Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:23 PM GMT

PDB ID	:	3ZBG
Title	:	Crystal structure of wild-type SCP2 thiolase from Leishmania mexicana at 1.85 A
Authors	:	Harijan, R.K.; Kiema, T.-R.; Weiss, M.S.; Michels, P.A.M.; Wierenga, R.K.
Deposited on	:	2012-11-09
Resolution	:	1.85 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:

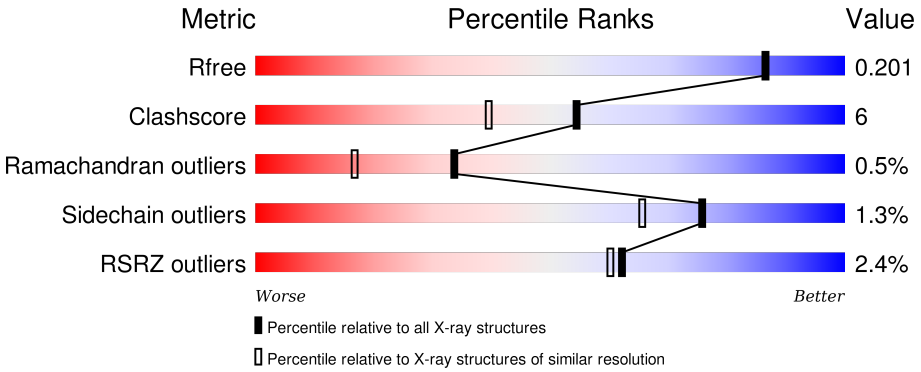
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 1.85 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	457	3% 84% 9% • 6%
1	B	457	2% 85% 8% • 6%

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	DMS	A	1443	-	-	X	X
2	DMS	A	1444	-	-	-	X
2	DMS	B	1445	-	-	-	X
2	DMS	B	1446	-	-	-	X
2	DMS	B	1448	-	-	-	X
2	DMS	B	1452	-	-	-	X
3	MPD	A	1446	-	-	-	X
3	MPD	B	1442	-	-	-	X
3	MPD	B	1451	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7220 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 3-KETOACYL-COA THIOLASE-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	7	0
			3277	2042	575	633	27			
1	B	431	Total	C	N	O	S	0	9	0
			3285	2048	573	637	27			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	HIS	-	EXPRESSION TAG	UNP E9AW84
A	-14	HIS	-	EXPRESSION TAG	UNP E9AW84
A	-13	HIS	-	EXPRESSION TAG	UNP E9AW84
A	-12	HIS	-	EXPRESSION TAG	UNP E9AW84
A	-11	HIS	-	EXPRESSION TAG	UNP E9AW84
A	-10	HIS	-	EXPRESSION TAG	UNP E9AW84
A	-9	SER	-	EXPRESSION TAG	UNP E9AW84
A	-8	SER	-	EXPRESSION TAG	UNP E9AW84
A	-7	GLY	-	EXPRESSION TAG	UNP E9AW84
A	-6	LEU	-	EXPRESSION TAG	UNP E9AW84
A	-5	VAL	-	EXPRESSION TAG	UNP E9AW84
A	-4	PRO	-	EXPRESSION TAG	UNP E9AW84
A	-3	ARG	-	EXPRESSION TAG	UNP E9AW84
A	-2	GLY	-	EXPRESSION TAG	UNP E9AW84
A	-1	SER	-	EXPRESSION TAG	UNP E9AW84
A	0	HIS	-	EXPRESSION TAG	UNP E9AW84
A	6	LEU	MET	SEE REMARK 999	UNP E9AW84
A	31	PRO	LYS	SEE REMARK 999	UNP E9AW84
A	34	ILE	VAL	SEE REMARK 999	UNP E9AW84
A	45	LYS	GLN	SEE REMARK 999	UNP E9AW84
A	61	MET	ILE	SEE REMARK 999	UNP E9AW84
A	63	HIS	ASN	SEE REMARK 999	UNP E9AW84
A	64	SER	VAL	SEE REMARK 999	UNP E9AW84
A	67	SER	LYS	SEE REMARK 999	UNP E9AW84
A	69	ARG	LYS	SEE REMARK 999	UNP E9AW84

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Chain	Residue	Modelled	Actual	Comment	Reference
A	107	SER	ALA	SEE REMARK 999	UNP E9AW84
A	112	MET	ILE	SEE REMARK 999	UNP E9AW84
A	134	MET	THR	SEE REMARK 999	UNP E9AW84
A	139	SER	ALA	SEE REMARK 999	UNP E9AW84
A	145	THR	VAL	SEE REMARK 999	UNP E9AW84
A	157	SER	THR	SEE REMARK 999	UNP E9AW84
A	176	GLN	LYS	SEE REMARK 999	UNP E9AW84
A	229	THR	SER	SEE REMARK 999	UNP E9AW84
A	268	VAL	ALA	SEE REMARK 999	UNP E9AW84
A	277	ARG	LYS	SEE REMARK 999	UNP E9AW84
A	327	ILE	VAL	SEE REMARK 999	UNP E9AW84
A	356	GLU	ASP	SEE REMARK 999	UNP E9AW84
A	368	ASP	GLU	SEE REMARK 999	UNP E9AW84
A	398	ILE	VAL	SEE REMARK 999	UNP E9AW84
A	410	GLU	GLY	SEE REMARK 999	UNP E9AW84
B	-15	HIS	-	EXPRESSION TAG	UNP E9AW84
B	-14	HIS	-	EXPRESSION TAG	UNP E9AW84
B	-13	HIS	-	EXPRESSION TAG	UNP E9AW84
B	-12	HIS	-	EXPRESSION TAG	UNP E9AW84
B	-11	HIS	-	EXPRESSION TAG	UNP E9AW84
B	-10	HIS	-	EXPRESSION TAG	UNP E9AW84
B	-9	SER	-	EXPRESSION TAG	UNP E9AW84
B	-8	SER	-	EXPRESSION TAG	UNP E9AW84
B	-7	GLY	-	EXPRESSION TAG	UNP E9AW84
B	-6	LEU	-	EXPRESSION TAG	UNP E9AW84
B	-5	VAL	-	EXPRESSION TAG	UNP E9AW84
B	-4	PRO	-	EXPRESSION TAG	UNP E9AW84
B	-3	ARG	-	EXPRESSION TAG	UNP E9AW84
B	-2	GLY	-	EXPRESSION TAG	UNP E9AW84
B	-1	SER	-	EXPRESSION TAG	UNP E9AW84
B	0	HIS	-	EXPRESSION TAG	UNP E9AW84
B	6	LEU	MET	SEE REMARK 999	UNP E9AW84
B	31	PRO	LYS	SEE REMARK 999	UNP E9AW84
B	34	ILE	VAL	SEE REMARK 999	UNP E9AW84
B	45	LYS	GLN	SEE REMARK 999	UNP E9AW84
B	61	MET	ILE	SEE REMARK 999	UNP E9AW84
B	63	HIS	ASN	SEE REMARK 999	UNP E9AW84
B	64	SER	VAL	SEE REMARK 999	UNP E9AW84
B	67	SER	LYS	SEE REMARK 999	UNP E9AW84
B	69	ARG	LYS	SEE REMARK 999	UNP E9AW84
B	107	SER	ALA	SEE REMARK 999	UNP E9AW84
B	112	MET	ILE	SEE REMARK 999	UNP E9AW84

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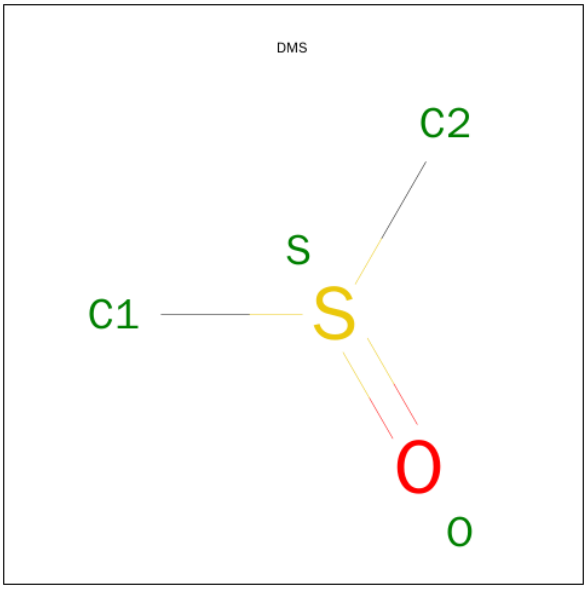
Chain	Residue	Modelled	Actual	Comment	Reference
B	134	MET	THR	SEE REMARK 999	UNP E9AW84
B	139	SER	ALA	SEE REMARK 999	UNP E9AW84
B	145	THR	VAL	SEE REMARK 999	UNP E9AW84
B	157	SER	THR	SEE REMARK 999	UNP E9AW84
B	176	GLN	LYS	SEE REMARK 999	UNP E9AW84
B	229	THR	SER	SEE REMARK 999	UNP E9AW84
B	268	VAL	ALA	SEE REMARK 999	UNP E9AW84
B	277	ARG	LYS	SEE REMARK 999	UNP E9AW84
B	327	ILE	VAL	SEE REMARK 999	UNP E9AW84
B	356	GLU	ASP	SEE REMARK 999	UNP E9AW84
B	368	ASP	GLU	SEE REMARK 999	UNP E9AW84
B	398	ILE	VAL	SEE REMARK 999	UNP E9AW84
B	410	GLU	GLY	SEE REMARK 999	UNP E9AW84

- Molecule 2 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



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

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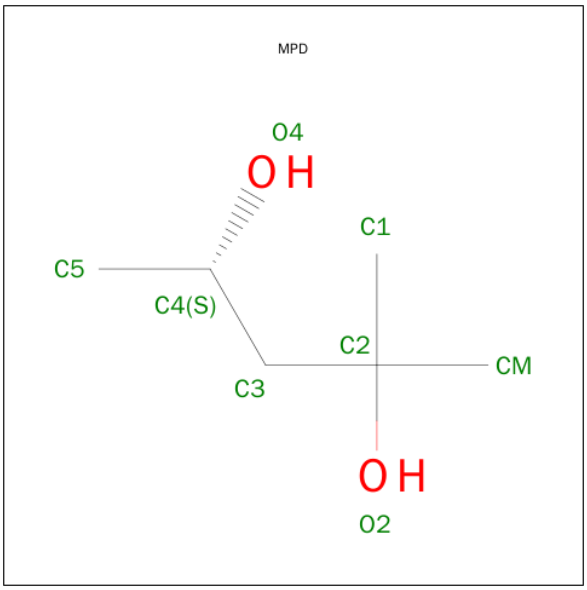
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4 2 1 1	0	0
2	B	1	Total C O S 4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

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 8 6 2	0	0
3	B	1	Total C O 8 6 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 8 6 2	0	0
3	B	1	Total C O 8 6 2	0	0

- Molecule 4 is water.

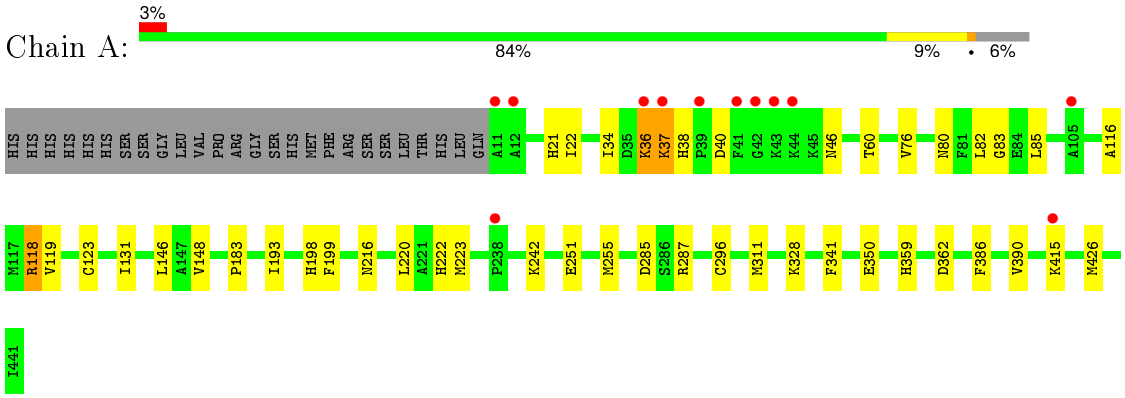
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	269	Total O 269 269	0	0
4	B	300	Total O 301 301	0	1

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.

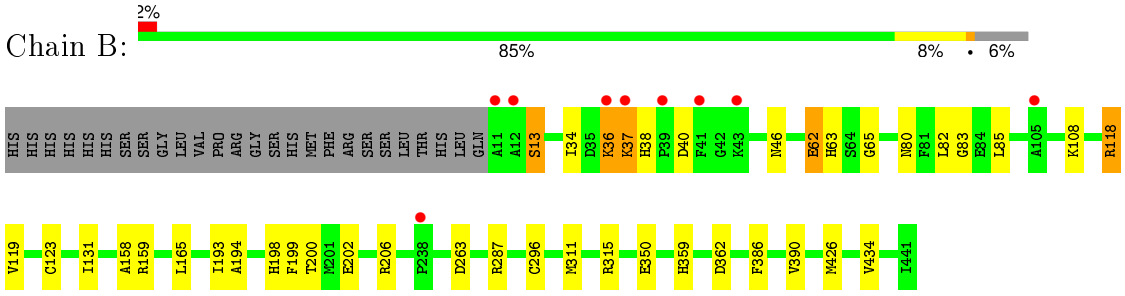
- Molecule 1: 3-KETOACYL-COA THIOLASE-LIKE PROTEIN

Chain A:



- Molecule 1: 3-KETOACYL-COA THIOLASE-LIKE PROTEIN

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	122.25Å 122.25Å 133.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	105.87 – 1.85 31.18 – 1.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (105.87-1.85) 100.0 (31.18-1.85)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.162 , 0.196 0.167 , 0.201	Depositor DCC
R_{free} test set	4796 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	23.4	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 47.9	EDS
Estimated twinning fraction	0.042 for h,-h-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 95892 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	7220	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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: OCS, DMS, MPD

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	0.77	0/3338	0.85	3/4497 (0.1%)
1	B	0.85	0/3349	0.88	7/4512 (0.2%)
All	All	0.81	0/6687	0.86	10/9009 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	118	ARG	NE-CZ-NH1	15.01	127.81	120.30
1	A	118	ARG	NE-CZ-NH2	-13.70	113.45	120.30
1	B	118	ARG	NE-CZ-NH1	12.51	126.56	120.30
1	B	118	ARG	NE-CZ-NH2	-11.68	114.46	120.30
1	B	311	MET	CG-SD-CE	-6.07	90.49	100.20
1	A	311	MET	CG-SD-CE	-6.05	90.53	100.20
1	B	263	ASP	CB-CG-OD1	5.92	123.62	118.30
1	B	159	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	B	315	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	B	159	ARG	NE-CZ-NH2	-5.19	117.70	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	3277	0	3265	43	0
1	B	3285	0	3273	37	0
2	A	24	0	36	9	0
2	B	32	0	48	5	0
3	A	8	0	14	1	0
3	B	24	0	42	10	0
4	A	269	0	0	2	0
4	B	301	0	0	12	0
All	All	7220	0	6678	85	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 6.

All (85) 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:146[B]:LEU:CD2	1:A:148:VAL:HG13	1.85	1.06
3:B:1451:MPD:H13	3:B:1451:MPD:H52	1.44	1.00
1:B:202:GLU:OE2	1:B:206[B]:ARG:NH2	1.96	0.99
1:A:146[B]:LEU:HD21	1:A:148:VAL:CG1	1.94	0.98
1:A:146[B]:LEU:HD21	1:A:148:VAL:HG13	1.45	0.98
1:A:34:ILE:H	1:A:46:ASN:HD21	1.15	0.93
1:B:34:ILE:H	1:B:46:ASN:HD21	1.17	0.89
1:B:194:ALA:CB	3:B:1442:MPD:H11	2.04	0.88
1:B:123:OCS:HA	1:B:390[B]:VAL:HG23	1.59	0.84
1:A:146[B]:LEU:HD23	1:A:148:VAL:HG13	1.60	0.83
1:A:21:HIS:HA	2:A:1443:DMS:H12	1.62	0.80
1:A:222:HIS:CD2	1:A:223:MET:HE2	2.18	0.77
1:B:131[A]:ILE:HG21	2:B:1445:DMS:H21	1.68	0.76
1:B:13:SER:HB2	4:B:2004:HOH:O	1.85	0.75
1:B:194:ALA:HB1	3:B:1442:MPD:H11	1.68	0.75
1:A:222:HIS:HD2	1:A:223:MET:HE2	1.51	0.73
2:B:1446:DMS:H21	4:B:2063:HOH:O	1.88	0.73
1:A:21:HIS:HA	2:A:1443:DMS:C1	2.20	0.71
1:B:165:LEU:HD12	4:B:2119:HOH:O	1.92	0.69
1:A:80:ASN:HD21	1:A:83:GLY:H	1.38	0.69
1:A:123:OCS:HA	1:A:390:VAL:HG13	1.75	0.69
1:A:255:MET:SD	3:A:1446:MPD:H53	2.33	0.68
1:B:13:SER:CB	4:B:2004:HOH:O	2.42	0.67
1:A:222:HIS:CD2	1:A:223:MET:CE	2.77	0.67
1:A:216:ASN:O	2:A:1445:DMS:H12	1.95	0.67
1:A:146[B]:LEU:CD2	1:A:148:VAL:CG1	2.61	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:OCS:OD2	4:B:2090:HOH:O	2.11	0.66
1:B:80:ASN:HD21	1:B:83:GLY:H	1.44	0.64
1:B:131[A]:ILE:HG21	2:B:1445:DMS:C2	2.28	0.64
1:A:123:OCS:HB2	1:A:390:VAL:HG13	1.81	0.63
1:A:222:HIS:HD2	1:A:223:MET:CE	2.11	0.62
1:A:146[B]:LEU:HD21	1:A:148:VAL:HG11	1.82	0.61
1:B:194:ALA:HB2	3:B:1442:MPD:H11	1.80	0.59
1:A:183:PRO:HD3	2:A:1442:DMS:H11	1.84	0.59
1:B:359:HIS:HE1	4:B:2271:HOH:O	1.87	0.57
1:B:359:HIS:HD2	1:B:362:ASP:OD2	1.88	0.57
1:B:198:HIS:HE1	1:B:350:GLU:OE1	1.88	0.56
1:A:183:PRO:HD3	2:A:1442:DMS:C1	2.36	0.55
1:B:65:GLY:HA3	3:B:1449:MPD:H53	1.88	0.54
1:A:198:HIS:HE1	1:A:350:GLU:OE1	1.91	0.53
1:B:193:ILE:HG23	1:B:198:HIS:HB3	1.92	0.52
1:A:34:ILE:H	1:A:46:ASN:ND2	1.97	0.52
1:B:200:THR:HA	3:B:1442:MPD:H12	1.91	0.52
1:A:38:HIS:HD2	1:A:40:ASP:H	1.58	0.51
1:B:38:HIS:HD2	1:B:40:ASP:H	1.57	0.51
1:B:194:ALA:HB2	3:B:1442:MPD:C1	2.40	0.51
1:B:62[B]:GLU:HA	4:B:2048:HOH:O	2.09	0.51
1:A:220:LEU:HD11	2:A:1443:DMS:C2	2.40	0.51
4:A:2104:HOH:O	2:B:1446:DMS:H11	2.10	0.50
1:B:63:HIS:CE1	4:B:2052:HOH:O	2.64	0.50
1:A:22:ILE:H	2:A:1443:DMS:C1	2.25	0.50
1:A:82:LEU:HD22	1:A:85:LEU:HD12	1.95	0.48
1:A:123:OCS:HA	1:A:390:VAL:CG1	2.42	0.48
1:B:131[A]:ILE:CD1	1:B:296:CYS:HB2	2.44	0.47
1:A:193:ILE:HG23	1:A:198:HIS:HB3	1.97	0.47
1:A:38:HIS:CD2	1:A:40:ASP:H	2.33	0.47
1:B:82:LEU:HD22	1:B:85:LEU:HD12	1.97	0.47
1:B:34:ILE:H	1:B:46:ASN:ND2	1.99	0.47
1:B:38:HIS:CD2	1:B:40:ASP:H	2.33	0.46
1:B:287:ARG:HD2	3:B:1449:MPD:HM1	1.96	0.46
1:B:36:LYS:O	1:B:37:LYS:CB	2.63	0.46
1:B:198:HIS:HD2	4:B:2153:HOH:O	1.97	0.46
1:A:119:VAL:HG12	1:B:119:VAL:HG12	1.96	0.46
1:B:426:MET:HE3	4:B:2088:HOH:O	2.16	0.46
1:A:220:LEU:HD11	2:A:1443:DMS:H22	1.96	0.46
3:B:1451:MPD:H13	3:B:1451:MPD:C5	2.25	0.45
1:A:60:THR:HG21	1:A:146[A]:LEU:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ASN:HD21	1:A:83:GLY:N	2.11	0.45
1:A:341:PHE:HZ	2:A:1442:DMS:H11	1.82	0.45
1:A:193:ILE:HD13	1:A:199:PHE:CZ	2.53	0.44
1:A:222:HIS:CD2	1:A:223:MET:HE3	2.53	0.43
1:A:359:HIS:HD2	1:A:362:ASP:OD2	2.01	0.43
1:A:36:LYS:O	1:A:37:LYS:CB	2.66	0.42
1:A:131:ILE:CD1	1:A:296:CYS:HB2	2.50	0.42
1:B:193:ILE:HD13	1:B:199:PHE:CZ	2.55	0.42
2:B:1452:DMS:H21	4:B:2169:HOH:O	2.19	0.42
1:A:242:LYS:HD3	1:A:251:GLU:HA	2.02	0.42
1:B:80:ASN:HD21	1:B:83:GLY:N	2.15	0.41
1:B:198:HIS:CE1	1:B:350:GLU:OE1	2.72	0.41
1:A:426:MET:HE3	4:A:2098:HOH:O	2.20	0.41
1:A:285:ASP:OD1	1:A:287:ARG:HG2	2.21	0.41
1:B:158:ALA:HB1	3:B:1451:MPD:H4	2.03	0.41
1:A:76:VAL:O	1:A:116:ALA:HA	2.21	0.41
1:B:131[A]:ILE:HD11	1:B:434:VAL:HG13	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	435/457 (95%)	426 (98%)	7 (2%)	2 (0%)	34	17
1	B	437/457 (96%)	427 (98%)	8 (2%)	2 (0%)	34	17
All	All	872/914 (95%)	853 (98%)	15 (2%)	4 (0%)	34	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	LYS

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Mol	Chain	Res	Type
1	B	37	LYS
1	A	36	LYS
1	B	36	LYS

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	345/362 (95%)	341 (99%)	4 (1%)	78	69
1	B	347/362 (96%)	341 (98%)	6 (2%)	68	54
All	All	692/724 (96%)	682 (99%)	10 (1%)	76	63

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	118	ARG
1	A	328	LYS
1	A	386	PHE
1	A	415	LYS
1	B	13	SER
1	B	62[A]	GLU
1	B	62[B]	GLU
1	B	108	LYS
1	B	118	ARG
1	B	386	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	46	ASN
1	A	58	GLN
1	A	63	HIS
1	A	80	ASN

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Mol	Chain	Res	Type
1	A	198	HIS
1	A	216	ASN
1	A	359	HIS
1	A	425	ASN
1	B	38	HIS
1	B	46	ASN
1	B	80	ASN
1	B	172	GLN
1	B	198	HIS
1	B	316	GLN
1	B	359	HIS
1	B	425	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	OCS	A	123	1	7,8,9	3.44	3 (42%)	7,11,13	10.93	5 (71%)
1	OCS	B	123	1	7,8,9	5.49	3 (42%)	7,11,13	13.79	6 (85%)

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
1	OCS	A	123	1	-	0/4/7/9	0/0/0/0
1	OCS	B	123	1	-	0/4/7/9	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	123	OCS	CB-SG	-6.91	1.67	1.77
1	A	123	OCS	CB-SG	-6.62	1.68	1.77
1	A	123	OCS	OD3-SG	2.96	1.54	1.45
1	B	123	OCS	OD3-SG	3.38	1.55	1.45
1	A	123	OCS	OD2-SG	4.66	1.58	1.46
1	B	123	OCS	OD2-SG	12.15	1.77	1.46

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	123	OCS	OD1-SG-CB	-31.43	80.45	106.94
1	B	123	OCS	OD2-SG-OD1	-9.22	90.15	111.61
1	A	123	OCS	OD2-SG-OD3	-8.90	90.89	111.61
1	A	123	OCS	OD2-SG-OD1	-5.62	98.53	111.61
1	B	123	OCS	OD3-SG-OD1	-4.55	96.89	113.48
1	B	123	OCS	O-C-CA	-2.14	119.92	125.49
1	B	123	OCS	CB-CA-C	2.79	119.12	111.46
1	A	123	OCS	CB-CA-C	3.10	119.95	111.46
1	A	123	OCS	OD1-SG-CB	12.54	117.51	106.94
1	B	123	OCS	OD3-SG-CB	15.02	119.61	106.94
1	A	123	OCS	OD3-SG-CB	23.58	126.82	106.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	123	OCS	3	0
1	B	123	OCS	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

18 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	DMS	A	1442	-	3,3,3	0.60	0	3,3,3	0.50	0
2	DMS	A	1443	-	3,3,3	0.67	0	3,3,3	0.60	0
2	DMS	A	1444	-	3,3,3	0.31	0	3,3,3	0.77	0
2	DMS	A	1445	-	3,3,3	0.52	0	3,3,3	0.74	0
3	MPD	A	1446	-	6,7,7	0.37	0	7,10,10	0.50	0
2	DMS	A	1447	-	3,3,3	0.30	0	3,3,3	1.09	0
2	DMS	A	1448	-	3,3,3	0.37	0	3,3,3	0.78	0
3	MPD	B	1442	-	6,7,7	1.17	1 (16%)	7,10,10	1.47	2 (28%)
2	DMS	B	1443	-	3,3,3	0.47	0	3,3,3	0.42	0
2	DMS	B	1444	-	3,3,3	0.33	0	3,3,3	1.06	0
2	DMS	B	1445	-	3,3,3	0.45	0	3,3,3	0.82	0
2	DMS	B	1446	-	3,3,3	0.51	0	3,3,3	0.81	0
2	DMS	B	1447	-	3,3,3	0.38	0	3,3,3	0.81	0
2	DMS	B	1448	-	3,3,3	0.29	0	3,3,3	0.89	0
3	MPD	B	1449	-	6,7,7	1.00	1 (16%)	7,10,10	1.69	3 (42%)
2	DMS	B	1450	-	3,3,3	0.40	0	3,3,3	0.88	0
3	MPD	B	1451	-	6,7,7	0.50	0	7,10,10	0.60	0
2	DMS	B	1452	-	3,3,3	0.34	0	3,3,3	0.73	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
2	DMS	A	1442	-	-	0/0/0/0	0/0/0/0
2	DMS	A	1443	-	-	0/0/0/0	0/0/0/0
2	DMS	A	1444	-	-	0/0/0/0	0/0/0/0
2	DMS	A	1445	-	-	0/0/0/0	0/0/0/0
3	MPD	A	1446	-	-	0/5/5/5	0/0/0/0
2	DMS	A	1447	-	-	0/0/0/0	0/0/0/0
2	DMS	A	1448	-	-	0/0/0/0	0/0/0/0
3	MPD	B	1442	-	-	0/5/5/5	0/0/0/0
2	DMS	B	1443	-	-	0/0/0/0	0/0/0/0
2	DMS	B	1444	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DMS	B	1445	-	-	0/0/0/0	0/0/0/0
2	DMS	B	1446	-	-	0/0/0/0	0/0/0/0
2	DMS	B	1447	-	-	0/0/0/0	0/0/0/0
2	DMS	B	1448	-	-	0/0/0/0	0/0/0/0
3	MPD	B	1449	-	-	0/5/5/5	0/0/0/0
2	DMS	B	1450	-	-	0/0/0/0	0/0/0/0
3	MPD	B	1451	-	-	0/5/5/5	0/0/0/0
2	DMS	B	1452	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1442	MPD	O2-C2	-2.39	1.38	1.44
3	B	1449	MPD	C5-C4	2.05	1.59	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	1449	MPD	CM-C2-C1	-2.64	104.48	110.24
3	B	1442	MPD	CM-C2-C1	-2.40	105.01	110.24
3	B	1449	MPD	O2-C2-C1	-2.25	99.85	108.09
3	B	1442	MPD	O2-C2-C1	-2.20	100.04	108.09
3	B	1449	MPD	C2-C3-C4	2.13	126.72	116.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1442	DMS	3	0
2	A	1443	DMS	5	0
2	A	1445	DMS	1	0
3	A	1446	MPD	1	0
3	B	1442	MPD	5	0
2	B	1445	DMS	2	0
2	B	1446	DMS	2	0
3	B	1449	MPD	2	0
3	B	1451	MPD	3	0
2	B	1452	DMS	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	430/457 (94%)	-0.23	12 (2%) 56 54	14, 26, 48, 80	0
1	B	430/457 (94%)	-0.40	9 (2%) 67 65	12, 21, 42, 75	0
All	All	860/914 (94%)	-0.31	21 (2%) 62 60	12, 23, 46, 80	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	ALA	9.7
1	B	11	ALA	6.9
1	A	12	ALA	6.5
1	A	41	PHE	4.6
1	A	36	LYS	3.9
1	A	238	PRO	3.6
1	A	39	PRO	3.6
1	A	43	LYS	3.5
1	B	12	ALA	3.4
1	B	36	LYS	3.4
1	A	105	ALA	3.1
1	B	43	LYS	3.0
1	B	41	PHE	2.7
1	A	415	LYS	2.6
1	B	105	ALA	2.6
1	B	39	PRO	2.6
1	A	44	LYS	2.4
1	A	42	GLY	2.4
1	A	37	LYS	2.3
1	B	37	LYS	2.1
1	B	238	PRO	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	OCS	A	123	9/10	0.95	0.09	-	15,18,41,41	0
1	OCS	B	123	9/10	0.94	0.10	-	14,17,36,38	0

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
3	MPD	B	1451	8/8	0.57	0.33	18.14	53,65,73,76	0
2	DMS	B	1452	4/4	0.83	0.28	7.92	60,67,75,90	0
2	DMS	A	1444	4/4	0.91	0.18	6.47	66,71,72,75	0
3	MPD	A	1446	8/8	0.74	0.21	6.44	61,72,78,79	0
2	DMS	A	1443	4/4	0.94	0.17	5.53	40,58,64,70	0
3	MPD	B	1442	8/8	0.92	0.22	4.60	22,39,53,54	0
2	DMS	B	1448	4/4	0.83	0.26	4.32	57,74,75,88	0
2	DMS	B	1446	4/4	0.91	0.14	3.27	47,62,66,72	0
2	DMS	B	1445	4/4	0.95	0.14	2.34	53,61,66,74	0
3	MPD	B	1449	8/8	0.92	0.11	1.95	26,29,32,36	0
2	DMS	A	1442	4/4	0.95	0.15	1.63	47,47,54,63	0
2	DMS	B	1443	4/4	0.96	0.11	0.64	36,42,43,48	0
2	DMS	B	1444	4/4	0.91	0.26	-	56,61,63,70	0
2	DMS	B	1447	4/4	0.91	0.19	-	73,76,78,82	0
2	DMS	B	1450	4/4	0.82	0.24	-	68,74,75,83	0
2	DMS	A	1448	4/4	0.73	0.34	-	80,90,93,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	DMS	A	1447	4/4	0.88	0.21	-	49,56,58,67	0
2	DMS	A	1445	4/4	0.83	0.30	-	73,75,78,88	0

6.5 Other polymers (i)

There are no such residues in this entry.