1:B:110:GLN:HA	1:B:114:GLU:HG3	2.01	0.41
1:B:96:LYS:HE3	1:B:96:LYS:HB2	1.89	0.41
1:B:169:ARG:O	1:B:173:GLU:HG3	2.21	0.41
1:B:100:ILE:CD1	1:B:233:LEU:HD21	2.45	0.41
1:B:271:ARG:HG3	1:B:271:ARG:HH11	1.85	0.41
1:B:237:GLY:O	1:B:292:GLU:HA	2.21	0.41
1:B:263:ARG:HG3	1:B:263:ARG:HH11	1.84	0.41
1:B:29:LEU:CG	1:B:97:VAL:HG11	2.51	0.41
1:B:80:VAL:HG22	1:B:81:SER:N	2.36	0.41
1:B:95:GLU:OE1	1:B:95:GLU:HA	2.21	0.41
1:B:150:LEU:HD21	1:B:171:ILE:HG21	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	294/301 (98%)	290 (99%)	4 (1%)	0	100 100
1	B	274/301 (91%)	252 (92%)	14 (5%)	8 (3%)	6 1
All	All	568/602 (94%)	542 (95%)	18 (3%)	8 (1%)	14 4

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	ASP
1	B	272	PRO
1	B	23	GLU
1	B	25	GLU
1	B	282	ARG

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Mol	Chain	Res	Type
1	B	72	SER
1	B	45	HIS
1	B	266	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	266/264 (101%)	259 (97%)	7 (3%)	54	45
1	B	235/264 (89%)	226 (96%)	9 (4%)	40	28
All	All	501/528 (95%)	485 (97%)	16 (3%)	46	35

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	152	ARG
1	A	200	LYS
1	A	219	LEU
1	A	228	LYS
1	A	275	GLU
1	A	280	ASN
1	B	40	ARG
1	B	44	GLU
1	B	46	CYS
1	B	73	ASP
1	B	87	PHE
1	B	133	GLU
1	B	219	LEU
1	B	266	THR
1	B	268	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	139	GLN
1	A	174	ASN
1	A	245	HIS
1	A	280	ASN
1	B	38	HIS
1	B	139	GLN
1	B	174	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

4 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	SAH	A	401	-	22,28,28	0.53	0	18,40,40	0.66	0
2	SO4	A	500	-	4,4,4	0.19	0	6,6,6	0.07	0
3	SAH	B	402	-	22,28,28	0.49	0	18,40,40	0.70	0
2	SO4	B	501	-	4,4,4	0.26	0	6,6,6	0.11	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
3	SAH	A	401	-	-	0/7/31/31	0/3/3/3
2	SO4	A	500	-	-	0/0/0/0	0/0/0/0
3	SAH	B	402	-	-	0/7/31/31	0/3/3/3
2	SO4	B	501	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	SAH	2	0
3	B	402	SAH	4	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, 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	289/301 (96%)	0.38	16 (5%) 29 32	10, 21, 43, 58	0
1	B	274/301 (91%)	2.45	124 (45%) 0 0	13, 64, 76, 79	0
All	All	563/602 (93%)	1.39	140 (24%) 1 1	10, 28, 75, 79	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	71	PHE	11.1
1	B	235	PRO	10.3
1	B	78	PHE	9.0
1	B	24	ASP	8.9
1	B	68	LEU	8.8
1	B	73	ASP	8.6
1	B	95	GLU	8.6
1	B	47	PRO	8.6
1	B	42	ILE	8.5
1	B	49	CYS	8.5
1	B	264	ILE	8.4
1	B	23	GLU	8.4
1	B	257	ARG	8.4
1	B	263	ARG	8.4
1	B	265	LEU	8.3
1	B	283	ALA	7.9
1	B	281	PRO	7.8
1	B	262	LEU	7.8
1	B	87	PHE	7.7
1	B	20	LEU	7.3
1	B	9	ILE	7.3
1	B	48	GLY	7.0
1	B	92	LEU	6.8
1	B	260	LYS	6.7

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Mol	Chain	Res	Type	RSRZ
1	B	70	GLU	6.6
1	B	27	ILE	6.6
1	B	29	LEU	6.5
1	B	25	GLU	6.5
1	B	50	ARG	6.5
1	B	76	SER	6.3
1	B	14	ARG	6.3
1	B	91	THR	6.3
1	A	2	ARG	6.2
1	B	227	LYS	6.2
1	B	40	ARG	6.2
1	B	272	PRO	6.1
1	A	278	ARG	6.0
1	B	88	LEU	6.0
1	B	19	PHE	6.0
1	B	22	PRO	5.8
1	B	93	GLY	5.7
1	B	75	VAL	5.7
1	B	18	GLU	5.5
1	B	282	ARG	5.5
1	B	271	ARG	5.4
1	B	261	LYS	5.4
1	B	233	LEU	5.2
1	A	7	ARG	5.0
1	B	46	CYS	5.0
1	A	284	ARG	5.0
1	B	268	LYS	4.8
1	B	237	GLY	4.8
1	B	101	LEU	4.8
1	B	285	SER	4.7
1	B	94	ILE	4.7
1	B	21	LYS	4.6
1	B	43	LEU	4.5
1	B	17	ILE	4.5
1	B	69	LYS	4.5
1	A	274	GLU	4.5
1	B	234	ASN	4.4
1	B	236	GLY	4.4
1	B	10	PRO	4.3
1	B	228	LYS	4.3
1	B	66	GLU	4.3
1	B	11	VAL	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	26	LYS	4.3
1	B	80	VAL	4.3
1	B	269	PRO	4.2
1	B	89	LEU	4.2
1	B	51	ILE	4.2
1	B	74	ARG	4.1
1	B	258	ASN	4.1
1	A	3	LYS	4.0
1	A	275	GLU	4.0
1	B	292	GLU	4.0
1	B	266	THR	4.0
1	B	83	ARG	4.0
1	A	6	GLN	3.9
1	B	13	VAL	3.9
1	A	200	LYS	3.9
1	B	259	SER	3.9
1	B	267	GLU	3.8
1	B	273	SER	3.8
1	B	256	PHE	3.8
1	B	85	ALA	3.7
1	B	84	GLU	3.7
1	B	41	ALA	3.7
1	B	77	LEU	3.6
1	B	16	VAL	3.5
1	B	97	VAL	3.4
1	B	247	LEU	3.4
1	B	254	GLU	3.3
1	B	100	ILE	3.3
1	B	291	ALA	3.2
1	B	135	GLU	3.2
1	B	8	HIS	3.2
1	B	44	GLU	3.2
1	B	52	ILE	3.2
1	B	63	ILE	3.2
1	B	111	LEU	3.1
1	B	28	ILE	3.1
1	B	72	SER	3.1
1	B	45	HIS	3.1
1	B	250	ARG	3.1
1	B	132	LEU	3.1
1	A	294	ILE	3.1
1	B	90	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	99	GLY	3.1
1	B	65	GLU	3.0
1	A	277	ILE	3.0
1	B	67	LYS	2.9
1	B	288	LEU	2.9
1	B	122	ARG	2.8
1	B	62	ARG	2.8
1	A	279	GLU	2.7
1	B	245	HIS	2.7
1	B	98	ASP	2.6
1	B	241	VAL	2.6
1	B	112	LYS	2.6
1	B	244	PHE	2.6
1	B	240	VAL	2.5
1	B	104	LEU	2.5
1	B	242	ILE	2.5
1	B	58	SER	2.5
1	A	5	SER	2.4
1	B	200	LYS	2.3
1	B	39	SER	2.3
1	B	61	LEU	2.3
1	B	183	LEU	2.3
1	B	225	PHE	2.2
1	B	133	GLU	2.2
1	B	286	GLY	2.2
1	B	38	HIS	2.1
1	A	260	LYS	2.1
1	B	103	ASP	2.1
1	B	229	ALA	2.1
1	A	14	ARG	2.1
1	A	268	LYS	2.1
1	B	33	VAL	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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	SAH	A	401	26/26	0.98	0.11	-0.11	10,14,18,21	0
3	SAH	B	402	26/26	0.87	0.14	-0.78	45,49,55,56	0
2	SO4	B	501	5/5	0.97	0.13	-	40,42,43,43	0
2	SO4	A	500	5/5	0.97	0.12	-	45,45,46,47	0

6.5 Other polymers

There are no such residues in this entry.