Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:53 AM GMT

PDB ID	:	2OKC
Title	:	Crystal structure of Type I restriction enzyme StySJI M protein (NP_813429.1) from Bacteroides thetaiotaomicron VPI-5482 at 2.20 A resolution
Authors	:	Joint Center for Structural Genomics (JCSG)
Deposited on	:	2007-01-16
Resolution	:	2.20 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:

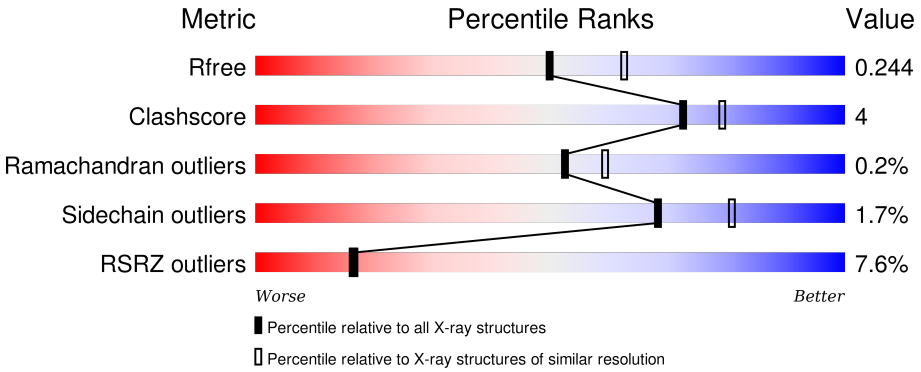
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	445	9% 85% 10% 5%
1	B	445	5% 86% 9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7069 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 Type I restriction enzyme StySJI M protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	Se	0	2	0
			3299	2110	542	632	5	10			
1	B	426	Total	C	N	O	S	Se	0	2	0
			3353	2146	548	643	5	11			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	LEADER SEQUENCE	UNP Q89Z59
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	44	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	51	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	116	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	125	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	162	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	170	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	192	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	225	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	292	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	293	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
A	295	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	0	GLY	-	LEADER SEQUENCE	UNP Q89Z59
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	44	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	51	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	116	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	125	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	162	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	170	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	192	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	225	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	292	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59
B	293	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59

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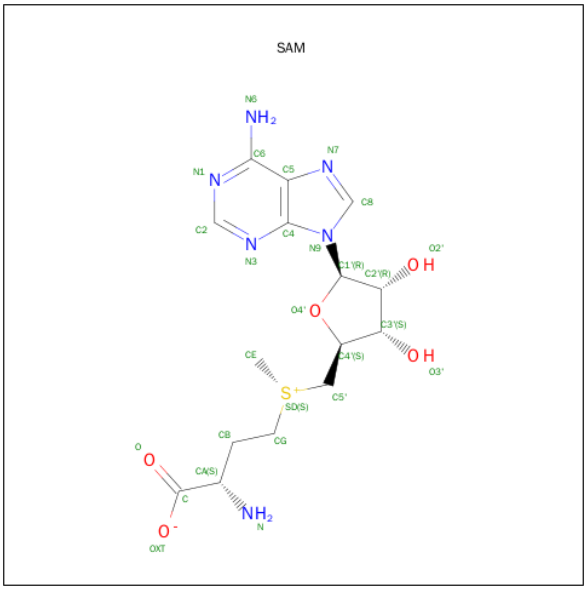
Chain	Residue	Modelled	Actual	Comment	Reference
B	295	MSE	MET	MODIFIED RESIDUE	UNP Q89Z59

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

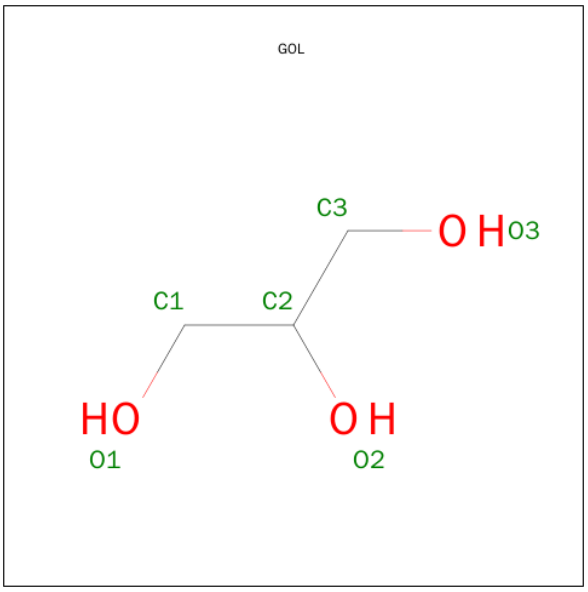
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Cl 1 1	0	0

- Molecule 3 is S-ADENOSYLMETHIONINE (three-letter code: SAM) (formula: $C_{15}H_{22}N_6O_5S$).



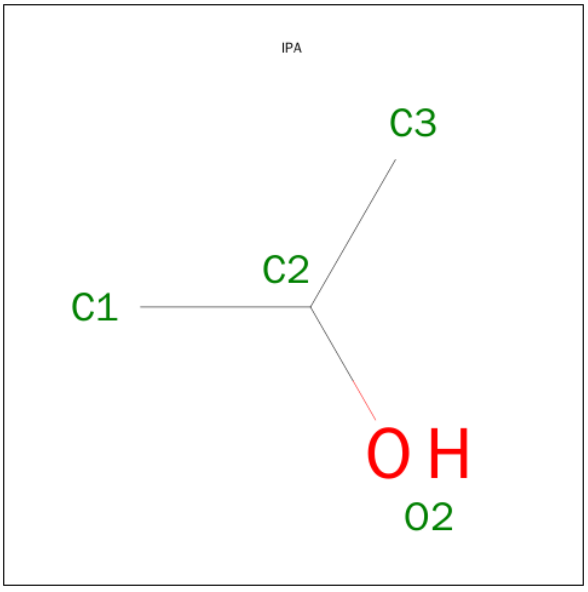
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O S 27 15 6 5 1	0	0
3	B	1	Total C N O S 27 15 6 5 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

- Molecule 5 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 3 1	0	0
5	B	1	Total C O 4 3 1	0	0

- Molecule 6 is water.

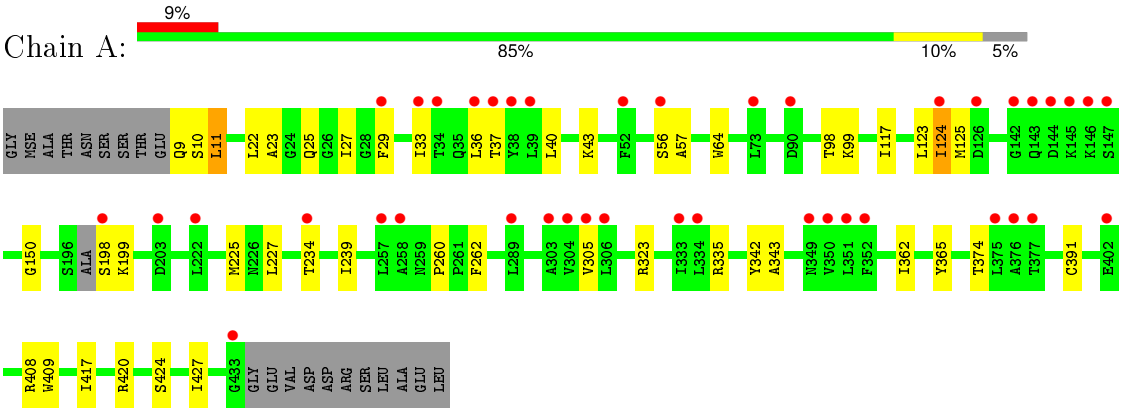
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	162	Total O 162 162	0	0
6	B	186	Total O 186 186	0	0

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.

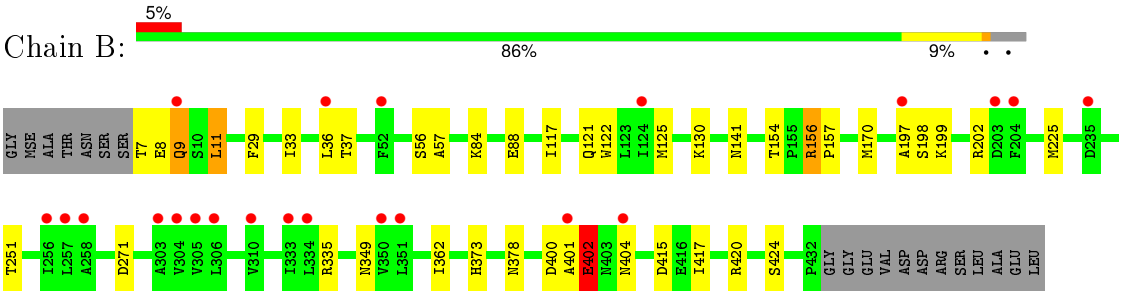
- Molecule 1: Type I restriction enzyme StySJI M protein

Chain A:



- Molecule 1: Type I restriction enzyme StySJI M protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	75.44Å 85.85Å 152.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.62 – 2.20 28.58 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.8 (28.62-2.20) 91.6 (28.58-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.182 , 0.232 0.194 , 0.244	Depositor DCC
R_{free} test set	2367 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	38.5	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 48.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 46666 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7069	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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: GOL, IPA, SAM, CL

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	0.70	1/3363 (0.0%)	0.73	1/4556 (0.0%)
1	B	0.81	4/3420 (0.1%)	0.79	1/4630 (0.0%)
All	All	0.76	5/6783 (0.1%)	0.76	2/9186 (0.0%)

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	B	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	402	GLU	CD-OE2	15.18	1.42	1.25
1	B	404	ASN	CG-ND2	10.97	1.60	1.32
1	B	402	GLU	CD-OE1	9.76	1.36	1.25
1	B	404	ASN	CG-OD1	8.17	1.42	1.24
1	A	262	PHE	CE1-CZ	5.65	1.48	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	404	ASN	CB-CG-OD1	-5.62	110.36	121.60
1	A	335	ARG	NE-CZ-NH1	5.39	123.00	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	197	ALA	Peptide
1	B	8	GLU	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	3299	0	3198	26	0
1	B	3353	0	3280	29	0
2	B	1	0	0	0	0
3	A	27	0	22	0	0
3	B	27	0	22	1	0
4	A	6	0	8	0	0
5	A	4	0	8	0	0
5	B	4	0	8	1	0
6	A	162	0	0	1	0
6	B	186	0	0	1	0
All	All	7069	0	6546	56	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 4.

All (56) 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:170:MSE:HE2	1:B:202:ARG:HA	1.53	0.88
1:A:23:ALA:O	1:A:25:GLN:O	2.04	0.74
1:A:362:ILE:HD12	1:A:417:ILE:HD13	1.69	0.74
1:A:150:GLY:HA3	1:A:342:TYR:CG	2.24	0.72
1:B:400:ASP:OD1	1:B:401:ALA:O	2.09	0.70
1:B:362:ILE:HD12	1:B:417:ILE:HD13	1.75	0.69
1:B:198:SER:HB2	1:B:199:LYS:HA	1.75	0.68
1:B:11:LEU:HD11	1:B:125:MSE:HE1	1.82	0.60
1:B:170:MSE:CE	1:B:202:ARG:HA	2.29	0.60
1:B:84:LYS:NZ	1:B:88:GLU:OE2	2.35	0.59
1:A:123:LEU:O	1:A:124:ILE:HB	2.03	0.57
1:A:342:TYR:CG	1:A:343:ALA:N	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:SER:O	1:A:57:ALA:HB3	2.06	0.56
1:A:198:SER:HB2	1:A:199:LYS:HA	1.87	0.55
1:B:420:ARG:HD3	1:B:424:SER:O	2.05	0.55
1:B:170:MSE:HE2	1:B:202:ARG:CA	2.35	0.53
1:B:401:ALA:O	1:B:402:GLU:HB2	2.07	0.53
1:A:123:LEU:O	1:A:124:ILE:CB	2.57	0.53
1:A:391:CYS:HB3	1:A:409:TRP:CE2	2.44	0.52
1:A:227:LEU:HD22	1:A:239:ILE:HD11	1.92	0.52
1:B:11:LEU:HD21	1:B:122:TRP:CH2	2.45	0.51
1:A:37:THR:HG23	1:A:225:MSE:HG2	1.92	0.51
1:A:198:SER:CB	1:A:199:LYS:HA	2.41	0.50
1:B:335:ARG:HD2	1:B:349:ASN:OD1	2.12	0.50
1:A:36:LEU:HD12	1:A:117:ILE:HD11	1.94	0.49
1:B:198:SER:HB2	1:B:199:LYS:CA	2.41	0.49
1:A:22:LEU:HB3	1:A:27:ILE:HB	1.94	0.49
1:B:36:LEU:HD12	1:B:117:ILE:HD11	1.94	0.49
1:B:29:PHE:HB3	1:B:141:ASN:ND2	2.28	0.48
1:B:29:PHE:CE1	1:B:33:ILE:HD11	2.49	0.47
1:B:36:LEU:CD1	1:B:117:ILE:HD11	2.44	0.47
1:B:11:LEU:HD11	1:B:125:MSE:CE	2.45	0.47
1:A:260:PRO:HD2	1:A:305:VAL:O	2.16	0.46
1:A:11:LEU:HD11	1:A:125:MSE:HE1	1.97	0.46
1:A:29:PHE:CE1	1:A:33:ILE:HD11	2.51	0.45
1:A:9:GLN:O	1:A:9:GLN:CD	2.55	0.45
1:A:362:ILE:HD12	1:A:417:ILE:CD1	2.44	0.45
1:B:29:PHE:CD1	1:B:33:ILE:HD11	2.52	0.45
1:B:362:ILE:CD1	1:B:417:ILE:HD13	2.45	0.44
1:A:323:ARG:NH1	6:A:588:HOH:O	2.49	0.44
1:B:154:THR:OG1	3:B:500:SAM:N	2.51	0.44
1:B:56:SER:O	1:B:57:ALA:HB3	2.18	0.44
1:B:373:HIS:HA	1:B:378:ASN:O	2.18	0.43
1:B:198:SER:CB	1:B:199:LYS:HA	2.42	0.42
1:B:125:MSE:HB2	1:B:130:LYS:HD2	2.01	0.42
1:A:98:THR:O	1:A:99:LYS:C	2.58	0.42
1:B:7:THR:O	1:B:11:LEU:HB2	2.19	0.42
1:A:420:ARG:HD3	1:A:424:SER:O	2.19	0.42
1:A:365:TYR:HA	1:A:408:ARG:O	2.20	0.42
5:B:501:IPA:H33	6:B:576:HOH:O	2.20	0.41
1:B:156:ARG:N	1:B:157:PRO:CD	2.83	0.41
1:B:198:SER:CB	1:B:199:LYS:CA	2.98	0.41
1:A:43:LYS:HD3	1:A:64:TRP:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:LEU:HD23	1:A:225:MSE:CE	2.51	0.41
1:A:420:ARG:HD2	1:A:427:ILE:HD11	2.03	0.41
1:B:37:THR:HG23	1:B:225:MSE:HG2	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	422/445 (95%)	396 (94%)	25 (6%)	1 (0%)	52 59
1	B	426/445 (96%)	409 (96%)	16 (4%)	1 (0%)	52 59
All	All	848/890 (95%)	805 (95%)	41 (5%)	2 (0%)	52 59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	124	ILE
1	B	9	GLN

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	348/372 (94%)	344 (99%)	4 (1%)	80 89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	359/372 (96%)	351 (98%)	8 (2%)	60 72
All	All	707/744 (95%)	695 (98%)	12 (2%)	68 81

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	11	LEU
1	A	234	THR
1	A	374	THR
1	B	9	GLN
1	B	11	LEU
1	B	121	GLN
1	B	156	ARG
1	B	251	THR
1	B	271	ASP
1	B	402	GLU
1	B	415	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	B	25	GLN
1	B	141	ASN
1	B	394	ASN
1	B	403	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 (i)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 for Mogul analysis.

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	SAM	A	500	-	21,29,29	1.11	2 (9%)	17,42,42	2.86	3 (17%)
4	GOL	A	501	-	5,5,5	0.39	0	5,5,5	0.51	0
5	IPA	A	502	-	3,3,3	0.59	0	3,3,3	0.20	0
3	SAM	B	500	-	21,29,29	1.23	2 (9%)	17,42,42	2.80	3 (17%)
5	IPA	B	501	-	3,3,3	0.72	0	3,3,3	0.24	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	SAM	A	500	-	-	0/8/33/33	0/3/3/3
4	GOL	A	501	-	-	0/4/4/4	0/0/0/0
5	IPA	A	502	-	-	0/0/0/0	0/0/0/0
3	SAM	B	500	-	-	0/8/33/33	0/3/3/3
5	IPA	B	501	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	500	SAM	C2-N1	2.69	1.39	1.33
3	B	500	SAM	C2-N1	2.70	1.39	1.33
3	A	500	SAM	C2-N3	3.26	1.38	1.32
3	B	500	SAM	C2-N3	3.72	1.38	1.32

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	500	SAM	N3-C2-N1	-10.68	120.72	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	500	SAM	N3-C2-N1	-10.47	120.88	128.89
3	A	500	SAM	C1'-N9-C4	-3.32	121.94	126.94
3	B	500	SAM	C4-C5-N7	-2.54	107.15	109.48
3	A	500	SAM	C4'-O4'-C1'	-2.48	106.99	109.72
3	B	500	SAM	O2'-C2'-C3'	2.12	118.71	111.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	500	SAM	1	0
5	B	501	IPA	1	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, 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	413/445 (92%)	0.34	41 (9%)	9	8	31, 43, 65, 84	0
1	B	415/445 (93%)	0.13	22 (5%)	30	29	32, 43, 61, 75	0
All	All	828/890 (93%)	0.23	63 (7%)	17	16	31, 43, 63, 84	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	376	ALA	6.4
1	A	433	GLY	6.0
1	A	145	LYS	5.4
1	A	304	VAL	4.7
1	A	351	LEU	4.7
1	A	126	ASP	4.3
1	A	305	VAL	4.2
1	A	350	VAL	4.2
1	A	124	ILE	4.1
1	A	37	THR	3.9
1	A	234	THR	3.9
1	B	304	VAL	3.9
1	A	146	LYS	3.8
1	B	351	LEU	3.8
1	A	143	GLN	3.7
1	B	350	VAL	3.7
1	B	401	ALA	3.6
1	A	52	PHE	3.6
1	A	402	GLU	3.5
1	B	305	VAL	3.4
1	A	144	ASP	3.3
1	B	124	ILE	3.3
1	A	333	ILE	3.2
1	A	90	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	333	ILE	3.0
1	A	306	LEU	3.0
1	A	303	ALA	3.0
1	A	33	ILE	2.9
1	B	52	PHE	2.9
1	B	306	LEU	2.8
1	A	36	LEU	2.7
1	B	203	ASP	2.7
1	B	258	ALA	2.7
1	B	404	ASN	2.7
1	A	38	TYR	2.7
1	B	235	ASP	2.6
1	B	197	ALA	2.6
1	A	352	PHE	2.6
1	A	39	LEU	2.6
1	B	36	LEU	2.6
1	A	147	SER	2.5
1	A	377	THR	2.5
1	A	142	GLY	2.5
1	B	257	LEU	2.5
1	A	29	PHE	2.4
1	A	257	LEU	2.4
1	A	334	LEU	2.4
1	A	73	LEU	2.4
1	B	310	VAL	2.4
1	B	334	LEU	2.3
1	B	303	ALA	2.3
1	B	204	PHE	2.3
1	B	256	ILE	2.3
1	A	375	LEU	2.2
1	A	34	THR	2.2
1	B	9	GLN	2.2
1	A	258	ALA	2.2
1	A	56	SER	2.2
1	A	349	ASN	2.1
1	A	198	SER	2.1
1	A	222	LEU	2.1
1	A	203	ASP	2.1
1	A	289	LEU	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, 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
5	IPA	A	502	4/4	0.84	0.27	1.84	51,57,62,67	0
3	SAM	A	500	27/27	0.95	0.10	-1.00	35,41,48,52	0
3	SAM	B	500	27/27	0.97	0.09	-1.32	23,29,34,38	0
2	CL	B	445	1/1	0.90	0.07	-	77,77,77,77	0
4	GOL	A	501	6/6	0.85	0.14	-	64,67,71,72	0
5	IPA	B	501	4/4	0.68	0.68	-	62,65,65,68	0

6.5 Other polymers (i)

There are no such residues in this entry.